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XAB2 links pre-mRNA splicing with the DNA damage response during mammalian development

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To my parents

Summary

RNA splicing and the DNA damage response are intriguingly linked in mammals but the underlying mechanisms remain poorly understood. Using an *in vivo* biotinylation tagging approach in mice we show that XAB2, the human homologue of the yeast pre-mRNA-splicing factor SYF1 has a functional role in Nucleotide Excision Repair (NER) and the DNA damage response (DDR) in mammals. XAB2 interacts with the spliceosome factors PRP19, BCAS2 and Aquarius; it is part of the core spliceosome and binds to spliceosomal U4 and U6 snRNAs during hepatic development. Ablation of XAB2 leads to defective NER, intron retention, the aberrant accumulation of pre-mRNAs and to a faulty ATM/ATR DDR signaling. Using functional approaches, we find that XAB2 dissociates from RNA targets upon persistent DNA damage or transcription blockage and from spliceosomal RNAs in NER-defective developing livers. We propose that XAB2 functionally links NER and the spliceosomal response to DNA damage with important ramifications for the developmental defects associated with transcription-coupled DNA repair disorders.

Περίληψη

Οι βλάβες του DNA προκαλούν την ενεργοποίηση σηματοδοτικών μονοπατιών, τα οποία ελέγχουν την επιδιόρθωση του DNA, την ρύθμιση της μεταγραφής καθώς και τις αποφάσεις για την προσωρινή ή μόνιμη αναστολή του κυτταρικού κύκλου ή την επαγωγή κυτταρικού θανάτου. Το σύνολο των μονοπατιών αυτών, από την αναγνώριση της βλάβης μέχρι την επιδιόρθωση του DNA και τις επιλογές για την τύχη του κυττάρου, συνιστά την απόκριση στις βλάβες τού DNA (DNA damage response, DDR). Τα τελευταία χρόνια, το μάτισμα του RNA έχει συσχετισθεί με την κυτταρική απόκριση στις βλάβες τού DNA, ωστόσο ο μηχανισμός με τον οποίο αυτά τα δύο μονοπάτια αλληλεπιδρούν συντονισμένα παραμένει άγνωστος. Η πρωτεΐνη XAB2 έχει εμπλακεί στο μάτισμα του RNA και ταυτόχρονα στο μονοπάτι επιδιόρθωσης του DNA μέσω της εκτομής νουκλεοτιδίων (Nucelotide excision repair, NER), ωστόσο η λειτουργική της συνεισφορά και στα δύο μονοπάτια παραμένει άγνωστη. Στην παρούσα διατριβή, χρησιμοποιήσαμε ένα νέο μοντέλο ποντικού προκειμένου να χαρακτηρίσουμε την λειτουργία της XAB2 κατά την ανάπτυξη του ποντικού *in vivo*. Η παραγωγή του νέου μοντέλου περιλαμβάνει την προσθήκη μίας ετικέτας συγγενείας στο ενδογενές γονίδιο μέσω γονιδιακής στόχευσης (knock in). Η συγκεκριμένη ετικέτα αναγνωρίζεται και βιοτινυλιώνεται από την βακτηριακή λιγάση BirA, με αποτέλεσμα σε ποντικούς που εκφράζουν τόσο το knock in αλλήλιο όσο και διαγονιδιακή λιγάση BirA, η XAB2 να βιοτινυλιώνεται in vivo, παρέχοντας έτσι ένα πολύτιμο εργαλείο για την απομόνωση της πρωτεΐνης μαζί με πρωτεϊνικούς ή DNA/RNA στόχους. Συνοπτικά βρήκαμε ότι η XAB2 αποτελεί κύριο συστατικό του μηχανισμού ματίσματος: αλληλεπιδρά με τους

παράγοντες ματίσματος PRP19, BCAS2 και Aquarius και προσδένεται σε pre-mRNAs καθώς και στα U4 και U6 snRNAs. Απώλεια της XAB2 οδηγεί σε ελαττωματική ωρίμαση του pre-mRNA μέσω της μειωμένης εκτομής ιντρονίων, μειωμένη επιδιορθωτική ικανότητα του NER και ανεπαρκή ενεργοποίηση του DDR. Επιπλέον, η επαγωγή βλαβών στο DNA προκαλεί την αποσύνδεση της XAB2 από τους RNA στόχους της· αντίστοιχη αποσύνδεση παρατηρήθηκε και σε ηπατικό ιστό αναπτυσσόμενων ποντικών με μεταλλαγές που προκαλούν ανεπάρκεια του μηχανισμού NER. Κατά συνέπεια, προτείνουμε ότι η XAB2 αποτελεί λειτουργικό σύνδεσμο μεταξύ των μηχανισμών ματίσματος, NER και γενικότερου DDR. Αυτή η λειτουργική σύνδεση σε συνδυασμό με τις παρατηρήσεις στον ηπατικό ιστό αναπτυσσόμενων ποντικών με ελαττωματικό NER, θα μπορούσε να εξηγήσει εν μέρει τις αναπτυξιακές ανωμαλίες που παρατηρούνται σε ασθένειες με παθολογική αιτιολογία την ανεπάρκεια μηχανισμών επιδιόρθωσης DNA.

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Abbreviations

ActD	Actinomycin D
AS	Alternative splicing
ATM	Ataxia Telangiectasia Mutated
ATR	ATM and RAD3 related
BER	Base Excision Repair
BPS	branch point sequence
CDK	cyclin-dependent kinase
COFS	cerebro-oculo-facio-skeletal syndrome
CPD	cyclobutane pyrimidine dimer
CRL	cullin 4A (CUL4A)–regulator of cullins 1 (ROC1) E3 ubiquitin ligase
CS	Cockayne Syndrome
CstF1	cleavage-stimulation factor 1
DCM	dilated cardiomyopathy
DDR	DNA Damage Response
DMD	Duchenne muscular dystrophy
DNA-PKcs	DNA protein kinase catalystic subunit
DRB	5,6-Dichloro-1-β-D-ribofuranosylbenzimidazole
DSB	double strand break
ESE	exonic splicing enhancer
ESS	exonic splicing silencer
EWS	Ewing sarcoma
FPLD2	familial partial lipodystrophy type 2
FTDP-17	frontotemporal dementia with parkinsonism linked to chromosome 17
GG-NER	Global Genome NER
HGPS	Hutchinson–Gilford progeria syndrome
hnRNP	heterogeneous nuclear ribonucleoprotein
HR	homologous recombination
ICL	interstrand crosslink
IR	ionizing radiation
IR	Intron retention
ISE	intronic splicing enhancer

ISS	intronic splicing silencer
LGMD1B	limb girdle muscular dystrophy type 1B
MAPT	microtubule-associated protein tau
MDS	myelodysplastic syndrome
MMC	Mitomycin C
MMR	Mismatch Repair
MOPD I	microcephalic osteodysplastic primordial dwarfism type I
MRN	MRE11-RAD50-NBS1
NER	Nucleotide Excision Repair
NHEJ	Non-Homologous End Joining repair
NMD	non-sense mediated decay
PI3K	phosphoinositide 3-kinase
PTC	premature termination codon
RFC	Replication factor C
RNP	ribonucleoprotein complexe
snoRNP	small nucleolar RNP
snRNP	small nuclear RNP
SR	serine-arginine-rich
SRPK	SR protein kinase
SS	splice site
SSB	single strand break
TC-NER	Transcription Coupled NER
TopBP1	Topoisomerase binding protein 1
TTD	trichothiodystrophy
UV	ultraviolet
UV-DDB	ultraviolet radiation–DNA damage-binding protein
UVsS	UV-sensitive syndrome
UVSSA	UV-stimulated scaffold protein A
XAB2	XPA binding protein 2
XP	Xeroderma Pigmentosum

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Introduction

1. Genome integrity is safeguarded by an integrated network

To sustain life, cells must be able to maintain and appropriately utilize their genome with the ultimate goal to produce the multitude of macromolecules ranging from small non-coding RNAs to large multisubunit proteins. Thus, every form of life aims at delivering its genetic material intact and unaltered to its progeny. To achieve this, chromosomes have to be precisely segregated, DNA must be accurately replicated and cells must be able to survive spontaneous and induced DNA damage while minimizing any heritable mutations. DNA in cells is subject to thousands of endogenously and exogenously induced lesions per day [1], which may impede genome replication and transcription. DNA lesions range from DNA base mismatches, base adducts and intra-strand crosslinks to inter-strand crosslinks and single and double strand breaks, the latter being the most deleterious ones. Some DNA lesions are formed by physiological cellular processes: DNA mismatches incorporated during DNA replication, DNA-base lesions produced by spontaneous hydrolytic reactions and non-enzymatic methylation, oxidative adducts produced by reactive oxygen species that are by-products of the oxidative respiration. DNA damage can be also caused by environmental agents. For example, genotoxic chemicals, such as tobacco products, generate DNA lesions and are thus associated with a risk of cancer initiation. The most pervasive environmental DNA-damaging agent is ultraviolet (UV) A and B radiation, which is not absorbed by the ozon layer unlike the most dangerous UVC spectrum. UV light induces nucleotide chemical modifications such as cyclobutane pyrimidine dimers (CPDs) 6-4 photoproducts. Cosmic ionizing radiation (IR), X-rays, exposure to radioactive

substances and chemotherapeutic drugs result in base and nucleotide modifications, interstrand crosslinks (ICLs), single (SSBs) and double strand breaks (DSBs). If these lesions are not restored, they may lead to mutations or broad genome abnormalities that threaten cell or organism viability. To counter this threat, life has evolved a network, collectively described as the DNA Damage Response (DDR): the DDR factors detect and signal the presence of DNA damage and promote DNA repair; in concert with this, DDR factors regulate chromatin structure, cell cycle progression (checkpoint activation) and gene expression (**Figure 1**). Ultimately DDR coordinates cell fate decisions in multicellular organisms: to prevent the proliferation of mutated cells that could lead to cancer or other pathologies, cells baring extensive DNA damage might either enter a state of permanent growth arrest and stop dividing (senescence) or undergo programmed cell death (apoptosis). Although usually examined separately, DNA repair and DNA damage signaling form an overlapping and interconnected network.

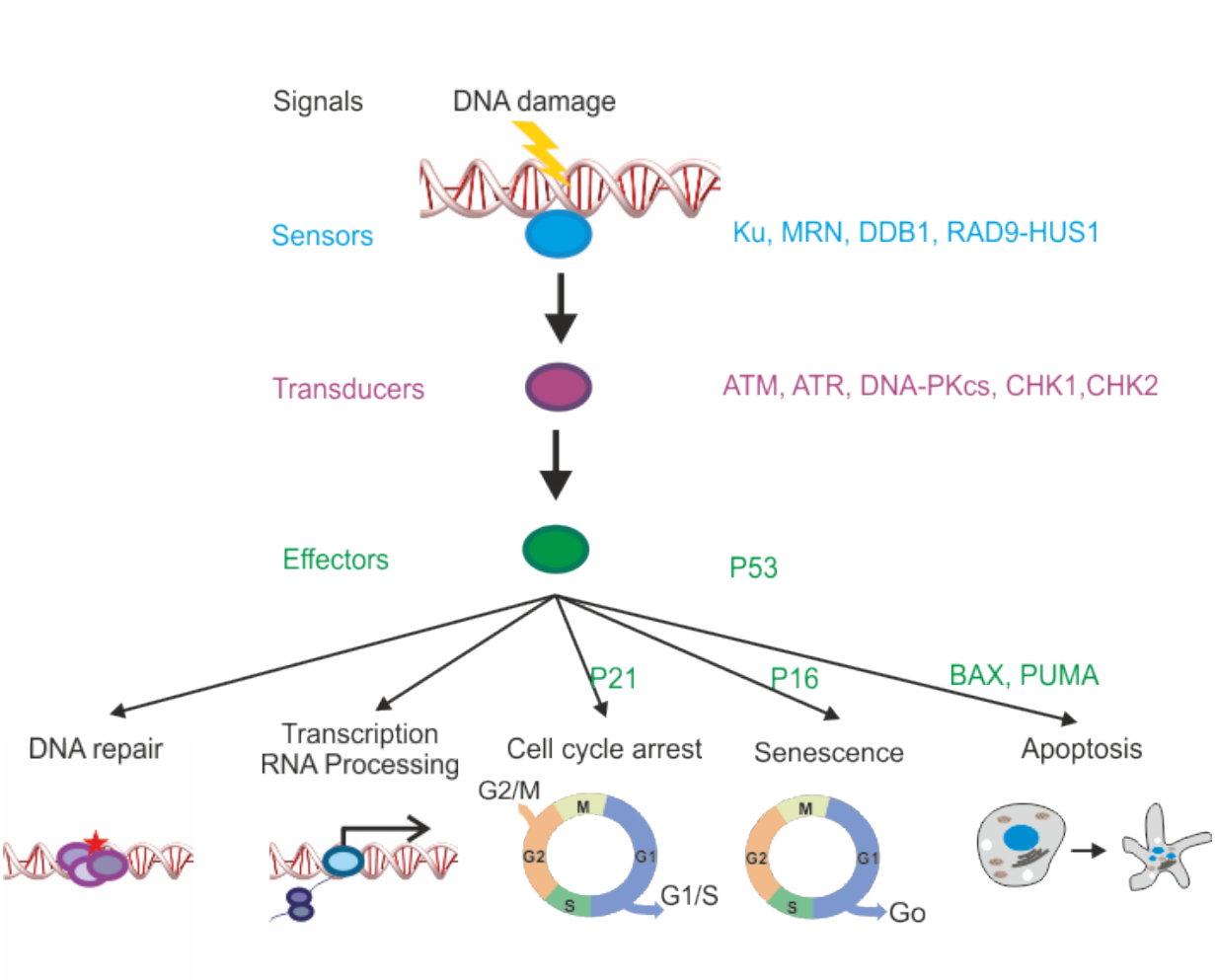


Figure 1. Outline of the DNA damage response (DDR)

1.1. DNA damage signalling

Activation of apical kinases. Upon DNA damage, recruitment and regulation of DDR factors is controlled by post-translational modifications (i.e. phosphorylation, ubiquitination, parylation, acetylation, sumoylation). The DDR itself is primarily driven by phosphorylation performed by the two apical DDR kinases ATM (Ataxia Telangiectasia Mutated) and ATR (ATM and RAD3 related) as well as the DNA-PKcs (DNA- Protein kinase catalytic subunit), the latter being primarily involved in Non-Homologous End Joining repair pathway (NHEJ). All three proteins are serine-threonine kinases and belong to the phosphoinositide 3-kinase (PI3K) family. Aberrant activation of the DDR

has been widely correlated with malignant pathologies, therefore ATM, ATR and DNA-PKcs must be tightly regulated. This regulation is mediated by a requirement of a specific co-factor tightly associated with the damaged DNA that allows for kinase recruitment at the site of damage and activation by autophosphorylation: NBS1 for ATM, ATRIP for ATR and Ku80 for DNA-PKcs.

DNA-PKcs is recruited by Ku protein binding to DSBs and subsequently autophosphorylated at several sites to stimulate NHEJ [2] . While DNA-PKcs activation mostly effects the sequestration of repair factors, substrate phosphorylation by ATM and ATR is essential for orchestrating DDR and cell fate decisions in response to genotoxic stress. ATM can be activated by several mechanisms, however the most well understood is the one in response to DSBs: the MRE11-RAD50-NBS1 (MRN) complex, via NBS1, recruits and activates ATM at the site of damage [2] [3] [4]. ATM activation can stimulate both DSB repair pathways, however the choice of the preferred mechanism in each occasion is still investigated.

ATR is the primary DNA replication stress response kinase, thus it is indispensable for replicating cells. In contrast to ATM and DNA-Pkcs, which are primarily activated in response to DSBs, ATR responds to a variety of genotoxic insults that are processed through ssDNA intermediates [5,6] and requires a multistep process for its activation. ATR is recruited by ATRIP to long tracts of ssDNA coated with the ssDNA binding complex, i.e. the replication protein A (RPA). Although RPA-ssDNA plays a fundamental role in ATR activation, this structure is not sufficient to fully activate the ATR signaling cascade. Optimal activation of ATR requires the presence of the activator Topoisomerase binding protein 1 (TopBP1), which by bridging ATR with ATRIP

stimulates ATR kinase activity [7,8]. TopBP1 is recruited at the site of damage independently but its interaction with the RAD9 subunit of the RAD9-RAD1-HUS1 (9-1-1) complex is considered to play an important role in full ATR activation [9,10,11]. The (9-1-1) complex is loaded on RPA-ssDNA/dsDNA junctions by RAD17 and Replication factor C (RFC) [12,13,14]. Only when these mechanisms function in concert ATR is fully activated and can efficiently signal DNA damage and replication stress.

Cell fate decisions. To orchestrate DDR and cell fate decisions in response to genotoxic stress, activated ATM/ATR phosphorylate many substrates including other protein kinases that in turn phosphorylate more substrates. Well characterized examples are CHK2 kinase for ATM and CHK1 kinase for ATR that regulate CDC25 and P53, which inactivate cyclin-dependent kinases (CDKs) and ultimately lead to cell cycle arrest or apoptosis, dependent on the DNA damage load: inhibition of cell cycle progress may be transient and is restored after efficient DNA repair; however, if DNA damage is persistent cells might undergo apoptosis or permanent exit of the cell cycle (cellular senescence) [15].

Chromatin changes. DNA repair pathways must function within the chromatin context to restore DNA lesions. While chromatin is the physiological substrate of all DNA metabolic reactions, chromatin compaction hinders the access of repair as well as replication and transcription factors. To bypass this physical barrier, activation of DDR results in transient chromatin changes to allow access of repair/transcription factors [16]. Such changes include post-translational modifications of chromatin associated proteins (histones and non-histones), histone variant replacement and nucleosome eviction or repositioning. One of the most well studied events is the phosphorylation of the H2A

variant H2AX (γH2AX), which is broadly used as a DNA damage marker. In response to DSBs, H2AX is rapidly phosphorylated primarily by ATM (DNA-PKcs also phosphorylates H2AX) to promote the relaxation of chromatin and the accumulation of repair factors at the sites of damage in a signaling cascade that involves phosphorylation, ubiquitination and other post-transcriptional modifications[17]. Phosphorylation of H2AX also occurs upon UV exposure, primarily mediated by ATR during G1 and S phases [18,19,16]. Although ATR is the key activated kinase in response to UV, ATM and DNA-PKcs are also stimulated and ATM is shown to contribute to H2AX phosphorylation during S-phase [20]. Although γH2AX contribution to DSBs repair and signaling has been well studied and understood, how γH2AX contributes to subsequent DDR upon UV still remains elusive.

Gene expression. DNA damage tends to globally repress gene expression at the transcriptional, pre-mRNA processing and translational level. Activation of the DDR triggers transcriptional silencing, possibly to avoid collision of the repair and transcription machineries and to compensate for the formation of RNA:DNA hybrids [21]. In response to DSBs, transcriptional inhibition expands several kilobases from the damaged site and may depend on DNA-PK [22,23] or ATM [24], while ATM is critical for nucleolar transcriptional silencing [25]. UV-induced DNA damage also results in genome wide transcriptional silencing [26] that maintains for several hours, while transcription levels are fully recovered only 24h-48h after UV exposure [27,28]. It is thought that transcriptional shut down is not just a consequence of DNA lesions that impede RNA polymerase II movement, but it is also mediated by signaling events [29,30]. Interestingly, transcriptional repression coincides with a hyper-phosphorylated form of RNAPII, while

recovery of RNA synthesis occurs when the hypo-phosphorylated form of RNAPII, necessary for transcription initiation, is generated [29]. Notably, transcription initiation rates recover faster (6-12h) than elongation rates (12-48h) in accordance with findings showing that larger genes (>20kb) are more affected than the shorter ones [31, 27, 28, 32]. Consistent with this, DNA damage affects co-transcriptional RNA-processing reactions such as pre-mRNA splicing (discussed later), 3' pre-mRNA processing and termination. In general, DNA damage decreases the expression of functional gene products by switching alternative splicing towards variants that contain premature stop codons and thus are degraded by the non-sense mediated decay pathway (NMD) [33,34]. Moreover, UV-induced damage represses 3' pre-mRNA processing via a mechanism mediated by the interaction of the 3' processing factor cleavage-stimulation factor 1 (CstF1) with the DNA repair factors BARD1 and BRCA1 in a P53-dependent manner [35-36]. UV-induced reduction of transcriptional rates also affects the mRNA polyadenylation site and termination [28]. On top of this, translational rates are dramatically decreased, at least in response to IR and doxorubicin, adding another level of gene expression regulation upon genotoxic stress [37,38].

While gene expression is globally repressed, individual genes, usually involved in DDR, apoptosis and cell cycle, are highly upregulated upon DNA damage; again, upregulation of gene expression occurs on transcriptional, pre-mRNA processing and translational levels. Activated ATM and ATR phosphorylate and subsequently activate transcription factors such as P53, NFκ-B and AP-1, thereby inducing transcription of target genes [39]. P53 provides an example of how the DDR may regulate gene expression of a specific gene at multiple levels. Under normal physiological conditions, P53 levels are kept low:

the interaction with the E3 ubiquitin ligase MDM2, ensures P53 export from the nucleus (monoubiquitinylation) and degradation (polyubiquitinylation) or inhibition of its transactivation domain [25]. Upon DNA damage, P53 is phosphorylated by ATM/ATR/DNA-PKcs [40] and as a consequence the MDM2-P53 interaction is disrupted, thus activating P53. In the nucleus, P53 upregulates transcription of cell cycle (e.g. *P21*) and apoptotic regulators (e.g. *BAX, PUMA*) transcribed by RNA pol II [2,4]. MDM2 has two opposing roles: MDM2 is the main ubiquitin ligase that drives P53 degradation but it also enhances, by direct binding to, *P53* mRNA translation [41]. In response to DNA damage, MDM2 is also phosphorylated by ATM/ATR [40]; this phosphorylation inhibits MDM2-P53 interaction but also enhances MDM2 binding on *P53* mRNA and therefore its *P53* translation [42].

Crosstalk of ATM, ATR and DNA-PKcs. While activation of each DDR kinase is described within the context of specific DNA lesions, it is known that DDR kinases crosstalk with each other to affect their localization to sites of damage and their activation[15]. For example, at DSBs ATM stimulates ATR activation by promoting DNA end resection that generates ssDNA [43-44]. Vice versa, ATR phosphorylates ATM in response to UV or replication stress [45]. ATM and ATR phosphorylate DNA-PKcs to stimulate DNA-PK complex disassembly from the damaged sites, thereby promoting repair [46-47]. Moreover, DNA-PKcs has been shown to phosphorylate ATM to reduce its activity [48]. ATM has been also shown to affect the function of ATR regulators. TopBP1 phosphorylation by ATM is thought to promote its interaction with ATR in response to DSBs [49] while RAD9 phosphorylation by ATM is also important for genome stability [50]. The functional crosstalk of the apical kinases is not limited only at their activation but

also at the substrate level. During the course of DDR, ATM and ATR function redundantly in the phosphorylation of their substrates [51]. ATM and ATR may phosphorylate the same or different sites of the same proteins in response to different genotoxic insults or during different stages of the DDR [51, 15].

1.2. DNA repair Pathways

DNA damage can affect either one or both DNA strands and is repaired by different, though overlapping, mechanisms most of which employ multiple proteins in a sequence of catalytic reactions to resolve the DNA lesion. Though carried out by different factors, all repair pathways share a common mechanism of repair: detection of the lesion, incision by one or more nucleases, synthesis by DNA polymerases and ligation to restore the integrity of DNA strands [52].

DNA damage in a single strand can be resolved by excision of either a base (Base Excision Repair, BER) or one (Mismatch Repair, MMR) or more nucleotides (Nucleotide Excision Repair, NER) and involves a break in the damaged strand. BER repairs alkylated, oxidated, deaminated or depurinated DNA bases by removing the damaged base, cleaving and removing the abasic site and eventually filling the gap by DNA polymerase and ligase activities [53]. Mismatches and insertion/deletion loops are repaired by MMR, where the detection of the lesion results in a single strand break that is subsequently repaired by polymerase and ligase proteins [54]. NER detects and repairs UV- and chemical-induced helix distorting lesions, by excising an oligonucleotide that contains the damage and filling the gap by synthesis and ligation [55].

DNA double strand breaks (DSBs) are highly cytotoxic lesions that interfere with transcription and DNA replication triggering large chromosomal rearrangements and

threatening cell survival. Persistent R-loops, endogenously generated free radicals and exposure of DNA to ionizing radiation or genotoxins e.g. bleomycin or zeocin may trigger DSBs. Eukaryotic cells have evolved two main pathways to resolve DSBs: the non-homologous end joining pathway (NHEJ) and the homologous recombination pathway (HR) (both reviewed in [52]). Alternative pathways for DSB repair have been also described, collectively referred to as alternative End Joining (a-EJ), though still poorly understood [56]. In mammalian cells, NHEJ is active throughout the cell cycle; instead, HR is active in late S and G2 phases when the sister chromatid provides the homologous template required for repair DNA synthesis. Inter-strand crosslinks are repaired by the concomitant action of the Fanconi anaemia pathway and HR. NHEJ starts when Ku protein (Ku70-Ku80) binds to DNA of a DSB; subsequently the DNA:Ku complex activates the DNA-dependent protein kinase catalytic subunit (DNA-PKcs) which in turn recruits and activates end processing enzymes and polymerase and ligase factors. In HR, the Mre11-Rad50-Nbs1 (MRN) complex accumulates at DSBs where, in combination with CtIP, resects the DNA ends. A sequence of events mediated by RAD51, BRCA1 and BRCA2 results in ssDNA invading the homologous strand and synthesis and ligation follow.

Interstrand crosslinks (ICLs) are generated by bifunctional alkylating agents, such as Mitomycin C (MMC) and Cisplatin, that form a linkage of the opposite strands of DNA; like DSBs, ICLs are also highly cytotoxic by interfering with transcription and replication [57, 58]. Repair of ICLs involves Fanconi Anemia, NER and HR factors.

1.2.1. The NER pathway

Nucleotide Excision Repair (NER) is a versatile DNA repair pathway that resolves double helix distorting lesions, including UV-induced cyclobutane pyrimidine dimers and 6-4 photoproducts, which impede transcription and DNA replication. It comprises over 30 proteins in two sub-pathways: Global Genome NER (GG-NER), which resolves DNA lesions throughout the genome, and Transcription Coupled NER (TC-NER) that is directed on the transcribed strand of active genes (**Figure 2**) (reviewed in [59,60]). In GG-NER, the UV-DDB (ultraviolet radiation–DNA damage-binding protein) complex, consisted of the DDB1 and DDB2 (XPE) proteins, binds directly to the UV-induced lesion and stimulates XPC binding to the DNA strand opposite the lesion. UV-DDB forms an E3 ubiquitin ligase complex with CRL (cullin 4A (CUL4A)–regulator of cullins 1 (ROC1) E3 ubiquitin ligase) to which the COP9 signalosome is attached; DDB2 offers substrate specificity while DDB1 forms the linker with CRL. Upon UV-DDB binding to the lesion, the COP9 signalosome is released allowing for CUL4A neddylation by NEDD8. This results in DDB2 polyubiquitylation, leading to its degradation, and to XPC ubiquitylation, thereby increasing its affinity for DNA and resulting in XPC binding to the DNA strand opposite the lesion. In TC-NER, DNA damage is detected indirectly by CSB binding to stalled RNA polymerase II elongating complexes. CSB then recruits CSA which together with DDB1 and CRL form an E3 ubiquitin ligase complex. The COP9 signalosome is also attached to CRL and is released upon CRL binding to CSA. Again this results in CRL activation by neddylation. It is thought that among others, CSB is a ubiquitylation target of CRL. In parallel, UV-stimulated scaffold protein A (UVSSA) is also associated with stalled RNAPII and recruits the deubiquitylation enzyme USP7, which stabilizes CSB by deubiquitylation. The coordinated ubiquitylation and

deubiquitylation of CSB by CSA-DDB1-CUL4A and UVSSA-USP7 respectively provide a mechanism to regulate the reaction. CSB and CSA are required for the subsequent recruitment of NER core factors.

Following damage recognition, TFIIH is recruited at the site of damage. TFIIH is a transcription initiation and repair factor, comprising 10 subunits. Its two DNA helicases, XPB and XPD, open the DNA conformation around the lesion once XPD verifies the existence of a lesion. RPA binds to exposed ssDNA opposite the lesion. TFIIH also stimulates XPA binding to ssDNA-dsDNA junctions, which subsequently recruits the structure specific endonuclease XPF-ERCC1 heterodimer and the endonuclease XPG to cleave at the 5’ and 3’ side of the lesion respectively. The excised 22-30nt oligonucleotide is displaced by TFIIH and the ssDNA gap is filled by DNA Polymerase d or e and sealed by DNA ligase I or IIIα-XRCC1.

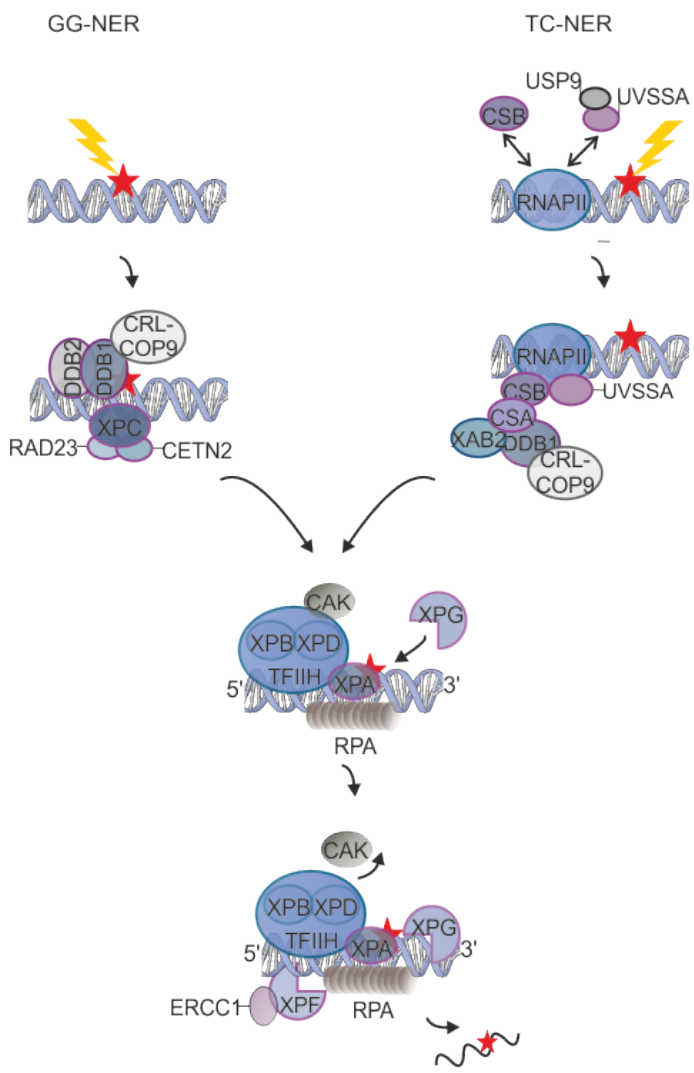


Figure 2. The NER pathway. The two NER subpathways differ in how the lesion is recognized with XPC-RAD23 being specific for GG-NER whereas, during TC-NER, CSA and CSB factors are recruited at the DNA damage-stalled RNA Pol II; both subpathways then merge to a common repair machinery, which restores DNA in a "cut and paste" manner, by unwinding the double helix, removing a 22-30 base oligonucleotide that contains the damage and filling the single strand gap by synthesis and ligation (not shown).

1.3. NER in mammalian development and disease

Defects in NER, apart from photosensitivity, have strikingly heterogeneous clinical outcomes, ranging from normal development with a high predisposition to skin cancer to progeroid-associated growth and neurodevelopmental defects but without susceptibility to cancer. The wide range of lesions repaired by NER, the existence of two subpathways and the additional roles of several NER factors probably contribute to this phenotypic diversity of NER-deficient patients.

In humans, Xeroderma Pigmentosum (XP) is caused by mutations in genes *XPA* through *XPG* and is characterized by photosensitivity and high cancer predisposition. Importantly, patients harboring defects only in GG-NER (i.e. *XPC* and *XPE/DDB2*), present with the highest susceptibility of cancer incidence among the Xeroderma Pigmentosum complementation groups: a >1000-fold increase in sun-induced skin cancer is observed along with a higher incidence of internal tumors [61], probably due to the accumulation of endogenously induced lesions that would otherwise be repaired by NER. Interestingly, XP caused by defects in all other complementation groups, which are part of the core NER and thus also affect TC-NER, is accompanied by neurological deficits of varying severity indicating a causative link between TC-NER and neurological traits [62,63].

Cockayne Syndrome ([CS] affected genes *CSA*, *CSB*, *UVSSA*, *XPB*, *XPD*, *XPF*, TFIIH subunit *TTDA* and certain mutations in *XPG*) and trichothiodystrophy ([TTD] affected genes: *XPB*, *XPD*, and TFIIH subunit *P8*) are both characterized by photosensitivity, neurological, developmental and progeroid traits but no cancer. CS patients present with impaired development of the nervous system, growth defects, progeroid traits and life expectancy of ~12 years, with symptoms varying from very severe in cerebro-oculo-facio-skeletal syndrome ([COFS] affected genes: *XPD*, *ERCC1*, *CSB*, *CSB*/*XPA*, *CSB*/*XPC*) with a life expectancy of less than two years, to milder in the UV-sensitive syndrome ([UVsS] affected genes: *CSB*, *CSA* and *UVSSA*). TTD is manifested by CS features together with ichtyosis and brittle hair and nails, deficits that probably arise from affected functions of TFIIH both in transcription initiation and repair.

While defects in GG-NER might well explain the cancer pre-disposition in XP patients and symptoms in TC-NER deficient patients could, at least partly, be explained by compromised transcription, mutations in genes of the common pathway result also in heterogeneous phenotypes, often dependent on the site of the mutation of a single gene; this could be mediated by additional roles-beyond NER- of the respective proteins. For example, XPG apart from NER is likely involved in BER and replication [64,65]; notably, mutations in *XPG* can lead to XP or to a syndrome that combines features from XP and CS (XPCS) [66]. The structure specific endonuclease XPF-ERCC1 heterodimer is also involved in interstrand crosslink repair, single strand annealing repair and the repair of transcription associated DNA lesions; intriguingly, depending on the mutation, patients can exhibit XP, severe CS, COFS and/or Fanconi anaemia [67].

To summarize, GG‑NER, by scanning the genome for helix-distorting lesions, prevents mutagenesis, while TC-NER, by removing transcription blocking lesions, ensures precise gene expression and thus cell viability. As a consequence, defective GG-NER results in high risk of cancer incidence while deficient TC-NER leads to a variety of diseases manifested by variable severity of developmental abnormalities and premature aging.

2. The RNA world

The central dogma of molecular biology holds that genetic information flows from DNA to protein through an intermediate RNA molecule. As a consequence, it has long been considered that DNA is the repository of the genetic information, RNA is a transient molecule that carries the information to the translation machinery, which subsequently produces proteins that carry out all the fundamental processes- structural, enzymatic and regulatory- of a cell. The discovery of tRNA and the ribozymes rRNA and snRNAs revealed the functional properties and potential of the RNA molecule and set the foundation of the RNA world hypothesis. Technological advances, however, allocated the RNA world from the past to the present. It is now generally accepted that RNAs and proteins highly collaborate to form ribonucleoprotein complexes (RNPs) that carry out fundamental cellular processes, such as maturation of RNA species and protein biosynthesis. Both molecules, though chemically diverse, share functional characteristics: both can act as catalysts (proteins-enzymes and RNA-ribozymes) and serve as scaffolding structures and binding platforms [68].

In an RNP, RNA can serve as an adaptor by annealing with another RNA molecule to direct specific alterations. For example, U7 snRNP directs the 3' end processing of the intronless non-polyadenylated histone pre-mRNAs (reviewed in [69]). Box C/D and box H/ACA small nucleolar RNPs (snoRNPs) direct modifications (2'-O-Methylation, pseudouridinylation, cleavage) essential for the maturation of ribosomal RNA [70]; a related family, small Cajal body RNPs (scaRNPs), modify small nuclear RNAs (snRNAs) [71]. Telomerase protects the ends of linear chromosomes from the loss of

critical coding sequences during its replication cycle. To do so, telomerase carries an RNA molecule that serves as a template to be reversely transcribed in multiple copies at the end of the chromosome [72]. The RNA molecule of an RNP can also serve as a scaffold that recruits proteins to regulate gene expression. The most prominent example is *Xist*, the RNA species that covers the whole X chromosome to completely inactivate it as a means for dosage compensation in female mammalian cells [73]. Enhancer RNAs (eRNAs) are RNAs transcribed at enhancer loci and are thought to recruit co-activator complexes that mediate chromosome looping and transcriptional activation [74,75].

In parallel, the RNA moiety of an RNP can act as a catalyst itself. The ribosome, which carries out protein biosynthesis, the spliceosome that excises introns from pre-mRNAs to produce mature mRNAs devoid of non-coding sequences and RNase P that generates the mature tRNA 5'end [76], are all ribonucleoproteins with an RNA-mediated enzymatic activity.

2.1. The splicing machinery

The spliceosome is a highly dynamic, ribonucleoprotein complex that comprises five small nuclear (sn) RNAs (the U1, U2, U4, U5, and U6 snRNAs) and a growing number of associated splicing factors that enables the selective intron excision of nascent pre-mRNA transcripts prior to mRNA translation [77]. Each snRNA (or two in the case of U4/U6) associates with a variable number of complex specific proteins forming a snRNP. The U1, U2, U4/U6 and U5 snRNPs are the main subunits of the major spliceosome that excises the majority of introns (U2 type introns). Some metazoan species and plants have an additional spliceosome (minor spliceosome) that removes a class of atypical introns (U12 introns) [78]. The minor spliceosome comprises U11, U12

and U4atac/U6atac snRNPs that are distinct but functionally equivalent to U1, U2 and U4/U6, whereas U5 is shared by both spliceosomes.

Pre-mRNA splicing involves two SN2-type transesterification reactions, implicating functional groups from three reactive regions of the intron and exon-intron boundaries. First, the phosphodiester bond at the 5' splice site (SS) is attacked by the 2'-hydroxyl of an adenosine of the branch point sequence (BPS) in the intron, which generates a free 5' exon and an intron lariat-3' exon. Subsequently, the 3'-hydroxyl of the 5' exon attacks the phosphodiester bond at the 3'SS, leading to exon ligation and excision of the lariat intron. The 5'SS, BPS, and 3'SS of pre-mRNA introns are defined by very short consensus elements that in metazoans are poorly conserved.

Splicing initiates with the recognition of the 5' and 3' splice sites (SS) that result in the formation of the spliceosomal E complex [79]. First, the U1 snRNP binds, in an ATP-independent manner and through base pairing, to the GU sequence at the 5' SS of an intron. This interaction is further stabilized by serine-arginine-rich (SR) and other proteins of the U1snRNP. In parallel, splicing factor 1 (SF1) and the U2 auxiliary factor (U2AF) bind to the intron branch point sequence (BPS) and the polypyrimidine tract just downstream of the BPS, respectively. The 65kd subunit of U2AF (U2AF65) interacts with SF1, while the 35kd subunit of U2AF (U2AF35) binds to the AG dinucleotide of the 3' SS. After the formation of the spliceosomal E complex, the U2 snRNP displaces SF1 and binds to the BPS in an ATP-dependent manner, leading to the formation of the A complex. Binding of U2snRNP to BPS is mediated by base pairing and further stabilized by SF3a and SF3b proteins of the U2 snRNP [80] as well as by U2AF65 [81]. Next, the U4/U6 and U5 snRNPs are sequestered as a preassembled U4/U6·U5 tri-

snRNP, resulting in the B complex. Intringuingly, the B complex, although containing all snRNPs, is still inactive; in order to be catalytically activated, major conformational and compositional changes must take place. The first step for spliceosome activation includes the release of U1 and U4, resulting in the formation of the activated B (B^{act}) complex, which performs the first transesterification reaction to generate the C complex. The C complex undergoes additional rearrangements before performing the second catalytic reaction [82]. After the second catalytic step, the mRNA is released as a mRNP and the resulting intron lariat is released with U2, U5, and U6 bound to it [83]. All snRNPs are eventually recycled and used in additional rounds of splicing reactions.

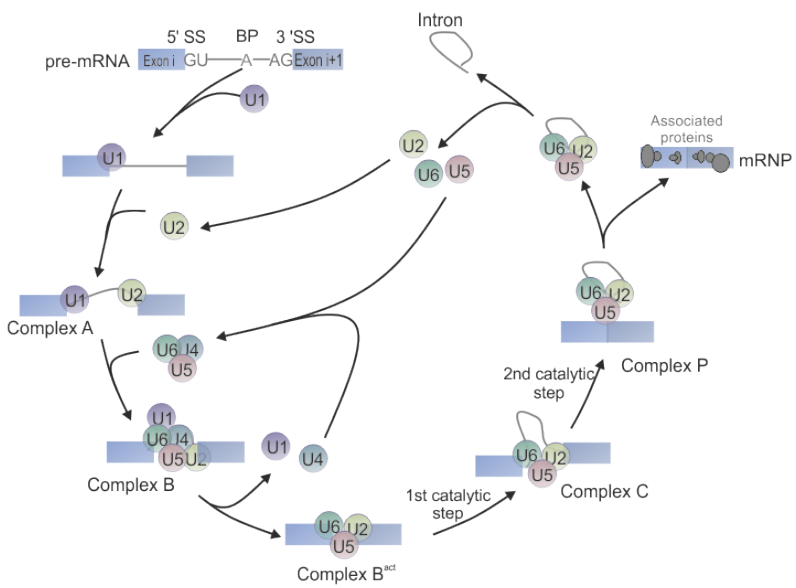
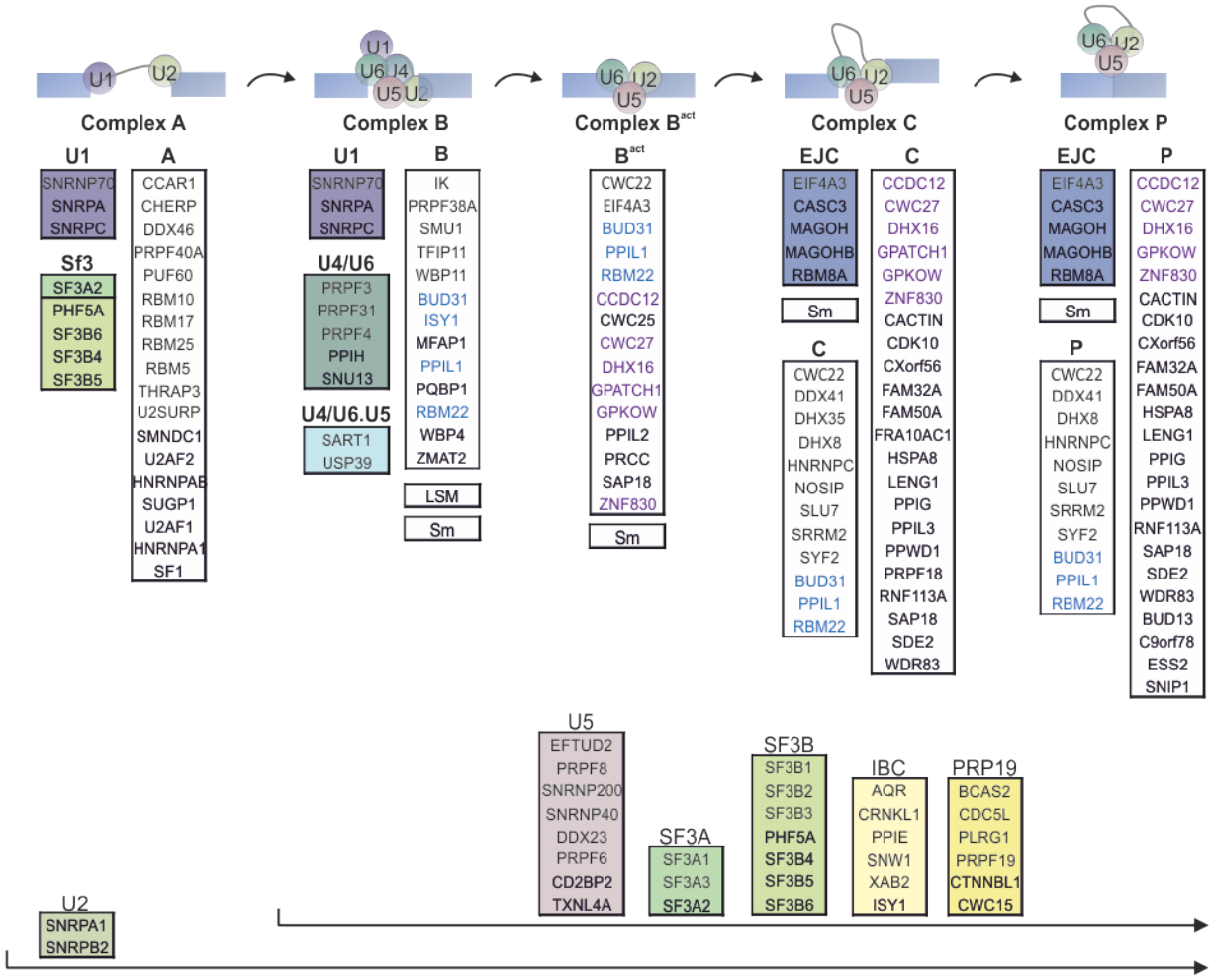


Figure 4. Core spliceosome assembly and composition. A. Diagram depicting the progressive assembly of the spliceosome on pre-mRNA. B. Major building blocks of the spliceosome. Protein names in blue and purple indicate factors involved in more than one spliceosome stages.



2.2. Regulation of the splicing complex and Alternative splicing

Although splicing involves a set of simple reactions, the spliceosome is assigned with the task to accurately identify authentic 5' and 3' SS; if SSs are not correctly recognized, even a single nucleotide mistake can lead to frameshift and ultimately result in mRNA degradation by the non-sense mediated decay (NMD) pathway or the production of non-functional proteins. This task becomes even more complicated if we account for the small size (<200bp) of the majority (~80%) of the exons that are dispersed in a sea of large introns [84]. Moreover, splicing is coupled with transcription [85] and is controlled by transcriptional elongation rates; slow RNA polymerase II elongation rate allows for recognition of weak splice sites and eventually the inclusion of "weak" exons [86]. This imposes an additional level of complexity as multiple regulatory mechanisms must cooperate to allow splice site selection.

In higher eukaryotes, many exons are differentially spliced, thus they are not present in every mRNA produced by a given pre-mRNA. Alternative splicing (AS) is considered a major regulator of gene expression as it generates variable mRNA molecules from a single pre-mRNA species, thereby increasing the complexity of the proteome of higher eukaryotes. AS generates protein isoforms that exert diverse biological properties concerning subcellular localization, potential interactions and catalytic ability [87]. Moreover, AS introduces another degree of complexity in the splicing process: the spliceosome must not only excise introns with great accuracy but also be able to guide inclusion or exclusion of specific exons in response to regulatory signals triggered by environmental and cellular changes.

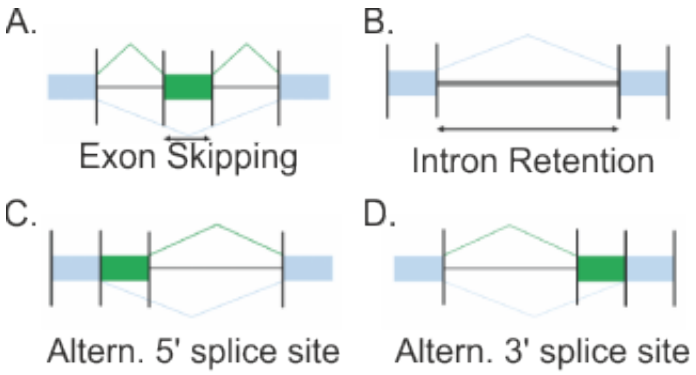


Figure 4. Alternative splicing events. (A) Exon skipping. (B). Intron retention. Alternative (C) 5' or (D) 3' splice site.

The requirements for efficient SS identification and differential SS choices impose the necessity for a splicing regulatory network. The spliceosome exerts certain characteristics that render it prone to regulation[68]. While the vast majority of RNPs are compositionally stable and harbor preformed active sites, the spliceosome forms stepwise on the pre-mRNA and in fact the substrate (pre-mRNA) is directly involved in building the active site of the spliceosome. Another unique principle of the spliceosome is that the RNA components of the active site are initially sequestered in an inactive conformation to allow for timely catalytic activation that involves substantial remodeling of the RNPs to allow for rearrangements of binding partners. This conformational plasticity of the spliceosome allows for splicing decisions: multiple factors (trans-acting) identify functional sites (cis-acting) on the mRNA precursor while multiple weak binary interactions contribute to allow or repress splicing.

Splice site decisions are primarily guided by the splice site sequences (5' SS, 3' SS, BPS), which are recognized and paired by the spliceosome. Consequently, a splice site with great affinity for U1 or U2AF will be more efficiently recognized and thus excised. However, as the splice site consensus sequences are loose, splice sites alone are not

sufficient to fully direct spliceosome assembly and splice choices. In higher eukaryotes, splicing decisions are assisted and directed by flanking pre-mRNA regulatory sequences (cis-acting elements) [88,89,90]. Cis-acting elements can have either positive (intronic or exonic splicing enhancers, ISEs or ESEs respectively) or negative (intronic or exonic splicing silencers, ISSs or ESSs respectively) effects on splice site usage.

Apart from the ~45 distinct snRNP-associated proteins, human spliceosomes also associate with approximately 125 or less factors at each stage of spliceosome assembly (170 in total) [91, 92, 93, 94, 95, 96, 97]. Many of the non-snRNP proteins are involved in coupling splicing with other cellular processes such as transcription, 3' end processing and quality control of mRNPs [77], while others function in splicing regulation. Splicing regulators (trans-acting elements) exhibit their regulatory effects by binding on cis-elements: positive trans-acting regulators bind on splicing enhancers and subsequently recruit the splicing machinery to the adjacent splice site while negative regulators bind to silencers and prevent the assembly of the spliceosome. For example, SR and hnRNP proteins, which often exert antagonistic effects: SR proteins tend to bind to ESEs while hnRNP proteins bind to ESSs; notably they can both bind concurrently on the same exon [98,99]. Ultimately, inclusion or exclusion of an exon is the result of multiple factors with antagonizing effects.

2.3. Splicing and Disease

Splicing requires the collaboration of multiple splicing factors that must be positioned at the right place at the right time to guide accurate splicing choices. This complexity that governs splicing renders it vulnerable to sequence polymorphisms and deleterious

mutations. Thus, it is not surprising that defects in splicing underlie a growing number of human diseases.

Generic splicing defects are considered not compatible with life, as null mutations in core spliceosomal factors often result in early embryonic lethality. There is currently, however, a growing number of reports that link mutations in core splicing factors with underlying pathologies, including Retinitis pigmentosa, microcephalic osteodysplastic primordial dwarfism type I (MOPD I) and myelodysplastic syndrome (MDS, discussed later). Retinitis pigmentosa is a progressive disease that is characterized by impaired night vision and decreased peripheral vision [100]. Numerous mutations cause autosomal dominant Retinitis pigmantosa (adRP), among which mutations in U4/U6·U5 tri-snRNP associated factors, namely PRPF31 [101,102], PRPF6 [103], PRP8 [104] or SNRNP200 [105]. Homozygous mutations in the U4atac snRNA of the minor spliceosome lead to microcephalic osteodysplastic primordial dwarfism type I (MOPD I, which is characterized by severe embryonic and postnatal growth retardation, microcephaly and skeletal anomalies that lead to early death [106,107,108].

The most common mutations, which alter splicing patterns and are associated with disease, are found in cis-acting elements, i.e. the core consensus sequences (5’ and 3’ SS and BPS) and the splicing enhancers and silencers that modulate spliceosome recruitment. For example, the generation of an alternative 3’ SS in the β-globin gene (*HBB*) by a point mutation results in β+ thalassaemia, which is characterized by reduced β-globin protein levels and aneamia [109,110,111]. Duchenne muscular dystrophy (DMD) is an X-linked heritable disease characterized by progressive muscle weakness and degeneration; DMD is caused by splice site mutations in the dystrophin-encoding gene

that lead to reduced dystrophin protein levels [112,113]. Mutations in an ESS of *MAPT* (microtubule-associated protein tau) exon 10 results in increased inclusion of exon 10 and dysfunction of the tau protein, leading to the neurodegenerative disorder frontotemporal dementia with parkinsonism linked to chromosome 17 (FTDP‑17) [114].

Aberrant splicing of the lamin A pre-mRNA (*LMNA)* is associated with four distinct disorders. 5' SS mutations result in retention of intron 9 or 8 accompanied by a premature termination codon (PTC) and cause limb girdle muscular dystrophy type 1B (LGMD1B) [115] or familial partial lipodystrophy type 2 (FPLD2) respectively [116]. Although the underlying mechanism of LGMD1B and FPLD2 is the same (intron retention that creates a pre-mature stop codon), they are characterized by diverse symptoms (muscle weakness and selective loss of fat tissue respectively), suggesting that different truncated proteins are produced. Moreover, Hutchinson–Gilford progeria syndrome (HGPS), a pre-mature aging disease, is caused by a mutation in *LMNA* exon 11 that activates an alternative 5' SS; this results in the excision of 150nt from exon 11 thus generating progerin that is causative for the disease. A point mutation in *LMNA* intron 4 generates an alternative 3' SS resulting in the in-frame addition of three amino acids, which leads to dilated cardiomyopathy (DCM) [117].

Alternative splicing offers a flexible way to regulate gene expression, as it allows for producing protein isoforms with different functions from a single gene. In particular, many protein isoforms that promote growth and cell survival are developmentally regulated by alternative splicing and are also found expressed in tumours. Thus it is not surprising that mis-regulation of alternative splicing has been widely associated with cancer [118]. Moreover, mutations that affect the expression of core spliceosomal factors

are also involved in cancer progression. For example, overexpression of *PRPF6*, a U4/U6·U5 tri-snRNP component, has been correlated to increased proliferation of colorectal carcinoma cells by preferential splicing of genes associated with growth regulation [119]. In contrast, reduced expression of *PRPF8* has been proposed to drive myelodysplstic syndromes (MDS) and promoting cancer cell proliferation [120].

3. At the crossroad of splicing and DNA Damage Response

Pre-mRNA splicing is functionally coupled to transcription [85, 121]. The process of mRNA synthesis is known to regulate constitutive and alternative splicing (AS) through the physical association of splicing factors to the elongating RNAPII [122], the 3D chromatin structure [123, 124] or through the fine-tuning of RNA polymerase II (RNAPII) elongation rates [125]. Recent findings support the notion that DNA damage affects splicing patterns [126]. The co-transcriptional recruitment of splicing factors to mRNA precursors as well as the regulation of AS by RNAPII elongation rates suggests that inhibition of RNA synthesis upon DNA damage will affect AS. Indeed, the presence of UV-induced DNA lesions has been shown to affect pre-mRNA splicing through the inhibition of the elongating RNAPII [127]. Moreover, the re-distribution of splicing factors can alter splicing patterns- especially of genes involved in the DDR- upon DNA damage: the Ewing sarcoma (EWS) protein is an RNA polymerase II-associated factor that binds co-transcriptionally to pre-mRNAs of genes involved in DDR and interacts with the YB-1 spliceosome-associated factor. In UV irradiated cells EWS translocates to nucleoli, thus is disengaged from both its target pre-mRNAs and YB-1. As a consequence, splicing patterns of EWS target transcripts change and are similar to the ones observed upon EWS depletion [128,129]. For example, proper splicing of *MDM2* transcripts requires the EWS: YB1 interaction; thus, upon DNA damage eight out of 12 exons of the *MDM2*

transcript are excluded thereby limiting full length *MDM2* mRNA and counteracting for MDM2 transcriptional upregulation. RNAPII stalling at DNA damage sites also causes the displacement of late-stage spliceosomes that ultimately results in ATM activation and altered splicing patterns [130].

Apart from direct or indirect effects of transcriptional inhibition, post transcriptional modifications of splicing regulators mediated by the DDR or downstream kinases (ATM, ATR, CHK1, CHK2, SR protein kinases (SRPK)) may also affect splicing decisions [131, 132]. For example, the spliceosome– associated factor THRAP3 is phosphorylated in an ATR-dependent manner and subsequently excluded from DNA lesions [133]; in response to cisplatin, the diverging actions of acetylation by Tip60 and phosphorylation by SRPK1 and SRPK2 kinases on SRSF2 (an SR regulator) determines whether cells undergo apoptosis or G2/M cell cycle arrest by regulating caspase-8 pre-mRNA splicing [134].

While DNA damage alters splicing patterns by regulating RNA synthesis and the spliceosome engagement with pre-mRNAs, splicing factors can also affect DDR by being directly involved in DNA repair. Many splicing factors have been reported to be recruited at sites of damage and subsequently promote DNA repair [135-136]. Though ncRNAs produced at sites of damage [137,138] could sequestrate RNA binding proteins at the lesion, an RNA-dependent mechanism has not yet been shown. On the contrary, splicing factors have been shown to be recruited at lesions by interacting with DNA or repair proteins. For example, YB-1 interacts with DNA that contains mis-paired bases or cisplatin adducts and exhibits strand separation and endonucleolytic activity in vitro [139]. Moreover, YB-1 binding to mismatched DNA has been shown to regulate MMR [140], while its interaction with several DNA repair factors (DNA polymerase delta, Ku80 and

WRN) potentiates YB-1 involvement in other repair pathways [139]. HnRNP C localizes at sites of IR-induced damage and interacts with the HR repair complex PALB2- BRCA2-BRCA1 to promote repair [141]; hnRNP U-like 1 and 2 interact with the MRN complex, stimulate DNA-end resection and promote ATR-dependent signaling and HR [142].

In addition to their role in regulating DDR gene expression at the post-transcriptional level, splicing factors also prevent DNA damage per se. In fact, each step in RNA production, from synthesis to export, has been associated with genome maintenance [143]. A major endogenous source of DNA damage leading to double strand breaks and associated with genome instability is the formation of R-loops. During transcription, nascent RNA may hybridize with the template DNA strand, thus leaving the other strand unpaired; such structures are called R-loops. R-loops are physiologically formed during cellular processes like V(D)J recombination; however unscheduled formation and accumulation of such structures leads to genome instability due to DSB formation by nucleases and/or transcription-replication conflicts [144,145]. Splicing factors, in addition to other mechanisms, contribute to genome maintenance by binding to nascent RNA, thereby preventing unscheduled R-loop formation [146]. For example, depletion of the SR splicing factor SF2[147] or MDS-associated point mutations in U2AF1 and SRSF2 [148,149] lead to accumulation of R-loops and subsequently to DNA damage.

3.1. XPA Binding protein (XAB2)

A NER factor that links DNA repair with transcription and pre-mRNA splicing is the XPA binding protein 2 (XAB2). XAB2 is the human homologue of the yeast pre-mRNA splicing factor Syf1. XAB2 is a predicted acidic protein of 855 amino acids (contains three stretches of acidic residues) and comprises 15 tetratricopeptide repeats, a

common domain of proteins involved in RNA processing [150, 151];. Sequence homology search using NCBI BLAST revealed conservation of the protein among lower and higher eukaryotes; indicatively, mouse XAB2 (mXAB2) shares 99% identity with the human homologue, 82% with that of zebrafish (*Danio rerio*), 61% with the fruitfly (*Drosophila melanogaster*), 49% with *Caenorhabditis elegans* and 28% with yeast (*Saccharomyces cerevisiae*). Disruption of the *Xab2* gene results in pre-implantation lethality in mice [152]. Thus, there are currently no available data to address the functional role of XAB2 in RNA biogenesis and the DDR *in vivo*. Using a yeast two-hybrid screen and *in vitro* pull-down assays XAB2 was shown to interact with the nucleotide excision repair factors XPA, CSA and CSB proteins and with RNAPII [153]. Microinjection of antibodies raised against XAB2 inhibited the recovery of RNA synthesis after UV irradiation and normal RNA synthesis in fibroblasts [153]. Follow-up work showed that XAB2 interacts with pre-mRNA splicing factors [154] and that the protein is functionally involved in homology-directed repair and single-strand annealing [155]. Moreover, XAB2 interacts with HDAC3 and the Retinoic Acid Receptor α (RARα) to form a co-repressor complex that inhibits gene activation by the RARα. Upon retinoic acid binding to its receptor XAB2 and HDAC3 dissociate, thus allowing transcription of RARα gene targets [156].

To dissect the functional contribution of XAB2 during mammalian development, we established an *in vivo* biotinylation tagging approach in mice. Our findings provide evidence that XAB2 is dispensable for NER or transcription. Instead, XAB2 interacts with the spliceosome factors PRP19, BCAS2 and Aquarius *in vivo*. We show that XAB2 binds on spliceosomal RNAs and the pre-mRNAs of selected gene targets during hepatic development and that the presence of persistent DNA lesions or transcription

blockage triggers the dissociation of XAB2 from spliceosomal RNAs and pre-mRNA targets leading to the aberrant accumulation of pre-mRNAs and to a defective DDR. Consistently, XAB2 is aberrantly released from RNA targets in the livers of developing mice with inborn NER defects. We propose that XAB2 functionally links the core spliceosome to DDR with important ramifications for mammalian development and the premature onset of inborn developmental defects associated with transcription-coupled DNA repair disorders.

Experimental Procedures

1. Generation of biotin-tagged XAB2 animals.

To generate the targeting vector for the insertion/knock-in of the Avi tag cassette before the stop codon of the last exon of the XAB2 gene, for the generation of the avXAB2 knock-in mice, the following approach was used: PCR products were amplified using Phusion High- Fidelity DNA Polymerase (NEB). The avi-tag was sub cloned in pBSSK (EcoRI/Hind III 0.18- kb). A triple ligation reaction was set up using the fragments: 5' homology sub cloned in two fragments (XbaI/BamHI 2.4kb and BamHI/ExoRI 1.2kb); avi tag (EcoRI/Hind III 0.18- kb); pBSSK-avi tag (XbaI/ExoRI 2.9kb). The lox-neomycin-lox cassette (HindIII/SalI 1.5-kb) was subsequently cloned into the vector followed by cloning of the 3' homology region (SalI fragment 3.3kb). Finally, the MC1-TK gene (SacII 1.8-kb) was inserted into the vector for negative selection. The final targeting vector was linearized using NotI and used for embryonic stem cell electroporation. 129/SV embryonic stem cells carrying the Protamine 1-Cre transgene were maintained in their undifferentiated state (LIF-ESGRO 10^7 units) and grown on a feeder layer of gamma-irradiated (3.500 rads) $G418^r$ primary mouse embryonic fibroblasts. Electroporation (400V, 25μF) of $0.8x10^7$ embryonic stem cells with 50μg of NotI linearized targeting vector (2mg mL^{-1}) was performed and homologous recombined clones were selected with G418 (300μg mL^{-1}) and ganciclovir (2μM). G418-resistant embryonic stem cell clones were subjected to Southern blot analysis and hybridized with 5' and 3' probes from their homology region. Genomic DNA from embryonic stem cell clones was digested overnight with EcoRV (MINOTECH Biotechnology) and

resolved on 1% agarose gels. Samples were immobilized on Hybond-NC nylon membranes (Amersham Bioscience) and hybridized with probes with [^{32}P] dCTP (Izotop). 5' (1.1kb NcoI/EcoRI) and 3' (1.2-kb BglII/Hind III) specific probes flanking the last exon of the Xab2 gene were used to identify the targeted (6.4-kb or 7.5-kb) and wild- type allele (15.8-kb). Clones with the correct homologous recombination were expanded to confirm their integrity and karyotyped to verify their euploid karyotype. Positive clones tested negative for mycoplasma (Venor GeM) were used for C57/BL6 blastocyst injection to generate chimeric mice. Chimeric males were bred to C57BL/6 wild-type females for germ-line transmission. Offspring were screened by PCR for neo-deletion using primers F1: 5'-AAGAACTGTCGCTCCCTGATGAAC-3' and R1 5'-CCTGGGGGGAAAGAATGAATTGCT-3' (Fig. 1a). Expression of Protamine-1 Cre transgene in the male germ line resulted in the deletion of the floxed neomycin gene in all the first pups born, leaving behind a single loxP site after the avi tag cassette. The Cre recombinase transgene, derived from the PC3 embryonic stem cell background, was bred out in the process of backcrossing to C57BL/6 mice. Biotin-tag XAB2 knock-in mice were further crossed to transgenic BirA transgenic mice [157]. Animals were kept on a regular diet and housed at the IMBB animal house, which operates in compliance with the `Animal Welfare Act' of the Greek government, using the `Guide for the Care and Use of Laboratory Animals' as its standard. As required by Greek law, formal permission to generate and use genetically modified animals was obtained from the responsible local and national authorities. All animal studies were approved by independent Animal Ethical Committees at FORTH and BSRC Al. Fleming.

2. Mass Spectrometry studies.

Proteins eluted from the beads were separated by SDS/PAGE electrophoresis on an 10% polyacrylamide gel and stained with Colloidal blue silver (ThermoFisher Scientific, USA; [158]. SDS-PAGE gel lanes were cut into 2-mm slices and subjected to in-gel reduction with dithiothreitol, alkylation with iodoacetamide and digested with trypsin (sequencing grade; Promega), as described previously [159, 160]. Nanoflow liquid chromatography tandem mass spectrometry (nLC-MS/MS) was performed on an EASY-nLC coupled to an Orbitrap Fusion Tribid mass spectrometer (Thermo) operating in positive mode. Peptides were separated on a ReproSil-C18 reversed-phase column (Dr. Maisch; 15 cm × 50µm) using a linear gradient of 0–80% acetonitrile (in 0.1% formic acid) during 90 min at a rate of 200 nl/min. The elution was directly sprayed into the electrospray ionization (ESI) source of the mass spectrometer. Spectra were acquired in continuum mode; fragmentation of the peptides was performed in data-dependent mode by HCD. Raw mass spectrometry data were analyzed with the MaxQuant software suite [161] (version 1.6.0.16) as described previously [160] with the additional options 'LFQ' and 'iBAQ' selected. The A false discovery rate of 0.01 for proteins and peptides and a minimum peptide length of 7 amino acids were set. The Andromeda search engine was used to search the MS/MS spectra against the Uniprot database (taxonomy: *Mus musculus*, release September 2017), concatenated with the reversed versions of all sequences. A maximum of two missed cleavages was allowed. The peptide tolerance was set to 10 ppm and the fragment ion tolerance was set to 0.6Da for HCD spectra. The enzyme specificity was set to trypsin and cysteine carbamidomethylation was set as a fixed modification. Both the PSM and protein FDR were set to 0.01. In case the identified peptides of two proteins were the same or the identified peptides of one

protein included all peptides of another protein, these proteins were combined by MaxQuant and reported as one protein group. The generated ‘proteingroups.txt’ table was filtered for contaminants and reverse hits. For interactor identification, t-test-based statistics was applied on LFQ. First, the logarithm (log 2) of the LFQ values were taken, resulting in a Gaussian distribution of the data. This allowed imputation of missing values by normal distribution (width=0.3, shift=1.8), assuming these proteins were close to the detection limit. Statistical outliers for the XAB2 samples compared to BirA control were then determined using two-tailed t-test. Multiple testing correction was applied by using a permutation-based false discovery rate (FDR) method in Perseus.

3. Cells, colony formation, trypan blue exclusion and unscheduled DNA synthesis assays.

Mouse embryonic stem cells JM8A3N.1 were cultured on gelatinized tissue culture dishes in medium containing Dulbecco's modified Eagle's medium (DMEM) supplemented with 15% fetal bovine serum (FBS), 50µg mL^{-1} streptomycin, 50 U mL^{-1} penicillin (Gibco), 2mM L-glutamine (Gibco), 1% non-essential amino acids (Gibco), 0.1mM β-Mercaptoethanol (Applichem), 1000U mL^{-1} LIF (Millipore), 1µM MEK inhibitor PD0325901 (Selleck), 3µM GSK inhibitor CHIR99021 (Selleck). Primary MEFs (P4) and HEPA cells were cultured in standard medium containing Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 50µg mL^{-1} streptomycin, 50 U mL^{-1} penicillin (Gibco), 2mM L-glutamine (Gibco). To knock down Xab2 an oligo RNA was designed at the position 1685 of the cDNA (Invitrogen). Mouse embryonic stem cells were transfected in suspension with Lipofectamine 2000 (Invitrogen) and subsequently plated in a 60mm plate. HEPA cells were transfected with Polyplus Jet prime according to the manufacturer’s protocol. As a non-targeting control,

AllStars negative (Qiagen) was used. Both siRNAs were used at a final concentration of 50nM.

For DNA damaging or transcription inhibition treatmens, cells were rinsed with PBS, exposed to UVC irradiation at the indicated doses, 10 μg mL^{-1} MMC (AppliChem), 100μM DRB or 1μM tryptolide and cultured at 37°C for 0.5 to 12h prior to subsequent experiments (as indicated). Pre-incubation with caffeine (10mM), ATM inhibitor (10μM) and ATR inhibitor (10μM) started 1 h before genotoxic treatments and lasted throughout the experiment. For cell survival experiments, a total of 200-300 HEPA cells or primary MEFs were seeded in 10 cm Petri dishes 24h post knock-down. The next day, MEFs were exposed to MMC treatment for 4 h or to UVC irradiation and incubated for 10 days. Colonies were stained with Coomassie blue (0.2% Coomassie blue, 50% methanol, 7% acetic acid) and the number of colonies was counted and expressed as a percentage of the treated cells relative to that of the untreated control. Three dishes per dose were used and at least three independent survival experiments were performed. For viability experiments, Trypan blue inclusion was used at selected time points post transfection. Culture medium was collected and centrifuged to precipitate dead cells. HEPA cells were detached from the tissue culture dish by trypsin-0.5% EDTA, resuspended in culture medium and merged with the fraction of cells from the medium. The cell suspension was subsequently diluted 1:5 with 0.4% Trypan blue and the number of viable and dead cells was counted in a Neubauer haemocytometer under the microscope. The number of viable cells was expressed as the percentage of viable cells relative to that of the control cells. At least three independent viability experiments per time point were performed. DNA repair synthesis was determined by 5-ethynyl-20-

deoxyuridine (EdU) incorporation. Primary MEFs grown on coverslips were globally UVC irradiated and incubated for 2.5 h in medium supplemented with 10μM EdU. After EdU incorporation, cells were washed with PBS followed by fixation with 2% formaldehyde in PBS. Coverslips were blocked for 30 min with 10% FBS in PBS, followed by 1h incubation with 10mM sodium ascorbate, 4mM CuSO4 containing Alexa Fluor594 azide (ThermoFischer Scientific A10270) and DAPI. The number of EdU-positive cells among at least 200 cells was counted, and the percentage of EdU-positive cells relative to the total number of cells was calculated.

4. Immunofluorescence, Antibodies, Westerns blots

Immunofluorescence experiments were performed as previously described [157]. Briefly, cells were fixed in 4% formaldehyde, permeabilized with 0,5% Triton-X and blocked with 1% BSA. After one-hour incubation with primary antibodies, secondary fluorescent antibodies were added and DAPI was used for nuclear counterstaining. Samples were imaged with SP8 confocal microscope (Leica). For local DNA damage infliction, cells were UV-irradiated (60 J/m^2) through isopore polycarbonate membranes containing 3-μm-diameter pores (Millipore). For CPD immunodetection, nuclear DNA was denatured with 1M HCl for 30min. For whole cell extract preparations, cell pellets were resuspended in 150mM NaCl, 50mM Tris pH=7.5, 5% Glycerol, 1% NP-40, 1mM MgCl) and incubated on ice for 30 min. Antibodies against XAB2 (wb: 1:2000, IF: 1:1000), PRP19 (wb: 1:1000, IF: 1:500), β-TUB (wb: 1:2000) were from Abcam. BCAS2 (wb: 1:5000, IF: 1:1000), ATM (wb: 1:300), ATR (wb: 1:500, IF: 1:500) and DDB1 (IF: 1:500) were from Novus. HA (Y-11, western blotting (wb): 1:500), ERCC1 (D-10, wb: 1:500), RAD9A (wb: 1:300), POLII (wb: 1:500, IF: 1:50), XPA (wb: 1:500) were from Santa Cruz Biotechnology. γH2AX (05-636, IF: 1:12.000) was from Millipore. DDB1 (wb: 1:5000),

XPC (wb: 1:1000) and CSB (wb: 1:1000) were from Bethyl Laboratories. Streptavidin-HRP (wb: 1:12,000) was from Upstate Biotechnology. pATM (wb: 1:1000, IF: 1:1000) was from Rockland. pATR (wb: 1:1000, IF: 1:500) was from Genetex.FLAGM2 (F3165, wb 1:2.000) was from Sigma-Aldrich. CPD (IF: 1:50) was from Cosmo Bio Ltd (TDM2).

5. Co-immunoprecipitation assays.

Nuclear protein extracts from 15-day-old livers or cells were prepared as previously described [157] using the high-salt extraction method (10mM HEPES-KOH pH 7.9, 380mM KCl, 3mM MgCl2, 0.2mM EDTA, 20% glycerol and protease inhibitors). For immunoprecipitation (IP) assays, nuclear lysates were diluted threefold by adding ice-cold HENG buffer (10mM HEPES-KOH pH 7.9, 1.5mM MgCl2, 0.25 mM EDTA, 20% glycerol) and precipitated with antibodies overnight at 4°C followed by incubation for 2 h with protein G Sepharose beads (Millipore). Normal mouse or rabbit IgG (Santa Cruz) was used as a negative control. Immunoprecipitates were washed five times (10mM HEPES-KOH pH7.9, 300mM KCl, 0.3% NP40, 1.5mM MgCl2, 0.25mM EDTA, 20% glycerol and protease inhibitors), eluted and resolved by SDS-PAGE. Pulldowns were performed with 0.6-0.7mg of nuclear extracts using M-280 paramagnetic streptavidin beads (Invitrogen) as previously described [157].

6. ChIP-sequencing and ChIP-qPCR analysis.

For ChIP assays, mESCs were cross-linked at room temperature for 2.5 min with 1% formaldehyde. Chromatin was prepared and sonicated on ice for 8 min using a Covaris S220 Focused-ultrasonicator. Samples were immunoprecipitated with antibodies (5-6µg) overnight at 4°C followed by incubation for 3 h with protein G Sepharose beads (Millipore) and washed sequentially [157]. The complexes were eluted and the crosslinking was heat reversed. Purified DNA fragments were analyzed by sequencing or qPCR. For

ChIPSeq data we followed the analysis pipeline proposed by ENCODE (https://www.encodeproject.org/pages/pipelines/#DNA-binding), using bowtie2 with–very- sensitive preset instead of bwa. After peak calling we used IDR (Irreproducible Discovery Rate - https://www.encodeproject.org/software/idr/) version 2.0.4.2 to identify (and exclude) false positives.

7. Differential alternative splicing analysis.

Global quality of FASTQ files with raw RNA-seq reads was analyzed using *fastqc* v.0.11.5 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). *Vast-tools* [162, 163] aligning and read processing software was used for quantification of alternative sequence inclusion levels from FASTQ files using VASTD-DB annotation [164] for mouse genome assembly mm9. To ensure sufficient read coverage for alternative splicing quantification, we considered only *vast-tools*' events with a minimum mapability-corrected read coverage score of "VLOW" across all samples. The relative inclusion of an alternative sequence (exon or intron), henceforth called alternative splicing event, is based on the number of junction reads supporting inclusion (#inc) and exclusion (#exc), used to quantify percent spliced-in (PSI) [165]values. The beta distribution (conjugate prior probability distribution for the binomial), constrained in the]0,1[interval and characterized by a mean value of $\alpha / (\alpha + \beta)$ from the distribution's shape parameters α and β, was exploited in modelling the precision of each PSI from its supporting coverage (#inc and #exc). We used R function *rbeta* to emit, for each sample, 500 values from a beta distribution with $\alpha = \#inc + 1$ and $\beta = \#exc + 1$, where 1 is added to ensure that both the shape parameters, α and β, are different from zero. Since beta distributions get narrower with increasing shape parameters (for the same PSI value), this

parametrization allows the scattering of emitted values to serve as a surrogate for that PSI's dispersion (given the original read coverage supporting it), while the distribution's mean value, (#inc + 1) / (#inc + 1 + #exc + 1), is an approximation of the empirical PSI. For each event, *rbeta*-emitted values were grouped per condition (Control and Xab2 siRNA) and used to fit, with the *fitdistr* function from R package *MASS* [166], (joint) beta distributions giving the global PSIs per condition and the difference between these, $\Delta PSI = PSI_{Xab2\ siRNA} - PSI_{Control}$. For each alternative splicing event, the joint beta distribution's 10 000 emitted values were used in calculating the significance of its ΔPSI. First, the difference between Xab2 siRNA and Control vectors of emitted values was calculated. The significance of each ΔPSI was set as the ratio between the number of differences that are greater than zero and the total number of differences, reflecting the probability of $PSI_{Xab2\ siRNA}$ being greater than $PSI_{Control}$. Differentially spliced events were considered as those with a probability of a $|\Delta PSI| > 0$ greater than 0.8. To assess the enrichment of differentially spliced events in positive or negative ΔPSI values within exon skipping and intron retention events, we tested the null hypothesis that the proportion of positive ΔPSI values (i.e. $PSI_{Xab2\ siRNA} > PSI_{Control}$) was equal to 0.5 using R function *prop.test*.

8. RNA immunoprecipitation studies.

RNA immunoprecipitation in HEPA cells and MEFs was performed as previously described [167] with a few modifications. In brief, cells (4x150mm plate) were harvested by trypsinization and the cell pellet was resuspended in NP-40 lysis buffer for 10min on ice. Nuclei were washed once in NP-40 Lysis buffer and subsequently resuspended in 1 ml RIP buffer (150mM Kcl, 25mM Tris pH 7.4, 5mM EDTA, 0.5mM DTT, 0.5% NP40, 1mM

PMSF, 40U/mL RNaseOut; Invitrogen). Resuspended nuclei were mechanically sheared using a syringe (26G) with 5-7 strokes. Nuclear membrane and debris were pelleted by centrifugation at 13,000 RPM for 10 min. Antibodies (5µg) were added to supernatant and incubated overnight at 4°C with gentle rotation. Fifty microliters of protein G Sepharose beads (Millipore) were added and incubated for 2hr at 4°C with gentle rotation. Beads were pelleted at 6,000 RPM for 3 min, the supernatant was removed, and beads were washed three times in 1 mL wash buffer (280mM KCl, 25mM Tris pH 7.4, 5mM EDTA, 0.5mM DTT, 0.5% NP40, 1mM PMSF, 40 U/mL RNaseOut; Invitrogen) for 10min at 4oC, followed by one wash in PBS. Beads were resuspended in 1 ml of Trizol and co-precipitated RNAs were isolated according to the manufacturer's protocol. Isolated RNA was treated with DNase I (Promega) followed by reverse transcription with random primers (Invitrogen). RNA immunoprecipitation in liver tissue was performed as previously described (Kaneko et al). In brief, livers from 15-days old mice were minced and subsequently cross-linked with 0.1% formaldehyde for 10 min at room temperature. After addition of 0.25 M glycine for 5 min, cells were harvested and lysed with RIPA buffer (50mM Tris-HCl [pH 7.4], 1% NP-40, 0.5% Na deoxycholate, 0.05% SDS, 1mM EDTA, and 150mM NaCl) followed by sonication at 4°C. Nuclear membrane and debris were pelleted by centrifugation at 13,000 RPM for 10 min. Antibodies (5µg) were added to supernatant and incubated overnight at 4°C with gentle rotation. Fifty microliters of protein G Sepharose beads (Millipore) were added and incubated for 2 hr at 4°C with gentle rotation. Beads were pelleted at 6,000 RPM for 3 min, the supernatant was removed, and beads were washed three times in 1 mL wash buffer (50mM Tris-HCl [pH 7.4], 1% NP-40, 0.5% Na deoxycholate, 0.05% SDS, 1mM

EDTA, and 350mM NaCl) for 10min at 4°C, followed by one wash with PBS. Crosslinks were reversed by adding 100µl elution buffer (50mM Tris-HCl pH 6.5, 5mM EDTA, 1% SDS, and 10mM DTT) and heating for 45 min at 70°C. RNA was purified with TRIzol reagent, treated with DNase I, and used for first-strand cDNA synthesis.

9. RNA-Seq and Quantitative PCR studies.

Total RNA was isolated from cells using a Total RNA isolation kit (Qiagen) as described by the manufacturer. For RNA-Seq studies, libraries were prepared using the Illumina® TruSeq® mRNA stranded sample preparation Kit for HEPA cells and for mESCs. Library preparation started with 1µg total RNA. After poly-A selection (using poly-T oligo-attached magnetic beads), mRNA was purified and fragmented using divalent cations under elevated temperature. The RNA fragments underwent reverse transcription using random primers. This is followed by second strand cDNA synthesis with DNA polymerase I and RNase H. After end repair and A-tailing, indexing adapters were ligated. The products were then purified and amplified to create the final cDNA libraries. After library validation and quantification (Agilent 2100 Bioanalyzer), equimolar amounts of all 12 libraries were pooled. The pool was quantified by using the Peqlab KAPA Library Quantification Kit and the Applied Biosystems 7900HT Sequence Detection System. The pool was sequenced by using an Illumina HiSeq 4000 sequencer with a paired-end (2x 75 cycles) protocol. Quantitative PCR (Q-PCR) was performed with a Biorad 1000-series thermal cycler according to the instructions of the manufacturer (Biorad) as previously described [157]. All relevant data and primer sequences for the genes tested by qPCR are available upon request. In order to quantify our transcriptomics data and identify possible different isoforms we decided to use cufflinks package (Differential gene and transcript expression analysis of RNA-seq

experiments with TopHat and Cufflinks, Cole Trapnell, Adam Roberts, Loyal Goff, Geo Pertea, Daehwan Kim, David R Kelley, Harold Pimentel, Steven L Salzberg, John L Rinn & Lior Pachter, *Nature Protocols* **volume 7**, pages 562–578 (2012)) for the RNASeq data analysis. Briefly, after sequencing the reads from every sample were checked for their quality using fastqc (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Next, separate transcriptome assemblies were constructed for every sample and then they were merged into a single assembly. Differential expressed genes were identified comparing data from each sample to this merged assembly. Quantitative PCR (Q-PCR) was performed with a Biorad 1000-series thermal cycler according to the instructions of the manufacturer (Biorad) as previously described [157].

10. Data analysis.

A two-tailed t-test was used to extract the statistically significant data by means of the IBM SPSS Statistics 19 (IBM), R-statistical package (www.r-project.org) or Microsoft Excel. Significant over-representation of pathways and gene networks was determined by Gene Ontology (http://geneontology.org/).

Results

1. Generation of biotin-tagged XAB2 mice.

Ablation of *Xab2* in the murine germline results in preimplantation lethality, indicating an essential role for XAB2 during mouse embryogenesis [152]. To delineate the functional role of XAB2 during mammalian development, we generated knock-in animals expressing XAB2 fused with a tandem affinity purification tag comprising two affinity moieties, a 3X FLAG tag and a 23aa Avitag sequence, separated by a Tobacco Etch Virus (TEV) site for easy tag removal. The tag was inserted before the stop codon of the last exon 19 (**Figure 5**).

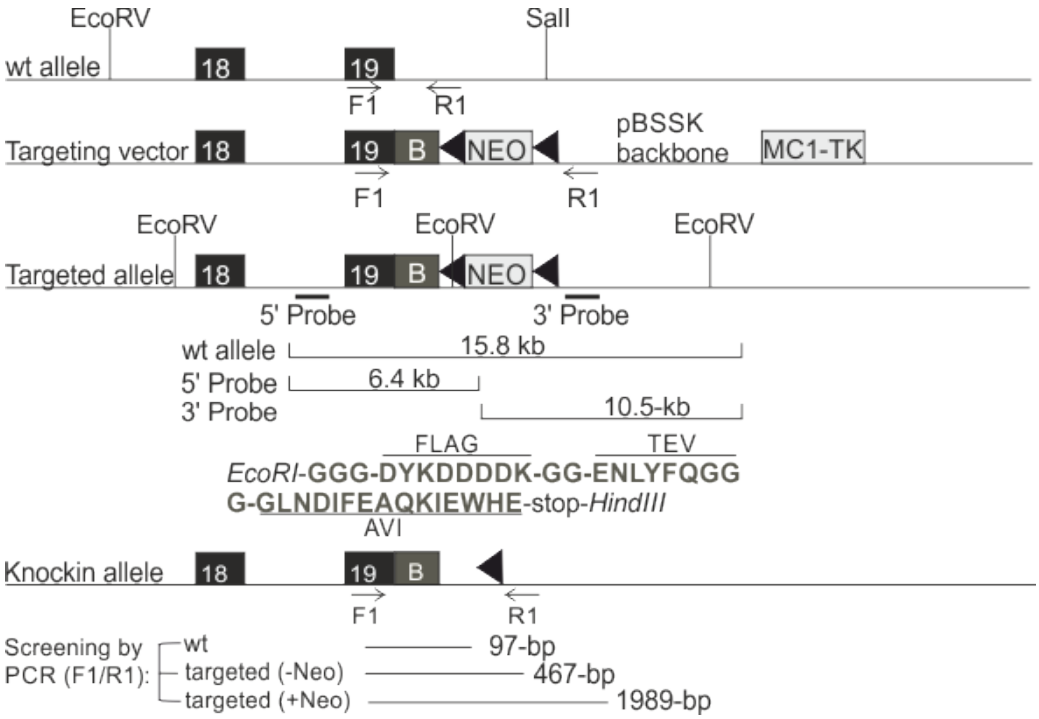


Figure 5. Schematic representation of knock-in mice expressing XAB2 fused with the 3xFLAG tag, a 15aa Avi tag sequence and a Tobacco Etch Virus (TEV) site separating the two tags. EcoRI and HindIII sites are synthetic; B: Flag-Tev-AVI fragment.

The targeting vector was transfected to 129/SV ES cells expressing the Protamine 1-Cre recombinase transgene, which efficiently excises the neomycin cassette in the male germ line [168]. After selecting properly targeted clones (**Figure 6A**; as indicated), two independently transfected clones were used to generate germ line-transmitting chimeras. Avitag-fused heterozygous males (*aviXab2*$^{+/-}$ mice) were backcrossed and maintained in a C57/BL6 background. Homozygous *aviXab2*$^{+/+}$ knock-in animals were then crossed with mice ubiquitously expressing the HA-tagged BirA biotin ligase transgene [157]. BirA is a bacterial ligase that specifically recognizes and successfully biotinylates the short 23aa biotinylation Avitag, thus creating a high affinity "handle" for the *in vivo* isolation of XAB2-bound protein complexes from biotin-tagged XAB2 (bXAB2) mice by binding to streptavidin. Importantly, the inserted Avitag sequence does not interfere with murine development as bXAB2 animals are born at the expected Mendelian frequency (**Figure 6B**), grow normally (**Figure 6C**) and show no developmental defects or other pathological features (**Figure 6D**). Nuclear extracts from P15 avXAB2 livers expressing either only aviXAB2 or aviXAB2 and BirA biotin ligase (bXAB2) were probed with streptavidin-HRP (stp-HRP) confirming the biotinylation of bXAB2 *in vivo* (**Figure 6E**). The use of anti-FLAG and anti-HA confirmed the presence of the knock-in allele and the BirA transgene, respectively. Pulldowns with 0.6 mg of nuclear extracts from P15 bXAB2$^{+/+}$ livers expressing the birA transgene and the use of M-280 paramagnetic beads (in excess) revealed the percentage of biotinylated XAB2 (90%) and flow through (fth; 10%) (**Figure 6F**).

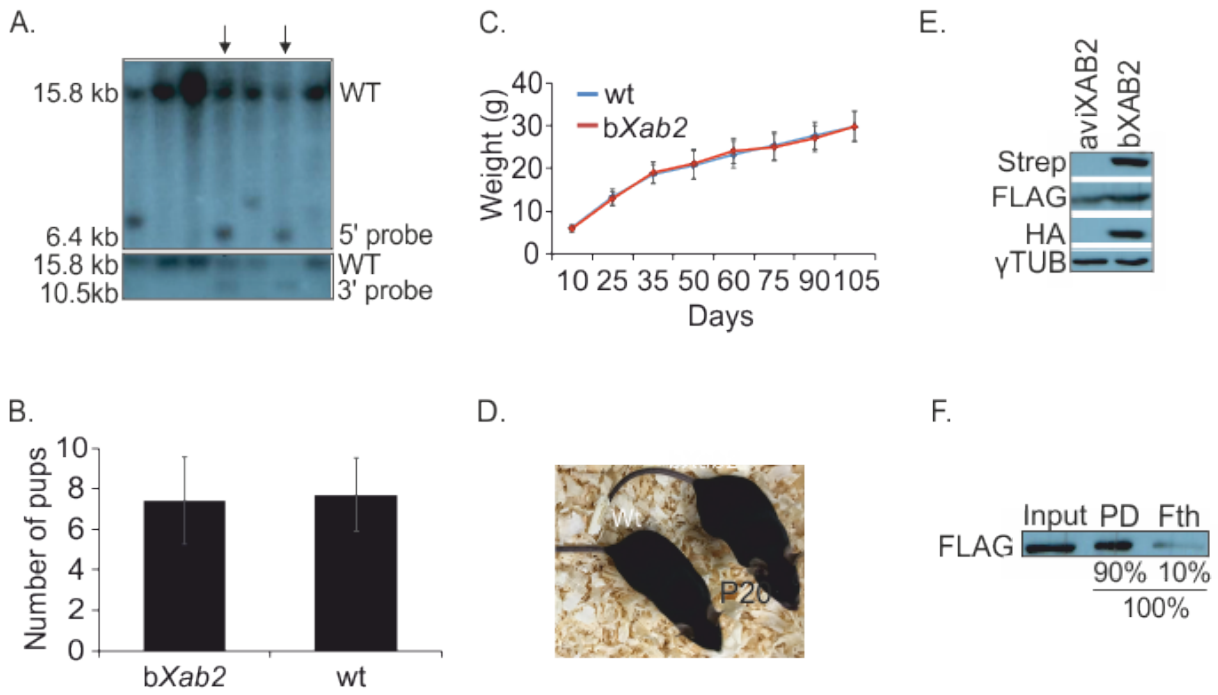


Figure 6. Generation of biotin-tagged XAB2 animals. (**A**). Two independently transfected ES clones (marked with arrow heads) were used to generate germline transmitting chimeras that were backcrossed with C57Bl/6 mice to generate *avXab2*$^{+/-}$ pups. (**B**). Number of wt. and bXAB2 pups born. (**C**). Weight (grams; g) of wt. and bXAB2 animals (n=8) at the indicated time points. (**D**). A photograph of P20 wt. and bXAB2 animals. (**E**). *In vivo* biotinylation of the short 15aa Avi-tag in bXAB2 animals. Nuclear extracts from P15 avXAB2 livers expressing either only avXAB2 (XAB2, MW: 110kDa) or avXAB2 and BirA biotin ligase (bXAB2) were tested by Western blot. The blot was probed with streptavidin-HRP (stp-HRP), which confirms biotinylation of XAB2 *in vivo*, with anti-FLAG and anti-HA confirming the presence of the knock-in allele and of the BirA transgene, respectively. (**F**). Biotinylation efficiency in bXAB2 livers. The percentage of biotinylated XAB2 (90%) and flow through (10%; fth) was calculated by performing pull-down with 0.7 mg of nuclear extract derived from 15-days old bXAB2$^{+/+}$;BirA livers and M-280 paramagnetic beads in excess.

Previous findings suggest that XAB2 is involved in the transcription-coupled repair (TC-NER) sub-pathway of nucleotide excision repair (NER) [153] and during the end resection step of homologous recombination repair [155]. To test whether the Avitag sequence interferes with the putative function of XAB2 in DNA repair *in vivo*, we further exposed mouse embryonic fibroblasts (MEFs) to ultraviolet irradiation (UV) as well as to mitomycin C (MMC), a potent genotoxic agent that introduces DNA inter-strand crosslinks that prevent dissociation of the strands, and thus inhibits replication and transcription of DNA. We find a similar percentage of UV-induced unscheduled DNA synthesis in bXAB2 cells compared to wild-type (wt.) controls (**Figure 7A**) and that bXAB2 MEFs are not hypersensitive to UV irradiation (**Figure 7B**) or to MMC (**Figure 7C**). Thus, bXAB2 animals develop normally to adulthood and are proficient at repairing UV-induced cyclobutane pyrimidine dimers (CPDs) and DNA interstrand cross-links (ICLs).

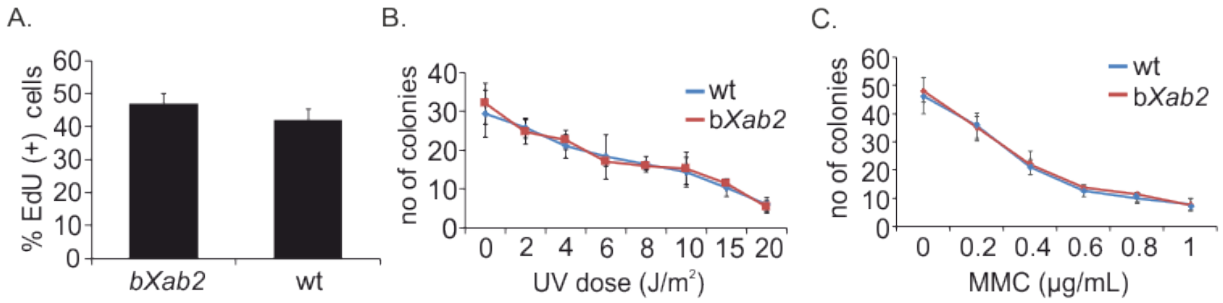


Figure 7. bXAB2 mice are NER and ICL efficient. (**A**) % of EdU (+) MEFs derived from bXAB2 and wt. mice (**B**). Survival of primary bXAB2 and wt. MEFs to UV (n ≥ 3 per time point) or (**C**). to MMC at the indicated doses (n ≥ 3 per dose point).

2. A proteomics strategy reveals XAB2-bound protein partners involved in RNA processing.

To isolate and characterize XAB2-associated protein complexes during postnatal hepatic development, we combined the *in vivo* biotinylation tagging approach [157] with a hypothesis-free, high-throughput proteomics strategy. To do this, we prepared nuclear extracts from P15 bXAB2; BirA livers (from now on designated as bXAB2) and livers expressing only the BirA transgene using high-salt extraction conditions (**Figure 8A**). The liver is a relatively homogeneous organ that accurately depicts the growth status of the developing animal. Nuclear extracts were treated with benzonase and RNase A, to ensure that DNA or RNA does not mediate the identified protein interactions. Nuclear extracts were further incubated with streptavidin-coated beads and bound proteins were eluted and subjected to Western blot analysis confirming that bXAB2 can still interact with the pre-mRNA-processing factor 19 (PRP19) [169] (**Figure 8B**). Next, the proteome was separated by 1D SDS-PAGE (~12 fractions) followed by in-gel digestion and peptides were analyzed with high-resolution liquid chromatography-tandem mass spectrometry (nLC MS/MS) on a hybrid linear ion trap Orbitrap instrument (**Figure 8C**). From three biological replicates, which comprised a total of 72 MS runs, we identified a total of 1167 proteins (**Appendix, Table 1**) with 636 proteins (54,49%) shared between all three measurements under stringent selection criteria (**Figure 8D, Appendix Table 2**; see methods).

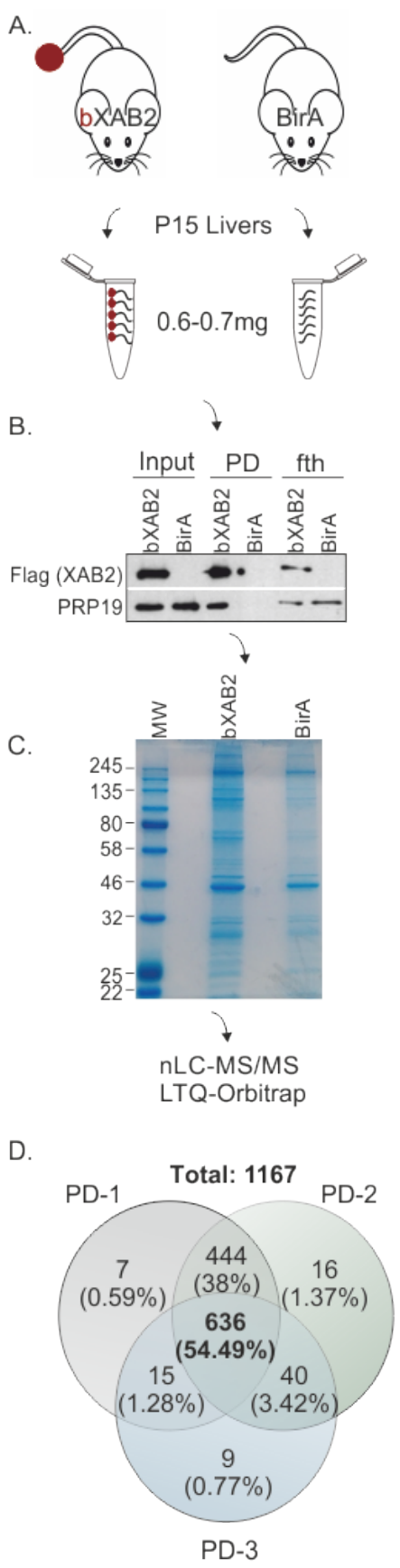


Figure 8. Schematic representation of the high-throughput MS analysis (**A**). in livers derived from P15 bXAB2 animals expressing the BirA transgene (n=8) and BirA transgenic control mice (n=8). (**B**). bXAB2 pulldowns (PD; n PD: Pulldown) and western blot with anti-FLAG (for XAB2) and anti-PRP19 in nuclear extracts derived from P15 bXab2 livers (n=3). (**C**). A representative 2D gel of proteins extracts derived from P15 XAB2 and BirA transgenic mice. (**D**). Venn's diagram of bXAB2-bound protein factors from three independent pull-downs (PD) and subsequent MS analyses; % depicts the percentage of XAB2-bound proteins involved in the indicated biological process over the total number of XAB2-bound proteins

To functionally characterize this dataset, we next subjected the 636-shared XAB2-bound proteins to gene ontology (GO) classification. Those biological processes (**Figure 9A**) or pathways (**Figure 9B**) containing a significantly disproportionate number of proteins relative to the murine proteome were flagged as significantly over-represented (FDR<0.05). At this confidence level, the over-represented biological processes and pathways involved 372 out of the initial 636 XAB2-bound core proteins; the latter set of proteins also showed a significantly higher number of known protein interactions (i.e. 958 interactions) than expected by chance (i.e. 531 interactions; **Figure 9C**) indicating a functionally relevant and highly interconnected protein network. Using this dataset, we were able to discern four major XAB2-associated protein complexes involved in i. pre-mRNA splicing ($p \leq 3.2 \times 10^{-38}$, e.g. AQR, BCAS2, PRP19, PRP8, SNRP40), ii. RNA transport ($p \leq 1.8 \times 10^{-7}$, e.g. NUP107, NUP133, NUP153, NUP160, NUP205, NUP210, NUP50, NUPl2), and iii. cell cycle ($p \leq 7.1 \times 10^{-6}$, e.g. ANAPC1, ANAPC 2, ANAPC 4, ANAPC 5, ANAPC 7, CDC23, CDC27, FZR1, RAD21, SMC1a, SMC3, STAG1, STAG2) and iv. ribosome biogenesis ($p \leq 4.8 \times 10^{-6}$, e.g. BMS1, GNL3, MDN1, NOP58, UTP15, WDR36, WDR43, WDR75, XRN2). Together, these findings indicate that the great majority of XAB2-bound protein partners are functionally involved in RNA processing and genome utilization processes.

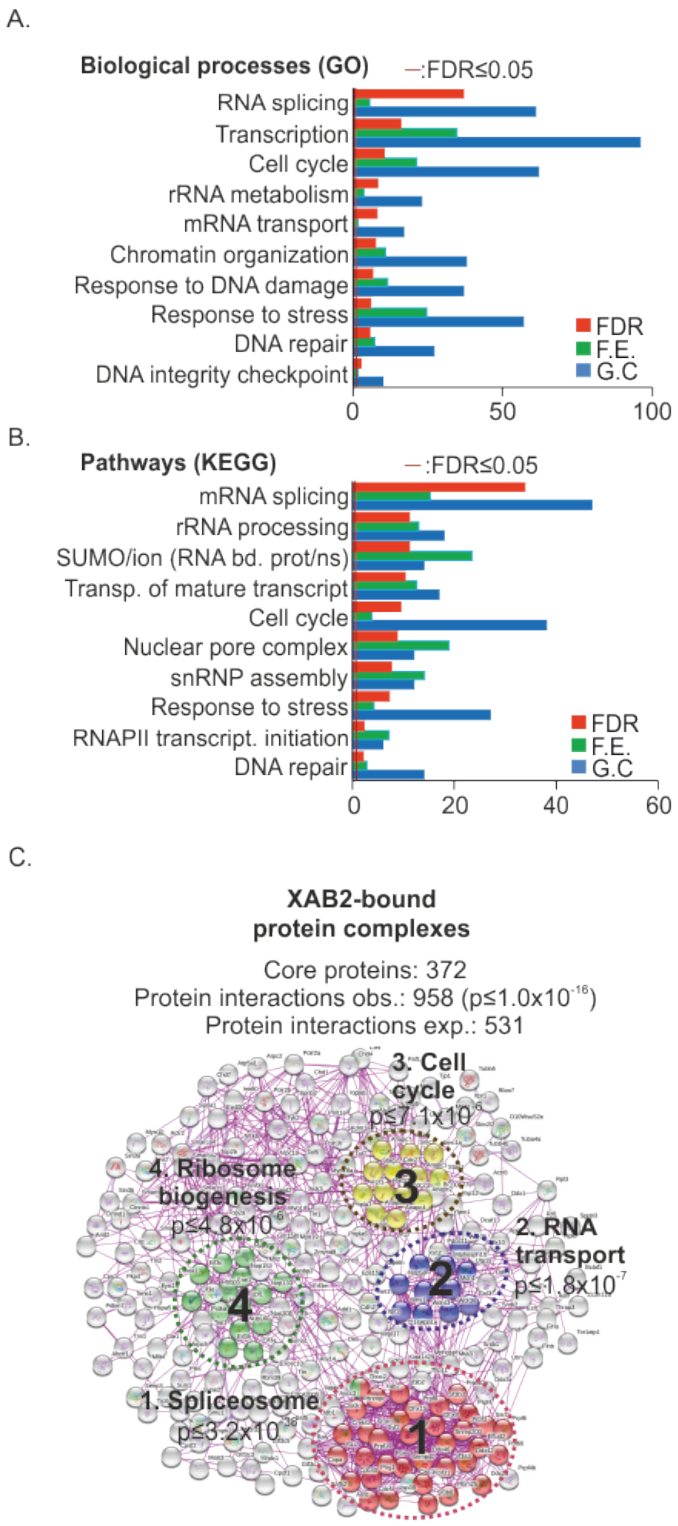


Figure 9. Functional characterization of XAB2-bound proteins. (**A**). List of significantly over-represented biological processes of 636 shared XAB2-bound proteins. Biological processes are sorted by the -log of FDR, which is calculated by Fisher's exact test right-tailed. The red-dotted line marks the threshold of significance at FDR ≤ 0.05. Count: the number of identified XAB2-bound protein factors involved in the indicated biological process. F.E. represents the ratio of XAB2-bound proteins involved in a process (sample frequency) to the total genes involved in the process (background frequency) (**B**). List of significantly over-represented pathways (KEGG). Data are shown as in (A). (**C**). Number of observed (obs.) and expected (exp.) known protein interactions within the core 372 XAB2

-bound protein set and schematic representation of the four significantly over-represented XAB2-bound protein complexes based on experimental evidence.

3. Abrogation of XAB2 leads to defective NER and DDR signaling.

Previous findings revealed that XAB2 is involved in transcription and the transcription-coupled sub-pathway of NER (TC-NER) [153, 170]. These data and the identification of several transcription factors in our bXAB2 MS data (**Appendix, Table 2**) prompted us to investigate whether XAB2 binds genome-wide on putative DNA elements e.g. enhancers, promoters that are known to regulate gene expression. An Illumina-based next generation sequencing approach on XAB2-co-immunoprecipitated DNA (ChIP-Seq) revealed, however, no significant peaks of DNA-binding enrichment in mouse embryonic stem cells (mESCs; **Figure 10A**). Similar findings were observed in the XAB2 ChIP-Seq profiles of mESCs treated with trans-retinoic acid (tRA), a pleiotropic factor known to activate transcription and regulate gene expression during cell differentiation and embryonic development [171] (**Figure 10A**; as indicated). To test whether XAB2 is required for transcription, we monitored native RNA synthesis in siXab2 cells. To do so, HEPA cells were transfected with dsRNA targeting the Xab2 transcript and assayed 48 hours (h) post-transfection to confirm the efficient reduction of XAB2 protein levels (Figure). Knockdown of XAB2 in si*Xab2* HEPA cells (**Figure 10B**) results in increased cell death at 72h post-transfection (**Figure 10C**) and reduced proliferative capacity (**Figure 10D**). Confocal microscopy experiments of fluorescently labelled BrU incorporation in nascent RNA [172] revealed lower transcription levels in si*Xab2* compared to control cells (**Figure 10E**). Importantly, RNAPII proteins levels are not affected by XAB2 abrogation (**Figure 10F**). We,

therefore, reason, that XAB2 has an indirect or transient role in transcription that is likely mediated through alternative mechanisms.

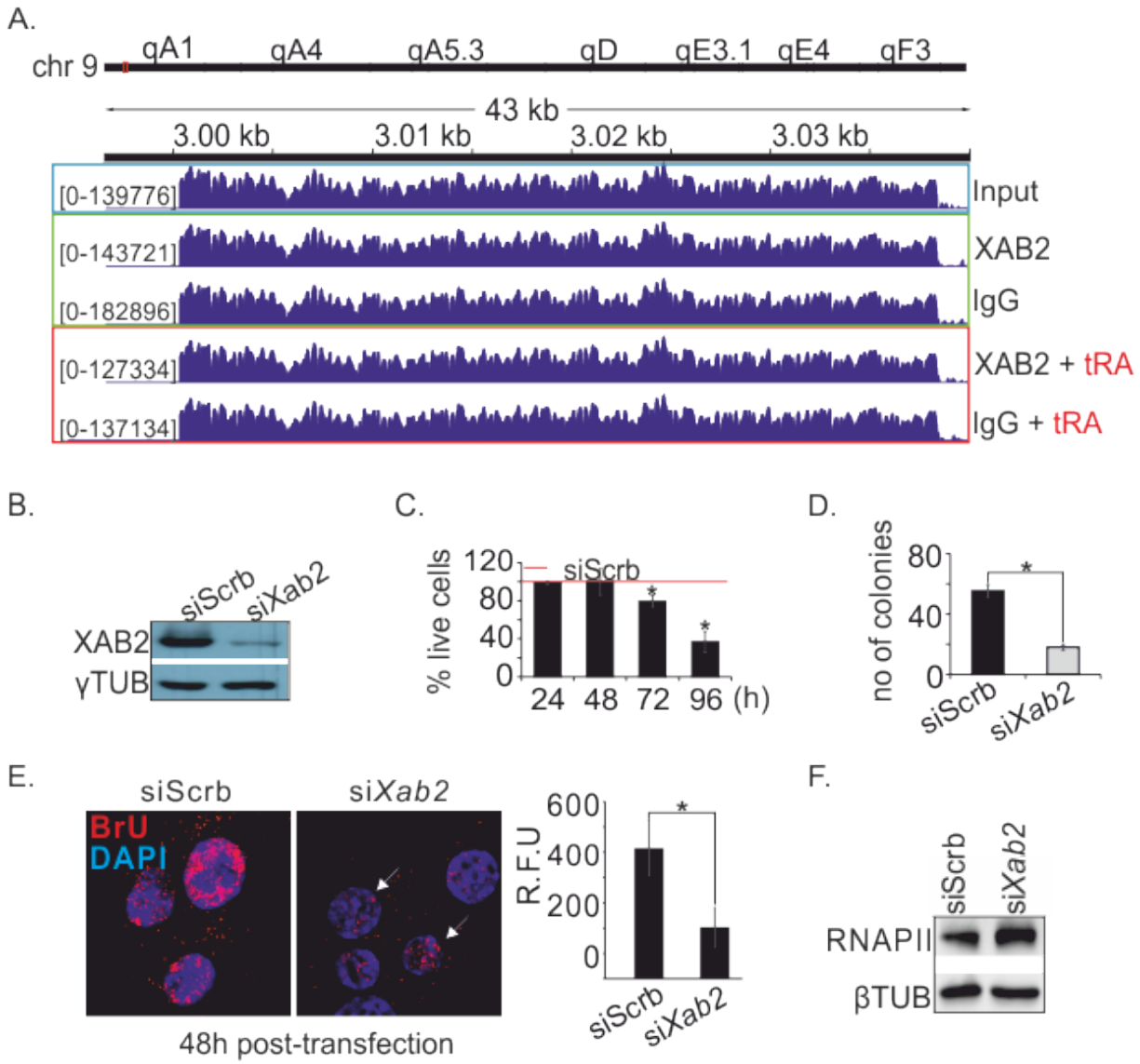


Figure 10. XAB2 has an indirect role in transcription. (A). XAB2 co-immunoprecipitated DNA (ChIP-Seq) profiles in mESCs treated with trans-retinoic acid (tRA) as indicated. (B). Western blot analysis of XAB2 protein levels in si*Xab2* cells and si Scramble (Scrb) cells at 48 hours (h) post-transfection (**C**). % of live si*Xab2* cells (Trypan blue inclusion) at the indicated time points post transfection. (**D**). Number (no) of colonies of si*Xab2* cells at seven days post-

transfection. (**E**). Immunofluorescence detection and quantification of nascent RNA synthesis in siScrb and siXab2 (white arrowhead) cells at 48h post-transfection. (**F**). Western blot analysis of RNAPII.

To test for the functional role of XAB2 in NER, we carried a series of pulldown assays in nuclear extracts of UV-irradiated (10J/m^2) and control bXAB2 primary mouse embryonic fibroblasts (MEFs). We find that bXAB2 interacts with the DNA damage-binding protein-1 (DDB1) involved in UV-induced DNA damage recognition [173], and with a portion of xeroderma pigmentosum, complementation group A protein (XPA) known to assemble the NER incision complex at sites of DNA damage [174], in control and UV-irradiated cells (**Figure 11A**). Confocal microscopy in UV-irradiated HEPA cells revealed that only a fraction of XAB2 co-localizes with the UV-induced CPDs (**Figure 11B**). The great majority of XAB2 is distributed throughout the nucleoplasm but is excluded from the denser DAPI-stained heterochromatin regions or the nucleolus and forms a punctuate staining that is distinctively adjacent to the DNA damage marker γH2Ax (**Figure 11C**).

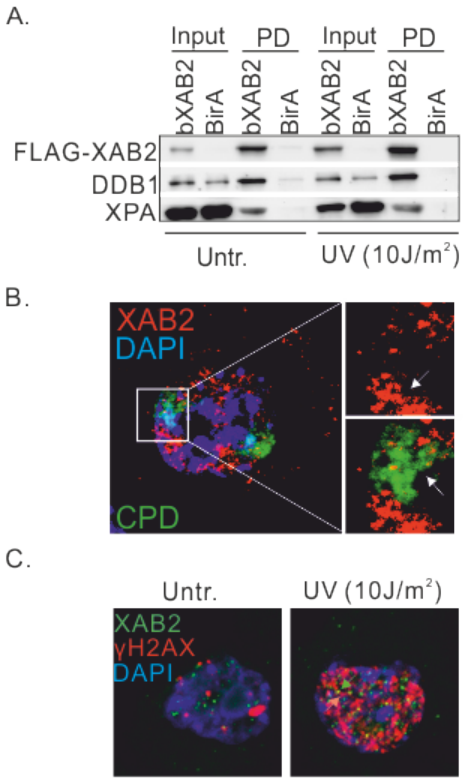


Figure 11. (**A**). bXAB2 pulldowns followed by western blot analysis with DDB1 or XPA in UV-irradiated (10J/m^2) and control primary MEFs. (**B**). Immunofluorescence detection of XAB2 with UV-induced CPDs; white arrowheads indicate the immunodetection of XAB2 and CPDs, respectively. (C). Immunofluorescence detection of XAB2 with γH2AX in HEPA cells exposed to UV-irradiation (10J/m^2).

To test whether XAB2 is required for repair of UV-unduced lesions by NER, we monitored the NER process in si*Xab2* cells. Unlike in wt. cells, we find that CPDs persist in si*Xab2* cells even 24h post UV irradiation (**Figure 12A**). In agreement with the defective repair of UV-induced CPDs, si*Xab2* cells manifest a noticeable decrease in unscheduled DNA synthesis at 2.5h post-UV irradiation (measuring global genome NER; **Figure 12B**) [175]. si*Xab2* cells also present with substantial delay in the recovery of RNA synthesis (assessing TC-NER; **Figure 12C)** as evaluated by the fluorescent detection of bromouridine (BrU) labelled nascent RNA at 4h post-UV irradiation. Importantly, with the exception of RAD9A (**Figure 12E)**, the protein levels of NER factors DDB1, XPC, XPA, ERCC1, RPA70 and XPD were comparable between untreated, UV-irradiated or MMC-treated si*Xab2* cells and the siScrb control (**Figure**

12D, 12F), suggesting that inefficient repair of UV-induced lesions does not result from a constitutive defect in NER upon *Xab2* abrogation.

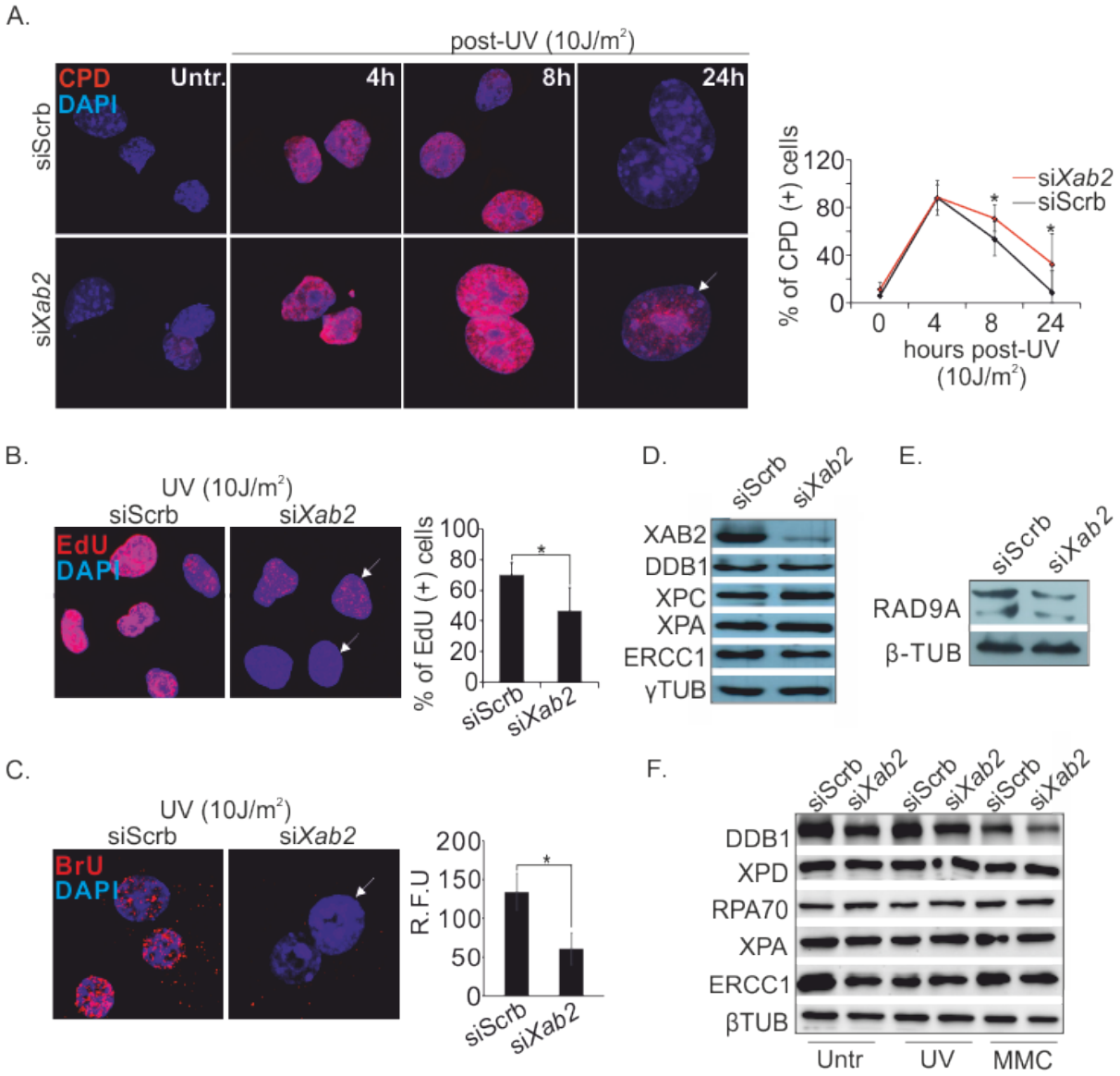


Figure 12. XAB2 is indispensable for efficient repair by NER. (**A**). Immunofluorescence detection and quantification of CPDs in siScrb and si*Xab2* cells at 4, 8 and 24h post UV irradiation (10J/m2); the white arrowhead indicates the presence of irreparable CPDs at 24h post-UV irradiation (**B**). Immunofluorescence detection and quantification of unscheduled DNA synthesis in siScrb and si*Xab2* cells treated with EdU at 48h post-transfection and 2.5h post

UV irradiation (10J/m^2). (**C**). Immunofluorescence detection of RNA synthesis recovery in siScrb and si*Xab2* cells treated with 5-Bromouridine (BrU) at 48h post-transfection and 4h post (Figure 12 legend) UV irradiation (10J/m^2). (**D-F**). Western blot analysis NER factors protein levels in siScrb and si*Xab2* cells at 48 hours (h) post-transfection and/or upon genotoxic stress. The asterisk "*" indicates a p-value ≤ 0.05 (n ≥ 3 per time point, treatment or genotype). R.F.U: Relative fluorescence units.

Next, we investigated whether DDB1 and XPA are efficiently recruited at DNA damage sites in UV-irradiated si*Xab2* HEPA cells. We find that DDB1 co-localizes competently with UV-induced CPDs in si*Xab2* cells (**Figure 13A**). Instead, XPA fails to form visible foci and properly recruit on UV-induced CPDs in these cells (**Figure 13B**).

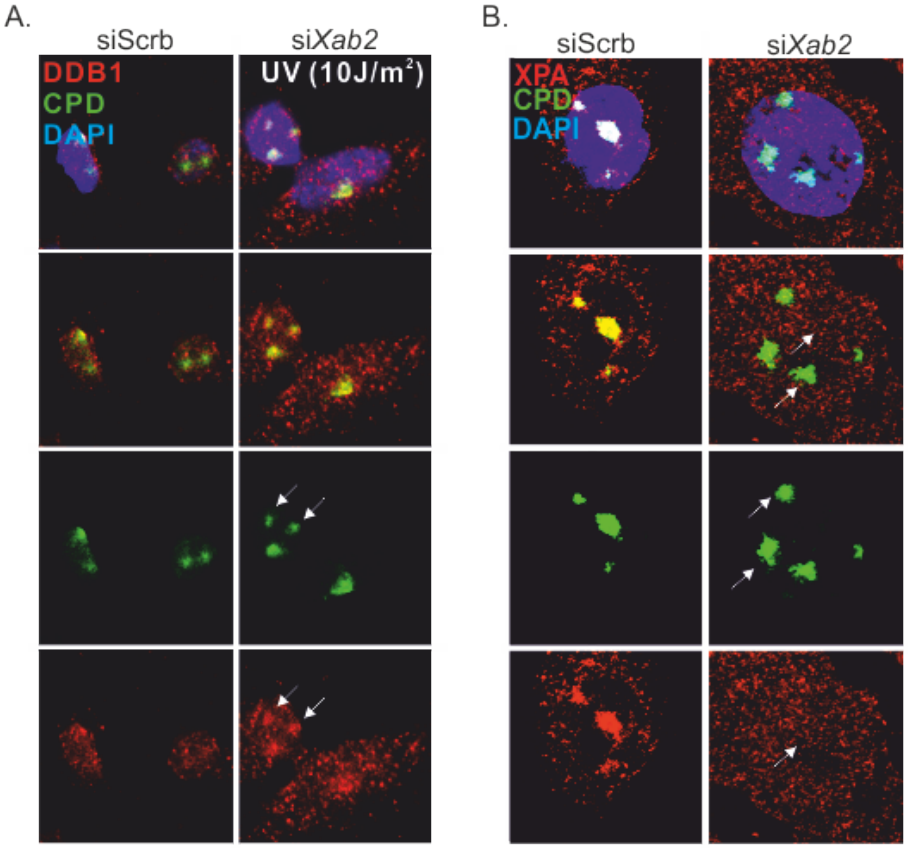


Figure 13. Xab2 abrogation is indispensable for core NER factors recruitment at UV-

induced lesions. Immunofluorescence analysis of CPDs and (**A**) DDB1 and (**B**) XPA in si*Xab2* and siScrb cells exposed to UV irradiation (10J/m^2).

The punctuate immunolocalization of XAB2 adjacent to γH2Ax (**Figure 11C**), prompted us to further test whether ablation of XAB2 affects proper DDR signaling. Confocal studies revealed the noticeable lack of γH2A.X foci in UV-irradiated or MMC-treated si*Xab2* cells (**Figure 14A**; as indicated)**.** Importantly, we did neither observe increased γH2AX foci in untreated si*Xab2* cells (**Figure 14A**) despite the presence of higher levels of RNA:DNA hybrids (**Figure 14B**), which are functionally linked with the formation of double-strand breaks and the activation of DDR [176]. Western blotting confirmed that the diminished detection of γH2Ax foci was not due to a constitutive defect in H2A.X protein expression levels in si*Xab2* cells (**Figure 14F**). Moderately higher γH2AX protein levels were only detected in untreated *siXab2* cells when compared to mock transfected control cells, indicating that transfection with dsRNA *per se* results in H2AX phosphorylation (**Figure 14C**). Depending on the type of DNA damage, phosphorylation of H2A.X is predominantly mediated by phosphorylated Ataxia telangiectasia-related (pATR) or Ataxia telangiectasia-mutated (pATM) kinases [3]. Consistent with these data and the lack of γH2AX foci in si*Xab2* cells, we find the substantial decrease in the number of pATR and pATM foci (**Figure 14E-F**; as indicated) as well as in pATM and pATR protein levels (**Figure 4D-E**) in MMC-treated or UV-irradiated si*Xab2* cells, respectively. Unlike with H2AX, however, we find that the ATR and ATM protein levels are markedly reduced in non-irradiated si*Xab2* cells (**Figure 14F**). Thus, ablation of XAB2 leads to defective NER, the accumulation of irreparable UV-induced DNA lesions,

the faulty recruitment of XPA at UV-induced DNA damaged sites and to the considerable decrease of ATM/ATR protein levels, pATM/pATR and γH2AX foci in mammalian cells.

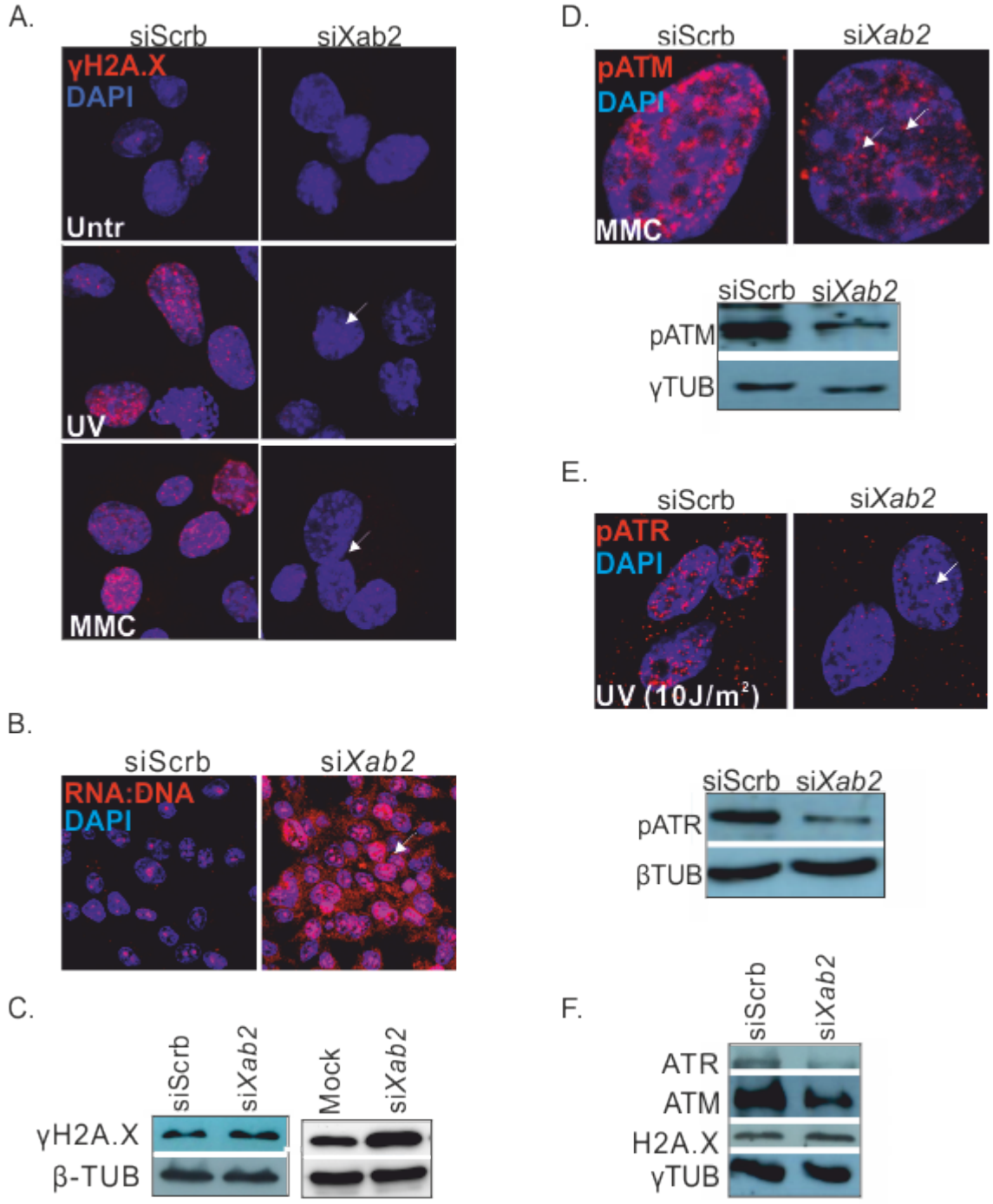


Figure 14. XAB2 is indispensable for DDR activation. (**A**). Immunofluorescence experiments showing the absence of γH2Ax foci in si*Xab2* cells (white arrowhead) untreated or exposed to UV-irradiation (10J/m^2) or MMC (as indicated) compared to siScrb cells. (**B**). Immunofluorescence detection of RNA:DNA hybrids in non-irradiated siScrb and si*Xab2* cells (indicated with the white arrowhead) at 48h post-transfection. (**C**). Western blot analysis of (Figure 14 legend) γH2AX in siScrb, mock transfected and si*Xab2* cells at 48h post-transfection. (**D**). Immunofluorescence detection and Western blot analysis of pATM in siScrb and si*Xab2* cells treated with MMC. (**E**). Immunofluorescence detection and Western blot analysis of pATR in siScrb and siXab2 cells exposed to UV irradiation (10J/m^2). (**F**). Western blot analysis of ATR, ATM and H2AX in siScrb and siXab2 cells at 48h post-transfection.

4. XAB2 is part of a core spliceosome complex that binds on U snRNAs.

Several factors involved in DNA repair and the DDR are now known to have functional roles in RNA processing [177, 178]. Spliceosomal factors were highly enriched in the bXAB2-bound proteome. As splicing factors are often non-specifically enriched in affinity enrichment-mass spectrometry approaches [179], we first challenged the specificity of XAB2 to the pre-mRNA splicing machinery by comparing the bXAB2 MS liver proteome to that derived previously from P15 biotin-tagged xeroderma pigmentosum complementation F (bXPF) livers under similar experimental conditions [157]. XPF is the obligatory interacting partner in the NER structure-specific ERCC1-XPF endonuclease complex [55]. Unlike bXPF, we find that bXAB2 co-immunoprecipitates several core spliceosome factors present in spliceosomal B through P complex and half of the proteins involved in the PRP19 and PRP19-related complex (nine out of 18 pre-mRNA splicing factors) (**Figure 5A**; colored in red). Follow-up pulldown experiments revealed that the endogenous bXAB2 interacts with Aquarius (AQR), an intron-binding spliceosomal factor that links pre-mRNA splicing to small nucleolar ribonucleoprotein biogenesis [180], PRP19, an ubiquitin-protein ligase involved in pre-mRNA splicing and

DNA repair [181, 182], and BCAS2, an integral component of the spliceosome that is required for activating pre-mRNA splicing [183] in P15 livers (**Figure 5B**). Consistently, BCAS2 immunoprecipitates XAB2, AQR and PRP19, thereby, establishing the reciprocity of protein-protein interactions and that XAB2 is part of the core spliceosome machinery (**Figure 5C**). Importantly, abrogation of XAB2 in si*Xab2* cells does not affect the protein levels of PRP19 or BCAS2 but it leads to the substantial decrease in AQR protein levels (**Figure 5D**). Further work revealed that PRP19 and BCAS2 do not co-localize with pATM in UV-irradiated or MMC-treated HEPA cells (**Figure 15E**) and that PRP19 only partially co-localizes with UV-induced CPD lesions (**Figure 15F**; as indicated).

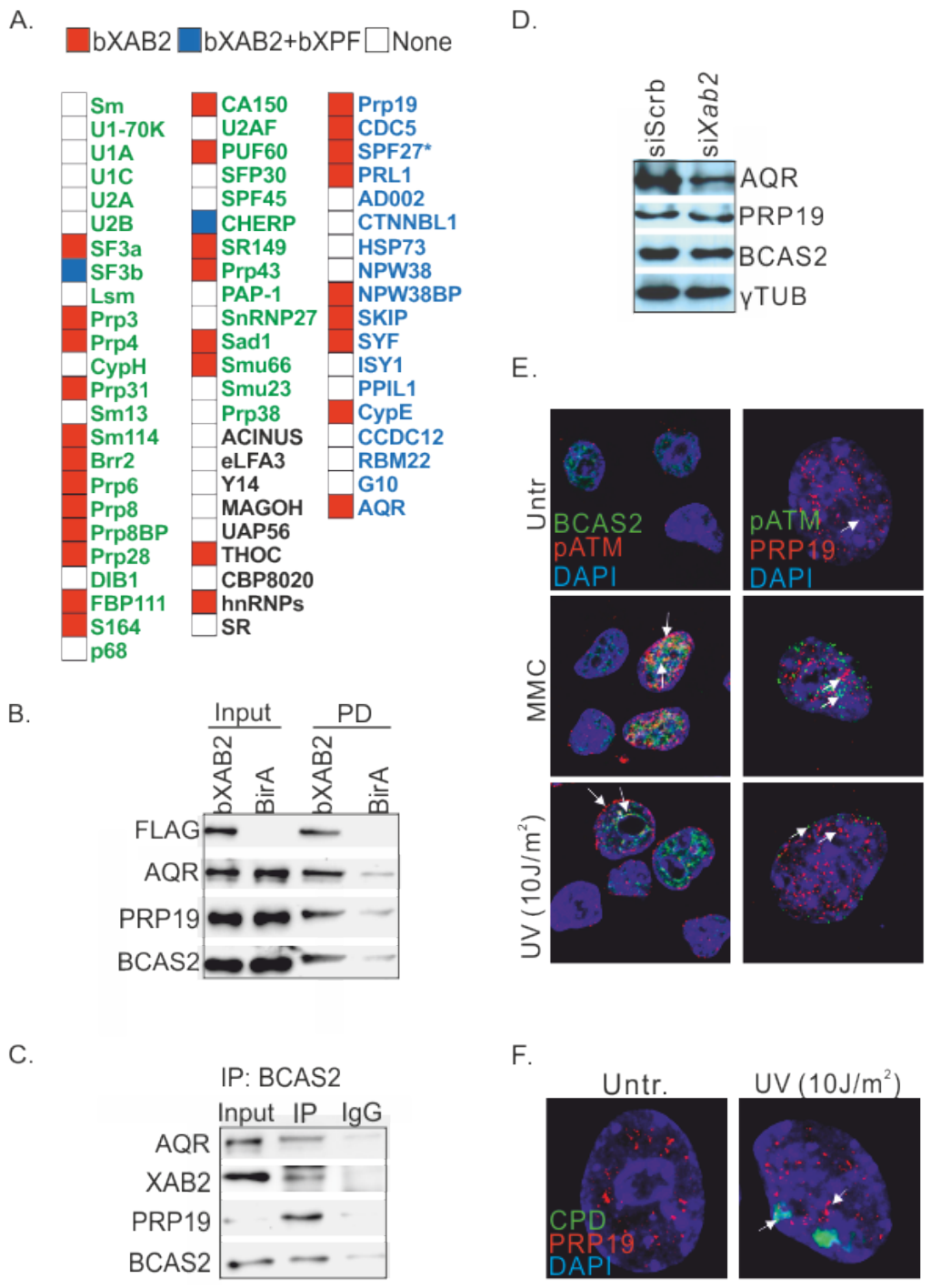


Figure 15. XAB2 is an integral part of the spliceosome. (**A**). Heat map representation of bXAB2- and bXPF-bound proteins involved in the core spliceosome in P15 bXAB2 and bXPF livers. Constitutive factors of snRNPs are shown in green-colored; the PRP19 and the

PRP19-(Figure 15 legend) related complex are shown in blue color. SPF27 (BCAS2) is marked with an "*" as it has been identified in two out of the 3 MS runs in P15 bXAB2 livers but has been further confirmed in downstream immunoprecipitation assays (**B**). bXAB2 pulldowns and western blot analysis of AQR, FLAG-tagged XAB2 (FLAG), PRP19 and BCAS2 proteins in P15 bXAB2 livers. (**C**). BCAS2 immunoprecipitation and western blot analysis of AQR, XAB2, PRP19 and BCAS2 proteins in P15 livers. (**D**). Western blot analysis of AQR, PRP19 and BCAS2 protein levels in siScrb and si*Xab2* HEPA cells. (**E**). Immunofluorescence detection of pATM and BCAS2 or PRP19 in UV-irradiated (10J/m^2) or MMC-treated cells (as indicated). (**F**). Immunofluorescence detection of PRP19 and CPDs in UV-irradiated cells (10J/m^2).

The interaction of bXAB2 with core spliceosome factors in P15 livers prompted us to test whether XAB2 binds RNA *in vivo*. To do so, we carried out a series of RNA immunoprecipitation (RIP) experiments in P15 bXAB2 liver nuclear extracts incubated with streptavidin-coated beads (for bXAB2). The co-precipitated RNA was eluted, reversely transcribed and quantified for spliceosomal U snRNAs by quantitative (q)PCR. We find that bXAB2 shows low specificity for U1 snRNA and no association with U2 snRNA or U3 small nucleolar RNAs (snoRNA). Instead, bXAB2 binds consistently to U4, U5 and U6 snRNAs (**Figure 16A**). Using U4 and U6 snRNAs in follow-up experiments, to exclude the possibility that the observed association is a false positive result of crosslinking, we carried out a series of native RNA immunoprecipitation assays in nuclear extracts of HEPA cells using antibodies raised against XAB2 or the XAB2 protein partners BCAS2 or AQR. Unlike BCAS2, we find that XAB2 and AQR bind on

U4 and U6 snRNAs (**Figure 16B**), indicating an indirect association of BCAS2 with these targets that is likely mediated through the XAB2-associated complex.

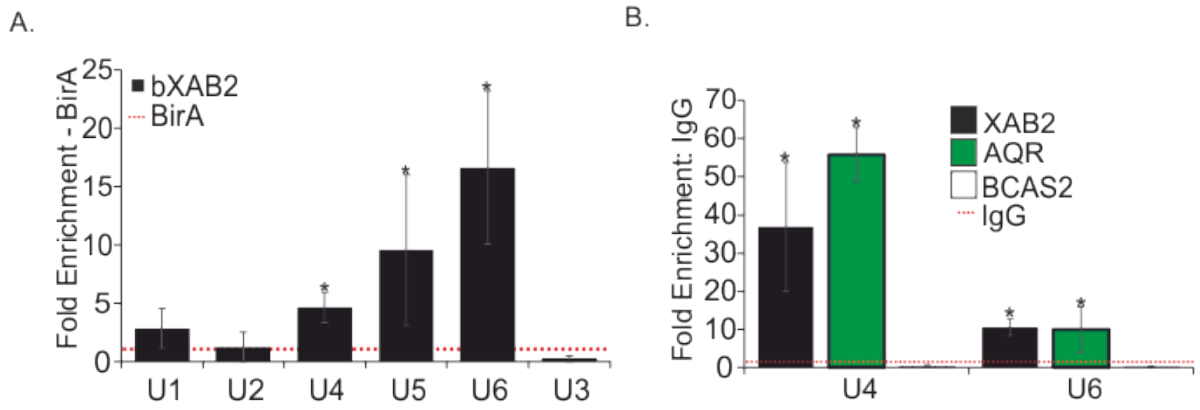


Figure 16. XAB2 binds to U snRNAs and pre-mRNAs. (**A**). RNA pulldowns with bXAB2 and BirA (control) on U1-U6 U sn(o)RNAs (as indicated). (**B**). RNA immunoprecipitation with XAB2, AQR and BCAS2 on U4 and U6 snRNAs (as indicated).

To assess the impact of XAB2 on gene expression, we next performed an RNA-Seq analysis on HEPA cells and mESCs transfected with dsRNA targeting the *Xab2* transcript. RNA-Seq analysis on si*Xab2* HEPA cells and mESCs revealed 255 differentially expressed genes (124 genes were upregulated; 131 downregulated genes; fold change: +/-1.2, q-value ≤ 0.05) (**Appendix, Table 3**) in si*Xab2* HEPA cells and 333 differentially expressed genes (41 upregulated and 291 downregulated; fold change: +/-1.2, q-value ≤ 0.05) (**Appendix, Table 4**) in si*Xab2* mESCs, with a striking overrepresentation of ribosomal protein genes. Using this dataset, we next tested whether knockdown of *Xab2* has an effect on splicing decisions i.e. exon skipping (ES), intron retention (IR) and alternative selection of 5' or 3' splice sites (**Figure 4**). Of the 126335 alternative spliced (AS) events detected in HEPA cells, 774 were found

differentially spliced in si*Xab2* cells (probability of differential splicing >0.8 and an absolute change in percent spliced-in (ΔPSI) greater than 5%) (**Figure 17A-C**). The great majority (i.e. 805 out of 849, 94.82%, $p \leq 10^{-16}$) of IR events with a significant probability of differential splicing are retained in si*Xab2* cells and 58,03% of alternative exons (i.e. 430 out of 741, $p \leq 10^{-5}$) are skipped upon *Xab2* ablation, indicating a global impairment of the splicing machinery in si*Xab2* cells (**Figure 17D-G, Appendix Table 5**). Similar to HEPA cells, si*Xab2* mESCs present with increased intron retention (i.e. 95,25% of significantly differentially spliced IR events are more retained in si*Xab2* cells) compared to control cells (**Figure 18 and Appendix Table 6**).

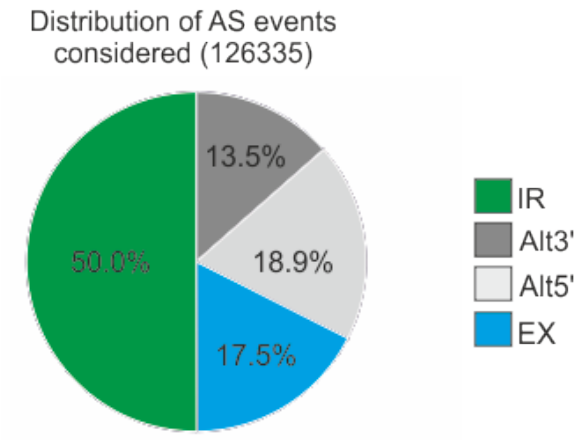
Figure 17. Analysis of alternative splicing events upon Xab2 abrogation in HEPA cells. (A). Table depicting details about splicing events considered for AS analysis. Distribution of (**B**). all considered AS events and (**C**). differentially spliced events. (**D**). Graph depicting the differences in PSI between si*Xab2* and siScrb HEPA cells (ΔPSI > 0: increased alternative exon/intron inclusion in *siXab2* and ΔPSI < 0: decreased alternative exon/intron inclusion in *siXab2* compared to control) . (**E**). Distribution of the direction of alternative splicing changes

between siXab2 and siScrb HEPA cells. Volcano plots of (**F**). all exon skipping events and (**G**). intron retention events considered in siScrb and si*Xab2* HEPA cells.

A.

	Considered	Pdiff>0.8	Volvano (all non redudant)	Violin plots (IR, EX, Pdiff >0.8)	Differentially spliced Pdiff>0.8 and |ΔPSI|>5
IR	63180	849	63180	849	262
EX	22160	741	22160	741	358
Alt3'	23892	434	10957		89
Alt5'	17103	240	7752		65
Total	126335	2264	104049	1590	774

B.



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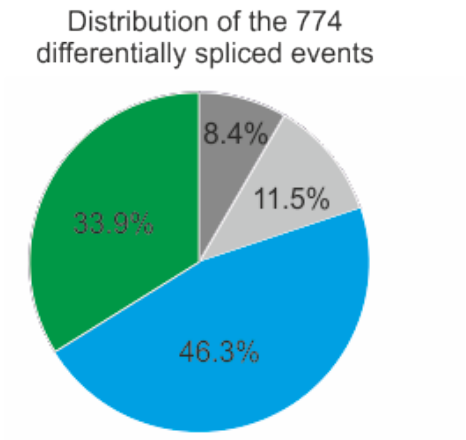

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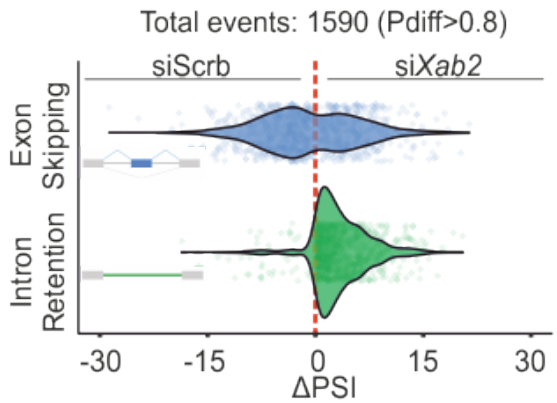

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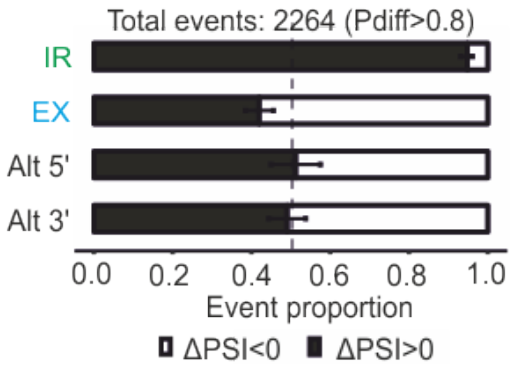

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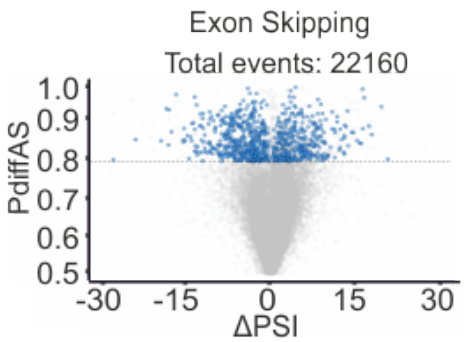


G.

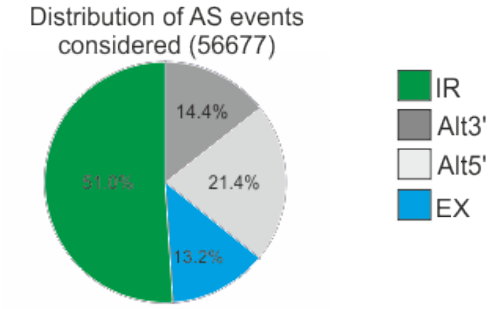
To investigate which GO biological processes are mostly affected by XAB2 knockdown-mediated AS, we subjected the AS events to GO classification. At the confidence level set in our analysis (FDR ≤ 0.05), we find that biological processes related, among others, to cell cycle, RNAPII-mediated transcription, DNA repair and RNA processing comprise a disproportional number of transcripts relative to the murine transcriptome (**Figure 19A**). Similarly, XAB2 knockdown-mediated AS in mESCs significantly affects fundamental biological processes related to *e.g.* DNA repair, ribosome biogenesis, chromosome organization and translation (**Figure 19B**). Further experiments revealed that XAB2 binds to the pre-mRNAs of several genes involved in e.g. DNA repair and/or the DDR in P15 livers (**Figure 19C**).

Figure 18. Analysis of alternative splicing events upon Xab2 abrogation in mESCs. (A). Table depicting details about splicing events considered for AS analysis. Distribution of (**B**). all considered AS events and (**C**). differentially spliced events. (**D**). Graph depicting the differences in PSI between si*Xab2* and siScrb mESCs (ΔPSI > 0: increased alternative exon/intron inclusion in *siXab2* and ΔPSI < 0: decreased alternative exon/intron inclusion in *siXab2* compared to control) . (**E**). Distribution of the direction of alternative splicing changes between siXab2 and siScrb mESCs. Volcano plots of (**F**). all exon skipping events and (**G**). intron retention events considered in siScrb and si*Xab2* HEPA cells.

A.

	Considered	Pdiff>0.8	Volvano (all non redudant)	Violin plots (IR, EX, Pdiff >0.8)	Differentially spliced Pdiff>0.8 and |ΔPSI|>5
IR	28917	1558	28917	1558	748
EX	7468	347	7468	347	207
Alt3'	12156	412	5545		123
Alt5'	8136	182	3676		56
Total	56677	2499	45606	1905	1134

B.



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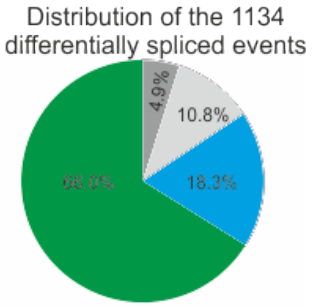

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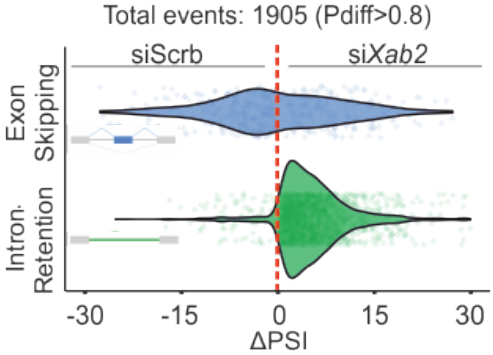

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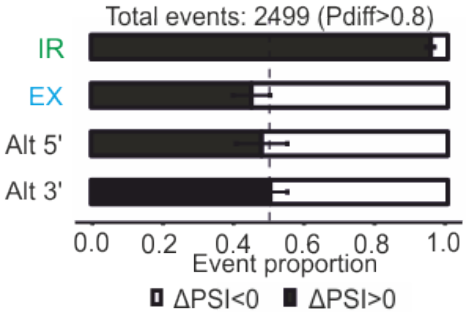

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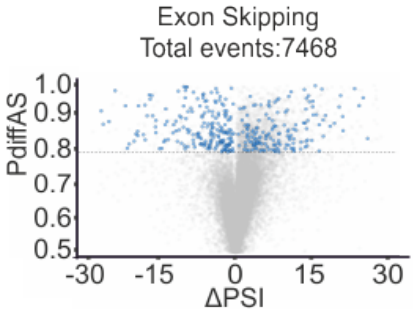

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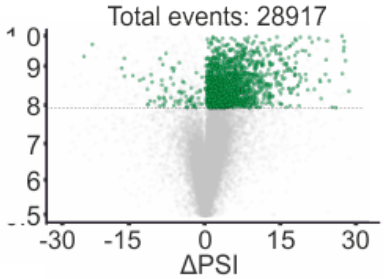

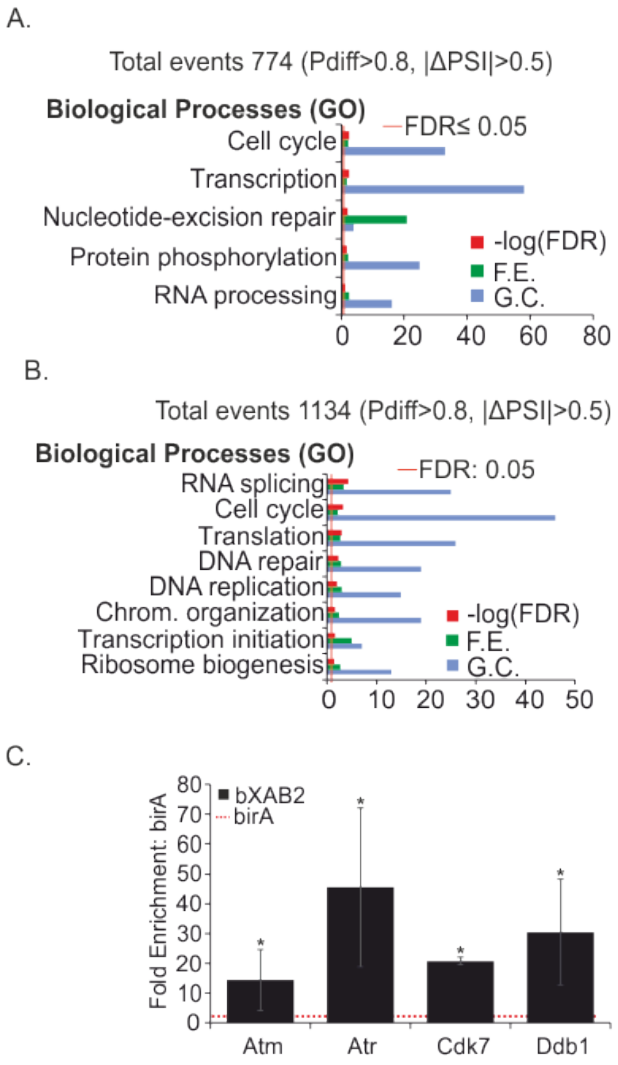

Figure 19. XAB2 affects fundamental cellular processes and binds to pre-mRNAs. (**A**). Over-representation of biological processes that are significantly affected by alternative splicing in si*Xab2* HEPA cells. (**B**). Over-representation of biological processes that are significantly affected by alternative splicing in si*Xab2* mESCs. (**C**). RNA pulldowns with bXAB2 and BirA (control) on selected pre-mRNAs (as indicated).

Transcripts with retained introns often contain premature stop codons (PTCs), which lead to their cytoplasmic degradation by the nonsense-mediated RNA decay machinery [184], [185] while a subset of these transcripts may be stably reserved within the nucleus for later processing [186]. Beginning at 48h post-transfection, we find that the pre-mRNA levels of transcripts with retained introns gradually accumulate (**Figure 6A**) whereas their corresponding mRNA levels progressively decrease in si*Xab2* cells (**Figure 6B**), indicating a defect in splicing rather than IR regulation in si*Xab2* cells. Taken together,

these results suggest that XAB2 is part of the core spliceosome complex and has a functional role in pre-mRNA splicing; it recruits on U snRNAs and pre-mRNAs and it is required for proper mRNA splicing early on during mammalian development.

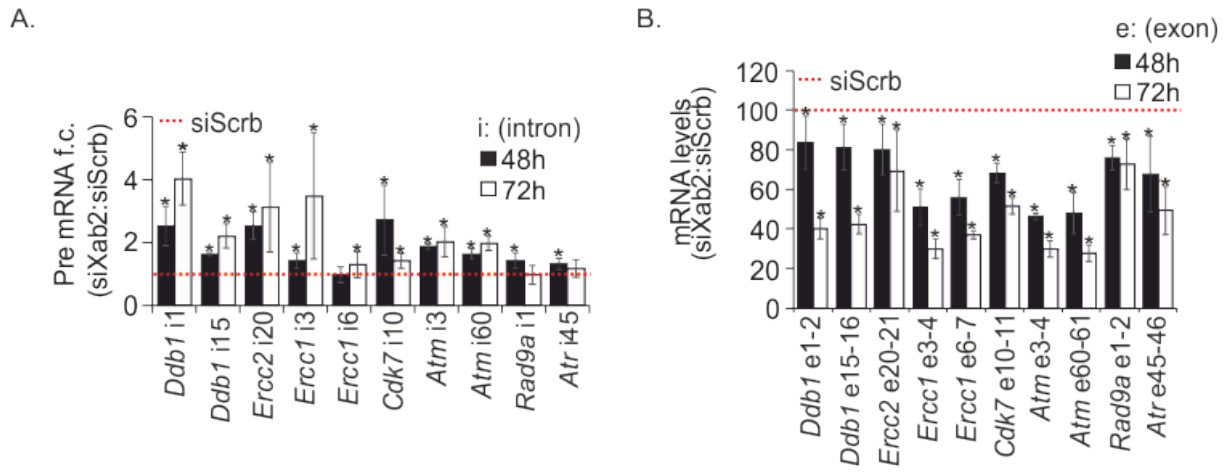

Figure 20. Xab2 abrogation results in accumulation of pre-mRNAs and progressive decrease of mRNAs. (**A**). Pre-mRNA levels and (**B**) mRNA levels of transcripts with retained introns in si*Xab2* and siScrb HEPA cells at 48h and 72h post-transfection (as indicated).

5. XAB2 is released from U snRNAs and pre-mRNAs upon DNA damage and transcription blockage.

To investigate the impact of persistent DNA damage on XAB2-mediated spliceosomal function, we assessed the recruitment of XAB2 on U snRNAs and pre-mRNAs in UV-irradiated or MMC-treated wt. cells. Our analysis revealed that DNA damage triggers the rapid release of XAB2 (**Figure 21A**) and AQR (**Figure 21B**) from U4 and U6 snRNAs and all pre-mRNAs tested (**Figure 21C**) which, in the case of UV-irradiation, persists for at least 6 hours (**Figure 21B**). Selective inhibition of ATM (ATMi) with KU-55933 inhibitor [187] or of ATR (ATRi) with NU6027 in cells treated with MMC or UV or exposure of cells to caffeine did not rescue the release of XAB2 from all RNA targets

tested indicating that the DNA damage-driven release of XAB2 from RNA is not mediated through DDR signaling (**Figure 21D**). Consistent with the DNA damage-driven dissociation of XAB2 from spliceosomal RNAs, we also evidence the substantial increase in intron retention for several, but not all, transcripts tested in UV-irradiated cells (**Figure 21E**). In contrast to Xab2 abrogation though, mRNA levels are not consistently affected by intron retention (**Figure 21F**).

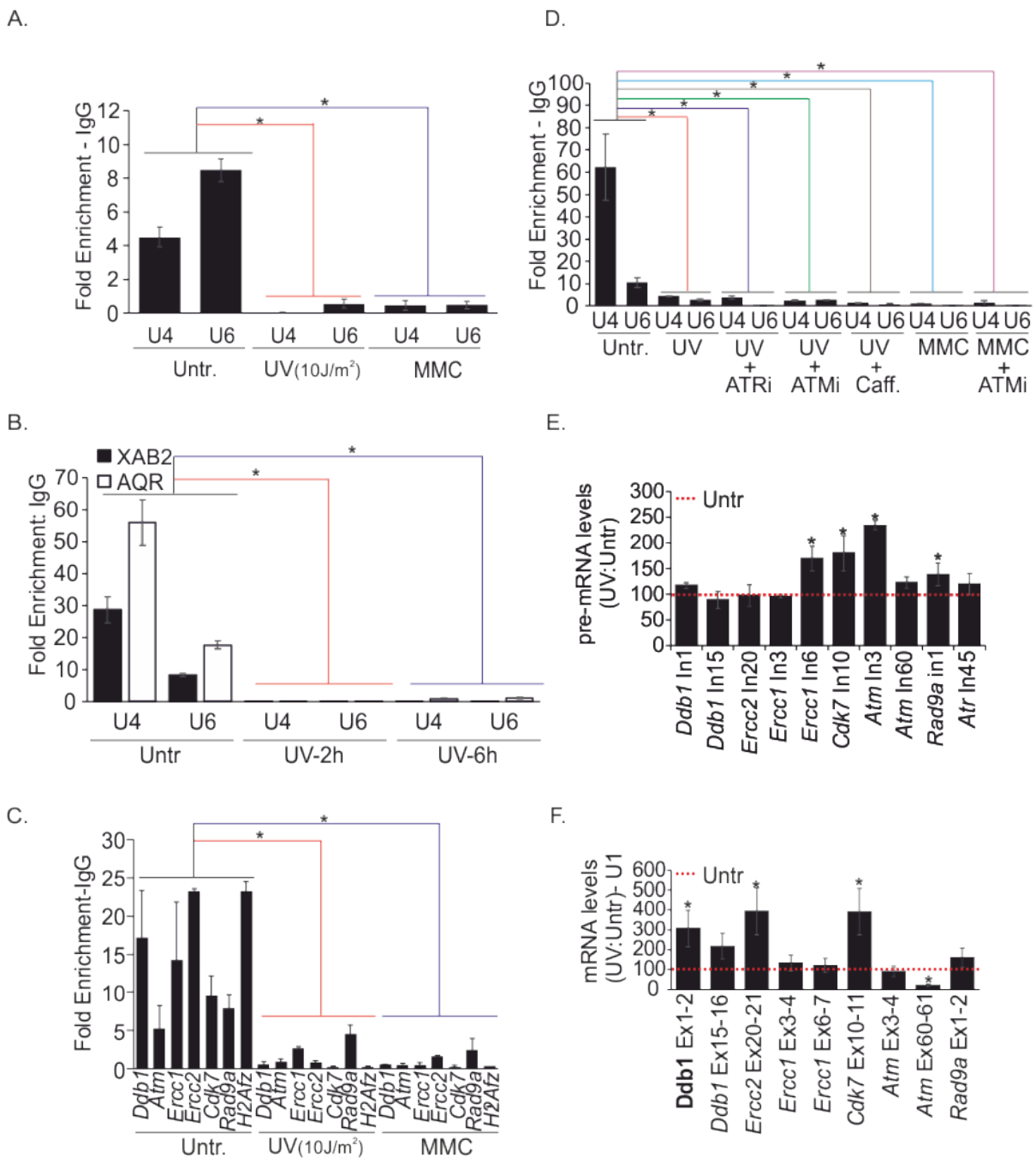

Figure 21. XAB2 dissociates from snRNAs and pre-mRNAs upon DNA damage. (**A**). RNA immunoprecipitation of XAB2 on U4 and U6 snRNAs. (B). (**B**) RNA immunoprecipitation of XAB2 and AQR on U4 and U6 snRNAs at 2 and 6h post UV-irradiation. (**C**) RNA immunoprecipitation of XAB2 on pre-mRNAs in UV-irradiated and MMC-treated HEPA cells

(as

(Figure 21 legend)

indicated). (**D**). RNA immunoprecipitation of XAB2 on U snRNAs in UV-irradiated and MMC-treated wt. cells treated with inhibitors against ATM (ATMi), ATR (ATRi; as indicated) or caffeine (Caff.). (**E**). Pre-mRNA and (**F**). mRNA levels of selected genes 6h after UV-irradiation.

We reasoned that DNA lesions altering the DNA double helix itself and/or interfering with transcription *in cis* are causal to the aberrant release of XAB2 from U snRNAs or the pre-mRNAs. To test this, we made use of mouse embryonic fibroblasts (MEFs) derived from CPD photolyase transgenic mice [188]. Photolyases directly revert photolesions into undamaged bases using visible light energy (i.e. photoreactivation; PR) and display substrate specificity for UV-induced 6-4PPs or CPDs [189]. Using this system, CPD photolyase transgenic MEFs were exposed to UV irradiation and were subsequently kept in the dark (UV-induced CPDs remain in the mammalian genome) or exposed to PR light (UV-induced CPDs are repaired) for 60min post-UV irradiation (**Figure 22A**). Importantly, we find that the exposure of UV-irradiated MEFs to PR light substantially rescues the XAB2 RIP signals in U4 and U6 snRNAs (**Figure 22B**) and the pre-mRNAs tested (**Figure 22C**) indicating that the presence of DNA helix-distorting lesions inadvertently affects the process of pre-mRNA splicing in the mammalian genome.

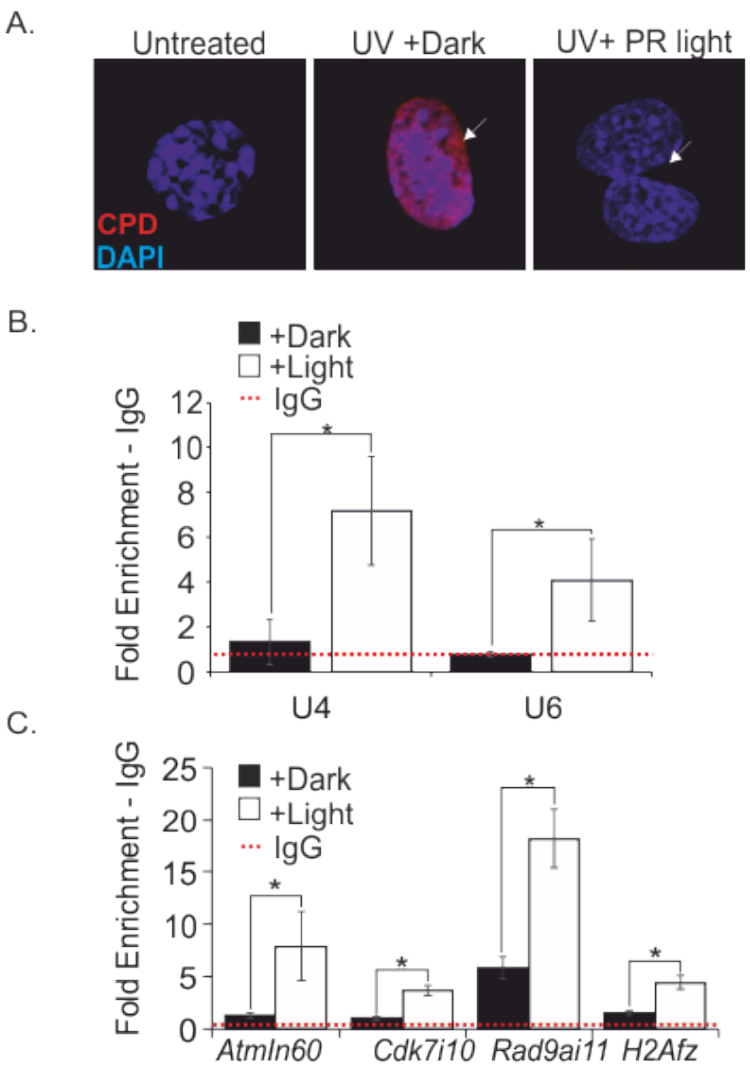

Figure 22. XAB2 re-associates with RNA targets after repair. (**A**). Immunofluorescence detection of UV-induced CPDs in UV-irradiated photolyase transgenic MEFs exposed to 1 hour of PR light (CPDs are repaired) or dark (CPDs remain) as indicated. (**B**). RNA immunoprecipitation of XAB2 on U4 and U6 snRNAs and (**C**) pre-mRNAs in UV-irradiated photolyase transgenic MEFs exposed to 1 hour of PR light (CPDs are repaired) or dark (CPDs remain).

Next, we test whether the release of XAB2 from snRNAs upon DNA damage also results in its dissociation from the spliceosome machinery itself. To do so, we performed bXAB2 pulldowns followed by western blot analysis with FLAG (for bXAB2), PRP8, PRP19, BCAS2 and the Small Nuclear Ribonucleoprotein U5 Subunit (SNRP) 40, a component of the U5 snRNP in UV-irradiated (10J/m^2) and untreated cells. PRP8 is a highly conserved protein identified in our MS approach (**Appendix** T**able 1**) that resides in the catalytic core of the spliceosome [190]. Unlike the mild or non-detectable interaction

of bXAB2 with PRP8 in untreated bXAB2 MEFs, follow-up pulldowns in UV-irradiated MEFs revealed the strong association of bXAB2 with PRP8, in UV-irradiated cells (**Figure 23A**). Furthermore, XAB2 still associates with PRP19, BCAS2, and SNRP40 in UV-irradiated cells. Similar to XAB2, PRP8 binding to U6 is significantly decreased at 2 hours post-UV irradiation but is restored 6h post-UV treatment. In contrast to XAB2, the PRP8 binding to U4 is significantly increased and remains so for at least 6 hours post UV-treatment (**Figure 23B**). Thus, XAB2 remains bound to the spliceosomal machinery despite dissociating from U4 and U6 RNAs.

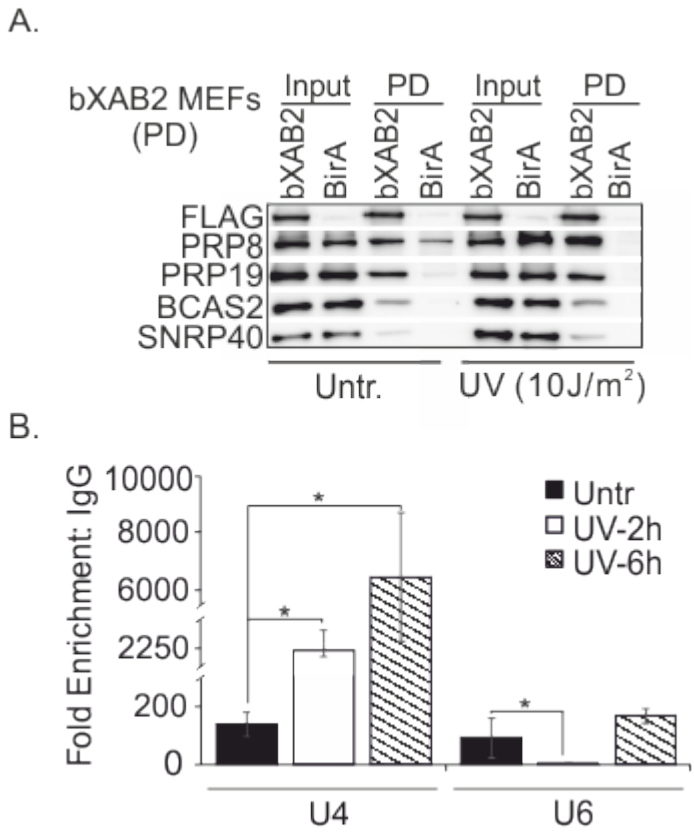

Figure 23. XAB2 remains associated with the spliceosome upon DNA damage. (I). bXAB2 pulldowns followed by western blot analysis with FLAG (for bXAB2), PRP8, PRP19, BCAS2 and SNRP40 in UV-irradiated (10J/m2) and control MEFs. (B). RNA immunoprecipitation of PRP8 on U snRNAs. The asterisk "*" indicates a p-value ≤ 0.05.

To test whether the dissociation of XAB2 from spliceosomal RNAs is also triggered upon inhibition of initiating or ongoing transcription, a consequence of persistent DNA damage itself [191, 192], cells were treated with 5,6-Dichloro-1-β-D-ribofuranosylbenzimidazole (DRB), an inhibitor of RNAPII-mediated transcription elongation [193] and tryptolide, a natural drug that interferes with the DNA-dependent ATPase activity of XPB helicase subunit of TFIIH [194] and inhibits RNAPI- and II-mediated transcription initiation [193]. We find that inhibition of transcription elongation (DRB-treated cells) triggers the substantial release of XAB2 and Aquarius from the U4 and U6 snRNAs (**Figure 7A**) and all pre-mRNAs (**Figure 7B**) tested. Similar findings, albeit to a lesser magnitude, were observed upon inhibition of transcription initiation (TPL-treated cells) (**Figure 7A-B**). To test whether XAB2 binding to U4 and U6 snRNAs is also altered in animal models with inborn defects in NER, we next test the XAB2 RIP signals on these snRNAs in P15 *bXab2*/*Xpc*$^{-/-}$ and *bXab2*/*Csb*$^{m/m}$ livers that are defective in the GG- or the TC-NER subpathway of NER, respectively. We find that XAB2 RIP signals on U4 snRNA are substantially decreased in the P15 livers of *bXab2*/*Xpc*$^{-/-}$ and *bXab2*/*Csb*$^{m/m}$ animals and for U6 snRNA only in *Csb*$^{m/m}$ mice (**Figure 7C**). Thus, XAB2 is released from the spliceosomal RNAs upon persistent DNA damage, due to transcription blockage and in developing, transcription-coupled repair-defective animals.

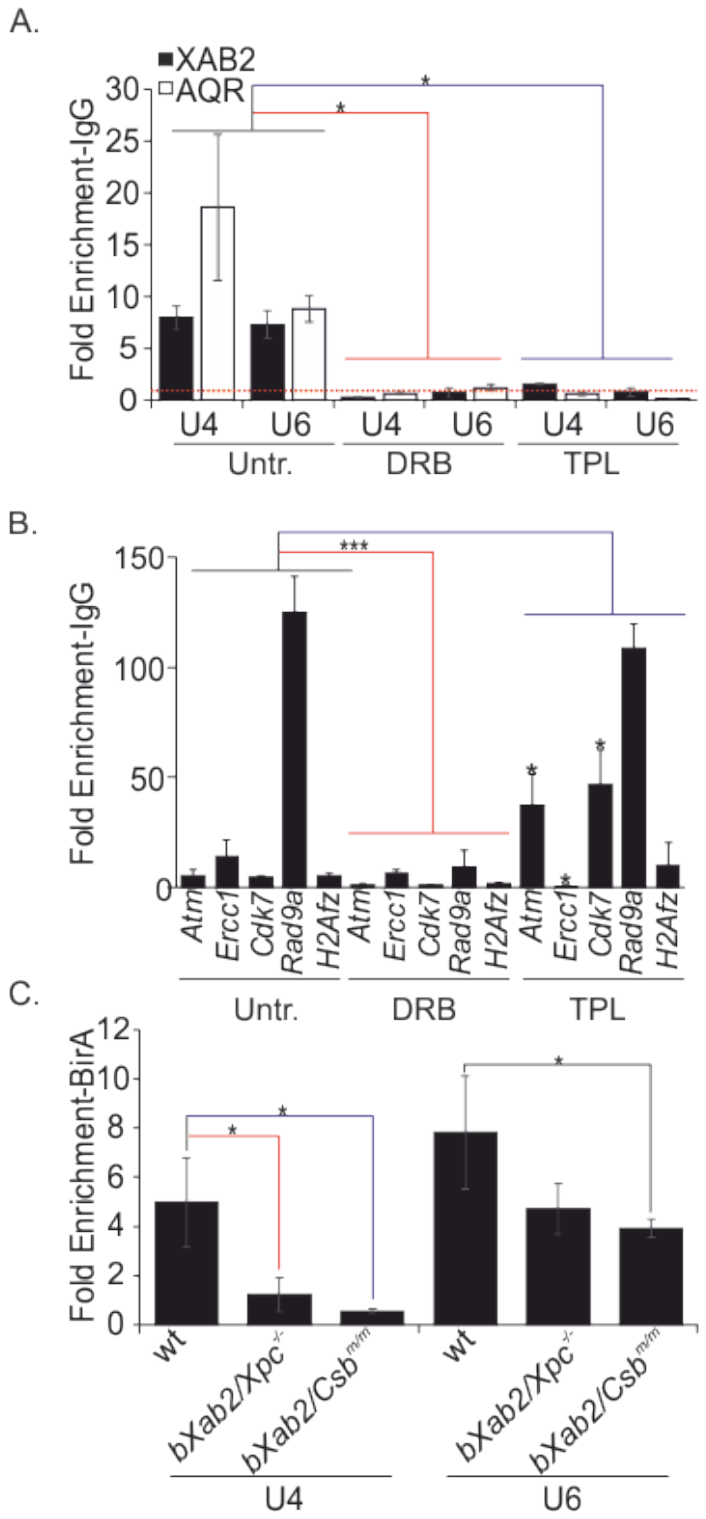

Figure 24. XAB2 is released from U snRNPs upon transcription blockage and in NER progeroid animals.

(**A**). RNA immunoprecipitation of XAB2 and AQR on U4 and U6 snRNAs (**B**). RNA immunoprecipitation of XAB2 on pre-mRNAs in wt. cells treated with the RNAPII transcription elongation inhibitor 5,6-Dichloro-1-β-D-ribofuranosylbenzimidazole (DRB) and the RNAPI- and II-mediated transcription initiation inhibitor tryptolide (TPL). (**C**). bXAB2 RNA pull downs on U4 and U6 snRNAs in P15 *bXab2;Xpc*$^{-/-}$ or *bXab2;Csb*$^{m/m}$ mouse livers.

Discussion

We used an *in vivo* biotinylation tagging approach in mice to dissect the functional role of XAB2 during mammalian development. Our evidence shows that XAB2 is part of the core spliceosome and binds on spliceosomal RNAs and pre-mRNAs during hepatic murine development. Consistently, we find that abrogation of XAB2 leads to defective NER, intron retention, the aberrant accumulation of pre-mRNAs and to a defective ATM/ATR DDR signaling. Persistent DNA damage in photolyase transgenic cells and the NER-defective animals or transcription blockage trigger the dissociation of XAB2 from RNA targets leading to altered splicing and intron retention. Thus, XAB2 functionally links NER with the core spliceosome and the DDR early on during hepatic development.

XAB2 is an essential core splicing factor. A high-throughput MS approach in developing livers revealed that bXAB2 co-immunoprecipitates with almost half (32/65) of the core spliceosome factors, verifying previous findings associating XAB2 with splicing complexes in human cells. Notably, we observed a significant enrichment of U5 and U4/U6 snRNP and U4/U6.U5 tri-snRNP associated factors; constistently, XAB2 specifically binds to U4, U5 and U6 snRNAs but not U1 and U2 snRNAs, suggesting that XAB2 predominantly associates with the U5, U4/U6 and/or the U4/U6.U5 snRNPs. Biochemical experiments conducted to identify snRNP constituents have not identified XAB2 [195-196], indicating that XAB2 interacts with the snRNP factors during the formation of the active spliceosome. In support with this notion, XAB2 also binds to pre-mRNAs, thus excluding the possibility that XAB2 binds to snRNAs during processes such as snRNA biogenesis. Interestingly, bXAB2 MS data are enriched for proteins involved in

all stages of the splicing reactions (spliceosome complex A through P), especially for complexes B through P (**Figure 25**); in agreement with previous findings, the PRP19 and the Intron binding complex (IBC or PRP19-related) that are both recruited to the spliceosome during complex B formation and remain until the release of mature mRNA, are also significantly enriched (**Figure 25**). Notably, IBC and PRP19 complex are considered to form two different pre-assembled building blocks that interact with each other after their association with the spliceosome [197], which is probably depicted in the relative enrichment of these factors in our immunoprecipitation experiments (XAB2-AQR vs BCAS-PRP19) (**Figure 15**). We also find that, like XAB2, AQR also binds to U4 and U6 snRNAs, while BCAS2 does not enrich for any snRNA and PRP19 has been shown not to bind to RNA [198], further supporting the notion for two separate complexes that are associated during certain stages of the splicing reaction rather than being constantly bound together.

In support with a fundamental role in splicing for XAB2, si*Xab2* cells manifest a genome-wide increase in intron retention accompanied with a gradual accumulation of pre-mRNA transcripts and a decrease in mRNA (spliced) transcripts, suggesting that XAB2 is indispensable for proper splicing. Importantly, both- PRP19 and IBC-complexes are indispensable for cell viability and, similar to XAB2, ablation of AQR, PRP19, PLRG1 and ZNF830 results in embryonic lethality or in the case of BCAS2 in early post-natal mortality (www.informatics.jax.org). Notably, we find that PRP19 and BCAS2 protein levels are not affected by XAB2 abrogation in contrast to AQR protein levels that are decreased, indicating that in si*Xab2* cells the IBC is primarily affected and possibly not properly recruited at the spliceosome. Whether under these

circumstances the PRP19 complex associates with the spliceosome or is still able to properly function within the spliceosome remains elusive.

Existing evidence suggest that the IBC binds to the BPS in a sequence-independent manner, thus requiring a mode of interactions between the IBC and other spliceosomal proteins residing at the BPS to guide AQR/IBC to its proper position on the intron. Cross-linking studies of B^{act} complexes have revealed multiple interactions between the IBC and SF3A/B proteins, which are located just upstream of the BSP and have been shown to play a key role in guiding AQR proper positioning on the intron [180]. Consistently, we have found that XAB2 interacts with SF3A/B proteins, implying a major role of XAB2 in guiding AQR to the BPS. Moreover, spliceosome activation and splicing reactions require a number of spliceosomal proteins and RNP rearrangements that may be mediated, in addition to other means, by post-translational modifications. PRP19 contains an N-terminal U-box/RING finger domain, indicative of E3 ubiquitin ligase activity [199]. The PRP19 complex ubiquitinates the U4/U6 snRNP protein PRP3 to enable the formation of the U4/U6.U5 tri-snRNP [182]. Although only PRP3 has been identified as a PRP19 substrate so far, PRP19 is considered as one of the potent mediators responsible for the conformational changes required for the splicing reaction. Importantly, during the course of splicing, IBC interacts with the PRP19 complex as well as other spliceosomal proteins, such as PRP8 [197]; this together with our findings could suggest that XAB2 plays an active role in mediating interactions necessary for the modifying activity of PRP19 and/or other proteins or vice versa PRP19 could modify components of the IBC to promote required rearrangements. Thus, XAB2 is a splicing

factor primarily associated with the IBC and the PRP19 complex to presumably coordinate timely interactions and remodeling of the spliceosome.

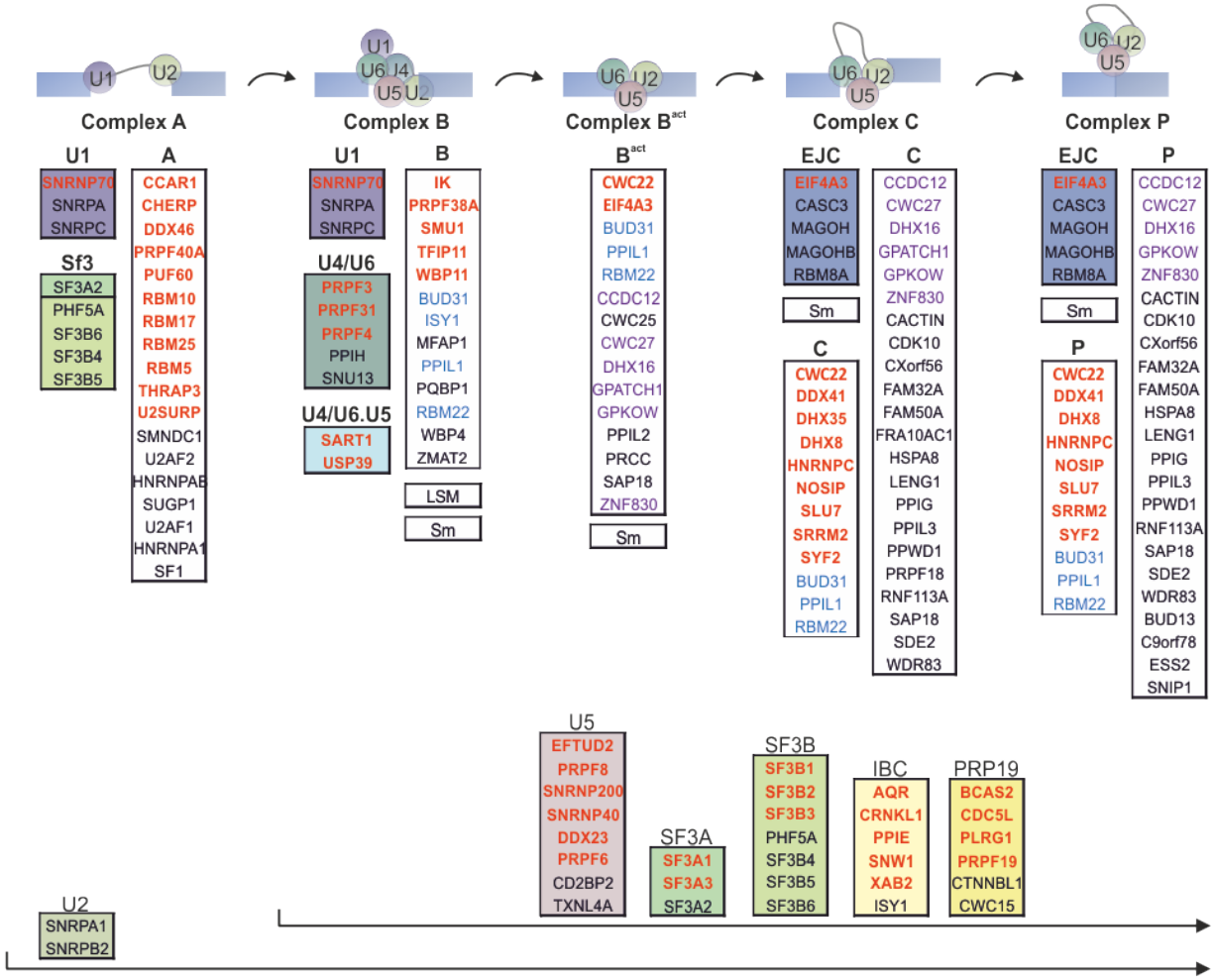

Figure 25. Shematic representation of the spliceosomal building blocks and the factors enriched in bXAB2 dataset. During the course of splicing multiple factors are exchanged or modified to allow structural changes, required for the trans-esterification reactions to take place. XAB2 coordinates interactions that are important for properly positioning the IBC on the intron and presumably for the enzyme activity of PRP19. Factors enriched in bXAB2 dataset are shown in red, factors remaining attached to the spliceosome during more than one stages are

shown in blue or purple.

XAB2 is required for NER and the DDR. Inborn defects in RNA processing or DNA repair associate with progeria [200-202], the metabolic syndrome [203-205], neurodegeneration [55, 88, 206, 207] and cancer [208-212], arguing for functional links between genome maintenance and the splicing machinery in development or disease. Similar to earlier *in vitro* findings in yeast two-hybrid screens [153] or in HeLa cells overexpressing XAB2 [154], we find that XAB2 interacts with NER factors. Although XAB2 partially co-localizes with UV-induced CPDs in irradiated cells, the endogenous bXAB2 interacts with DDB1 and XPA involved in UV-induced DNA damage recognition and the assembly of the NER incision complex at sites of DNA damage during NER [55, 59]. Whether these interactions are fundamental for NER function remains elusive. For example, DDB1 is successfully recruited to UV-induced CPDs in the absence of XAB2 supporting the notion that XAB2 is dispensable for lesion recognition during NER. In contrast, in si*Xab2* cells, XPA fails to form visible foci and recruit at sites of UV-induced DNA damage. In support of a defect in NER, si*XAB2* cells have decreased UDS and associate with a delay in RNA synthesis recovery following UV-induced DNA damage induction. Moreover, UV-induced CPDs remain unrepaired even 24h post-UV irradiation in si*Xab2* cells. Besides NER, we reasoned that ablation of XAB2 triggers spliceosome-driven defects affecting primarily apical DNA damage sensors with a high protein turnover. Intriguingly, BCAS2 is involved in DNA damage repair through the replication protein A (RPA) complex during mouse embryonic development [213]. In line, PRP19 acts as a sensor of RPA-ssDNA, thereby, driving ATR activation upon DNA damage [181]. Similar to XAB2, AQR is required for RAD51/RPA repair foci formation during HR but is dispensable for the recognition of DSBs [214]. Consistent with these data, we find the substantial decrease in

pATM/ATM and pATR/ATR proteins levels matched with the accumulation of ATM/ATR pre-mRNAs and the substantial decrease of the respective mRNAs; the reduced formation of pATR and pATM foci and the noticeable absence of γH2A.X foci in UV-irradiated or MMC-treated si*Xab2* cells. Importantly, phosphorylation of XPA by ATR enhances nuclear import of XPA so that it can be localized to the sites of damage [215]. Whether decreased localization of XPA at damaged DNA, upon *Xab2* ablation, is due to lack of its interaction with XAB2 or reduced phosphorylation by ATR remains elusive. Although the role of XAB2 in NER remains questionable, a plausible role in the DNA damage signaling is revealed: XAB2 plays an indirect role in regulating the DDR by ensuring proper splicing and thus appropriate mRNA and protein levels of the apical DDR kinases (**Figure 26C**). Importantly, ATR reduced levels might as well contribute to the cell death phenotype observed in si*Xab2* cells, as ATR mediates replication stress responses and thus is indispensable for dividing cells. Thus, the XAB2-PRP19-BCAS2 complex likely assists in coordinating DNA repair with the spliceosomal response to DNA damage.

XAB2 is released from RNA targets upon DNA damage, transcription blockage and in NER-defective animals. Nascent pre-mRNAs that associate with transcription complexes blocked at DNA lesions are released from late-spliceosome components and hybridize to the template strand of the melted DNA to form RNA/DNA duplexes (R-loops), a structure that slows transcription and activates DDR [177]. In line, we find the pronounced accumulation of RNA:DNA hybrids and a sharp decrease in nascent RNA synthesis in si*Xab2* cells. DNA damaging agents are known to affect the subcellular localization of several splicing factors and/or their association with nascent transcripts

[177, 216-218]. In this work, the DNA damage-driven release of XAB2 from RNA targets is not limited to UV-induced DNA lesions; it is also profound in the presence of DNA ICLs that prevent the separation of two DNA strands hampering DNA replication and transcription. Importantly, we find that the dissociation of XAB2 from RNA targets is not rescued when ATM or ATR are inhibited but only when UV-induced CPDs are efficiently removed through PR-dependent repair. The latter is in line with previous findings indicating that ATM (and likely ATR) function downstream of the spliceosome displacement [130,127]. Spliceosome displacement from nascent pre-mRNAs, as indicated by XAB2 release from its target RNAs, and from sites of damage, as indicated by the absence of XAB2:CPD colocalization, could contribute to increased formation of R-loops and subsequent ATM activation[130]. DNA damage is known to induce alternative splicing and a preference for intron-less or shorter genes. Consistently, we find that while XAB2 is released from its RNA targets upon DNA damage, it remains attached with the spliceosomal factor PRP8, which still associates with snRNAs, supporting the concept that XAB2 is still recruited to the spliceosome. Notably, we observe a moderate accumulation of pre-mRNA transcripts, which, in contrast to siXab2 cells, is not universal and is not accompanied by a decrease in mRNA levels. Taken together these observations indicate that XAB2 release from its RNA targets is tolerated by the cell and is probably required for alternative splicing decisions within the context of the DDR (**Figure 26B**).

DNA helix-distorting lesions (and likely DNA ICLs) interfere with proper pre-mRNA splicing through the transcription blockage of elongating RNAPII or the inhibition of mRNA synthesis upon DNA damage [219]. Consistently, XAB2 is released from snRNAs

in NER-defective developing livers whereas inhibition of transcription elongation (by DRB) or initiation (by TPL) also triggers the substantial release of XAB2 from snRNAs and pre-mRNAs in cells. As a core spliceosomal component that functionally links NER and splicing with RNAPII transcription blockage and the DDR, XAB2 could serve to coordinate the temporary release of spliceosome upon DNA damage repair. The latter would enable the reversible sliding of RNAPII from a productive to a backtracked state, thereby, allowing the efficient recognition and repair of transcription-blocking DNA lesions [220]. However, in the case of the NER mutant animals, the presence of irreparable DNA lesions (in view of the DNA repair defect) would trigger a vicious cycle of irreversible spliceosomal changes hampering the timely execution of developmental gene expression programs. In this respect, it would be attractive to test the extent to which defects in the spliceosomal response to DNA damage are causal to the premature onset of TCR progeroid syndromes and natural ageing.

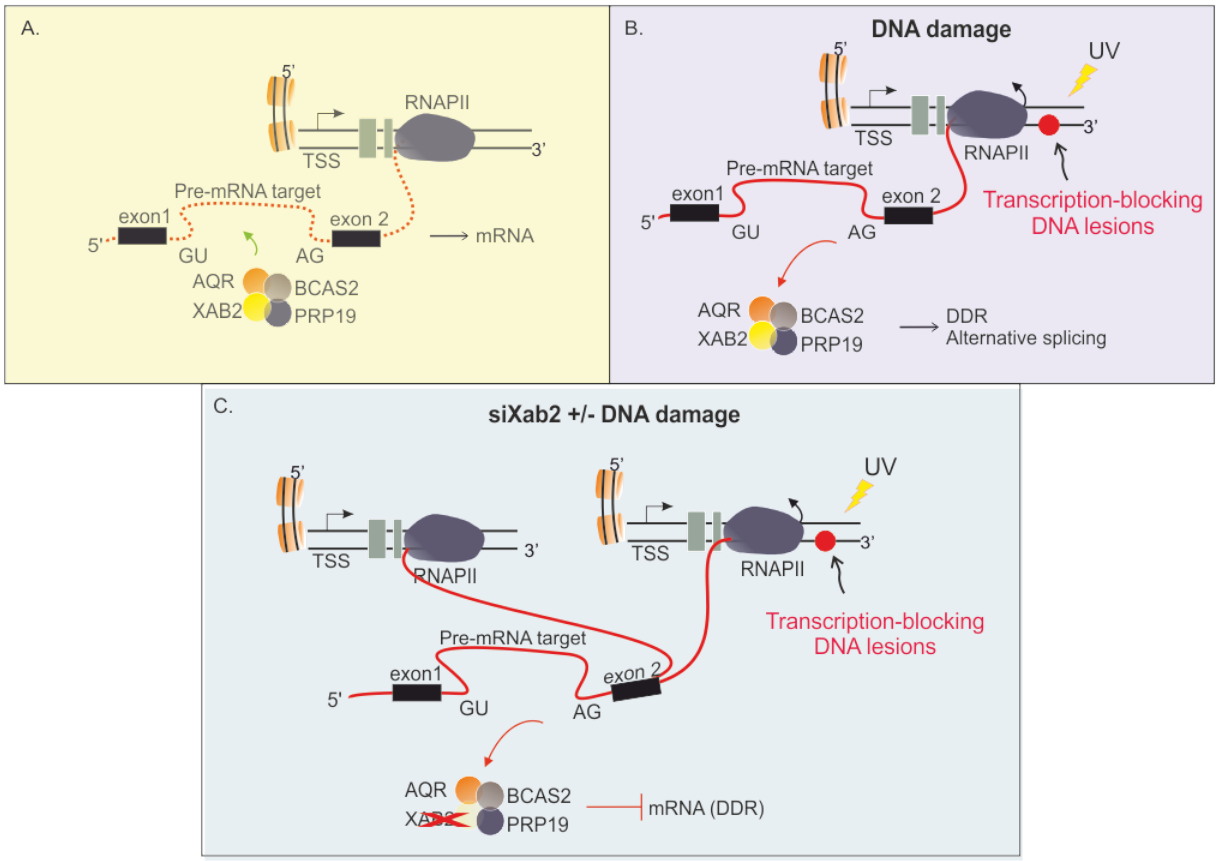

Figure 26. Schematic representation of XAB2 role in DDR. A. Under physiological conditions XAB2 and its interacting proteins associate with spliceosome allowing for proper splicing and consequently for proper gene expression. B. DNA damage results in XAB2 release from its RNA targets, which results in alternative splicing that regulates and is being regulated by the DDR. C. In the absence of XAB2, pre-mRNA splicing is hampered, pre-mRNA transcripts accumulate and mRNA levels are decreased, resulting in aberrant gene expression. The DDR kinases are primarily affected, thus leading to defective DNA damage signaling and repair which could ultimately result in cell death.

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Appendix

Table 1. A list of 1167 XAB2-bound proteins identified in the P15 bXAB2 biological replicates compared to BirA control livers.

Access. no	Symbol	bXab UP1	bXab_UP3	bXab_UP2	BirA UP1	BirA UP3	BirA UP2
Q9QXS1	Actn4	188	197	202	44	62	193
E9Q447	Sptan1	158	159	0.01	60	83	156
P16546	Sptan1	157	0.01	175	61	83	0.01
Q5YD48	A1cf	8	8	16	1	0.01	6
Q3UH59	Myh10	121	131	136	44	82	134
O35452	Tnxb	116	130	137	30	58	124
E9QPE7	Myh11	112	135	132	36	77	133
O08638	Myh11	108	130	128	0.01	73	127
Q68FG2	Sptbn2	103	111	118	31	49	101
E9PZ16	Hspg2	97	115	115	27	44	105
E9QP46	Syne2	97	187	235	6	38	154
Q6URW6	Myh14	96	89	87	19	40	95
G3UW82	Myh2	95	120	124	61	93	140
F6XCT0	Macf1	40	48	44	0.01	0.01	0.01
Q921L6	Cttn	23	24	27	0.01	0.01	0.01
A0A0R4J0V1	Ints10	8	10	11	0.01	0.01	0.01
E9Q360	Ints10	8	10	11	0.01	0.01	0.01
A2A9P6	Cdk11b	7	10	9	0.01	0.01	0.01
A0A1B0GS91	Svil	72	82	82	14	33	85
Q9JKX4	Aatf	6	10	14	0.01	0.01	7
P13542	Myh8	72	101	106	43	76	134
E9QMC1	Cgn	69	72	71	32	41	68
E9Q8N1	Ttn	61	138	186	17	61	236
F6RND9	Mprip	61	65	0.01	11	27	63
E9Q8K5	Ttn	61	138	186	17	61	236
E9PWQ3	Col6a3	60	67	66	34	26	52
A0A087WR50	Fn1	59	72	74	23	32	64
Q3UHL6	Fn1	59	72	74	23	32	64
B7ZNH7	Col14a1	57	63	71	33	46	62
A0A1D5RLS1	Eps15l1	4	8	8	0.01	0.01	0.01
D3Z315	Cope	6	7	6	0.01	0.01	0.01
A0A0R4J0I6	Acad11	17	20	17	10	9	17
Q80XL6	Acad11	17	20	17	10	9	17
E9QNH7	Acbd5	8	9	7	0.01	0.01	4
E9PUJ6	Mycbp2	52	0.01	0.01	0.01	5	0.01
Q5XG73	Acbd5	8	9	7	0.01	0.01	4
B2RSU6	Cgnl1	50	49	44	8	16	56

Q91Z83	Myh7	50	78	70	23	52	99
Q5XG73	Acbd5	8	9	7	0.01	0.01	4
E9PVU0	Myo6	49	50	57	11	20	49
Q5XG73	Acbd5	8	9	7	0.01	0.01	4
F6RJ39	Acin1	25	33	43	6	20	33
Q8JZR0	Acsl5	17	15	17	6	6	15
P57780	Actn4	51	55	55	24	26	53
Q5SYD0	Myo1d	47	55	55	16	26	51
Q80US4	Actr5	12	13	14	1	7	11
P20152	Vim	45	50	50	30	35	48
Q80YX1	Tnc	44	51	54	16	15	48
Q8R2S9	Actr8	20	24	23	2	10	19
Q9QYC0	Add1	14	21	23	3	5	17
Q9QYB5	Add3	14	15	17	3	3	15
Q9Z103	Adnp	8	16	21	0.01	0.01	13
Q640N1	Aebp1	19	20	21	2	7	24
Q9QZQ1	Afdn	40	53	59	5	9	0.01
Q9QZQ1	Afdn	40	53	59	5	9	46
Q8CJF7	Ahctf1	32	59	61	5	15	48
Q9Z0X1	Aifm1	21	20	22	12	9	20
A1BN54	Actn1	38	45	39	11	16	36
Q6PDN3	Mylk	36	0.01	0.01	4	9	0.01
Q8CAQ8	Immt	36	40	33	18	14	30
F6TFN2	Lmo7	36	47	44	8	18	45
P53995	Anapc1	19	31	41	0.01	8	27
Q91W96	Anapc4	14	13	18	0.01	2	14
O35488	Slc27a2	34	32	35	28	22	31
Q8BTZ4	Anapc5	9	13	17	0.01	4	10
B7ZWM6	Sorbs2	33	37	35	0.01	18	37
Q8BTZ4	Anapc5	9	13	17	0.01	4	10
Q9ERG0	Lima1	33	37	40	16	20	40
Q9WVM3	Anapc7	17	17	23	0.01	6	16
A0A0R4J1N7	Ank1	11	20	21	0.01	0.01	9
Q8C8R3	Ank2	11	25	28	0.01	0.01	14
Z9Z044		33	0.01	29	38	0.01	0.01
E9Q634	Myo1e	32	29	26	7	13	32
Z9Z173		31	28	29	22	19	27
E9Q5J9	Tpm3	31	28	33	0.01	17	33
E9QPN7	Dock6	30	0.01	48	0.01	0.01	35
P26231	Ctnna1	30	41	42	19	19	36
P97449	Anpep	5	10	15	0.01	0.01	10
Q8BP43	Tpm1	30	0.01	36	12	19	0.01
B2RXQ9	Sorbs2	29	31	29	0.01	16	31
F8WID5	Tpm1	28	0.01	34	0.01	0.01	0.01

Q8CFQ3	Aqr	32	40	39	1	14	29
A2AQA7	Aqr	32	40	39	1	14	29
E9Q7E2	Arid2	13	20	17	0.01	0.01	9
P63268	Actg2	26	25	29	0.01	21	28
Q9WTL8	Arntl	7	7	12	0.01	0.01	5
Q60598	Cttn	26	26	30	9	15	27
P21981	Tgm2	26	25	25	15	15	26
Q9WTL8	Arntl	7	7	12	0.01	0.01	5
Q8BI84	Mia3	26	54	40	0.01	4	19
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
Q80YQ1	Thbs1	25	34	35	6	11	31
A0A1L1STC6	Syne1	25	70	77	0.01	2	40
Q9EP89	Lactb	25	24	26	10	12	22
P47757	Capzb	24	25	27	13	14	26
A2AMW0	Capzb	24	25	27	13	14	26
Q3U741	Ddx17	24	28	30	13	17	25
E9PZJ8	Ascc3	13	18	14	0.01	0.01	10
G5E8R1	Tpm1	24	0.01	24	0.01	12	0.01
P47757	Capzb	24	25	27	13	14	26
E9Q166	Atad2b	36	19	27	2	11	34
Q925I1	Atad3	32	32	29	10	12	24
P58774	Tpm2	22	26	28	8	17	32
O55143	Atp2a2	27	31	29	16	16	28
P58774	Tpm2	22	27	29	8	17	33
O55143	Atp2a2	27	31	29	16	16	28
M0QWP1	Agrn	22	40	43	3	3	39
P56480	Atp5b	19	19	21	14	11	16
Q61687	Atrx	35	60	55	3	20	52
B1AU25	Aifm1	21	20	22	12	9	20
A2AS05	Helz2	21	12	11	0.01	0.01	3
A2AS03	Helz2	21	12	11	0.01	0.01	3
G3X973	Stab1	21	21	24	0.01	0.01	18
A2AKD7	Snta1	5	8	8	0.01	0.01	2
Q03265	Atp5a1	20	20	21	15	12	15
Z9Z146		20	23	21	15	10	18
E9Q5F4	Actb	20	0.01	0.01	0.01	0.01	0.01
Q8R4H2	Arhgef12	11	15	14	0.01	0.01	4
F8VQN6	Arhgef12	11	15	14	0.01	0.01	4
A2A839	Epb41	20	23	20	6	7	21
P49290	Epx	20	18	22	4	11	21
A2A838	Epb41	20	23	20	6	7	21

P19001	krt19	20	23	21	15	10	18
Q9JI91	Actn2	20	31	26	5	13	35
Q0KL02	Trio	19	21	0.01	0.01	3	17
P08032	Spta1	17	13	13	0.01	0.01	5
Q9D287	Bcas2	13	12	12	2	5	12
Q8K019	Bclaf1	9	25	27	0.01	5	19
Q8K019	Bclaf1	9	25	27	0.01	5	19
Q3TL44	Nlrx1	9	12	12	1	0.01	3
A0A140T8T7	Col6a5	9	10	4	0.01	0.01	3
A6H584	Col6a5	9	10	4	0.01	0.01	3
A0A140T8W1	Col6a5	9	10	4	0.01	0.01	3
Q8CCJ3	Ufl1	8	11	9	0.01	0.01	3
Q99JY9	Actr3	19	19	21	10	10	17
Q7TQG1	Plekha6	29	33	0.01	4	7	0.01
Q6PAL0	Bend3	25	29	34	0.01	8	29
Q9QXX4	Slc25a13	18	26	25	10	11	22
P35441	Thbs1	24	33	35	6	10	0.01
Q6PGF5	Bms1	17	19	23	0.01	2	19
Q921S7	Mrpl37	8	11	8	0.01	0.01	4
P47757	Capzb	18	0.01	21	0.01	11	0.01
E9Q6A7	Bptf	19	36	39	0.01	3	23
A2A654	Bptf	19	36	0.01	0.01	3	23
A2A655	Bptf	19	36	0.01	0.01	3	23
E9QQ10	Akap9	7	12	10	0.01	0.01	4
Q6NWW9	Fndc3b	17	23	22	0.01	9	21
A0A0R4J0H8	Fndc3b	17	23	22	0.01	9	22
B7ZNJ1	Fn1	57	69	0.01	23	0.01	0.01
O88665	Brd7	6	14	13	0.01	0.01	12
Q80YE7	Dapk1	16	12	8	0.01	0.01	5
Q80YE7	Dapk1	16	12	8	0.01	0.01	5
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
Q8K1N2	Phldb2	17	26	28	0.01	7	25
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
Q8K1N2	Phldb2	17	26	28	0.01	7	25
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
F8VPU2	Farp1	17	22	21	8	5	20
E9Q397	Sptb	27	24	20	0.01	0.01	11
O54825	Bysl	15	14	14	0.01	5	14
E9Q3C1	C2cd2	15	17	15	5	5	13
O35646	Capn6	11	12	19	3	5	13
O70589	Cask	6	14	7	0.01	0.01	4
O70589	Cask	6	14	7	0.01	0.01	4
O70589	Cask	6	14	7	0.01	0.01	4
O70589	Cask	6	14	7	0.01	0.01	4

A0A067XG53	Cask	6	14	7	0.01	0.01	4
Q9JKF7	Mrpl39	9	11	7	0.01	0.01	4
Q5SUA5	Myo1g	16	24	19	3	7	25
Q8JZQ9	Eif3b	7	13	7	0.01	0.01	4
Z4YJU8	Golga2	16	25	0.01	4	4	13
Q9CVB6	Arpc2	16	21	19	10	8	15
Q9R112	Sqor	16	22	24	13	10	21
E9Q2E4	Hectd4	16	19	18	0.01	0.01	9
Q8VCB3	Gys2	16	21	18	4	7	17
Q8CH18	Ccar1	14	22	32	0.01	4	14
Z9Z153		15	19	21	7	10	19
Q8VDP4	Ccar2	15	18	18	0.01	2	12
Q9D312	krt20	15	19	21	7	10	19
P39061	Col18a1	15	17	16	5	7	15
Q5SV80	Myo19	6	9	8	0.01	0.01	4
P82198	Tgfbi	15	18	18	9	7	13
E9QPX1	Col18a1	15	17	16	5	7	15
Q8BZ09	Slc25a21	15	12	14	6	4	12
Q02788	Col6a2	15	17	15	7	7	12
Q9JLB2	Mpp5	15	21	21	3	9	19
P39061	Col18a1	15	17	16	5	7	15
Q8BGH2	Samm50	15	16	14	4	4	15
Q8R349	Cdc16	11	13	15	3	4	13
A0A1D5RLQ9	Cdc42bpa	12	21	18	0.01	0.01	8
D3YYN8	Cdc42bpa	12	21	18	0.01	0.01	8
A2A6Q5	Cdc27	9	14	17	1	4	9
H7BX44	Cdc42bpa	12	21	18	0.01	0.01	8
B6CI26	Slc25a21	15	12	14	6	4	12
E9PVY0	Cdc42bpa	12	21	18	0.01	0.01	8
P61161	Actr2	15	15	18	6	9	14
Q3UU96	Cdc42bpa	12	21	18	0.01	0.01	8
Q80TN4	Dnajc16	7	13	19	0.01	0.01	7
J3JS23	Zfp62	14	23	23	0.01	6	19
Q63918	Cavin2	14	14	16	0.01	6	16
A2A6Q5	Cdc27	9	14	17	1	4	9
A2A6Q5	Cdc27	0.01	14	17	1	0.01	9
Q9DC48	Cdc40	23	26	26	0.01	6	21
S4R1B9	Taf1	14	30	30	0.01	6	17
P15331	Prph	14	14	11	0.01	0.01	10
G5E846	Prph	14	14	11	0.01	0.01	10
Q6A068	Cdc5l	26	31	37	5	12	27
Q8JZM7	Cdc73	17	21	25	3	13	23
P09803	Cdh1	5	13	7	0.01	1	4
B1Q2W7	Taf1	14	30	30	0.01	6	17

P15331	Prph	14	14	11	0.01	0.01	10
A0A0R4IZW5	Cdh1	5	13	7	0.01	1	4
P24788	Cdk11b	7	10	9	0.01	0.01	0.01
E9Q3L2	Pi4ka	6	8	9	0.01	0.01	4
A0A140T8I9	Pi4ka	6	8	9	0.01	0.01	4
Q6ZWZ7	Rpl17	14	17	13	6	5	14
A2AWT5	Ubtf	14	24	28	4	8	20
Q9CR57	Rpl14	14	17	21	5	6	18
F7CGG2	Trrap	13	0.01	45	0.01	6	22
A2ADB1	Spen	13	26	35	0.01	2	26
A0A0R4J046	Cebpz	30	32	34	4	11	34
Q8BX10	Pgam5	13	18	19	6	4	17
O70194	Eif3d	9	13	9	0.01	0.01	7
Q62009	Postn	13	15	11	2	3	15
E9QLK7	Trrap	13	0.01	46	0.01	6	22
Q62009	Postn	13	15	11	2	3	15
P68368	Tuba4a	13	13	14	0.01	0.01	10
Q8BH59	Slc25a12	13	16	13	4	5	14
Q62009	Postn	13	15	11	2	3	15
O35218	Cpsf2	13	22	29	1	5	19
A0A0A0MQA5	Tuba4a	13	13	14	0.01	0.01	10
Q62009	Postn	13	15	11	2	3	15
Q9CRB9	Chchd3	13	16	15	8	6	11
P40201	Chd1	24	36	39	0.01	8	29
Q920A7	Afg3l1	6	11	14	0.01	0.01	5
E9PZM4	Chd2	23	21	30	1	8	27
Q5SUH7	Clint1	9	14	11	0.01	0.01	7
E9Q614	Chd3	0.01	17	21	0.01	0.01	13
B1AR17	Chd3	0.01	17	21	0.01	0.01	13
Q6PDQ2	Chd4	40	56	60	4	16	50
E9QAS5	Chd4	40	56	60	4	16	50
E9QAS4	Chd4	40	56	60	4	16	50
A3KFM7	Chd6	16	27	29	0.01	2	29
A3KFM7	Chd6	16	27	29	0.01	2	29
D3YVL0	Mov10	12	12	8	0.01	0.01	9
A0A0A0MQ89	Actr5	12	13	14	1	7	11
A2AJK6	Chd7	13	29	33	0.01	0.01	21
Q09XV5	Chd8	19	26	26	2	0.01	26
F8WHU7	Stag1	12	23	26	0.01	4	9
E9PW39	Mov10	12	12	8	0.01	0.01	9
Q8BYH8	Chd9	9	15	12	0.01	0.01	11
Q8BYH8	Chd9	9	15	12	0.01	0.01	11
Q8CGZ0	Cherp	14	18	20	0.01	4	14
A0A1D5RL92	Cherp	14	18	20	0.01	4	14

P02535	krt10	12	12	0.01	0.01	0.01	0.01
Q8BU03	Pwp2	12	15	15	4	6	13
Q61233	Lcp1	11	16	11	0.01	0.01	8
P23249	Mov10	12	12	8	0.01	0.01	9
Q8C147	Dock8	12	23	22	0.01	0.01	11
Q5SUH6	Clint1	9	14	11	0.01	0.01	7
E9PVA8	Gcn1	12	26	14	0.01	0.01	12
F7AA26	Pakap	12	21	20	0.01	2	19
D3Z3E8	Mov10	12	12	8	0.01	0.01	9
O08746	Matn2	11	22	20	0.01	3	18
B1AYU7	Cwc22	16	17	21	0.01	0.01	12
E9QMQ3	Triobp	8	16	14	0.01	0.01	9
G5E8J2	Ank1	11	20	21	0.01	0.01	9
G8JL84	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q5NBX1	Cobl	10	14	11	0.01	0.01	10
Q5NBX1	Cobl	10	14	11	0.01	0.01	10
Q5NBX1	Cobl	10	14	11	0.01	0.01	10
Q8R1B4	Eif3c	9	17	13	1	0.01	7
B1AX58	Pls3	10	9	7	0.01	0.01	6
A0A1W2P711	Mia2	11	25	16	0.01	0.01	6
A0A1C7CYV0	Pls3	10	9	7	0.01	0.01	6
B7ZW98	Ank1	11	20	21	0.01	0.01	9
Q99K51	Pls3	10	9	7	0.01	0.01	6
E9QNT8	Ank1	11	20	21	0.01	0.01	9
Q91ZV0	Mia2	11	25	16	0.01	0.01	6
D3YTV8	Ank1	11	20	21	0.01	0.01	9
Q0VGY9	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
A0A0A0MQM7	Matn2	11	22	20	0.01	3	18
Q02357	Ank1	11	20	21	0.01	0.01	9
Q8C196	Cps1	37	32	28	18	10	18
Q9R0Q6	Arpc1a	11	9	13	6	0.01	8
Q9EPU4	Cpsf1	27	39	49	0.01	11	34
S4R2F3	Ank2	11	25	28	0.01	0.01	14
Q9QXK7	Cpsf3	13	17	23	0.01	7	13
Q02357	Ank1	11	20	21	0.01	0.01	9
E9PUM4	Tln2	31	41	48	0.01	0.01	26
A0A1L1SQ51	Tln2	31	41	48	0.01	0.01	26
Q02357	Ank1	11	20	21	0.01	0.01	9
D3Z5M4	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q71LX4	Tln2	30	41	47	0.01	0.01	26
Q8BG67	Efr3a	7	9	11	0.01	0.01	6

Q8BG67	Efr3a	7	9	11	0.01	0.01	6
A0A1D5RLL3	Efr3a	7	9	11	0.01	0.01	6
Q3TXE3	Tyk2	9	12	14	0.01	0.01	8
Q8CIZ8	Vwf	19	20	25	2	0.01	13
E9QPU1	Vwf	19	20	25	2	0.01	13
Q8VE19	Mios	14	17	16	0.01	0.01	10
A0A0R4J1W7	Cdc23	10	19	24	4	6	14
P63154	Crnkl1	19	23	25	0.01	12	16
A0A140LI54	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
A0A0A0MQ73	Kmt2d	9	11	15	0.01	0.01	8
Q8BGZ4	Cdc23	10	19	24	4	6	14
Q61164	Ctcf	13	18	14	0.01	6	17
Q02248	Ctnnb1	24	27	29	7	12	23
P30999	Ctnnd1	36	41	42	12	18	35
P30999	Ctnnd1	36	42	43	0.01	0.01	35
A2AS45	Pkp4	13	17	16	0.01	0.01	10
Q62018	Ctr9	31	36	43	2	15	32
O55029	Copb2	15	25	16	0.01	0.01	13
Q8C5N3	Cwc22	16	17	21	0.01	0.01	12
Q8C5N3	Cwc22	16	17	21	0.01	0.01	12
Q6NV66	Zfp646	9	22	24	0.01	0.01	21
Q8JZS0	Lin7a	9	9	10	0.01	0.01	8
Q9JHU4	Dync1h1	58	84	65	2	6	45
Q9D0G0	Mrps30	9	11	9	0.01	0.01	6
A0A171EBL2	Rnf213	9	26	5	0.01	0.01	8
P49222	Epb42	10	14	17	0.01	0.01	11
Q6PAC3	Dcaf13	10	11	13	0.01	0.01	7
E0CYM1	Filip1l	9	20	20	0.01	1	16
H3BK65	Eps15	8	11	12	0.01	0.01	7
Q5JC28	Eps15	8	11	12	0.01	0.01	7
P42567	Eps15	8	11	12	0.01	0.01	7
Q3U1J4	Ddb1	10	14	9	0.01	0.01	4
Q91VR5	Ddx1	13	17	17	0.01	0.01	13
A7TU71	Shroom2	13	24	29	0.01	0.01	18
Q80Y44	Ddx10	8	20	23	0.01	4	17
A0A0R4J047	Luc7l	9	9	10	0.01	0.01	9
A2ALU4	Shroom2	13	24	29	0.01	0.01	18
Q501J6	Ddx17	24	28	30	13	17	25
Q9JIK5	Ddx21	23	26	33	0.01	7	27
D3Z0M9	Ddx23	26	33	36	0.01	6	32
F8WJA0	Ddx24	17	23	21	0.01	6	24

Q9ESV0	Ddx24	17	23	21	0.01	6	24
Q921N6	Ddx27	13	6	14	0.01	0.01	12
Q8R0Y6	Aldh1l1	9	15	2	1	0.01	3
Q62167	Ddx3x	30	31	34	10	16	30
Q62095	Ddx3y	27	0.01	26	0.01	0.01	24
Q91VN6	Ddx41	17	21	24	0.01	5	21
Q810A7	Ddx42	6	9	10	0.01	0.01	6
Q569Z5	Ddx46	5	11	12	0.01	0.01	5
Q8BSE0	Rmdn2	8	12	11	0.01	0.01	8
E9PVZ8	Golgb1	9	22	14	0.01	0.01	12
P97927	Lama4	9	17	12	2	2	14
Q61656	Ddx5	29	32	36	21	17	33
Q8BTS0	Ddx5	29	32	36	21	17	33
Q99MJ9	Ddx50	18	17	21	3	6	20
Q6P9R1	Ddx51	22	28	28	2	13	27
Q8K4L0	Ddx54	23	20	24	1	7	22
E0CYH7	Filip1l	9	20	20	0.01	1	16
E9QAH1	Golgb1	9	22	14	0.01	0.01	12
Q5F2E8	Taok1	12	11	11	0.01	0.01	7
P31001	Des	32	32	36	19	17	30
O35286	Dhx15	28	33	36	8	20	29
O55111	Dsg2	8	15	13	3	0.01	8
Q8VDC1	Fyco1	8	14	6	0.01	0.01	9
Q99PU8	Dhx30	18	20	22	0.01	3	20
Q99PU8	Dhx30	18	20	22	0.01	3	20
Q99PU8	Dhx30	18	20	22	0.01	3	20
Q9CPR5	Mrpl15	8	8	6	0.01	0.01	3
A2ACQ1	Dhx35	10	15	17	0.01	2	10
Q6NZL1	Dhx37	12	14	18	0.01	2	18
Q8C8Z9	Dtnb	10	13	13	0.01	2	7
O70585	Dtnb	10	13	13	0.01	2	7
A2A4P0	Dhx8	19	20	29	0.01	4	16
A0A087WPL5	Dhx9	50	53	62	26	0.01	0.01
O70133	Dhx9	0.01	52	61	26	34	0.01
Q8C6K9	Col6a6	8	11	8	2	0.01	4
Q9CZJ2	Hspa12b	9	8	11	0.01	0.01	8
Q91X77	Cyp2c50	8	8	4	0.01	0.01	0.01
Q9ESX5	Dkc1	17	17	21	7	9	19
Q811D0	Dlg1	11	16	13	2	2	8
Q811D0	Dlg1	11	15	13	2	2	8
Q3UNN4	Smarcc1	8	17	16	3	0.01	10
P11531	Dmd	13	23	23	0.01	4	13
P63037	Dnaja1	10	9	14	1	2	7
Q9QYI4	Dnajb12	9	14	9	0.01	0.01	10

H3BLH0	Smarca2	29	34	35	0.01	0.01	25
E9Q6A6	Col6a6	8	11	8	2	0.01	4
Q7TT50	Cdc42bpb	40	48	42	3	5	30
A0A0G2JDM7	Anapc5	9	13	17	0.01	4	10
A0A0G2JE03	Anapc5	9	13	17	0.01	4	10
J3KMH5	Mia3	8	22	17	0.01	0.01	0.01
Q3TWF7	Anapc5	9	13	17	0.01	4	10
B2LVG5	Cpsf4	7	10	11	0.01	1	7
Q8R2M2	Dnttip2	7	9	14	0.01	0.01	11
Q8VDR9	Dock6	30	0.01	48	0.01	0.01	35
G5E8K2	Ank3	7	19	23	0.01	3	13
G5E8K5	Ank3	7	19	23	0.01	3	13
A0A0R4J2B6	Rbbp5	7	13	12	1	2	5
G5E8K5	Ank3	7	19	23	0.01	3	13
G3UWY3	Cobl	10	14	11	0.01	0.01	10
G5E8P4	Cobl	10	14	11	0.01	0.01	10
Q9D903	Ebna1bp2	13	11	12	1	5	12
K3W4P2	Ints1	8	12	19	0.01	0.01	12
A0A0G2JH17	Ints1	8	12	19	0.01	0.01	12
G5E8K5	Ank3	7	19	23	0.01	3	13
O08810	Eftud2	33	44	45	18	23	36
P23116	Eif3a	19	29	24	0.01	4	14
D3Z7I0	Gtf3c2	14	21	21	0.01	2	15
P60229	Eif3e	6	11	10	0.01	0.01	5
Q8QZY1	Eif3l	8	9	11	0.01	0.01	5
Q91VC3	Eif4a3	17	23	22	5	14	20
G5E8K3	Ank3	7	19	23	0.01	3	13
Q9DBR7	Ppp1r12a	7	21	16	0.01	4	14
Q8BYC6	Taok3	11	12	13	2	0.01	9
Z9Z174		12	8	9	0.01	0.01	9
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q66JV4	Rbm12b2	20	23	32	0.01	0.01	23
O70318	Epb41l2	22	34	31	0.01	3	23
Q8R0W0	Eppk1	16	22	18	0.01	4	14
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
A0A1W2P812	Ank3	7	19	23	0.01	3	13
Q9DBR7	Ppp1r12a	7	20	16	0.01	4	14
Q3V1V3	Esf1	9	14	14	0.01	4	10

Q0KL02	Trio	19	21	28	0.01	3	17
Q0KL02	Trio	19	21	28	0.01	3	17
Q9D1C9	Rrp7a	8	10	11	0.01	0.01	10
S4R2K9	Ank3	7	19	23	0.01	3	13
P56960	Exosc10	18	20	22	1	3	18
Q8K366	Exosc10	0.01	0.01	22	1	3	0.01
Q8BTW3	Exosc6	9	8	9	0.01	0.01	7
Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q9Z1T2	Thbs4	12	12	15	0.01	2	11
F6WL90	Sp100	8	11	10	0.01	0.01	8
Q6A0A9	FAM120A	26	27	27	12	4	26
Q69ZR9	Fam208a	27	43	0.01	0.01	10	0.01
Q69ZR9	Fam208a	27	44	54	0.01	10	44
P48725	Pcnt	6	12	11	0.01	0.01	5
A0A1L1SQR4	Dock6	30	40	48	0.01	0.01	35
P35550	Fbl	19	19	19	8	13	18
Q7TPD1	Fbxo11	6	9	7	0.01	3	0.01
A0A0G2JEP4	Lrrfip2	15	9	12	0.01	2	11
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q6P6L0	Filip1l	9	20	20	0.01	1	16
Q6P6L0	Filip1l	9	20	20	0.01	1	16
P08121	Col3a1	8	12	11	0.01	1	8
Q9JJ28	Flii	22	22	19	5	4	21
Q8BTM8	Flna	83	94	97	13	37	84
B7FAU9	Flna	83	94	97	13	37	84
Q80X90	Flnb	74	88	82	4	20	73
Q9Z1T1	Ap3b1	13	20	14	0.01	3	11
O35231	Kifc3	7	12	12	0.01	1	9
E9PWU7	Kifc3	7	12	12	0.01	1	9
Q8VHX6	Flnc	19	31	27	0.01	0.01	25
Q8VHX6	Flnc	19	31	27	0.01	0.01	25
D3YUX2	Mpdz	6	26	27	0.01	0.01	15
A0A1D5RLV1	Epb41	13	15	10	0.01	0.01	13
Q80U35	Arhgef17	6	13	20	0.01	2	14
Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q61584	Fxr1	25	27	24	5	13	21
Q61584	Fxr1	25	27	24	5	13	21
Q91Z49	Fyttd1	11	16	20	5	7	14
Q8C8U0	Ppfibp1	6	20	17	0.01	0.01	14
Q9R1K5	Fzr1	5	9	11	0.01	0.01	6
F8VPV0	Pcnt	6	12	11	0.01	0.01	5

Q4VAA7	Snx33	6	11	10	0.01	0.01	5
P26039	Tln1	36	50	51	3	5	40
A0A1W2P737	Pcnt	6	12	11	0.01	0.01	5
Q8C8U0	Ppfibp1	6	20	17	0.01	0.01	14
Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q8R322	Gle1	9	16	22	0.01	0.01	16
D3YYT1	Glyr1	11	17	21	6	8	15
A2AWL7	Mga	5	12	21	0.01	2	14
A2ATP6	Myef2	16	22	22	0.01	0.01	20
Q8BPB5	Efemp1	5	12	9	0.01	0.01	6
Q99LH1	Gnl2	15	9	14	0.01	3	13
Q8CI11	Gnl3	14	18	17	1	6	12
Q921M4	Golga2	16	25	0.01	4	4	13
Q921M4	Golga2	16	25	0.01	4	4	13
E9Q361	Ints10	8	10	11	0.01	0.01	9
P51655	Gpc4	14	13	15	0.01	2	13
G5E8T6	Magi3	11	12	16	0.01	0.01	12
F6T2Z7	Cald1	9	11	11	0.01	0.01	9
F6SMY7	Mycbp2	52	74	75	0.01	5	61
A0A087WP63	Gm42715	5	12	11	0.01	0.01	6
Q80X80	C2cd2l	11	15	15	3	2	9
Q99MI1	Erc1	5	16	13	0.01	0.01	6
Q6P5H2	Nes	24	34	40	0.01	0.01	34
Q8K284	Gtf3c1	46	64	65	0.01	10	49
Q3TMP1	Gtf3c3	20	25	25	6	6	21
Q8BMQ2	Gtf3c4	26	36	38	3	9	29
Q8R2T8	Gtf3c5	13	17	17	2	7	11
Q2PFD7	Psd3	5	11	10	0.01	1	3
E9QNH6	Myo1b	55	54	57	0.01	0.01	55
E9Q580	Myo1b	55	54	57	0.01	0.01	55
Q8R2T8	Gtf3c5	13	17	17	2	7	11
Q99ME9	Gtpbp4	16	21	21	0.01	5	18
V9GWT6	Erc1	5	14	0.01	0.01	0.01	0.01
V9GXP8	Erc1	5	16	13	0.01	0.01	6
B1ARU1	Macf1	82	75	82	0.01	0.01	80
G3X922	Dnajc13	35	51	51	0.01	6	41
Q2PFD7	Psd3	5	11	10	0.01	1	3
A0A0R4J0J8	Specc1l	20	28	33	1	5	24
Q2KN98	Specc1l	20	28	33	1	5	24
O09106	Hdac1	12	14	14	2	4	12
P70288	Hdac2	10	12	13	2	0.01	11
Q8BVW3	Trim14	10	12	11	2	2	8
A2AWL7	Mga	5	12	21	0.01	2	14
E9QLG3	Mga	5	12	21	0.01	2	14

G3X9B1	Heatr1	39	43	54	5	19	49
E9QAM5	Helz2	21	12	11	0.01	0.01	3
Q4U2R1	Herc2	12	20	27	0.01	0.01	24
Q4U2R1	Herc2	12	20	27	0.01	0.01	24
Q9R1Y5	Hic1	7	14	19	0.01	4	12
A0A0R4J008	Hdac2	10	12	13	2	0.01	11
Z4YJP0	Hic1	7	14	19	0.01	4	12
F8VPM7	Erc1	5	16	13	0.01	0.01	6
Q8C4C9	Dnajb12	9	14	9	0.01	0.01	10
A0A1D5RM59	Tns1	26	37	39	0.01	3	32
A0A087WQS0	Tns1	26	37	39	0.01	3	32
E9Q0S6	Tns1	26	37	39	0.01	3	32
Q4VAC9	Plekhg3	15	24	23	0.01	0.01	23
V9GXF0	Erc1	5	15	13	0.01	0.01	0.01
V9GXH3	Erc1	5	15	13	0.01	0.01	0.01
H9KV01	Son	36	49	49	2	0.01	46
B2RUE8	Map4k4	8	12	9	0.01	2	8
Q2PFD7	Psd3	5	11	10	0.01	1	3
A0A0A6YWM8	Map4k4	8	12	9	0.01	2	8
Q8BJA3	Hmbox1	9	12	17	0.01	7	11
H3BKM3	Hmbox1	9	12	17	0.01	7	11
H3BKF8	Hmbox1	9	12	17	0.01	7	11
A0A087WS56	Fn1	59	72	0.01	23	32	0.01
Q64727	Vcl	24	24	16	0.01	3	18
O88569	Hnrnpa2b1	11	10	13	4	2	10
E9PUQ5	Golga2	16	25	21	4	4	13
E9Q0A3	Arhgef11	11	20	22	0.01	2	17
Q9Z204	Hnrnpc	23	26	28	12	14	24
Q9Z204	Hnrnpc	23	26	28	12	14	24
Q9Z204	Hnrnpc	22	24	26	12	14	23
Q9Z204	Hnrnpc	22	24	26	12	14	23
G3X9W0	Hnrnpd	11	0.01	13	0.01	0.01	0.01
G5E8G0	Hnrnpd	11	0.01	13	0.01	0.01	0.01
E9QNA7	Sorbs1	21	22	21	1	3	19
P15116	Cdh2	9	12	12	3	2	8
D3YYT0	Cdh2	9	12	12	3	2	8
P14873	Map1b	4	15	14	0.01	0.01	9
Q8VHE0	Sec63	10	10	11	0.01	2	9
P70333	Hnrnph2	12	12	14	0.01	4	9
E9PVP1	Crybg1	15	20	22	0.01	3	15
A0A0G2JG52	Crybg1	15	20	22	0.01	3	15
P61979	Hnrnpk	12	13	15	2	1	12
B2M1R6	Hnrnpk	12	13	15	2	1	12
G5E924	Hnrnpl	12	16	22	2	2	13

Q9D0E1	Hnrnpm	48	48	55	29	34	52
Q9D0E1	Hnrnpm	48	48	55	29	34	52
Q8VHM5	Hnrnpr	11	10	14	0.01	0.01	9
Q8VEK3	Hnrnpu	27	22	31	15	11	28
Q8VEK3	Hnrnpu	27	22	31	15	11	28
Q00PI9	Hnrnpul2	43	42	48	24	22	41
Z4YKB8	Hp1bp3	21	20	21	13	9	17
Q3TEA8	Hp1bp3	21	20	21	13	9	17
P11499	Hsp90ab1	12	12	13	4	4	10
P20029	Hspa5	27	33	34	15	15	29
P38647	Hspa9	15	20	17	12	9	12
Q9Z1M8	Ik	13	25	31	4	9	18
D3YU58	Anapc7	17	17	23	0.01	6	16
Q9Z1X4	Ilf3	30	36	40	8	11	33
Q9Z1X4	Ilf3	30	36	40	8	11	33
G5E8I8	Cherp	14	18	20	0.01	4	14
F8VQC7	Ktn1	11	16	13	0.01	2	12
A0A087WS29	Ktn1	11	16	13	0.01	2	12
A0A087WPX0	Ktn1	11	16	13	0.01	2	12
Q6ZPV2	Ino80	23	31	44	2	11	30
Q6ZPV2	Ino80	23	31	44	2	11	30
A0A087WP14	Ktn1	11	16	13	0.01	2	12
A0A087WQQ5	Ktn1	11	16	13	0.01	2	12
A0A087WP85	Ktn1	11	16	13	0.01	2	12
F7AL76	Chd8	19	26	26	2	0.01	26
Q6P4S8	Ints1	8	12	19	0.01	0.01	12
Q8K2A7	Ints10	8	10	11	0.01	0.01	9
Q8QZV7	IntS13	4	13	11	0.01	0.01	9
Q3UQ44	Iqgap2	42	50	47	5	10	39
E9Q9B7	Kidins220	4	12	11	0.01	1	7
S4R1P5	Dst	4	14	19	0.01	0.01	7
Q8BZQ7	Anapc2	11	18	18	0.01	3	14
Q9JKF1	Iqgap1	20	27	28	0.01	4	19
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
Q9Z329	Itpr2	65	67	78	14	23	65
P70227	Itpr3	13	19	17	0.01	0.01	10
Q8C1D8	Iws1	12	13	16	0.01	4	12

A2AQ25	Skt	8	14	17	0.01	0.01	15
E9QAU4	Etl4	8	14	17	0.01	0.01	15
E9Q238	Kank1	9	16	15	0.01	0.01	13
A0A087WS23	Ktn1	10	16	12	0.01	2	12
A0A087WQ25	Ktn1	10	16	12	0.01	2	12
A0A087WP48	Ktn1	10	16	12	0.01	2	12
A0A087WQI3	Ktn1	10	16	12	0.01	2	12
A0A087WS04	Ktn1	10	16	12	0.01	2	12
A0A087WQF8	Ktn1	10	16	12	0.01	2	12
A0A087WQD0	Ktn1	10	16	12	0.01	2	12
Q6NZF1	Zc3h11a	4	16	21	0.01	4	13
A0A087WPW5	Ktn1	10	16	12	0.01	2	12
A0A087WQG4	Ktn1	10	16	12	0.01	2	12
A0A087WRS1	Ktn1	10	16	12	0.01	2	12
A0A087WNW3	Ktn1	10	16	12	0.01	2	12
A2AQD5	Ssfa2	17	22	22	2	2	17
A0A1Y7VMH7	Kidins220	4	12	11	0.01	1	7
A3KG93	Kdm1a	6	9	12	0.01	0.01	7
Q6ZQ88	Kdm1a	6	9	12	0.01	0.01	7
Q3UXZ9	Kdm5a	20	24	28	0.01	5	27
A0A1Y7VME9	Kidins220	4	12	11	0.01	1	7
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
Q6PDK2	Kmt2d	9	11	15	0.01	0.01	8
Q80YR9	Rbm12b1	24	28	33	2	6	27
G5E8D6	Efemp2	11	8	9	0.01	0.01	9
Q9WVJ9	Efemp2	11	8	9	0.01	0.01	9
P05784	krt18	31	28	29	22	19	27
Q9DCV7	krt7	12	8	9	0.01	0.01	9
P11679	krt8	39	37	37	31	29	35
Q99L88	Sntb1	19	22	24	4	5	17
A0A0G2JGL8	Dhx30	18	20	22	0.01	3	20
Q61001	Lama5	16	23	24	4	0.01	24
P02469	Lamb1	14	20	19	2	0.01	19
A2BE28	Las1l	17	21	22	4	13	20
A2BE28	Las1l	17	21	22	4	13	20
Q68FD5	Cltc	39	38	35	8	8	28
Q3U9G9	Lbr	18	17	19	10	9	16
Q5SXR6	Cltc	39	38	35	8	8	28
Q6P5B5	Fxr2	20	17	23	2	4	19
P20918	Plg	23	31	26	3	6	24
E9PU96	Urb1	45	53	72	3	13	55

G5E8G6	Myo5b	54	54	64	3	10	51
P21271	Myo5b	54	54	64	3	10	51
Q5XJE5	Leo1	12	16	22	3	7	13
Q8BH80	Vapb	12	12	12	4	3	8
Q9QY76	Vapb	12	12	12	4	3	8
P48678	Lmna	54	49	52	30	35	48
P14733	Lmnb1	44	44	46	30	36	47
Q61586	Gpam	21	22	24	6	4	19
A0A0R4J0Q5	Lmnb2	36	34	33	14	24	35
P21619	Lmnb2	36	34	33	14	24	35
O88322	Nid2	25	33	35	3	8	28
Q91ZX7	Lrp1	44	57	55	3	4	36
A0A0R4J0I9	Lrp1	44	57	55	3	4	36
Q8BWT1	Acaa2	14	17	15	6	4	11
Q3UM18	Lsg1	11	16	13	0.01	2	12
Q9CYI4	Luc7l	9	9	10	0.01	0.01	9
Q7TNC4	Luc7l2	12	11	13	0.01	0.01	11
Q7TNC4	Luc7l2	12	11	13	0.01	0.01	11
Q7TNC4	Luc7l2	12	11	13	0.01	0.01	11
Q7TNC4	Luc7l2	12	11	13	0.01	0.01	11
Q9WTX8	Mad1l1	15	24	24	0.01	2	23
Q6RHR9	Magi1	7	15	15	0.01	0.01	11
Q60847	Col12a1	55	50	53	4	12	46
E9PX70	Col12a1	55	50	53	4	12	46
Q6RHR9	Magi1	7	15	15	0.01	0.01	0.01
Q60847	Col12a1	55	50	53	4	12	46
Q60847	Col12a1	55	50	53	4	12	46
A0A0N4SUZ0	Magi1	7	15	15	0.01	0.01	0.01
Q9EQJ9	Magi3	11	12	16	0.01	0.01	12
Q61554	Fbn1	3	21	13	10	0.01	6
Q3V3W4	Zbtb2	11	13	12	1	3	11
E9QN70	Lamb1	14	20	19	2	0.01	19
Q8K310	Matr3	48	48	55	16	17	49
Q91VS8	Farp2	19	23	23	2	5	19
Q99L90	Mcrs1	12	12	13	0.01	4	13
J3QMC5	Mdn1	7	29	40	0.01	0.01	16
A2ANY6	Mdn1	7	29	40	0.01	0.01	16
A0A1B0GR85	2900026A02Rik	15	23	24	0.01	2	24
F7BGR7	Gm21992	11	14	19	0.01	3	14
A5D6P2	Pard3	26	40	37	3	6	37
C0HKD8	Mfap1a	11	16	18	1	5	12
C0HKD9	Mfap1b	11	16	18	1	5	12
H7BX50	Mga	5	12	21	0.01	2	14
Q8BML1	Mical2	7	14	18	0.01	0.01	13

Q3UID0	Smarcc2	16	23	19	3	7	17
D3Z598	Ltbp4	29	36	40	2	11	35
Q8K4G1	Ltbp4	29	36	40	2	11	35
A0A087WSN6	Fn1	57	69	71	23	0.01	62
B9EHT6	Fn1	57	69	71	23	0.01	62
Q810V0	Mphosph10	9	7	12	0.01	0.01	8
Q3TYA6	Mphosph8	7	13	17	0.01	5	12
P11247	Mpo	6	12	16	0.01	2	9
Q9JMH9	Myo18a	76	86	86	13	23	71
Q9JMH9	Myo18a	76	86	86	13	23	71
Q9D7N3	Mrps9	8	10	10	0.01	0.01	9
P46978	Stt3a	16	12	15	5	4	8
F8WHY8	Mta1	7	19	15	0.01	8	14
Q9R190	Mta2	16	28	27	2	8	21
Q924K8	Mta3	4	16	13	0.01	4	9
Q3UII8	Mta3	4	16	13	0.01	4	9
Q80WJ7	Mtdh	19	21	25	3	8	20
Q7TPV4	Mybbp1a	48	54	60	31	36	57
A0A0U1RNK7	Dock7	36	50	51	6	10	44
Q7TPH6	Mycbp2	52	0.01	0.01	0.01	5	0.01
Q7TPH6	Mycbp2	52	0.01	0.01	0.01	5	0.01
Q8C854	Myef2	16	23	23	6	8	20
Q5SX40	Myh1	98	129	132	65	95	150
Q61879	Myh10	121	131	136	44	82	134
Q8VDD5	Myh9	164	167	169	90	126	169
F8VQB6	Myo10	12	13	22	0.01	0.01	17
P46735	Myo1b	55	54	57	24	32	55
Q8R1A4	Dock7	36	50	51	6	10	44
Q7TQD7	Myo1b	55	54	57	24	32	55
Q9WTI7	Myo1c	48	47	54	23	33	51
A2A9M5	Dock7	36	50	51	6	10	44
Q9WTI7	Myo1c	48	47	54	0.01	33	51
E9PX48	Dock7	36	50	51	6	10	44
Q9QY06	Myo9b	3	7	9	0.01	0.01	0.01
Q8R1A4	Dock7	36	50	51	6	10	44
A2A9M4	Dock7	36	50	51	6	10	44
Q5SWZ5	Mprip	77	80	82	0.01	25	78
F8WHL2	Copa	31	43	37	7	11	29
Q8CIE6	Copa	31	43	37	7	11	29
Q8BPM0	Daam1	16	16	16	7	3	12
Q8BPM0	Daam1	16	16	16	7	3	12
Q62383	Supt6h	46	54	61	4	15	47
P97479	Myo7a	29	28	27	0.01	3	32
Q5MJ56	Myo7a	29	28	27	0.01	3	32

Q8K224	Nat10	33	36	36	7	19	38
Q8BZR9	Ncbp3	12	16	16	4	7	15
A0A0R4J113	Myo7a	29	28	27	0.01	3	32
P09405	Ncl	17	22	21	4	11	17
P97479	Myo7a	29	28	27	0.01	3	32
Q91W39	Ncoa5	17	19	19	1	6	18
A0A0U1RPX7	Myo7a	29	28	27	0.01	3	32
P46935	Nedd4	23	22	21	2	5	19
A2AL85	Asph	14	19	18	6	5	14
Q8BSY0	Asph	14	19	18	6	5	14
P70257	Nfix	14	0.01	14	3	7	0.01
Q6PIJ4	Nfrkb	14	33	34	5	11	27
Q8BY02	Nkrf	9	10	18	0.01	2	13
H9KV00	Son	39	53	58	2	19	49
J3QK52	Noc2l	14	13	16	0.01	6	15
Q8BJW5	Nol11	15	16	19	2	4	16
Q8R5K4	Nol6	12	18	18	2	5	17
Q8R5K4	Nol6	12	18	18	2	5	17
E9Q8Z8	Ctnnd1	36	42	0.01	0.01	0.01	35
Q8R3N1	Nop14	16	19	21	0.01	3	22
Q9D6Z1	Nop56	33	35	37	11	21	35
Q6DFW4	Nop58	16	22	24	4	10	19
Q9D6T0	Nosip	4	10	12	0.01	0.01	5
Q8BX02	Kank2	19	26	22	5	5	20
Q6IRU2	Tpm4	16	13	16	2	3	16
B1B1A8	Mylk	36	43	46	4	9	43
Q99PL5	Rrbp1	34	35	25	7	7	28
A2AVJ7	Rrbp1	34	35	25	7	7	28
Q3TJY1	Mcrs1	12	12	13	0.01	4	13
P48776	Tdo2	15	16	15	4	5	12
Q9CSB4	Pard3b	10	11	13	0.01	0.01	13
Q9CSB4	Pard3b	10	11	13	0.01	0.01	13
Q8CG29	Myo1f	15	16	12	0.01	5	16
E9Q7G0	Numa1	65	102	107	31	68	97
F6ZQA3	Numa1	18	32	36	0.01	23	32
Q9QZS3	Numb	6	10	11	0.01	0.01	8
Q9QZS3	Numb	6	10	11	0.01	0.01	8
Q9QZS3	Numb	6	10	11	0.01	0.01	8
Q9QZS3	Numb	6	10	11	0.01	0.01	8
E9Q4V9	Nup107	34	36	0.01	9	14	0.01
Q8BH74	Nup107	34	36	39	9	14	34
Q8R0G9	Nup133	30	32	38	8	13	29
E9Q3G8	Nup153	13	22	26	3	10	19
Q99104	Myo5a	19	27	21	0.01	2	26

D3YZ62	Myo5a	19	27	21	0.01	2	26
Q99P88	Nup155	18	17	20	0.01	4	17
Q9Z0W3	Nup160	34	38	46	8	14	38
Q6ZQH8	Nup188	15	11	16	0.01	0.01	14
D3Z4J3	Myo5a	19	27	21	0.01	2	26
A0A0J9YUD5	Nup205	29	26	37	2	5	32
B9EJ54	Nup205	29	26	37	2	5	32
Q9QY81	Nup210	14	17	21	3	4	15
A0A0R4J1I6	Nup210	14	17	21	3	4	15
Q9QXS6	Dbn1	15	19	18	0.01	7	15
Q9QXS6	Dbn1	15	19	18	0.01	7	15
Q9JIH2	Nup50	6	16	15	0.01	2	8
Q8R480	Nup85	20	21	23	6	13	21
P10493	Nid1	17	23	20	3	3	22
Q8BJ71	Nup93	26	27	27	2	8	26
A0A1B0GSX7	Nup98	38	50	52	8	14	37
Q8CIC2	Nupl2	9	9	12	0.01	0.01	8
E9QL43	Nupl2	9	9	12	0.01	0.01	8
Q99JX7	Nxf1	7	12	13	0.01	2	10
Q61235	Sntb2	22	26	26	4	10	21
A0A0R4J150	Osbpl8	6	11	10	0.01	0.01	6
B9EJ86	Osbpl8	6	12	10	0.01	0.01	6
Q8K2T8	Paf1	18	22	26	3	10	21
Q921K2	Parp1	10	15	17	3	4	15
Q63ZW7	Patj	28	31	41	2	5	28
P58501	Paxbp1	19	27	30	0.01	3	18
Q8BSQ9	Pbrm1	28	38	37	2	8	35
Q8BSQ9	Pbrm1	28	38	37	2	8	35
E9Q7L3	Pbrm1	28	38	37	2	8	35
E9Q7L2	Pbrm1	28	38	37	2	8	35
D3Z1N4	Pbrm1	28	38	37	2	8	35
F8VQD1	Pbrm1	28	38	37	2	8	35
E9Q4Y5	Pbrm1	28	38	37	2	8	35
P49586	Pcyt1a	7	9	9	0.01	0.01	5
Q6NS46	Pdcd11	28	38	49	0.01	11	39
Q3TJD7	Pdlim7	9	14	15	0.01	3	9
Q4VA53	Pds5b	14	15	19	0.01	4	14
Q9CQ73	Pkp2	16	17	16	5	4	15
Q9QY23	Pkp3	6	14	14	0.01	0.01	10
Q9QY23	Pkp3	6	14	14	0.01	0.01	10
Q68FH0	Pkp4	13	17	16	0.01	0.01	10
B7ZC24	Ncoa5	13	15	15	1	5	14
Q68FH0	Pkp4	13	17	0.01	0.01	0.01	10
A0A0N4SWD7	Plekha5	20	29	0.01	3	2	0.01

E9Q6H8	Plekha5	20	29	25	3	2	19
Q3UIL6	Plekha7	29	30	28	3	7	30
Q8VCQ8	Cald1	24	31	33	4	10	25
Q922V4	Plrg1	20	24	26	3	10	20
Q60953	Pml	20	30	29	10	12	22
Q60953	Pml	0.01	0.01	26	0.01	0.01	0.01
Q99KG5	Lsr	17	16	18	5	4	14
Q61292	Lamb2	27	27	25	9	4	26
Q3TUQ5	Pnn	22	27	30	4	11	24
O35691	Pnn	22	27	30	4	11	24
A2AJ88	Pnpla7	7	14	13	0.01	0.01	7
A2AJ88	Pnpla7	7	14	13	0.01	0.01	7
P51660	Hsd17b4	15	15	12	4	5	12
O35134	Polr1a	6	17	19	0.01	0.01	7
P70700	Polr1b	5	12	10	0.01	0.01	3
Q8C0T5	Sipa1l1	26	25	31	0.01	3	34
P08775	Polr2a	34	50	54	4	15	40
A0A0R4J0V5	Polr2a	34	50	54	4	15	40
Q8CFI7	Polr2b	26	38	35	5	11	30
Q8K2H1	Pphln1	9	12	11	0.01	2	10
Q8K2H1	Pphln1	9	12	11	0.01	2	10
Q9QZH3	Ppie	10	12	12	0.01	3	6
E9Q9C7	Ablim1	22	23	25	4	7	22
E9Q9C1	Ablim1	22	23	25	4	7	22
E9Q9C2	Ablim1	22	23	25	4	7	22
E9Q9C0	Ablim1	22	23	25	4	7	22
Q8K4G5	Ablim1	22	23	25	4	7	22
Q8K4G5	Ablim1	22	23	25	4	7	22
E9QK41	Ablim1	22	23	25	4	7	22
Q8R4U0	Stab2	31	24	25	8	3	26
Q6R891	Ppp1r9b	16	25	20	0.01	5	17
Q5FWX6	Prkd3	5	8	11	0.01	0.01	4
Q8K1Y2	Prkd3	5	8	11	0.01	0.01	4
P48437	Prox1	15	24	27	2	13	26
Q99KP6	Prpf19	10	15	16	2	6	12
Q922U1	Prpf3	18	23	26	3	14	20
Q8CCF0	Prpf31	11	12	15	2	4	11
Q4FK66	Prpf38a	10	10	12	0.01	2	10
Q9DAW6	Prpf4	18	20	26	4	12	19
F8VQJ3	Lamc1	28	38	39	8	7	36
Q9R1C7	Prpf40a	20	23	34	3	6	24
Q61136	Prpf4b	8	15	23	0.01	3	12
Q91YR7	Prpf6	29	42	42	14	19	33
Q99PV0	Prpf8	92	109	117	32	53	94

Q14C51	Ptcd3	9	9	9	0.01	0.01	5
Q3UEB3	Puf60	12	11	15	0.01	4	10
Q3UEB3	Puf60	12	11	15	0.01	4	10
G3UWZ0	Baz1a	17	19	27	0.01	5	24
P68040	Rack1	9	12	10	0.01	0.01	10
Q61550	Rad21	12	20	20	1	4	14
Q8C570	Rae1	11	11	15	1	2	10
Q9EP71	Rai14	43	47	52	9	18	44
Q64012	Raly	20	23	25	10	11	20
Q9ERU9	Ranbp2	52	84	95	12	28	74
Q8BX09	Rbbp5	7	13	12	1	2	5
P97434	Mprip	0.01	0.01	66	11	26	0.01
Q99KG3	Rbm10	23	27	32	2	11	26
Q8C2Q3	Rbm14	21	27	32	10	16	26
Q0VBL3	Rbm15	14	14	19	2	7	13
Q8JZX4	Rbm17	21	25	24	5	8	21
B2RY56	Rbm25	22	28	33	6	10	26
Q8VH51	Rbm39	11	15	18	3	6	14
Q8VH51	Rbm39	11	15	18	3	6	14
Q8VE92	Rbm4b	10	11	17	0.01	0.01	14
Q91YE7	Rbm5	17	25	29	5	8	24
Q91YE7	Rbm5	17	25	29	5	8	24
S4R1W5	Rbm6	19	24	30	2	9	25
Q9CQT2	Rbm7	8	11	11	0.01	0.01	7
Q9WV02	Rbmx	16	19	24	11	11	18
Q91VM5	Rbmxl1	18	19	26	11	10	19
F6VG99	Lmo7	0.01	46	44	8	18	45
Q6PR54	Rif1	9	20	27	0.01	4	21
Q6PR54	Rif1	9	20	27	0.01	4	21
Q6PR54	Rif1	9	20	27	0.01	4	21
Q9JJF3	Riox1	9	13	14	0.01	4	12
Q3UJU9	Rmdn3	12	16	14	4	3	10
E9Q555	Rnf213	9	26	5	0.01	0.01	8
P47963	Rpl13	18	19	20	5	11	19
P19253	Rpl13a	19	23	21	5	9	20
Q9CPR4	Rpl17	14	17	13	6	5	14
Q4VBF8	Sipa1l1	0.01	25	0.01	0.01	3	0.01
P27659	Rpl3	28	29	29	10	15	24
Q9D8E6	Rpl4	34	37	40	9	14	34
P47962	Rpl5	25	23	20	13	14	22
D3Z080	Sorbs2	0.01	0.01	35	12	0.01	0.01
P47911	Rpl6	21	24	30	11	12	23
P14148	Rpl7	32	31	30	17	19	33
P12970	Rpl7a	23	25	27	11	13	23

P62754	Rps6	13	13	16	5	5	14
Q6P5B0	Rrp12	14	22	30	2	3	22
Q91YK2	Rrp1b	8	14	19	0.01	3	16
Q9CYH6	Rrs1	9	11	12	0.01	0.01	13
Q8BVY0	Rsl1d1	10	13	13	0.01	1	12
P97434	Mprip	0.01	0.01	66	11	26	0.01
Q99LF4	Rtcb	12	14	19	0.01	1	10
P60122	Ruvbl1	21	21	26	8	11	21
Q9WTM5	Ruvbl2	30	30	33	14	21	29
D3YXK2	Safb	28	33	39	5	16	29
Q80YR5	Safb2	40	47	53	9	21	44
Q9ER74	Sall1	5	13	19	0.01	1	10
Q6P5E3	Sall1	5	13	19	0.01	1	10
Q9Z315	Sart1	40	48	51	11	21	44
E9PZM7	Scaf11	14	24	26	0.01	5	20
Q80U72	Scrib	24	34	33	2	4	27
Q80U72	Scrib	0.01	34	0.01	2	4	0.01
Q80U72	Scrib	0.01	34	0.01	2	4	0.01
Q80U72	Scrib	0.01	34	0.01	2	4	0.01
Q9EP97	Senp3	5	10	13	0.01	2	7
E9Q5F9	Setd2	6	21	33	0.01	0.01	15
E9Q5F9	Setd2	6	21	33	0.01	0.01	15
Q8K4Z5	Sf3a1	28	35	35	9	16	33
Q9D554	Sf3a3	14	18	19	2	7	12
Q99NB9	Sf3b1	48	55	58	17	30	53
G5E866	Sf3b1	48	55	58	17	30	53
Q3UJB0	Sf3b2	31	37	38	10	19	32
Q921M3	Sf3b3	36	42	47	15	24	40
Q9QXS1	Plec	0.01	197	202	44	62	193
Q9QXS1	Plec	0.01	197	202	44	62	193
Q3USH5	Sfswap	5	19	22	0.01	3	14
Q3TFD0	Shmt2	13	6	11	0.01	1	8
Q9CZN7	Shmt2	13	6	11	0.01	1	8
E9QAX2	Myo18a	0.01	85	0.01	13	23	0.01
Q60520	Sin3a	12	27	22	0.01	3	17
Q60520	Sin3a	12	27	22	0.01	3	17
Q62141	Sin3b	6	10	10	0.01	0.01	0.01
Q62141	Sin3b	6	10	10	0.01	0.01	6
Q9CZU3	Skiv2l2	29	33	36	2	9	26
Q9QXS1	Plec	0.01	197	202	44	62	193
P51881	Slc25a5	20	26	26	13	13	23
Q8CH25	Sltm	20	0.01	34	0.01	9	25
Q8CH25	Sltm	20	28	34	0.01	9	25
Q8BHJ9	Slu7	12	15	18	0.01	0.01	12

Q6DIC0	Smarca2	29	34	35	0.01	0.01	25
F2Z4A9	Smarca2	29	34	35	0.01	0.01	25
A0A0R4J170	Smarca4	23	29	28	2	7	21
Q3TKT4	Smarca4	23	29	28	2	7	21
Q3TKT4	Smarca4	23	29	28	2	7	21
Q91ZW3	Smarca5	35	50	42	15	25	42
P97496	Smarcc1	8	17	16	3	0.01	10
P97496	Smarcc1	8	17	16	3	0.01	10
Q6PDG5	Smarcc2	16	23	19	3	7	17
Q6PDG5	Smarcc2	16	23	19	3	7	17
Q99JR8	Smarcd2	9	17	16	0.01	0.01	7
Q99JR8	Smarcd2	9	17	16	0.01	0.01	7
O54941	Smarce1	9	13	13	2	4	8
Q9CU62	Smc1a	41	57	58	9	25	52
Q9CW03	Smc3	41	49	53	9	19	41
Q3UKJ7	Smu1	11	16	19	2	6	12
E9PX43	Plekha6	0.01	34	32	4	7	32
Q78PY7	Snd1	5	14	7	0.01	0.01	4
Q6P4T2	Snrnp200	69	90	103	30	50	91
Q6PE01	Snrnp40	9	14	16	2	4	10
Q62376	Snrnp70	9	13	13	0.01	0.01	10
A0A0B4J1E2	Snw1	18	25	24	4	8	19
Q9QX47	Son	36	49	49	2	0.01	46
Q9QX47	Son	0.01	43	43	0.01	19	41
Q3UTJ2	Sorbs2	37	41	40	12	0.01	40
Q3UTJ2	Sorbs2	0.01	0.01	35	12	0.01	0.01
Q9R1Z8	Sorbs3	12	15	16	0.01	2	14
Q8C405	Sp100	18	23	23	0.01	7	20
Q6NXI6	Rprd2	0.01	6	16	0.01	0.01	2
A2ADB0	Spen	13	26	35	0.01	2	26
Q62504	Spen	13	26	0.01	0.01	2	0.01
Q62504	Spen	13	26	0.01	0.01	2	0.01
Q62504	Spen	13	26	0.01	0.01	2	0.01
Q62261	Sptbn1	123	136	140	44	71	131
A0A087WNL7	Srcap	5	12	11	0.01	0.01	6
A0A087WQ44	Srcap	5	12	11	0.01	0.01	6
A0A087WNX7	Srcap	5	12	11	0.01	0.01	6
Q8BTI8	Srrm2	2	8	15	0.01	0.01	5
Q8BTI8	Srrm2	2	8	15	0.01	0.01	5
H7BX95	Srsf1	15	14	15	4	5	14
Q9QXS1	Plec	0.01	197	202	44	62	193
Q6PDM2	Srsf1	15	14	15	4	5	14
Q3TWW8	Srsf6	10	11	13	0.01	3	12
Q9D0B0	Srsf9	15	15	16	2	6	15

Q922B9	Ssfa2	17	22	22	2	2	17
Q08943	Ssrp1	20	22	22	2	7	19
Q08943	Ssrp1	20	22	22	2	7	19
Q9D3E6	Stag1	12	23	26	0.01	4	9
Q9JMH9	Myo18a	0.01	85	0.01	13	23	0.01
O35638	Stag2	14	21	18	0.01	0.01	11
A2AFF6	Stag2	14	21	18	0.01	0.01	11
Q9QXS1	Plec	0.01	197	202	44	62	193
Q9D666	Sun1	6	10	10	1	2	5
B2RQG2	Phf3	0.01	12	19	0.01	2	5
G3X956	Supt16	26	35	29	7	9	27
Q920B9	Supt16h	26	35	0.01	7	9	27
O55201	Supt5h	13	27	32	0.01	4	19
P70279	Surf6	11	18	15	2	4	15
Q8K4L3	Svil	72	82	82	14	33	85
Q8K4L3	Svil	0.01	78	81	14	33	81
Q9D198	Syf2	8	9	12	0.01	1	6
Q6ZWQ0	Syne2	97	187	235	6	38	154
Q6DFZ2	Syne2	0.01	61	76	0.01	0.01	55
Q8VCR2	Hsd17b13	0.01	9	10	0.01	0.01	0.01
E9Q1U2	Synpo2	13	21	17	0.01	1	16
Q80UV9	Taf1	14	30	30	0.01	6	17
Q80UV9	Taf1	14	30	30	0.01	6	17
E9QAP7	Taf4	9	12	14	1	3	10
F8VPY2	Taf5	10	19	20	2	8	16
Q62311	Taf6	17	24	27	1	6	16
Q9R1C0	Taf7	6	8	11	1	2	3
Q02566	Myh6	0.01	80	73	0.01	43	76
Q6ZQ29	Taok2	6	13	13	0.01	2	10
Q6ZQ29	Taok2	0.01	12	12	0.01	2	0.01
P36371	Tap2	11	14	10	2	4	10
Q80UE5	Epb41l2	0.01	30	27	0.01	3	0.01
Q8C4J7	Tbl3	18	18	31	4	9	28
Q8CGF7	Tcerg1	9	16	20	0.01	1	9
Q8CGF7	Tcerg1	9	16	20	0.01	1	9
Q9QXS1	Plec	0.01	197	202	44	62	193
Q9QXS1	Plec	0.01	197	202	44	62	193
Q3URQ0	Tex10	11	18	19	0.01	0.01	16
Q9ERA6	Tfip11	21	26	33	0.01	2	28
B2RRE2	Myo18a	0.01	85	0.01	13	23	0.01
Q8R3N6	Thoc1	2	9	16	0.01	0.01	6
B1AZI6	Thoc2	7	12	17	0.01	2	8
Q569Z6	Thrap3	20	30	31	3	12	27
Q0VBL1	Tigd2	8	11	9	0.01	0.01	9

Q9WV92	Epb41l3	0.01	13	9	0.01	0.01	0.01
P39447	Tjp1	59	62	71	17	25	61
Q9QXS1	Plec	0.01	197	202	44	62	193
B9EHJ3	Tjp1	58	61	70	17	26	60
Q9Z0U1	Tjp2	35	43	41	7	16	36
Q921G9	Tjp3	23	24	22	7	12	24
Q61029	Tmpo	13	18	19	10	10	0.01
Q61033	Tmpo	10	15	16	0.01	5	14
P58871	Tnks1bp1	29	47	53	2	8	40
Q04750	Top1	23	23	21	15	9	17
Q01320	Top2a	13	20	26	4	11	20
Q9QXS1	Plec	0.01	197	202	44	62	193
Q64511	Top2b	39	55	63	9	23	44
Q9QXS1	Plec	0.01	197	202	44	62	193
Q921T2	Tor1aip1	13	16	22	4	6	17
P70399	Tp53bp1	12	25	27	0.01	3	15
K3W4L0	Myo18a	0.01	85	0.01	13	23	0.01
P70399	Tp53bp1	12	25	27	0.01	3	15
Q7M739	Tpr	23	29	33	2	6	29
F6ZDS4	Tpr	23	29	33	2	6	29
Q62318	Trim28	16	22	21	9	11	20
Q99KW3	Triobp	8	16	14	0.01	0.01	9
Q99KW3	Triobp	8	16	14	0.01	0.01	9
Q99KW3	Triobp	8	16	14	0.01	0.01	9
G5E870	Trip12	5	28	34	0.01	3	22
A2ASS6	Ttn	61	138	185	17	61	0.01
P68369	Tuba1a	16	16	16	0.01	4	13
P68373	Tuba1c	16	16	15	0.01	4	13
Q7TMM9	Tubb2a	16	17	20	0.01	7	17
P68372	Tubb4b	17	17	21	5	0.01	16
P99024	Tubb5	15	16	20	7	9	15
Q922F4	Tubb6	11	10	12	0.01	0.01	9
Q8BFR5	Tufm	11	11	13	2	3	11
E9QJS1	Tyk2	9	12	14	0.01	0.01	8
Q9R117	Tyk2	9	12	14	0.01	0.01	8
Q6NV83	U2surp	27	34	36	6	14	30
Q6NV83	U2surp	27	34	36	6	14	30
Q6NV83	U2surp	0.01	33	35	6	0.01	0.01
Q811S7	Ubp1	13	17	19	2	4	14
Q9EPU0	Upf1	16	27	22	0.01	0.01	17
Q9EPU0	Upf1	16	27	22	0.01	0.01	17
Q571H0	Urb1	45	53	72	3	13	55
E9Q7L1	Urb2	17	28	34	6	14	29
Q3TIX9	Usp39	13	18	17	1	3	12

Q9CZJ1	Utp11	13	8	13	0.01	5	10
Q640M1	Utp14a	18	22	24	1	8	25
Q9QXS1	Plec	0.01	197	202	44	62	193
Q8C7V3	Utp15	19	20	24	4	8	17
Q5SSI6	Utp18	14	14	14	0.01	7	14
Q5XG71	Utp20	48	56	72	2	16	61
E9QK83	Utp20	48	56	72	2	16	61
E9Q6R7	Utrn	121	139	150	25	60	128
A0A1W2P8A5	Utrn	0.01	28	31	0.01	0.01	26
Q01853	Vcp	14	17	23	1	4	14
E9PZY8	Virma	9	19	26	0.01	0.01	17
A2AIV2	Virma	9	19	26	0.01	0.01	17
Q923D5	Wbp11	4	6	17	0.01	2	6
Q8C0T5	Sipa1l1	0.01	25	0.01	0.01	3	0.01
Q8BHB4	Wdr3	16	18	24	4	8	21
Q8K4P0	Wdr33	5	15	21	0.01	4	13
Q3TA68	Wdr36	20	28	29	6	11	24
Q3TAQ9	Wdr36	20	28	29	6	11	24
Q6ZQL4	Wdr43	13	18	20	0.01	6	16
Q9Z0H1	Wdr46	12	13	12	0.01	4	13
F6R6A4	Svil	0.01	0.01	45	0.01	19	0.01
Q3U821	Wdr75	14	16	25	3	6	20
Q9DCD2	Xab2	17	22	27	0.01	7	22
P27641	Xrcc5	15	19	21	1	3	18
P23475	Xrcc6	15	14	17	1	6	17
A0A0R4J187	Xrcc6	15	14	17	1	6	17
Q9DBR1	Xrn2	6	11	16	0.01	0.01	7
Q9DBR1	Xrn2	6	11	16	0.01	0.01	7
D3YWX2	Ylpm1	19	33	45	0.01	6	27
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
P62259	Ywhae	10	16	11	0.01	0.01	8
Q8K0L9	Zbtb20	13	20	20	0.01	3	15
O88990	Actn3	0.01	17	14	0.01	0.01	0.01
Q8K0L9	Zbtb20	13	20	20	0.01	3	15
O88939	Zbtb7a	11	13	13	3	4	11
E9Q784	Zc3h13	4	19	24	0.01	0.01	14
Q8BJ05	Zc3h14	12	21	24	0.01	5	15
Q0P678	Zc3h18	19	25	28	8	12	25
G3X8T2	Zc3h18	19	25	28	8	12	25
Q9CYA6	Zcchc8	9	11	15	0.01	2	8
E9Q7Q3	Tpm3	0.01	24	27	0.01	0.01	0.01
A0A0R4J098	Zfp326	25	26	30	6	11	27

E9Q175	Myo6	0.01	50	57	11	20	49
Q8C827	Zfp62	14	23	0.01	0.01	6	0.01
Q8C827	Zfp62	14	23	23	0.01	6	19
Q8C827	Zfp62	14	23	23	0.01	6	19
E9QML5	Zfp638	18	45	55	0.01	10	35
A0A0N4SV80	Zfp638	18	45	0.01	0.01	10	35
Q9CZP3	Zfp655	10	12	13	0.01	2	11
O88532	Zfr	11	19	21	0.01	0.01	12
P70121	Zhx1	2	12	11	0.01	0.01	3
Q8C0C0	Zhx2	1	15	16	0.01	1	8
A0A0A0MQD5	Shank3	0.01	11	15	0.01	0.01	4
A0A0R4J1L3	Zkscan3	16	19	22	5	9	23
Q91VW9	Zkscan3	16	19	22	5	9	23
A3KGU9	Sptan1	0.01	0.01	176	60	83	0.01
A2A482	Zmynd8	11	0.01	23	0.01	3	0.01
A2A484	Zmynd8	11	0.01	23	0.01	3	0.01
A2A483	Zmynd8	11	17	23	0.01	3	16
Q3UH28	Zmynd8	11	17	23	0.01	3	16
E9Q8D1	Zmynd8	11	17	23	0.01	3	16
Q3U1M7	Zmynd8	11	17	23	0.01	3	16
Q61624	Znf148	4	12	18	0.01	4	9
A0A0U1RP81	Immt	0.01	26	0.01	0.01	0.01	0.01
Q9QXS1	Plec	0.01	197	202	44	62	193
Q9ERU3	Znf22	11	8	10	0.01	0.01	7
Q91VN1	Znf24	9	12	11	0.01	3	9
O88291	Znf326	25	26	30	6	11	27
Q69Z99	Znf512	16	16	16	0.01	6	17
Q8BHZ4	Znf592	7	16	19	0.01	3	18
Q9QXS1	Plec	0.01	197	202	44	62	193
Q9QXS1	Plec	0.01	197	202	44	62	193

Table 2. A list of the 636 XAB2-bound proteins identified in P15 livers shared across the three bXAB2 biological replicates compared to BirA control livers.

Access. no	Symbol	bXab UP1	bXab_UP3	bXab_UP2	BirA UP1	BirA UP3	BirA UP2
Q9QXS1	Actn4	188	197	202	44	62	193
Q5YD48	A1cf	8	8	16	1	0.01	6
O35452	Tnxb	116	130	137	30	58	124
Q68FG2	Sptbn2	103	111	118	31	49	101
E9PZ16	Hspg2	97	115	115	27	44	105
E9QP46	Syne2	97	187	235	6	38	154
F6XCT0	Macf1	40	48	44	0.01	0.01	0.01
Q921L6	Cttn	23	24	27	0.01	0.01	0.01
A0A0R4J0V1	Ints10	8	10	11	0.01	0.01	0.01
E9Q360	Ints10	8	10	11	0.01	0.01	0.01
A2A9P6	Cdk11b	7	10	9	0.01	0.01	0.01
Q9JKX4	Aatf	6	10	14	0.01	0.01	7
E9PWQ3	Col6a3	60	67	66	34	26	52
A0A087WR50	Fn1	59	72	74	23	32	64
Q3UHL6	Fn1	59	72	74	23	32	64
B7ZNH7	Col14a1	57	63	71	33	46	62
A0A1D5RLS1	Eps15l1	4	8	8	0.01	0.01	0.01
D3Z315	Cope	6	7	6	0.01	0.01	0.01
E9PVU0	Myo6	49	50	57	11	20	49
F6RJ39	Acin1	25	33	43	6	20	33
Q5SYD0	Myo1d	47	55	55	16	26	51
Q80YX1	Tnc	44	51	54	16	15	48
Q8R2S9	Actr8	20	24	23	2	10	19
Q9QYC0	Add1	14	21	23	3	5	17
Q9Z103	Adnp	8	16	21	0.01	0.01	13
Q9QZQ1	Afdn	40	53	59	5	9	0.01
Q9QZQ1	Afdn	40	53	59	5	9	46
Q8CJF7	Ahctf1	32	59	61	5	15	48
P53995	Anapc1	19	31	41	0.01	8	27
Q91W96	Anapc4	14	13	18	0.01	2	14
O35488	Slc27a2	34	32	35	28	22	31
Q8BTZ4	Anapc5	9	13	17	0.01	4	10
Q8BTZ4	Anapc5	9	13	17	0.01	4	10
Q9WVM3	Anapc7	17	17	23	0.01	6	16
A0A0R4J1N7	Ank1	11	20	21	0.01	0.01	9
Q8C8R3	Ank2	11	25	28	0.01	0.01	14
P26231	Ctnna1	30	41	42	19	19	36
P97449	Anpep	5	10	15	0.01	0.01	10
Q8CFQ3	Aqr	32	40	39	1	14	29
A2AQA7	Aqr	32	40	39	1	14	29

E9Q7E2	Arid2	13	20	17	0.01	0.01	9
Q9WTL8	Arntl	7	7	12	0.01	0.01	5
Q9WTL8	Arntl	7	7	12	0.01	0.01	5
Q8BI84	Mia3	26	54	40	0.01	4	19
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
P98203	Arvcf	19	23	23	0.01	3	17
Q80YQ1	Thbs1	25	34	35	6	11	31
A0A1L1STC6	Syne1	25	70	77	0.01	2	40
Q9EP89	Lactb	25	24	26	10	12	22
Q3U741	Ddx17	24	28	30	13	17	25
E9PZJ8	Ascc3	13	18	14	0.01	0.01	10
Q925I1	Atad3	32	32	29	10	12	24
M0QWP1	Agrn	22	40	43	3	3	39
P56480	Atp5b	19	19	21	14	11	16
A2AS05	Helz2	21	12	11	0.01	0.01	3
A2AS03	Helz2	21	12	11	0.01	0.01	3
G3X973	Stab1	21	21	24	0.01	0.01	18
A2AKD7	Snta1	5	8	8	0.01	0.01	2
Q03265	Atp5a1	20	20	21	15	12	15
Q8R4H2	Arhgef12	11	15	14	0.01	0.01	4
F8VQN6	Arhgef12	11	15	14	0.01	0.01	4
P08032	Spta1	17	13	13	0.01	0.01	5
Q8K019	Bclaf1	9	25	27	0.01	5	19
Q8K019	Bclaf1	9	25	27	0.01	5	19
Q3TL44	Nlrx1	9	12	12	1	0.01	3
Q8CCJ3	Ufl1	8	11	9	0.01	0.01	3
Q99JY9	Actr3	19	19	21	10	10	17
Q6PAL0	Bend3	25	29	34	0.01	8	29
P35441	Thbs1	24	33	35	6	10	0.01
Q6PGF5	Bms1	17	19	23	0.01	2	19
Q921S7	Mrpl37	8	11	8	0.01	0.01	4
E9Q6A7	Bptf	19	36	39	0.01	3	23
E9QQ10	Akap9	7	12	10	0.01	0.01	4
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
Q8C5W0	Clmn	10	12	9	0.01	0.01	5
E9Q397	Sptb	27	24	20	0.01	0.01	11
O35646	Capn6	11	12	19	3	5	13
Q9CVB6	Arpc2	16	21	19	10	8	15
E9Q2E4	Hectd4	16	19	18	0.01	0.01	9
Q8CH18	Ccar1	14	22	32	0.01	4	14
Q8VDP4	Ccar2	15	18	18	0.01	2	12

Q5SV80	Myo19	6	9	8	0.01	0.01	4
P82198	Tgfbi	15	18	18	9	7	13
A0A1D5RLQ9	Cdc42bpa	12	21	18	0.01	0.01	8
D3YYN8	Cdc42bpa	12	21	18	0.01	0.01	8
A2A6Q5	Cdc27	9	14	17	1	4	9
H7BX44	Cdc42bpa	12	21	18	0.01	0.01	8
E9PVY0	Cdc42bpa	12	21	18	0.01	0.01	8
P61161	Actr2	15	15	18	6	9	14
Q3UU96	Cdc42bpa	12	21	18	0.01	0.01	8
Q80TN4	Dnajc16	7	13	19	0.01	0.01	7
J3JS23	Zfp62	14	23	23	0.01	6	19
A2A6Q5	Cdc27	9	14	17	1	4	9
Q9DC48	Cdc40	23	26	26	0.01	6	21
S4R1B9	Taf1	14	30	30	0.01	6	17
Q6A068	Cdc5l	26	31	37	5	12	27
B1Q2W7	Taf1	14	30	30	0.01	6	17
P24788	Cdk11b	7	10	9	0.01	0.01	0.01
E9Q3L2	Pi4ka	6	8	9	0.01	0.01	4
A0A140T8I9	Pi4ka	6	8	9	0.01	0.01	4
A2AWT5	Ubtf	14	24	28	4	8	20
A2ADB1	Spen	13	26	35	0.01	2	26
P68368	Tuba4a	13	13	14	0.01	0.01	10
O35218	Cpsf2	13	22	29	1	5	19
A0A0A0MQA5	Tuba4a	13	13	14	0.01	0.01	10
Q9CRB9	Chchd3	13	16	15	8	6	11
P40201	Chd1	24	36	39	0.01	8	29
Q920A7	Afg3l1	6	11	14	0.01	0.01	5
Q5SUH7	Clint1	9	14	11	0.01	0.01	7
Q6PDQ2	Chd4	40	56	60	4	16	50
E9QAS5	Chd4	40	56	60	4	16	50
E9QAS4	Chd4	40	56	60	4	16	50
A2AJK6	Chd7	13	29	33	0.01	0.01	21
F8WHU7	Stag1	12	23	26	0.01	4	9
Q8CGZ0	Cherp	14	18	20	0.01	4	14
A0A1D5RL92	Cherp	14	18	20	0.01	4	14
Q8C147	Dock8	12	23	22	0.01	0.01	11
Q5SUH6	Clint1	9	14	11	0.01	0.01	7
B1AYU7	Cwc22	16	17	21	0.01	0.01	12
E9QMQ3	Triobp	8	16	14	0.01	0.01	9
G5E8J2	Ank1	11	20	21	0.01	0.01	9
G8JL84	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q8R1B4	Eif3c	9	17	13	1	0.01	7
A0A1W2P711	Mia2	11	25	16	0.01	0.01	6

B7ZW98	Ank1	11	20	21	0.01	0.01	9
E9QNT8	Ank1	11	20	21	0.01	0.01	9
Q91ZV0	Mia2	11	25	16	0.01	0.01	6
D3YTV8	Ank1	11	20	21	0.01	0.01	9
Q0VGY9	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q8C196	Cps1	37	32	28	18	10	18
Q9R0Q6	Arpc1a	11	9	13	6	0.01	8
Q9EPU4	Cpsf1	27	39	49	0.01	11	34
S4R2F3	Ank2	11	25	28	0.01	0.01	14
Q9QXK7	Cpsf3	13	17	23	0.01	7	13
Q02357	Ank1	11	20	21	0.01	0.01	9
E9PUM4	Tln2	31	41	48	0.01	0.01	26
A0A1L1SQ51	Tln2	31	41	48	0.01	0.01	26
Q02357	Ank1	11	20	21	0.01	0.01	9
D3Z5M4	Ank1	11	20	21	0.01	0.01	9
Q02357	Ank1	11	20	21	0.01	0.01	9
Q71LX4	Tln2	30	41	47	0.01	0.01	26
Q8BG67	Efr3a	7	9	11	0.01	0.01	6
Q8BG67	Efr3a	7	9	11	0.01	0.01	6
A0A1D5RLL3	Efr3a	7	9	11	0.01	0.01	6
Q3TXE3	Tyk2	9	12	14	0.01	0.01	8
Q8CIZ8	Vwf	19	20	25	2	0.01	13
E9QPU1	Vwf	19	20	25	2	0.01	13
Q8VE19	Mios	14	17	16	0.01	0.01	10
A0A0R4J1W7	Cdc23	10	19	24	4	6	14
P63154	Crnkl1	19	23	25	0.01	12	16
A0A140LI54	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
Q3TRM4	Pnpla6	14	17	21	0.01	2	12
A0A0A0MQ73	Kmt2d	9	11	15	0.01	0.01	8
Q8BGZ4	Cdc23	10	19	24	4	6	14
Q02248	Ctnnb1	24	27	29	7	12	23
P30999	Ctnnd1	36	41	42	12	18	35
P30999	Ctnnd1	36	42	43	0.01	0.01	35
A2AS45	Pkp4	13	17	16	0.01	0.01	10
Q62018	Ctr9	31	36	43	2	15	32
Q8C5N3	Cwc22	16	17	21	0.01	0.01	12
Q8C5N3	Cwc22	16	17	21	0.01	0.01	12
Q9JHU4	Dync1h1	58	84	65	2	6	45
P49222	Epb42	10	14	17	0.01	0.01	11
Q6PAC3	Dcaf13	10	11	13	0.01	0.01	7

E0CYM1	Filip1l	9	20	20	0.01	1	16
H3BK65	Eps15	8	11	12	0.01	0.01	7
Q5JC28	Eps15	8	11	12	0.01	0.01	7
P42567	Eps15	8	11	12	0.01	0.01	7
Q3U1J4	Ddb1	10	14	9	0.01	0.01	4
Q91VR5	Ddx1	13	17	17	0.01	0.01	13
A7TU71	Shroom2	13	24	29	0.01	0.01	18
Q80Y44	Ddx10	8	20	23	0.01	4	17
A2ALU4	Shroom2	13	24	29	0.01	0.01	18
Q501J6	Ddx17	24	28	30	13	17	25
Q9JIK5	Ddx21	23	26	33	0.01	7	27
D3Z0M9	Ddx23	26	33	36	0.01	6	32
Q62167	Ddx3x	30	31	34	10	16	30
Q810A7	Ddx42	6	9	10	0.01	0.01	6
Q569Z5	Ddx46	5	11	12	0.01	0.01	5
E0CYH7	Filip1l	9	20	20	0.01	1	16
Q5F2E8	Taok1	12	11	11	0.01	0.01	7
P31001	Des	32	32	36	19	17	30
O35286	Dhx15	28	33	36	8	20	29
O55111	Dsg2	8	15	13	3	0.01	8
A2ACQ1	Dhx35	10	15	17	0.01	2	10
Q8C8Z9	Dtnb	10	13	13	0.01	2	7
O70585	Dtnb	10	13	13	0.01	2	7
A2A4P0	Dhx8	19	20	29	0.01	4	16
A0A087WPL5	Dhx9	50	53	62	26	0.01	0.01
Q8C6K9	Col6a6	8	11	8	2	0.01	4
Q91X77	Cyp2c50	8	8	4	0.01	0.01	0.01
Q811D0	Dlg1	11	16	13	2	2	8
Q811D0	Dlg1	11	15	13	2	2	8
Q3UNN4	Smarcc1	8	17	16	3	0.01	10
P11531	Dmd	13	23	23	0.01	4	13
P63037	Dnaja1	10	9	14	1	2	7
H3BLH0	Smarca2	29	34	35	0.01	0.01	25
E9Q6A6	Col6a6	8	11	8	2	0.01	4
Q7TT50	Cdc42bpb	40	48	42	3	5	30
A0A0G2JDM7	Anapc5	9	13	17	0.01	4	10
A0A0G2JE03	Anapc5	9	13	17	0.01	4	10
J3KMH5	Mia3	8	22	17	0.01	0.01	0.01
Q3TWF7	Anapc5	9	13	17	0.01	4	10
B2LVG5	Cpsf4	7	10	11	0.01	1	7
G5E8K2	Ank3	7	19	23	0.01	3	13
G5E8K5	Ank3	7	19	23	0.01	3	13
A0A0R4J2B6	Rbbp5	7	13	12	1	2	5
G5E8K5	Ank3	7	19	23	0.01	3	13

K3W4P2	Ints1	8	12	19	0.01	0.01	12
A0A0G2JH17	Ints1	8	12	19	0.01	0.01	12
G5E8K5	Ank3	7	19	23	0.01	3	13
O08810	Eftud2	33	44	45	18	23	36
P23116	Eif3a	19	29	24	0.01	4	14
D3Z7I0	Gtf3c2	14	21	21	0.01	2	15
P60229	Eif3e	6	11	10	0.01	0.01	5
Q8QZY1	Eif3l	8	9	11	0.01	0.01	5
G5E8K3	Ank3	7	19	23	0.01	3	13
Q8BYC6	Taok3	11	12	13	2	0.01	9
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q8CHI8	Ep400	4	10	13	0.01	0.01	8
Q66JV4	Rbm12b2	20	23	32	0.01	0.01	23
O70318	Epb41l2	22	34	31	0.01	3	23
Q8R0W0	Eppk1	16	22	18	0.01	4	14
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
Q60902	Eps15l1	4	8	8	0.01	0.01	0.01
A0A1W2P812	Ank3	7	19	23	0.01	3	13
Q3V1V3	Esf1	9	14	14	0.01	4	10
Q0KL02	Trio	19	21	28	0.01	3	17
Q0KL02	Trio	19	21	28	0.01	3	17
S4R2K9	Ank3	7	19	23	0.01	3	13
P56960	Exosc10	18	20	22	1	3	18
Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q9Z1T2	Thbs4	12	12	15	0.01	2	11
Q69ZR9	Fam208a	27	44	54	0.01	10	44
P48725	Pcnt	6	12	11	0.01	0.01	5
A0A1L1SQR4	Dock6	30	40	48	0.01	0.01	35
Q7TPD1	Fbxo11	6	9	7	0.01	3	0.01
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q8CGB6	Tns2	17	27	37	0.01	5	24
Q6P6L0	Filip1l	9	20	20	0.01	1	16
Q6P6L0	Filip1l	9	20	20	0.01	1	16
Q8BTM8	Flna	83	94	97	13	37	84
B7FAU9	Flna	83	94	97	13	37	84
Q80X90	Flnb	74	88	82	4	20	73
D3YUX2	Mpdz	6	26	27	0.01	0.01	15
Q80U35	Arhgef17	6	13	20	0.01	2	14

Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q91Z49	Fyttd1	11	16	20	5	7	14
Q9R1K5	Fzr1	5	9	11	0.01	0.01	6
F8VPV0	Pcnt	6	12	11	0.01	0.01	5
Q4VAA7	Snx33	6	11	10	0.01	0.01	5
P26039	Tln1	36	50	51	3	5	40
A0A1W2P737	Pcnt	6	12	11	0.01	0.01	5
Q8VBX6	Mpdz	6	26	27	0.01	0.01	15
Q8R322	Gle1	9	16	22	0.01	0.01	16
D3YYT1	Glyr1	11	17	21	6	8	15
A2AWL7	Mga	5	12	21	0.01	2	14
Q8CI11	Gnl3	14	18	17	1	6	12
G5E8T6	Magi3	11	12	16	0.01	0.01	12
F6SMY7	Mycbp2	52	74	75	0.01	5	61
A0A087WP63	Gm42715	5	12	11	0.01	0.01	6
Q80X80	C2cd2l	11	15	15	3	2	9
Q99MI1	Erc1	5	16	13	0.01	0.01	6
Q6P5H2	Nes	24	34	40	0.01	0.01	34
Q8K284	Gtf3c1	46	64	65	0.01	10	49
Q3TMP1	Gtf3c3	20	25	25	6	6	21
Q8BMQ2	Gtf3c4	26	36	38	3	9	29
Q8R2T8	Gtf3c5	13	17	17	2	7	11
Q2PFD7	Psd3	5	11	10	0.01	1	3
Q8R2T8	Gtf3c5	13	17	17	2	7	11
V9GXP8	Erc1	5	16	13	0.01	0.01	6
G3X922	Dnajc13	35	51	51	0.01	6	41
Q2PFD7	Psd3	5	11	10	0.01	1	3
A0A0R4J0J8	Specc1l	20	28	33	1	5	24
Q2KN98	Specc1l	20	28	33	1	5	24
A2AWL7	Mga	5	12	21	0.01	2	14
E9QLG3	Mga	5	12	21	0.01	2	14
G3X9B1	Heatr1	39	43	54	5	19	49
E9QAM5	Helz2	21	12	11	0.01	0.01	3
Q9R1Y5	Hic1	7	14	19	0.01	4	12
Z4YJP0	Hic1	7	14	19	0.01	4	12
F8VPM7	Erc1	5	16	13	0.01	0.01	6
A0A1D5RM59	Tns1	26	37	39	0.01	3	32
A0A087WQS0	Tns1	26	37	39	0.01	3	32
E9Q0S6	Tns1	26	37	39	0.01	3	32
V9GXF0	Erc1	5	15	13	0.01	0.01	0.01
V9GXH3	Erc1	5	15	13	0.01	0.01	0.01
Q2PFD7	Psd3	5	11	10	0.01	1	3
Q8BJA3	Hmbox1	9	12	17	0.01	7	11
H3BKM3	Hmbox1	9	12	17	0.01	7	11

H3BKF8	Hmbox1	9	12	17	0.01	7	11
E9PUQ5	Golga2	16	25	21	4	4	13
E9Q0A3	Arhgef11	11	20	22	0.01	2	17
Q9Z204	Hnrnpc	23	26	28	12	14	24
Q9Z204	Hnrnpc	23	26	28	12	14	24
P15116	Cdh2	9	12	12	3	2	8
D3YYT0	Cdh2	9	12	12	3	2	8
P14873	Map1b	4	15	14	0.01	0.01	9
P70333	Hnrnph2	12	12	14	0.01	4	9
E9PVP1	Crybg1	15	20	22	0.01	3	15
A0A0G2JG52	Crybg1	15	20	22	0.01	3	15
G5E924	Hnrnpl	12	16	22	2	2	13
Q8VHM5	Hnrnpr	11	10	14	0.01	0.01	9
Q00PI9	Hnrnpul2	43	42	48	24	22	41
Z4YKB8	Hp1bp3	21	20	21	13	9	17
Q3TEA8	Hp1bp3	21	20	21	13	9	17
P20029	Hspa5	27	33	34	15	15	29
Q9Z1M8	Ik	13	25	31	4	9	18
D3YU58	Anapc7	17	17	23	0.01	6	16
Q9Z1X4	Ilf3	30	36	40	8	11	33
Q9Z1X4	Ilf3	30	36	40	8	11	33
G5E8I8	Cherp	14	18	20	0.01	4	14
Q6ZPV2	Ino80	23	31	44	2	11	30
Q6ZPV2	Ino80	23	31	44	2	11	30
Q6P4S8	Ints1	8	12	19	0.01	0.01	12
Q3UQ44	Iqgap2	42	50	47	5	10	39
E9Q9B7	Kidins220	4	12	11	0.01	1	7
S4R1P5	Dst	4	14	19	0.01	0.01	7
Q8BZQ7	Anapc2	11	18	18	0.01	3	14
Q9JKF1	Iqgap1	20	27	28	0.01	4	19
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
P11881	Itpr1	40	44	47	7	8	30
Q9Z329	Itpr2	65	67	78	14	23	65
P70227	Itpr3	13	19	17	0.01	0.01	10
Q8C1D8	Iws1	12	13	16	0.01	4	12
Q6NZF1	Zc3h11a	4	16	21	0.01	4	13
A2AQD5	Ssfa2	17	22	22	2	2	17
A0A1Y7VMH7	Kidins220	4	12	11	0.01	1	7

A3KG93	Kdm1a	6	9	12	0.01	0.01	7
Q6ZQ88	Kdm1a	6	9	12	0.01	0.01	7
A0A1Y7VME9	Kidins220	4	12	11	0.01	1	7
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
A2AAE1	Kiaa1109	21	37	37	0.01	4	22
Q6PDK2	Kmt2d	9	11	15	0.01	0.01	8
Q80YR9	Rbm12b1	24	28	33	2	6	27
Q99L88	Sntb1	19	22	24	4	5	17
Q68FD5	Cltc	39	38	35	8	8	28
Q5SXR6	Cltc	39	38	35	8	8	28
Q6P5B5	Fxr2	20	17	23	2	4	19
E9PU96	Urb1	45	53	72	3	13	55
G5E8G6	Myo5b	54	54	64	3	10	51
P21271	Myo5b	54	54	64	3	10	51
Q5XJE5	Leo1	12	16	22	3	7	13
Q8BH80	Vapb	12	12	12	4	3	8
Q9QY76	Vapb	12	12	12	4	3	8
P48678	Lmna	54	49	52	30	35	48
Q61586	Gpam	21	22	24	6	4	19
O88322	Nid2	25	33	35	3	8	28
Q91ZX7	Lrp1	44	57	55	3	4	36
A0A0R4J0I9	Lrp1	44	57	55	3	4	36
Q8BWT1	Acaa2	14	17	15	6	4	11
Q6RHR9	Magi1	7	15	15	0.01	0.01	11
Q60847	Col12a1	55	50	53	4	12	46
E9PX70	Col12a1	55	50	53	4	12	46
Q6RHR9	Magi1	7	15	15	0.01	0.01	0.01
Q60847	Col12a1	55	50	53	4	12	46
Q60847	Col12a1	55	50	53	4	12	46
A0A0N4SUZ0	Magi1	7	15	15	0.01	0.01	0.01
Q9EQJ9	Magi3	11	12	16	0.01	0.01	12
Q8K310	Matr3	48	48	55	16	17	49
Q91VS8	Farp2	19	23	23	2	5	19
J3QMC5	Mdn1	7	29	40	0.01	0.01	16
A2ANY6	Mdn1	7	29	40	0.01	0.01	16
F7BGR7	Gm21992	11	14	19	0.01	3	14
C0HKD8	Mfap1a	11	16	18	1	5	12
C0HKD9	Mfap1b	11	16	18	1	5	12
H7BX50	Mga	5	12	21	0.01	2	14
Q8BML1	Mical2	7	14	18	0.01	0.01	13
D3Z598	Ltbp4	29	36	40	2	11	35
Q8K4G1	Ltbp4	29	36	40	2	11	35

A0A087WSN6	Fn1	57	69	71	23	0.01	62
B9EHT6	Fn1	57	69	71	23	0.01	62
Q810V0	Mphosph10	9	7	12	0.01	0.01	8
Q3TYA6	Mphosph8	7	13	17	0.01	5	12
P11247	Mpo	6	12	16	0.01	2	9
Q9JMH9	Myo18a	76	86	86	13	23	71
Q9JMH9	Myo18a	76	86	86	13	23	71
P46978	Stt3a	16	12	15	5	4	8
Q9R190	Mta2	16	28	27	2	8	21
Q924K8	Mta3	4	16	13	0.01	4	9
Q3UII8	Mta3	4	16	13	0.01	4	9
Q80WJ7	Mtdh	19	21	25	3	8	20
A0A0U1RNK7	Dock7	36	50	51	6	10	44
F8VQB6	Myo10	12	13	22	0.01	0.01	17
Q8R1A4	Dock7	36	50	51	6	10	44
A2A9M5	Dock7	36	50	51	6	10	44
E9PX48	Dock7	36	50	51	6	10	44
Q8R1A4	Dock7	36	50	51	6	10	44
A2A9M4	Dock7	36	50	51	6	10	44
Q5SWZ5	Mprip	77	80	82	0.01	25	78
F8WHL2	Copa	31	43	37	7	11	29
Q8CIE6	Copa	31	43	37	7	11	29
Q8BPM0	Daam1	16	16	16	7	3	12
Q8BPM0	Daam1	16	16	16	7	3	12
Q62383	Supt6h	46	54	61	4	15	47
P09405	Ncl	17	22	21	4	11	17
A2AL85	Asph	14	19	18	6	5	14
Q8BSY0	Asph	14	19	18	6	5	14
Q6PIJ4	Nfrkb	14	33	34	5	11	27
Q8BY02	Nkrf	9	10	18	0.01	2	13
H9KV00	Son	39	53	58	2	19	49
Q6DFW4	Nop58	16	22	24	4	10	19
Q9D6T0	Nosip	4	10	12	0.01	0.01	5
E9Q7G0	Numa1	65	102	107	31	68	97
F6ZQA3	Numa1	18	32	36	0.01	23	32
Q8BH74	Nup107	34	36	39	9	14	34
Q8R0G9	Nup133	30	32	38	8	13	29
E9Q3G8	Nup153	13	22	26	3	10	19
Q9Z0W3	Nup160	34	38	46	8	14	38
A0A0J9YUD5	Nup205	29	26	37	2	5	32
B9EJ54	Nup205	29	26	37	2	5	32
Q9QY81	Nup210	14	17	21	3	4	15
A0A0R4J1I6	Nup210	14	17	21	3	4	15
Q9JIH2	Nup50	6	16	15	0.01	2	8

A0A1B0GSX7	Nup98	38	50	52	8	14	37
Q8CIC2	Nupl2	9	9	12	0.01	0.01	8
E9QL43	Nupl2	9	9	12	0.01	0.01	8
Q61235	Sntb2	22	26	26	4	10	21
A0A0R4J150	Osbpl8	6	11	10	0.01	0.01	6
B9EJ86	Osbpl8	6	12	10	0.01	0.01	6
Q8K2T8	Paf1	18	22	26	3	10	21
Q63ZW7	Patj	28	31	41	2	5	28
P58501	Paxbp1	19	27	30	0.01	3	18
P49586	Pcyt1a	7	9	9	0.01	0.01	5
Q6NS46	Pdcd11	28	38	49	0.01	11	39
Q3TJD7	Pdlim7	9	14	15	0.01	3	9
Q4VA53	Pds5b	14	15	19	0.01	4	14
Q9QY23	Pkp3	6	14	14	0.01	0.01	10
Q9QY23	Pkp3	6	14	14	0.01	0.01	10
Q68FH0	Pkp4	13	17	16	0.01	0.01	10
E9Q6H8	Plekha5	20	29	25	3	2	19
Q8VCQ8	Cald1	24	31	33	4	10	25
Q922V4	Plrg1	20	24	26	3	10	20
Q60953	Pml	20	30	29	10	12	22
Q99KG5	Lsr	17	16	18	5	4	14
Q3TUQ5	Pnn	22	27	30	4	11	24
O35691	Pnn	22	27	30	4	11	24
A2AJ88	Pnpla7	7	14	13	0.01	0.01	7
A2AJ88	Pnpla7	7	14	13	0.01	0.01	7
O35134	Polr1a	6	17	19	0.01	0.01	7
P70700	Polr1b	5	12	10	0.01	0.01	3
P08775	Polr2a	34	50	54	4	15	40
A0A0R4J0V5	Polr2a	34	50	54	4	15	40
Q8CFI7	Polr2b	26	38	35	5	11	30
Q9QZH3	Ppie	10	12	12	0.01	3	6
Q5FWX6	Prkd3	5	8	11	0.01	0.01	4
Q8K1Y2	Prkd3	5	8	11	0.01	0.01	4
Q99KP6	Prpf19	10	15	16	2	6	12
Q922U1	Prpf3	18	23	26	3	14	20
Q8CCF0	Prpf31	11	12	15	2	4	11
Q9DAW6	Prpf4	18	20	26	4	12	19
Q9R1C7	Prpf40a	20	23	34	3	6	24
Q61136	Prpf4b	8	15	23	0.01	3	12
Q91YR7	Prpf6	29	42	42	14	19	33
Q99PV0	Prpf8	92	109	117	32	53	94
Q14C51	Ptcd3	9	9	9	0.01	0.01	5
Q3UEB3	Puf60	12	11	15	0.01	4	10
Q3UEB3	Puf60	12	11	15	0.01	4	10

Q61550	Rad21	12	20	20	1	4	14
Q8C570	Rae1	11	11	15	1	2	10
Q9EP71	Rai14	43	47	52	9	18	44
Q64012	Raly	20	23	25	10	11	20
Q9ERU9	Ranbp2	52	84	95	12	28	74
Q8BX09	Rbbp5	7	13	12	1	2	5
Q99KG3	Rbm10	23	27	32	2	11	26
Q8C2Q3	Rbm14	21	27	32	10	16	26
Q0VBL3	Rbm15	14	14	19	2	7	13
B2RY56	Rbm25	22	28	33	6	10	26
Q8VH51	Rbm39	11	15	18	3	6	14
Q8VH51	Rbm39	11	15	18	3	6	14
Q91YE7	Rbm5	17	25	29	5	8	24
Q91YE7	Rbm5	17	25	29	5	8	24
S4R1W5	Rbm6	19	24	30	2	9	25
Q9CQT2	Rbm7	8	11	11	0.01	0.01	7
Q9WV02	Rbmx	16	19	24	11	11	18
Q91VM5	Rbmxl1	18	19	26	11	10	19
Q6PR54	Rif1	9	20	27	0.01	4	21
Q6PR54	Rif1	9	20	27	0.01	4	21
Q6PR54	Rif1	9	20	27	0.01	4	21
Q3UJU9	Rmdn3	12	16	14	4	3	10
P27659	Rpl3	28	29	29	10	15	24
Q9D8E6	Rpl4	34	37	40	9	14	34
P47911	Rpl6	21	24	30	11	12	23
P12970	Rpl7a	23	25	27	11	13	23
Q6P5B0	Rrp12	14	22	30	2	3	22
Q99LF4	Rtcb	12	14	19	0.01	1	10
P60122	Ruvbl1	21	21	26	8	11	21
Q9WTM5	Ruvbl2	30	30	33	14	21	29
D3YXK2	Safb	28	33	39	5	16	29
Q80YR5	Safb2	40	47	53	9	21	44
Q9ER74	Sall1	5	13	19	0.01	1	10
Q6P5E3	Sall1	5	13	19	0.01	1	10
Q9Z315	Sart1	40	48	51	11	21	44
E9PZM7	Scaf11	14	24	26	0.01	5	20
Q80U72	Scrib	24	34	33	2	4	27
Q9EP97	Senp3	5	10	13	0.01	2	7
E9Q5F9	Setd2	6	21	33	0.01	0.01	15
E9Q5F9	Setd2	6	21	33	0.01	0.01	15
Q9D554	Sf3a3	14	18	19	2	7	12
Q99NB9	Sf3b1	48	55	58	17	30	53
G5E866	Sf3b1	48	55	58	17	30	53
Q3UJB0	Sf3b2	31	37	38	10	19	32

Q921M3	Sf3b3	36	42	47	15	24	40
Q3USH5	Sfswap	5	19	22	0.01	3	14
Q60520	Sin3a	12	27	22	0.01	3	17
Q60520	Sin3a	12	27	22	0.01	3	17
Q62141	Sin3b	6	10	10	0.01	0.01	0.01
Q62141	Sin3b	6	10	10	0.01	0.01	6
Q9CZU3	Skiv2l2	29	33	36	2	9	26
Q8CH25	Sltm	20	28	34	0.01	9	25
Q8BHJ9	Slu7	12	15	18	0.01	0.01	12
Q6DIC0	Smarca2	29	34	35	0.01	0.01	25
F2Z4A9	Smarca2	29	34	35	0.01	0.01	25
A0A0R4J170	Smarca4	23	29	28	2	7	21
Q3TKT4	Smarca4	23	29	28	2	7	21
Q3TKT4	Smarca4	23	29	28	2	7	21
P97496	Smarcc1	8	17	16	3	0.01	10
P97496	Smarcc1	8	17	16	3	0.01	10
Q99JR8	Smarcd2	9	17	16	0.01	0.01	7
Q99JR8	Smarcd2	9	17	16	0.01	0.01	7
O54941	Smarce1	9	13	13	2	4	8
Q9CU62	Smc1a	41	57	58	9	25	52
Q9CW03	Smc3	41	49	53	9	19	41
Q3UKJ7	Smu1	11	16	19	2	6	12
Q6P4T2	Snrnp200	69	90	103	30	50	91
Q6PE01	Snrnp40	9	14	16	2	4	10
A0A0B4J1E2	Snw1	18	25	24	4	8	19
A2ADB0	Spen	13	26	35	0.01	2	26
Q62261	Sptbn1	123	136	140	44	71	131
A0A087WNL7	Srcap	5	12	11	0.01	0.01	6
A0A087WQ44	Srcap	5	12	11	0.01	0.01	6
A0A087WNX7	Srcap	5	12	11	0.01	0.01	6
Q922B9	Ssfa2	17	22	22	2	2	17
Q9D3E6	Stag1	12	23	26	0.01	4	9
O35638	Stag2	14	21	18	0.01	0.01	11
A2AFF6	Stag2	14	21	18	0.01	0.01	11
Q9D666	Sun1	6	10	10	1	2	5
O55201	Supt5h	13	27	32	0.01	4	19
Q9D198	Syf2	8	9	12	0.01	1	6
Q6ZWQ0	Syne2	97	187	235	6	38	154
Q80UV9	Taf1	14	30	30	0.01	6	17
Q80UV9	Taf1	14	30	30	0.01	6	17
E9QAP7	Taf4	9	12	14	1	3	10
F8VPY2	Taf5	10	19	20	2	8	16
Q62311	Taf6	17	24	27	1	6	16
Q9R1C0	Taf7	6	8	11	1	2	3

Q8CGF7	Tcerg1	9	16	20	0.01	1	9
Q8CGF7	Tcerg1	9	16	20	0.01	1	9
Q9ERA6	Tfip11	21	26	33	0.01	2	28
B1AZI6	Thoc2	7	12	17	0.01	2	8
Q569Z6	Thrap3	20	30	31	3	12	27
P39447	Tjp1	59	62	71	17	25	61
B9EHJ3	Tjp1	58	61	70	17	26	60
Q9Z0U1	Tjp2	35	43	41	7	16	36
P58871	Tnks1bp1	29	47	53	2	8	40
Q04750	Top1	23	23	21	15	9	17
Q01320	Top2a	13	20	26	4	11	20
Q64511	Top2b	39	55	63	9	23	44
Q921T2	Tor1aip1	13	16	22	4	6	17
P70399	Tp53bp1	12	25	27	0.01	3	15
P70399	Tp53bp1	12	25	27	0.01	3	15
Q7M739	Tpr	23	29	33	2	6	29
F6ZDS4	Tpr	23	29	33	2	6	29
Q99KW3	Triobp	8	16	14	0.01	0.01	9
Q99KW3	Triobp	8	16	14	0.01	0.01	9
Q99KW3	Triobp	8	16	14	0.01	0.01	9
G5E870	Trip12	5	28	34	0.01	3	22
A2ASS6	Ttn	61	138	185	17	61	0.01
P68372	Tubb4b	17	17	21	5	0.01	16
P99024	Tubb5	15	16	20	7	9	15
E9QJS1	Tyk2	9	12	14	0.01	0.01	8
Q9R117	Tyk2	9	12	14	0.01	0.01	8
Q6NV83	U2surp	27	34	36	6	14	30
Q6NV83	U2surp	27	34	36	6	14	30
Q811S7	Ubp1	13	17	19	2	4	14
Q9EPU0	Upf1	16	27	22	0.01	0.01	17
Q9EPU0	Upf1	16	27	22	0.01	0.01	17
Q571H0	Urb1	45	53	72	3	13	55
E9Q7L1	Urb2	17	28	34	6	14	29
Q3TIX9	Usp39	13	18	17	1	3	12
Q8C7V3	Utp15	19	20	24	4	8	17
Q5XG71	Utp20	48	56	72	2	16	61
E9QK83	Utp20	48	56	72	2	16	61
E9Q6R7	Utrn	121	139	150	25	60	128
Q01853	Vcp	14	17	23	1	4	14
E9PZY8	Virma	9	19	26	0.01	0.01	17
A2AIV2	Virma	9	19	26	0.01	0.01	17
Q923D5	Wbp11	4	6	17	0.01	2	6
Q8K4P0	Wdr33	5	15	21	0.01	4	13
Q3TA68	Wdr36	20	28	29	6	11	24

Q3TAQ9	Wdr36	20	28	29	6	11	24
Q6ZQL4	Wdr43	13	18	20	0.01	6	16
Q3U821	Wdr75	14	16	25	3	6	20
Q9DCD2	Xab2	17	22	27	0.01	7	22
Q9DBR1	Xrn2	6	11	16	0.01	0.01	7
Q9DBR1	Xrn2	6	11	16	0.01	0.01	7
D3YWX2	Ylpm1	19	33	45	0.01	6	27
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
E9Q5K9	Ythdc1	9	13	17	0.01	4	12
Q8K0L9	Zbtb20	13	20	20	0.01	3	15
Q8K0L9	Zbtb20	13	20	20	0.01	3	15
E9Q784	Zc3h13	4	19	24	0.01	0.01	14
Q8BJ05	Zc3h14	12	21	24	0.01	5	15
Q9CYA6	Zcchc8	9	11	15	0.01	2	8
Q8C827	Zfp62	14	23	23	0.01	6	19
Q8C827	Zfp62	14	23	23	0.01	6	19
E9QML5	Zfp638	18	45	55	0.01	10	35
O88532	Zfr	11	19	21	0.01	0.01	12
A2A483	Zmynd8	11	17	23	0.01	3	16
Q3UH28	Zmynd8	11	17	23	0.01	3	16
E9Q8D1	Zmynd8	11	17	23	0.01	3	16
Q3U1M7	Zmynd8	11	17	23	0.01	3	16
Q61624	Znf148	4	12	18	0.01	4	9

Table 3. A list of 255 differentially expressed genes in HEPA cells transfected with dsRNA targeting the *Xab2* transcript vs. scramble control cells

Gene ID	Gene symbol	FC	P value	Q value
XLOC_024651	Arglu1	5.493774	5.00E-05	0.00581
XLOC_000040	Gsta3	2.790866	5.00E-05	0.00581
XLOC_008926	Kmt2d	2.585648	5.00E-05	0.00581
XLOC_002682	Mbd6	2.577908	5.00E-05	0.00581
XLOC_005261	Mir8099-1	2.437726	5.00E-05	0.00581
XLOC_024417	Nlrc5	2.114796	5.00E-05	0.00581
XLOC_013555	Lrp4	2.055607	5.00E-05	0.00581
XLOC_022045	Lmtk3	1.943463	5.00E-05	0.00581
XLOC_018507	Cacna2d1	1.858967	5.00E-05	0.00581
XLOC_026663	Ptpn23	1.79707	5.00E-05	0.00581
XLOC_016963	Col27a1	1.755826	5.00E-05	0.00581
XLOC_017857	Szt2	1.673532	5.00E-05	0.00581
XLOC_020480	Kbtbd8	1.608034	5.00E-05	0.00581
XLOC_025836	Gsta4	1.604497	0.0002	0.016562
XLOC_006331	Lhfpl2	1.58489	0.0001	0.009797
XLOC_018736	Ugt2b35	1.567962	5.00E-05	0.00581
XLOC_005623	Zfyve26	1.553334	5.00E-05	0.00581
XLOC_000021	Xkr9	1.535324	0.0003	0.022372
XLOC_022746	Gltscr1	1.530128	5.00E-05	0.00581
XLOC_019430	Ugt2b34	1.491004	5.00E-05	0.00581
XLOC_016830	Mdn1	1.485966	5.00E-05	0.00581
XLOC_008711	BC024139,Eppk1	1.44005	5.00E-05	0.00581
XLOC_014615	Prr5l	1.439003	5.00E-05	0.00581
XLOC_014061	Ss18l1	1.435786	0.00095	0.047465
XLOC_027448	Clcn5	1.43536	5.00E-05	0.00581
XLOC_012449	Lcor	1.434183	5.00E-05	0.00581
XLOC_018944	Gm15800	1.432854	5.00E-05	0.00581
XLOC_001101	Lamc2	1.427963	5.00E-05	0.00581
XLOC_007943	Abcc4	1.422403	5.00E-05	0.00581
XLOC_026981	Maoa	1.419764	5.00E-05	0.00581
XLOC_017062	Usp24	1.415167	5.00E-05	0.00581
XLOC_011820	Nrep	1.408701	0.0005	0.032871
XLOC_019713	Cldn4	1.408596	5.00E-05	0.00581
XLOC_014755	Cep152	1.402274	5.00E-05	0.00581
XLOC_022963	Kmt2b	1.400677	5.00E-05	0.00581
XLOC_010712	Igf2r	1.398307	0.00015	0.013544
XLOC_026949	Xk	1.396522	0.00055	0.03435
XLOC_022366	Ampd3	1.391766	5.00E-05	0.00581
XLOC_000809	Fam126b	1.391417	5.00E-05	0.00581
XLOC_027346	Vsig1	1.386022	0.0001	0.009797
XLOC_017307	Hspg2	1.380663	5.00E-05	0.00581

XLOC_016055	Slc7a11	1.379557	5.00E-05	0.00581
XLOC_025789	Vps13c	1.37503	5.00E-05	0.00581
XLOC_003308	Per1	1.370714	5.00E-05	0.00581
XLOC_020684	Mgst1	1.36819	5.00E-05	0.00581
XLOC_006435	Gpr137b	1.367162	0.0009	0.046358
XLOC_018597	Depdc5	1.364187	0.00035	0.024863
XLOC_009821	Plcxd2	1.359702	5.00E-05	0.00581
XLOC_003187	Fnip1	1.357773	5.00E-05	0.00581
XLOC_011902	Cep120	1.355205	5.00E-05	0.00581
XLOC_009352	Map3k13	1.349688	0.0003	0.022372
XLOC_019058	Gigyf1	1.346598	5.00E-05	0.00581
XLOC_008878	Gxylt1	1.343211	5.00E-05	0.00581
XLOC_017329	Ubr4	1.328262	5.00E-05	0.00581
XLOC_024318	Hmox1	1.327338	5.00E-05	0.00581
XLOC_000272	Spp2	1.3259	0.0003	0.022372
XLOC_022076	Herc2	1.323041	5.00E-05	0.00581
XLOC_000432	Dennd1b	1.322424	5.00E-05	0.00581
XLOC_021898	Zfp568	1.315545	5.00E-05	0.00581
XLOC_023213	Chd2	1.314641	0.00025	0.019827
XLOC_006116	Serpinb9b	1.314554	5.00E-05	0.00581
XLOC_000775	Slc40a1	1.312906	5.00E-05	0.00581
XLOC_019427	Tmprss11f	1.312184	0.00015	0.013544
XLOC_027257	Atp7a	1.309026	0.0001	0.009797
XLOC_013985	Ctsa	1.308774	0.00015	0.013544
XLOC_012748	Vps13a	1.307794	5.00E-05	0.00581
XLOC_027336	Trap1a	1.303909	5.00E-05	0.00581
XLOC_022423	Tnrc6a	1.299229	5.00E-05	0.00581
XLOC_011491	Dsg2	1.29913	5.00E-05	0.00581
XLOC_016225	Sprr1b	1.297888	5.00E-05	0.00581
XLOC_018109	Vps13d	1.297219	0.0004	0.027503
XLOC_027335	Mum1l1	1.296291	0.0001	0.009797
XLOC_000169	Pikfyve	1.296196	0.0001	0.009797
XLOC_010845	Dusp1	1.295962	5.00E-05	0.00581
XLOC_016792	Trp53inp1	1.294208	5.00E-05	0.00581
XLOC_026625	Sema3b	1.293413	0.00095	0.047465
XLOC_010812	Mapk8ip3	1.292875	0.00015	0.013544
XLOC_003479	Ccl2	1.292831	0.0001	0.009797
XLOC_020275	Gpnmb	1.290966	5.00E-05	0.00581
XLOC_009427	Iqcb1	1.290603	0.00045	0.030247
XLOC_023585	Cln3	1.290531	0.0002	0.016562
XLOC_011181	Ankrd12	1.289866	0.0001	0.009797
XLOC_009982	Tmprss2	1.289174	0.0001	0.009797
XLOC_023092	Ftl1	1.287422	0.0001	0.009797
XLOC_018614	Htt	1.285363	0.0002	0.016562

XLOC_006341	Gcnt4	1.284224	0.00055	0.03435
XLOC_002173	Ankrd52	1.284211	0.0002	0.016562
XLOC_016368	Csf1	1.278774	5.00E-05	0.00581
XLOC_013130	Arl5b	1.278176	0.00035	0.024863
XLOC_010248	Clcn7	1.27778	0.00025	0.019827
XLOC_015063	Lama5	1.277136	0.0001	0.009797
XLOC_001185	Uhmk1	1.275072	5.00E-05	0.00581
XLOC_006866	Zswim6	1.273725	0.0001	0.009797
XLOC_024867	Ifi30	1.273377	0.00035	0.024863
XLOC_006015	Elmo1	1.27002	0.0005	0.032871
XLOC_009003	Itga5	1.270012	0.00025	0.019827
XLOC_010980	Vars2	1.269703	0.0003	0.022372
XLOC_024169	Ppp1r3b	1.267551	0.0005	0.032871
XLOC_001729	Rev3l	1.266697	0.0007	0.039297
XLOC_004995	Dnmt3a	1.265839	0.00045	0.030247
XLOC_020984	Atoh8	1.262073	0.00045	0.030247
XLOC_016954	Snx30	1.260936	0.0002	0.016562
XLOC_008560	Trio	1.260702	0.0001	0.009797
XLOC_001742	Ostm1	1.259171	0.00035	0.024863
XLOC_017753	Jun	1.258725	0.0006	0.036118
XLOC_014303	Zbtb26	1.256416	0.0004	0.027503
XLOC_013154	Acbd5	1.256192	0.0006	0.036118
XLOC_018757	Slc4a4	1.256003	0.0002	0.016562
XLOC_009984	Prdm15	1.25379	0.00055	0.03435
XLOC_003372	Zzef1	1.252404	0.0009	0.046358
XLOC_005130	Fam179b	1.250555	0.0009	0.046358
XLOC_025888	Xrn1	1.249861	0.00075	0.04133
XLOC_020991	Tgoln1	1.248898	0.00075	0.04133
XLOC_003067	Cpeb4	1.248767	0.0008	0.043604
XLOC_015620	Gba	1.24312	0.0003	0.022372
XLOC_000831	Fzd5	1.240482	0.00075	0.04133
XLOC_014835	Flrt3	1.239705	0.00075	0.04133
XLOC_008671	Ago2	1.237956	0.0003	0.022372
XLOC_007203	Ercc6	1.237761	0.0008	0.043604
XLOC_002169	Stat2	1.236765	0.00085	0.045665
XLOC_000527	Olfml2b	1.235798	0.0006	0.036118
XLOC_000152	Nbeal1	1.232953	0.00055	0.03435
XLOC_007140	Zswim8	1.226879	0.0009	0.046358
XLOC_019125	Trrap	1.222326	0.00055	0.03435
XLOC_019654	Camkk2	-1.20376	0.00055	0.03435
XLOC_016880	Ccdc107	-1.21111	0.00085	0.045665
XLOC_022093	Tarsl2	-1.22344	0.00065	0.037763
XLOC_027434	Arhgap6	-1.22856	0.00055	0.03435
XLOC_023705	Ifitm3	-1.22894	0.0007	0.039297

XLOC_010419	H2-Q1	-1.23057	0.00035	0.024863
XLOC_023256	Btbd1	-1.23403	0.00065	0.037763
XLOC_019480	Antxr2	-1.23838	0.0007	0.039297
XLOC_012402	Papss2	-1.23967	0.00095	0.047465
XLOC_026398	Lingo1	-1.24033	0.00045	0.030247
XLOC_018489	Abcb1b	-1.24221	0.0006	0.036118
XLOC_014354	Grb14	-1.24339	0.0002	0.016562
XLOC_014881	Sox12	-1.24567	0.00085	0.045665
XLOC_003620	Cisd3	-1.24802	0.00055	0.03435
XLOC_013229	Rapgef1	-1.2529	0.00015	0.013544
XLOC_019453	Btc	-1.25334	0.0004	0.027503
XLOC_010867	Fkbp5	-1.25482	0.0003	0.022372
XLOC_004745	Faap100	-1.25511	0.00015	0.013544
XLOC_012669	Uqcc3	-1.25594	0.0006	0.036118
XLOC_024291	Slc27a1	-1.25636	0.0009	0.046358
XLOC_023518	Galnt18	-1.25668	0.00015	0.013544
XLOC_017681	Rnf183	-1.25714	0.00035	0.024863
XLOC_004564	Aarsd1	-1.25749	0.0003	0.022372
XLOC_013063	Itih5	-1.25799	0.0001	0.009797
XLOC_024334	Inpp4b	-1.258	0.0001	0.009797
XLOC_020814	Podxl	-1.25823	0.0007	0.039297
XLOC_000904	Pid1	-1.25986	0.0005	0.032871
XLOC_026554	1190002N15Rik	-1.26041	0.00035	0.024863
XLOC_012394	Il33	-1.26332	0.00055	0.03435
XLOC_010924	Angptl4	-1.26643	0.00075	0.04133
XLOC_019782	Psmg3	-1.26695	0.0009	0.046358
XLOC_005094	Foxg1	-1.26852	0.00065	0.037763
XLOC_009911	Adamts1	-1.26854	0.0009	0.046358
XLOC_019338	Qdpr	-1.27211	5.00E-05	0.00581
XLOC_015417	Bhlhe22	-1.27223	0.0004	0.027503
XLOC_013275	Ptges2	-1.27357	0.0006	0.036118
XLOC_005752	Ccdc85c	-1.27378	0.00055	0.03435
XLOC_025617	Pvrl1	-1.27421	0.00065	0.037763
XLOC_024879	Nr2f6	-1.27526	0.00025	0.019827
XLOC_024568	Irf8	-1.27637	0.0004	0.027503
XLOC_004759	Pycr1	-1.27802	0.0002	0.016562
XLOC_016443	Enpep	-1.2848	5.00E-05	0.00581
XLOC_003648	Igfbp4	-1.29022	0.0001	0.009797
XLOC_024938	Nfix	-1.29184	5.00E-05	0.00581
XLOC_002545	Cry1	-1.29276	0.00065	0.037763
XLOC_019327	Hs3st1	-1.29297	0.0001	0.009797
XLOC_009707	Etv5	-1.29736	0.0002	0.016562
XLOC_003691	Tmem106a	-1.30111	0.00095	0.047465
XLOC_005480	1700030C10Rik	-1.30183	0.00085	0.045665

XLOC_010829	Metrn	-1.30319	0.0007	0.039297
XLOC_004406	Stxbp4	-1.30426	0.00065	0.037763
XLOC_001099	Rgl1	-1.30833	0.0004	0.027503
XLOC_012917	Shtn1	-1.30889	5.00E-05	0.00581
XLOC_022953	Sdhaf1	-1.3094	0.0001	0.009797
XLOC_011977	Ctif	-1.31107	0.0002	0.016562
XLOC_012460	Marveld1	-1.31284	5.00E-05	0.00581
XLOC_014200	Agpat2	-1.31857	5.00E-05	0.00581
XLOC_003740	Tcam1	-1.32276	5.00E-05	0.00581
XLOC_023626	Bcl7c	-1.32373	0.00015	0.013544
XLOC_017266	Map3k6	-1.32992	0.0006	0.036118
XLOC_008755	Il2rb	-1.33001	5.00E-05	0.00581
XLOC_004666	Cd300lb	-1.33065	5.00E-05	0.00581
XLOC_001318	G0s2	-1.33151	0.0001	0.009797
XLOC_009804	Tigit	-1.33194	5.00E-05	0.00581
XLOC_022220	Lipt2	-1.33285	5.00E-05	0.00581
XLOC_022452	Zfp771	-1.3348	0.00015	0.013544
XLOC_009611	Dexi	-1.33516	0.0003	0.022372
XLOC_022437	Ccdc101	-1.33528	0.0002	0.016562
XLOC_004246	Spns2	-1.33602	0.0003	0.022372
XLOC_016969	6330416G13Rik	-1.33835	5.00E-05	0.00581
XLOC_022750	Inafm1	-1.34141	0.0009	0.046358
XLOC_019482	Prkg2	-1.34323	5.00E-05	0.00581
XLOC_021212	Grcc10	-1.34412	5.00E-05	0.00581
XLOC_003051	Fancl	-1.34449	0.00035	0.024863
XLOC_003919	Igfbp3	-1.349	5.00E-05	0.00581
XLOC_006591	Mcur1	-1.35569	5.00E-05	0.00581
XLOC_018828	Lrrc8b	-1.35616	5.00E-05	0.00581
XLOC_009650	Sdf2l1	-1.35769	0.00015	0.013544
XLOC_021829	Tgfb1	-1.35833	5.00E-05	0.00581
XLOC_006828	Tmem171	-1.36459	5.00E-05	0.00581
XLOC_019492	Plac8	-1.36711	5.00E-05	0.00581
XLOC_000292	Twist2	-1.37114	5.00E-05	0.00581
XLOC_009385	Cep19	-1.38222	0.0002	0.016562
XLOC_023008	Kctd15	-1.38716	0.0001	0.009797
XLOC_024578	Zfpm1	-1.38907	5.00E-05	0.00581
XLOC_020448	Txnrd3	-1.39076	5.00E-05	0.00581
XLOC_004677	Fdxr	-1.39135	0.0004	0.027503
XLOC_008876	Abcd2	-1.39297	5.00E-05	0.00581
XLOC_013163	Il1rn	-1.39331	5.00E-05	0.00581
XLOC_007920	Tbc1d4	-1.39678	0.00025	0.019827
XLOC_026302	Oaf	-1.40583	5.00E-05	0.00581
XLOC_009259	Rbfox1	-1.41625	0.0006	0.036118
XLOC_021223	Ptms	-1.42134	5.00E-05	0.00581

XLOC_021068	H1fx	-1.42328	5.00E-05	0.00581
XLOC_010899	Notch3	-1.42502	0.00035	0.024863
XLOC_014925	Scand1	-1.44548	5.00E-05	0.00581
XLOC_014373	Mettl8	-1.45232	5.00E-05	0.00581
XLOC_020504	Lmcd1	-1.45715	5.00E-05	0.00581
XLOC_013579	Lrrc4c	-1.4692	0.0009	0.046358
XLOC_000478	Tnr	-1.46958	5.00E-05	0.00581
XLOC_022758	Calm3	-1.47282	5.00E-05	0.00581
XLOC_004539	Hap1	-1.47942	5.00E-05	0.00581
XLOC_025624	H2afx	-1.48535	5.00E-05	0.00581
XLOC_005401	Tnfaip2	-1.49665	5.00E-05	0.00581
XLOC_000117	Osgepl1	-1.50134	5.00E-05	0.00581
XLOC_014910	Ggt7	-1.50398	0.0001	0.009797
XLOC_025406	Mmp10	-1.50667	5.00E-05	0.00581
XLOC_002587	Socs2	-1.52788	5.00E-05	0.00581
XLOC_016216	Npr1	-1.53653	0.001	0.049632
XLOC_007173	Wnt5a	-1.54269	5.00E-05	0.00581
XLOC_009695	Clcn2	-1.55145	0.0003	0.022372
XLOC_021720	Pglyrp1	-1.56003	5.00E-05	0.00581
XLOC_019322	Slc2a9	-1.56081	0.0009	0.046358
XLOC_005593	Gpr135,L3hypdh	-1.57489	0.0001	0.009797
XLOC_008330	H1f0	-1.58099	5.00E-05	0.00581
XLOC_023537	Syt17	-1.58359	0.00025	0.019827
XLOC_012242	Rcor2	-1.59586	5.00E-05	0.00581
XLOC_017708	Ptprd	-1.60272	5.00E-05	0.00581
XLOC_000339	Serpinb2	-1.63868	5.00E-05	0.00581
XLOC_020096	Ppp1r9a	-1.66783	5.00E-05	0.00581
XLOC_016370	Gstm7	-1.68108	5.00E-05	0.00581
XLOC_004761	Notum	-1.69305	5.00E-05	0.00581
XLOC_014775	Mal	-1.69854	5.00E-05	0.00581
XLOC_026190	Epor	-1.71145	0.0009	0.046358
XLOC_001061	Pkp1	-1.74101	5.00E-05	0.00581
XLOC_010531	Trerf1	-1.74822	5.00E-05	0.00581
XLOC_004525	Krt33b	-1.86845	0.00095	0.047465
XLOC_016058	Ndufc1	-2.16564	5.00E-05	0.00581
XLOC_024633	Xab2	-2.51335	5.00E-05	0.00581
XLOC_017267	Slc9a1	-6.86589	5.00E-05	0.00581
XLOC_012228	Mir192,Mir194-2	-76.5398	5.00E-05	0.00581

Table 4. A list of 333 differentially expressed genes in mES cells transfected with dsRNA targeting the *Xab2* transcript vs. scramble control cells

Gene ID	Gene symbol	FC	P value	Q value
XLOC_039582	Gm21978	ND in Scrbl cells	0.00445	0.039699
XLOC_024521	Gm9959	ND in Scrbl cells	0.00345	0.031132
XLOC_021960	Gm23332	ND in Scrbl cells	0.00305	0.027701
XLOC_012490	Ighv1-60	ND in Scrbl cells	0.0022	0.020359
XLOC_027409	Scarna17	ND in Scrbl cells	0.00215	0.019965
XLOC_046725	1700065J11Rik	ND in Scrbl cells	0.00175	0.018436
XLOC_031461	Gm16355	ND in Scrbl cells	0.0017	0.018436
XLOC_062989	Gm15378	ND in Scrbl cells	0.0015	0.01775
XLOC_014722	Gm9742	ND in Scrbl cells	0.00145	0.01775
XLOC_064030	Gm14614	ND in Scrbl cells	0.001	0.01775
XLOC_018145	Ube2e2	13805.92565	5.00E-05	0.004846
XLOC_031542	Uckl1os	28.79786594	0.00135	0.01775
XLOC_050684	Rnf225	16.70073856	5.00E-05	0.004846
XLOC_034754	Gm27403,Gm27611	6.900782679	0.0045	0.040089
XLOC_010057	Cep131	6.692382944	5.00E-05	0.004846
XLOC_037000	4933431E20Rik	6.437542269	0.00055	0.01775
XLOC_032450	Cd82	5.290595065	0.00055	0.01775
XLOC_047412	Gata2	3.902260257	0.0001	0.009173
XLOC_048031	Arntl2	3.720973201	0.00285	0.025922
XLOC_011292	AC099934.1	3.641745236	5.00E-05	0.004846
XLOC_020851	Kansl2	3.144803774	5.00E-05	0.004846
XLOC_031779	Snhg7,Snora17	2.924500022	0.001	0.01775
XLOC_047707	A2m	2.796476099	0.0002	0.0177
XLOC_052192	RP23-370I17.3	2.401357168	0.00175	0.018436
XLOC_031529	Birc7	2.388508482	0.0027	0.024623
XLOC_035717	Pitx2	2.168563968	0.00275	0.025055
XLOC_030395	Platr26	2.046204022	0.0015	0.01775
XLOC_040624	Ldha-ps2	1.925259613	0.005	0.044365
XLOC_020671	Card10	1.827123307	0.00335	0.030266
XLOC_054102	Cemip	1.82286788	0.00265	0.024191
XLOC_032409	Ptprj	1.778874831	0.00265	0.024191
XLOC_012282	Ahnak2	1.763738896	0.0027	0.024623
XLOC_007498	Adam19	1.763103295	0.0005	0.01775
XLOC_024886	Notch3	1.694334825	0.00365	0.032772
XLOC_041150	Klhl17,Plekhn1	1.670464125	0.0044	0.039272

XLOC_036591	Kirrel	1.651607643	0.001	0.01775
XLOC_058850	Ldlr	1.566986771	0.0033	0.029864
XLOC_035347	Rps10-ps1 (retro)	-1.48949884	0.00375	0.033614
XLOC_042975	Gm5869	-1.503349034	0.0043	0.038407
XLOC_001865	Gm7658	-1.503737766	0.004	0.035803
XLOC_006017	Rpsa-ps2	-1.506622521	0.0047	0.041762
XLOC_052303	RP23-136A14.1	-1.508114536	0.00335	0.030266
XLOC_024624	Pabpc6	-1.514249568	0.00515	0.045631
XLOC_012147	Gm6863	-1.514338787	0.0045	0.040089
XLOC_035742	Gm43524	-1.517747714	0.00435	0.038835
XLOC_059966	Rpl15-ps3	-1.51931709	0.0041	0.036681
XLOC_040956	Gm13050	-1.520677264	0.0055	0.048561
XLOC_029031	Rpl9-ps6	-1.523728643	0.00465	0.041337
XLOC_063032	Rps24-ps3	-1.525971481	0.00355	0.031912
XLOC_026674	Gm10036	-1.527824678	0.004	0.035803
XLOC_002196	Sumo1	-1.528014252	0.0037	0.033189
XLOC_057302	Gm7901	-1.530228396	0.00545	0.048153
XLOC_044891	Gm15484	-1.531851025	0.00565	0.04985
XLOC_001348	Rpsa-ps1	-1.533866581	0.0028	0.02548
XLOC_056561	2310036O22Rik	-1.540718184	0.00525	0.046441
XLOC_015341	Gm10260	-1.542733645	0.00325	0.029419
XLOC_028250	Fau	-1.54305662	0.0043	0.038407
XLOC_057161	Gm8623	-1.544910219	0.0026	0.023769
XLOC_045158	Rps16-ps2	-1.548252741	0.00325	0.029419
XLOC_027132	Gm10269	-1.550020182	0.0052	0.046031
XLOC_062956	Rpl3-ps2	-1.552164001	0.00195	0.018855
XLOC_059156	Rpp25	-1.553327461	0.00205	0.01925
XLOC_054828	Ifitm2	-1.55532923	0.0031	0.028108
XLOC_026625	Rpl27-ps3	-1.560841454	0.0017	0.018436
XLOC_020476	Eif3h	-1.563210432	0.00205	0.01925
XLOC_038868	Gm11263	-1.566829287	0.00275	0.025055
XLOC_014531	Rps23	-1.569189949	0.0014	0.01775
XLOC_058756	Gm10709	-1.575761291	0.0036	0.032338
XLOC_037023	Sars	-1.577929775	0.0045	0.040089
XLOC_011096	Gm4294	-1.579168371	0.0017	0.018436
XLOC_027343	Rps2-ps10	-1.583365147	0.00105	0.01775
XLOC_034793	Rps23-ps1	-1.584780463	0.0032	0.02898
XLOC_032949	Rps15a-ps7	-1.585269365	0.00185	0.01851
XLOC_059387	Rps27a-ps2	-1.585957378	0.00225	0.020761
XLOC_008657	Uqcr10	-1.593111232	0.00515	0.045631
XLOC_002692	Gm6170	-1.595784679	0.0018	0.018436
XLOC_002446	Gm6136	-1.595988217	0.0022	0.020359
XLOC_053487	Rps11	-1.599411316	0.00095	0.01775

XLOC_047229	Rpl34-ps1	-1.601615676	0.00085	0.01775
XLOC_029179	Rpl13a-ps1	-1.602002057	0.0021	0.019685
XLOC_004906	Rps15	-1.603276219	0.00115	0.01775
XLOC_036830	Rpl21-ps11	-1.605803096	0.0042	0.03754
XLOC_045388	Atp5j2	-1.605839827	0.0031	0.028108
XLOC_048287	Ybx1-ps2	-1.606334112	0.0011	0.01775
XLOC_018406	Gm6055	-1.607422298	0.00265	0.024191
XLOC_043605	Gm10051	-1.60791707	0.00115	0.01775
XLOC_017841	Gm10233	-1.611192642	0.0026	0.023769
XLOC_017576	Rps19-ps1	-1.61660588	0.0051	0.04522
XLOC_056848	Rps23-ps2	-1.621816955	0.0016	0.018404
XLOC_060483	Gm5619	-1.622153113	0.00215	0.019965
XLOC_008214	Gm11539	-1.624715372	0.00185	0.01851
XLOC_007801	Rpl26	-1.626567846	0.00095	0.01775
XLOC_009544	Gm11478	-1.628568045	0.0036	0.032338
XLOC_037363	Rpsa-ps10	-1.628650452	0.0031	0.028108
XLOC_020029	Rpl8	-1.63132587	0.0052	0.046031
XLOC_034678	Gm7536	-1.632151525	0.00185	0.01851
XLOC_011266	Gm5786	-1.63233481	0.0006	0.01775
XLOC_020387	Basp1	-1.632669753	0.0017	0.018436
XLOC_012020	Gm7862	-1.632999105	0.00345	0.031132
XLOC_006011	Rps26	-1.634771503	0.00105	0.01775
XLOC_022313	Sod1	-1.635994616	0.00125	0.01775
XLOC_059624	Rpl29	-1.639569434	0.0004	0.01775
XLOC_014438	Gm9625	-1.63973764	0.00095	0.01775
XLOC_052888	RP24-490A22.9	-1.641137366	0.00125	0.01775
XLOC_026823	Pabpc2	-1.641747206	0.0055	0.048561
XLOC_049488	Rpl38-ps2	-1.644376888	0.00055	0.01775
XLOC_034941	Rpl13-ps6	-1.644925221	0.0012	0.01775
XLOC_024814	Gm8186	-1.644985651	0.00125	0.01775
XLOC_034705	Rpl22l1	-1.646551915	0.005	0.044365
XLOC_039746	Aurkaip1	-1.648768674	0.0029	0.026371
XLOC_019921	Gm5045	-1.649766675	0.00145	0.01775
XLOC_012082	Gm5436	-1.650434633	0.0005	0.01775
XLOC_043832	Rpl21	-1.651470272	0.0031	0.028108
XLOC_051031	Blvrb	-1.652420656	0.00445	0.039699
XLOC_017541	Rps19-ps2	-1.652819293	0.00235	0.021609
XLOC_011479	Rpl30-ps8	-1.653221464	0.00345	0.031132
XLOC_036601	Apoa1bp	-1.657145179	0.00535	0.047303
XLOC_020478	Gm10020	-1.657786248	0.00065	0.01775
XLOC_064183	Gm14681	-1.657936785	0.0007	0.01775
XLOC_030034	Rpsa-ps9	-1.659934138	0.0006	0.01775
XLOC_064838	Gm6472,Rpl7a-ps12	-1.661159956	0.0022	0.020359

XLOC_011965	Rpl36al	-1.661439777	0.00065	0.01775
XLOC_003139	Gm10171	-1.662952545	0.00295	0.026812
XLOC_039448	Id3	-1.664053711	0.00475	0.042196
XLOC_049113	Rpl32	-1.667791569	0.0012	0.01775
XLOC_024835	Rps10	-1.66859173	0.001	0.01775
XLOC_050844	Zfp296	-1.669071779	0.00455	0.040505
XLOC_060211	Rps6-ps3	-1.670290453	0.00125	0.01775
XLOC_046718	Gm13864	-1.676160151	0.0042	0.03754
XLOC_030100	Gm13611	-1.676640054	0.0008	0.01775
XLOC_063314	Gm16373	-1.677318892	0.00315	0.028548
XLOC_039969	Bag1	-1.677944503	0.0017	0.018436
XLOC_048567	Gm9794	-1.679533998	0.0014	0.01775
XLOC_001822	Rpl7	-1.681298634	0.0007	0.01775
XLOC_039148	Gm12848	-1.68456839	0.0025	0.02291
XLOC_062660	Gm6274	-1.689373119	0.00025	0.01775
XLOC_063984	Rpl39	-1.694520394	0.0001	0.009173
XLOC_047051	Rps15-ps2	-1.697429905	0.00045	0.01775
XLOC_018725	Gm16409	-1.699155632	0.00165	0.018404
XLOC_051433	Rpl14-ps1	-1.705344251	0.0005	0.01775
XLOC_001308	Mrps14	-1.707267356	0.00085	0.01775
XLOC_058936	Gm10177	-1.711874572	0.0023	0.021206
XLOC_036359	Gm6394	-1.71311856	0.0004	0.01775
XLOC_038398	Gm11824	-1.713506898	0.0003	0.01775
XLOC_025265	Rpl7a-ps5	-1.717807053	0.0011	0.01775
XLOC_014150	Gm11353	-1.724626556	0.0003	0.01775
XLOC_064384	Gm6977	-1.726542682	0.00025	0.01775
XLOC_005610	Gm6419	-1.727095669	0.00235	0.021609
XLOC_006007	Rpl41	-1.728000937	0.00025	0.01775
XLOC_009086	Gm12254	-1.728741311	0.0001	0.009173
XLOC_020726	Ndufa6	-1.729790117	0.00335	0.030266
XLOC_059794	Rpsa	-1.730470083	0.00065	0.01775
XLOC_027217	Pfdn1	-1.731621958	0.0001	0.009173
XLOC_008261	Rpl19	-1.732641286	0.0001	0.009173
XLOC_040696	Rpl28-ps3	-1.733267107	0.0007	0.01775
XLOC_049378	Ybx3	-1.736239537	0.0036	0.032338
XLOC_022853	Gm9843	-1.740541243	0.0003	0.01775
XLOC_059805	Rpl14	-1.74333642	0.0001	0.009173
XLOC_038363	Gm12918	-1.744440028	0.001	0.01775
XLOC_007395	Rpsa-ps5	-1.747751411	0.0003	0.01775
XLOC_048715	Mrpl35	-1.747954947	0.00145	0.01775
XLOC_040275	Gm10154	-1.752718127	0.00055	0.01775
XLOC_033201	Gm14303	-1.756226596	0.0012	0.01775
XLOC_051528	Rps12l1	-1.757822014	0.0006	0.01775

XLOC_032132	Mrpl23-ps1	-1.757962139	0.0022	0.020359
XLOC_064783	Gm15066	-1.759574989	5.00E-05	0.004846
XLOC_057536	Rps18-ps3	-1.764439545	5.00E-05	0.004846
XLOC_051915	Ndufc2	-1.766826039	0.004	0.035803
XLOC_017967	Gm10076	-1.7705321	5.00E-05	0.004846
XLOC_001278	Gm2000	-1.770794748	0.0001	0.009173
XLOC_001880	Tubb4b-ps2	-1.775614014	0.00245	0.022479
XLOC_058788	Gm5611	-1.777027491	0.0001	0.009173
XLOC_049450	Dynlt1-ps1	-1.78264694	0.00015	0.013338
XLOC_009054	Anxa6	-1.782735908	0.00555	0.048991
XLOC_034781	Gm12583	-1.783829837	0.00015	0.013338
XLOC_063677	Gm7331	-1.784596604	5.00E-05	0.004846
XLOC_031032	Gm14036	-1.788275483	0.0013	0.01775
XLOC_042648	Gm4754	-1.793767616	0.00095	0.01775
XLOC_041051	Rpsa-ps12	-1.804441035	0.00065	0.01775
XLOC_014482	Gm4149	-1.811866927	5.00E-05	0.004846
XLOC_018771	Rps3a2	-1.819617229	0.00025	0.01775
XLOC_060367	Gm7866	-1.825513073	0.0001	0.009173
XLOC_026932	Rps14	-1.825937014	0.00015	0.013338
XLOC_052806	Rps8-ps4	-1.828742566	0.00375	0.033614
XLOC_064277	Gm15361	-1.829777211	0.00045	0.01775
XLOC_004908	Reep6	-1.833519996	0.0042	0.03754
XLOC_011651	Rps19-ps6	-1.834308123	0.00015	0.013338
XLOC_064100	Gm14586	-1.840293661	5.00E-05	0.004846
XLOC_020011	Rps6-ps1	-1.844663926	0.0008	0.01775
XLOC_054197	Gm15501	-1.847016814	0.0008	0.01775
XLOC_054653	Nupr1	-1.848218084	0.00125	0.01775
XLOC_004508	Gm10335	-1.854394253	0.00065	0.01775
XLOC_017784	Rpl13-ps3	-1.855514146	0.0002	0.0177
XLOC_018023	Gm2904	-1.858290435	0.001	0.01775
XLOC_057234	Ndufa13	-1.861957315	5.00E-05	0.004846
XLOC_051455	Rpl18	-1.862864836	5.00E-05	0.004846
XLOC_011829	Rps7	-1.863754712	0.0005	0.01775
XLOC_057539	Rps26-ps1	-1.868718162	0.00335	0.030266
XLOC_055991	RP24-74L7.3	-1.870146125	0.0005	0.01775
XLOC_054283	Gm7027	-1.873944207	5.00E-05	0.004846

XLOC_044441	Rpl9	-1.876663517	0.00465	0.041337
XLOC_062914	Rpl30-ps10	-1.879788045	5.00E-05	0.004846
XLOC_000026	Gm37108	-1.880536098	5.00E-05	0.004846
XLOC_063168	Tpt1-ps6	-1.889017412	5.00E-05	0.004846
XLOC_014912	Acot13	-1.889821535	0.00225	0.020761
XLOC_001009	Gm8392	-1.895806868	5.00E-05	0.004846
XLOC_012038	Vti1b	-1.896674355	0.0039	0.034933
XLOC_020802	Rpl31-ps8	-1.905421272	5.00E-05	0.004846
XLOC_005520	Rps8-ps1	-1.913776029	0.0001	0.009173
XLOC_014341	Gm6344	-1.918830132	0.0009	0.01775
XLOC_005716	Timm13	-1.925052778	0.00065	0.01775
XLOC_033240	Rps8-ps2	-1.929375565	5.00E-05	0.004846
XLOC_001121	Gm15454	-1.931195206	0.0016	0.018404
XLOC_031489	Gm14414	-1.932382912	5.00E-05	0.004846
XLOC_040228	Rps18-ps1	-1.93616647	0.0037	0.033189
XLOC_039776	Gm11808	-1.937268606	5.00E-05	0.004846
XLOC_020052	Nol12	-1.945528346	0.00265	0.024191
XLOC_017160	Gm17048	-1.946306607	0.0028	0.02548
XLOC_049011	Gm6681	-1.946461757	0.00285	0.025922
XLOC_036687	Gm5851	-1.94976331	5.00E-05	0.004846
XLOC_018745	Gm10132	-1.955530449	0.0006	0.01775
XLOC_036685	Gm5850	-1.958574491	0.00015	0.013338
XLOC_064525	Rpl30-ps9	-1.962501831	5.00E-05	0.004846
XLOC_025344	Gm6548	-1.97366892	5.00E-05	0.004846
XLOC_009518	Aatf	-1.978864734	0.0009	0.01775
XLOC_031462	Gm14438	-1.979799045	5.00E-05	0.004846
XLOC_044990	Gm13841	-1.985659154	5.00E-05	0.004846
XLOC_039204	Gm12857	-1.98598813	5.00E-05	0.004846
XLOC_039772	Rps20	-1.99189003	5.00E-05	0.004846
XLOC_059912	Gm7808	-2.003302104	5.00E-05	0.004846

XLOC_036999	Gm5075	-2.009198356	0.0032	0.02898
XLOC_017158	Gm17046	-2.012724903	0.003	0.027254
XLOC_036435	Gm37009	-2.016229689	5.00E-05	0.004846
XLOC_019775	Capsl	-2.035721211	0.00335	0.030266
XLOC_031950	Rpl35	-2.041840255	0.00075	0.01775
XLOC_037415	Gm6520	-2.043652637	0.0034	0.030703
XLOC_018394	Bmp4	-2.049014225	0.00095	0.01775
XLOC_000314	Gm8210	-2.057410966	5.00E-05	0.004846
XLOC_045008	Gm3786	-2.058466543	0.0007	0.01775
XLOC_003119	Rpl27-ps1	-2.059365636	0.0001	0.009173
XLOC_033083	Gtsf1l	-2.064181743	5.00E-05	0.004846
XLOC_008978	Gm12191	-2.065555751	0.0055	0.048561
XLOC_043683	Gm16089	-2.067833463	0.001	0.01775
XLOC_064304	Gm8692	-2.074120913	0.00165	0.018404
XLOC_030834	Gm14016	-2.077963049	0.00125	0.01775
XLOC_018749	Dnajc15	-2.086608587	0.0045	0.040089
XLOC_020899	Bin2	-2.090502835	0.00505	0.044787
XLOC_058944	Tpt1-ps5	-2.094607604	0.0052	0.046031
XLOC_026983	Gm17669	-2.101471659	5.00E-05	0.004846
XLOC_020438	Gm3362	-2.115443274	5.00E-05	0.004846
XLOC_054352	Dnajc19-ps	-2.118421986	0.00035	0.01775
XLOC_053489	Rpl13a	-2.130762802	5.00E-05	0.004846
XLOC_030136	Gm13408	-2.141260024	5.00E-05	0.004846
XLOC_036764	Rpl31-ps11	-2.146371792	5.00E-05	0.004846
XLOC_003368	Gm19777	-2.153509966	5.00E-05	0.004846
XLOC_050978	Rps19	-2.156153665	0.0007	0.01775
XLOC_032778	Gm14044	-2.159354337	0.00015	0.013338
XLOC_035723	Rpl7a-ps7	-2.176168095	0.00035	0.01775
XLOC_009165	Rps13-ps5	-2.178039321	5.00E-05	0.004846
XLOC_052242	E130201H02Rik	-2.182452115	0.00025	0.01775
XLOC_036577	Rps3a1	-2.184162204	5.00E-05	0.004846
XLOC_017150	Gm3348	-2.184434731	0.0037	0.033189
XLOC_028431	Prune2	-2.184798154	0.0006	0.01775
XLOC_020933	Itgb7	-2.193690507	0.00565	0.04985

XLOC_014603	Rpl31-ps13	-2.195668113	5.00E-05	0.004846
XLOC_063124	Rpl17-ps8	-2.205292468	5.00E-05	0.004846
XLOC_024543	Rpl31-ps16	-2.224575403	0.00165	0.018404
XLOC_017339	Rpl23a-ps3	-2.225392791	5.00E-05	0.004846
XLOC_022879	Rpl31-ps4	-2.239970916	0.00195	0.018855
XLOC_053112	Gm4613	-2.269209801	0.0022	0.020359
XLOC_053968	Rpl17-ps10	-2.284423293	5.00E-05	0.004846
XLOC_022482	Rpl31-ps12	-2.285120113	5.00E-05	0.004846
XLOC_020887	Gm9763	-2.299308426	0.00155	0.01812
XLOC_035524	Gm4540	-2.301508866	5.00E-05	0.004846
XLOC_051250	Rpl17-ps9	-2.309691232	5.00E-05	0.004846
XLOC_054162	Rps13-ps2	-2.343703391	5.00E-05	0.004846
XLOC_048012	Rps25-ps1	-2.358010267	5.00E-05	0.004846
XLOC_060808	Rps27rt	-2.358369873	5.00E-05	0.004846
XLOC_050570	Rps9	-2.3690358	5.00E-05	0.004846
XLOC_011642	Dio3	-2.375712077	0.00245	0.022479
XLOC_054218	Aamdc	-2.377853775	0.0034	0.030703
XLOC_008572	Ccdc40	-2.390562293	0.0037	0.033189
XLOC_002271	Rpl31-ps14	-2.392518367	5.00E-05	0.004846
XLOC_009436	Rpl23a	-2.398279828	5.00E-05	0.004846
XLOC_002678	Gm8451	-2.41119779	0.00025	0.01775
XLOC_002845	Gm7266	-2.413940305	5.00E-05	0.004846
XLOC_051460	Ccdc114	-2.414425587	0.00075	0.01775
XLOC_014037	Hist1h2ai	-2.463774128	0.0024	0.022042
XLOC_014126	Hist1h2ab	-2.466696126	0.0011	0.01775
XLOC_064432	Zc4h2	-2.486092542	0.00135	0.01775
XLOC_038702	Gm12482	-2.487230133	5.00E-05	0.004846
XLOC_030898	Rps12-ps10	-2.509152227	0.00135	0.01775
XLOC_008026	Gm11204	-2.548220287	0.00275	0.025055
XLOC_023997	Gm8225	-2.592924143	5.00E-05	0.004846

XLOC_056590	Rps13-ps1	-2.61204545	5.00E-05	0.004846
XLOC_053209	RP24-471H15.4	-2.648581679	5.00E-05	0.004846
XLOC_014824	Hist1h2ah	-2.697849744	0.00485	0.043074
XLOC_017272	Gm7565	-2.880341757	5.00E-05	0.004846
XLOC_014878	Hist1h2ae	-3.058533335	0.00165	0.018404
XLOC_057615	Rps13-ps4	-3.099939372	0.0023	0.021206
XLOC_019856	Rps19-ps5	-3.147573353	5.00E-05	0.004846
XLOC_014884	Hist1h2ac	-3.233955888	0.001	0.01775
XLOC_022752	Dubr	-3.316450516	0.0054	0.047734
XLOC_014826	Hist1h2ag	-3.338823893	0.0003	0.01775
XLOC_001415	Gm7299	-3.363166024	0.0012	0.01775
XLOC_036291	Ndufc1	-3.459203769	0.0053	0.046872
XLOC_027008	Myo5b	-3.526336133	0.00095	0.01775
XLOC_014115	Hist1h2ad	-3.830014887	5.00E-05	0.004846
XLOC_031601	9230102O04Rik,Gata3	-3.894019207	0.0004	0.01775
XLOC_014815	Hist1h2ap	-4.043262863	5.00E-05	0.004846
XLOC_056849	Xab2	-4.173882536	5.00E-05	0.004846
XLOC_002874	Pla2g4a	-4.211838155	0.0013	0.01775
XLOC_014047	Hist1h2ao	-4.229684341	5.00E-05	0.004846
XLOC_056788	Vat1l	-4.31230733	0.00265	0.024191
XLOC_040846	Man1c1	-4.454983227	0.0001	0.009173
XLOC_038474	Gm11918	-4.531127227	0.00055	0.01775
XLOC_001830	Jph1	-5.117999477	0.00505	0.044787
XLOC_006071	Gm20746,Gm26445	-5.781925421	0.0001	0.009173
XLOC_064058	Smarca1	-7.355584564	0.00015	0.013338
XLOC_014340	Unc5a	-8.241060486	0.0031	0.028108
XLOC_014498	A830082K12Rik	-9.031026631	0.0024	0.022042
XLOC_063433	Tceal3	-9.597375898	0.00105	0.01775
XLOC_036993	Slc6a17	-11.07212323	0.0001	0.009173
XLOC_052247	Vwa3a	-12.10918614	0.00145	0.01775
XLOC_031015	AU019990	-12.41532394	0.0014	0.01775
XLOC_059042	C1qtnf5,Mfrp	-28.79207779	5.00E-05	0.004846
XLOC_042512	Kcnk3	-30.82715829	0.0047	0.041762
XLOC_009585	Hlf	-31.60235135	0.0018	0.018436
XLOC_018791	Gm25130	ND in si*Xab2* cells	0.0013	0.01775
XLOC_052323	RP23-421P23.5	ND in si*Xab2* cells	0.0013	0.01775

XLOC_004025		ND in si*Xab2* cells	0.00105	0.01775
XLOC_060788	Rp31-ps19	ND in si*Xab2* cells	0.001	0.01775
XLOC_053450	RP23-361A18.17	ND in si*Xab2* cells	5.00E-05	0.004846

Table 5. *Xab2*-induced differential splicing events in HEPA cells

GENE	EVENT	COORD	Complex	β_siRNA	β_Ctrl	β_siRNA_Ctrl	P_xzero
Atp6v1a	MmuALTD0001887-1/3	chr16:44139075-44139093	Alt5	0.1090087	0.7996605	-0.690651737	0.922
Cyp4f16	MmuALTA0004959-1/2	chr17:32673943-32674141	Alt3	0.35937	0.9639825	-0.604612448	0.838
Ncor1	MmuEX0031185	chr11:62147165-62147658	C1	0.5356821	0.9895236	-0.453841488	0.82333333
Atf2	MmuEX0006584	chr2:73684254-73684432	C2	0.6880473	0.9750753	-0.287027975	0.80533333
Serpinb6a	MmuALTD0012645-1/5	chr13:34027636-34027663	Alt5	0.0785913	0.3655519	-0.28696058	0.92933333
Mr1	MmuALTD0008714-1/2	chr1:156984829-156984904	Alt5	0.0804305	0.3341185	-0.253687984	0.96533333
Tmem161a	MmuEX0047784	chr8:72698202-72698305	S	0.5361885	0.7826644	-0.24647598	0.85933333
Git2	MmuALTA0007752-1/2	chr5:115202288-115202336	Alt3	0.4584876	0.6987804	-0.240292837	0.804
Fmr1	MmuALTA0007321-1/2	chrX:65965442-65965480	Alt3	0.1628548	0.395801	-0.232946172	0.91
Mier2	MmuALTA0010968-1/2	chr10:79012381-79012424	Alt3	0.6986348	0.917274	-0.218639214	0.86533333
Nfya	MmuALTD0009355-1/2	chr17:48538310-48538363	Alt5	0.1562663	0.3699905	-0.213724207	0.90333333
Rbm14	MmuALTD0011633-1/2	chr19:4793816-4793849	Alt5	0.565482	0.7791952	-0.213713145	0.83133333
Alkbh7	MmuEX0004696	chr17:57137812-57137985	S	0.7540418	0.9539332	-0.199891474	0.856
D19Wsu162e	MmuEX0013522	chr19:46681202-46681249	S	0.6695706	0.8598263	-0.190255669	0.942
Arhgef12	MmuALTA0001960-1/2	chr9:42816099-42816191	Alt3	0.3999025	0.5895391	-0.189636567	0.84066667
Mtif3	MmuALTD0008893-1/3	chr5:147775299-147775319	Alt5	0.4193444	0.6079851	-0.188640649	0.84733333
Fanca	MmuINT0062263	chr8:125792738-125792842	IR-C	0.3356849	0.5219056	-0.186220661	0.91266667
Tpcn2	MmuEX0048557	chr7:152441356-152441438	S	0.7927872	0.9789566	-0.186169376	0.84466667
Tmem38b	MmuEX0047954	chr4:53853499-53853655	S	0.7359678	0.9215461	-0.185578221	0.93933333
Zfp740	MmuALTA0020740-1/2	chr15:102038703-102038773	Alt3	0.3971194	0.5807793	-0.18365998	0.91733333
Ubr4	MmuEX0050365	chr4:138997107-138997211	S	0.6823619	0.8633006	-0.180938727	0.88
BC017643	MmuALTD0002029-1/2	chr11:121090373-121090409	Alt5	0.2559084	0.4348297	-0.178921364	0.80133333
Cdk12	MmuALTA0003745-1/2	chr11:98111024-98111414	Alt3	0.6222564	0.8000865	-0.177830112	0.862
Ankzf1	MmuEX0005222	chr1:75190753-75190859	S	0.8046241	0.9769959	-0.172371803	0.98
Atp6v1e1	MmuALTD0001895-1/3	chr6:120772610-	Alt5	0.1445453	0.3162145	-0.171669252	0.96
Actr5	MmuALTD0000932-1/2	chr2:158457365-158457416	Alt5	0.7795977	0.9511359	-0.171538247	0.892
Eed	MmuALTD0004652-1/2	chr7:97104854-97104923	Alt5	0.1313608	0.3024625	-0.171101681	0.926
Smek1	MmuALTD0013244-1/2	chr12:102291678-102291794	Alt5	0.6204392	0.7910117	-0.170572583	0.80333333
1110057K04Rik	MmuALTD0000068-1/3	chr12:-8214998	Alt5	0.2262214	0.3938678	-0.1676464	0.808
Clasrp	MmuALTD0003224-1/2	chr7:20170133-20170172	Alt5	0.6606028	0.8255283	-0.164925491	0.82866667
Tubgcp2	MmuALTD0015006-1/5	chr7:147222246-	Alt5	0.2273246	0.3920411	-0.164716461	0.88266667
Trrap	MmuALTA0018970-1/2	chr5:145552143-145552237	Alt3	0.2511486	0.4152459	-0.164097284	0.858
Bmp4	MmuINT0025192	chr14:47005770-47006830	IR-S	0.072019	0.2340737	-0.16205473	0.958
Fam48a	MmuALTA0006920-1/3	chr3:54526479-54526562	Alt3	0.1799672	0.3417749	-0.161807718	0.81666667
Acot8	MmuEX0003517	chr2:164628497-164628633	S	0.6458656	0.8053368	-0.159471221	0.85266667
Ddx6	MmuALTD0004130-1/6	chr9:-44413010	Alt5	0.2108359	0.3700148	-0.159178893	0.85866667
Mef2d	MmuEX0028565	chr3:87971960-87972266	S	0.6627814	0.8216785	-0.158897152	0.858
Mef2a	MmuEX0028561	chr7:74412953-74413090	C3	0.3623816	0.5202061	-0.15782453	0.88933333
Uqcc	MmuEX0050723	chr2:155727034-155727091	C3	0.8071934	0.9633238	-0.156130393	0.85666667
Senp6	MmuALTA0016126-1/2	chr9:79946700-79946713	Alt3	0.0288114	0.1836152	-0.154803855	0.81133333
Ift52	MmuALTD0006914-1/2	chr2:-162843269	Alt5	0.7147012	0.867003	-0.152301798	0.84933333
Dlg4	MmuEX0014814	chr11:69857160-69857269	S	0.4193698	0.5711075	-0.15173777	0.87
Atf2	MmuEX0006585	chr2:73683496-73683610	C1	0.6891787	0.8379289	-0.148750189	0.808
Cep55	MmuALTD0003039-1/2	chr19:-38129571	Alt5	0.5879371	0.7358439	-0.147906807	0.81333333
Mtpap	MmuALTA0011446-1/2	chr18:4383187-4383411	Alt3	0.7592401	0.9056124	-0.146372269	0.83866667
Thap7	MmuEX0047170	chr16:17530323-17530478	C2	0.5922371	0.738304	-0.146066897	0.866
Banp	MmuEX0007671	chr8:124513855-124513971	S	0.6597408	0.8038098	-0.144069008	0.856
Setd5	MmuEX0041847	chr6:113055911-113056135	C1	0.550027	0.6936253	-0.143598346	0.902
Nr2f2	MmuALTD0009542-1/2	chr7:77504774-77505479	Alt5	0.730448	0.8720211	-0.141573183	0.87133333
Pcyt2	MmuEX0034099	chr11:120474344-120474397	S	0.4387014	0.5794984	-0.14079701	0.904
Odf2	MmuALTD0009758-1/2	chr2:29748964-29749032	Alt5	0.4045722	0.5439274	-0.139355163	0.876
Fam53a	MmuEX0018352	chr5:33971502-33971626	S	0.8441551	0.9826355	-0.138480319	0.97333333
Acbd5	MmuEX0003421	chr2:22931010-22931130	S	0.8325246	0.9709464	-0.138421792	0.828
Senp6	MmuEX0041679	chr9:79946693-79946713	S	0.6422916	0.7805176	-0.13822596	0.88666667
Prpf40b	MmuEX0037345	chr15:99135597-99135624	S	0.7811273	0.918409	-0.137281671	0.84266667
Hgfac	MmuEX0022853	chr5:35389138-35389277	S	0.7169644	0.8533042	-0.136339872	0.828
1810031K17Rik	MmuINT0001713	chr1:75138078-75138631	IR-C	0.4049344	0.5403648	-0.135430444	0.874
Hsd17b7	MmuEX0023306	chr1:171889554-171889610	S	0.8118881	0.9469799	-0.135091849	0.952
Stim1	MmuEX0045370	chr7:109577288-109577380	S	0.3353827	0.4696332	-0.134250429	0.818

Rif1	MmuEX0039819	chr2:51972188-51972265	S	0.3597079	0.4935274	-0.133819493	0.83933333
Pus10	MmuALTA0014590-1/3	chr11:23628975-23629071	Alt3	0.7909149	0.92387	-0.132955151	0.81266667
D930015E06Rik	MmuALTA0005042-1/3	chr3:83704249-83704337	Alt3	0.106469	0.2387084	-0.132239347	0.84266667
Ubr3	MmuALTA0019357-1/2	chr2:69789404-69789465	Alt3	0.1049374	0.2357565	-0.130819101	0.84333333
Fbxw5	MmuEX0018961	chr2:25357921-25358078	S	0.6564712	0.7871617	-0.130690505	0.82466667
Cacnb3	MmuALTA0003082-1/2	chr15:98471878-98471889	Alt3	0.0162489	0.1462584	-0.130009467	0.80133333
Ttc19	MmuEX0049456	chr11:62097633-62097671	S	0.7870955	0.9164614	-0.129365881	0.896
Rpl23	MmuALTA0015503-1/2	chr11:97642718-97642744	Alt3	0.6148007	0.7436096	-0.128808889	0.86066667
Wbp1	MmuEX0051721	chr6:83070766-83070867	S	0.2637117	0.3921128	-0.128401096	0.928
Kbtbd4	MmuALTD0007324-1/2	chr2:-90744969	Alt5	0.0728694	0.200331	-0.12746162	0.83933333
Luc7l	MmuEX0027311	chr17:26390919-26390989	S	0.2907271	0.4173451	-0.126618061	0.89533333
Cln6	MmuEX0011748	chr9:62688292-62688398	S	0.0896504	0.2160062	-0.12635584	0.82466667
Tmem161a	MmuEX0047786	chr8:72701140-72701237	C3	0.661919	0.7879595	-0.126040528	0.85733333
Pan3	MmuALTA0012718-1/2	chr5:148348038-148348116	Alt3	0.0720857	0.1974971	-0.125411449	0.80133333
Plekha6	MmuEX0035729	chr1:135195497-135195620	C1	0.8082256	0.9323877	-0.124162094	0.916
Tsc2	MmuEX0049266	chr17:24743169-24743297	S	0.5000818	0.6241061	-0.12402428	0.80266667
Sept6	MmuALTD0012613-1/2	chrX:34482077-34482211	Alt5	0.0800657	0.2040751	-0.124009373	0.846
Dsn1	MmuALTD0004496-1/2	chr2:156832711-	Alt5	0.7990031	0.9224673	-0.123464172	0.802
Abcc1	MmuEX0003090	chr16:14413314-14413475	S	0.8501773	0.9732794	-0.123102125	0.92866667
Rap1gap	MmuEX0038750	chr4:137279661-137279738	S	0.1544303	0.2772729	-0.122842639	0.88933333
Senp1	MmuEX0041653	chr15:97892381-97892458	S	0.2325932	0.3539959	-0.12140271	0.85266667
Zfp568	MmuINT0179471	chr7:30774127-30782768	IR-S	0.1157406	0.2365569	-0.120816282	0.846
Sbf1	MmuEX0041054	chr15:89126383-89126460	S	0.518793	0.6389842	-0.120191155	0.87133333
Tmem131	MmuALTA0018335-1/2	chr1:36850889-36851040	Alt3	0.201343	0.3214679	-0.120124887	0.80666667
Palm	MmuEX0033522	chr10:79279537-79279668	S	0.4573629	0.5774638	-0.120100887	0.83533333
Stk25	MmuEX0045410	chr1:95521611-95521725	S	0.7834155	0.9030233	-0.119607809	0.82666667
Nol11	MmuALTA0012107-1/3	chr11:107034524-107034715	Alt3	0.3342629	0.4522152	-0.11795233	0.81933333
Myo9b	MmuALTA0011588-1/2	chr8:73883563-	Alt3	0.0964731	0.2120939	-0.115620823	0.824
Rock2	MmuEX0040276	chr12:16965434-16965680	S	0.8760814	0.9916898	-0.115608465	0.824
Cnot1	MmuALTA0004327-1/2	chr8:98278885-98279008	Alt3	0.2163931	0.3317658	-0.115372705	0.80666667
0610037P05Rik	MmuEX0000067	chr16:14311140-14311224	C2	0.7928753	0.9060622	-0.113186937	0.90066667
Ccdc80	MmuINT0031273	chr16:45118363-45122959	IR-S	0.1911747	0.3035195	-0.112344827	0.872
Arntl	MmuEX0006229	chr7:120422971-120423096	C2	0.8389886	0.951268	-0.112279349	0.85
Arfgap1	MmuALTA0001881-1/2	chr2:180702307-180702519	Alt3	0.5865742	0.6985279	-0.111953688	0.84933333
Cdc16	MmuEX0010339	chr8:13758998-13759052	S	0.806557	0.9182388	-0.111681717	0.85266667
Pstk	MmuEX0037613	chr7:138517050-138517344	S	0.6811754	0.7926626	-0.11148717	0.84733333
Prrc2c	MmuALTA0014278-1/2	chr1:164653241-164653412	Alt3	0.2437823	0.3551295	-0.111347172	0.85933333
Tmem39a	MmuEX0047961	chr16:38575856-38575939	S	0.8366273	0.9477744	-0.111147156	0.93333333
Mtmr11	MmuEX0030063	chr3:95968356-95968491	S	0.8471985	0.9582376	-0.111039059	0.914
Eif2ak4	MmuEX0016515	chr2:118230783-118230885	S	0.8684732	0.9792872	-0.110813963	0.82933333
Zfml	MmuEX0053002	chr6:83931678-83931779	C1	0.2949814	0.4055253	-0.110543931	0.82533333
Cgnl1	MmuALTD0003083-1/2	chr9:71619316-	Alt5	0.7599611	0.8679934	-0.108032235	0.83666667
Plb1	MmuEX0035556	chr5:32627766-32627809	S	0.8209311	0.9284829	-0.107551786	0.84133333
Igdcc4	MmuEX0023770	chr9:64972419-64972583	S	0.8320373	0.9395162	-0.107478857	0.92133333
Arfgap3	MmuALTA0001885-1/2	chr15:83140680-83140811	Alt3	0.1483152	0.2554752	-0.107160007	0.80733333
Ncor2	MmuALTD0009193-1/2	chr5:125507172-125507294	Alt5	0.5100857	0.6168141	-0.106728338	0.80066667
Plb1	MmuEX0035557	chr5:32628472-32628580	S	0.800764	0.9066867	-0.105922718	0.82133333
Nelf	MmuEX0031485	chr2:24913485-24913490	MIC	0.065704	0.1713461	-0.105642009	0.83533333
Kif4	MmuALTA0009695-1/2	chrX:97909220-97909346	Alt3	0.0648301	0.1700661	-0.105236014	0.80866667
Cda	MmuEX0010292	chr4:137907099-137907210	S	0.8257685	0.9299397	-0.104171155	0.91
5730469M10Rik	MmuALTA0000599-1/2	chr14:41817330-41817492	Alt3	0.6603025	0.7638922	-0.103589723	0.90133333
Plcg1	MmuINT0121525	chr2:160579748-160580020	IR-S	0.1149734	0.2182585	-0.103285028	0.882
Phf6	MmuEX0034779	chrX:50270343-50270444	C2	0.8504822	0.9533676	-0.102885395	0.836
Ssh3	MmuEX0045049	chr19:4267747-4267978	C3	0.795896	0.8984539	-0.102557869	0.83333333
Plekhj1	MmuEX0035798	chr10:80260655-80260722	S	0.672185	0.7738169	-0.101631882	0.888
Ikbkap	MmuEX0023862	chr4:56787889-56787962	S	0.8565629	0.9580132	-0.101450315	0.88
Strada	MmuEX0045526	chr11:106032268-106032391	S	0.8681843	0.9686617	-0.100477445	0.892
Sgsm3	MmuALTD0012747-1/2	chr15:80833790-80833875	Alt5	0.8585732	0.9565324	-0.097959155	0.84133333
Tnpo3	MmuALTA0018602-1/2	chr6:29504883-29504962	Alt3	0.8661573	0.9638323	-0.097675057	0.99066667
Map4k3	MmuEX0027789	chr17:81028626-81028688	S	0.6408269	0.737983	-0.097156033	0.83133333
Nhej1	MmuEX0031694	chr1:75014743-75014849	S	0.8041598	0.9006952	-0.096535403	0.84533333

Ypel3	MmuEX0052574	chr7:133921568-133921611	S	0.8358928	0.9318137	-0.095920955	0.926
Aldoc	MmuEX0004623	chr11:78139437-78139636	S	0.8649017	0.9606447	-0.095743036	0.92333333
Crtc2	MmuEX0012798	chr3:90063076-90063144	S	0.6226972	0.718181	-0.095483787	0.82133333
Dgka	MmuEX0014397	chr10:128168380-128168468	S	0.8314131	0.9268635	-0.09545043	0.82266667
Pkmyt1	MmuINT0120788	chr17:23869792-23870789	IR-S	0.0721441	0.1673	-0.095155873	0.85466667
Hcfc1	MmuALTA0008418-1/2	chrX:71192534-71192853	Alt3	0.6523508	0.7471562	-0.094805424	0.81466667
Ankrd11	MmuEX0005001	chr8:125424502-125424598	S	0.1575116	0.2520934	-0.094581864	0.842
Tpx2	MmuALTD0014706-1/2	chr2:-152673845	Alt5	0.5687491	0.6627698	-0.094020696	0.85466667
Supv3l1	MmuALTD0013858-1/3	chr10:61906143-61906311	Alt5	0.8693623	0.9626975	-0.093335273	0.80733333
Gm98	MmuEX0021244	chr19:10303143-10303406	S	0.7326759	0.8257307	-0.093054758	0.814
Ccnt1	MmuEX0010085	chr15:98377176-98377339	S	0.8565989	0.9496098	-0.093010995	0.84466667
Ercc1	MmuINT0058725	chr7:19940522-19940641	IR-S	0.1079107	0.2004439	-0.092533172	0.812
Nae1	MmuEX0030804	chr8:107051278-107051349	S	0.850793	0.9427523	-0.091959279	0.856
Tmem161a	MmuEX0047785	chr8:72700744-72700824	C3	0.779516	0.870924	-0.091407944	0.844
Ubp1	MmuEX0050295	chr9:113868494-113868601	S	0.3630995	0.4544094	-0.091309857	0.81733333
Tle6	MmuEX0047448	chr10:81062780-81062860	C1	0.873347	0.9643958	-0.09104888	0.89733333
Tank	MmuINT0156890	chr2:61488346-61491435	IR-C	0.1363223	0.2271398	-0.090817461	0.86733333
Gmpr2	MmuINT0071744	chr14:56294570-56295591	IR-S	0.0609904	0.151763	-0.090772581	0.87266667
Eml2	MmuEX0016785	chr7:19787179-19787276	S	0.5593494	0.6499512	-0.090601843	0.82466667
Nup214	MmuEX0032768	chr2:31845755-31845881	S	0.8869195	0.9772394	-0.090319981	0.91066667
Phf20l1	MmuEX0034753	chr15:66462429-66462528	S	0.8921779	0.9815791	-0.089401182	0.80066667
Rbm5	MmuEX0039182	chr9:107662107-107662180	S	0.8966366	0.9859963	-0.089359659	0.93733333
Tspan17	MmuEX0049335	chr13:54897327-54897443	S	0.8586109	0.9477367	-0.08912578	0.87533333
Tpcn2	MmuEX0048563	chr7:152442419-152442501	C2	0.8929207	0.981913	-0.088992317	0.81733333
0610037P05Rik	MmuEX0000066	chr16:14313909-14314106	C2	0.8302135	0.918782	-0.08856846	0.90933333
Crtc2	MmuEX0012795	chr3:90061039-90061140	C2	0.682401	0.7707774	-0.088376408	0.80733333
Zfp334	MmuALTA0020582-1/2	chr2:-165207383	Alt3	0.0383216	0.1262951	-0.087973586	0.83266667
Sema3f	MmuALTD0012567-1/2	chr9:107592017-107592110	Alt5	0.8850566	0.97219	-0.087133431	0.87466667
Slc39a10	MmuEX0043270	chr1:46874908-46874988	S	0.8896325	0.9762224	-0.086589877	0.91666667
Mgat5	MmuALTA0010915-1/2	chr1:129203214-129203593	Alt3	0.1594591	0.2453861	-0.085926956	0.81333333
2310037I24Rik	MmuEX0000923	chr15:98361754-98361868	C3	0.0799454	0.1654669	-0.085521544	0.82133333
Tnrc6a	MmuEX0048382	chr7:130318940-130318972	S	0.8829847	0.9684413	-0.085456613	0.86933333
Rer1	MmuALTD0011754-1/2	chr4:154457241-154457345	Alt5	0.0717396	0.1570057	-0.08526614	0.886
Mdm2	MmuEX0028331	chr10:117146756-117146840	S	0.8355692	0.9202132	-0.084644036	0.90266667
Baiap2	MmuEX0007649	chr11:119858803-119859004	S	0.8813238	0.9657221	-0.084398334	0.84266667
Rin1	MmuALTA0015265-1/2	chr19:5051774-5051832	Alt3	0.0633696	0.1476444	-0.084274778	0.81733333
Srek1	MmuEX0044884	chr13:104554376-104554499	S	0.1142729	0.1983654	-0.084092409	0.81466667
Tcf4	MmuEX0046677	chr18:69506933-69507024	C2	0.8884951	0.9725733	-0.084078171	0.90733333
Trp53bp1	MmuEX0049084	chr2:121095955-121096045	S	0.8710434	0.9548362	-0.083792717	0.832
Fbxo9	MmuEX0018925	chr9:77942952-77943066	S	0.8855864	0.9691353	-0.083548917	0.86066667
Nt5c	MmuEX0032475	chr11:115352452-115352512	S	0.8442576	0.9274049	-0.083147248	0.94866667
Taz	MmuEX0046361	chrX:71534444-71534521	C2	0.8914998	0.9743221	-0.082822279	0.86733333
Zfp740	MmuEX0053594	chr15:102039184-102039307	S	0.79732	0.8800224	-0.082702417	0.874
Lipa	MmuALTA0010065-1/2	chr19:34599228-34599332	Alt3	0.0691366	0.1517978	-0.082661255	0.82866667
Crtc2	MmuEX0012796	chr3:90061217-90061333	C3	0.7017613	0.7839038	-0.082142475	0.83866667
Mfsd11	MmuALTD0008478-1/2	chr11:116722837-116722981	Alt5	0.8915589	0.9731993	-0.081640444	0.864
Ablim3	MmuINT0009131	chr18:61968616-61970964	IR-S	0.0518255	0.1332581	-0.081432638	0.81466667
Naga	MmuEX0030814	chr15:82168668-82168744	S	0.898523	0.9799032	-0.081380242	0.92133333
Med22	MmuINT0097426	chr2:26761514-26763612	IR-S	0.8866078	0.9678484	-0.081240667	0.854
Bag6	MmuEX0007606	chr17:35283702-35283848	S	0.5108394	0.5917009	-0.080861455	0.86133333
Crtc2	MmuEX0012797	chr3:90062387-90062448	C3	0.6969783	0.7776384	-0.080660051	0.822
Pcyox1l	MmuEX0034095	chr18:61863007-61863048	S	0.1317144	0.2120427	-0.080328371	0.83666667
Chd2	MmuALTD0003110-1/2	chr7:80586655-80586685	Alt5	0.0286812	0.1089589	-0.080277684	0.81133333
Mtss1	MmuEX0030166	chr15:58778881-58779075	C3	0.8298963	0.9096934	-0.079797066	0.87466667
Zfml	MmuEX0053001	chr6:83928988-83929903	C1	0.8762065	0.9559297	-0.079723108	0.88066667
D6Wsu116e	MmuEX0013632	chr6:116204431-116204511	S	0.8614894	0.9408365	-0.079347104	0.90133333
E130309D02Rik	MmuALTD0004586-1/2	chr5:144076582-	Alt5	0.8417398	0.9209925	-0.079252694	0.812
Rrp36	MmuEX0040605	chr17:46809655-46809796	C2	0.7772997	0.8563711	-0.079071396	0.83866667
Tbcel	MmuEX0046565	chr9:42252490-42252671	S	0.815544	0.8944391	-0.078895142	0.87533333
Sun1	MmuALTA0017589-1/2	chr5:139714785-139714893	Alt3	0.2646829	0.3434744	-0.078791503	0.83066667
2700029M09Rik	MmuEX0001175	chr8:63375535-63375633	C3	0.8654866	0.9440122	-0.078525639	0.81133333

Hsdl2	MmuEX0023325	chr4:59606109-59606207	S	0.8456623	0.9235314	-0.07786905	0.82533333
Lyn	MmuEX0027367	chr4:3669589-3669634	C1	0.8983439	0.9760818	-0.077737948	0.82
Nptn	MmuALTD0009528-1/2	chr9:58491339-58491491	Alt5	0.1213367	0.1982069	-0.076870145	0.82666667
Prmt5	MmuEX0037247	chr14:55135334-55135452	S	0.8355651	0.9124284	-0.076863394	0.866
Kirrel	MmuEX0025646	chr3:86901664-86901828	S	0.8994507	0.9760516	-0.07660085	0.88733333
Ankrd13b	MmuINT0015420	chr11:77285381-77285515	IR-S	0.8828828	0.9592844	-0.076401565	0.88
Clcn7	MmuEX0011608	chr17:25293746-25293797	S	0.8565431	0.9328127	-0.076269541	0.84733333
Ttf2	MmuALTA0019095-1/2	chr3:100758114-100758242	Alt3	0.0327104	0.1089258	-0.076215353	0.82066667
Fam114a2	MmuALTD0005173-1/2	chr11:57327597-57327790	Alt5	0.8902454	0.9664043	-0.076158926	0.87266667
Ppip5k2	MmuALTA0013876-1/2	chr1:99637401-99637519	Alt3	0.1084772	0.1846021	-0.076124886	0.82133333
Tada2a	MmuEX0046146	chr11:83931750-83931809	S	0.8936759	0.9696512	-0.075975295	0.86333333
Napg	MmuINT0105631	chr18:63151534-63153965	IR-S	0.0255005	0.1014431	-0.075942627	0.87866667
Ipo13	MmuALTA0009268-1/2	chr4:117576403-117576509	Alt3	0.0316015	0.1074845	-0.07588298	0.846
Pcif1	MmuINT0116133	chr2:164704990-164708274	IR-S	0.0846829	0.1605082	-0.075825334	0.80866667
Gale	MmuINT0067228	chr4:135522032-135522284	IR-S	0.060263	0.1358746	-0.075611593	0.85333333
Ide	MmuEX0023575	chr19:37364534-37364678	C3	0.0393236	0.1144393	-0.075115737	0.89933333
0610007P22Rik	MmuEX0000030	chr17:25379104-25379167	S	0.8209081	0.8958068	-0.074898676	0.92066667
Asl	MmuINT0019804	chr5:130499967-130500163	IR-S	0.1980609	0.2727898	-0.074728942	0.81133333
Mtmr14	MmuEX0030080	chr6:113219495-113219553	S	0.8812172	0.9559015	-0.074684357	0.842
Cnot1	MmuALTA0004325-1/2	chr8:98285223-98285336	Alt3	0.056235	0.1308714	-0.074636417	0.87933333
Ift80	MmuEX0023730	chr3:68739769-68739843	S	0.9020276	0.9766171	-0.074589425	0.88266667
Adck5	MmuINT0011724	chr15:76425697-76425766	IR-S	0.0467649	0.1208047	-0.074039806	0.82266667
Snx14	MmuEX0044238	chr9:88295561-88295587	S	0.0885921	0.1626251	-0.074033037	0.818
Echdc2	MmuEX0016195	chr4:107842320-107842387	S	0.8927867	0.9667281	-0.07394143	0.89533333
Hsdl2	MmuEX0023328	chr4:59610129-59610227	C2	0.9071617	0.9808165	-0.073654845	0.87266667
4933427D14Rik	MmuEX0001873	chr11:72015914-72016052	S	0.8975653	0.9711757	-0.073610486	0.85866667
Picalm	MmuALTA0013222-1/2	chr7:97330750-97330878	Alt3	0.102073	0.1754313	-0.073358363	0.844
Trp53inp1	MmuEX0049097	chr4:11095044-11095081	S	0.5699951	0.643016	-0.07302088	0.81866667
Mef2a	MmuEX0028559	chr7:74389407-74389430	S	0.0398313	0.1124604	-0.072629028	0.91466667
Stxbp5	MmuEX0045641	chr10:9497819-9497869	C1	0.9057084	0.9780467	-0.072338317	0.90533333
Atg16l2	MmuEX0006630	chr7:108447520-108447622	S	0.8868871	0.9589537	-0.072066611	0.83733333
Ap3d1	MmuEX0005453	chr10:80179219-80179364	C2	0.8967651	0.9685243	-0.071759211	0.824
Nthl1	MmuEX0032515	chr17:24771670-24771840	S	0.9084683	0.9801912	-0.071722898	0.91666667
Pnpla6	MmuEX0036053	chr8:3537969-3538085	C3	0.895969	0.9675259	-0.071556899	0.85533333
Irak1	MmuEX0024482	chrX:71268405-71268536	S	0.8865139	0.9577614	-0.07124752	0.898
Tdrd7	MmuEX0046837	chr4:46031402-46031488	S	0.9107171	0.9818913	-0.071174215	0.908
Ubxn8	MmuEX0050426	chr8:34743974-34744099	S	0.9127998	0.9838115	-0.071011615	0.92933333
Cdk2ap2	MmuALTD0002919-1/2	chr19:4097817-4097907	Alt5	0.1330213	0.2039503	-0.070929071	0.876
Anapc16	MmuEX0004851	chr10:59465166-59465215	C1	0.2331475	0.3040312	-0.070883762	0.82133333
Hsf1	MmuEX0023331	chr15:76330561-76330626	S	0.7951784	0.8660618	-0.070883479	0.86266667
ORF61	MmuALTA0012469-1/3	chr10:79441141-79441169	Alt3	0.0798433	0.1500755	-0.070232196	0.864
Med14	MmuALTA0010782-1/3	chrX:12324975-12325103	Alt3	0.9076454	0.9776828	-0.070037412	0.864
Zmynd8	MmuEX0053991	chr2:165709679-165709739	S	0.0709462	0.140737	-0.06979072	0.81333333
Acer3	MmuEX0003470	chr7:105366566-105366611	S	0.9109092	0.9804519	-0.069542682	0.89466667
Fanca	MmuEX0018526	chr8:125796220-125796332	S	0.9098238	0.9784116	-0.068587743	0.89466667
Chka	MmuEX0011300	chr19:3871003-3871062	C2	0.1504018	0.2186319	-0.068230097	0.85333333
Stx5a	MmuALTD0013798-1/2	chr19:8817843-8817913	Alt5	0.890502	0.9587237	-0.068221672	0.85666667
Rbm39	MmuEX0039147	chr2:156004616-156004688	S	0.2218962	0.2900972	-0.068200945	0.88266667
Impact	MmuEX0024095	chr18:13134488-13134540	S	0.8981259	0.9662241	-0.068098213	0.914
Fam176b	MmuEX0018106	chr4:125826128-125826289	S	0.7928569	0.8609372	-0.068080265	0.92333333
Prpf40a	MmuALTA0014214-1/2	chr2:53004858-53004949	Alt3	0.755817	0.8238891	-0.068072156	0.80733333
Irak1	MmuEX0024486	chrX:71267524-71267588	C3	0.9015151	0.9693237	-0.067808512	0.83266667
Megf8	MmuEX0028608	chr7:26119811-26119974	S	0.9144313	0.9817313	-0.067300061	0.842
Stx16	MmuEX0045570	chr2:173919430-173919573	S	0.9151827	0.9818932	-0.066710509	0.91733333
Rhebl1	MmuEX0039725	chr15:98709439-98709486	S	0.8059649	0.8725565	-0.066591589	0.82666667
Klhdc5	MmuEX0025728	chr6:147050088-147050281	S	0.9115647	0.9779717	-0.06640696	0.85733333
Map4k4	MmuEX0027796	chr1:40068495-40068686	S	0.6736001	0.7400021	-0.066401988	0.816
Zyx	MmuEX0054111	chr6:42301269-42301361	S	0.7424483	0.8088151	-0.066366845	0.81066667
Picalm	MmuEX0035018	chr7:97342783-97342806	S	0.3407291	0.4069238	-0.066194758	0.832
Sgta	MmuALTD0012748-1/3	chr10:80522873-	Alt5	0.8329168	0.8990918	-0.066175067	0.88666667
Top1mt	MmuINT0163850	chr15:75487645-75488113	IR-S	0.0339897	0.0998191	-0.06582939	0.814

Vegfb	MmuEX0051323	chr19:7060780-7060976	S	0.9113588	0.9771387	-0.065779895	0.90666667
Fblim1	MmuEX0018705	chr4:141157898-141158005	C3	0.095138	0.1608837	-0.065745716	0.88466667
Exo1	MmuALTA0006647-1/2	chr1:177823104-177823192	Alt3	0.040973	0.1066379	-0.065664901	0.80933333
Polr3a	MmuEX0036306	chr14:25295235-25295338	S	0.9062238	0.9718768	-0.065653019	0.84733333
Dph1	MmuALTD0004436-1/4	chr11:75003901-75004021	Alt5	0.8870615	0.9526318	-0.065570282	0.80866667
Ccnt1	MmuINT0031772	chr15:98377026-98377175	IR-S	0.0405382	0.1059673	-0.065429112	0.826
Bnip2	MmuEX0008099	chr9:69852113-69852148	S	0.1870393	0.2524149	-0.065375575	0.842
Myef2	MmuEX0030334	chr2:124923299-124923370	S	0.3917399	0.4569664	-0.065226542	0.852
Kntc1	MmuEX0025859	chr5:124205683-124205803	S	0.9036859	0.9686462	-0.06496024	0.80333333
Gtf3c1	MmuALTA0008284-1/2	chr7:132802571-132802725	Alt3	0.0301008	0.0949765	-0.064875781	0.91133333
Ctdp1	MmuEX0013022	chr18:80630905-80631067	S	0.9191807	0.9839871	-0.064806366	0.90333333
Dapk3	MmuEX0013762	chr10:80653787-80653813	S	0.8439674	0.9082761	-0.064308773	0.82066667
Susd1	MmuEX0045801	chr4:59382403-59382509	C3	0.8312409	0.8953062	-0.064065297	0.806
Trrap	MmuINT0166368	chr5:145598193-145600269	IR-S	0.0462986	0.1102209	-0.06392229	0.86866667
Dgka	MmuEX0014395	chr10:128171144-128171193	S	0.8978061	0.9616759	-0.063869797	0.82933333
Myst2	MmuEX0030642	chr11:95152834-95152896	S	0.7020155	0.7652955	-0.063280076	0.814
Hsdl2	MmuEX0023327	chr4:59609735-59609838	C3	0.9175584	0.980716	-0.063157538	0.85733333
Sec24b	MmuEX0041495	chr3:129723456-129723560	S	0.5625496	0.6254742	-0.062924574	0.806
Sf1	MmuEX0041898	chr19:6375658-6375862	S	0.334966	0.3976079	-0.062641841	0.84666667
Ppox	MmuEX0036654	chr1:173210000-173210132	S	0.9257774	0.9883304	-0.062553016	0.93333333
Yipf1	MmuEX0052538	chr4:107009042-107009129	S	0.9245796	0.9862429	-0.061663333	0.928
Plekha5	MmuEX0035717	chr6:140521386-140521487	S	0.8971594	0.9583842	-0.061224779	0.85666667
Pigx	MmuEX0035099	chr16:32087380-32087593	S	0.8798613	0.941061	-0.061199713	0.83933333
Trim24	MmuALTD0014777-1/2	chr6:37895521-37895687	Alt5	0.7167443	0.7778556	-0.061111319	0.82066667
Zfp516	MmuEX0053402	chr18:83162462-83162581	S	0.921829	0.9827088	-0.060879772	0.90266667
D6Wsu116e	MmuEX0013631	chr6:116177364-116177552	S	0.8805798	0.9414338	-0.060854023	0.83733333
Tcof1	MmuEX0046741	chr18:60991820-60991963	S	0.8629627	0.9233767	-0.060413978	0.91933333
Sun1	MmuEX0045737	chr5:139706727-139706792	C3	0.9309874	0.9911346	-0.060147129	0.898
Map2k7	MmuEX0027697	chr8:4244861-4245003	S	0.9180676	0.9781436	-0.060076	0.93733333
Prune	MmuINT0127594	chr3:95072246-95085506	IR-S	0.0565985	0.1166417	-0.060043172	0.83
Dido1	MmuEX0014686	chr2:180425227-180425338	S	0.0467828	0.1066938	-0.059910976	0.804
Clcn7	MmuEX0011609	chr17:25294434-25294519	S	0.9271042	0.9869035	-0.059799266	0.932
Fcho2	MmuALTA0007148-1/2	chr13:99513366-99513490	Alt3	0.021065	0.0806856	-0.059620617	0.844
Tmem50b	MmuEX0047998	chr16:91583521-91583633	S	0.9241752	0.9833821	-0.059206874	0.82866667
Drap1	MmuALTA0005846-1/2	chr19:5423607-5423653	Alt3	0.8715319	0.9303197	-0.058787822	0.93666667
Sipa1	MmuINT0143848	chr19:5652874-5653998	IR-C	0.0383053	0.0970273	-0.058722013	0.812
Htra2	MmuEX0023442	chr6:83002692-83002797	S	0.8781887	0.9366253	-0.058436537	0.898
Lmo7	MmuEX0026624	chr14:102317157-102317261	S	0.9082141	0.9664919	-0.058277746	0.83933333
Sigirr	MmuALTD0012812-1/2	chr7:148282519-148282535	Alt5	0.8730359	0.9309578	-0.057921869	0.87733333
Gtpbp2	MmuEX0022162	chr17:46302727-46302946	S	0.9249384	0.9827025	-0.057764067	0.89333333
Rock2	MmuEX0040284	chr12:16935740-16935840	S	0.9178161	0.9750796	-0.057263549	0.85
Snapc1	MmuEX0044080	chr12:75083465-75083566	S	0.8988441	0.9560499	-0.0572058	0.828
Fastkd2	MmuEX0018663	chr1:63782419-63782542	S	0.8817543	0.9389018	-0.057147483	0.80266667
Gnl3	MmuALTD0006118-1/2	chr14:31830013-31830093	Alt5	0.8805983	0.9374256	-0.056827229	0.846
Tnrc6a	MmuEX0048379	chr7:130316747-130316923	S	0.9191078	0.9757779	-0.056670114	0.86
Prpsap1	MmuALTA0014241-1/2	chr11:116340966-116341138	Alt3	0.9220242	0.9786462	-0.056621982	0.872
Clk3	MmuEX0011722	chr9:57606434-57606530	S	0.8876653	0.9442267	-0.056561364	0.92
Atf7	MmuEX0006593	chr15:102393745-102393841	S	0.9306796	0.9870104	-0.056330871	0.82133333
Tmem20	MmuEX0047880	chr19:38474924-38475104	S	0.9090442	0.9651301	-0.056085948	0.82266667
P2rx4	MmuEX0033383	chr5:123174603-123174683	S	0.8217096	0.8777302	-0.056020608	0.844
Otud4	MmuALTA0012620-1/2	chr8:82190615-82190738	Alt3	0.9258557	0.9817891	-0.055933383	0.862
Unc5b	MmuEX0050631	chr10:60240138-60240302	C1	0.8792162	0.9348975	-0.05568135	0.95333333
Metap1d	MmuEX0028695	chr2:71360590-71360687	S	0.9287198	0.9843217	-0.055601927	0.89133333
Atg9a	MmuEX0006681	chr1:75181030-75181147	S	0.9022147	0.9575551	-0.055340391	0.84466667
Psen1	MmuEX0037504	chr12:85040305-85040371	S	0.923603	0.9788145	-0.055211492	0.896
Cntrob	MmuEX0012034	chr11:69116354-69116468	S	0.9217556	0.9769495	-0.055193931	0.85466667
Lrrc14	MmuEX0026925	chr15:76543831-76544415	S	0.91037	0.9652892	-0.054919257	0.81133333
Isyna1	MmuEX0024549	chr8:73118519-73118647	S	0.9045155	0.9594028	-0.054887319	0.91733333
Tnk2	MmuALTD0014613-1/2	chr16:32670039-32670302	Alt5	0.0350653	0.0898962	-0.05483084	0.82933333
Inf2	MmuEX0024138	chr12:113841923-113842064	S	0.9318404	0.9866197	-0.054779354	0.938
Sgsm3	MmuEX0042101	chr15:80837877-80838020	S	0.9314712	0.9860522	-0.054580939	0.80333333

Vegfb	MmuEX0051324	chr19:7060511-7060584	S	0.9238792	0.9783441	-0.054464921	0.93933333
Fbf1	MmuEX0018697	chr11:116012103-116012161	S	0.9323616	0.9866009	-0.054239296	0.808
Papola	MmuEX0033600	chr12:107071310-107071372	S	0.889698	0.9435887	-0.053890676	0.80333333
Terf2	MmuEX0046964	chr8:109618722-109618852	S	0.9239508	0.9777862	-0.053835428	0.82
Aatf	MmuEX0002922	chr11:84324985-84325080	S	0.921951	0.9754157	-0.053464745	0.90066667
Med20	MmuEX0028520	chr17:47755758-47756011	C1	0.911816	0.9648627	-0.053046732	0.81
Blm	MmuEX0008028	chr7:87618915-87619110	S	0.9208838	0.9736118	-0.05272796	0.82333333
Plaa	MmuEX0035534	chr4:94256572-94256765	S	0.9053482	0.9579092	-0.052560964	0.836
Lztr1	MmuEX0027436	chr16:17524401-17524550	S	0.901482	0.9538453	-0.052363298	0.82333333
Npr2	MmuEX0032213	chr4:43656207-43656281	S	0.9341341	0.9857696	-0.051635497	0.89266667
AA408296	MmuALTD0000665-1/3	chr1:194956238-	Alt5	0.923652	0.9752804	-0.051628384	0.81466667
Cpt1c	MmuEX0012628	chr7:52220454-52220636	S	0.933221	0.9847986	-0.051577695	0.86466667
Azin1	MmuEX0007181	chr15:38436942-38437101	S	0.1780855	0.2292625	-0.051177063	0.81733333
Flot1	MmuEX0019350	chr17:35961224-35961314	S	0.8765688	0.9276	-0.051031245	0.886
Lepre1	MmuALTA0009994-1/3	chr4:118914288-118914409	Alt3	0.933772	0.9847588	-0.050986772	0.88533333
Rnf34	MmuEX0040181	chr5:123311698-123311916	S	0.9336067	0.9841651	-0.050558435	0.866
Srrm1	MmuEX0044966	chr4:134902231-134902360	S	0.0201509	0.0705394	-0.050388584	0.85533333
Mllt6	MmuEX0029243	chr11:97537453-97537519	S	0.9277897	0.977953	-0.050163313	0.84
5730469M10Rik	MmuALTD0000562-1/2	chr14:41826987-	Alt5	0.9070016	0.8567972	0.050204366	0.82133333
Mtmr11	MmuINT0101894	chr3:95974570-95975008	IR-S	0.092044	0.0414674	0.050576607	0.80266667
Stk25	MmuINT0154086	chr1:95522184-95522357	IR-S	0.1648711	0.1141689	0.050702197	0.80533333
Sh2b1	MmuINT0142937	chr7:133612843-133614635	IR-S	0.0948951	0.0440791	0.050816028	0.82
Thop1	MmuALTA0018165-1/2	chr10:80540661-80540760	Alt3	0.0724702	0.0214363	0.051033816	0.83866667
Tnpo3	MmuINT0163475	chr6:29504963-29505152	IR-S	0.0918527	0.0407077	0.051144951	0.866
Xrcc1	MmuINT0176964	chr7:25352946-25355234	IR-S	0.1106431	0.0594393	0.051203739	0.80533333
Lrrc42	MmuINT0093029	chr4:106906590-106908404	IR-S	0.074224	0.0230065	0.051217547	0.86933333
Pkn1	MmuINT0120799	chr8:86196232-86197200	IR-S	0.0737856	0.0224177	0.051367904	0.802
Mfge8	MmuEX0028788	chr7:86288164-86288274	S	0.2707689	0.2191984	0.051570559	0.93
Rexo4	MmuEX0039487	chr2:26813999-26814087	C2	0.9787914	0.9271728	0.051618663	0.85
Nfat5	MmuEX0031580	chr8:109871567-109871757	C3	0.9626324	0.9109333	0.05169913	0.804
Arhgef5	MmuINT0018639	chr6:43215743-43222303	IR-S	0.084003	0.0320916	0.05191135	0.80733333
Bpnt1	MmuEX0008140	chr1:187161985-187162111	S	0.9162525	0.8642913	0.051961235	0.86333333
Pan3	MmuEX0033551	chr5:148331081-148331328	C3	0.9579407	0.9059168	0.052023924	0.83333333
Tbrg4	MmuINT0157805	chr11:6520147-6520744	IR-S	0.2091838	0.1569318	0.052251967	0.812
Aurkb	MmuINT0022300	chr11:68863979-68864401	IR-S	0.0974391	0.0451841	0.052254957	0.89266667
Marveld1	MmuINT0095940	chr19:42224050-42225287	IR-S	0.1100797	0.057675	0.052404644	0.82066667
Clasrp	MmuINT0036794	chr7:20166508-20166729	IR-S	0.0772263	0.0246872	0.052539133	0.872
Hsf1	MmuINT0079205	chr15:76330767-76330846	IR-S	0.1249457	0.0723902	0.052555545	0.82466667
Trmt2a	MmuINT0165646	chr16:18252342-18252494	IR-S	0.118647	0.065908	0.052738981	0.814
Hjurp	MmuINT0077956	chr1:90166875-90169303	IR-C	0.1343469	0.081531	0.052815865	0.89466667
Tuft1	MmuINT0168279	chr3:94426068-94426609	IR-S	0.0977568	0.0447678	0.05298897	0.84
2500003M10Rik	MmuINT0002587	chr3:90304030-90306037	IR-S	0.1023592	0.0493571	0.05300215	0.83466667
Acadvl	MmuINT0009473	chr11:69826586-69826673	IR-S	0.0812593	0.0282269	0.053032475	0.83266667
Traf7	MmuEX0048730	chr17:24653450-24653541	C1	0.8549857	0.8017595	0.053226185	0.84133333
Ppp1r16a	MmuEX0036712	chr15:76523869-76523944	S	0.9608965	0.9076181	0.053278412	0.808
Traf7	MmuINT0164563	chr17:24647317-24647400	IR-S	0.0785362	0.0251755	0.05336067	0.93466667
Cacnb3	MmuINT0027924	chr15:98471182-98471389	IR-S	0.0820453	0.0286218	0.053423503	0.86266667
Gga1	MmuINT0068629	chr15:78716375-78718540	IR-S	0.0973421	0.0438131	0.053528942	0.84
Fam195a	MmuINT0061458	chr17:26001298-26001538	IR-S	0.080721	0.0271197	0.05360138	0.82933333
Hsf1	MmuEX0023336	chr15:76328584-76328720	S	0.8971121	0.8434704	0.053641683	0.82
Zfp498	MmuEX0053380	chr5:146047177-146047378	S	0.9675719	0.9139247	0.053647163	0.83866667
Pcif1	MmuEX0033977	chr2:164714886-164714972	C3	0.9568075	0.9030128	0.053794695	0.82733333
Atxn7l3	MmuINT0022253	chr11:102153522-102153755	IR-S	0.0864964	0.0326163	0.053880079	0.82333333
Cdk11b	MmuEX0010536	chr4:155016594-155016684	S	0.9850335	0.9309614	0.054072191	0.88066667
Grk6	MmuINT0074221	chr13:55553205-55553495	IR-S	0.085863	0.0317038	0.054159231	0.906
Zranb1	MmuEX0054026	chr7:140162869-140163022	C2	0.989543	0.9352383	0.054304642	0.84533333
Phrf1	MmuALTA0013192-1/2	chr7:148443243-148443397	Alt3	0.9718447	0.9175295	0.05431518	0.80066667
1810032O08Rik	MmuINT0001724	chr11:116534053-116535251	IR-S	0.1044883	0.0500333	0.054454999	0.802
Ercc1	MmuINT0058724	chr7:19938055-19939674	IR-S	0.0837965	0.029308	0.054488476	0.80666667
Oxa1l	MmuINT0114193	chr14:54983180-54986392	IR-C	0.0887778	0.0339921	0.054785696	0.86933333
Adrbk1	MmuINT0012180	chr19:4291331-4291589	IR-S	0.089615	0.0345387	0.055076315	0.85733333

Usp21	MmuINT0171436	chr1:173213873-173214092	IR-C	0.1129805	0.0578902	0.055090308	0.81266667
Cinp	MmuEX0011439	chr12:112115051-112115180	S	0.9691636	0.9140597	0.055103817	0.83933333
Csnk1e	MmuINT0043069	chr15:79251441-79255269	IR-C	0.1203181	0.0650453	0.055272763	0.83066667
Fbrs	MmuINT0062998	chr7:134628757-134628866	IR-C	0.0804732	0.0251673	0.05530589	0.832
1810014F10Rik	MmuINT0001673	chr7:147285606-147285777	IR-S	0.1401394	0.0847458	0.055393629	0.822
Agxt2l2	MmuEX0004351	chr11:51412153-51412242	S	0.9809492	0.9254912	0.05545802	0.86266667
Cep55	MmuALTD0003042-1/2	chr19:38132279-38132473	Alt5	0.9490901	0.8935969	0.055493173	0.812
Ppan	MmuINT0124382	chr9:20695457-20695526	IR-S	0.1170112	0.0612728	0.055738457	0.84466667
Lhpp	MmuEX0026395	chr7:139822165-139822352	S	0.9724688	0.9166234	0.055845413	0.828
Fbrs	MmuEX0018747	chr7:134631388-134631468	S	0.9894576	0.9336113	0.05584627	0.94
Ephx1	MmuALTA0006488-1/2	chr1:182924010-182924176	Alt3	0.0694498	0.0134603	0.0559895	0.92066667
Alg8	MmuINT0014149	chr7:104532317-104535311	IR-S	0.1204432	0.064415	0.056028194	0.88666667
Arhgap27	MmuEX0005853	chr11:103200339-103200422	S	0.9720185	0.915975	0.056043483	0.88933333
Crim1	MmuEX0012728	chr17:78680586-78680706	C2	0.9525291	0.8964131	0.056116015	0.80533333
Hira	MmuEX0022943	chr16:18947237-18947335	S	0.0857214	0.0294787	0.056242698	0.84
Mrps2	MmuEX0029731	chr2:28324741-28324848	S	0.0713263	0.0150221	0.056304148	0.932
Pcif1	MmuEX0033976	chr2:164714594-164714766	C2	0.9568668	0.9001551	0.056711688	0.83333333
Rxrb	MmuINT0138112	chr17:34173910-34174111	IR-S	0.0878396	0.0311211	0.056718478	0.81266667
Ipo4	MmuINT0082786	chr14:56247825-56247903	IR-S	0.1192524	0.0623795	0.056872902	0.80866667
Nol7	MmuINT0109458	chr13:43494165-43494879	IR-S	0.095118	0.0382316	0.056886382	0.84133333
Pvt1	MmuINT0129846	chr15:62007104-62073728	IR-S	0.0960882	0.0391585	0.056929646	0.81933333
Spag9	MmuINT0150947	chr11:93973461-93975486	IR-S	0.118452	0.0615078	0.056944178	0.818
Dusp6	MmuINT0054000	chr10:98726726-98727177	IR-S	0.0716378	0.0146591	0.056978707	0.99533333
Commd10	MmuEX0012374	chr18:47123314-47123424	C3	0.9862819	0.9292659	0.057016031	0.928
Tatdn1	MmuEX0046340	chr15:58755460-58755523	S	0.9496299	0.8925251	0.057104774	0.832
Ska1	MmuEX0042478	chr18:74362244-74362341	S	0.9712165	0.914041	0.05717554	0.826
Ranbp3	MmuINT0131512	chr17:56846662-56847273	IR-S	0.0939629	0.0367296	0.057233265	0.86466667
Ercc1	MmuEX0017237	chr7:19937982-19938054	S	0.9355209	0.8782526	0.057268342	0.812
Spsb3	MmuEX0044809	chr17:25027513-25027700	S	0.9816605	0.9242004	0.057460091	0.88866667
Sigirr	MmuINT0143637	chr7:148277401-148277701	IR-S	0.3132091	0.2556435	0.057565602	0.866
Kat5	MmuINT0085267	chr19:5605684-5607550	IR-S	0.0819885	0.0242191	0.057769323	0.858
Rin1	MmuINT0135051	chr19:5053276-5053598	IR-S	0.0931067	0.035275	0.057831736	0.822
Git1	MmuINT0068966	chr11:77314617-77316330	IR-S	0.0917318	0.033782	0.057949819	0.83933333
Zfyve27	MmuEX0053824	chr19:42263687-42263733	S	0.9747899	0.9166441	0.058145832	0.86133333
Dgka	MmuEX0014392	chr10:128165312-128165397	S	0.9825221	0.9243554	0.058166618	0.904
Parp3	MmuINT0115442	chr9:106375538-106375763	IR-S	0.1161416	0.0579083	0.058233382	0.80133333
Gstm2	MmuINT0074614	chr3:107788601-107788951	IR-S	0.0713821	0.0130099	0.058372233	0.92266667
Rab6	MmuEX0038387	chr7:107778352-107778457	C3	0.8427674	0.7842701	0.058497362	0.834
Psrc1	MmuINT0128262	chr3:108187204-108187291	IR-S	0.2728287	0.2142918	0.058536855	0.82666667
Fam119a	MmuINT0060622	chr1:64661784-64662846	IR-S	0.0812377	0.0226777	0.058559966	0.826
Ncln	MmuINT0106543	chr10:80956285-80958824	IR-S	0.0859421	0.0273661	0.058576002	0.92733333
Nudt1	MmuEX0032597	chr5:140808377-140808427	S	0.9048131	0.8461495	0.058663529	0.812
Cxxc1	MmuINT0044416	chr18:74378310-74378385	IR-S	0.0844981	0.025788	0.058710152	0.91133333
Polrmt	MmuINT0124031	chr10:79200255-79200344	IR-S	0.1025777	0.043844	0.058733752	0.81133333
Rnpepl1	MmuINT0136062	chr1:94813049-94813287	IR-S	0.0773048	0.0184385	0.058866318	0.878
Haus6	MmuINT0076035	chr4:86250194-86251540	IR-S	0.0881754	0.0292811	0.058894289	0.808
Gbf1	MmuEX0020159	chr19:46344748-46344841	S	0.9812119	0.9222916	0.058920313	0.87933333
Psip1	MmuINT0127791	chr4:83107146-83109498	IR-C	0.1235875	0.0646021	0.058985427	0.83133333
Nubp2	MmuINT0111394	chr17:25022563-25022663	IR-S	0.1007979	0.0416678	0.059130113	0.83266667
Otud5	MmuINT0114115	chrX:7451080-7451358	IR-S	0.0817627	0.0226014	0.059161219	0.852
Ide	MmuEX0023574	chr19:37365160-37365304	S	0.976757	0.917286	0.059470936	0.91933333
Micall1	MmuINT0098687	chr15:78953417-78954930	IR-S	0.0897975	0.0302548	0.059542654	0.80266667
2700007P21Rik	MmuEX0001172	chr2:106812925-106813319	C2	0.1033494	0.043802	0.059547374	0.81533333
Ddx17	MmuALTD0004079-1/3	chr15:79362108-79362298	Alt5	0.7583282	0.6986605	0.059667671	0.84333333
Ampd3	MmuEX0004816	chr7:117934702-117934861	C3	0.9788842	0.9190907	0.059793564	0.81066667
Inf2	MmuINT0082086	chr12:113843074-113843583	IR-S	0.089777	0.0299727	0.059804311	0.88266667
Csnk1g2	MmuINT0043093	chr10:80101979-80102324	IR-S	0.1118794	0.0518776	0.060001819	0.91133333
Id1	MmuINT0080143	chr2:152562482-152562707	IR-S	0.0922599	0.0322343	0.06002561	0.99933333
Scly	MmuEX0041234	chr1:93206374-93206480	S	0.9622991	0.9021627	0.060136369	0.86066667
Apba3	MmuINT0016991	chr10:80732330-80733712	IR-S	0.0883143	0.0279831	0.060331156	0.854
Tmem134	MmuINT0161475	chr19:4127640-4127759	IR-S	0.1189764	0.0585952	0.060381157	0.854

R3hdm2	MmuEX0038219	chr10:126899262-126899339	S	0.9512997	0.8908595	0.060440196	0.84666667
Eml3	MmuINT0057207	chr19:9011978-9012052	IR-S	0.1204689	0.0600277	0.060441219	0.81466667
Zmynd8	MmuINT0180616	chr2:165646189-165653707	IR-C	0.1139522	0.0529135	0.061038747	0.836
Hgs	MmuINT0077598	chr11:120344416-120344702	IR-S	0.1521313	0.0910582	0.061073086	0.806
Alg9	MmuEX0004668	chr9:50591363-50591433	S	0.9542773	0.893094	0.061183314	0.82466667
Snhg1	MmuINT0149687	chr19:8799537-8799711	IR-S	0.2299587	0.1687266	0.061232075	0.85066667
Mff	MmuEX0028787	chr1:82743658-82743717	C2	0.5469946	0.4857098	0.061284796	0.826
Llgl1	MmuINT0091354	chr11:60522396-60522936	IR-S	0.1064659	0.0451699	0.061296033	0.80866667
Eif4g2	MmuINT0056593	chr7:118219227-118220209	IR-C	0.1153149	0.0539695	0.06134537	0.87866667
Pcsk7	MmuEX0034084	chr9:45734817-45734911	C1	0.9865739	0.9251535	0.061420478	0.84333333
Aph1a	MmuINT0017118	chr3:95700284-95700616	IR-S	0.9202598	0.8587794	0.061480383	0.95
Rpp21	MmuINT0136861	chr17:36394652-36394727	IR-S	0.1769545	0.1152755	0.061678951	0.80466667
Acin1	MmuEX0003479	chr14:55272051-55272115	S	0.2053971	0.143678	0.061719109	0.81933333
Ranbp10	MmuEX0038697	chr8:108298187-108298335	S	0.9823311	0.920438	0.061893147	0.828
Ftsjd2	MmuINT0066431	chr17:29835675-29836164	IR-C	0.0984449	0.0365352	0.061909703	0.87866667
Dtx3	MmuINT0053774	chr10:126631691-126632749	IR-S	0.0782592	0.0163058	0.06195341	0.92066667
Cd97	MmuINT0032583	chr8:86253425-86257312	IR-C	0.1005087	0.0385017	0.062007045	0.81
Fam49b	MmuEX0018344	chr15:63802485-63802523	C2	0.86899	0.8069792	0.062010764	0.83266667
Cast	MmuEX0009297	chr13:74917951-74918022	S	0.9796	0.9171789	0.062421066	0.81533333
Bet1l	MmuINT0024795	chr7:148040721-148040972	IR-S	0.1455856	0.0831392	0.062446401	0.84133333
Spns1	MmuINT0151896	chr7:133517588-133518580	IR-S	0.1702246	0.107772	0.062452646	0.82266667
Cx3cl1	MmuEX0013248	chr8:97301928-97302048	S	0.9807558	0.9182741	0.062481774	0.868
Tia1	MmuINT0160065	chr6:86375065-86375443	IR-S	0.1107139	0.0480267	0.062687206	0.842
Clk3	MmuINT0037424	chr9:57599635-57599921	IR-S	0.0925189	0.0297779	0.062740939	0.86666667
Adrbk1	MmuINT0012165	chr19:4290006-4290073	IR-S	0.0833389	0.0203444	0.06299447	0.94866667
Sri	MmuEX0044919	chr5:8059353-8059422	S	0.9549121	0.8917781	0.063134007	0.88266667
Gltscr2	MmuINT0069537	chr7:16523239-16523522	IR-S	0.1227324	0.059388	0.063344376	0.86733333
Cxxc1	MmuINT0044419	chr18:74379222-74379491	IR-S	0.1345044	0.0708536	0.063650851	0.848
Znf512b	MmuALTA0020891-1/3	chr2:181323784-181323949	Alt3	0.0886273	0.0249604	0.063666887	0.844
Egr1	MmuINT0055886	chr18:35021441-35022118	IR-S	0.1013937	0.0373911	0.06400258	0.85733333
Gtse1	MmuINT0075106	chr15:85702012-85704069	IR-S	0.0951432	0.0310676	0.064075595	0.85733333
Hnrnpd	MmuEX0023101	chr5:100405553-100405609	S	0.5671751	0.5029533	0.064221806	0.86066667
Hgsnat	MmuALTA0008585-1/2	chr8:27083314-27083423	Alt3	0.0876475	0.023303	0.064344473	0.83
Nxf1	MmuINT0112178	chr19:8839522-8841286	IR-S	0.3454367	0.2810845	0.064352194	0.82333333
Top2a	MmuINT0163887	chr11:98854728-98855077	IR-S	0.3283833	0.2638778	0.064505505	0.84
Lysmd2	MmuINT0094108	chr9:75483525-75485018	IR-S	0.1001622	0.0356472	0.064514984	0.80133333
Foxm1	MmuINT0065643	chr6:128322622-128322794	IR-S	0.1765812	0.1117783	0.064802871	0.808
Grpel2	MmuINT0074315	chr18:61879510-61885879	IR-S	0.1045877	0.0397554	0.06483228	0.80733333
Lypla2	MmuINT0094085	chr4:135525445-135525515	IR-S	0.122587	0.057534	0.065052947	0.83066667
Rbbp5	MmuINT0132414	chr1:134386306-134386999	IR-S	0.0962656	0.0310969	0.065168687	0.83866667
Map4k4	MmuEX0027798	chr1:40060608-40060832	C2	0.5342253	0.4690072	0.065218063	0.846
Actn1	MmuEX0003624	chr12:81271170-81271235	C3	0.4643682	0.3991421	0.065226088	0.83533333
Rnpep	MmuEX0040242	chr1:137168939-137169055	S	0.8612515	0.7959294	0.06532211	0.816
Thop1	MmuINT0159914	chr10:80539796-80540657	IR-S	0.1024555	0.0369024	0.065553014	0.84533333
Usp21	MmuINT0171433	chr1:173215170-173215385	IR-C	0.1048465	0.0390078	0.06583871	0.86666667
4933424B01Rik	MmuINT0004974	chr6:146498508-146498608	IR-S	0.1204428	0.0542566	0.06618618	0.81533333
Cxxc1	MmuINT0044414	chr18:74377651-74377739	IR-S	0.128468	0.0620623	0.066405703	0.81733333
Syvn1	MmuINT0156325	chr19:6050686-6050940	IR-C	0.1092955	0.0428799	0.066415632	0.838
Pan2	MmuINT0114946	chr10:127756095-127757303	IR-S	0.0921731	0.0257382	0.066434878	0.85333333
Jub	MmuINT0085080	chr14:55190671-55192228	IR-C	0.1248484	0.058366	0.066482325	0.814
2310021P13Rik	MmuINT0002177	chr14:21537215-21537648	IR-S	0.1020802	0.0354234	0.066656878	0.914
Plxnb1	MmuINT0122681	chr9:108998160-109001784	IR-S	0.1058321	0.0391609	0.066671201	0.806
Magt1	MmuINT0094619	chrX:103166366-103166774	IR-S	0.9296865	0.8629742	0.066712324	0.86466667
Mbnl1	MmuEX0028097	chr3:60418605-60418658	S	0.291869	0.2251207	0.066748315	0.808
Hspa13	MmuEX0023366	chr16:75758877-75758972	S	0.1627082	0.0959474	0.066760814	0.82533333
Rrp1b	MmuALTD0012250-1/2	chr17:32182874-32182956	Alt5	0.9231743	0.8563959	0.066778469	0.816
Slc9a8	MmuINT0148011	chr2:167249798-167260281	IR-C	0.1197066	0.0529281	0.066778495	0.80066667
Trim47	MmuINT0165258	chr11:115969323-115969579	IR-C	0.109404	0.0425805	0.066823533	0.83666667
2610301G19Rik	MmuEX0001138	chr14:70542732-70542895	S	0.984782	0.9173447	0.067437328	0.92066667
Rbm5	MmuALTA0014985-1/2	chr9:107652039-107652127	Alt3	0.1021621	0.0343395	0.067822645	0.80866667
Itfg3	MmuINT0083542	chr17:26351673-26352129	IR-S	0.0993948	0.031454	0.067940767	0.83666667

Srsf6	MmuINT0152721	chr2:162757879-162759161	IR-S	0.1679852	0.0999854	0.06799986	0.98266667
Mapkap1	MmuEX0027862	chr2:34274628-34274785	C2	0.0985336	0.0304419	0.068091691	0.828
Hdac6	MmuINT0076412	chrX:7516659-7516731	IR-C	0.1514744	0.0832811	0.068193313	0.85066667
Sec24c	MmuEX0041502	chr14:21494953-21495081	S	0.1172782	0.0488434	0.068434781	0.89333333
Dido1	MmuINT0049507	chr2:180419882-180422180	IR-S	0.1082657	0.0396917	0.068574001	0.856
Lmnb2	MmuINT0091567	chr10:80367519-80367630	IR-S	0.1251825	0.0562315	0.068951026	0.822
Racgap1	MmuALTA0014746-1/2	chr15:99473314-99473398	Alt3	0.1631816	0.0938957	0.069285872	0.848
Mff	MmuALTA0010879-1/2	chr1:82731994-82732082	Alt3	0.5987742	0.5292961	0.069478127	0.86533333
Gcn1l1	MmuINT0068236	chr5:116065609-116066359	IR-S	0.1115988	0.0421083	0.069490549	0.85266667
Commd4	MmuINT0040778	chr9:57004363-57004581	IR-S	0.1145417	0.0445284	0.070013391	0.852
Hdac7	MmuINT0076453	chr15:97640471-97641283	IR-S	0.1308466	0.0606727	0.070173921	0.87666667
Slc25a44	MmuEX0042934	chr3:88219910-88220037	S	0.9418334	0.8715297	0.070303773	0.81533333
Ehmt1	MmuEX0016475	chr2:24708185-24708322	S	0.9786136	0.9081446	0.070468947	0.82266667
Med24	MmuINT0097479	chr11:98577840-98579223	IR-S	0.1443417	0.0736573	0.070684323	0.82733333
Sltm	MmuEX0043731	chr9:70431739-70431919	S	0.9899901	0.9192874	0.0707027	0.846
Mark3	MmuEX0027961	chr12:112856529-112856594	S	0.9849615	0.9142356	0.07072595	0.94866667
Pnma5	MmuINT0123081	chrX:70279667-70280502	IR-S	0.4836766	0.4127696	0.070907009	0.88
Nfat5	MmuEX0031586	chr8:109890079-109890227	C3	0.9644071	0.8932618	0.071145223	0.84466667
Slc12a4	MmuINT0144551	chr8:108471852-108473037	IR-S	0.1493486	0.0778233	0.071525297	0.90333333
Igsf9	MmuEX0023844	chr1:174420792-174420903	C3	0.967502	0.8958207	0.071681259	0.90866667
Atxn7l2	MmuEX0007104	chr3:108007419-108007540	S	0.9765835	0.9048378	0.071745706	0.80666667
Dtx3	MmuINT0053776	chr10:126630414-126630785	IR-C	0.1761181	0.1038548	0.0722633	0.84533333
Csf1	MmuEX0012866	chr3:107559907-107560046	S	0.1309285	0.058641	0.072287476	0.82733333
Isg20l2	MmuINT0083411	chr3:87734534-87735252	IR-S	0.1367704	0.0644521	0.072318305	0.85666667
Orc4	MmuINT0113508	chr2:48789143-48792291	IR-S	0.0954598	0.0230498	0.07240999	0.898
Dvl1	MmuINT0054028	chr4:155227868-155228091	IR-S	0.169412	0.0967597	0.072652369	0.876
Rbm28	MmuINT0132749	chr6:29105190-29107067	IR-S	0.1509651	0.0780669	0.07289823	0.87333333
Smtn	MmuINT0149363	chr11:3417831-3420754	IR-S	0.1912504	0.1182994	0.072951014	0.856
Wdr67	MmuEX0052001	chr15:57751486-57751601	S	0.8537658	0.7807858	0.07298	0.81733333
Gon4l	MmuEX0021473	chr3:88662309-88662428	S	0.9658858	0.8927874	0.073098428	0.81
Hmha1	MmuINT0078331	chr10:79487597-79488153	IR-S	0.1823968	0.1091975	0.073199265	0.894
Pold1	MmuINT0123476	chr7:51789168-51789254	IR-S	0.1352978	0.0620475	0.073250314	0.824
Gigyf2	MmuEX0020409	chr1:89230845-89230909	S	0.9786783	0.9053678	0.07331043	0.85933333
Mark3	MmuEX0027960	chr12:112853607-112853655	C1	0.985441	0.9119569	0.07348418	0.84333333
Mpnd	MmuINT0100349	chr17:56151767-56151838	IR-S	0.1296785	0.0561361	0.073542436	0.83466667
Wdr11	MmuINT0174948	chr7:136744125-136746512	IR-S	0.1168472	0.0430546	0.073792607	0.81466667
Mtx1	MmuINT0102245	chr3:89014106-89014187	IR-S	0.1430152	0.0688602	0.074154986	0.908
Cherp	MmuALTA0004076-1/4	chr8:74985900-74985944	Alt3	0.2148929	0.1402158	0.074677078	0.82
Tsen54	MmuINT0166510	chr11:115676394-115676488	IR-S	0.1648376	0.0899974	0.074840221	0.80066667
Xab2	MmuINT0176563	chr8:3613710-3613798	IR-S	0.1373014	0.0619824	0.07531903	0.82
Glipr1	MmuINT0069262	chr10:111422739-111422833	IR-C	0.3313286	0.2558261	0.075502517	0.92933333
Cpt1c	MmuINT0041893	chr7:52215307-52215419	IR-S	0.2042594	0.1287331	0.07552628	0.806
Tm9sf1	MmuINT0160864	chr14:56256970-56259221	IR-C	0.163959	0.0883164	0.075642611	0.85266667
Gas8	MmuALTA0007571-1/2	chr8:126054733-126054936	Alt3	0.1432626	0.0673603	0.075902293	0.83533333
Tlcd1	MmuINT0160470	chr11:77993125-77993448	IR-S	0.1644801	0.0885224	0.075957765	0.80066667
Ilkap	MmuEX0024066	chr1:93287709-93287774	S	0.9426429	0.8665802	0.076062728	0.85533333
Snhg12	MmuINT0149697	chr4:131864823-131865752	IR-S	0.1738396	0.0976594	0.076180202	0.82466667
Tcfap4	MmuALTD0014106-1/2	chr16:4559487-	Alt5	0.1022286	0.026007	0.076221637	0.81866667
Sbf1	MmuINT0139006	chr15:89125744-89125825	IR-S	0.0969699	0.0207233	0.07624654	0.956
Ncoa3	MmuALTA0011807-1/2	chr2:165874009-165874055	Alt3	0.1456405	0.0693283	0.076312129	0.806
Cyth4	MmuINT0045563	chr15:78440305-78441878	IR-C	0.1673002	0.090626	0.076674126	0.804
Zfr	MmuEX0053757	chr15:12047994-12048093	S	0.9254986	0.8488075	0.076691076	0.922
Mcm3ap	MmuALTD0008318-1/2	chr10:75952080-75952321	Alt5	0.9548696	0.8781562	0.076713379	0.82266667
H2-T10	MmuINT0075658	chr17:36257232-36257242	IR-C	0.0927356	0.0159476	0.076788032	0.926
Smyd5	MmuINT0149486	chr6:85390739-85391553	IR-S	0.1640009	0.0871004	0.07690045	0.87733333
Naa35	MmuEX0030749	chr13:59710122-59710205	S	0.9682817	0.8912073	0.077074369	0.81933333
Lrrc68	MmuEX0027071	chr7:20122719-20122816	S	0.9447315	0.8672789	0.077452671	0.878
Prpf38b	MmuEX0037322	chr3:108713261-108713313	S	0.1606365	0.0831268	0.077509742	0.86933333
Ppan	MmuINT0124378	chr9:20693884-20694077	IR-S	0.2171025	0.1393778	0.077724713	0.836
N4bp2l2	MmuEX0030701	chr5:151449576-151449652	S	0.9288168	0.8508835	0.077933362	0.89933333
Cd47	MmuEX0010235	chr16:49908167-49908191	C1	0.1857464	0.1075285	0.078217889	0.85133333

Polrmt	MmuINT0124032	chr10:79200108-79200201	IR-S	0.129461	0.0512115	0.078249473	0.82933333
Igsf9	MmuEX0023846	chr1:174421996-174422141	C3	0.9640827	0.8855529	0.078529779	0.90466667
Kdelc2	MmuEX0025246	chr9:53202041-53202237	S	0.9803448	0.9016892	0.078655512	0.81733333
Mre11a	MmuEX0029633	chr9:14614248-14614328	S	0.8899892	0.8111424	0.078846809	0.84133333
March7	MmuINT0095819	chr2:60083318-60085946	IR-S	0.1372753	0.058267	0.079008342	0.81133333
Sdccag3	MmuINT0140196	chr2:26241130-26241509	IR-C	0.1934352	0.1141435	0.079291695	0.81066667
Tuft1	MmuEX0049920	chr3:94443317-94443391	C1	0.8068491	0.7275503	0.079298861	0.84
Nedd4l	MmuEX0031402	chr18:65327168-65327227	S	0.2075422	0.1278083	0.079733902	0.90333333
Ikbkb	MmuINT0081086	chr8:23770932-23771873	IR-S	0.110594	0.0300561	0.080537888	0.876
Gpaa1	MmuINT0072449	chr15:76163530-76163606	IR-S	0.1828326	0.1021767	0.080655975	0.89
Tnr	MmuINT0163502	chr1:161780677-161782087	IR-S	0.1226352	0.041864	0.080771225	0.83466667
Crim1	MmuEX0012727	chr17:78679313-78679555	S	0.9612274	0.8804003	0.080827096	0.88333333
Ncor1	MmuEX0031180	chr11:62203193-62203294	C1	0.9828088	0.901602	0.081206803	0.81666667
Tlk2	MmuEX0047474	chr11:105101675-105101770	S	0.9070461	0.8257524	0.081293604	0.87133333
Tjap1	MmuINT0160350	chr17:46396433-46396885	IR-S	0.2347667	0.1534205	0.081346212	0.80733333
Slc25a37	MmuINT0145664	chr14:69863412-69865637	IR-S	0.1490192	0.0676147	0.081404473	0.92666667
Mrs2	MmuINT0101017	chr13:25085058-25085538	IR-S	0.1304588	0.0486111	0.08184771	0.80266667
Gtf3a	MmuINT0074921	chr5:147766760-147766943	IR-C	0.478461	0.3965043	0.081956686	0.91133333
Senp1	MmuEX0041655	chr15:97907343-97907473	S	0.1191087	0.0371502	0.081958519	0.902
Eif4g3	MmuINT0056627	chr4:137733926-137736461	IR-C	0.2335836	0.1512667	0.082316955	0.814
Abhd6	MmuEX0003237	chr14:8860751-8860903	C1	0.9660437	0.8833261	0.082717649	0.844
Mospd2	MmuINT0100134	chrX:161385287-161385998	IR-S	0.1191455	0.0362872	0.082858271	0.844
Llgl1	MmuALTA0010072-1/2	chr11:60519943-60520075	Alt3	0.1444517	0.0611898	0.083261869	0.84466667
Gm2382	MmuEX0021047	chr9:88598764-88598974	C1	0.1384934	0.0550913	0.083402118	0.862
Nde1	MmuINT0106827	chr16:14190326-14191810	IR-C	0.2626074	0.1787619	0.083845526	0.87133333
Fbf1	MmuEX0018696	chr11:116007750-116007935	S	0.9130781	0.8289527	0.084125391	0.89333333
Stx5a	MmuINT0154631	chr19:8823068-8823144	IR-S	0.1635214	0.0793842	0.084137201	0.826
Abi1	MmuEX0003242	chr2:22818734-22818748	MIC	0.1436753	0.0595042	0.084171096	0.84666667
Taz	MmuINT0157185	chrX:71529033-71529270	IR-C	0.1500669	0.0657287	0.084338178	0.85466667
5730455O13Rik	MmuINT0005364	chr19:38296404-38298451	IR-S	0.1584526	0.0740909	0.084361621	0.808
Mbnl1	MmuEX0028095	chr3:60400641-60400751	S	0.1794726	0.0950729	0.084399755	0.81266667
Rpe	MmuALTD0012056-1/2	chr1:-66747591	Alt5	0.1370095	0.052504	0.084505566	0.86133333
Igsf9	MmuEX0023845	chr1:174421746-174421887	C3	0.9562561	0.8716784	0.084577716	0.88666667
Tgds	MmuALTA0018115-1/2	chr14:118511133-118512281	Alt3	0.1117969	0.0271826	0.0846143	0.818
2410004B18Rik	MmuINT0002460	chr3:145601293-145601861	IR-S	0.1260991	0.0411118	0.084987255	0.866
Dgcr8	MmuINT0048675	chr16:18283377-18283789	IR-S	0.1415659	0.056571	0.084994946	0.81133333
Eri3	MmuEX0017312	chr4:117237232-117237503	C2	0.9151893	0.8300318	0.085157499	0.89
Usp21	MmuINT0171428	chr1:173212934-173213145	IR-C	0.2220605	0.1368749	0.085185582	0.844
Rhebl1	MmuINT0134588	chr15:98708966-98709438	IR-S	0.3315201	0.2459796	0.085540479	0.85666667
Anapc1	MmuEX0004845	chr2:128505845-128505945	S	0.9583478	0.8726952	0.085652594	0.80533333
Pum2	MmuEX0038043	chr12:8740079-8740315	S	0.7883708	0.7023811	0.085989703	0.824
Sco2	MmuINT0139878	chr15:89204034-89204113	IR-C	0.191198	0.1050229	0.086175063	0.842
Sft2d2	MmuEX0041979	chr1:167118100-167118185	S	0.8708461	0.7846283	0.086217824	0.92866667
1810032O08Rik	MmuINT0001725	chr11:116535386-116535613	IR-S	0.1929923	0.1067458	0.086246472	0.832
Gatad2a	MmuEX0020135	chr8:72474552-72474653	C2	0.9537086	0.8673296	0.086379009	0.96666667
C230081A13Rik	MmuEX0008505	chr9:56166470-56166627	S	0.9692038	0.8827756	0.086428181	0.86066667
Cspp1	MmuEX0012969	chr1:10106099-10106165	C2	0.9776924	0.8906823	0.087010093	0.892
Cald1	MmuINT0028216	chr6:34696016-34703442	IR-S	0.2719601	0.1849078	0.087052242	0.84333333
Exosc2	MmuINT0059851	chr2:31531425-31532187	IR-S	0.1318593	0.0443316	0.087527667	0.81866667
Safb	MmuALTA0015782-1/2	chr17:56744980-56745080	Alt3	0.901788	0.8140731	0.08771492	0.854
Erf	MmuINT0058824	chr7:26030551-26030652	IR-S	0.2487525	0.1609929	0.087759561	0.94733333
Taf1d	MmuINT0156671	chr9:15117281-15118433	IR-S	0.2630985	0.175081	0.088017433	0.80866667
Ift52	MmuINT0080570	chr2:162843270-162848110	IR-S	0.1462855	0.0580342	0.088251374	0.83866667
Arhgap23	MmuALTA0001927-1/2	chr11:97309484-97309579	Alt3	0.9553613	0.8669664	0.088394971	0.828
BC003331	MmuALTA0002510-1/2	chr1:152235653-152235749	Alt3	0.145169	0.0565731	0.088595888	0.80866667
Ing4	MmuINT0082105	chr6:124997606-124997810	IR-S	0.3048046	0.2157425	0.089062049	0.814
Aim2	MmuEX0004445	chr1:175357890-175358029	C1	0.7940641	0.7049465	0.08911757	0.86866667
Dbr1	MmuEX0013797	chr9:99478860-99478940	S	0.9662237	0.877066	0.089157762	0.83866667
Scaf1	MmuINT0139153	chr7:52268645-52268849	IR-S	0.1864567	0.0972741	0.089182594	0.814
Arfip2	MmuINT0017796	chr7:112784908-112785324	IR-S	0.2420649	0.152533	0.089531868	0.83866667
Dph1	MmuINT0052839	chr11:74994447-74994794	IR-S	0.1390794	0.0490201	0.090059323	0.828

Clk4	MmuEX0011723	chr11:51080673-51080833	C1	0.9448811	0.8543343	0.090546867	0.90933333
Irak1	MmuINT0083219	chrX:71267589-71267811	IR-S	0.2509778	0.1602676	0.090710203	0.87
Dhx30	MmuINT0049139	chr9:109988383-109988453	IR-S	0.1598615	0.0690619	0.0907996	0.84866667
Cby1	MmuINT0029856	chr15:79496182-79496260	IR-S	0.1393244	0.0484905	0.090833899	0.81866667
Zfml	MmuALTD0016024-1/2	chr6:-83864473	Alt5	0.9446024	0.8537172	0.090885239	0.852
Chrnb1	MmuEX0011383	chr11:69609097-69609175	S	0.810087	0.7191448	0.090942246	0.81533333
Rhebl1	MmuINT0134585	chr15:98709919-98710207	IR-S	0.2268013	0.1358334	0.090967862	0.86533333
St6galnac6	MmuINT0153256	chr2:32463617-32464745	IR-C	0.1738341	0.0823231	0.091510956	0.80866667
Yes1	MmuEX0052527	chr5:32942704-32942976	S	0.9723264	0.8806271	0.091699301	0.89733333
Igsf9	MmuEX0023843	chr1:174420420-174420574	C3	0.9636968	0.871959	0.091737806	0.954
Dcaf6	MmuEX0013850	chr1:167341595-167341730	S	0.9815461	0.8894828	0.092063249	0.86733333
9430008C03Rik	MmuINT0006146	chr2:158181778-158182933	IR-S	0.1929969	0.1008868	0.092110101	0.91866667
Hook2	MmuINT0078678	chr8:87522424-87525053	IR-C	0.174999	0.0828396	0.092159457	0.83666667
Sart1	MmuINT0138866	chr19:5382360-5382714	IR-S	0.2410462	0.1485549	0.092491247	0.80733333
Golph3l	MmuEX0021465	chr3:95395639-95395827	S	0.9707232	0.8779859	0.092737235	0.88733333
Sirt6	MmuINT0143981	chr10:81085618-81086736	IR-S	0.1554679	0.0626925	0.092775484	0.82533333
BC037034	MmuINT0023193	chr5:138701936-138702062	IR-S	0.1875847	0.094662	0.092922638	0.80866667
Midn	MmuALTA0010964-1/2	chr10:79617079-79617217	Alt3	0.379792	0.2867663	0.09302569	0.87
Rab24	MmuINT0130449	chr13:55421576-55421672	IR-S	0.1364975	0.0433509	0.093146604	0.962
Ssbp4	MmuINT0152818	chr8:73121668-73121911	IR-S	0.7622352	0.6689352	0.093300001	0.92733333
Magi1	MmuEX0027545	chr6:93644002-93644169	S	0.9494457	0.8560893	0.093356378	0.81533333
Kdm1a	MmuEX0025261	chr4:136137955-136138014	S	0.5856106	0.4921069	0.093503718	0.854
Atp9b	MmuEX0006985	chr18:80933551-80933583	S	0.2344563	0.14063	0.09382627	0.804
Trip6	MmuINT0165591	chr5:137754318-137754578	IR-S	0.2701666	0.1763321	0.093834545	0.864
Arhgap22	MmuINT0017989	chr14:34172512-34175628	IR-S	0.1379991	0.0439578	0.094041352	0.86
Ift81	MmuALTD0006923-1/2	chr5:123064447-	Alt5	0.9455176	0.8513383	0.094179295	0.80133333
Rce1	MmuINT0133172	chr19:4624182-4624684	IR-S	0.1786244	0.0843429	0.094281528	0.90066667
Athl1	MmuINT0020568	chr7:148132328-148132400	IR-S	0.1619887	0.067607	0.094381683	0.856
Mettl10	MmuEX0028729	chr7:140023043-140023259	C1	0.9783788	0.8835486	0.094830268	0.92933333
Dtx3	MmuALTA0005895-1/2	chr10:126631466-126631529	Alt3	0.1891188	0.0941445	0.094974278	0.818
Use1	MmuALTA0019551-1/2	chr8:73893031-73893202	Alt3	0.8983651	0.80256	0.095805073	0.90333333
Gpr172b	MmuINT0073135	chr15:76371010-76371101	IR-S	0.2280601	0.132235	0.095825161	0.824
Tns3	MmuEX0048432	chr11:8500558-8500595	S	0.9742752	0.8778489	0.096426235	0.81133333
Tmem87a	MmuEX0048105	chr2:120200224-120200295	C3	0.4604897	0.3640101	0.096479639	0.80466667
Tecpr1	MmuINT0158726	chr5:144957121-144957220	IR-S	0.1714745	0.0748174	0.0966571	0.88133333
C230081A13Rik	MmuEX0008507	chr9:56222183-56222246	S	0.9636418	0.8666551	0.096986622	0.87866667
Cchcr1	MmuINT0031500	chr17:35666092-35667092	IR-S	0.2331386	0.1361514	0.096987208	0.848
Skiv2l	MmuINT0144279	chr17:34978164-34978386	IR-S	0.1720031	0.0745359	0.097467166	0.81533333
Gtf2ird1	MmuEX0022126	chr5:134842706-134842765	S	0.5664876	0.4690168	0.097470791	0.82066667
2310037I24Rik	MmuEX0000927	chr15:98352067-98352193	S	0.2616243	0.1639597	0.097664583	0.852
Lzts2	MmuALTA0010402-1/3	chr19:45096096-45096326	Alt3	0.1546912	0.05645	0.098241174	0.87666667
Gcat	MmuINT0068051	chr15:78867305-78867572	IR-C	0.135199	0.0367941	0.098404923	0.84866667
Git2	MmuEX0020455	chr5:115193785-115193889	S	0.7486963	0.6502748	0.098421568	0.85333333
Toe1	MmuINT0163718	chr4:116478351-116478589	IR-S	0.1489127	0.0498154	0.099097306	0.87133333
Ercc2	MmuINT0058738	chr7:19979050-19979124	IR-S	0.1685199	0.0692327	0.099287269	0.82666667
Entpd2	MmuINT0057671	chr2:25253034-25253520	IR-S	0.1347206	0.0349637	0.099756899	0.84933333
Dnm2	MmuINT0051794	chr9:21310160-21310779	IR-S	0.1411197	0.0413379	0.099781807	0.86
Stxbp1	MmuEX0045617	chr2:32650108-32650233	S	0.2147982	0.1149387	0.099859482	0.84866667
5730419I09Rik	MmuINT0005332	chr6:143048317-143048452	IR-C	0.150036	0.0498591	0.100176896	0.832
Ercc5	MmuALTD0004996-1/2	chr1:44214989-44215104	Alt5	0.9464284	0.8458808	0.100547622	0.82133333
Tmem168	MmuEX0047810	chr6:13555787-13555959	C1	0.2677	0.1671394	0.100560535	0.80866667
Kirrel	MmuEX0025651	chr3:86944899-86945041	S	0.9713259	0.8706877	0.100638128	0.91333333
Pgm5	MmuINT0118482	chr19:24783853-24802158	IR-S	0.3529745	0.2515704	0.10140409	0.824
Ogg1	MmuALTD0009774-1/2	chr6:113278403-113278473	Alt5	0.1851295	0.0834096	0.101719858	0.81666667
Papd5	MmuALTA0012735-1/2	chr8:90776426-90776472	Alt3	0.2474741	0.1454458	0.102028281	0.808
Lnp	MmuEX0026643	chr2:74366149-74366231	S	0.3745931	0.2712384	0.10335467	0.81133333
Dcaf8	MmuALTD0003997-1/3	chr1:-174078299	Alt5	0.6396813	0.5362079	0.103473438	0.83
Malt1	MmuEX0027588	chr18:65623695-65623769	S	0.972198	0.867452	0.104745998	0.818
Nf2	MmuEX0031553	chr11:4680581-4680625	S	0.9215042	0.8166129	0.10489134	0.81666667
Lpin2	MmuINT0092041	chr17:71588494-71590151	IR-S	0.1756235	0.0706669	0.104956639	0.81866667
Gpr124	MmuINT0072935	chr8:28221071-28221523	IR-S	0.2105634	0.1055446	0.105018803	0.91466667

1300001I01Rik	MmuALTA0000080-1/2	chr11:74477289-74477390	Alt3	0.2242024	0.1183646	0.10583779	0.81
Strn4	MmuINT0154497	chr7:17416488-17416813	IR-C	0.1577957	0.0515256	0.106270147	0.82866667
Tle6	MmuALTA0018241-1/2	chr10:81061822-81061883	Alt3	0.9663804	0.8600717	0.10630874	0.80266667
Canx	MmuINT0028590	chr11:50110640-50110775	IR-S	0.1805933	0.0736397	0.106953564	0.83133333
Rif1	MmuALTA0015254-1/2	chr2:51972362-51972470	Alt3	0.1754467	0.0683777	0.107068984	0.826
Pitpnm1	MmuINT0120267	chr19:4108194-4108422	IR-S	0.1835022	0.0761087	0.107393525	0.818
Nub1	MmuALTD0009618-1/3	chr5:-24191840	Alt5	0.9580616	0.8501953	0.107866337	0.85066667
Usp15	MmuEX0050842	chr10:122590097-122590183	S	0.6627488	0.5533333	0.109415539	0.83866667
9130404D08Rik	MmuINT0006049	chr8:72552674-72553106	IR-S	0.222681	0.1126689	0.110012095	0.90133333
Acot8	MmuINT0009931	chr2:164620680-164621151	IR-S	0.2323245	0.1221607	0.110163839	0.82
Ncor2	MmuALTA0011820-1/2	chr5:125531281-125531428	Alt3	0.7831923	0.6728603	0.11033206	0.828
Wee1	MmuEX0052129	chr7:117274343-117274489	S	0.9713598	0.8591169	0.112242889	0.93333333
Dlg4	MmuEX0014813	chr11:69840425-69840490	S	0.8749818	0.7623945	0.112587282	0.888
D10Ertd610e	MmuINT0045684	chr10:126621269-126621447	IR-S	0.2000382	0.0874467	0.112591502	0.87333333
Ccnl1	MmuINT0031750	chr3:65752713-65754401	IR-C	0.3029351	0.1898807	0.113054448	0.88066667
2310022A10Rik	MmuINT0002202	chr7:28365711-28366369	IR-S	0.9722806	0.8589698	0.113310779	0.83866667
Fibp	MmuINT0064520	chr19:5463305-5463603	IR-S	0.2823538	0.168753	0.113600788	0.81533333
Safb2	MmuINT0138607	chr17:56715436-56716300	IR-S	0.2607887	0.1453462	0.115442501	0.872
Pxk	MmuALTA0014604-1/2	chr14:8987800-8987859	Alt3	0.5422425	0.4265622	0.115680244	0.822
Igsf9	MmuINT0081000	chr1:174420904-174421745	IR-C	0.187597	0.0718666	0.115730388	0.85266667
Rere	MmuALTA0015114-1/2	chr4:149990868-149991588	Alt3	0.6983648	0.5819608	0.11640408	0.836
Kdm4c	MmuEX0025318	chr4:73926801-73926915	S	0.9657154	0.8491409	0.116574524	0.88666667
Ubr2	MmuEX0050335	chr17:47117269-47117367	C3	0.7578447	0.6406627	0.117181976	0.81066667
2810403A07Rik	MmuINT0003063	chr3:88514775-88515551	IR-S	0.5684822	0.451092	0.117390155	0.93666667
Gas2l1	MmuINT0067671	chr11:4964482-4964839	IR-C	0.7843065	0.6665696	0.117736889	0.92533333
Slc25a16	MmuEX0042839	chr10:62395467-62395530	S	0.9206415	0.802713	0.117928564	0.87866667
Mrpl40	MmuALTA0011257-1/2	chr16:18875417-18875500	Alt3	0.9482699	0.8278741	0.120395877	0.862
Tatdn1	MmuALTD0014009-1/2	chr15:58741132-58741204	Alt5	0.1856037	0.0648008	0.120802818	0.82266667
Zfp740	MmuINT0179805	chr15:102039308-102039585	IR-S	0.1983438	0.0770936	0.12125026	0.868
Prrc2b	MmuEX0037403	chr2:32084783-32084864	S	0.3711154	0.2496312	0.121484224	0.90666667
Clcn7	MmuEX0011607	chr17:25292313-25292482	S	0.8700041	0.7483302	0.121673948	0.92066667
Rnf123	MmuALTA0015329-1/2	chr9:107964085-107964190	Alt3	0.1653079	0.0434658	0.121842109	0.87666667
Eml3	MmuINT0057212	chr19:9013995-9015068	IR-S	0.1789372	0.0565621	0.122375069	0.90933333
Wdr74	MmuALTD0015694-1/2	chr19:8812338-8812352	Alt5	0.1324167	0.0100313	0.122385417	0.84133333
Asb8	MmuALTA0002103-1/2	chr15:97973082-97973241	Alt3	0.3442245	0.2202541	0.123970448	0.82533333
D2Wsu81e	MmuINT0045983	chr2:30030810-30031233	IR-S	0.2014134	0.0766717	0.124741716	0.87066667
Ets1	MmuEX0017458	chr9:32545684-32545944	S	0.994463	0.869087	0.125375954	0.832
Ldb1	MmuINT0090373	chr19:46107832-46108521	IR-C	0.6474918	0.5220538	0.12543804	0.846
Ints3	MmuINT0082557	chr3:90195834-90195914	IR-S	0.9084923	0.7829711	0.125521204	0.878
Ncor2	MmuINT0106748	chr5:125506175-125507171	IR-S	0.4271202	0.3006092	0.126511037	0.82333333
Susd1	MmuINT0155279	chr4:59337780-59342334	IR-C	0.2463954	0.1197297	0.126665739	0.83266667
Cdc42bpa	MmuEX0010395	chr1:182024075-182024317	S	0.7681745	0.6413013	0.12687319	0.83733333
Rbbp5	MmuALTD0011614-1/2	chr1:134394510-134394584	Alt5	0.8433908	0.7162279	0.127162942	0.85066667
Zbtb38	MmuEX0052674	chr9:96631711-96632161	C2	0.8434165	0.7161021	0.127314333	0.88733333
Stard3	MmuINT0153680	chr11:98240313-98241286	IR-S	0.2115694	0.0826069	0.128962506	0.83466667
Gcfc1	MmuINT0068106	chr16:91027575-91030677	IR-S	0.3318565	0.2023473	0.129509154	0.82533333
Zfp68	MmuEX0053548	chr5:139057698-139057787	S	0.7114357	0.5818803	0.129555397	0.86
Mknk2	MmuALTD0008560-1/2	chr10:80138868-	Alt5	0.9028697	0.7721994	0.13067025	0.846
Klc3	MmuINT0087636	chr7:19980517-19980587	IR-C	0.3840167	0.252842	0.131174768	0.81933333
Ssh3	MmuINT0152874	chr19:4264109-4264313	IR-S	0.2672813	0.1354968	0.131784462	0.81933333
Mef2a	MmuEX0028560	chr7:74413155-74413286	C3	0.6135948	0.4799287	0.133666101	0.82533333
Rnpepl1	MmuINT0136064	chr1:94813838-94814210	IR-S	0.2184971	0.08467	0.133827152	0.93866667
Klc3	MmuINT0087637	chr7:19980298-19980409	IR-C	0.4569387	0.3229695	0.133969165	0.874
Msh3	MmuEX0029790	chr13:93123180-93123297	S	0.7662206	0.6314531	0.134767525	0.86333333
Pcm1	MmuEX0033988	chr8:42360349-42360522	S	0.9082845	0.7734773	0.134807191	0.87
5430435G22Rik	MmuEX0001980	chr1:133602173-133602298	C1	0.5940483	0.4592097	0.134838606	0.82066667
Rab11fip5	MmuEX0038272	chr6:85290337-85290491	C2	0.3989762	0.263807	0.135169208	0.898
Nup88	MmuINT0112037	chr11:70758488-70758704	IR-C	0.2157204	0.0801019	0.135618504	0.81333333
Fibp	MmuINT0064523	chr19:5464216-5464333	IR-S	0.2709194	0.1350897	0.13582966	0.916
Irf3	MmuINT0083304	chr7:52253279-52254074	IR-C	0.2095747	0.0722046	0.137370092	0.97466667
Clasp1	MmuEX0011507	chr1:120438252-120438275	S	0.1891587	0.0515258	0.137632923	0.894

Atxn7l3	MmuALTA0002430-1/2	chr11:102154590-102154635	Alt3	0.8978321	0.7585421	0.139290048	0.84466667
Igsf9	MmuEX0023842	chr1:174419644-174419796	C2	0.951005	0.8106519	0.140353094	0.936
Trim3	MmuINT0165094	chr7:112759984-112761120	IR-S	0.3676723	0.2268679	0.140804465	0.88533333
Wrb	MmuEX0052257	chr16:96374583-96374645	S	0.9652827	0.8234751	0.141807608	0.84266667
Trim11	MmuINT0164965	chr11:58795726-58802226	IR-S	0.3649832	0.2230205	0.141962647	0.87133333
Slc25a37	MmuINT0145663	chr14:69865695-69867450	IR-S	0.6885801	0.5436866	0.144893435	0.928
Zfp598	MmuINT0179513	chr17:24817977-24818053	IR-S	0.2628259	0.1168237	0.146002154	0.862
Fam133b	MmuALTA0006793-1/4	chr5:3559138-3559159	Alt3	0.1939526	0.0476906	0.146261986	0.80133333
Kif2a	MmuALTD0007462-1/2	chr13:107778090-107778155	Alt5	0.5517139	0.4044529	0.147260936	0.802
Syvn1	MmuINT0156329	chr19:6052480-6052547	IR-S	0.2517794	0.1044071	0.147372357	0.96266667
Usp1	MmuEX0050811	chr4:98593146-98593365	S	0.7694125	0.6213254	0.148087087	0.87866667
Pitpnm1	MmuINT0120274	chr19:4111699-4111865	IR-S	0.3148845	0.1660081	0.148876406	0.942
Dbnl	MmuALTA0005093-1/4	chr11:5697290-5697338	Alt3	0.6311117	0.4800965	0.15101517	0.89
Stoml1	MmuEX0045502	chr9:58102741-58102847	C1	0.9162442	0.7649631	0.151281131	0.87866667
Slc25a22	MmuINT0145559	chr7:148617813-148617919	IR-S	0.3365945	0.185057	0.151537426	0.87133333
Terf2	MmuALTA0018073-1/2	chr8:109600779-109600896	Alt3	0.3666741	0.2137821	0.152892001	0.86866667
Rbm15	MmuINT0132595	chr3:107129223-107133132	IR-S	0.4087696	0.25561	0.153159601	0.88933333
Ncor2	MmuALTA0011823-1/2	chr5:125517644-125517746	Alt3	0.2406819	0.0859379	0.154743994	0.854
Sipa1	MmuINT0143835	chr19:5661112-5663603	IR-C	0.2440785	0.0869072	0.157171367	0.93866667
1810063B07Rik	MmuALTD0000212-1/2	chr14:20902100-	Alt5	0.8932792	0.735326	0.157953265	0.96
Dhrsx	MmuEX0014516	NT_166291:31370-31471	C1	0.8170732	0.658967	0.158106197	0.85666667
Nup88	MmuALTA0012434-1/2	chr11:70758347-70758472	Alt3	0.7839401	0.6244217	0.159518461	0.94
Zfp7	MmuINT0179739	chr15:76718778-76720436	IR-S	0.3536458	0.1929014	0.16074432	0.91866667
Diap1	MmuEX0014636	chr18:38066042-38066068	S	0.8375693	0.6747997	0.162769615	0.85
Nat10	MmuEX0030922	chr2:103566873-103567045	S	0.8339928	0.6682544	0.165738376	0.84866667
Ttll4	MmuEX0049665	chr1:74719418-74719584	S	0.9673515	0.799379	0.16797248	0.99466667
Mink1	MmuEX0029044	chr11:70422910-70422933	S	0.362034	0.1936096	0.168424447	0.88866667
Gpr124	MmuINT0072933	chr8:28220245-28220412	IR-S	0.455733	0.2858032	0.169929796	0.83533333
Atp6v1e1	MmuEX0006911	chr6:120768352-120768417	C1	0.870825	0.6998187	0.171006315	0.97133333
Ogg1	MmuINT0112996	chr6:113278607-113279222	IR-S	0.4419171	0.2656175	0.176299521	0.90066667
Mfap3	MmuALTD0008457-1/3	chr11:-57332214	Alt5	0.7919435	0.6150726	0.176870868	0.81866667
Pcnxl3	MmuALTA0012873-1/3	chr19:5681432-5681553	Alt3	0.6526103	0.4741171	0.178493252	0.83866667
Plekhg3	MmuEX0035767	chr12:77672591-77672629	S	0.9442094	0.7645407	0.179668755	0.89533333
Sec61g	MmuALTD0012549-1/3	chr11:16408103-	Alt5	0.4500681	0.2665522	0.183515941	0.908
Tank	MmuALTA0017805-1/2	chr2:61464963-61465071	Alt3	0.7587042	0.5747137	0.183990568	0.89333333
Amn1	MmuEX0004800	chr6:149133514-149133646	C1	0.9366184	0.7522014	0.184417056	0.87266667
Zfp428	MmuALTA0020637-1/2	chr7:25300095-25300121	Alt3	0.6151911	0.4261129	0.189078225	0.83733333
Chpf2	MmuINT0036144	chr5:24095480-24096126	IR-S	0.4342334	0.2423701	0.191863266	0.946
6330503K22Rik	MmuALTA0000628-1/2	chr7:125867972-125868099	Alt3	0.2586236	0.0654822	0.193141493	0.86933333
AU019823	MmuEX0002794	chr9:50424763-50424789	S	0.3287905	0.1264678	0.202322706	0.94733333
Setd6	MmuINT0142186	chr8:98240942-98241820	IR-S	0.3510388	0.1458754	0.205163405	0.936
Nat10	MmuEX0030920	chr2:103568157-103568253	S	0.7848231	0.5707078	0.214115364	0.80666667
Igdcc4	MmuALTA0009019-1/2	chr9:64974565-64974735	Alt3	0.7301875	0.4493135	0.280873977	0.84533333
Taf4a	MmuALTD0013961-1/3	chr2:179666721-179666930	Alt5	0.7643013	0.4588023	0.305499017	0.95

Table 6. *Xab2*-induced differential splicing events in mES cells

GENE	EVENT	COORD	Complex	β_siRNA	β_Ctrl	β_siRNA_Ctrl	P_xzero
Atg2b	MmuALTA0002215-1/2	chr12:106874657-106874762	Alt3	0.202691978	0.637078343	-0.434386365	0.944
1110012J17Rik	MmuALTD0000043-1/2	chr17:66717634-66717800	Alt5	0.12325943	0.484573053	-0.361313623	0.878
Stk30	MmuALTA0017477-1/2	chr12:112046415-112046609	Alt3	0.174236766	0.534848126	-0.36061136	0.951333333
Cpsf1	MmuALTA0004583-1/2	chr15:-76426337	Alt3	0.03700922	0.372280287	-0.335271067	0.868
Chtf18	MmuALTA0004131-1/2	chr17:-25856227	Alt3	0.206105031	0.498371294	-0.292266263	0.861333333
Prpf38b	MmuALTD0011071-1/2	chr3:108711254-108711322	Alt5	0.661523578	0.939925841	-0.278402263	0.806666667
Mark3	MmuEX0027963	chr12:112891601-112891645	C2	0.674561504	0.950206303	-0.2756448	0.924
Picalm	MmuEX0035017	chr7:97330729-97330878	S	0.165463865	0.436938117	-0.271474252	0.884
Sgta	MmuALTD0012748-1/3	chr10:80522873-	Alt5	0.584991349	0.844991812	-0.260000463	0.860666667
Fetub	MmuEX0019085	chr16:22929148-22929382	S	0.65767743	0.917396472	-0.259719042	0.892
Rad9	MmuINT0131107	chr19:4197587-4197670	IR-S	0.123841347	0.375685668	-0.251844321	0.943333333
Dpp7	MmuEX0015605	chr2:25209128-25209246	S	0.716314734	0.963327392	-0.247012658	0.984666667
Scyl2	MmuALTA0015976-1/2	chr10:89108207-89108299	Alt3	0.382156214	0.627659969	-0.245503755	0.868666667
Rab12	MmuINT0130380	chr17:66846789-66847358	IR-S	0.110290761	0.344966937	-0.234676177	0.976666667
Trpc2	MmuALTA0018934-1/2	chr7:109219733-109219875	Alt3	0.090080041	0.320830039	-0.230749998	0.808
Trub2	MmuEX0049247	chr2:29638832-29638893	S	0.669457396	0.895392622	-0.225935226	0.939333333
Usp9x	MmuALTA0019709-1/2	chrX:12693750-12693883	Alt3	0.624215737	0.848044947	-0.22382921	0.806
Prrc2c	MmuALTA0014278-1/2	chr1:164653241-164653412	Alt3	0.2793126	0.502537317	-0.223224716	0.967333333
Serpinb6a	MmuEX0041782	chr13:34027496-34027663	C1	0.093757648	0.315681003	-0.221923355	0.812
Dnm1l	MmuEX0015292	chr16:16318857-16318934	C2	0.515207595	0.733560308	-0.218352713	0.824666667
Ggnbp2	MmuALTD0005895-1/2	chr11:84654923-84655126	Alt5	0.476332456	0.694140729	-0.217808273	0.868666667
Haus6	MmuALTA0008398-1/2	chr4:86228785-86229618	Alt3	0.230260129	0.441497636	-0.211237507	0.825333333
Usp11	MmuEX0050820	chrX:20288875-20288984	S	0.780932748	0.988967767	-0.208035019	0.833333333
Chd9	MmuALTA0004065-1/2	chr8:93558807-93558964	Alt3	0.171555608	0.375968354	-0.204412747	0.806
Ap2b1	MmuEX0005428	chr11:83178297-83178338	S	0.236916597	0.441105855	-0.204189258	0.854666667
Ylpm1	MmuEX0052560	chr12:86401213-86401264	S	0.7775214	0.9783933	-0.2008719	0.862666667
Ube3a	MmuEX0050212	chr7:66496337-66496403	C3	0.199925935	0.40063874	-0.200712805	0.85
Zfp106	MmuEX0053021	chr2:120359247-120361415	C1	0.715938034	0.915069373	-0.199131339	0.939333333
Mff	MmuALTA0010879-1/2	chr1:82731994-82732082	Alt3	0.603608308	0.802579436	-0.198971128	0.884
Slc3a2	MmuALTA0016711-1/2	chr19:8782684-8782767	Alt3	0.771021066	0.968000806	-0.196979746	0.956
Stk11	MmuEX0045388	chr10:79588820-79588910	S	0.799687218	0.988626219	-0.188939	0.852666667

Ndufs1	MmuALTD0009254-1/2	chr1:63223160-	Alt5	0.447018692	0.635164326	-0.188145634	0.885333333
Pank2	MmuEX0033562	chr2:131108328-131108504	C2	0.753315765	0.939195021	-0.185879256	0.941333333
Zfp7	MmuALTA0020728-1/2	chr15:76718664-76718777	Alt3	0.093533108	0.279109566	-0.185576458	0.878666667
Ppil3	MmuEX0036587	chr1:58495188-58495255	S	0.777317044	0.962666093	-0.185349049	0.837333333
Ddx49	MmuALTD0004111-1/2	chr8:72820282-72820357	Alt5	0.795952513	0.980162298	-0.184209784	0.908
Stag1	MmuEX0045215	chr9:100853905-100854015	S	0.719025294	0.900309329	-0.181284035	0.909333333
Tmpo	MmuALTD0014572-1/2	chr10:90628692-90628814	Alt5	0.161817712	0.341510324	-0.179692611	0.857333333
Gm14444	MmuEX0020870	chr2:174838929-174838983	S	0.290027844	0.466895733	-0.176867889	0.972
Zfp498	MmuALTD0016143-1/2	chr5:-146044649	Alt5	0.762350414	0.938281031	-0.175930617	0.821333333
AC111135.1	MmuEX0002619	chr9:72330254-72330336	S	0.803442367	0.978663608	-0.175221241	0.959333333
Agrn	MmuINT0012847	chr4:155551551-155552537	IR-S	0.058152935	0.231875604	-0.17372267	0.910666667
Celf1	MmuALTA0003834-1/2	chr2:90849362-90849472	Alt3	0.675666764	0.847566389	-0.171899625	0.907333333
Rnf138	MmuEX0040030	chr18:21176320-21176376	S	0.791610804	0.963376053	-0.171765249	0.97
Clybl	MmuEX0011817	chr14:122710466-122710652	C1	0.794022918	0.963854389	-0.16983147	0.909333333
4921513D23Rik	MmuINT0003601	chr16:14138615-14140275	IR-S	0.045108637	0.213159061	-0.168050424	0.938
Mthfd1	MmuINT0101740	chr12:77404969-77408208	IR-S	0.080864206	0.24877379	-0.167909584	0.888
Hif1a	MmuALTA0008596-1/2	chr12:75027544-75027734	Alt3	0.422444576	0.589422777	-0.166978201	0.816
Sap130	MmuALTA0015805-1/2	chr18:31841664-31841838	Alt3	0.537821166	0.704230418	-0.166409252	0.805333333
9030409G11Rik	MmuALTA0000655-1/2	chr4:141702938-141703060	Alt3	0.561016134	0.726755575	-0.165739441	0.824666667
Arhgap1	MmuALTA0001908-1/2	chr2:91491921-91491980	Alt3	0.805332091	0.970532811	-0.165200721	0.978
9030409G11Rik	MmuEX0002278	chr4:141702721-141702827	C1	0.054805129	0.219160827	-0.164355698	0.876
Ubqln1	MmuEX0050301	chr13:58282183-58282266	S	0.497242845	0.660714284	-0.163471439	0.858666667
Ube3a	MmuEX0050213	chr7:66498720-66498839	C1	0.319553554	0.482914476	-0.163360922	0.895333333
Setd5	MmuALTA0016203-1/2	chr6:113060368-113060519	Alt3	0.782826115	0.943848635	-0.161022521	0.844
Prrc2a	MmuALTA0014260-1/2	chr17:35287762-35287847	Alt3	0.289085405	0.448852065	-0.159766661	0.951333333
Herc4	MmuALTA0008554-1/3	chr10:62745961-62746089	Alt3	0.051241949	0.209141167	-0.157899218	0.81
Fxr1	MmuEX0019783	chr3:33967083-33967174	S	0.484905081	0.640807576	-0.155902495	0.810666667
Fryl	MmuEX0019677	chr5:73416010-73416027	S	0.012086104	0.163588956	-0.151502852	0.811333333
Actr6	MmuALTA0001105-1/2	chr10:89188513-89188648	Alt3	0.818465395	0.969225187	-0.150759791	0.852666667
Man2c1	MmuINT0094884	chr9:56985182-56985275	IR-S	0.124428685	0.274940016	-0.150511331	0.89
Tanc1	MmuALTD0013981-1/2	chr2:59628833-59628934	Alt5	0.806419155	0.956875824	-0.150456669	0.922
Jmjd1c	MmuEX0024903	chr10:66679731-66679855	S	0.540727651	0.68774025	-0.147012599	0.831333333
2610101N10Rik	MmuALTD0000361-1/2	chr9:95391687-95391719	Alt5	0.397820084	0.544279305	-0.146459221	0.811333333

Pum1	MmuEX0038035	chr4:130309857-130310093	S	0.773197282	0.917728874	-0.144531592	0.836666667
Rnps1	MmuEX0040247	chr17:24551986-24552107	C1	0.250701341	0.394978185	-0.144276844	0.882666667
Tnrc6a	MmuALTA0018605-1/2	chr7:130324902-130324961	Alt3	0.10328035	0.246531056	-0.143250706	0.834
Melk	MmuEX0028647	chr4:44338513-44338611	C2	0.819684468	0.96288434	-0.143199872	0.93
Dgkz	MmuALTA0005407-1/2	chr2:91776859-91776928	Alt3	0.682404694	0.823983704	-0.14157901	0.826
Tnpo3	MmuALTA0018602-1/2	chr6:29504883-29504962	Alt3	0.855656642	0.996496789	-0.140840147	0.928
Qrich1	MmuEX0038156	chr9:108421098-108421157	C2	0.227464998	0.36813107	-0.140666072	0.892666667
Gemin5	MmuEX0020277	chr11:57952997-57953110	S	0.839223449	0.97727115	-0.138047701	0.838
Pick1	MmuINT0119453	chr15:79078727-79079150	IR-S	0.059470703	0.195575863	-0.13610516	0.876666667
Elp3	MmuALTD0004837-1/2	chr14:66211819-	Alt5	0.067346247	0.203093866	-0.135747619	0.898
Ckap2l	MmuALTA0004170-1/2	chr2:129096311-129096494	Alt3	0.177295147	0.31268827	-0.135393123	0.86
Ncor1	MmuALTD0009188-1/2	chr11:62167885-62167974	Alt5	0.055713076	0.184925395	-0.129212319	0.898
Hbp1	MmuINT0076101	chr12:32612373-32613448	IR-C	0.042084041	0.17095292	-0.128868879	0.881333333
Mllt10	MmuEX0029217	chr2:18092670-18092702	S	0.807137614	0.935426194	-0.12828858	0.858
Abcf2	MmuALTD0000811-1/4	chr5:24083165-	Alt5	0.780221821	0.907872001	-0.12765018	0.834666667
Kdm5c	MmuEX0025334	chrX:148674173-148674295	S	0.850138426	0.977082901	-0.126944474	0.882666667
Fubp1	MmuALTD0005693-1/2	chr3:151889044-151889172	Alt5	0.254926906	0.381129413	-0.126202507	0.887333333
Taf2	MmuALTD0013958-1/2	chr15:54878973-54879038	Alt5	0.856574613	0.980749293	-0.124174682	0.884
Man2c1	MmuEX0027640	chr9:56986661-56986776	S	0.500760388	0.622929723	-0.122169335	0.893333333
Atf2	MmuEX0006578	chr2:73661258-73661363	S	0.858177882	0.980198942	-0.122021061	0.864
Trub1	MmuINT0166386	chr19:57561812-57562498	IR-S	0.095133789	0.215440009	-0.120306229	0.852
Ccdc9	MmuALTA0003480-1/2	chr7:16861411-16861456	Alt3	0.502354092	0.622007089	-0.119652997	0.802666667
Vrk1	MmuEX0051614	chr12:107289970-107290057	C3	0.844967642	0.964259972	-0.119292329	0.832666667
Leng8	MmuINT0090549	chr7:4096416-4096496	IR-S	0.071753113	0.190978777	-0.119225664	0.809333333
Rsrc2	MmuINT0137658	chr5:124192866-124193646	IR-C	0.170524904	0.289724722	-0.119199818	0.809333333
Slc38a10	MmuALTA0016683-1/2	chr11:-119967347	Alt3	0.053708713	0.172374466	-0.118665755	0.823333333
Ccdc77	MmuEX0009926	chr6:120281830-120282049	S	0.846935431	0.964434177	-0.117498746	0.983333333
Aff4	MmuEX0004154	chr11:53194088-53194174	S	0.850838231	0.966654364	-0.115816133	0.866666667
Got1	MmuALTA0008039-1/2	chr19:43577398-43577535	Alt3	0.428073213	0.543217263	-0.11514405	0.962666667
Chd8	MmuINT0035790	chr14:52832395-52832498	IR-S	0.162043189	0.276875573	-0.114832385	0.819333333
A430005L14Rik	MmuEX0002491	chr4:153333865-153333971	S	0.868648556	0.983368964	-0.114720409	0.908666667
Usp16	MmuALTD0015364-1/2	chr16:87471957-87472076	Alt5	0.060755928	0.173455197	-0.112699269	0.82
Chd8	MmuINT0035803	chr14:52821999-52822178	IR-S	0.059076601	0.1717669	-0.112690299	0.892666667

Exo1	MmuALTA0006648-1/2	chr1:177823872-177823920	Alt3	0.863236484	0.975814364	-0.112577879	0.89
Fbxw5	MmuALTA0007130-1/2	chr2:25358391-25358565	Alt3	0.839497309	0.951886757	-0.112389448	0.912
Tpd52l2	MmuEX0048580	chr2:181237581-181237640	S	0.615108652	0.726384228	-0.111275576	0.904
Tnrc6c	MmuEX0048401	chr11:117582264-117584864	S	0.871298622	0.982138475	-0.110839854	0.827333333
Mapk1	MmuALTD0008180-1/2	chr16:17015991-17016171	Alt5	0.248084199	0.358808273	-0.110724074	0.890666667
Zmynd8	MmuINT0180617	chr2:165640970-165646041	IR-S	0.871884662	0.982347219	-0.110462557	0.872
Sept1	MmuALTA0016135-1/2	chr7:134359399-134359483	Alt3	0.875855262	0.986234571	-0.110379309	0.866
Ubr3	MmuEX0050340	chr2:69797624-69797720	S	0.873108498	0.980012896	-0.106904398	0.875333333
Tsc2	MmuALTA0019000-1/2	chr17:24764936-24765050	Alt3	0.086752028	0.193629392	-0.106877364	0.812666667
Ddx3y	MmuEX0014098	chrY:619344-619391	S	0.872820423	0.979370192	-0.106549769	0.938666667
Birc5	MmuEX0007996	chr11:117711068-117711177	S	0.885860954	0.991978426	-0.106117472	0.996666667
Ilk	MmuINT0081839	chr7:112889382-112889473	IR-S	0.106281956	0.212257941	-0.105975985	0.818
Cbfb	MmuEX0009355	chr8:107718375-107718491	S	0.883747734	0.988231906	-0.104484173	0.819333333
Trpc2	MmuEX0049113	chr7:109218411-109218505	S	0.869618227	0.973214715	-0.103596488	0.81
Herc4	MmuEX0022799	chr10:62737745-62737836	S	0.889303149	0.992487495	-0.103184346	0.963333333
Setdb1	MmuALTA0016209-1/2	chr3:95143829-95143984	Alt3	0.132189122	0.235190489	-0.103001367	0.803333333
Hk2	MmuEX0022972	chr6:82710098-82710260	S	0.887826081	0.990618898	-0.102792817	0.985333333
Dclk2	MmuALTA0005126-1/2	chr3:86620280-86620352	Alt3	0.698126401	0.799926835	-0.101800435	0.806
Golga4	MmuEX0021439	chr9:118446360-118446443	S	0.818772249	0.920501548	-0.1017293	0.900666667
Ncl	MmuALTD0009174-1/5	chr1:88255781-	Alt5	0.799247915	0.900577479	-0.101329565	0.802666667
Taf15	MmuEX0046179	chr11:83310764-83310798	S	0.880245737	0.981402691	-0.101156954	0.995333333
Gpr108	MmuALTA0008084-1/2	chr17:57382364-57382536	Alt3	0.344710680	0.445474559	-0.100763878	0.801333333
Nras	MmuEX0032299	chr3:102868039-102868080	S	0.892805372	0.992888714	-0.100083342	0.996
Ccar1	MmuEX0009438	chr10:62227072-62227282	S	0.864091622	0.963013067	-0.098921445	0.868666667
Myst2	MmuEX0030640	chr11:95137757-95137863	S	0.630360795	0.728240974	-0.097880179	0.816666667
St14	MmuEX0045085	chr9:30914074-30914109	S	0.888515622	0.986041274	-0.097525651	0.922
Gemin5	MmuALTA0007665-1/2	chr11:57977296-57977412	Alt3	0.028421533	0.125780419	-0.097358886	0.931333333
Mpdu1	MmuALTA0011169-1/2	chr11:69471438-69471523	Alt3	0.887569822	0.984902392	-0.097332569	0.823333333
Agfg1	MmuEX0004229	chr1:82882950-82883042	S	0.659809305	0.756799404	-0.096990099	0.858666667
Plxnb2	MmuINT0122738	chr15:88989214-88989388	IR-S	0.088699747	0.185510464	-0.096810717	0.83
Rere	MmuALTA0015112-1/2	chr4:149987834-149987995	Alt3	0.855301946	0.951448369	-0.096146423	0.820666667
Brms1	MmuALTD0002311-1/2	chr19:-5041490	Alt5	0.863582726	0.958395229	-0.094812503	0.802666667
Pcnp	MmuEX0034007	chr16:56024647-56024750	S	0.077276481	0.171967908	-0.094691428	0.865333333

Tars2	MmuALTD0014000-1/2	chr3:95549708-95549785	Alt5	0.883575983	0.978255643	-0.09467966	0.908
Pitpnb	MmuINT0120248	chr5:111814625-111815522	IR-S	0.023747331	0.118368257	-0.094620926	0.826
Gm4902	MmuINT0070679	chr14:59940121-59940290	IR-S	0.336262262	0.430339317	-0.094077055	0.805333333
Tmem144	MmuINT0161519	chr3:79629320-79630744	IR-S	0.028236236	0.122111655	-0.093875418	0.937333333
Hnrnph1	MmuALTD0006709-1/3	chr11:50197182-50197232	Alt5	0.008861475	0.102350987	-0.093489512	0.996
Alg11	MmuALTD0001213-1/3	chr8:23172442-23172588	Alt5	0.831126257	0.923420617	-0.09229436	0.850666667
Pum1	MmuEX0038033	chr4:130286193-130286463	C1	0.836340311	0.927901447	-0.091561136	0.932
Nop2	MmuINT0109583	chr6:125091177-125091291	IR-S	0.122383609	0.212766862	-0.090383253	0.877333333
Gns	MmuINT0072124	chr10:120811621-120813263	IR-S	0.029216043	0.119110778	-0.089894735	0.864
Ankrd52	MmuEX0005156	chr10:127820625-127820765	S	0.891536563	0.980488573	-0.08895201	0.922
Scrib	MmuALTA0015943-1/2	chr15:75896520-75896633	Alt3	0.030277276	0.118916031	-0.088638755	0.852
Atp13a1	MmuINT0020899	chr8:72329462-72329544	IR-S	0.087884252	0.176108983	-0.088224731	0.920666667
Eps15l1	MmuALTD0004968-1/2	chr8:74896925-74896975	Alt5	0.890503518	0.977659737	-0.087156219	0.930666667
Fancl	MmuEX0018591	chr11:26303322-26303378	S	0.901621705	0.988723312	-0.087101607	0.852666667
Smc1a	MmuEX0043822	chrX:148457289-148457477	C1	0.587160779	0.674121307	-0.086960528	0.836666667
Arid3b	MmuINT0018775	chr9:57640493-57642742	IR-C	0.056519426	0.143313547	-0.086794121	0.811333333
Dgcr2	MmuINT0048661	chr16:17845229-17849683	IR-S	0.022741696	0.109377786	-0.086636084	0.829333333
Wdr62	MmuALTA0020079-1/3	chr7:31028852-31028925	Alt3	0.056047139	0.142629399	-0.08658226	0.801333333
Cdc123	MmuEX0010315	chr2:5754127-5754159	S	0.901018915	0.987378847	-0.086359932	0.98
Rnf149	MmuEX0040054	chr1:39615160-39615256	S	0.808681726	0.894913776	-0.08623205	0.825333333
Wdr46	MmuINT0175329	chr17:34085479-34085587	IR-S	0.053358318	0.139530776	-0.086172458	0.806
Lass5	MmuALTA0009935-1/2	chr15:99569096-99569161	Alt3	0.112144828	0.198044441	-0.085899614	0.825333333
Rbm33	MmuINT0132774	chr5:28679184-28684813	IR-C	0.067459786	0.152492288	-0.085032502	0.826
Dtx1	MmuALTD0004515-1/2	chr5:121132589-121132747	Alt5	0.792001123	0.876333817	-0.084332694	0.835333333
Acin1	MmuEX0003478	chr14:55268397-55269724	S	0.078262098	0.162024658	-0.08376256	0.815333333
App	MmuALTA0001831-1/2	chr16:85043825-85043986	Alt3	0.06608679	0.149694727	-0.083607937	0.879333333
Mrpl9	MmuALTA0011271-1/2	chr3:94248823-94248873	Alt3	0.894757881	0.977833762	-0.083075881	0.815333333
Ergic3	MmuINT0058861	chr2:155834172-155834299	IR-S	0.058292423	0.14077309	-0.082480667	0.847333333
Chmp2a	MmuINT0036063	chr7:13617552-13617637	IR-S	0.076619041	0.158978998	-0.082359958	0.818
Papola	MmuINT0115109	chr12:107047873-107049246	IR-C	0.051956447	0.134090315	-0.082133867	0.854666667
Hdlbp	MmuINT0076551	chr1:95305075-95305265	IR-S	0.032989873	0.114603901	-0.081614028	0.952
Rsrc2	MmuALTA0015699-1/2	chr5:124190681-124190871	Alt3	0.916219042	0.994872094	-0.078653052	0.992666667
Capn10	MmuEX0009055	chr1:94841594-94841855	S	0.902969575	0.981352064	-0.078382489	0.855333333

Nuf2	MmuALTD0009653-1/3	chr1:171445043-171445116	Alt5	0.892450383	0.970699141	-0.078248758	0.840666667
Actn4	MmuEX0003639	chr7:29696509-29696594	C3	0.888919042	0.966865226	-0.077946183	0.960666667
Cnot3	MmuALTA0004348-1/3	chr7:3604802-3605021	Alt3	0.776882007	0.854631335	-0.077749328	0.847333333
2810004N23Rik	MmuEX0001218	chr8:127378802-127378928	S	0.026644607	0.104386629	-0.077742022	0.845333333
Hnrnpul2	MmuEX0023139	chr19:8905378-8905451	S	0.911819458	0.989471418	-0.077651959	0.852666667
Glb1	MmuEX0020475	chr9:114329471-114329621	C3	0.912355127	0.987882145	-0.075527018	0.857333333
Tmem63b	MmuEX0048040	chr17:45815912-45815950	S	0.91241495	0.985623901	-0.073208951	0.938666667
Rbm5	MmuEX0039181	chr9:107658184-107658244	S	0.902195226	0.975111367	-0.07291614	0.846
Erf	MmuEX0017276	chr7:26031107-26031341	S	0.91494309	0.987367665	-0.072424575	0.824
Parp1	MmuALTA0012760-1/2	chr1:182529088-182529211	Alt3	0.025558489	0.097752133	-0.072193644	0.906666667
Sbno1	MmuINT0139090	chr5:124831787-124831867	IR-S	0.012075063	0.083924607	-0.071849543	0.883333333
Vps41	MmuALTA0019886-1/2	chr13:18831315-18831415	Alt3	0.021419069	0.092707402	-0.071288333	0.836666667
Spint1	MmuINT0151590	chr2:119063209-119063436	IR-C	0.060139767	0.131372644	-0.071232877	0.829333333
Supt5h	MmuEX0045763	chr7:29102756-29102840	S	0.922454375	0.993151763	-0.070697388	0.840666667
Uba3	MmuEX0050075	chr6:97155300-97155341	S	0.8321025	0.902637045	-0.070534545	0.824666667
Jam2	MmuALTA0009451-1/2	chr16:84823032-	Alt3	0.918234839	0.988448519	-0.070213679	0.954
Zfand3	MmuEX0052966	chr17:30197755-30197795	S	0.903447708	0.973352859	-0.069905151	0.825333333
Akap1	MmuINT0013298	chr11:88693144-88693621	IR-S	0.013454615	0.082931202	-0.069476587	0.911333333
Fancl	MmuEX0018592	chr11:26307548-26307648	C2	0.916243758	0.984962383	-0.068718624	0.905333333
Gnl2	MmuEX0021365	chr4:124714766-124714905	S	0.908080637	0.976298512	-0.068217875	0.876666667
Neo1	MmuEX0031504	chr9:58732277-58732371	S	0.900963759	0.969062688	-0.068098929	0.91
Bub1b	MmuALTA0002956-1/2	chr2:118448806-118448921	Alt3	0.848919331	0.916794858	-0.067875528	0.862666667
Naa35	MmuEX0030749	chr13:59710122-59710205	S	0.925461263	0.992503362	-0.067042098	0.972666667
R3hdm2	MmuEX0038219	chr10:126899262-126899339	S	0.911051326	0.977601385	-0.06655006	0.963333333
Ythdc2	MmuINT0177415	chr18:45016746-45017841	IR-S	0.022150387	0.088528978	-0.066378591	0.866
Pitrm1	MmuINT0120352	chr13:6554895-6555787	IR-S	0.018229758	0.084194723	-0.065964965	0.902
Mms19	MmuALTD0008647-1/2	chr19:42055489-	Alt5	0.913074747	0.978809147	-0.0657344	0.874
Pml	MmuEX0035974	chr9:58082160-58082740	S	0.921263137	0.986823944	-0.065560806	0.819333333
Prrc2c	MmuEX0037415	chr1:164618247-164618348	C3	0.881685469	0.947150851	-0.065465382	0.974666667
Rfc1	MmuINT0133844	chr5:65667021-65668595	IR-S	0.018937033	0.084366675	-0.065429643	0.806666667
Stt3b	MmuINT0154529	chr9:115163163-115163906	IR-S	0.018874204	0.083505404	-0.064631201	0.91
Ubl7	MmuEX0050267	chr9:57759524-57759632	S	0.124288815	0.188906242	-0.064617427	0.888
Mrpl9	MmuEX0029711	chr3:94251182-94251265	S	0.923015475	0.98661167	-0.063596194	0.918

Setx	MmuEX0041879	chr2:29029839-29030003	S	0.01512371	0.078340517	-0.063216806	0.827333333
Fuca2	MmuEX0019744	chr10:13232424-13232532	S	0.928151117	0.990600345	-0.062449228	0.952666667
Cep192	MmuEX0010944	chr18:68014939-68015029	S	0.927087062	0.989516278	-0.062429216	0.822
Hspg2	MmuINT0079548	chr4:137125280-137125406	IR-S	0.021662335	0.083760273	-0.062097939	0.817333333
Scaf1	MmuALTD0012407-1/2	chr7:52261211-52261293	Alt5	0.908943571	0.971016977	-0.062073399	0.802666667
Prr14	MmuEX0037378	chr7:134617893-134617936	S	0.929351893	0.991090778	-0.061738885	0.833333333
Fxr1	MmuALTA0007451-1/3	chr3:33960828-33960911	Alt3	0.029802878	0.091208552	-0.061405673	0.827333333
Baz2a	MmuALTD0002128-1/2	chr10:127560822-127561044	Alt5	0.902290406	0.962334932	-0.060044526	0.808
Atf7ip	MmuALTD0001751-1/2	chr6:136512281-136512358	Alt5	0.868734601	0.928242398	-0.059507798	0.826
Dnajc11	MmuEX0015163	chr4:151343955-151344077	S	0.929754566	0.989105382	-0.059350816	0.954666667
Snrpa1	MmuEX0044159	chr7:73215005-73215084	S	0.929960924	0.988988778	-0.059027854	0.935333333
Safb2	MmuALTA0015786-1/2	chr17:56710823-56710972	Alt3	0.930135692	0.988576488	-0.058440796	0.970666667
Zmym1	MmuEX0053911	chr4:126736037-126736267	C3	0.928649846	0.987080783	-0.058430937	0.876
Anxa6	MmuEX0005344	chr11:54812037-54812115	S	0.932723632	0.990833078	-0.058109446	0.811333333
Twf1	MmuALTD0015028-1/2	chr15:94420183-	Alt5	0.924695772	0.982742472	-0.058046699	0.802
Prpsap1	MmuALTA0014241-1/2	chr11:116340966-116341138	Alt3	0.920922206	0.978090054	-0.057167994	0.818666667
Rod1	MmuEX0040288	chr4:59514182-59514346	S	0.921742716	0.977741393	-0.055998677	0.885333333
Ubap2l	MmuINT0168968	chr3:89805791-89806200	IR-C	0.032119078	0.088049675	-0.055930597	0.818666667
Shcbp1	MmuALTA0016353-1/2	chr8:4741848-4741966	Alt3	0.936806412	0.992583341	-0.05577693	0.854666667
Srp72	MmuINT0152459	chr5:77409457-77409539	IR-S	0.030349973	0.085500066	-0.055150086	0.844666667
Erp44	MmuEX0017362	chr4:48249745-48249860	S	0.936833452	0.991846978	-0.055013526	0.923333333
Trip12	MmuINT0165551	chr1:84724865-84727106	IR-S	0.041147857	0.095608718	-0.054460861	0.811333333
Sod2	MmuALTA0017080-1/2	chr17:13206299-13206478	Alt3	0.935222145	0.989523642	-0.054301496	0.844
Chmp4b	MmuINT0036070	chr2:154515432-154516945	IR-S	0.013421855	0.067332182	-0.053910328	0.926
Rbm25	MmuEX0039099	chr12:84983352-84983469	C3	0.105367501	0.159224697	-0.053857195	0.81
2310008H04Rik	MmuEX0000869	chr16:16140099-16140165	S	0.917531943	0.971020557	-0.053488614	0.820666667
Gab1	MmuEX0019855	chr8:83300060-83300149	S	0.096153535	0.149582365	-0.053428835	0.818
Vars	MmuEX0051254	chr17:35142195-35142295	S	0.940594991	0.992873669	-0.052278678	0.813333333
Prpf40a	MmuEX0037336	chr2:53012998-53013106	S	0.941126923	0.9931015	-0.051974577	0.826
Trim24	MmuEX0048872	chr6:37858217-37858364	S	0.907096906	0.958613142	-0.051516233	0.856666667
Ppp2cb	MmuINT0125236	chr8:34721337-34722219	IR-S	0.026365385	0.077822213	-0.051456833	0.846
Zmym1	MmuEX0053910	chr4:126736754-126736903	S	0.935585725	0.986862152	-0.051276428	0.834666667
Akap8	MmuINT0013431	chr17:32451090-32452386	IR-S	0.03354052	0.084479027	-0.050938507	0.822

Qk	MmuALTA0014623-1/3	chr17:10409030-10409300	Alt3	0.052910889	0.10346725	-0.05055636	0.812
Eapp	MmuEX0016145	chr12:55786847-55786958	C3	0.939326843	0.989706825	-0.050379982	0.866
Msh6	MmuINT0101225	chr17:88388602-88388766	IR-S	0.074061344	0.023946055	0.050115289	0.844
Agpat6	MmuINT0012761	chr8:24285133-24285811	IR-S	0.072131641	0.021937019	0.050194622	0.807333333
Kat2a	MmuINT0085222	chr11:100568283-100569522	IR-S	0.068318265	0.018067471	0.050250795	0.813333333
Sars	MmuINT0138847	chr3:108230851-108231091	IR-S	0.095287239	0.045034514	0.050252726	0.922666667
Scamp3	MmuINT0139196	chr3:88983146-88983238	IR-C	0.076123497	0.025862774	0.050260723	0.806
Por	MmuINT0124197	chr5:136208470-136208555	IR-S	0.071585387	0.021310581	0.050274806	0.806666667
Tmpo	MmuINT0162598	chr10:90615926-90616022	IR-C	0.078432221	0.028104742	0.050327479	0.824666667
Stoml2	MmuINT0154308	chr4:43043408-43043842	IR-S	0.065869364	0.015451514	0.05041785	0.864
Hsf2bp	MmuEX0023344	chr17:32150263-32150412	S	0.988739098	0.938260573	0.050478525	0.846666667
Ilf3	MmuEX0024059	chr9:21207580-21207945	S	0.978425764	0.927687473	0.050738291	0.804
Xrcc1	MmuINT0176967	chr7:25355946-25356033	IR-S	0.063561542	0.012792896	0.050768646	0.935333333
Pltp	MmuINT0122515	chr2:164672417-164677012	IR-S	0.0665386	0.015633287	0.050905313	0.810666667
Rsrc2	MmuINT0137661	chr5:124183645-124186567	IR-S	0.059287615	0.00815681	0.051130804	0.936666667
Ccna2	MmuINT0031594	chr3:36465597-36465921	IR-S	0.059335527	0.008155427	0.051180101	0.959333333
Tbrg4	MmuINT0157801	chr11:6516718-6517310	IR-S	0.067084618	0.015858112	0.051226507	0.807333333
Scrib	MmuINT0139955	chr15:75897185-75897249	IR-S	0.082088074	0.03085357	0.051234504	0.809333333
Scrib	MmuALTD0012463-1/2	chr15:75897040-75897184	Alt5	0.990296068	0.938941349	0.051354719	0.837333333
Map2k4	MmuINT0094989	chr11:65507073-65509789	IR-S	0.075739916	0.024367286	0.051372635	0.804666667
Edc4	MmuINT0055206	chr8:108411304-108411405	IR-S	0.063635172	0.012150393	0.051484779	0.821333333
Fkbp9	MmuINT0064705	chr6:56825827-56828027	IR-S	0.084764824	0.033154477	0.051610343	0.806666667
Ddx58	MmuINT0047984	chr4:40155956-40156911	IR-S	0.078485971	0.026804146	0.051681825	0.814666667
Cars	MmuEX0009191	chr7:150745554-150745613	S	0.982726041	0.930904891	0.05182115	0.942
Dync1h1	MmuINT0054153	chr12:111900057-111900727	IR-S	0.06510167	0.013236771	0.051864899	0.961333333
Tmem199	MmuINT0161865	chr11:78321308-78321820	IR-S	0.067680995	0.015664315	0.052016675	0.899333333
Nckap1	MmuINT0106448	chr2:80342472-80346329	IR-C	0.071285885	0.019245535	0.05204035	0.860666667
Abcf2	MmuINT0008764	chr5:24073131-24073318	IR-S	0.063592879	0.011452592	0.052140287	0.858
Tuba4a	MmuINT0168086	chr1:75214010-75215767	IR-S	0.074860902	0.022715313	0.052145593	0.855333333
Pcbp2	MmuINT0115856	chr15:102318709-102320182	IR-C	0.105771929	0.053474816	0.052297113	0.83
Mrps22	MmuINT0100934	chr9:98494576-98495088	IR-S	0.078765042	0.026377272	0.052387768	0.814666667
Cenpt	MmuINT0034513	chr8:108373824-108375770	IR-S	0.073127782	0.020656682	0.052471102	0.929333333
Pop4	MmuINT0124171	chr7:39049449-39050918	IR-S	0.085218023	0.032615193	0.05260283	0.819333333

Erp29	MmuINT0059040	chr5:121897289-121902199	IR-S	0.075112555	0.02248397	0.052628585	0.828666667
Kif20a	MmuINT0086965	chr18:34790081-34790175	IR-S	0.071070632	0.018420689	0.052649943	0.922666667
Parvb	MmuINT0115551	chr15:84134334-84139282	IR-S	0.063414753	0.010647331	0.052767422	0.838666667
Dynll1	MmuINT0054321	chr5:115748843-115750521	IR-S	0.058705829	0.005930852	0.052774977	0.862
Gm13242	MmuINT0070119	chr4:145286139-145289146	IR-C	0.181949418	0.129040234	0.052909184	0.830666667
Ddx27	MmuINT0047691	chr2:166859158-166859233	IR-S	0.071359659	0.018413571	0.052946088	0.890666667
Trip12	MmuINT0165529	chr1:84755703-84757337	IR-C	0.082662845	0.029559378	0.053103467	0.826666667
Mpdu1	MmuINT0100221	chr11:69471346-69471437	IR-S	0.084059836	0.030929904	0.053129932	0.930666667
Atp2a3	MmuINT0021199	chr11:72786044-72786323	IR-S	0.071455385	0.018312305	0.05314308	0.864666667
Sip1	MmuINT0143829	chr12:60122724-60125989	IR-S	0.079683178	0.026468081	0.053215097	0.811333333
Arhgdia	MmuINT0018300	chr11:120441059-120441280	IR-S	0.079868785	0.026639783	0.053229002	0.811333333
Spns1	MmuINT0151898	chr7:133516405-133517283	IR-S	0.07225513	0.019011562	0.053243568	0.930666667
Trim28	MmuINT0165072	chr7:13614945-13615024	IR-S	0.107976977	0.054667128	0.053309849	0.83
Gm949	MmuINT0071519	chr18:47081547-47085635	IR-S	0.066978618	0.013618659	0.053359959	0.898666667
Hmgxb4	MmuINT0078326	chr8:77547204-77547896	IR-S	0.073772042	0.020310595	0.053461447	0.807333333
Ubxn1	MmuINT0169769	chr19:8948746-8949649	IR-S	0.110266987	0.056795025	0.053471962	0.873333333
Ctdspl2	MmuEX0013035	chr2:121823183-121823592	S	0.081030924	0.027532416	0.053498508	0.824666667
Esyt1	MmuINT0059247	chr10:127960172-127962519	IR-S	0.072136032	0.018603835	0.053532197	0.819333333
Fkbp8	MmuINT0064696	chr8:73058514-73058765	IR-S	0.083090203	0.02953153	0.053558673	0.813333333
D14Ertd668e	MmuINT0045797	chr14:59974027-59975153	IR-C	0.077216939	0.023655685	0.053561254	0.82
Rif1	MmuEX0039819	chr2:51972188-51972265	S	0.665958685	0.612376926	0.053581759	0.806666667
Nup188	MmuINT0111788	chr2:30192926-30195018	IR-S	0.076932178	0.0232896	0.053642578	0.810666667
BC049349	MmuINT0023296	chr8:74490060-74491797	IR-S	0.071175784	0.017383963	0.053791821	0.896666667
Nek2	MmuINT0107582	chr1:193653397-193655015	IR-S	0.068744509	0.014780615	0.053963894	0.932
Fen1	MmuINT0063899	chr19:10275588-10278177	IR-S	0.085023752	0.030983492	0.05404026	0.809333333
Uqcrc1	MmuINT0170946	chr9:108850679-108850983	IR-S	0.066501145	0.012456437	0.054044708	0.888
Spcs1	MmuINT0151198	chr14:31813951-31814029	IR-S	0.074117114	0.019962938	0.054154177	0.812
Eif4a2	MmuINT0056471	chr16:23107894-23108660	IR-S	0.078350282	0.024088827	0.054261455	0.994
Ap1g1	MmuINT0016637	chr8:112379634-112382698	IR-S	0.07099976	0.016709215	0.054290545	0.81
March7	MmuINT0095818	chr2:60081728-60083268	IR-S	0.073130921	0.018771872	0.054359049	0.912
Fancm	MmuALTA0007006-1/2	chr12:66222644-66223077	Alt3	0.072185569	0.017820197	0.054365372	0.844666667
Vars	MmuINT0172575	chr17:35149981-35150066	IR-S	0.092519758	0.037978152	0.054541606	0.872666667
Arid1a	MmuINT0018712	chr4:133240481-133240788	IR-S	0.07648399	0.021926535	0.054557455	0.868666667

Grn	MmuINT0074308	chr11:102296141-102296372	IR-S	0.07684611	0.022280255	0.054565855	0.914
Nubp2	MmuINT0111393	chr17:25022783-25023223	IR-S	0.079514028	0.024912206	0.054601823	0.81
Smarcal1	MmuINT0148691	chr1:72673220-72674674	IR-C	0.06645556	0.011842013	0.054613547	0.810666667
Sulf2	MmuINT0154936	chr2:165901306-165903017	IR-S	0.080068604	0.025446532	0.054622071	0.844
Hcfc1	MmuINT0076181	chrX:71197408-71197511	IR-S	0.087579736	0.032897107	0.054682628	0.815333333
Traf7	MmuINT0164571	chr17:24650878-24651069	IR-S	0.068136513	0.013444503	0.05469201	0.9
Ubap2	MmuINT0168923	chr4:41152771-41153185	IR-S	0.078575794	0.023871791	0.054704003	0.847333333
Polr3e	MmuINT0123978	chr7:128078408-128081116	IR-S	0.074956759	0.020194201	0.054762559	0.836666667
Trpm7	MmuINT0166176	chr2:126624971-126625048	IR-S	0.075846552	0.021040615	0.054805937	0.81
Ncor1	MmuINT0106706	chr11:62134720-62134893	IR-S	0.087288915	0.032447256	0.054841659	0.81
Dus3l	MmuINT0053914	chr17:56906712-56907055	IR-C	0.157117796	0.102231861	0.054885935	0.806666667
Taf15	MmuINT0156631	chr11:83302548-83310763	IR-C	0.11486053	0.059939699	0.054920831	0.838666667
Flna	MmuINT0064818	chrX:71469317-71470090	IR-S	0.067962211	0.01302415	0.054938061	0.929333333
Sept1	MmuINT0141455	chr7:134361257-134361484	IR-S	0.182541437	0.127589033	0.054952404	0.884
Psmc5	MmuINT0127976	chr11:106123817-106123894	IR-S	0.068853571	0.013869841	0.05498373	0.964666667
Cops3	MmuINT0040978	chr11:59632002-59633506	IR-S	0.105280914	0.050288791	0.054992122	0.838
Ltv1	MmuINT0093864	chr10:12899130-12899460	IR-S	0.074798781	0.019772065	0.055026716	0.855333333
Cnot2	MmuINT0038151	chr10:115944245-115954372	IR-C	0.074742841	0.01968933	0.055053511	0.827333333
Grn	MmuINT0074301	chr11:102297563-102297648	IR-S	0.061911572	0.006767214	0.055144358	0.841333333
Klhdc2	MmuINT0087732	chr12:70411027-70411139	IR-S	0.075282676	0.020059524	0.055223152	0.820666667
Orc2	MmuINT0113474	chr1:58537998-58540486	IR-S	0.074121639	0.018882365	0.055239274	0.808666667
Fgfr1op	MmuINT0064251	chr17:8384303-8385049	IR-S	0.071758861	0.016487555	0.055271306	0.816
Tmem131	MmuINT0161420	chr1:36851044-36851648	IR-S	0.070518414	0.01510294	0.055415474	0.890666667
Ireb2	MmuINT0083270	chr9:54748380-54751697	IR-S	0.095174772	0.039579914	0.055594858	0.846666667
Gpx4	MmuINT0073489	chr10:79516461-79517258	IR-C	0.080539939	0.024927058	0.05561288	0.882666667
Agrn	MmuINT0012827	chr4:155547240-155547651	IR-S	0.081597335	0.02595247	0.055644866	0.805333333
Prim1	MmuINT0126131	chr10:127455139-127455203	IR-S	0.114005804	0.058336246	0.055669558	0.858666667
Srp72	MmuINT0152461	chr5:77411292-77413142	IR-C	0.070268423	0.01448135	0.055787073	0.848666667
Rtn4	MmuINT0137797	chr11:29636499-29640980	IR-S	0.085834659	0.030009993	0.055824665	0.827333333
Rangap1	MmuINT0131563	chr15:81547132-81549172	IR-S	0.067747077	0.01188283	0.055864247	0.878
Hprt	MmuINT0078864	chrX:50369607-50373281	IR-S	0.063749366	0.007841595	0.055907771	0.845333333
Gga2	MmuINT0068645	chr7:129145727-129146180	IR-C	0.096033916	0.040116709	0.055917207	0.823333333
Ndufv1	MmuINT0107150	chr19:4007916-4008047	IR-S	0.066608087	0.010618633	0.055989454	0.935333333

Mynn	MmuINT0103858	chr3:30511475-30512473	IR-S	0.09238752	0.036298353	0.056089167	0.816
Yars	MmuINT0177179	chr4:128874533-128877969	IR-S	0.069350054	0.013092926	0.056257128	0.935333333
Mcm4	MmuINT0096641	chr16:15626358-15627741	IR-S	0.064538931	0.008254399	0.056284531	0.914
Gtf2ird1	MmuEX0022118	chr5:134877981-134878064	S	0.98997369	0.933589761	0.05638393	0.86
Lsm14b	MmuINT0093555	chr2:179766577-179766765	IR-S	0.081006809	0.024467851	0.056538958	0.878
Tcerg1	MmuINT0158011	chr18:42730849-42731477	IR-S	0.107461236	0.050858074	0.056603162	0.82
Kif18b	MmuINT0086812	chr11:102768391-102769426	IR-S	0.083152113	0.026521033	0.05663108	0.878
Nol7	MmuINT0109458	chr13:43494165-43494879	IR-S	0.095146798	0.038513815	0.056632983	0.814666667
Nsmce4a	MmuINT0111054	chr7:137676207-137677090	IR-S	0.085818549	0.029170903	0.056647646	0.811333333
Reps1	MmuINT0133642	chr10:17840036-17840838	IR-S	0.071588084	0.014930553	0.056657531	0.809333333
Mcm7	MmuINT0096695	chr5:138609401-138609560	IR-S	0.082379626	0.025655348	0.056724278	0.826
Cetn3	MmuINT0035226	chr13:81922357-81923639	IR-S	0.068397135	0.011669834	0.0567273	0.829333333
Trpc4ap	MmuINT0165935	chr2:155465300-155466209	IR-S	0.087230523	0.030462234	0.056768289	0.849333333
Psmd7	MmuINT0128121	chr8:110109698-110110524	IR-S	0.070078924	0.013134231	0.056944694	0.848666667
Ptp4a2	MmuINT0128717	chr4:129522437-129523708	IR-S	0.071220395	0.014249112	0.056971283	0.800666667
Nhlrc2	MmuALTA0012026-1/2	chr19:56666917-56667005	Alt3	0.088907703	0.031852887	0.057054816	0.906
Pcf11	MmuINT0116060	chr7:99797542-99797965	IR-S	0.072602102	0.015446094	0.057156008	0.896666667
Gtf2f1	MmuINT0074756	chr17:57143477-57143544	IR-S	0.090323268	0.033138775	0.057184493	0.889333333
Usp7	MmuINT0172091	chr16:8693212-8693794	IR-S	0.083932785	0.026747648	0.057185137	0.894
Chmp5	MmuINT0036077	chr4:40895710-40896486	IR-S	0.079549361	0.022349186	0.057200175	0.838
Stub1	MmuALTA0017516-1/4	chr17:25968741-25968854	Alt3	0.073635665	0.016405213	0.057230452	0.955333333
Nfkbia	MmuINT0108171	chr12:56590957-56591392	IR-S	0.084375928	0.027081348	0.05729458	0.827333333
Atp6v1c1	MmuINT0021602	chr15:38616865-38618879	IR-S	0.085177045	0.027658902	0.057518143	0.808
Lphn1	MmuINT0091954	chr8:86461225-86461359	IR-S	0.074682329	0.017061033	0.057621296	0.818666667
Commd4	MmuINT0040781	chr9:57003396-57003708	IR-S	0.077396277	0.019703878	0.057692399	0.815333333
Vps72	MmuINT0174155	chr3:94922686-94923052	IR-S	0.074469659	0.016544203	0.057925456	0.866
Sdc4	MmuINT0140141	chr2:164255227-164256686	IR-S	0.075679662	0.017748349	0.057931313	0.886666667
Mlf2	MmuINT0099099	chr6:124884438-124884603	IR-S	0.103068607	0.04484632	0.058222288	0.938
Supt5h	MmuINT0155194	chr7:29114672-29115036	IR-S	0.080352082	0.022101851	0.058250231	0.828
Pou5f1	MmuINT0124341	chr17:35647085-35647232	IR-S	0.113642547	0.055146326	0.058496222	0.854
Apoa1bp	MmuINT0017203	chr3:87861760-87861842	IR-S	0.082254099	0.023738049	0.05851605	0.846
Dhx36	MmuINT0049217	chr3:62284842-62288052	IR-S	0.094778637	0.036220431	0.058558206	0.866
Senp1	MmuINT0141323	chr15:97907141-97912673	IR-S	0.082190503	0.023627178	0.058563325	0.824666667

Ralbp1	MmuINT0131226	chr17:66203540-66207001	IR-S	0.074269009	0.015509596	0.058759412	0.930666667
Qtrt1	MmuALTA0014634-1/2	chr9:21224486-	Alt3	0.086261236	0.027399522	0.058861714	0.843333333
Impact	MmuINT0081933	chr18:13146895-13148253	IR-S	0.095961502	0.037093284	0.058868218	0.824666667
Slc19a2	MmuINT0145038	chr1:166192371-166192750	IR-S	0.082238095	0.023368933	0.058869162	0.865333333
Napa	MmuINT0105602	chr7:16698539-16698698	IR-S	0.077617	0.018742317	0.058874682	0.962
Sgta	MmuINT0142921	chr10:80510422-80511124	IR-S	0.074404063	0.015416342	0.058987722	0.844
Decr2	MmuEX0014187	chr17:26224967-26225018	S	0.985810584	0.926805246	0.059005338	0.804666667
Eif3l	MmuINT0056439	chr15:78920392-78923766	IR-S	0.080772873	0.021638857	0.059134016	0.816
Eps15l1	MmuINT0058419	chr8:74906312-74906578	IR-S	0.083483508	0.024132649	0.059350859	0.882666667
Cars	MmuEX0009188	chr7:150756869-150756983	C3	0.083551894	0.024174786	0.059377108	0.805333333
Ap3d1	MmuINT0016859	chr10:80185708-80186277	IR-S	0.079679428	0.020235879	0.059443549	0.849333333
Tfpt	MmuINT0159311	chr7:3572586-3572664	IR-S	0.088108294	0.028515308	0.059592986	0.834666667
Thoc6	MmuINT0159896	chr17:23807328-23807415	IR-S	0.09152606	0.031898359	0.0596277	0.843333333
Lig1	MmuINT0090972	chr7:13885697-13886279	IR-S	0.11508026	0.055195275	0.059884985	0.801333333
Gnl3	MmuINT0072021	chr14:31825976-31826352	IR-S	0.13068452	0.070617753	0.060066766	0.886666667
Cdkn1a	MmuINT0033897	chr17:29230807-29235341	IR-C	0.126293338	0.066118542	0.060174796	0.850666667
Cherp	MmuINT0035897	chr8:74993915-74993988	IR-S	0.137707661	0.077471193	0.060236468	0.837333333
Tpd52l2	MmuINT0164139	chr2:181246321-181247743	IR-S	0.081093405	0.020769593	0.060323812	0.913333333
Zfp598	MmuINT0179515	chr17:24814131-24814354	IR-S	0.096108492	0.035768508	0.060339985	0.856666667
Ccni	MmuINT0031722	chr5:93616845-93617105	IR-S	0.086606708	0.026187693	0.060419015	0.865333333
Ehmt2	MmuINT0056007	chr17:35048424-35048523	IR-S	0.080380393	0.019953117	0.060427277	0.877333333
Ltbp4	MmuINT0093771	chr7:28113882-28113986	IR-S	0.077831571	0.017271838	0.060559734	0.864
Afg3l1	MmuEX0004159	chr8:126023892-126024007	S	0.992862717	0.932207151	0.060655566	0.826
E2f4	MmuINT0054711	chr8:107824517-107825152	IR-S	0.092005055	0.031289059	0.060715995	0.858
Taf1d	MmuINT0156673	chr9:15118709-15119545	IR-S	0.110231044	0.049448182	0.060782862	0.901333333
Ikbkap	MmuINT0081060	chr4:56787963-56788296	IR-S	0.084690769	0.023891396	0.060799373	0.92
Lrrc59	MmuINT0093153	chr11:94502708-94504607	IR-S	0.077893928	0.017083704	0.060810223	0.897333333
Dnm1l	MmuINT0051772	chr16:16341562-16346090	IR-C	0.087126186	0.026270351	0.060855835	0.875333333
Usp7	MmuINT0172086	chr16:8696010-8696769	IR-S	0.129776571	0.068834946	0.060941624	0.838
Adar	MmuINT0011626	chr3:89543894-89544015	IR-S	0.097218021	0.036219452	0.060998569	0.822
Mybbp1a	MmuINT0102887	chr11:72263336-72263494	IR-S	0.073088224	0.012077233	0.061010994	0.903333333
Copg	MmuINT0040940	chr6:87842714-87843789	IR-S	0.083814601	0.022751683	0.061062918	0.891333333
Wdr61	MmuINT0175499	chr9:54568160-54570640	IR-S	0.080410577	0.019203554	0.061207023	0.87

Bat3	MmuINT0024019	chr17:35282185-35282273	IR-S	0.093911398	0.032686267	0.061225131	0.888666667
Snhg1	MmuINT0149686	chr19:8799212-8799503	IR-S	0.080208678	0.018950103	0.061258575	0.988666667
Aup1	MmuINT0022280	chr6:83006429-83006535	IR-S	0.097236859	0.03595564	0.06128122	0.883333333
Dus1l	MmuINT0053882	chr11:120652665-120653168	IR-S	0.080100394	0.018713685	0.061386709	0.870666667
Def8	MmuALTA0005311-1/2	chr8:125982251-125982331	Alt3	0.985205613	0.923791513	0.0614141	0.907333333
Bax	MmuINT0024062	chr7:52718874-52720558	IR-S	0.069812059	0.008352583	0.061459476	0.924
Spint1	MmuINT0151593	chr2:119071019-119071245	IR-S	0.08460863	0.023136234	0.061472396	0.876666667
Gnl3	MmuINT0072028	chr14:31828213-31828460	IR-S	0.087025001	0.025528398	0.061496603	0.896666667
Ppan	MmuINT0124381	chr9:20695160-20695348	IR-S	0.103471207	0.041950726	0.061520481	0.828666667
Brd2	MmuINT0025650	chr17:34249924-34250121	IR-S	0.093354373	0.03180492	0.061549452	0.857333333
Adh5	MmuINT0012038	chr3:138108356-138110046	IR-S	0.087944557	0.026382359	0.061562198	0.812
Nub1	MmuINT0111379	chr5:24201409-24202822	IR-S	0.083477384	0.021785353	0.061692031	0.81
Frmd8	MmuALTA0007397-1/2	chr19:5873169-5873333	Alt3	0.090731543	0.028922418	0.061809124	0.841333333
Dynlrb1	MmuALTA0005962-1/2	chr2:155068471-155068542	Alt3	0.075795412	0.013972394	0.061823018	0.898666667
Psmd12	MmuINT0128038	chr11:107353245-107353330	IR-S	0.078367466	0.016504363	0.061863104	0.836666667
Ppp4r1	MmuEX0036811	chr17:66163894-66163984	S	0.078174922	0.016289699	0.061885224	0.840666667
Etnk1	MmuINT0059402	chr6:143151673-143151903	IR-S	0.105905085	0.043979302	0.061925783	0.843333333
Dvl2	MmuINT0054043	chr11:69819049-69819163	IR-S	0.080396058	0.018460497	0.061935561	0.909333333
Ganab	MmuINT0067515	chr19:8981885-8982340	IR-S	0.162275622	0.100271929	0.062003692	0.815333333
Hirip3	MmuINT0077925	chr7:134008000-134008076	IR-S	0.123524478	0.061320345	0.062204133	0.840666667
Ssbp3	MmuINT0152796	chr4:106710256-106710826	IR-S	0.078598617	0.01635284	0.062245778	0.816666667
Ptcd3	MmuINT0128369	chr6:71848450-71851189	IR-S	0.075625741	0.013102157	0.062523584	0.914666667
Cuedc2	MmuINT0043999	chr19:46405471-46405541	IR-S	0.081190349	0.01859926	0.062591089	0.904
Rbm19	MmuEX0039080	chr5:120569904-120569939	C3	0.983893524	0.921210844	0.06268268	0.85
Chordc1	MmuINT0036133	chr9:18108831-18109736	IR-S	0.085097857	0.022370644	0.062727213	0.862666667
Ufd1l	MmuINT0169936	chr16:18827811-18834328	IR-S	0.112175413	0.049445995	0.062729419	0.822
Urm1	MmuINT0171029	chr2:29698290-29698622	IR-S	0.077925712	0.015143755	0.062781957	0.888
Prc1	MmuALTA0014037-1/2	chr7:87458416-87458454	Alt3	0.075260959	0.012453241	0.062807717	0.871333333
Ccar1	MmuINT0029954	chr10:62226272-62227071	IR-S	0.168595279	0.105773787	0.062821492	0.822
Sh3bp1	MmuINT0143032	chr15:78731934-78732984	IR-C	0.086213194	0.023386425	0.062826768	0.814
Shmt1	MmuINT0143451	chr11:60608455-60611026	IR-C	0.073928352	0.011095078	0.062833275	0.941333333
Kars	MmuEX0024963	chr8:114532107-114532286	S	0.166855975	0.103934599	0.062921376	0.913333333
Ubap2	MmuALTA0019255-1/3	chr4:41152557-41152628	Alt3	0.078369826	0.015413304	0.062956522	0.844666667

Matr3	MmuINT0096186	chr18:35738112-35738558	IR-S	0.111163838	0.047987964	0.063175874	0.912
Eif3g	MmuINT0056397	chr9:20698887-20699076	IR-S	0.077302265	0.013977428	0.063324837	0.9
Smyd5	MmuINT0149489	chr6:85392212-85392592	IR-S	0.081235447	0.017900609	0.063334838	0.943333333
Sap30bp	MmuINT0138781	chr11:115821906-115822669	IR-S	0.07908949	0.015743195	0.063346295	0.898666667
Glb1	MmuINT0069075	chr9:114373417-114382955	IR-C	0.07820488	0.01477162	0.06343326	0.910666667
Cops5	MmuINT0040997	chr1:10025245-10027750	IR-S	0.086388513	0.022944858	0.063443655	0.872666667
Gigyf1	MmuINT0068832	chr5:137965337-137965416	IR-C	0.095390532	0.031780546	0.063609986	0.867333333
Spns1	MmuINT0151897	chr7:133517351-133517435	IR-S	0.121660978	0.057870113	0.063790865	0.820666667
Nop56	MmuINT0109597	chr2:130100883-130101398	IR-S	0.081199311	0.017359585	0.063839725	0.933333333
Snx17	MmuINT0150053	chr5:31497287-31497787	IR-S	0.074912791	0.011065384	0.063847407	0.953333333
Mtap4	MmuINT0101521	chr9:109965628-109966731	IR-S	0.115549641	0.051394107	0.064155534	0.852666667
R3hdm1	MmuINT0130262	chr1:130087317-130090036	IR-S	0.092527248	0.02826713	0.064260118	0.818666667
Atp6v0b	MmuINT0021536	chr4:117558286-117558408	IR-S	0.142233251	0.077861475	0.064371776	0.935333333
Atp6ap1	MmuINT0021458	chrX:71548926-71549135	IR-S	0.080071052	0.015683477	0.064387575	0.885333333
2410006H16Rik	MmuINT0002464	chr11:62417149-62417904	IR-S	0.072355001	0.00784254	0.064512461	0.882666667
Dap3	MmuEX0013753	chr3:88732369-88732449	C3	0.98028223	0.915750082	0.064532148	0.850666667
Mcoln1	MmuINT0096735	chr8:3507567-3508318	IR-S	0.085028843	0.020470935	0.064557907	0.888
Mrps10	MmuEX0029712	chr17:47506978-47507107	C1	0.084174877	0.01955456	0.064620317	0.817333333
Mybl2	MmuINT0102918	chr2:162887332-162888192	IR-S	0.122052571	0.057427267	0.064625312	0.894666667
Bat2l	MmuINT0023965	chr2:32082557-32084782	IR-C	0.085400295	0.020680474	0.064719821	0.899333333
Parl	MmuINT0115312	chr16:20297807-20298203	IR-S	0.087325091	0.022573951	0.064751139	0.818
Agtrap	MmuINT0012894	chr4:147454714-147455671	IR-S	0.089717676	0.024939898	0.064777778	0.829333333
Cox4nb	MmuINT0041265	chr8:123182975-123184683	IR-S	0.095747012	0.030940619	0.064806393	0.838666667
1600002H07Rik	MmuINT0000717	chr17:24353386-24354625	IR-S	0.081642586	0.016700664	0.064941922	0.878
2310008H04Rik	MmuINT0002135	chr16:15895734-15897316	IR-S	0.0890219	0.023889272	0.065132628	0.808666667
Spc25	MmuINT0151196	chr2:69032603-69035191	IR-S	0.08651551	0.021318157	0.065197353	0.856666667
Lonp1	MmuINT0091726	chr17:56753987-56754058	IR-S	0.09817041	0.032931951	0.065238459	0.816
Srfbp1	MmuINT0152296	chr18:52647248-52647904	IR-S	0.105584349	0.040326974	0.065257376	0.830666667
Prr14	MmuINT0127301	chr7:134617501-134617892	IR-C	0.089445975	0.024103547	0.065342429	0.837333333
Ktn1	MmuINT0089060	chr14:48323953-48324094	IR-S	0.079638086	0.014285978	0.065352108	0.920666667
Sf3b1	MmuINT0142382	chr1:55071407-55073219	IR-S	0.12376087	0.058376066	0.065384804	0.9
Cdc16	MmuINT0032686	chr8:13768635-13769376	IR-C	0.079849708	0.014354862	0.065494846	0.974666667
Ncaph2	MmuINT0106341	chr15:89194121-89194196	IR-S	0.088784926	0.023218056	0.06556687	0.824

Mfsd1	MmuINT0098217	chr3:67402048-67403861	IR-S	0.08182107	0.015980523	0.065840547	0.94
Wiz	MmuINT0176159	chr17:32494930-32495887	IR-C	0.121656956	0.055784883	0.065872074	0.814
Vps41	MmuINT0174032	chr13:18919603-18921091	IR-S	0.08024082	0.014346795	0.065894025	0.884
Dhx38	MmuINT0049262	chr8:112082211-112082543	IR-C	0.078218899	0.01221531	0.06600359	0.89
Jtb	MmuINT0085077	chr3:90036434-90037844	IR-S	0.108399173	0.042228306	0.066170868	0.81
Tcfe3	MmuINT0158236	chrX:7348197-7349574	IR-S	0.093232812	0.027005555	0.066227257	0.85
Abcb6	MmuINT0008305	chr1:75168563-75168687	IR-S	0.103853697	0.037580405	0.066273291	0.834
Mcm3	MmuINT0096600	chr1:20793736-20794897	IR-S	0.082123641	0.015730249	0.066393392	0.898
Hap1	MmuALTA0008382-1/3	chr11:100212732-100212839	Alt3	0.089042047	0.022512472	0.066529575	0.81
Pelp1	MmuINT0117824	chr11:70215569-70219128	IR-C	0.084746286	0.018145807	0.066600479	0.847333333
Eed	MmuINT0055349	chr7:97104924-97110765	IR-S	0.094691496	0.028002795	0.066688701	0.832666667
Ctsa	MmuINT0043709	chr2:164664231-164664344	IR-S	0.07955015	0.012820846	0.066729304	0.978
Kdm3a	MmuINT0086159	chr6:71545648-71546649	IR-S	0.083900814	0.017117492	0.066783322	0.915333333
Pdcd2	MmuINT0116674	chr17:15658758-15658879	IR-S	0.077599707	0.010810032	0.066789676	0.834666667
Prmt1	MmuINT0126767	chr7:52232354-52232873	IR-S	0.083574939	0.016703507	0.066871432	0.942
Add1	MmuINT0011980	chr5:34971822-34973118	IR-C	0.103343321	0.03626706	0.067076262	0.957333333
Rrp1b	MmuINT0137470	chr17:32192943-32193500	IR-S	0.113203468	0.046007946	0.067195523	0.805333333
Aaas	MmuINT0007280	chr15:102176965-102177108	IR-S	0.115606681	0.048310735	0.067295946	0.812
Dut	MmuINT0054013	chr2:125076754-125082584	IR-S	0.09081744	0.023472592	0.067344848	0.808
Agfg1	MmuINT0012641	chr1:82876703-82878802	IR-S	0.08743514	0.020042302	0.067392838	0.892666667
Mrpl38	MmuINT0100804	chr11:115993871-115994056	IR-S	0.082718538	0.015164444	0.067554094	0.810666667
Snx17	MmuEX0044249	chr5:31497579-31497652	S	0.09249312	0.024865049	0.067628071	0.942
Gak	MmuALTA0007504-1/2	chr5:109045928-109046065	Alt3	0.101231203	0.033143906	0.068087297	0.848666667
Atp6v1h	MmuINT0021657	chr1:5074645-5079089	IR-S	0.096221581	0.028096524	0.068125057	0.825333333
Efna3	MmuEX0016365	chr3:89119730-89119807	S	0.972955976	0.904816951	0.068139025	0.808666667
Sltm	MmuINT0148449	chr9:70422433-70424528	IR-C	0.268642409	0.200390022	0.068252387	0.843333333
Zfp259	MmuINT0178812	chr9:46087839-46087998	IR-S	0.105198992	0.036914824	0.068284168	0.842
Umps	MmuINT0170374	chr16:33959254-33960262	IR-S	0.082166039	0.013830645	0.068335394	0.854666667
Ap3d1	MmuEX0005450	chr10:80195596-80195691	S	0.967549337	0.899200741	0.068348596	0.856
Rnf114	MmuINT0135428	chr2:167336483-167336711	IR-S	0.093878217	0.025510024	0.068368193	0.821333333
Ebna1bp2	MmuINT0054972	chr4:118294139-118294674	IR-S	0.094762192	0.02631093	0.068451262	0.874666667
Usp11	MmuINT0171261	chrX:20296541-20296718	IR-S	0.098428813	0.029790786	0.068638027	0.854
Vdac1	MmuINT0172821	chr11:52200976-52201933	IR-S	0.095478897	0.026837662	0.068641235	0.926

Tjap1	MmuINT0160350	chr17:46396433-46396885	IR-S	0.088000918	0.019341517	0.068659401	0.838666667
Timm50	MmuINT0160265	chr7:29091998-29092571	IR-S	0.087513772	0.018738211	0.068775562	0.858
Tulp3	MmuINT0168315	chr6:128275097-128275894	IR-S	0.091977114	0.023147949	0.068829165	0.864666667
C030048B08Rik	MmuINT0026530	chr5:3590804-3591669	IR-S	0.103806679	0.034966314	0.068840365	0.814666667
Atp6v1e1	MmuEX0006910	chr6:120746416-120746482	S	0.107982619	0.039135363	0.068847256	0.952
Qars	MmuINT0130122	chr9:108417564-108418126	IR-S	0.106259375	0.037396439	0.068862937	0.850666667
Gatad2a	MmuEX0020135	chr8:72474552-72474653	C2	0.956252817	0.887363875	0.068888942	0.901333333
Hras1	MmuINT0078987	chr7:148378190-148378340	IR-S	0.088758705	0.019623835	0.069134874	0.854
Rpusd4	MmuINT0137277	chr9:35081151-35082648	IR-S	0.099024675	0.029715564	0.069309106	0.848
Dcaf4	MmuINT0046887	chr12:84878765-84878893	IR-S	0.089410468	0.019987931	0.069422538	0.878666667
Orc6	MmuINT0113532	chr8:87826859-87827260	IR-S	0.099124239	0.029684283	0.069439956	0.977333333
Pdcd2l	MmuINT0116680	chr7:34969831-34971312	IR-S	0.119844326	0.050382223	0.069462102	0.842
Atp5j2	MmuEX0006867	chr5:145949062-145949127	S	0.094111954	0.024509651	0.069602303	0.937333333
Wtip	MmuINT0176419	chr7:34903825-34903955	IR-S	0.094775349	0.025078324	0.069697025	0.861333333
Psmd4	MmuINT0128097	chr3:94839247-94839731	IR-S	0.082172301	0.012370796	0.069801505	0.948
2310057J16Rik	MmuINT0002339	chr8:3602426-3602553	IR-C	0.093720093	0.023909893	0.0698102	0.894666667
Hddc2	MmuINT0076493	chr10:31036202-31040073	IR-S	0.090934515	0.020929366	0.070005149	0.826
Surf2	MmuINT0155263	chr2:26774576-26774711	IR-S	0.101630666	0.031609346	0.07002132	0.804666667
Nxn	MmuINT0112259	chr11:76087574-76088016	IR-S	0.097405404	0.02729515	0.070110254	0.810666667
Cdk2	MmuINT0033678	chr10:128139640-128140762	IR-S	0.094664119	0.024496625	0.070167493	0.852
Upf1	MmuINT0170824	chr8:72862220-72862295	IR-S	0.097168383	0.026935602	0.070232781	0.87
Dhx38	MmuINT0049269	chr8:112078652-112078812	IR-S	0.086115611	0.015846593	0.070269019	0.866666667
2310035C23Rik	MmuINT0002257	chr1:107647621-107650079	IR-S	0.098969895	0.028500179	0.070469716	0.812666667
AU018091	MmuALTA0000788-1/2	chr7:3163894-3164295	Alt3	0.465623962	0.395069581	0.070554382	0.880666667
Clk1	MmuINT0037407	chr1:58471529-58473856	IR-C	0.103350478	0.032752273	0.070598205	0.841333333
ORF19	MmuINT0112293	chr17:66466784-66467402	IR-S	0.097681348	0.027006155	0.070675193	0.846
Ganab	MmuINT0067516	chr19:8982407-8983167	IR-S	0.13554704	0.06484276	0.070704279	0.902666667
Tceal8	MmuINT0157980	chrX:132705589-132706174	IR-C	0.114860572	0.044116807	0.070743765	0.829333333
Dhx36	MmuINT0049218	chr3:62283341-62284723	IR-S	0.088060711	0.017265242	0.07079547	0.926
Asns	MmuINT0019833	chr6:7630212-7631249	IR-S	0.19376179	0.122870621	0.070891168	0.844666667
Tbx3	MmuINT0157876	chr5:120125714-120127509	IR-S	0.086104245	0.015077033	0.071027212	0.970666667
Sept2	MmuALTA0016139-1/2	chr1:95385705-95385731	Alt3	0.089684257	0.018647497	0.07103676	0.856
Gpa33	MmuINT0072439	chr1:168087800-168093903	IR-S	0.093604759	0.022489934	0.071114825	0.883333333

Gabbr1	MmuINT0066890	chr17:37199722-37200274	IR-S	0.20284585	0.131573888	0.071271962	0.852666667
Eif5	MmuINT0056658	chr12:112778784-112779916	IR-S	0.088139418	0.01684938	0.071290038	0.954666667
Mosc2	MmuINT0100112	chr1:186646430-186656454	IR-C	0.09889238	0.027534009	0.07135837	0.816666667
Blm	MmuEX0008028	chr7:87618915-87619110	S	0.963571064	0.892181391	0.071389673	0.842666667
Abcd4	MmuINT0008713	chr12:85944360-85944898	IR-S	0.154576097	0.082772109	0.071803988	0.85
Stra13	MmuINT0154341	chr11:120573071-120573157	IR-S	0.092841278	0.020653414	0.072187864	0.888
Apeh	MmuINT0017095	chr9:107988661-107988753	IR-S	0.129857313	0.057660705	0.072196608	0.88
Ttf2	MmuINT0167469	chr3:100749874-100751320	IR-C	0.107344169	0.03514493	0.072199238	0.805333333
Tex19.1	MmuINT0159170	chr11:121007916-121008042	IR-S	0.109221168	0.037008731	0.072212437	0.822666667
Hnrnph3	MmuINT0078508	chr10:62480086-62480271	IR-C	0.099370328	0.027090114	0.072280214	0.886
M6pr	MmuINT0094233	chr6:122263444-122265074	IR-S	0.097129075	0.02477175	0.072357325	0.919333333
Dusp1	MmuINT0053929	chr17:26643596-26643929	IR-S	0.085985066	0.013593647	0.072391419	0.931333333
Pfdn4	MmuINT0118140	chr2:170341347-170342049	IR-S	0.099438599	0.026994505	0.072444094	0.840666667
Ik	MmuINT0081028	chr18:36904443-36905264	IR-S	0.093040608	0.020574626	0.072465982	0.848
Tada2a	MmuINT0156552	chr11:83907150-83916554	IR-S	0.097485537	0.024937106	0.07254843	0.811333333
2510006D16Rik	MmuINT0002598	chr4:129279506-129284330	IR-S	0.089738883	0.016657909	0.073080974	0.887333333
2900064A13Rik	MmuINT0003170	chr2:112299737-112302957	IR-S	0.088632472	0.015426028	0.073206444	0.916
Ergic3	MmuINT0058868	chr2:155842539-155842624	IR-S	0.11576944	0.042408645	0.073360795	0.812666667
Acox1	MmuINT0009957	chr11:116040159-116040921	IR-S	0.093914876	0.020336606	0.07357827	0.935333333
Usp19	MmuINT0171371	chr9:108400368-108400453	IR-S	0.090881738	0.017117726	0.073764012	0.872
Rtel1	MmuINT0137710	chr2:181086659-181086745	IR-S	0.136220062	0.062451903	0.073768159	0.808
Tspan31	MmuALTD0014919-1/2	chr10:126505964-126505973	Alt5	0.98085206	0.907078192	0.073773868	0.803333333
Ostf1	MmuINT0113885	chr19:18659234-18661036	IR-S	0.087125432	0.013191513	0.073933919	0.879333333
Gm505	MmuINT0070717	chr8:127424236-127425524	IR-S	0.096750386	0.022749351	0.074001035	0.91
Ireb2	MmuINT0083278	chr9:54730264-54731703	IR-S	0.130292887	0.056290647	0.07400224	0.822
Mybbp1a	MmuINT0102878	chr11:72260803-72261054	IR-S	0.099441295	0.025221313	0.074219982	0.922666667
Atp5g3	MmuINT0021416	chr2:73747999-73749011	IR-S	0.088537903	0.014245476	0.074292427	0.91
D2Ertd750e	MmuINT0045972	chr2:118657364-118659735	IR-S	0.1175062	0.043163116	0.074343084	0.822
Asah1	MmuINT0019454	chr8:42434979-42437247	IR-C	0.086693408	0.012302992	0.074390416	0.878
Gsk3a	MmuINT0074494	chr7:26016761-26016852	IR-S	0.120312352	0.045815987	0.074496365	0.809333333
Nqo1	MmuINT0110391	chr8:109915047-109916021	IR-S	0.11137348	0.036831507	0.074541973	0.946
Sec23a	MmuALTA0016023-1/2	chr12:60108034-60108218	Alt3	0.106203063	0.031617243	0.074585819	0.898666667
Ctsa	MmuINT0043710	chr2:164664450-164664650	IR-S	0.110075014	0.035440853	0.074634162	0.943333333

0610007P22Rik	MmuINT0000034	chr17:25378203-25378632	IR-S	0.102612259	0.027865366	0.074746894	0.842666667
Zranb2	MmuINT0180795	chr3:157206209-157207927	IR-S	0.166030479	0.091140882	0.074889597	0.865333333
Hnrnpl	MmuINT0078535	chr7:29600372-29603479	IR-S	0.134636668	0.05970994	0.074926728	0.848
Ehmt2	MmuINT0056008	chr17:35048611-35049333	IR-S	0.094716877	0.019754884	0.074961993	0.896666667
1700061G19Rik	MmuINT0001454	chr17:57026111-57028059	IR-S	0.140198161	0.06520906	0.074989101	0.910666667
Epn1	MmuEX0017111	chr7:5041605-5041770	S	0.923990031	0.848939742	0.075050289	0.867333333
G3bp1	MmuINT0066779	chr11:55299241-55300980	IR-S	0.093356997	0.018176199	0.075180798	0.94
0610007C21Rik	MmuINT0000005	chr5:31355258-31356333	IR-S	0.092070636	0.016753271	0.075317366	0.908
Prkcsh	MmuINT0126414	chr9:21816548-21816662	IR-S	0.104691915	0.029365066	0.075326849	0.888666667
Nfyb	MmuINT0108337	chr10:82213193-82213482	IR-S	0.103538067	0.028112981	0.075425086	0.821333333
Rrp1	MmuINT0137423	chr10:77871965-77873710	IR-S	0.127244319	0.051725041	0.075519278	0.870666667
Prpf40b	MmuINT0127142	chr15:99146580-99146673	IR-S	0.139924111	0.064364177	0.075559934	0.850666667
Ulk1	MmuINT0170258	chr5:111225520-111227900	IR-S	0.100417132	0.024832245	0.075584886	0.816666667
Adipor2	MmuINT0012096	chr6:119309128-119309368	IR-S	0.098510967	0.02292537	0.075585596	0.813333333
Abcc4	MmuEX0003118	chr14:118906815-118906904	S	0.970396511	0.894609471	0.075787039	0.808
Rtel1	MmuINT0137695	chr2:181073947-181075200	IR-S	0.124704331	0.048800823	0.075903508	0.847333333
Spns1	MmuINT0151895	chr7:133518718-133520187	IR-S	0.11211188	0.036169942	0.075941938	0.895333333
Smpd4	MmuEX0043985	chr16:17620805-17620855	S	0.09594801	0.019975272	0.075972738	0.894666667
Parl	MmuINT0115316	chr16:20285909-20286992	IR-S	0.104765918	0.028730729	0.076035189	0.859333333
Dctn2	MmuINT0047229	chr10:126714582-126714750	IR-S	0.094684049	0.01849458	0.076189468	0.960666667
Sec23b	MmuINT0140570	chr2:144405140-144407679	IR-S	0.091795409	0.015510828	0.076284581	0.844
Git1	MmuINT0068965	chr11:77314244-77314573	IR-S	0.107698648	0.031413505	0.076285142	0.83
D10Wsu52e	MmuINT0045713	chr10:85409096-85409921	IR-S	0.093737556	0.017450687	0.076286869	0.854666667
Ilf3	MmuINT0081823	chr9:21207946-21208503	IR-S	0.118621487	0.04230647	0.076315016	0.972
Tial1	MmuALTA0018177-1/2	chr7:135592135-135592233	Alt3	0.906373373	0.830055655	0.076317719	0.828
Mpdu1	MmuINT0100220	chr11:69471524-69472067	IR-S	0.166891752	0.090550124	0.076341628	0.806666667
Tmem8	MmuINT0162410	chr17:26257631-26258484	IR-S	0.113460059	0.036966251	0.076493808	0.852666667
Rnf10	MmuALTA0015313-1/2	chr5:115691788-115692067	Alt3	0.153720141	0.077095508	0.076624633	0.973333333
Gdf15	MmuINT0068324	chr8:73154074-73155231	IR-S	0.088108944	0.011481074	0.076627871	0.976
Map2k2	MmuINT0094964	chr10:80580975-80581853	IR-S	0.115040944	0.038330209	0.076710734	0.844666667
Agfg1	MmuALTA0001309-1/2	chr1:82882689-82882762	Alt3	0.217405176	0.140545418	0.076859758	0.828666667
Trim25	MmuINT0165050	chr11:88876505-88876846	IR-S	0.125028541	0.048117877	0.076910664	0.823333333
Vac14	MmuINT0172508	chr8:113236728-113239326	IR-C	0.102750965	0.025806749	0.076944216	0.878666667

Cenph	MmuEX0010803	chr13:101541429-101541521	S	0.114427537	0.037385323	0.077042214	0.874
Snhg12	MmuINT0149698	chr4:131865819-131866065	IR-S	0.120317912	0.042997996	0.077319916	0.952
Cpsf6	MmuEX0012610	chr10:116798830-116798940	S	0.113731875	0.036396335	0.07733554	0.835333333
Fus	MmuINT0066544	chr7:135124806-135124924	IR-S	0.115137956	0.037715757	0.077422199	0.915333333
Rnasen	MmuINT0135339	chr15:12837150-12842265	IR-S	0.114950155	0.037422068	0.077528086	0.841333333
Tbcel	MmuINT0157652	chr9:42251159-42252489	IR-S	0.109494535	0.031779251	0.077715284	0.849333333
Kdelr3	MmuINT0086067	chr15:79355393-79356096	IR-S	0.085196315	0.00740804	0.077788276	0.963333333
Prr11	MmuINT0127278	chr11:86905368-86910464	IR-S	0.111115025	0.033276578	0.077838446	0.803333333
Ppil2	MmuINT0124766	chr16:17089747-17090194	IR-S	0.10977741	0.031729222	0.078048189	0.818666667
Uap1l1	MmuINT0168763	chr2:25217658-25218182	IR-S	0.155223561	0.07695354	0.078270021	0.826
Rrp36	MmuINT0137484	chr17:46807135-46809284	IR-S	0.096444034	0.018105472	0.078338562	0.854666667
Naa40	MmuEX0030756	chr19:7304438-7304596	S	0.968489631	0.890143428	0.078346203	0.822
Mybbp1a	MmuINT0102880	chr11:72261385-72261457	IR-S	0.110442707	0.031877041	0.078565667	0.935333333
Nup85	MmuINT0112032	chr11:115431435-115439243	IR-S	0.092057879	0.013343575	0.078714304	0.946666667
Psmg1	MmuINT0128223	chr16:96205599-96208899	IR-S	0.114960729	0.036245686	0.078715043	0.845333333
Capn10	MmuINT0028666	chr1:94841856-94843350	IR-C	0.11601853	0.037202121	0.078816408	0.808666667
Mta1	MmuINT0101422	chr12:114374040-114374491	IR-S	0.114865824	0.035982278	0.078883546	0.848
Osgep	MmuINT0113817	chr14:51539467-51539604	IR-S	0.117379316	0.038491894	0.078887422	0.841333333
Gclc	MmuINT0068174	chr9:77634657-77635083	IR-S	0.095864232	0.0169236	0.078940633	0.958
Prkcsh	MmuINT0126411	chr9:21815698-21815881	IR-S	0.143707251	0.064755277	0.078951974	0.853333333
Xrcc5	MmuINT0177003	chr1:72428303-72429931	IR-S	0.149373683	0.070420017	0.078953666	0.811333333
Rpap1	MmuINT0136427	chr2:119608968-119609469	IR-S	0.102643732	0.023539914	0.079103818	0.885333333
Rgl2	MmuINT0134168	chr17:34072979-34073807	IR-S	0.124984813	0.045672801	0.079312012	0.820666667
Apoa1bp	MmuINT0017204	chr3:87861056-87861645	IR-S	0.115681968	0.036329091	0.079352877	0.804
Tcn2	MmuINT0158317	chr11:3819409-3822013	IR-S	0.106763125	0.027382572	0.079380552	0.806666667
Ppm1a	MmuINT0124885	chr12:73891729-73893764	IR-S	0.093530686	0.014145266	0.07938542	0.938666667
Cc2d1b	MmuINT0029902	chr4:108305909-108306127	IR-S	0.10330942	0.023762366	0.079547054	0.897333333
Ints10	MmuEX0024260	chr8:71348089-71348166	C1	0.164758513	0.085146089	0.079612424	0.804
Tmpo	MmuEX0048159	chr10:90615373-90615483	C1	0.808961448	0.729256954	0.079704494	0.88
Cdc42bpg	MmuINT0032921	chr19:6321755-6321826	IR-S	0.104762614	0.025005135	0.079757479	0.903333333
Snrnp25	MmuINT0149773	chr11:32108409-32108684	IR-S	0.103143085	0.023366644	0.079776441	0.862666667
Abcf1	MmuINT0008743	chr17:36097675-36097759	IR-S	0.102774812	0.022855611	0.079919201	0.917333333
Kdm3a	MmuINT0086151	chr6:71557601-71561498	IR-S	0.111844869	0.031688866	0.080156003	0.828666667

Atp6v0a1	MmuINT0021483	chr11:100910791-100916339	IR-S	0.105034211	0.024870003	0.080164208	0.831333333
Phc1	MmuINT0118601	chr6:122271071-122271889	IR-S	0.114381931	0.034198941	0.08018299	0.814666667
Brca1	MmuINT0025580	chr11:101369545-101371234	IR-S	0.101759122	0.021559464	0.080199657	0.894666667
2410076I21Rik	MmuINT0002505	chr9:58508179-58513639	IR-S	0.107775657	0.027352505	0.080423151	0.813333333
Tbx3	MmuEX0046615	chr5:120125252-120125311	S	0.333577733	0.253018847	0.080558886	0.950666667
Ubr5	MmuALTA0019392-1/2	chr15:37943197-37943320	Alt3	0.187086935	0.106490825	0.08059611	0.808
Becn1	MmuINT0024728	chr11:101155462-101156283	IR-S	0.123223537	0.042385438	0.080838099	0.868666667
Pcm1	MmuALTA0012855-1/2	chr8:42407310-42407405	Alt3	0.108163127	0.027266326	0.080896801	0.806
Use1	MmuALTA0019551-1/2	chr8:73893031-73893202	Alt3	0.832335007	0.751350449	0.080984558	0.877333333
Ints10	MmuINT0082495	chr8:71346150-71351175	IR-C	0.120243867	0.039216264	0.081027602	0.806666667
Ddx46	MmuINT0047838	chr13:55760460-55762077	IR-S	0.144992812	0.063959229	0.081033583	0.864
Nop56	MmuINT0109602	chr2:130102869-130103211	IR-C	0.208445039	0.127307977	0.081137062	0.948
Tax1bp1	MmuEX0046353	chr6:52692686-52692832	S	0.983650019	0.90242108	0.081228939	0.822666667
Fbxl3	MmuINT0063115	chr14:103488691-103491520	IR-S	0.156576673	0.07526244	0.081314233	0.804666667
Acp6	MmuINT0010040	chr3:96979717-96980253	IR-S	0.097373467	0.016015354	0.081358114	0.863333333
Dusp1	MmuINT0053927	chr17:26644665-26644901	IR-S	0.096740369	0.015273346	0.081467023	0.955333333
Ftsjd2	MmuINT0066434	chr17:29837227-29837915	IR-C	0.138761291	0.057196055	0.081565236	0.807333333
Ranbp9	MmuEX0038733	chr13:43531459-43531511	S	0.989465471	0.907803795	0.081661676	0.802
Nob1	MmuINT0109301	chr8:109945513-109948637	IR-S	0.097774575	0.016107139	0.081667436	0.822666667
St3gal3	MmuINT0153167	chr4:117613106-117631032	IR-S	0.141653968	0.059957003	0.081696965	0.864
Slc3a2	MmuINT0146812	chr19:8786419-8787219	IR-S	0.101947267	0.020183674	0.081763594	0.962666667
Dhx38	MmuINT0049272	chr8:112086037-112086343	IR-S	0.105463941	0.023684666	0.081779276	0.899333333
Cops7a	MmuINT0041016	chr6:124912716-124914741	IR-S	0.095071983	0.013270854	0.081801129	0.992
Spns1	MmuINT0151902	chr7:133514791-133515054	IR-S	0.1315488	0.049710331	0.081838469	0.854
Rps6kb1	MmuINT0137151	chr11:86316465-86317767	IR-S	0.110887114	0.029013907	0.081873208	0.910666667
Bat2l	MmuINT0023966	chr2:32084865-32086130	IR-C	0.108336776	0.026444193	0.081892583	0.896666667
Ubap2l	MmuINT0168966	chr3:89807235-89812177	IR-C	0.119651935	0.037745172	0.081906763	0.895333333
Mta2	MmuINT0101432	chr19:9016873-9017954	IR-S	0.108123755	0.026021668	0.082102087	0.894666667
Coq7	MmuINT0041099	chr7:125668809-125669337	IR-S	0.108101145	0.025960093	0.082141052	0.844
Ubxn2a	MmuINT0169791	chr12:4887578-4890628	IR-S	0.112207316	0.030029075	0.082178241	0.872
Aars	MmuINT0007389	chr8:113567242-113567542	IR-S	0.10189724	0.019623434	0.082273807	0.948666667
Kpna1	MmuEX0025871	chr16:36015973-36016095	S	0.12290284	0.040454097	0.082448743	0.878
Dus3l	MmuINT0053911	chr17:56908862-56908956	IR-S	0.149554322	0.067082735	0.082471587	0.822

Echdc2	MmuINT0055072	chr4:107842554-107844693	IR-C	0.109943674	0.027386913	0.082556761	0.884666667
Prpf3	MmuINT0127038	chr3:95636546-95637675	IR-S	0.097376591	0.014760627	0.082615963	0.95
Mrpl24	MmuINT0100758	chr3:87725971-87726052	IR-S	0.10626533	0.023487564	0.082777767	0.821333333
Dusp12	MmuALTD0004538-1/2	chr1:172810261-172810357	Alt5	0.982649445	0.899785908	0.082863536	0.846666667
Zwilch	MmuINT0180967	chr9:63994728-63995076	IR-S	0.163174488	0.080258049	0.082916439	0.806666667
Rbm28	MmuINT0132750	chr6:29104894-29105026	IR-S	0.107573435	0.024314828	0.083258607	0.818666667
Akap11	MmuALTD0001163-1/2	chr14:78916154-78916264	Alt5	0.117041816	0.033548962	0.083492853	0.828666667
Dnajc11	MmuINT0051430	chr4:151353439-151353552	IR-S	0.135283578	0.051729106	0.083554473	0.847333333
Txnl4a	MmuEX0049995	chr18:80416996-80417053	S	0.111298736	0.027680108	0.083618628	0.812666667
Adprh	MmuINT0012140	chr16:38447689-38450208	IR-S	0.143952675	0.060306529	0.083646146	0.806666667
Emg1	MmuINT0057119	chr6:124655235-124655532	IR-S	0.136002406	0.052285799	0.083716607	0.965333333
Neo1	MmuINT0107766	chr9:58826569-58829882	IR-S	0.148841902	0.065109828	0.083732074	0.811333333
Acss1	MmuINT0010299	chr2:150447369-150450534	IR-S	0.127465893	0.04353657	0.083929323	0.836
Cdk9	MmuINT0033815	chr2:32565136-32565292	IR-S	0.11436932	0.03007291	0.08429641	0.866
Sars	MmuINT0138843	chr3:108234539-108235935	IR-S	0.12105075	0.036697947	0.084352803	0.969333333
Mrpl38	MmuINT0100800	chr11:115996431-115996504	IR-S	0.158673717	0.074064144	0.084609573	0.865333333
Usp21	MmuINT0171437	chr1:173213573-173213768	IR-C	0.11889262	0.034243175	0.084649446	0.802666667
Trim6	MmuINT0165300	chr7:111380654-111380880	IR-S	0.132178147	0.046814085	0.085364062	0.875333333
Mllt6	MmuINT0099396	chr11:97539978-97540278	IR-S	0.111997362	0.026526875	0.085470486	0.896
Smarcad1	MmuEX0043790	chr6:65061770-65061879	S	0.991152562	0.905604821	0.085547741	0.956666667
Zp3	MmuINT0180734	chr5:136461533-136463124	IR-S	0.111539925	0.025809801	0.085730124	0.843333333
Mpv17	MmuINT0100523	chr5:31448462-31456040	IR-S	0.120878826	0.03497065	0.085908176	0.832
Psmd3	MmuINT0128086	chr11:98556728-98556836	IR-S	0.110797216	0.024792316	0.0860049	0.890666667
Trp53inp1	MmuEX0049097	chr4:11095044-11095081	S	0.308419045	0.222350835	0.086068211	0.919333333
Tm9sf4	MmuALTA0018271-1/2	chr2:153013267-153013399	Alt3	0.978767222	0.892548201	0.08621902	0.816
Hes1	MmuINT0077423	chr16:30066013-30066248	IR-S	0.10435649	0.018132627	0.086223863	0.864
Vps16	MmuINT0173866	chr2:130267638-130267908	IR-S	0.115341321	0.029091856	0.086249466	0.831333333
Abcd4	MmuINT0008708	chr12:85946914-85947049	IR-S	0.128210149	0.041884865	0.086325283	0.911333333
Shmt2	MmuINT0143464	chr10:126955437-126955526	IR-S	0.129169345	0.042785649	0.086383696	0.868666667
Xab2	MmuINT0176552	chr8:3611237-3611393	IR-S	0.095203239	0.008697078	0.08650616	0.986666667
Eif2b1	MmuINT0056147	chr5:125026924-125027024	IR-S	0.107393254	0.020872957	0.086520298	0.898
Uap1l1	MmuINT0168762	chr2:25218369-25218763	IR-S	0.105796279	0.019091407	0.086704873	0.934
Mms19	MmuALTA0011108-1/2	chr19:42037478-42037524	Alt3	0.109968909	0.02314106	0.086827849	0.902666667

Tbl1x	MmuINT0157714	chrX:74898681-74900744	IR-S	0.109076443	0.022088973	0.08698747	0.878666667
Sema4b	MmuINT0141119	chr7:87368903-87369481	IR-S	0.141607812	0.054589936	0.087017876	0.848
Ddx41	MmuINT0047795	chr13:55637166-55637246	IR-S	0.13731978	0.050274707	0.087045073	0.841333333
Galk2	MmuINT0067250	chr2:125801198-125808790	IR-S	0.114865999	0.027802301	0.087063697	0.828666667
Edc4	MmuINT0055217	chr8:108413998-108414139	IR-S	0.105442405	0.018178947	0.087263458	0.93
Smg5	MmuINT0149139	chr3:88163561-88164252	IR-S	0.14990688	0.062534456	0.087372424	0.816666667
Epb4.1	MmuEX0016979	chr4:131518839-131518901	C1	0.142044002	0.054605124	0.087438877	0.826666667
Immt	MmuINT0081895	chr6:71801875-71802723	IR-S	0.207510419	0.119942466	0.087567954	0.83
Spry2	MmuINT0152069	chr14:106293019-106295804	IR-S	0.104262505	0.016645657	0.087616848	0.983333333
Chtf8	MmuEX0011409	chr8:109410820-109410937	S	0.876894203	0.789261845	0.087632357	0.808666667
Tnk2	MmuINT0163208	chr16:32675803-32677979	IR-S	0.107527541	0.019737298	0.087790244	0.934
Adar	MmuINT0011622	chr3:89554678-89554850	IR-S	0.117202217	0.029269669	0.087932548	0.857333333
Dus3l	MmuINT0053915	chr17:56907098-56907205	IR-S	0.109430929	0.021421135	0.088009794	0.878666667
Adsl	MmuINT0012220	chr15:80794160-80794309	IR-S	0.122229189	0.034103839	0.08812535	0.870666667
Echdc2	MmuEX0016196	chr4:107850976-107851023	S	0.995208505	0.907065195	0.08814331	0.855333333
Ebna1bp2	MmuINT0054973	chr4:118294799-118295902	IR-S	0.122794	0.034492795	0.088301205	0.842666667
Ipo7	MmuINT0082836	chr7:117193208-117194293	IR-S	0.118145788	0.029829548	0.08831624	0.864
Fars2	MmuEX0018632	chr13:36299496-36299615	S	0.114454846	0.025919399	0.088535447	0.834666667
Auh	MmuEX0007114	chr13:53014568-53014635	C2	0.988080984	0.899462611	0.088618373	0.960666667
Zwilch	MmuINT0180966	chr9:63995214-63997205	IR-S	0.113498547	0.024712537	0.088786004	0.877333333
Glb1	MmuEX0020472	chr9:114329987-114330101	S	0.119061476	0.030087851	0.088973625	0.800666667
Xaf1	MmuINT0176566	chr11:72116965-72118167	IR-S	0.126107842	0.037013927	0.089093915	0.82
Pip5k1c	MmuINT0120160	chr10:80777864-80780070	IR-C	0.133021031	0.043672592	0.089348439	0.849333333
Zfp740	MmuALTD0016228-1/2	chr15:102039184-102039307	Alt5	0.920601392	0.831188333	0.089413062	0.835333333
Cep57	MmuINT0034873	chr9:13617155-13617853	IR-S	0.172195213	0.082689603	0.089505607	0.813333333
Tecr	MmuINT0158764	chr8:86096355-86096447	IR-S	0.162568266	0.072903025	0.089665241	0.996
Bscl2	MmuINT0026001	chr19:8914275-8915597	IR-C	0.120267739	0.030555605	0.089712134	0.870666667
Cds2	MmuINT0033976	chr2:132126378-132126967	IR-S	0.147352587	0.057503133	0.089849454	0.822
Triml1	MmuEX0048955	chr8:44221891-44221913	C1	0.974016462	0.883988558	0.090027904	0.856666667
Smarcb1	MmuINT0148702	chr10:75377939-75379517	IR-C	0.133683019	0.043482199	0.090200829	0.818
Brms1	MmuINT0025837	chr19:5047485-5048508	IR-C	0.114824427	0.024539612	0.090284815	0.816666667
Galnt6	MmuINT0067386	chr15:100527080-100527549	IR-S	0.140703897	0.050407751	0.090296146	0.954
Cpsf1	MmuINT0041741	chr15:76431223-76431367	IR-S	0.121763809	0.031389 65	0.090374159	0.892

Fnip2	MmuINT0065500	chr3:79283566-79284480	IR-S	0.1366338	0.04596632	0.09066748	0.800666667
BC088983	MmuINT0023550	chr8:59011698-59017407	IR-S	0.129741029	0.038804587	0.090936442	0.868666667
Ccnt2	MmuINT0031778	chr1:129691895-129694417	IR-C	0.130380508	0.039220315	0.091160193	0.894
Mtss1	MmuINT0102166	chr15:58779998-58783024	IR-C	0.16429759	0.072893193	0.091404398	0.856666667
Orc3	MmuINT0113490	chr4:34519822-34522280	IR-S	0.11671421	0.025288402	0.091425808	0.919333333
Dctn6	MmuINT0047267	chr8:35160349-35169395	IR-S	0.127772419	0.036299976	0.091472443	0.851333333
Larp1	MmuINT0089897	chr11:57856409-57857407	IR-S	0.122719432	0.031171456	0.091547976	0.858666667
Cul4a	MmuEX0013174	chr8:13106194-13106309	S	0.973421058	0.881846849	0.091574209	0.823333333
Slc25a1	MmuINT0145429	chr16:17927560-17927637	IR-S	0.134552243	0.042950132	0.091602112	0.884
Tsta3	MmuINT0166818	chr15:75757526-75758858	IR-S	0.161419787	0.069701287	0.0917185	0.898
Vti1b	MmuINT0174323	chr12:80261570-80265934	IR-S	0.107407828	0.015506059	0.091901769	0.876
Fam48a	MmuALTA0006916-1/3	chr3:54519079-54519178	Alt3	0.106776274	0.014824949	0.091951325	0.834666667
Zc3h7a	MmuINT0177915	chr16:11152024-11153151	IR-S	0.146887135	0.054597026	0.092290108	0.809333333
Spop	MmuINT0151997	chr11:95343406-95346605	IR-S	0.110551398	0.018184657	0.092366742	0.92
Actr8	MmuINT0010569	chr14:30804942-30806146	IR-S	0.121860046	0.029417111	0.092442935	0.800666667
Smc2	MmuINT0148871	chr4:52491385-52494541	IR-S	0.128198762	0.035734481	0.092464281	0.848
Traf7	MmuINT0164557	chr17:24649032-24649113	IR-S	0.114888135	0.022309909	0.092578226	0.825333333
Aifm1	MmuINT0013110	chrX:45858130-45866412	IR-C	0.120431298	0.027660065	0.092771234	0.824
Ptpn23	MmuINT0128969	chr9:110293770-110294137	IR-S	0.136403858	0.043608511	0.092795347	0.808666667
Mlh3	MmuINT0099128	chr12:86586873-86588561	IR-S	0.128208273	0.035379936	0.092828338	0.832666667
Kif15	MmuINT0086735	chr9:122913812-122916431	IR-S	0.134771996	0.041787838	0.092984158	0.826666667
Mars	MmuINT0095931	chr10:126733690-126733772	IR-C	0.142642229	0.049278406	0.093363823	0.922666667
Lsg1	MmuINT0093519	chr16:30565596-30567796	IR-S	0.108861171	0.015356840	0.093504331	0.946
Neu1	MmuINT0107811	chr17:35069774-35070947	IR-S	0.409786163	0.315941235	0.093844928	0.833333333
Fermt2	MmuINT0063970	chr14:46088228-46088914	IR-S	0.117608187	0.023695349	0.093912838	0.879333333
Cdc42bpb	MmuINT0032885	chr12:112534505-112534590	IR-S	0.121855215	0.027725297	0.094129917	0.827333333
Cdh11	MmuINT0033118	chr8:105194073-105197711	IR-S	0.156846068	0.062550263	0.094295806	0.843333333
Idua	MmuALTA0008979-1/2	chr5:109109414-109109516	Alt3	0.118154195	0.023794488	0.094359707	0.863333333
Ddx19a	MmuINT0047594	chr8:113502606-113502935	IR-S	0.114543451	0.02007199	0.094471462	0.936666667
Cln3	MmuINT0037475	chr7:133721436-133722686	IR-C	0.14697608	0.052223757	0.094752324	0.807333333
Prosc	MmuINT0126990	chr8:28156472-28159645	IR-S	0.147134137	0.051789988	0.095344149	0.928666667
Mllt4	MmuINT0099377	chr17:14025985-14033094	IR-S	0.158175352	0.062590187	0.095585165	0.805333333
Nsmce4a	MmuINT0111057	chr7:137682625-137683327	IR-S	0.113465424	0.017864184	0.095601239	0.845333333

Man2b1	MmuINT0094830	chr8:87608403-87608539	IR-S	0.127081476	0.031390338	0.095691138	0.894
Ngdn	MmuINT0108360	chr14:55640446-55640657	IR-S	0.109261561	0.013511745	0.095749816	0.960666667
Dctn1	MmuINT0047214	chr6:83145108-83145541	IR-S	0.122819551	0.026820059	0.095999492	0.874
Chtf18	MmuALTD0003169-1/2	chr17:25863914-25864065	Alt5	0.145726898	0.049241654	0.096485244	0.807333333
Top2a	MmuINT0163887	chr11:98854728-98855077	IR-S	0.309230329	0.212612125	0.096618204	0.856
1300001I01Rik	MmuINT0000505	chr11:74477634-74478275	IR-S	0.131866946	0.035099107	0.09676784	0.893333333
Trappc3	MmuINT0164722	chr4:125939782-125949921	IR-S	0.124769457	0.02793805	0.096831407	0.889333333
Sun1	MmuALTA0017589-1/2	chr5:139714785-139714893	Alt3	0.312530993	0.215626985	0.096904008	0.834666667
Tsta3	MmuINT0166820	chr15:75756888-75757228	IR-S	0.115408282	0.018180285	0.097227997	0.978666667
Cyth2	MmuALTA0004968-1/3	chr7:53063743-53063819	Alt3	0.182830279	0.08552642	0.097303859	0.800666667
Baz2a	MmuINT0024115	chr10:127558382-127558646	IR-C	0.118676463	0.021089758	0.097586705	0.931333333
Sec31a	MmuINT0140698	chr5:100817631-100818086	IR-S	0.123906269	0.025770742	0.098135527	0.870666667
Nae1	MmuINT0105399	chr8:107050290-107050982	IR-S	0.124675708	0.026539332	0.098136376	0.832
Wdr48	MmuINT0175361	chr9:119828873-119829674	IR-S	0.131617226	0.033289768	0.098327459	0.81
Trim39	MmuINT0165202	chr17:36399078-36400673	IR-C	0.137067559	0.038731106	0.098336453	0.813333333
Rnf167	MmuINT0135638	chr11:70463520-70463627	IR-S	0.130114164	0.031342745	0.098771418	0.946666667
Mcm10	MmuINT0096565	chr2:4915729-4916766	IR-S	0.120885478	0.022025816	0.098859662	0.881333333
Sfxn2	MmuINT0142629	chr19:46664692-46664973	IR-S	0.127632656	0.028503666	0.09912899	0.893333333
Dhx15	MmuINT0049076	chr5:52548817-52551468	IR-S	0.17542139	0.076264297	0.099157093	0.817333333
Lars	MmuINT0089975	chr18:42374525-42376505	IR-S	0.189730637	0.090554717	0.09917592	0.956
Tinf2	MmuINT0160320	chr14:56299545-56299631	IR-S	0.204718536	0.105402401	0.099316134	0.889333333
Dpp7	MmuINT0052969	chr2:25210343-25210412	IR-S	0.216727161	0.117017911	0.099709251	0.956666667
Psma1	MmuINT0127811	chr7:121413918-121414567	IR-C	0.121603474	0.021872429	0.099731044	0.818
Snhg5	MmuEX0044127	chr9:88417145-88417219	S	0.989599305	0.889752953	0.099846354	0.881333333
Pigq	MmuINT0119578	chr17:26068519-26068618	IR-S	0.126539076	0.026586544	0.099952532	0.852
Spats2	MmuINT0151163	chr15:99036139-99039263	IR-C	0.126956913	0.026803883	0.100153031	0.825333333
Exosc9	MmuINT0059882	chr3:36464219-36464350	IR-C	0.361417465	0.261055903	0.100361562	0.811333333
Smpd4	MmuINT0149308	chr16:17625956-17626036	IR-S	0.18140786	0.080694779	0.100713081	0.820666667
Wdr26	MmuALTA0020015-1/3	chr1:183127706-183127818	Alt3	0.138357624	0.037631067	0.100726557	0.859333333
L1td1	MmuALTA0009836-1/2	chr4:98399834-98400251	Alt3	0.70447051	0.603540915	0.100929595	0.908
Mllt4	MmuINT0099380	chr17:14036235-14039536	IR-S	0.142809535	0.041783234	0.101026301	0.836666667
Mrpl21	MmuINT0100743	chr19:3285396-3286874	IR-S	0.1430898	0.041882412	0.101207387	0.830666667
Ndufa7	MmuINT0107018	chr17:33961626-33962545	IR-S	0.129000447	0.027743147	0.1012573	0.984666667

Ipo4	MmuINT0082786	chr14:56247825-56247903	IR-S	0.117179375	0.015762182	0.101417193	0.864666667
Hexa	MmuINT0077455	chr9:59408885-59409749	IR-S	0.129279594	0.027859537	0.101420057	0.91
Acaa1a	MmuINT0009223	chr9:119255687-119256847	IR-S	0.123770146	0.022120678	0.101649468	0.868
Polr1c	MmuINT0123782	chr17:46384750-46384843	IR-S	0.114070159	0.012132429	0.10193773	0.928
Atp6v0b	MmuINT0021534	chr4:117558751-117558880	IR-S	0.164570325	0.062534642	0.102035683	0.896
Prpf38b	MmuINT0127071	chr3:108711002-108711253	IR-S	0.143473309	0.041432043	0.102041266	0.822666667
Pcid2	MmuINT0116130	chr8:13086327-13090656	IR-S	0.166410821	0.064346089	0.102064732	0.92
Usp5	MmuALTA0019683-1/2	chr6:124774574-124774665	Alt3	0.120989418	0.018909634	0.102079784	0.875333333
Gigyf1	MmuINT0068831	chr5:137965110-137965189	IR-C	0.147980051	0.045874163	0.102105888	0.814
Cox4nb	MmuEX0012510	chr8:123183859-123183917	S	0.132035645	0.029811504	0.102224142	0.92
Hmgxb4	MmuEX0023060	chr8:77522734-77522837	S	0.863141029	0.760553595	0.102587434	0.810666667
Rpl8	MmuINT0136808	chr15:76734540-76734732	IR-S	0.127077108	0.024458954	0.102618155	0.953333333
Gpn3	MmuINT0072789	chr5:122831504-122832056	IR-S	0.155851902	0.053097793	0.102754109	0.842
4931406P16Rik	MmuINT0004540	chr7:35024257-35024762	IR-S	0.13773405	0.034724656	0.103009394	0.882666667
Tcn2	MmuALTA0017984-1/2	chr11:3831396-3831587	Alt3	0.131591379	0.028268457	0.103322922	0.912
Nbr1	MmuINT0106129	chr11:101438566-101439245	IR-S	0.155872213	0.052510494	0.103361719	0.843333333
Ncor1	MmuINT0106705	chr11:62134948-62138988	IR-S	0.132691909	0.029223991	0.103467919	0.887333333
Sec24c	MmuALTD0012534-1/3	chr14:-21493610	Alt5	0.977468361	0.873939175	0.103529191	0.85
Rtcd1	MmuINT0137679	chr3:116207387-116209752	IR-S	0.123019944	0.019467954	0.10355199	0.956666667
Aup1	MmuALTA0002435-1/3	chr6:83006781-83006872	Alt3	0.1456685	0.041706982	0.103961518	0.85
Dna2	MmuALTA0005598-1/2	chr10:62425161-62425253	Alt3	0.127283782	0.023308119	0.103975663	0.825333333
Snrpb	MmuINT0149822	chr2:129998911-129999342	IR-S	0.215034436	0.110814953	0.104219483	0.92
Snhg6	MmuINT0149705	chr1:9932237-9932403	IR-S	0.129182089	0.024906169	0.104275919	0.896666667
Hdgfrp2	MmuINT0076517	chr17:56236587-56236657	IR-S	0.155804312	0.051510631	0.104293681	0.907333333
Srsf6	MmuEX0044998	chr2:162758551-162758715	S	0.252448417	0.148002359	0.104446058	0.822666667
Ctsa	MmuINT0043714	chr2:164660249-164660337	IR-S	0.218704946	0.114221047	0.104483899	0.909333333
Hsf1	MmuINT0079210	chr15:76328260-76328381	IR-C	0.147810181	0.043113168	0.104697013	0.829333333
Wdr67	MmuINT0175614	chr15:57786964-57789891	IR-S	0.158992963	0.054056128	0.104936835	0.802666667
Hnrnph1	MmuINT0078495	chr11:50193126-50193322	IR-S	0.338840084	0.233499921	0.105340163	0.914
Lypla1	MmuEX0027388	chr1:4829468-4829569	S	0.794526096	0.688852732	0.105673364	0.926666667
Imp4	MmuINT0081906	chr1:34500769-34500841	IR-S	0.112211968	0.00648725	0.105724718	0.999333333
Hnrnpm	MmuINT0078545	chr17:33785810-33786539	IR-S	0.229752053	0.12388869	0.105863362	0.802666667
Slc6a8	MmuINT0147681	chrX:70925772-70925843	IR-S	0.193893841	0.087987001	0.105906841	0.834666667

Brd4	MmuALTD0002289-1/2	chr17:32361032-32361167	Alt5	0.920907194	0.81486635	0.106040844	0.957333333
Safb	MmuINT0138572	chr17:56740395-56740470	IR-S	0.165873402	0.059291279	0.106582123	0.812
Rnf181	MmuINT0135701	chr6:72311534-72312234	IR-S	0.177446238	0.07083132	0.106614918	0.844666667
Fam49b	MmuEX0018346	chr15:63788155-63788237	C1	0.898605418	0.791810308	0.106795109	0.848666667
Lrrc2	MmuINT0092917	chr9:110863514-110865018	IR-S	0.135554431	0.028732434	0.106821996	0.921333333
Pdxdc1	MmuEX0034348	chr16:13836479-13836708	S	0.797532893	0.690700632	0.106832262	0.862
2410002O22Rik	MmuALTA0000313-1/2	chr13:104934484-104934631	Alt3	0.454848804	0.347898189	0.106950615	0.838666667
Maz	MmuINT0096204	chr7:134168454-134168817	IR-C	0.182991973	0.075925296	0.107066676	0.889333333
Ssr4	MmuINT0153008	chrX:71035460-71035697	IR-S	0.188866591	0.081649818	0.107216773	0.875333333
Qtrt1	MmuINT0130239	chr9:21224157-21224479	IR-S	0.126039874	0.018754616	0.107285257	0.914666667
Cdca8	MmuINT0033073	chr4:124596944-124597502	IR-S	0.137239142	0.029805008	0.107434134	0.962666667
Abcf1	MmuINT0008749	chr17:36095303-36096013	IR-S	0.148282318	0.040691098	0.10759122	0.929333333
Ect2	MmuALTA0006066-1/2	chr3:27047915-27047991	Alt3	0.128086957	0.020335783	0.107751174	0.859333333
Pum1	MmuALTD0011321-1/2	chr4:130224978-130225118	Alt5	0.258756683	0.150838579	0.107918104	0.887333333
Rpn2	MmuEX0040423	chr2:157148959-157149006	S	0.136752858	0.028298353	0.108454505	0.866666667
Usp11	MmuINT0171255	chrX:20294080-20294880	IR-S	0.200619726	0.092050689	0.108569038	0.925333333
Pfdn5	MmuINT0118143	chr15:102156967-102157248	IR-S	0.177810563	0.069206335	0.108604228	0.872
Ncor1	MmuINT0106699	chr11:62144427-62147164	IR-S	0.157999191	0.049309767	0.108689424	0.892
Trip6	MmuINT0165595	chr5:137751634-137751880	IR-S	0.178021684	0.069300815	0.108720868	0.814
Dap3	MmuINT0046611	chr3:88732450-88733317	IR-S	0.156850068	0.047965448	0.10888462	0.822666667
Clasp2	MmuEX0011521	chr9:113796163-113796165	MIC	0.634967851	0.525972345	0.108995506	0.821333333
Usf2	MmuINT0171088	chr7:31732079-31739762	IR-S	0.122160409	0.013035757	0.109124651	0.968666667
Rsrc2	MmuEX0040662	chr5:124185831-124185905	S	0.121002634	0.011742854	0.109259781	0.967333333
Snhg1	MmuINT0149688	chr19:8799747-8799974	IR-S	0.274152139	0.164595486	0.109556653	0.863333333
Ap2s1	MmuINT0016777	chr7:17328718-17332609	IR-S	0.141343178	0.031118588	0.110224581	0.890666667
Fam48a	MmuINT0061758	chr3:54518719-54519075	IR-S	0.147266694	0.036947623	0.11031907	0.843333333
Limk2	MmuINT0091122	chr11:3255920-3258112	IR-C	0.156112925	0.045593113	0.110519813	0.956666667
Mrpl17	MmuINT0100724	chr7:112958659-112958963	IR-S	0.141308198	0.030567315	0.110740883	0.801333333
Ptcd3	MmuEX0037650	chr6:71844815-71844875	S	0.994361161	0.883599129	0.110762032	0.843333333
Spns1	MmuEX0044750	chr7:133517436-133517487	S	0.99048701	0.8793665	0.11112051	0.838
Fnta	MmuINT0065518	chr8:27110413-27111441	IR-S	0.150007176	0.038466923	0.111540253	0.929333333
Pole	MmuINT0123556	chr5:110753103-110753178	IR-S	0.142538928	0.030942799	0.11159613	0.881333333
Triml2	MmuINT0165408	chr8:44275724-44278556	IR-S	0.159718582	0.048007181	0.111711401	0.87

Polr2i	MmuINT0123886	chr7:31017424-31017500	IR-S	0.127843731	0.016102008	0.111741722	0.953333333
Mrpl28	MmuINT0100764	chr17:26260795-26261500	IR-S	0.128970211	0.017173443	0.111796767	0.857333333
Kctd9	MmuINT0086038	chr14:68351500-68352197	IR-C	0.16647166	0.053615328	0.112856331	0.876666667
Abtb1	MmuINT0009192	chr6:88790760-88790831	IR-S	0.148754787	0.035458661	0.113296125	0.872
Nrd1	MmuINT0110701	chr4:108716086-108717152	IR-S	0.155472637	0.042068765	0.113403873	0.845333333
App	MmuEX0005606	chr16:85103451-85103580	S	0.897968995	0.784332476	0.113636519	0.850666667
Acox1	MmuEX0003523	chr11:116044778-116044938	C3	0.985628852	0.871772769	0.113856083	0.981333333
Mt1	MmuINT0101405	chr8:96703239-96703722	IR-S	0.185582968	0.071546658	0.11403631	0.854
Tcfe3	MmuEX0046715	chrX:7347900-7347956	C3	0.985696109	0.871534213	0.114161899	0.811333333
Gatad2a	MmuALTD0005812-1/2	chr8:72440468-72440599	Alt5	0.950806067	0.836619137	0.11418693	0.883333333
Dhx36	MmuINT0049225	chr3:62276042-62276649	IR-S	0.134443321	0.020047139	0.114396181	0.946666667
Chd2	MmuINT0035574	chr7:80592200-80594042	IR-S	0.231187893	0.116356973	0.11483092	0.802666667
Prpsap1	MmuINT0127252	chr11:116339430-116339838	IR-S	0.159050361	0.04410094	0.11494942	0.9
Nop14	MmuINT0109559	chr5:34987464-34989810	IR-S	0.141707952	0.026193888	0.115514064	0.882666667
Nubp2	MmuINT0111395	chr17:25021501-25022363	IR-S	0.168390068	0.052185095	0.116204974	0.922
Zfp598	MmuINT0179512	chr17:24817744-24817825	IR-S	0.164194686	0.047939383	0.116255304	0.980666667
Usp11	MmuINT0171258	chrX:20295551-20295804	IR-S	0.14639885	0.030029806	0.116369045	0.926666667
Cpsf7	MmuINT0041843	chr19:10607414-10607782	IR-S	0.165021424	0.048635776	0.116385648	0.873333333
Eif4enif1	MmuINT0056539	chr11:3130105-3134464	IR-C	0.156440436	0.039594878	0.116845558	0.867333333
Trrap	MmuINT0166380	chr5:145614494-145617755	IR-S	0.202271416	0.084787595	0.117483821	0.858666667
Cdk16	MmuINT0033629	chrX:20272888-20273143	IR-S	0.239103733	0.121559792	0.117543941	0.920666667
Ap3d1	MmuINT0016832	chr10:80183914-80184335	IR-S	0.155255282	0.037706078	0.117549204	0.916666667
Brd7	MmuALTA0002864-1/2	chr8:90858004-90858115	Alt3	0.841725888	0.724110851	0.117615037	0.819333333
Ddhd2	MmuINT0047409	chr8:26843595-26845187	IR-S	0.171550606	0.05377926	0.117771346	0.85
Hnrnpf	MmuALTD0006707-1/3	chr6:117857822-117857897	Alt5	0.228330447	0.110534445	0.117796002	0.808
Ppp1r12c	MmuINT0125092	chr7:4436919-4436990	IR-S	0.177807905	0.059727995	0.11807991	0.814666667
Tmf1	MmuINT0162536	chr6:97111555-97113512	IR-S	0.152686193	0.034560605	0.118125588	0.886666667
Mdm4	MmuEX0028335	chr1:134915931-134916008	S	0.196354154	0.078111498	0.118242657	0.807333333
Glb1	MmuEX0020473	chr9:114313639-114318427	C1	0.153272242	0.034956364	0.118315878	0.827333333
Mdc1	MmuINT0096877	chr17:35987951-35988057	IR-S	0.154443585	0.035780024	0.118663561	0.892
Cep57l1	MmuEX0010995	chr10:41441363-41441507	S	0.985416025	0.866672246	0.118743779	0.869333333
Tcfe3	MmuEX0046716	chrX:7348121-7348196	C2	0.985699996	0.866680243	0.119019753	0.812
Spata5	MmuEX0044561	chr3:37428905-37428941	S	0.14732484	0.028111298	0.119213543	0.840666667

Ncor1	MmuINT0106700	chr11:62143642-62144297	IR-S	0.175782617	0.055998957	0.11978366	0.925333333
Rqcd1	MmuINT0137283	chr1:74573665-74574165	IR-C	0.156158218	0.036284017	0.1198742	0.876
Top3a	MmuALTD0014661-1/2	chr11:60559323-60559462	Alt5	0.13957325	0.019687205	0.119886045	0.830666667
Tpp2	MmuEX0048617	chr1:44006157-44006252	S	0.967114617	0.847220138	0.119894479	0.803333333
Trim6	MmuINT0165296	chr7:111375419-111376659	IR-C	0.174924023	0.054462065	0.120461958	0.935333333
Brd8	MmuINT0025712	chr18:34767710-34768071	IR-S	0.145875125	0.025079113	0.120796012	0.857333333
Pak1ip1	MmuINT0114761	chr13:41104308-41104587	IR-S	0.1876419	0.066358979	0.121282921	0.919333333
Spns1	MmuINT0151901	chr7:133515121-133515471	IR-S	0.193400919	0.071974701	0.121426219	0.98
Arhgap17	MmuINT0017911	chr7:130423631-130430011	IR-C	0.18923405	0.06761727	0.121616781	0.824666667
Metap1	MmuINT0097938	chr3:138136952-138137950	IR-S	0.13400062	0.012164728	0.121835892	0.836666667
Vps16	MmuALTA0019849-1/2	chr2:130267353-130267441	Alt3	0.180237697	0.057843019	0.122394678	0.886666667
Acad9	MmuINT0009403	chr3:35986722-35987409	IR-S	0.141501764	0.018586255	0.122915509	0.966666667
Son	MmuINT0150348	chr16:91671711-91675645	IR-S	0.20472046	0.081778732	0.122941729	0.868
Rbm39	MmuEX0039149	chr2:156002139-156002193	S	0.169321261	0.046065372	0.123255888	0.882
Hnrnph2	MmuINT0078503	chrX:131137302-131137456	IR-S	0.145792308	0.02248674	0.123305567	0.831333333
Utp15	MmuINT0172264	chr13:99023684-99024873	IR-S	0.196596682	0.073004046	0.123592636	0.840666667
Fat1	MmuEX0018678	chr8:46135196-46135231	S	0.895135148	0.771178904	0.123956244	0.866
Uba1	MmuALTD0015078-1/3	chrX:20240024-20240251	Alt5	0.963260165	0.838417549	0.124842617	0.834
Pdhb	MmuINT0117275	chr14:9002334-9002674	IR-S	0.163700399	0.038426902	0.125273497	0.890666667
1500032L24Rik	MmuINT0000707	chr15:82176700-82178329	IR-S	0.213878455	0.088464528	0.125413926	0.860666667
Usp10	MmuINT0171245	chr8:122466039-122470974	IR-S	0.173912154	0.048039397	0.125872757	0.812
Atad3a	MmuINT0020151	chr4:155122851-155123265	IR-S	0.175888562	0.049935143	0.125953419	0.96
Cryzl1	MmuINT0042636	chr16:91712513-91714993	IR-S	0.152732696	0.026700114	0.126032582	0.868
Wdr74	MmuALTD0015694-1/2	chr19:8812338-8812352	Alt5	0.150261071	0.022772618	0.127488453	0.833333333
Fgfr1op2	MmuINT0064264	chr6:146537380-146538415	IR-S	0.182390777	0.054885422	0.127505355	0.864
Orc1	MmuINT0113450	chr4:108276095-108276569	IR-S	0.198703784	0.070920472	0.127783312	0.849333333
Epb4.1l4a	MmuALTA0006454-1/2	chr18:33962167-33962211	Alt3	0.171000883	0.042611625	0.128389258	0.850666667
Maged1	MmuINT0094512	chrX:91783095-91783312	IR-S	0.179433732	0.050924864	0.128508868	0.896
Psmd4	MmuINT0128103	chr3:94836907-94837403	IR-S	0.157670056	0.028760458	0.128909599	0.944666667
Parp2	MmuINT0115429	chr14:51434642-51435026	IR-S	0.255785887	0.126123785	0.129662102	0.859333333
Acss1	MmuINT0010304	chr2:150455630-150463582	IR-S	0.171559921	0.041764028	0.129795892	0.866
Fzr1	MmuINT0066747	chr10:80831502-80831818	IR-S	0.218187821	0.088217825	0.129969997	0.866666667
Dhx9	MmuALTA0005499-1/2	chr1:155325996-155326108	Alt3	0.16338109	0.033117227	0.130263863	0.820666667

Mreg	MmuINT0100655	chr1:72207594-72208895	IR-S	0.199231119	0.068267663	0.130963456	0.832666667
Actr1b	MmuINT0010514	chr1:36758359-36758529	IR-S	0.184401465	0.052999558	0.131401906	0.906666667
Cldnd1	MmuINT0037096	chr16:58728198-58729550	IR-C	0.155922407	0.024219117	0.13170329	0.84
Dscr3	MmuINT0053420	chr16:94723840-94725908	IR-S	0.234416142	0.102421199	0.131994944	0.828
Gigyf1	MmuINT0068837	chr5:137966588-137966657	IR-C	0.405008005	0.273002269	0.132005735	0.824
Rnf25	MmuINT0135850	chr1:74641876-74642204	IR-S	0.178126866	0.045924249	0.132202617	0.815333333
Idh3g	MmuINT0080222	chrX:71026047-71026236	IR-S	0.165542633	0.033245898	0.132296734	0.948666667
Srsf7	MmuINT0152728	chr17:80603728-80604601	IR-C	0.254709198	0.121728836	0.132980361	0.99
Ddrgk1	MmuINT0047486	chr2:130487926-130489083	IR-S	0.187306722	0.054271429	0.133035292	0.831333333
Scpep1	MmuINT0139907	chr11:88797266-88798327	IR-S	0.315675648	0.182418049	0.133257599	0.928666667
Dmap1	MmuEX0014847	chr4:117349214-117349372	C1	0.980704968	0.847257046	0.133447922	0.809333333
Appbp2	MmuINT0017365	chr11:85005402-85008076	IR-S	0.149094923	0.015430763	0.133664156	0.837333333
Fam50a	MmuINT0061804	chrX:71564209-71564388	IR-S	0.225003329	0.090848485	0.134154845	0.924
Fbxw9	MmuINT0063609	chr8:87588396-87588479	IR-S	0.352775939	0.218267171	0.134508769	0.840666667
Atp13a3	MmuEX0006791	chr16:30321892-30321981	S	0.599076447	0.464485983	0.134590464	0.830666667
Manba	MmuINT0094890	chr3:135226314-135229451	IR-S	0.210135282	0.075493722	0.134641561	0.827333333
Neurl4	MmuINT0107844	chr11:69721005-69721338	IR-S	0.233720282	0.098778268	0.134942014	0.856666667
Blm	MmuINT0025074	chr7:87605739-87608658	IR-S	0.169752434	0.034640873	0.135111561	0.918
Dolpp1	MmuINT0052628	chr2:30253078-30254661	IR-S	0.275756014	0.140332382	0.135423632	0.862666667
Lrp1	MmuINT0092453	chr10:126979358-126979622	IR-S	0.173604597	0.038121375	0.135483222	0.893333333
Setd6	MmuINT0142186	chr8:98240942-98241820	IR-S	0.234980096	0.099468423	0.135511673	0.814
Rfc2	MmuINT0133868	chr5:135067090-135069058	IR-S	0.155455501	0.019831546	0.135623955	0.921333333
Chkb	MmuALTA0004097-1/3	chr15:89257811-89257830	Alt3	0.154697011	0.018830554	0.135866457	0.874666667
Neu1	MmuINT0107812	chr17:35071131-35071227	IR-S	0.210788613	0.074028038	0.136760574	0.866
Trmt2a	MmuINT0165647	chr16:18252571-18252811	IR-C	0.168114776	0.030919626	0.13719515	0.959333333
Cln3	MmuINT0037470	chr7:133724379-133725159	IR-S	0.18025719	0.04209007	0.13816712	0.968
Ubl7	MmuALTD0015166-1/5	chr9:-57758814	Alt5	0.813162876	0.673960366	0.139202511	0.912
Akap8l	MmuINT0013441	chr17:32473684-32475215	IR-S	0.163272775	0.02385225	0.139420525	0.922
Rexo1	MmuINT0133817	chr10:80011279-80012077	IR-S	0.173662466	0.034077902	0.139584564	0.807333333
Carm1	MmuEX0009179	chr9:21392295-21392363	S	0.884477915	0.744866064	0.139611851	0.888
Far1	MmuINT0062471	chr7:120695517-120697155	IR-C	0.222491338	0.082864695	0.139626643	0.922
Rpl10	MmuINT0136608	chrX:71516214-71516317	IR-C	0.305135415	0.165299554	0.139835861	0.831333333
Hdgfrp2	MmuALTA0008463-1/4	chr17:56236274-56236427	Alt3	0.210468483	0.070328054	0.140140429	0.833333333

Srsf10	MmuINT0152642	chr4:135414325-135417688	IR-C	0.20129953	0.061009418	0.140290112	0.833333333
Ilf3	MmuEX0024061	chr9:21193750-21193927	S	0.96980543	0.828669838	0.141135592	0.988
St3gal3	MmuEX0045104	chr4:117630040-117630123	S	0.251992524	0.109895057	0.142097467	0.887333333
Nme4	MmuEX0031892	chr17:26229452-26229502	S	0.189444874	0.046366077	0.143078797	0.816
Slc7a1	MmuINT0147707	chr5:149144120-149145465	IR-S	0.1863179	0.043026611	0.143291289	0.969333333
Fastk	MmuINT0062628	chr5:23947642-23947741	IR-S	0.200221402	0.056548278	0.143673124	0.897333333
Slc38a10	MmuALTA0016682-1/2	chr11:119967748-119967921	Alt3	0.211767183	0.067930482	0.143836701	0.946666667
Mrps10	MmuEX0029713	chr17:47507237-47507319	C1	0.17691695	0.032597349	0.144319601	0.929333333
Edc4	MmuEX0016231	chr8:108413573-108413629	S	0.985307183	0.840559384	0.1447478	0.832666667
Pdcd2l	MmuEX0034112	chr7:34971313-34971461	S	0.943031395	0.79770235	0.145329045	0.961333333
Epb4.1l1	MmuEX0016987	chr2:156337521-156337556	S	0.192601634	0.047143345	0.145458289	0.870666667
Gas5	MmuINT0067691	chr1:162968169-162968355	IR-S	0.196666187	0.051137724	0.145528463	0.881333333
D2Ertd750e	MmuINT0045971	chr2:118654751-118657288	IR-S	0.17962841	0.033911996	0.145716414	0.962
Stk38	MmuINT0154219	chr17:29119132-29121021	IR-S	0.255013062	0.109120084	0.145892978	0.958666667
Casc3	MmuINT0029248	chr11:98690743-98692601	IR-S	0.203666581	0.05767211	0.145994471	0.884666667
Ints2	MmuEX0024267	chr11:86069939-86069999	C1	0.216074588	0.069679537	0.146395051	0.819333333
Got1	MmuINT0072389	chr19:43575048-43577397	IR-S	0.184195361	0.036841677	0.147353685	0.974
Ndufs1	MmuEX0031308	chr1:63223002-63223098	C2	0.392168133	0.244684721	0.147483412	0.836666667
Nolc1	MmuINT0109495	chr19:46158117-46158240	IR-S	0.218395424	0.070785205	0.147610219	0.951333333
Zfp655	MmuEX0053538	chr5:145996606-145996732	C3	0.237413297	0.089460603	0.147952694	0.894666667
Mib2	MmuINT0098599	chr4:155033375-155033496	IR-S	0.267393615	0.119289002	0.148104613	0.862
Acox3	MmuINT0009983	chr5:35952472-35954663	IR-C	0.286473625	0.138354032	0.148119593	0.896666667
Trmt1	MmuINT0165615	chr8:87214472-87214709	IR-S	0.319949718	0.171678464	0.148271255	0.870666667
Cnpy3	MmuALTA0004365-1/3	chr17:46874124-46874222	Alt3	0.189913739	0.04151714	0.1483966	0.81
Zfp259	MmuINT0178820	chr9:46084562-46084874	IR-S	0.178263752	0.029827365	0.148436387	0.896
Prim1	MmuINT0126135	chr10:127460029-127460638	IR-S	0.234973742	0.086425407	0.148548335	0.892
Adamtsl5	MmuALTA0001187-1/2	chr10:79808258-79808448	Alt3	0.953661047	0.804824996	0.148836051	0.820666667
Slc3a2	MmuINT0146813	chr19:8784274-8786323	IR-S	0.161527083	0.012659193	0.148867891	0.997333333
Cstf2	MmuALTA0004748-1/2	chrX:130607753-130607816	Alt3	0.180640914	0.031465435	0.149175479	0.907333333
Zfp568	MmuALTA0020671-1/2	chr7:30798862-30798908	Alt3	0.23265374	0.083337258	0.149316482	0.816666667
Actn4	MmuEX0003640	chr7:29694922-29695007	C3	0.235904367	0.086257191	0.149647176	0.969333333
Manba	MmuALTD0008136-1/3	chr3:135210514-135210600	Alt5	0.763837206	0.614188537	0.149648668	0.821333333
Sdcbp	MmuALTA0015987-1/2	chr4:6312176-6312204	Alt3	0.263000025	0.113227896	0.149772128	0.955333333

Slc1a5	MmuINT0145088	chr7:17381302-17381372	IR-S	0.329708574	0.178125796	0.151582779	0.900666667
Ncam1	MmuEX0031041	chr9:49358645-49358674	S	0.195122038	0.043518361	0.151603677	0.951333333
Coil	MmuALTD0003402-1/3	chr11:-88831586	Alt5	0.949572566	0.797908527	0.15166404	0.933333333
Exoc1	MmuINT0059649	chr5:76996182-76996991	IR-S	0.218231443	0.06628662	0.151944823	0.871333333
P2rx4	MmuINT0114305	chr5:123174684-123174998	IR-S	0.272038377	0.117650649	0.154387728	0.848
Terf2	MmuINT0158994	chr8:109603370-109604992	IR-C	0.166444435	0.011972041	0.154472394	0.973333333
Pip5k1a	MmuINT0120137	chr3:94869783-94871303	IR-S	0.228195126	0.073465556	0.15472957	0.813333333
Sykb	MmuINT0155707	chr13:52738522-52741091	IR-C	0.244887227	0.089599466	0.155287761	0.864
Acads	MmuINT0009441	chr5:115562037-115562248	IR-S	0.188680778	0.033102324	0.155578454	0.949333333
Ddx41	MmuINT0047798	chr13:55635850-55636649	IR-S	0.260324729	0.104631035	0.155693694	0.952666667
Rnaseh1	MmuINT0135290	chr12:29343161-29343857	IR-C	0.222675676	0.06687664	0.155799036	0.936
Atp13a1	MmuINT0020898	chr8:72329277-72329346	IR-S	0.335798429	0.179901705	0.155896724	0.932666667
Epb4.1l1	MmuALTA0006444-1/3	chr2:156336493-156336617	Alt3	0.326404845	0.17030931	0.156095535	0.942666667
Zfp532	MmuEX0053435	chr18:65811214-65811376	C3	0.321868608	0.165367221	0.156501387	0.835333333
Qtrt1	MmuINT0130237	chr9:21223811-21223882	IR-S	0.338163139	0.181090727	0.157072411	0.84
Cuta	MmuINT0044187	chr17:27075563-27075671	IR-S	0.391141906	0.233959487	0.157182419	0.865333333
Klc3	MmuINT0087637	chr7:19980298-19980409	IR-C	0.979544155	0.821853173	0.157690977	0.81
Cobl	MmuALTD0003385-1/2	chr11:12153092-12154974	Alt5	0.776711343	0.618518749	0.158192594	0.955333333
Zfpl1	MmuINT0180065	chr19:6082328-6082398	IR-S	0.192341905	0.034099843	0.158242061	0.810666667
Rbm26	MmuEX0039116	chr14:105538308-105538379	S	0.305719221	0.147409194	0.158310027	0.936666667
Eif4enif1	MmuEX0016604	chr11:3133991-3134062	S	0.434399276	0.275599725	0.158799552	0.952666667
Gclc	MmuINT0068162	chr9:77635707-77635994	IR-S	0.376201169	0.216936554	0.159264615	0.888666667
App	MmuEX0005609	chr16:85040496-85040552	C2	0.826218985	0.666919966	0.159299018	0.912
Qars	MmuINT0130121	chr9:108417365-108417437	IR-S	0.296496729	0.135499871	0.160996858	0.854
Polb	MmuINT0123449	chr8:23747627-23750405	IR-S	0.24869649	0.087414657	0.161281832	0.88
Noc4l	MmuINT0109341	chr5:111078003-111078084	IR-S	0.206626806	0.045154093	0.161472714	0.935333333
Sept1	MmuINT0141461	chr7:134358554-134358794	IR-S	0.406059632	0.243192937	0.162866695	0.922666667
Med17	MmuEX0028515	chr9:15071858-15071995	S	0.992024686	0.828500603	0.163524084	0.999333333
Tfpt	MmuINT0159310	chr7:3572735-3576200	IR-S	0.253820447	0.090197243	0.163623204	0.900666667
Ttc4	MmuINT0167377	chr4:106340183-106340641	IR-S	0.243206595	0.078281305	0.16492529	0.882666667
Hnrpdl	MmuEX0023143	chr5:100464654-100464758	S	0.550946257	0.385039957	0.1659063	0.912666667
Wdr77	MmuINT0175753	chr3:105768792-105769274	IR-S	0.243039909	0.075594141	0.167445768	0.965333333
Cirbp	MmuINT0036513	chr10:79633510-79633726	IR-S	0.444298816	0.276770838	0.167527978	0.920666667

Carkd	MmuINT0029167	chr8:11511998-11512894	IR-S	0.244766574	0.076930303	0.167836271	0.923333333
Suds3	MmuINT0154859	chr5:117549332-117549485	IR-S	0.317675381	0.149220742	0.16845464	0.802
Cenpv	MmuINT0034526	chr11:62347457-62349783	IR-S	0.196410511	0.027728806	0.168681705	0.923333333
Cnot1	MmuALTA0004327-1/2	chr8:98278885-98279008	Alt3	0.36718661	0.198090916	0.169095694	0.834666667
Csrp2	MmuINT0043199	chr10:110372373-110374792	IR-S	0.240790151	0.071457377	0.169332774	0.904
Eral1	MmuINT0058556	chr11:77889337-77889491	IR-S	0.218958252	0.048196877	0.170761375	0.912666667
Bcl2l1	MmuALTA0002708-1/2	chr2:152655493-152655838	Alt3	0.975657078	0.804670641	0.170986437	0.969333333
D4Wsu53e	MmuEX0013588	chr4:134481692-134481736	C1	0.379940725	0.208499923	0.171440801	0.804
Eif2d	MmuEX0016550	chr1:133060980-133061083	S	0.972421905	0.800684984	0.171736921	0.882666667
Aaas	MmuINT0007271	chr15:102180512-102180926	IR-C	0.22385312	0.050781013	0.173072107	0.94
Man1b1	MmuINT0094772	chr2:25203747-25204090	IR-S	0.535471222	0.361752914	0.173718308	0.852666667
Fn1	MmuINT0065262	chr1:71650504-71651543	IR-C	0.250964759	0.0772254	0.17373936	0.854666667
Gnb2	MmuINT0071907	chr5:137970994-137971073	IR-S	0.219058299	0.045112397	0.173945902	0.904666667
Iars	MmuALTD0006865-1/2	chr13:-49777572	Alt5	0.850640094	0.676246807	0.174393287	0.936666667
Taf6l	MmuINT0156771	chr19:8853416-8856490	IR-C	0.216486449	0.041130103	0.175356346	0.972
Rtel1	MmuINT0137713	chr2:181088881-181089057	IR-S	0.294974971	0.119396264	0.175578707	0.972
Dclk2	MmuINT0047083	chr3:86597222-86597738	IR-S	0.224056276	0.048116582	0.175939694	0.908666667
Nudt1	MmuINT0111465	chr5:140811413-140813546	IR-S	0.213498543	0.036988059	0.176510485	0.806
Hirip3	MmuINT0077924	chr7:134007765-134007833	IR-S	0.411287773	0.234249202	0.17703857	0.843333333
Cnot2	MmuEX0011916	chr10:115954373-115954439	C1	0.934288605	0.757140496	0.17714811	0.989333333
Emg1	MmuINT0057120	chr6:124655107-124655175	IR-S	0.276737002	0.098643156	0.178093846	0.841333333
Senp6	MmuEX0041676	chr9:79937656-79937713	C2	0.87556754	0.696090853	0.179476686	0.896666667
Npdc1	MmuINT0110058	chr2:25264207-25264424	IR-S	0.23832979	0.058596678	0.179733112	0.902666667
Ttc13	MmuEX0049422	chr8:127219536-127219652	C3	0.538700467	0.358624956	0.180075511	0.848
Rfc2	MmuINT0133870	chr5:135070145-135071152	IR-S	0.226919396	0.045732508	0.181186888	0.979333333
Birc5	MmuINT0024962	chr11:117714095-117716538	IR-S	0.223686301	0.042175001	0.181511301	0.852
Pycr2	MmuALTA0014610-1/3	chr1:182836297-182836515	Alt3	0.357758453	0.17395236	0.183806093	0.899333333
Rpap1	MmuINT0136439	chr2:119599956-119600688	IR-S	0.267847608	0.083896462	0.183951146	0.854666667
Dnm1l	MmuEX0015293	chr16:16318538-16318570	C2	0.449722504	0.265480065	0.184242439	0.91
Foxm1	MmuINT0065643	chr6:128322622-128322794	IR-S	0.402419364	0.216739927	0.185679437	0.89
Rela	MmuINT0133506	chr19:5639951-5640302	IR-S	0.235013221	0.049164025	0.185849196	0.911333333
Lta4h	MmuINT0093641	chr10:92943532-92944994	IR-S	0.220922242	0.034672622	0.18624962	0.946
Trib3	MmuINT0164956	chr2:152164424-152165450	IR-S	0.259933987	0.073494539	0.186439448	0.910666667

Sbf1	MmuINT0139006	chr15:89125744-89125825	IR-S	0.30438002	0.117879747	0.186500272	0.892
Ubr7	MmuINT0169730	chr12:104004562-104006279	IR-S	0.233174815	0.046647947	0.186526869	0.894666667
Pfkp	MmuINT0118259	chr13:6587900-6597104	IR-S	0.488121742	0.301547886	0.186573856	0.992
1700029I01Rik	MmuINT0001303	chr4:146245836-146549955	IR-C	0.202691419	0.014090457	0.188600962	0.988
Rpap1	MmuINT0136421	chr2:119597633-119598223	IR-S	0.225440539	0.036835596	0.188604944	0.926
Prpsap1	MmuINT0127253	chr11:116338662-116339373	IR-C	0.232237879	0.041101686	0.191136193	0.955333333
9430015G10Rik	MmuINT0006152	chr4:155497779-155498084	IR-S	0.410378793	0.218925077	0.191453715	0.86
Gnl3	MmuINT0072030	chr14:31827414-31827775	IR-S	0.295770057	0.103745697	0.192024353	0.837333333
Exoc1	MmuINT0059642	chr5:76983231-76986843	IR-S	0.272813752	0.079918177	0.192895574	0.863333333
Mtf2	MmuEX0029979	chr5:108502326-108502473	C2	0.541463928	0.34746909	0.193994837	0.878
Hnrpdl	MmuINT0078609	chr5:100464004-100465122	IR-C	0.517463228	0.322735598	0.194727629	0.806
2610318N02Rik	MmuINT0002826	chr16:17121645-17123604	IR-S	0.244608412	0.049419212	0.1951892	0.892666667
Usp21	MmuINT0171438	chr1:173213225-173213485	IR-C	0.380540396	0.183925378	0.196615019	0.872666667
Tbrg4	MmuINT0157802	chr11:6515770-6516560	IR-S	0.986627679	0.78920131	0.197426369	0.996666667
Cnot10	MmuINT0038131	chr9:114502631-114506596	IR-C	0.316155879	0.117138345	0.199017534	0.883333333
Trmt1	MmuINT0165619	chr8:87219440-87220725	IR-S	0.318072025	0.116685227	0.201386798	0.96
Cnot10	MmuEX0011905	chr9:114505723-114505789	S	0.283029361	0.080287601	0.20274176	0.886666667
Snap23	MmuALTD0013290-1/2	chr2:-120393497	Alt5	0.24310444	0.038626573	0.204477867	0.915333333
Ddx39	MmuINT0047725	chr8:86243839-86244447	IR-S	0.257058359	0.048969953	0.208088406	0.958666667
Clk1	MmuINT0037404	chr1:58476578-58476964	IR-C	0.289393164	0.08111808	0.208275084	0.893333333
Adpgk	MmuINT0012136	chr9:59158156-59160846	IR-S	0.308381479	0.099156428	0.209225052	0.878
Dnajc21	MmuALTD0004346-4/4	chr15:10389705-10389861	Alt5	0.282513855	0.071286171	0.211227683	0.842
Raly	MmuEX0038685	chr2:154685647-154685694	S	0.324340408	0.11198431	0.212356097	0.936
Rabggtb	MmuINT0130842	chr3:153573331-153573654	IR-S	0.341708433	0.128762494	0.212945939	0.850666667
Tcf3	MmuALTA0017960-1/2	chr10:79878110-79878265	Alt3	0.273603075	0.060041061	0.213562014	0.930666667
Atxn2l	MmuEX0007082	chr7:133635963-133636122	C2	0.503252085	0.287717908	0.215534177	0.97
9130404D08Rik	MmuINT0006049	chr8:72552674-72553106	IR-S	0.312068673	0.096048163	0.216020507	0.947333333
Dnajc21	MmuALTA0005652-1/3	chr15:10384527-10384607	Alt3	0.290057614	0.073496678	0.216560937	0.843333333
Suv420h2	MmuINT0155347	chr7:4693890-4694220	IR-S	0.286248611	0.069516645	0.216731966	0.996
Cpsf4	MmuALTA0004597-1/4	chr5:145939705-145939747	Alt3	0.285189292	0.067267112	0.217922181	0.806666667
Ttk	MmuALTA0019098-1/2	chr9:83746694-83746782	Alt3	0.782367119	0.562759001	0.219608118	0.844666667
Prrc2b	MmuEX0037403	chr2:32084783-32084864	S	0.626713725	0.407021117	0.219692608	0.907333333
Cep70	MmuEX0011013	chr9:99154674-99154796	S	0.817976133	0.597464819	0.220511314	0.864666667

Qtrt1	MmuINT0130238	chr9:21223993-21224068	IR-S	0.316371073	0.094586538	0.221784535	0.983333333
Ints7	MmuINT0082607	chr1:193431939-193434242	IR-C	0.257361455	0.030735511	0.226625944	0.852
Rnf25	MmuALTA0015388-1/2	chr1:74641783-74641872	Alt3	0.309873226	0.078478788	0.231394438	0.964
1500010J02Rik	MmuALTA0000098-1/2	chr11:68844916-68845055	Alt3	0.597616661	0.363273381	0.23434328	0.923333333
Chtf8	MmuINT0036373	chr8:109410427-109410819	IR-S	0.276869047	0.041073935	0.235795112	0.992666667
Arfgap1	MmuINT0017671	chr2:180707501-180708165	IR-S	0.326024045	0.088065722	0.237958324	0.878
Klc1	MmuALTA0009722-1/2	chr12:113027560-113027670	Alt3	0.334821372	0.096074434	0.238746939	0.837333333
Gfer	MmuINT0068488	chr17:24832396-24832775	IR-S	0.331012865	0.09196383	0.239049034	0.872666667
Kifc5b	MmuINT0087493	chr17:27059669-27059849	IR-S	0.291787537	0.05110983	0.240677707	0.826
Cuta	MmuALTA0004873-1/2	chr17:27075672-27075726	Alt3	0.299767988	0.055744324	0.244023664	0.812666667
Ktn1	MmuEX0025968	chr14:48336549-48336635	S	0.35967314	0.115436916	0.244236224	0.990666667
Dync1h1	MmuALTA0005942-1/2	chr12:111897654-111897726	Alt3	0.331469267	0.082540898	0.248928369	0.856666667
2410022L05Rik	MmuINT0002489	chr8:13885882-13887759	IR-S	0.315132449	0.065403309	0.24972914	0.893333333
Ranbp3	MmuINT0131515	chr17:56848758-56849510	IR-C	0.321190987	0.070289944	0.250901043	0.934
Top3b	MmuINT0163961	chr16:16883657-16884331	IR-C	0.353077053	0.100187625	0.252889429	0.986666667
Ndufs1	MmuEX0031310	chr1:63218728-63218831	C2	0.440672376	0.18725193	0.253420445	0.94
Haus8	MmuALTA0008404-1/2	chr8:73780358-73780450	Alt3	0.334563933	0.078244498	0.256319436	0.878666667
Nsun5	MmuINT0111098	chr5:135851356-135851424	IR-S	0.30690306	0.049422963	0.257480097	0.875333333
Zfp740	MmuALTD0016227-1/3	chr15:102035211-102035314	Alt5	0.285310484	0.026812985	0.258497499	0.984666667
Zfp655	MmuEX0053537	chr5:145996175-145996260	C2	0.53872086	0.27686527	0.26185559	0.963333333
Zfp276	MmuINT0178852	chr8:125791600-125791669	IR-S	0.632018082	0.368406022	0.26361206	0.802
Snrnp70	MmuEX0044157	chr7:52638495-52638554	S	0.453086691	0.182205553	0.270881138	0.841333333
Pcyt2	MmuINT0116608	chr11:120473916-120474343	IR-S	0.342705742	0.071560564	0.271145178	0.800666667
Farsa	MmuALTD0005371-1/2	chr8:87384805-87384856	Alt5	0.411329897	0.132361756	0.278968142	0.834
Ndc80	MmuALTD0009203-1/2	chr17:71856642-71856752	Alt5	0.357959359	0.075037214	0.282922146	0.943333333
Abcd4	MmuINT0008707	chr12:85947259-85949519	IR-S	0.503690434	0.219516026	0.284174408	1
Aspscr1	MmuINT0019946	chr11:120570024-120570243	IR-S	0.358976451	0.074215585	0.284760865	0.895333333
Scaf8	MmuALTA0015879-1/2	chr17:3169330-3169406	Alt3	0.359584587	0.072895503	0.286689084	0.840666667
Snapin	MmuINT0149596	chr3:90294195-90294469	IR-S	0.358903527	0.071645608	0.287257919	0.958666667
Dclk2	MmuINT0047084	chr3:86596034-86597140	IR-S	0.487833246	0.19973296	0.288100286	0.968666667
Zfp598	MmuINT0179518	chr17:24815659-24815981	IR-S	0.524862911	0.236304018	0.288558893	0.985333333
Polr2f	MmuALTA0013764-1/2	chr15:78976486-78976516	Alt3	0.316203899	0.026029581	0.290174318	0.958
Chtf18	MmuALTD0003172-1/2	chr17:25856313-25856370	Alt5	0.801902048	0.511590197	0.290311851	0.884666667

Trim11	MmuINT0164967	chr11:58802432-58803688	IR-S	0.525958945	0.234730674	0.291228271	0.931333333
Rnf19b	MmuALTA0015361-1/2	chr4:128750746-128750887	Alt3	0.915399094	0.623339044	0.292060053	0.838666667
Safb2	MmuINT0138607	chr17:56715436-56716300	IR-S	0.566665574	0.268327532	0.298338042	0.846666667
Zwilch	MmuALTA0020923-1/2	chr9:64010467-64010566	Alt3	0.359202812	0.055752043	0.303450769	0.862
Prdx2	MmuINT0125920	chr8:87493662-87494138	IR-C	0.627386779	0.316516067	0.310870711	0.885333333
Mon2	MmuALTA0011130-1/2	chr10:122468096-122468177	Alt3	0.872512	0.551696686	0.320815314	0.809333333
Ndufa7	MmuINT0107019	chr17:33962596-33966611	IR-S	0.412645229	0.089286309	0.323358921	0.957333333
1700061G19Rik	MmuINT0001460	chr17:57022114-57022202	IR-S	0.715380523	0.356331259	0.359049264	0.874666667
Sp2	MmuALTA0017130-1/2	chr11:96824679-96824755	Alt3	0.830298208	0.461714226	0.368583981	0.836
Ckb	MmuALTD0003211-1/2	chr12:112910074-112910152	Alt5	0.507053012	0.135825996	0.371227016	0.806666667
Naga	MmuEX0030813	chr15:82167200-82167371	S	0.544787875	0.154228293	0.390559582	0.920666667
Rnf115	MmuEX0039991	chr3:96558258-96558316	C3	0.867198225	0.461467584	0.405730641	0.868666667
Cyb5r1	MmuINT0044453	chr1:136307170-136307483	IR-S	0.665175943	0.209338844	0.455837099	0.876
Zfp473	MmuALTA0020647-1/4	chr7:51993336-51993401	Alt3	0.618201684	0.08851059	0.529691094	0.930666667

Table 7. pre-mRNA and mRNA primers

Gene	Name	Sequence
ATM	ATM_IN60_F	TGGCTGCATCTACCTGTGAC
	ATM_IN60_R	TGCTAGTCAGCCCTCCTCAT
	ATM_Ex60_R	ACCCAGGTCTATGTGCACAA
	ATM_Ex61_R	CCCCTGTTCAAAAGCCACTC
ERCC1	ERCC1_IN6_F	CTAAGCCAAGCATGGTGACA
	ERCC1_IN6_R	TGGGGAGAACAGAACAAACC
	ERCC1_Ex6_F	AAAGATCCCCAGCAGGCTC
	ERCC1_Ex7_R	ATAAGGAGGTCGGCTGGCTT
CDK7	CDK7_IN10_F	TTTCTCGTGTCATCCTGGCT
	CDK7_IN10_R	TTAAGCACTTGGGAGGCAGA
	CDK7_Ex10_F	ACTGCAGCACATCTTCATCG
	CDK7_Ex11_R	GGGGCGGTTACTGAAGTACT
RAD9a	RAD9a_Ex1_F	GTAGTAGCTGCTGGGACTCA
	RAD9a_Ex2_R	TTCGGGATAGCGAATGGACA
	RAD9a_IN1_F	GGCAACGTGAAGGGTAAGTT
	RAD9a_IN1_R	CGGGGAGGAGAACAGAAAGT
ATM	ATM_Ex3_F	TATCAGCCACCACACAGAGC
Atm-205 short	ATM_In3_R	acacgcagccaaggttactt
	ATM_Ex4_R	CAAGAGGTCTTGACATTTTAGCC
ERCC1	ERCC1_Ex3_F	GTGTGCTGCTGGTTCAAGTG
Ercc1-209 short	ERCC1_In3_R	cattctgcactgaggtcctg
	ERCC1_Ex4_R	GGTGCAGTCAGCCAAGATG
DDB1	DDB1_Ex1_F	AGTGAACGGCTGTGTGACC
	DDB1_In1_R	gtgggaacagctcctttgag
	DDB1_Ex2_R	GCCTGAAGAGCTCCATGACT
	DDB1_Ex15_F	CCTCGATCCATCCTGATGAC
	DDB1_In15_R	agctgcttggttaaggctca
	DDB1_Ex16_R	AGAGCAAGCAAAGACGTTGG

ERCC2	ERCC2_Ex20_F	GGCTGTGATCATGTTTGGAG
	ERCC2_In20_R	ccctgacagcactgtttcc
	ERCC2_Ex21_R	CAGCAAAGACCATGAGTCCA
Atr	ATR_Ex45_F	ATGGGTCCTATGGGAACAGA
	ATR_In45_R	CAGTATTTACATTCGAGGCCACT
	ATR_Ex46_R	TGCTTTGGAGTGTCCTTTCA
Hprt	Ex7_F	CGAAGTGTTGGATACAGGCC
	3UTR	GGCAACATCAACAGGACTCC

Table 8. sn(o)RNA primers

Gene	Name	Sequence
U1 snRNA	RNU1_F	GATCACGAAGGTGGTTTTCC
	RNU1_R	CAGTCCCCCACTACCACAAA
U2 snRNA	RNU2_F	GCCTTTCGGCTAAGATCAAG
	RNU2_R	GGAGCAAGCTCCTATTCCAA
U4 snRNA	RNU4_F	GCAGTGGCAGTATCGTAGCC
	RNU4_R	AAAATTGCCAATGCCGACTA
U5 snRNA	RNU5_F	CTTTCGGCTTTACAAAGATTCC
	RNU5_R	CCTTGTTGGAGCAGAACCTC
U6 snRNA	RNU6_F	CGCTTCGGCAGCACATATAC
	RNU6_R	ATGGAACGCTTCACGAATTT
U3 snoRNA	snoU3_F	AGAGCACCTGAAACCACGAG
	snoU3_R	CTGCAATCAAGCAGCACCTA