Supplementary information for Materials and Methods

Sequencing splicing sites of IAP-derived Fancd2

To validate the RNA-seq data and detect the aberrant chimeric transcripts, a part of cDNA synthesized for RNA-seq analysis was subjected to PCR using a primer set and TaKaRa Ex Taq Hot Start Version (#RR006A; Takara). PCR products of IAP-derived *Fancd2* were cloned into a pGEM-T Easy Vector (#1360; Promega, Madison, WI, USA), and plasmids were subjected to DNA sequencing analysis using SP6 and T7 primers. Sequencing of the cloned amplicon was performed using an ABI PRISM 3130 platform (Thermo Fisher Scientific). The sequence was viewed using SnapGene® software (Insightful Science LLC, San Diego, CA, USA; available at snapgene.com). The primers used for PCR are shown in Supplementary Table 2.

*Bisulfite sequencing analysis*

FACS-purified gonocytes from 1 dpp mice and spermatogenic cells of 2-week-old mice were subjected to DNA extraction using the QIAamp DNA Micro Kit (#56304; Qiagen) and subsequent bisulfite treatment with EpiTect Bisulfite Kits (#59104; Qiagen) for DNA methylation analysis. DNA was extracted from three biologically independent cell pools, and PCR products were cloned into the pGEM-T Easy vector. Plasmids were amplified from single colonies using a TempliPhi 500 Amplification Kit (#25640050; Cytiva, Tokyo, Japan) and sequenced using an ABI PRISM 3130 platform (Thermo Fisher Scientific). DNA methylation was analyzed using QUMA [38].

All the primers used for bisulfite sequencing analysis are shown in Supplementary Table 2.
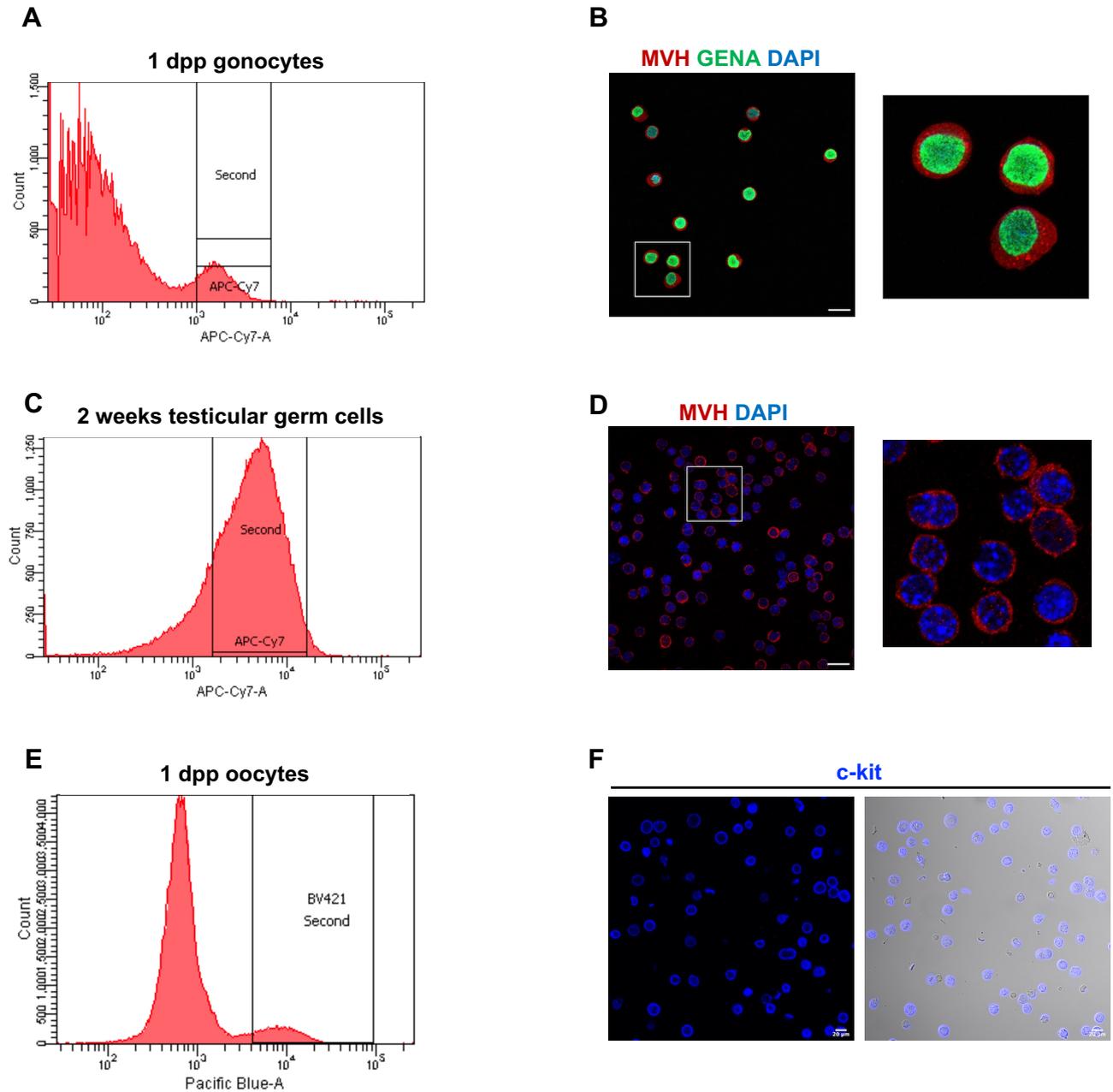
Supplementary Fig. 1. Purification of germ cells by FACS

(A, C, E) A flow cytometric analysis for gonocytes from 1dpp mice, spermatogenic cells from 2-week-old mice, and non-growing oocytes from 1 dpp mice. An anti-EpCAM antibody labeled with deep-red fluorescence was used for FACS purification of gonocytes and spermatogenic cells. An anti-c-kit antibody labeled with blue fluorescence was used for FACS purification of non-growing oocytes. The horizontal axis indicates the fluorescence intensity of labeled cells. **(B)** Immunofluorescence analysis of germ cell-specific markers, DDX4/MVH (red) and GENA/TRA98 (green) in gonocytes purified by FACS. Nuclei (blue) were counterstained with DAPI. **(D)** Immunofluorescence analysis of DDX4/MVH (red) in spermatogenic cells purified by FACS. Nuclei (blue) were counterstained with DAPI. **(F)** Confocal microscopy images of purified non-growing oocytes by FACS. Scale bars indicate 20 μm.
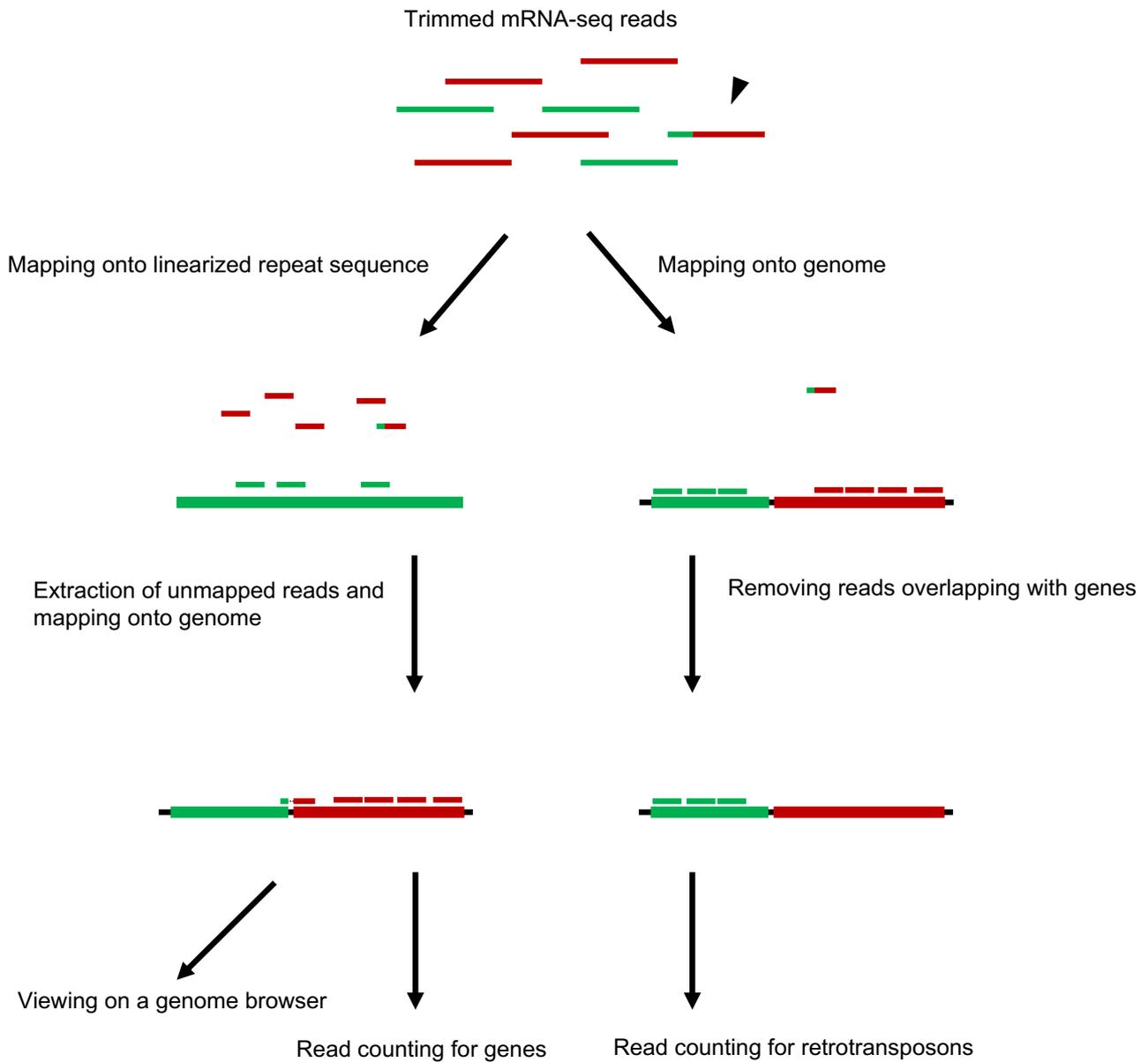
Supplementary Fig. 2. Schematic representation of read mapping of retrotransposons and other genes

To count reads separately for retrotransposons and the other genes, trimmed RNA-seq reads were mapped onto the genome using two different strategies. The arrowhead indicates an aberrant chimeric read composed of a part of a retrotransposon (green) and an adjacent gene (red). To assess the expression levels of genes other than retrotransposons, reads were mapped on a linearized repeat sequence, and all reads that were defined as retrotransposon RNA were removed. Thereafter, the remaining reads were mapped onto the genomic sequence and subjected to read counts. Chimeric reads were counted during this process because they were not mapped onto the linearized repeat sequence. On the other hand, to assess expression levels of retrotransposons, RNA-seq reads were mapped onto the genome, excluding splicing junctions. Subsequently, reads overlapping with genes other than retrotransposons were removed. Chimeric reads were excluded from the analysis.
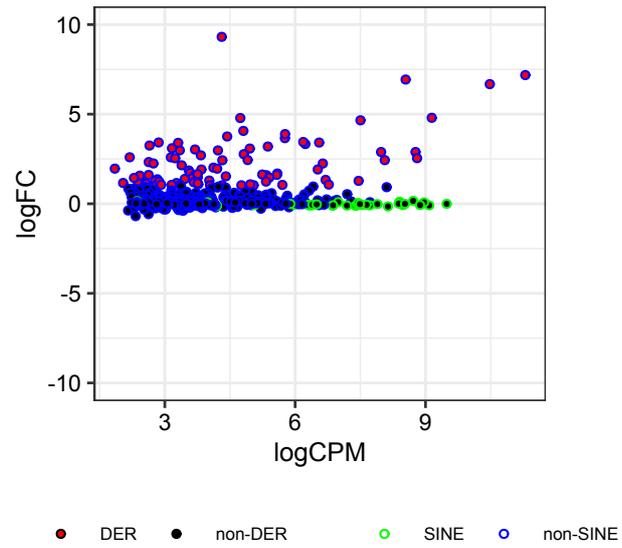
Supplementary Fig. 3. Expression fold changes of SINE elements

The MA plot represents the same data as that shown in Fig. 4A. Dots with green and blue borders indicate the SINE and non-SINE elements, respectively. Differentially expressed retrotransposons are shown as red dots (FDR < 0.01, |fold-change| > 2).
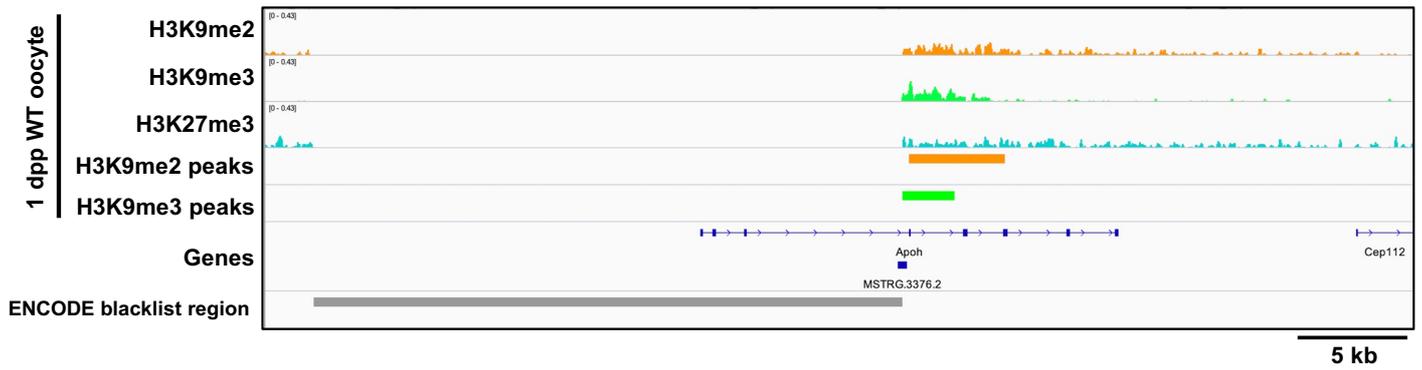
Supplementary Fig. 4. Enrichment of repressive histone marks in non-growing oocytes in the *Apoh* region

MSTRG.3376.2 is an aberrant exon of *IAP-Apoh.* Reads on the ENCODE blacklist region were removed and excluded from ChIP-seq analysis because of their low complexity. Details of the analysis are described in the Materials and Methods section. Previously published ChIP-seq datasets (DRA006633) were used.
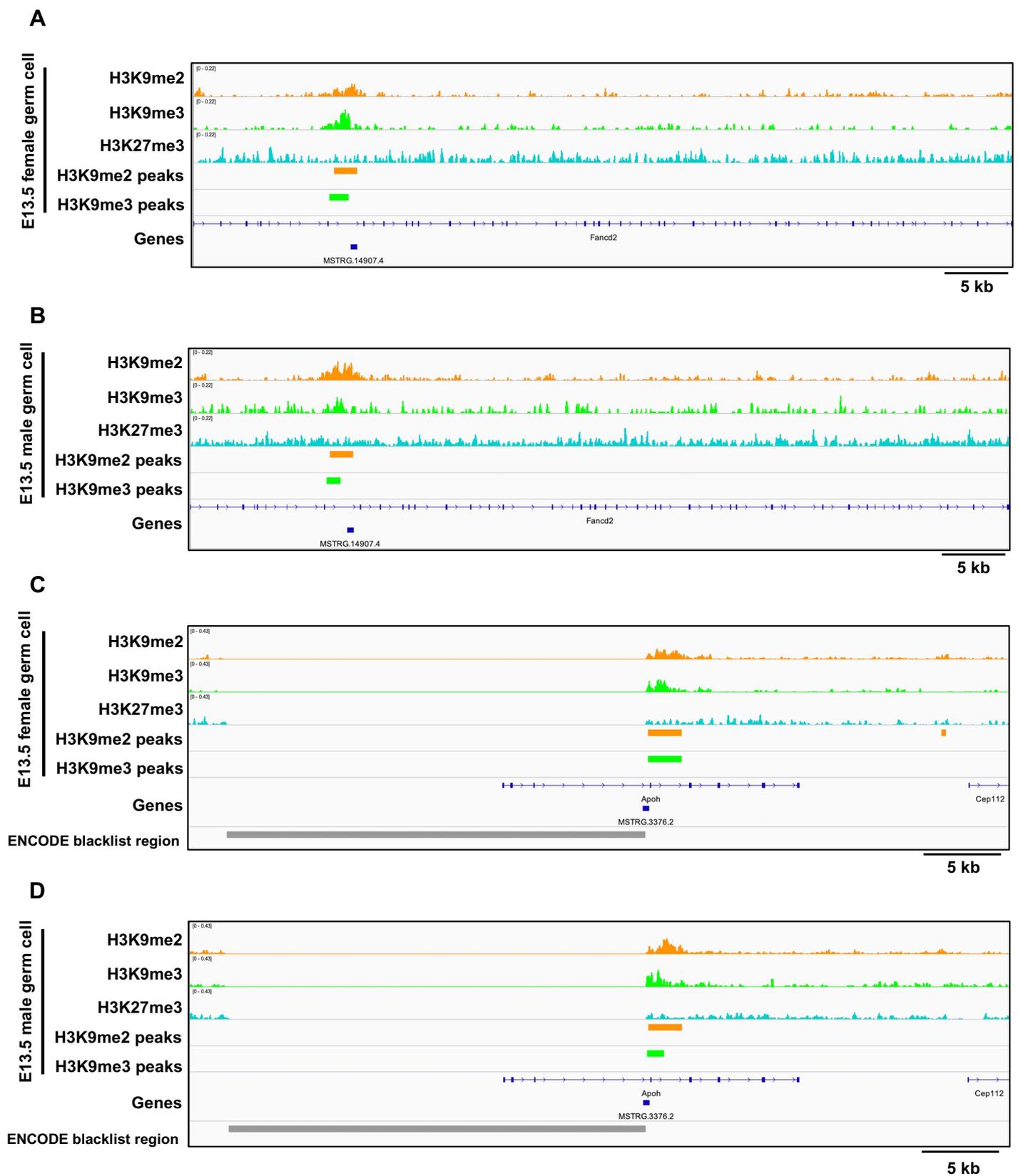
Supplementary Fig. 5. Enrichment of repressive histone marks in early germline

(A-B) Enrichment of H3K9me2, H3K9me3, and H3K27me3 in female (A) and male germ cells (B) of E13.5 fetuses in the *Fancd2* region. **(C-D)** Enrichment of H3K9me2, H3K9me3, and H3K27me3 in female (C) and male germ cells (D) of E13.5 fetuses in the *Apoh* region. Previously published ChIP-seq data sets (DRA006633) were used.

A

1 dpp WT gonocyte

H3K9me2
H3K9me3
H3K27me3
H3K9me2 peaks
H3K9me3 peaks
Genes

[0 - 0.22]
[0 - 0.22]
[0 - 0.22]

Fancd2

MSTRG.14907.4

5 kb

B

1 dpp WT gonocyte

H3K9me2
H3K9me3
H3K27me3
H3K9me2 peaks
H3K9me3 peaks
Genes
ENCODE blacklist region

[0 - 0.43]
[0 - 0.43]
[0 - 0.43]

Apoh

Cep112

MSTRG.3376.2

5 kb
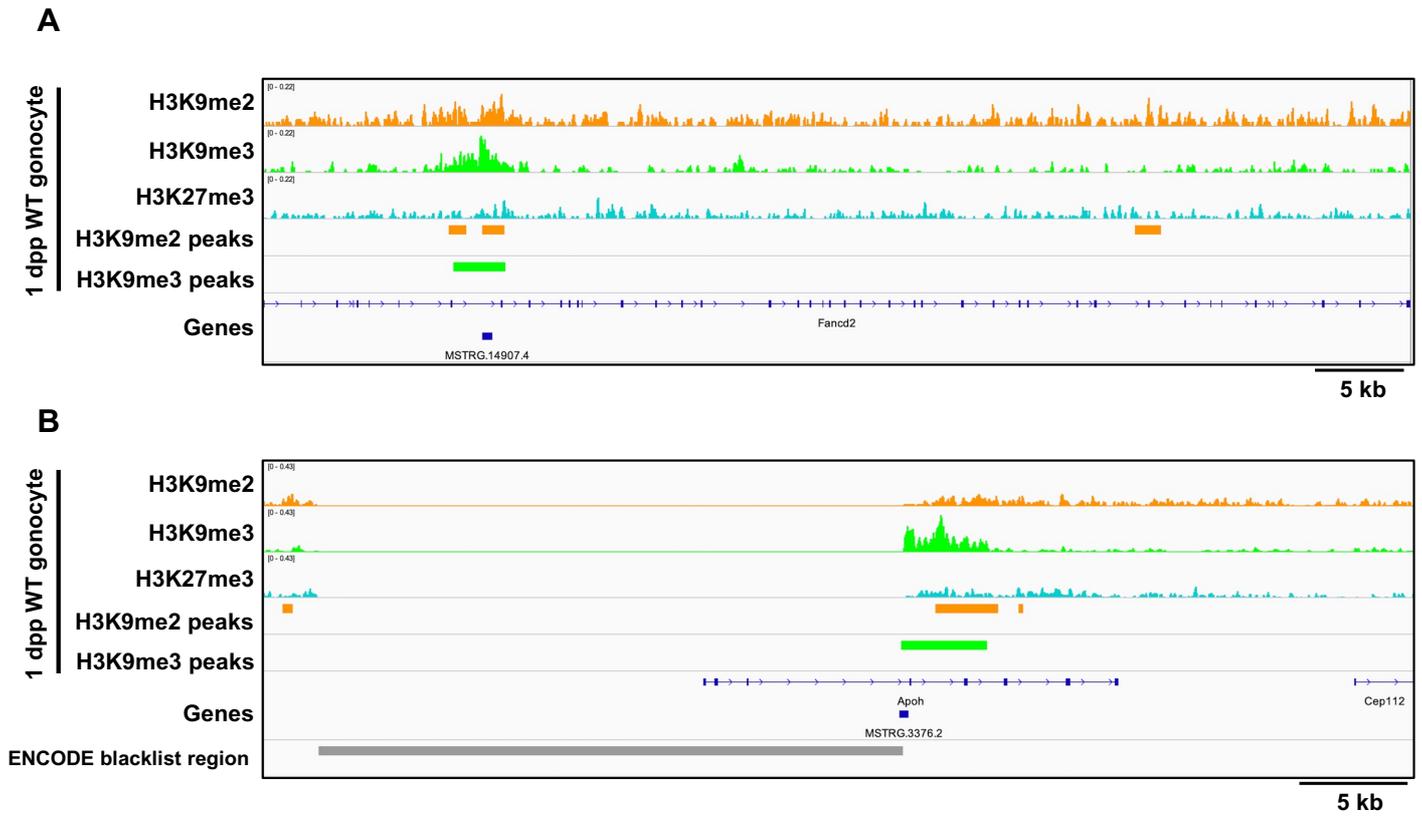
Supplementary Fig. 6. Enrichment of repressive histone marks in gonocytes

(A-B) Enrichment of H3K9me2, H3K9me3, and H3K27me3 in the *Fancd2* region (A) and the *Apoh* region (B) in gonocytes of 1 dpp wild-type mice. Previously published ChIP-seq data sets (DRA006633) were used.

Supplementary Table 1. Antibodies used for immunofluorescence, western blotting, and FACS.

Primary antibodies	Supplier	Reference	Species	Type	Dilution		
					Immunofluorescense	Western blotting	FACS
ASZ1	GeneTex	GTX111618	rabbit	polyclonal		1/1000	
MVH (DDX4)	abcam	ab13840	rabbit	polyclonal	1/500	1/1000	
GENA	BioAcademia	73-003	rat	monoclonal	1/500		
SCP1	abcam	ab15090	rabbit	polyclonal	1/500		
SCP3	abcam	ab97672	mouse	monoclonal	1/500		
PIWIL4 (MIWI2)	abcam	ab21869	rabbit	polyclonal	1/500		
L1ORF1p	abcam	ab216324	rabbit	monoclonal	1/500		
CD16/32	BioLegend	101301	rat	monoclonal			1/200
EpCAM (APC/Fire750-conjugated)	BioLegend	118229	rat	monoclonal			1/200
c-kit (Brilliant Violet 421-conjugated)	BioLegend	135123	rat	monoclonal			1/200
GAPDH	Trevigen	2275-PC-100	rabbit	polyclonal		1/1000	
Secondary antibodies	**Supplier**	**Reference**	**Species**	**Type**	**Dilution**		
					Immunofluorescense	Western blotting	FACS
Alexa Fluor 488 Donkey anti-Mouse IgG (H+L)	Thermo Fisher Scientific	A-21202	mouse	polyclonal	1/500		
Alexa Fluor 594 Goat anti-Rabbit IgG (H+L)	ThermoFisherScientific	A-11012	rabbit	polyclonal	1/500		
Anti-Rabbit IgG, HRP-Linked Whole Ab Donkey	Cytiva	NA934V	rabbit	polyclonal		1/10000	
Anti-Mouse IgG, HRP-Linked Whole Ab Sheep	Cytiva	NA931VS	mouse	polyclonal		1/10000	

Supplementary Table 2. Primers used for bisulfite sequencing, q-RT-PCR, and sequencing of PCR products.

Name	sequence (5'- 3')	Splicing site sequencing	Bisulfite sequencing	qRT-PCR
Cdh12-F	ATGTTTGTTTGTATATTGTTTATTTT		✓	
Cdh12-R	AACATTACCTATTCTATTTTCCTAA		✓	
Inadl-F	GTTATGTTTGGTTGTATTGTT		✓	
Inadl-R	CTTAAAAAACATTCTCCTTC		✓	
Apoh-F	AGAGAGAAGTAAGAGAGAGAGAAAA		✓	
Apoh-R	TACCAAATAAAAAAACTAAAAAACC		✓	
Zfp72_F	GAGAAGTTGTTTTTTTTATGTG		✓	
Zfp72_R	TTAAAATTTTTCTACCTCCC		✓	
Fancd2-F	GAATTTTAGAAATATAAGGAATG		✓	
Fancd2-R	CAAACAATACCTCAAATAAAC		✓	
Spag16-F	TTTAGGGAGGATATTTAGGAGA		✓	
Spag16-R	CAAACAACAAATACCAAAAA		✓	
Sult2a5-F	ATTAGGTTTGGGTAGTTTGTTTT		✓	
Sult2a5-R	TATAAATTCTAAAATACTTCTT		✓	
Fam135a-F	GTTGTGTTGTATAAGGTTTTGTT		✓	
Fam135a-R	ATATTCATTTCTTTTCTCCC		✓	
Sec11a-F	ATAGTTGTGTTTTAAGTGGT		✓	
Sec11a-R	CAATCTAAAATCTAATTATT		✓	
Hibch-F	ATTTTGTTGGTAAGGAAGTT		✓	
Hibch-R	AAAATATTCTACAAAACTAAAC		✓	
IAP-Fancd2_1_F	CATCTTGCAACGGCGAATGA	✓		✓
IAP-Fancd2_1_R	GTTGGGGTCAAGTCGGAGAC	✓		✓
SP6	ATTTAGGTGACACTATAGAA	✓		
T7	TAATACGACTCACTATAGGG	✓		

Supplementary Table 3. Significantly up- and down-regulated genes in *Asz1*$^{-/-}$ mice gonocytes compared with those of wild-type mice.

Upregulated Genes in *Asz1*$^{-/-}$ gonocytes				
gene_id	logFC	logCPM	PValue	FDR
Apoh	6.87894841	5.22198548	1.51E-176	3.77E-173
Cdh12	8.45543075	4.08760179	1.02E-105	1.27E-102
4930558C23I	6.39170013	4.1705752	1.78E-85	1.71E-82
Cbx5	2.01856378	7.81599404	4.31E-66	2.99E-63
Tfcp2l1	2.73997758	5.73106356	6.72E-62	4.41E-59
Gm16897	4.9700051	3.69141476	4.21E-56	2.28E-53
Gm9733	10.7830501	2.7052466	4.50E-53	2.25E-50
AW551984	3.3243023	4.4763667	3.12E-52	1.44E-49
Gyltl1b	1.85338787	6.90663231	6.19E-52	2.66E-49
Ms4a6d	5.70268118	3.50123867	1.21E-50	5.01E-48
Cd93	2.3289957	5.94660073	1.90E-50	7.63E-48
Spag16	3.1546635	4.24822131	1.42E-47	5.20E-45
Fancd2	1.48146623	7.42639077	2.11E-47	7.51E-45
Mup3	6.28045094	2.88925469	3.57E-45	1.20E-42
Polr1a	1.42176268	7.13048199	4.48E-44	1.47E-41
Clec2g	6.61337356	2.66345346	8.55E-43	2.73E-40
Sult2a5	7.51757615	2.64630744	1.46E-39	4.44E-37
Abcb11	4.25839768	3.85361299	5.14E-39	1.53E-36
Tmppe	1.65913114	5.90181699	2.10E-37	5.69E-35
Bcl6b	1.74233201	7.94634637	2.41E-37	6.38E-35
Cd82	1.39170539	6.90581052	1.13E-33	2.81E-31
Sez6	1.34276098	7.59284084	1.20E-33	2.92E-31
AA792892	10.1027647	2.04707938	3.12E-32	7.33E-30
Itga7	1.50786181	6.19604428	5.79E-31	1.30E-28
Samd9l	3.82819352	3.12564986	5.86E-31	1.30E-28
Gm6329	2.41754246	4.21605564	5.93E-31	1.30E-28
Cntn6	2.30880626	4.33300407	4.84E-29	1.02E-26
Tmem232	1.72711291	5.21841503	5.10E-29	1.06E-26
Adtrp	2.25226292	4.15589707	2.28E-28	4.59E-26
Sidt1	2.15611241	4.46114776	3.39E-28	6.70E-26
BC051019	3.42375303	2.8626333	4.28E-27	7.97E-25
Wbp2nl	2.65883403	3.39538363	9.65E-25	1.64E-22
Gabrr1	2.56493201	3.75288696	9.76E-25	1.64E-22
Cdc14b	1.17645942	6.40364149	2.45E-24	3.97E-22
Cks2	1.05743725	6.71963356	1.82E-22	2.80E-20
E330020D12	3.93921365	2.01795216	2.01E-22	3.05E-20
Atp13a4	4.03866909	1.82410565	2.79E-22	4.18E-20
Zfp72	2.94513306	2.85362196	3.04E-22	4.52E-20
Ryr1	1.27748351	6.17725606	5.00E-22	7.32E-20
Inadl	1.33536647	6.06725635	2.72E-21	3.85E-19
Six1	1.80908531	4.39513511	4.04E-21	5.66E-19
Gm14296	2.29053542	3.59412416	7.21E-21	9.98E-19
Gm6182	2.29053524	3.59412416	7.29E-21	9.98E-19
Cdkl4	2.64050623	3.23831732	2.30E-20	3.11E-18
Zfp53	1.54275423	4.94990945	2.58E-20	3.46E-18
Ripk3	1.28911932	6.16374427	5.44E-20	7.06E-18
Dpp4	3.30216479	3.13973605	1.07E-19	1.35E-17
Tmc2	3.31077496	2.58122805	1.27E-19	1.56E-17
Pdk1	1.25053942	7.20982995	1.88E-19	2.30E-17
4930481A15I	2.99916371	2.28604451	4.71E-19	5.54E-17
Hmmr	1.63276152	4.74034748	1.81E-18	2.01E-16
Ccdc127	1.0700891	6.73681635	1.97E-18	2.18E-16
Slc35e1	1.18806173	5.60984361	2.88E-18	3.15E-16
Eva1b	1.22832145	5.47023281	3.42E-18	3.71E-16
Gabpb2	1.35598388	5.56472554	4.78E-18	5.05E-16
Lpp	1.09982804	6.16916465	7.88E-18	8.19E-16
Mkl2	1.10894313	5.75023815	3.19E-17	3.13E-15
Plekho2	1.13671905	5.99051292	1.70E-16	1.61E-14
Gm14326	2.10547661	3.83090855	2.68E-16	2.48E-14
Naip5	2.56597883	2.45786799	1.12E-15	1.01E-13
Eps8l1	2.2250619	3.02672439	1.45E-15	1.30E-13
D17H6S56E-	1.30501698	4.7995196	1.83E-15	1.63E-13

Downregulated Genes in *Asz1*$^{-/-}$ gonocytes				
gene_id	logFC	logCPM	PValue	FDR
Asz1	-7.5110766	6.66971389	0	0
Lmna	-1.826733	7.86647621	9.20E-62	5.73E-59
Inha	-2.8536438	4.46970522	1.95E-45	6.75E-43
Adgrg1	-1.6000895	6.27491838	9.02E-37	2.34E-34
Magea8	-1.7637567	5.93105652	4.93E-34	1.25E-31
Chic2	-1.1835006	7.52496583	2.05E-30	4.40E-28
Ehmt2	-1.2688152	7.92610669	4.92E-28	9.57E-26
Axl	-1.552368	5.51048035	2.27E-24	3.72E-22
Ecm1	-1.1773188	6.64619325	3.07E-23	4.84E-21
Magea5	-1.5023911	5.14348738	5.05E-22	7.32E-20
Cftr	-3.7638401	3.58175943	4.55E-20	6.03E-18
Sdc3	-1.1949642	6.66564719	1.26E-19	1.56E-17
Gstm2	-2.0149187	4.03823729	1.51E-18	1.71E-16
Gpd2	-1.3333776	5.18321231	1.73E-18	1.94E-16
Sult5a1	-1.1832245	5.80440994	2.31E-17	2.30E-15
Cst9	-3.8047878	1.62094378	8.78E-17	8.42E-15
Prss35	-2.7430257	2.35108919	2.99E-16	2.74E-14
Garnl3	-1.0741896	5.99717312	8.06E-16	7.33E-14
Dscaml1	-1.2393136	5.25063927	3.09E-14	2.45E-12
Hsd17b1	-2.7592124	1.76980478	3.24E-14	2.54E-12
Haus7	-1.1783757	5.01045044	3.28E-14	2.56E-12
Magea3	-1.9723907	3.16269202	7.00E-14	5.22E-12
Gm773	-1.0519945	5.81735223	1.13E-13	8.21E-12
Prdx2	-1.0772495	5.35289998	1.54E-13	1.09E-11
Lama4	-1.3671772	4.61840606	3.03E-13	2.08E-11
Hcfc2	-1.0459514	5.36381702	3.65E-13	2.48E-11
Arap3	-1.3862196	4.15351421	6.48E-13	4.29E-11
Bcar3	-1.1549737	4.79512658	1.64E-12	1.01E-10
Cdkn1a	-1.1571868	4.68987396	3.72E-12	2.19E-10
Jam2	-2.2632423	2.27776063	3.81E-12	2.22E-10
Bhlhe40	-1.0597659	5.36340849	7.17E-12	3.99E-10
Luzp4	-1.0124592	5.23789617	8.51E-12	4.67E-10
Tmem184a	-1.3209092	4.18180843	9.12E-12	4.99E-10
Fbln1	-1.1804648	6.16772588	9.29E-12	5.05E-10
Gm1140	-1.7220909	3.67307546	1.01E-11	5.47E-10
Pet2	-1.7133234	4.34996034	1.02E-11	5.50E-10
Amh	-2.572667	2.33444398	1.12E-11	5.96E-10
Mslnl	-2.1718847	2.85102531	2.10E-11	1.07E-09
Wnt3	-1.0374744	5.00873306	2.25E-11	1.14E-09
Magea2	-1.6534338	3.73037101	2.79E-11	1.40E-09
Etfb	-1.1660373	4.63297257	2.88E-11	1.44E-09
Aldh1a1	-2.5752663	3.35415147	3.28E-11	1.62E-09
Gatm	-1.2727435	4.40545807	4.36E-11	2.03E-09
Magea1	-1.7714343	2.98043111	5.15E-11	2.39E-09
Akr1cl	-2.1827875	2.40270809	5.85E-11	2.67E-09
S100a6	-1.2350553	4.624746	6.26E-11	2.83E-09
Gja1	-2.0860624	3.37013305	6.97E-11	3.11E-09
Egr3	-1.5217279	3.78805741	8.42E-11	3.72E-09
Gm14692	-1.6971271	3.3070011	9.76E-11	4.25E-09
Hnrnph3	-1.1584263	4.40137516	1.10E-10	4.73E-09
1700029J07F	-1.6425175	3.22122933	1.51E-10	6.26E-09
Kctd14	-2.2385584	2.37945549	2.14E-10	8.67E-09
Erdr1	-2.6019867	2.00242368	2.67E-10	1.06E-08
Def8	-1.3215387	3.98152964	2.90E-10	1.14E-08
Nxt2	-1.7058054	2.8243848	3.60E-10	1.39E-08
Igdcc4	-1.1025601	4.39277267	6.16E-10	2.26E-08
Rhox13	-1.038716	4.73355472	6.45E-10	2.36E-08
Speg	-1.4237871	3.4288845	9.33E-10	3.34E-08
Rara	-1.0197345	4.65931894	9.85E-10	3.50E-08
Pnma5	-1.3110947	3.89796761	1.18E-09	4.17E-08
Adgrg6	-1.3923938	3.96738421	1.29E-09	4.51E-08
Sbsn	-1.885348	2.80227121	1.76E-09	5.99E-08

Supplementary Table 3. Significantly up- and down-regulated genes in *Asz1* [-/-] mice gonocytes compared with those of wild-type mice.

Upregulated Genes in *Asz1* [-/-] gonocytes					Downregulated Genes in *Asz1* [-/-] gonocytes			
Rnf125	1.94668788	3.91148628	1.88E-15	1.66E-13	Gngt2	-1.3027328	4.06323105	2.04E-09	6.76E-08
Scn7a	2.10181038	4.42561529	4.74E-15	4.11E-13	Scd1	-1.3895235	3.77491635	2.41E-09	7.93E-08
Zfp882	2.16291833	3.21587827	8.39E-15	7.21E-13	Cntnap4	-1.5888844	2.93260369	2.69E-09	8.76E-08
Flt4	1.64752069	4.20891109	1.01E-14	8.60E-13	Myh8	-1.3996892	3.89246926	2.76E-09	8.95E-08
Atp9b	1.18021958	5.94564414	1.27E-14	1.05E-12	Gm15097	-1.1187958	4.30348093	3.19E-09	1.02E-07
Cyp20a1	1.79609779	4.17930537	1.45E-14	1.19E-12	Rufy2	-1.0924326	4.33504197	4.07E-09	1.28E-07
Tek	1.22929768	5.03546653	2.04E-14	1.63E-12	Postn	-1.5448673	3.22129854	4.11E-09	1.29E-07
Alx4	2.03990891	3.24707637	3.15E-14	2.48E-12	Aard	-1.5629994	2.91287879	4.13E-09	1.29E-07
Colec12	1.09431513	5.36905239	4.27E-14	3.29E-12	Trim47	-1.3980493	3.57089776	4.43E-09	1.37E-07
Mfap3	1.23570125	6.36057488	4.83E-14	3.67E-12	Thbs2	-1.01839	4.50803439	5.39E-09	1.64E-07
Aig1	1.1745335	5.61202738	6.89E-14	5.17E-12	Lgals7	-1.168275	4.3791012	5.51E-09	1.67E-07
Nrros	1.31503776	4.54287487	9.52E-14	7.02E-12	Hspb7	-1.4294413	3.32614399	6.57E-09	1.96E-07
Slc24a2	1.6516704	4.10551553	9.79E-14	7.18E-12	Tep1	-1.1070292	4.11119242	1.02E-08	2.92E-07
Sorcs2	1.9070006	3.16577707	2.29E-13	1.61E-11	Lad1	-1.00375	4.97890839	1.21E-08	3.44E-07
Thbd	2.70987264	2.86225461	5.22E-13	3.51E-11	Itih2	-2.0447679	2.06307087	1.45E-08	4.02E-07
Fam219b	1.33360275	4.72712323	6.72E-13	4.43E-11	Igsf9b	-1.2827364	3.70336247	1.55E-08	4.26E-07
Slc43a2	1.02616467	5.32844579	7.00E-13	4.59E-11	Brcc3	-1.0051722	4.38781274	1.66E-08	4.52E-07
Glrx2	1.09838653	5.16768094	1.38E-12	8.60E-11	Pdk4	-2.0833921	2.25206301	1.67E-08	4.54E-07
C920006O11	1.90020331	3.12556963	3.39E-12	2.01E-10	Crygs	-1.4409746	3.37928331	1.95E-08	5.25E-07
Xrcc2	1.20377974	4.69068313	3.57E-12	2.11E-10	Hsd17b10	-1.1085777	4.03260985	1.97E-08	5.28E-07
Cercam	1.28968443	4.32424278	3.92E-12	2.27E-10	Bcat2	-1.274945	3.74719396	2.11E-08	5.60E-07
Gm14322	1.89997563	2.97034775	4.15E-12	2.39E-10	Magea6	-1.6409526	3.31098182	2.92E-08	7.52E-07
Creg2	1.37854914	4.22171474	4.53E-12	2.60E-10	Mid1	-1.6476633	2.38184905	3.30E-08	8.42E-07
Fam206a	1.04716756	5.38652838	4.70E-12	2.69E-10	Magea10	-1.0014096	4.47186055	4.28E-08	1.07E-06
Derl3	1.36880765	4.15140729	4.77E-12	2.72E-10	Gata4	-1.2643452	3.64326792	4.82E-08	1.18E-06
Nrip3	1.35384107	4.15397947	5.35E-12	3.03E-10	Sfn	-1.1744538	3.88285735	4.84E-08	1.19E-06
Clvs1	2.30807337	1.98977518	8.38E-12	4.62E-10	Rcor1	-1.4671101	4.09253028	6.11E-08	1.47E-06
Zfp346	1.02467785	5.76165441	1.20E-11	6.34E-10	Cd68	-1.4558293	3.12664178	6.36E-08	1.52E-06
Ccnb3	1.06214687	5.74426115	1.36E-11	7.10E-10	Crtam	-1.5830729	2.99662677	7.58E-08	1.77E-06
Tmem40	2.82166944	1.80730851	2.00E-11	1.03E-09	Dnajc6	-1.0015194	4.28504018	9.61E-08	2.17E-06
Orai3	1.26942028	5.30131973	2.57E-11	1.30E-09	Vwa1	-1.8254062	2.29348268	9.88E-08	2.22E-06
6820431F20	1.59078125	3.49747762	2.59E-11	1.30E-09	Sparc	-1.5239138	5.30022145	1.18E-07	2.60E-06
Zfp953	1.93830866	2.58287021	3.28E-11	1.62E-09	Tmem160	-1.0053716	4.15680396	1.24E-07	2.70E-06
Kndc1	1.88966457	3.73919946	3.84E-11	1.85E-09	Kctd15	-1.5324829	2.54331849	1.39E-07	2.99E-06
Gm6710	1.71302112	3.58497359	3.93E-11	1.87E-09	Cd300lb	-1.6881018	2.44068325	1.42E-07	3.05E-06
Fstl4	1.30213749	4.90048669	3.95E-11	1.87E-09	Inhbb	-1.5912527	2.52425137	1.65E-07	3.51E-06
Fam84b	1.37488426	4.30436147	5.22E-11	2.41E-09	Gabra2	-1.717626	2.52715811	1.86E-07	3.91E-06
Gm14325	1.85241599	3.34840605	5.46E-11	2.51E-09	Endod1	-1.3045832	3.22184633	1.88E-07	3.94E-06
Tomm7	1.00875737	5.05765539	6.17E-11	2.79E-09	Col6a5	-1.1193465	3.9391983	2.02E-07	4.21E-06
Upk1b	1.23701421	4.37943674	6.82E-11	3.07E-09	Qprt	-1.0438967	3.91055841	2.09E-07	4.33E-06
Myof	1.03105098	5.88352687	7.05E-11	3.14E-09	Cfi	-1.3874475	2.78681625	3.01E-07	6.00E-06
9330102E08	1.48068788	3.67516932	9.76E-11	4.25E-09	Tnfrsf11a	-1.727192	2.0459758	3.06E-07	6.08E-06
Ano4	1.60909944	3.60979722	1.03E-10	4.47E-09	Efhd1	-1.5788653	1.91298063	5.86E-07	1.09E-05
Mtap7d3	1.24712339	4.39403155	1.07E-10	4.60E-09	Trim46	-1.165904	3.37787942	5.91E-07	1.09E-05
Col22a1	1.21696339	4.60946587	1.25E-10	5.29E-09	AI607873	-1.8153532	2.18664628	6.54E-07	1.19E-05
Nuggc	2.4837937	2.30346646	1.25E-10	5.29E-09	S100a3	-1.5441303	2.44827247	6.69E-07	1.21E-05
Pamr1	2.68320426	1.8698371	1.31E-10	5.52E-09	Tmem80	-1.6456453	2.55263172	9.86E-07	1.69E-05
Tmem53	1.23699345	4.23047669	1.38E-10	5.78E-09	Apoa1	-1.3662653	2.68347079	1.25E-06	2.09E-05
Cdk5rap1	1.1213579	5.32205911	1.85E-10	7.57E-09	Sult1c1	-1.4820186	2.85866844	1.32E-06	2.20E-05
A4galt	1.98556253	2.99309293	2.13E-10	8.63E-09	Pla2g1b	-1.3877995	2.4915224	1.36E-06	2.26E-05
L1cam	1.33536839	4.16411868	2.15E-10	8.68E-09	S100a16	-1.1910892	3.63674225	1.51E-06	2.46E-05
Cyp1b1	1.99739027	2.79367086	2.40E-10	9.64E-09	Adgrf1	-1.3637074	2.59825608	1.61E-06	2.60E-05
Pnpla1	1.02897284	4.94589138	3.55E-10	1.38E-08	Dab2	-1.3037129	3.29951852	1.61E-06	2.60E-05
Ky	2.00941512	2.19853862	4.29E-10	1.62E-08	Ror2	-1.0272813	5.00970516	1.75E-06	2.80E-05
Glyctk	1.10363883	5.08733473	5.67E-10	2.11E-08	Gucy2g	-1.5347265	1.92438442	1.91E-06	3.02E-05
Fam109b	1.99253304	2.21039645	5.86E-10	2.17E-08	Cpeb2	-1.1473529	4.51788904	2.07E-06	3.23E-05
2610005L07	1.60237666	3.19923604	8.30E-10	2.99E-08	S100a13	-1.5897566	2.12700216	2.08E-06	3.24E-05
Ccdc28b	2.14667032	1.93842692	9.14E-10	3.28E-08	Gpc6	-1.3815505	2.8792447	2.25E-06	3.45E-05
Slc5a4a	1.83201696	2.55084175	1.22E-09	4.29E-08	Klhl32	-1.0521806	3.66962097	2.52E-06	3.83E-05
Rassf4	1.15388852	4.19106707	1.37E-09	4.77E-08	Sox9	-1.6314796	2.1404261	2.57E-06	3.90E-05
Ap5b1	2.03611048	2.47656953	1.41E-09	4.90E-08	Abca8a	-1.1907716	3.68018193	2.78E-06	4.17E-05
Gm14430	1.8031456	2.43233282	1.85E-09	6.24E-08	Cpe	-1.1856198	4.05089805	2.85E-06	4.24E-05
Gm4724	1.80314548	2.43233282	1.86E-09	6.25E-08	Sh3bp5	-1.228519	3.24483558	3.29E-06	4.84E-05

Supplementary Table 3. Significantly up- and down-regulated genes in *Asz1* $^{-/-}$ mice gonocytes compared with those of wild-type mice.

Upregulated Genes in *Asz1* $^{-/-}$ gonocytes					Downregulated Genes in *Asz1* $^{-/-}$ gonocytes				
Gm14308	1.80314545	2.43233282	1.86E-09	6.25E-08	Nat14	-1.4870576	2.08773471	3.82E-06	5.53E-05
Gm14434	1.80314543	2.43233282	1.87E-09	6.25E-08	Phf2	-1.1015653	3.48642894	4.05E-06	5.82E-05
0610010B08I	1.80314535	2.43233282	1.87E-09	6.26E-08	Tnnt2	-1.5856386	2.30261816	4.10E-06	5.88E-05
4932435O22	2.21437158	2.29472189	2.21E-09	7.30E-08	1110001J03F	-1.4080202	2.90008726	4.73E-06	6.68E-05
B430306N03	1.10507347	4.40706206	2.55E-09	8.33E-08	Zfp326	-1.2164425	3.24158064	4.75E-06	6.68E-05
Mertk	1.24601592	4.21303606	2.91E-09	9.40E-08	1700012D01	-1.4067696	2.26195339	4.95E-06	6.89E-05
Cdh26	2.22822803	2.28049176	5.05E-09	1.55E-07	Bicd1	-1.5057237	2.17320979	4.96E-06	6.89E-05
Pars2	1.45021011	3.7655722	5.78E-09	1.75E-07	Cadm4	-1.3044211	3.70915643	5.76E-06	7.94E-05
Ttc26	1.16806609	4.06075772	6.41E-09	1.92E-07	Tnfaip2	-1.2210551	2.75215986	5.87E-06	8.06E-05
4930539E08I	1.26143602	3.71407053	6.79E-09	2.02E-07	Trim52	-1.0854764	3.54793243	5.96E-06	8.16E-05
Gm14403	1.78797195	2.61587307	7.24E-09	2.15E-07	Vrk2	-1.0840792	3.34924034	6.63E-06	8.94E-05
Srxn1	1.46551236	3.53954859	7.63E-09	2.26E-07	Ier5	-1.0524243	3.76720717	7.32E-06	9.74E-05
Il10ra	1.80721552	2.69741766	8.72E-09	2.53E-07	Shc4	-1.0590605	4.08902587	7.62E-06	0.00010055
Adra2a	1.62195129	2.6773278	9.50E-09	2.73E-07	Rbmx	-1.2572166	2.80321124	8.44E-06	0.0001101
Tigd3	1.53806518	3.05481213	1.13E-08	3.22E-07	1700021F07I	-1.1112939	3.19736056	8.93E-06	0.00011584
Adgrv1	1.12634531	4.79094583	1.14E-08	3.26E-07	Syt7	-1.4668992	2.11843069	1.05E-05	0.00013278
Ttc38	1.31370125	3.86871937	1.26E-08	3.55E-07	Sfxn1	-1.0759807	3.56932032	1.06E-05	0.00013444
Slc7a4	1.49940313	3.44204504	1.35E-08	3.76E-07	St8sia3	-1.0337495	3.53289223	1.08E-05	0.0001368
Sspn	1.50062569	3.17029861	1.44E-08	3.99E-07	Zp2	-1.6224175	2.11660378	1.12E-05	0.0001409
Slc29a3	1.23702661	3.71049018	1.86E-08	5.03E-07	Thra	-1.2418124	2.64274736	1.15E-05	0.00014401
Rspo2	1.19980363	3.87471537	2.03E-08	5.43E-07	Pfkfb3	-1.0286947	3.94009024	1.18E-05	0.00014728
Cep128	1.1497371	4.00517039	2.14E-08	5.66E-07	BC021891	-1.2518764	2.57103832	1.24E-05	0.00015342
H6pd	1.95792891	2.31722742	2.22E-08	5.85E-07	Pros1	-1.3707343	2.51806329	1.26E-05	0.00015529
Exoc8	1.02192829	4.35336316	2.60E-08	6.78E-07	Slc27a5	-1.3196481	2.34575045	1.55E-05	0.00018536
Ccdc28a	1.17370159	3.82155967	2.63E-08	6.84E-07	Ccser1	-1.1131008	3.18096481	1.72E-05	0.00020229
Ube2u	1.6181461	2.88973895	3.82E-08	9.61E-07	4931414P19I	-1.3367427	2.22527436	1.82E-05	0.00021347
Pkhd1	1.90150379	2.35117784	3.84E-08	9.64E-07	Vsx1	-1.097885	3.01812894	2.12E-05	0.000245
Neil3	1.37496064	3.65898404	4.03E-08	1.01E-06	Anxa5	-1.0779641	3.35088114	2.16E-05	0.00024888
Cbln2	1.15914756	3.8416161	4.55E-08	1.13E-06	Col6a1	-1.5338717	3.57456303	2.33E-05	0.00026603
Eomes	1.08723567	4.45311294	4.67E-08	1.15E-06	Klf6	-1.0195962	3.68799096	2.69E-05	0.00029935
Upp2	1.59454224	2.83270973	5.46E-08	1.32E-06	Morn2	-1.0629034	3.09126621	3.10E-05	0.00033999
OTTMUSG00	1.66266342	2.22927796	6.21E-08	1.49E-06	Mtmr1	-1.177641	3.59847505	3.66E-05	0.00039154
Fam19a4	1.6181291	2.38907559	7.21E-08	1.70E-06	Tnni1	-1.0955802	3.21505989	4.00E-05	0.00042152
Zfp119a	1.37146478	3.19422736	7.48E-08	1.75E-06	Nap1l3	-1.2598939	2.26621973	4.04E-05	0.00042413
Htra1	1.2921555	3.98368897	8.25E-08	1.91E-06	Cst12	-1.4254656	2.11639317	4.41E-05	0.00045808
Cnr1	1.03699931	4.26937225	9.15E-08	2.09E-06	Snap25	-1.1601022	2.42137756	5.60E-05	0.00056046
Sstr5	1.1559345	4.65984999	9.54E-08	2.16E-06	Cdhr2	-1.2878179	2.63608813	5.67E-05	0.00056595
Kcnc2	1.36317187	4.23329407	1.01E-07	2.25E-06	Tbx4	-1.0612199	3.55312014	5.71E-05	0.00056844
Gm14391	1.56504229	2.62925729	1.03E-07	2.29E-06	Adora1	-1.183875	2.89959607	6.10E-05	0.00060114
Xkrx	1.5034505	3.07696857	1.17E-07	2.57E-06	Il10rb	-1.2039515	2.29521513	6.21E-05	0.00060926
Zfp931	1.60447594	2.39544803	1.65E-07	3.51E-06	Col5a2	-1.5085109	2.34525058	7.76E-05	0.00074101
BC026585	1.19621655	4.00171394	2.38E-07	4.87E-06	Ptprz1	-1.2940951	3.16857482	8.90E-05	0.00083555
Cptp	1.08452841	4.41919046	2.47E-07	5.00E-06	Srcin1	-1.2048279	2.68943576	9.28E-05	0.00086444
Gpa33	1.44864019	2.6287114	2.49E-07	5.03E-06	Vamp8	-1.0361361	2.99577626	9.32E-05	0.00086654
Kdm8	1.07463145	3.84845379	2.72E-07	5.46E-06	Trps1	-1.1710963	2.17531905	9.34E-05	0.00086798
Bik	1.1177026	4.13138782	2.88E-07	5.78E-06	Fam131b	-1.0316096	3.23154668	9.69E-05	0.00089292
Deptor	1.13633912	3.95254679	3.38E-07	6.62E-06	Cd3e	-1.4740349	2.27308268	0.00011833	0.00105789
Efcab6	1.39942133	3.07896955	3.40E-07	6.65E-06	5031425E22I	-1.2166287	2.18100381	0.00012411	0.0011025
Cntn2	1.75382556	2.37341464	4.12E-07	7.92E-06	Slc7a10	-1.1625712	2.11576096	0.00012582	0.00111448
Pld1	1.3185046	3.17834616	4.63E-07	8.80E-06	Sorbs2	-1.0706707	2.72212915	0.00013754	0.00120378
Dffa	1.04884396	4.1086591	4.74E-07	8.99E-06	Gm13544	-1.2570301	2.50708022	0.00013844	0.00120995
2610524H06	1.57273036	3.32688809	5.29E-07	9.90E-06	Cfap69	-1.1207236	2.94703235	0.00013918	0.00121558
2410012E07I	1.45745772	2.66193951	5.71E-07	1.06E-05	Dusp27	-1.1452649	2.34864267	0.00014349	0.00124795
Slc10a4	1.45217255	2.68315048	5.73E-07	1.07E-05	Nfix	-1.268351	3.0248791	0.00015167	0.00130467
Tagln	1.20734555	3.31292553	6.23E-07	1.14E-05	2210010C04I	-1.1623638	2.19869155	0.00015169	0.00130467
Zfp820	1.14681985	3.64308572	6.27E-07	1.15E-05	Rpia	-1.1267196	2.29921097	0.00015613	0.00133551
Rltpr	1.00296755	3.98699415	7.05E-07	1.27E-05	Notch4	-1.2189105	2.21704256	0.00018144	0.00151964
St8sia5	1.19182861	3.79108986	7.19E-07	1.29E-05	Tph2	-1.1877752	2.37282024	0.00018314	0.0015313
Spag6	1.29534966	3.16835735	7.53E-07	1.34E-05	Efcab2	-1.0936702	3.24549886	0.00018885	0.00156887
Fras1	1.16383159	3.34501623	7.84E-07	1.39E-05	Cd274	-1.073539	2.94061647	0.00019789	0.00163437
Mfsd4	1.12816962	3.50558501	8.45E-07	1.48E-05	Alox12b	-1.0762574	2.53665337	0.0002049	0.00168764
Sec14l4	2.08245198	2.07826549	8.68E-07	1.51E-05	Clca1	-1.1185525	3.03276298	0.0002124	0.00173698
Sppl2b	1.11024687	4.79798197	9.13E-07	1.58E-05	Fam187b	-1.1318783	2.48468055	0.00022178	0.00179716

Supplementary Table 3. Significantly up- and down-regulated genes in *Asz1* $^{-/-}$ mice gonocytes compared with those of wild-type mice.

Upregulated Genes in *Asz1* $^{-/-}$ gonocytes			
Pax9	1.643349	3.36448099	9.66E-07	1.66E-05
Exog	1.04479896	4.10211445	1.06E-06	1.81E-05
Actc1	1.78879802	2.2411266	1.08E-06	1.84E-05
Gm9112	1.60487294	2.1451409	1.17E-06	1.97E-05
Map6d1	1.23191644	3.18139319	1.19E-06	2.00E-05
Syn3	1.10009536	3.93935881	1.23E-06	2.07E-05
Ybey	1.36650121	3.30798404	1.29E-06	2.15E-05
Fem1a	1.41892452	3.15464073	1.30E-06	2.16E-05
Gm5091	1.1037438	3.5407654	1.57E-06	2.55E-05
Hs3st1	1.1514783	3.40325316	1.70E-06	2.73E-05
Fam46b	1.2201427	3.56835456	1.88E-06	2.97E-05
Kcnh1	1.22694985	3.08820924	1.95E-06	3.07E-05
Fgf9	1.15471267	3.41844133	1.99E-06	3.13E-05
Klhl26	1.63238336	2.99241706	2.20E-06	3.41E-05
D430020J02	1.47275251	2.32448441	2.58E-06	3.91E-05
Cyp2u1	1.03146141	3.75840968	2.59E-06	3.92E-05
Lca5l	1.31001026	2.8313633	2.83E-06	4.23E-05
Nrn1l	1.11368835	3.87810691	2.87E-06	4.26E-05
Cfb	1.4966886	2.28531042	2.97E-06	4.39E-05
Nos2	1.47753506	2.35328307	3.00E-06	4.44E-05
Etohi1	1.51170434	2.08470019	3.35E-06	4.91E-05
Dnah7b	1.15740127	3.74190626	3.45E-06	5.04E-05
Fitm2	1.09704355	3.56513422	4.27E-06	6.08E-05
Zbtb20	1.02395132	4.7370392	4.29E-06	6.10E-05
Abcc10	1.15945641	3.36116921	5.08E-06	7.06E-05
Pde4c	1.34869809	2.46358664	6.22E-06	8.48E-05
Zfp799	1.04484906	3.88587991	6.28E-06	8.54E-05
Lhfpl5	1.50352199	2.07222208	6.80E-06	9.12E-05
Tecpr2	1.11307007	3.99615531	7.20E-06	9.62E-05
Alg6	1.32411576	2.63835416	7.94E-06	0.00010451
Itpripl1	1.00221375	3.65801742	8.07E-06	0.00010595
9830147E19	1.18163973	3.18954	8.79E-06	0.00011427
Slc18a3	1.19603348	3.10929706	9.18E-06	0.00011868
Zdhhc25	1.86261596	2.12649515	1.00E-05	0.00012761
Depdc1a	1.20525526	3.64546985	1.02E-05	0.00012955
Smug1	1.25786324	3.11589747	1.12E-05	0.0001409
Slc38a3	1.21729573	3.12130559	1.33E-05	0.00016163
9930014A18	1.13423376	3.29782838	1.36E-05	0.00016498
Mas1	1.32614862	2.40804844	1.36E-05	0.00016541
Htr3a	1.32125493	2.69415633	1.45E-05	0.00017528
Efcab8	1.64837621	2.59938369	1.73E-05	0.00020369
Tmem176b	1.336546	3.25080445	2.42E-05	0.00027422
Rasl10b	1.11164288	3.35429687	2.54E-05	0.00028482
Gm3604	1.21724528	3.15595196	2.84E-05	0.00031467
Mfsd3	1.16648039	2.97789471	3.10E-05	0.00033999
Dram1	1.11128011	3.02668789	3.15E-05	0.00034376
Slfn9	1.03632747	3.27160467	3.61E-05	0.00038778
Pllp	1.24821068	2.23589984	3.85E-05	0.00040783
Glmp	1.30896788	3.29877512	3.90E-05	0.00041209
Ctdsp1	1.00072956	3.3300604	4.32E-05	0.00045141
D030018L15	1.34411209	2.33521538	4.39E-05	0.00045754
Scg5	1.22410146	2.7713525	4.46E-05	0.00046109
Hsd17b11	1.22606797	2.21988321	4.76E-05	0.00048871
A530064D06	1.02120794	3.31627495	4.84E-05	0.00049562
Prrt3	1.11613185	2.6643065	5.21E-05	0.00052754
AA414768	1.31953954	2.15747887	5.53E-05	0.00055488
Ctag2	1.24594499	2.52555269	6.12E-05	0.00060337
Afmid	1.21594267	2.45969367	7.55E-05	0.00072353
Ccdc155	1.20368395	2.1433358	8.02E-05	0.00076341
Rhbdl1	1.22315786	1.99639765	8.04E-05	0.00076393
Cdh20	1.00482895	2.98698141	9.45E-05	0.00087547
Gm5113	1.02704826	3.16757164	0.00010269	0.00094037
Pla2g2d	1.16595426	2.53962099	0.00011063	0.00099981

Downregulated Genes in *Asz1* $^{-/-}$ gonocytes			
Zfp275	-1.0617811	2.63412941	0.00022341	0.00180803
Serpinc1	-1.1079316	2.64143642	0.00023433	0.00188419
4933402E13	-1.204501	2.78521901	0.00024459	0.00195031
Kitl	-1.3280851	2.6987501	0.00026127	0.00205572
Plp1	-1.3106186	1.85958112	0.00027309	0.0021299
Syce1l	-1.0940325	2.36244597	0.00028063	0.00218047
Rin1	-1.1035399	2.26614264	0.00029348	0.00226291
Fam114a1	-1.2870303	2.46705666	0.00029906	0.00229874
Kazald1	-1.8304188	2.11755019	0.00030972	0.00236235
Nr5a1	-1.0288375	2.70534653	0.00032326	0.00244908
Trappc6a	-1.0210933	2.4819844	0.00032986	0.00248702
Cd7	-1.1085912	2.20129955	0.00033368	0.00250694
AI854517	-1.041527	2.45875316	0.00034715	0.00258958
Rhox2d	-1.0836461	2.67689696	0.00036529	0.00270824
Slc22a23	-1.0410207	2.42471691	0.0003813	0.00280526
Zfpm2	-1.157357	2.98414833	0.00041088	0.00298417
Pappa2	-1.0273348	3.37582928	0.00042973	0.00310295
Tecta	-1.0980309	2.11446464	0.00044923	0.00321871
Amhr2	-1.0811351	2.35839598	0.00055524	0.00382741
Igf2os	-1.189105	2.34333131	0.00066478	0.0044211
Nedd9	-1.1402662	3.51436612	0.00073408	0.00480004
Col3a1	-1.166546	3.87349462	0.00082835	0.00529152
Fosb	-1.7087219	2.59054699	0.00087286	0.00553048
Il20rb	-1.0128593	2.09817777	0.00089182	0.00562769
Dsg2	-1.1886754	2.69010617	0.00094086	0.00587177
Pomc	-1.0414269	1.94895131	0.00095325	0.0059372
Pvrl2	-1.0260855	2.95773822	0.00095418	0.00593739
Mbtps2	-1.1349426	2.18660208	0.0015308	0.00877873
Akr1c12	-1.0303262	2.50632184	0.00156662	0.00893583

Supplementary Table 3. Significantly up- and down-regulated genes in *Asz1*^{-/-} mice gonocytes compared with those of wild-type mice.

Upregulated Genes in *Asz1*^{-/-} gonocytes					Downregulated Genes in *Asz1*^{-/-} gonocytes
Pts	1.04417683	3.54379918	0.00011736	0.00105304	
Sfi1	1.45291534	2.68719344	0.00013176	0.0011589	
Gcnt1	1.02894831	3.63222514	0.00015205	0.00130692	
Btnl9	1.07534017	2.44474206	0.00018623	0.00155144	
Tspyl3	1.01508708	2.68994318	0.00018895	0.00156887	
Ankrd42	1.00614367	3.04436994	0.00019371	0.00160302	
Gdap1	1.09981931	2.58851885	0.00022655	0.00183107	
Pomgnt2	1.1099916	2.48058521	0.0002572	0.00202748	
1700011M02	1.08653379	2.41364698	0.00026246	0.00206116	
Vipr1	1.02516757	3.28707543	0.00026875	0.00210234	
Gm5878	1.21645707	2.56553106	0.00027265	0.00212773	
Acer2	1.07982494	2.40997096	0.00029141	0.00224884	
Gm13238	1.05064983	2.62674161	0.00030474	0.00233289	
Vrtn	1.19256663	1.98309242	0.00031179	0.00237379	
Pik3r5	1.17183347	3.54136416	0.00032551	0.00246167	
Them6	1.02949771	2.58546603	0.00034148	0.00255454	
Azin2	1.05220094	2.67202935	0.00041312	0.0029969	
Tmem202	1.06865893	2.09922517	0.00043352	0.00312668	
Car4	1.14607823	2.23975147	0.00043747	0.00314971	
Slc16a9	1.00938917	2.84679917	0.00052259	0.00363655	
Ulbp1	1.03260766	2.26267478	0.0005761	0.00394503	
Wdfy2	1.08717979	2.87008547	0.00060486	0.00409917	
Cnga3	1.13936383	2.96351365	0.00098675	0.00609708	
Zfp345	1.01168075	2.48300926	0.00145843	0.00843563	

Supplementary Table 4. Genomic locations of aberrant chimeric transcript variant 5' exons.

Transcripts	Positions of 5' exons of aberrant chimeric transcript variants			strand
Gm9733	chr3	15334826	15335106	-
Fancd2	chr6	113543997	113544539	+
Cdh12	chr15	21565466	21565647	+
Rsrc1	chr3	67029941	67030201	+
4930558C23Rik	chr3	95406554	95406818	-
Hibch	chr1	52893921	52894101	+
Inadl	chr4	98454560	98454822	+
Grid1	chr14	35514545	35514841	+
Apoh	chr11	108404308	108404732	+
Eps8l1	chr7	4460644	4461024	+
Ccdc117	chr11	5535356	5535491	-
Spag16	chr1	69831740	69831850	+
Adtrp	chr13	41817115	41818458	-
l7Rn6	chr7	89943847	89944037	-
Zfp72	chr13	74384065	74384330	-
Mup3	chr4	62101373	62101531	-
Gabrr1	chr4	33123718	33124099	+
Gm16897	chr1	194970593	194970843	-
Ano4	chr10	89171040	89171506	-
Sec11a	chr7	80935296	80935446	-
Nrros	chr16	32148059	32148324	-
Abcb11	chr2	69268366	69268487	-
Sult2a5	chr7	13597405	13597722	+
Tomm7	chr5	23847706	23848012	-
Fam135a	chr1	24068223	24068622	-
Cyp20a1	chr1	60375742	60375925	+
Raver2	chr4	101128894	101129392	+
Esco2	chr14	65833536	65833651	-
Rb1cc1	chr1	6223598	6223745	+
Glrx2	chr1	143739814	143739979	+
Usp44	chr10	93833252	93833891	+
Aig1	chr10	13692246	13692427	-

Supplementary Table 5. Retrotransposons located within 1 kb upstream of the aberrant chimeric transcript variants.

Aberrant chimeric transcript variants	Retrotransposons within 1kb upstream of the transcripts
Gm9733	IAPLTR2_Mm,L1_Mus3,L1_Mus3
Rsrc1	IAPEz-int,IAPLTR1_Mm
Gm16897	IAP1-MM_LTR,PB1D11,MIRb
4930558C23Rik	IAPLTR2b,MuLV-int
Aig1	Lx7,L1_Rod,RLTR10A,RMER19B
Gabrr1	Lx9,Lx9,ORR1B1,RLTR10C,RLTR10C
Mup3	IAPLTR2b,B3A
Inadl	IAPLTR1_Mm
Raver2	IAPEz-int,IAPLTR1_Mm
Rb1cc1	PB1,B1_Mus2,B1_Mur2
Tomm7	LTRIS2,RLTR10A,B1_Mus2
Fancd2	IAPLTR2a,B3,B1_Mur3
Eps8l1	IAPEz-int,IAPLTR1_Mm
Sult2a5	L1Md_A
Sec11a	IAPLTR1a_Mm,MTE2a,ID_B1,B1_Mus1,B3
I7Rn6	IAPLTR2a,RLTR15,RLTR15,MYSERV16_I-int
Ano4	IAPLTR2a
Usp44	B3
Ccdc117	IAPLTR2_Mm,B2_Mm2,B3
Hibch	L1Md_A
Cyp20a1	RSINE1,IAPLTR2b,B2_Mm2
Apoh	IAPEz-int,IAPLTR1_Mm
Spag16	MTC,MTD,MTD,IAPLTR2b,B1_Mur4
Adtrp	IAPLTR2a,MIR,B4A
Zfp72	Lx7,Lx7,IAPLTR2b,RMER6BA
Grid1	ORR1A4,IAPLTR2_Mm
Esco2	B3A,MIRb
Cdh12	ORR1B1-int,ORR1B1,IAPLTR2b
Nrros	IAPLTR1_Mm,IAPEz-int
Glrx2	B1_Mm
Fam135a	Lx8,IAPLTR2_Mm,B1F2
Abcb11	IAPLTR2b