

Table A Summary of read number

Mapping Summary	R1	R2	L1	L2	M1	M2
Total Reads	81823434	97229756	56366502	95095060	47101384	49566142
Total Mapped Reads	69433435	83783153	48600531	81573996	33190081	34540993
Uniq-Mapped Reads	63971761	81782329	47417172	79577620	31726185	33063076
Muilti- Mapped Reads	1848499	2000824	11833859	1996367	1463896	1463896
Read-1	32512972	41181824	23814353	39774016	15867742	16513211
Read-2	31458789	40600505	23602819	38903604	15858443	16513211
Reads map to ‘+’	31940565	40823334	23666171	39741296	15846826	16536620
Reads map to ‘-’	32031196	40958995	23751001	39836324	15879359	16526456
Non-splice reads	52162994	65545223	38343370	64320295	31620334	32822369
Splice reads	11808767	16237106	9073802	15257325	105851	240707
Splice rate	18.50%	19.85%	19.14%	19.17%	0.33%	0.73%
Map_ Rate	84.86%	86.17%	86.22%	85.78%	70.47%	69.69%

Table B Common alternative splicing events in short and elongated spermatids and sperm during spermiogenesis

Alternative transcript events	Number detected (R1)	Number detected (R2)	Number detected (L1)	Number detected (L2)	Number detected (M1)	Number detected (M2)
Exon skipping	2298	2606	2180	2216	6	122
SKIP	1886	2126	1760	1822	4	102
XSKIP	166	226	222	190	0	14
MSKIP	208	218	176	174	0	6
XMSKIP	38	36	22	30	2	0

Intron retention	380	444	344	376	44	114
IR	278	328	246	286	20	60
XIR	92	106	92	80	22	52
MIR	6	6	6	4	0	2
XMIR	4	4	0	6	2	0
Alternative exon ends (5', 3', or both)	882	927	795	830	15	89
AE	818	871	757	778	12	76
XAE	64	56	38	52	3	13
Alternative first exon	24208	25935	21881	25257	2518	6006
Alternative last exon	23027	24733	20870	24299	2491	5846
Total	50795	54645	46070	52978	5074	12177

Table C Fifteen functional categories of DEGs in mouse spermatids during spermiogenesis

Functional Category	Terms Included	Number of Genes
Golgi apparatus	GO:0005794 GO:0044431 GO:0005802 GO:0048193 GO:0006888 GO:0005802 GO:0048193 GO:0005798	119
Acrosomal	GO:0043159 GO:0001669 GO:0001669	17
Centriole	GO:0005814	13
Mitochondrion	GO:0005739 GO:0005761 GO:0005759	118
Microtubule	GO:0007017 GO:0000226 GO:0044450	71

Flagellum	GO:0005930 GO:0019861	19
histone degradation	GO:0004386 GO:0042826	57
	GO:0043967 GO:0016570	
Protamine synthetizing	mmu00330	13
Ankyrin	IPR002110	17
chromosome condensing	GO:0006461 GO:0000794	76
	GO:0000793 GO:0016585	
	IPR000408	
transcription factor	GO:0006351 GO:0008134	41
	mmu03022 GO:0030528	
translation initiation factor activity	GO:0003743	19
MAPK signaling pathway	mmu04010	11
ncRNA metabolic process	GO:0034660	15
Spliceosome	mmu03040	23

Table D Primer sequences used for qPCR and relative levels of expression of ten genes in mature sperm, round spermatid and elongated spermatid of *Mus musculus*

Gene Name	Primers Sequence (5'-3')	Size (bp)
<i>Gkap1</i>	Forward: TGGGAAACAAAGCAACCT Reverse: CAAATGGAATGGGAGGAT	136
<i>Gabarap</i>	Forward: ACAATGTCATTCCACCCA Reverse: ACAGACCATAGACGCTTTC	111
<i>Tbpl1</i>	Forward: TCATGCCAGCTATGAACC Reverse: CAGTCGCCACAGCCTTTA	131
<i>Spaca4</i>	Forward: GCCTCACATACAGTCTCACCA Reverse: TGAAGCAGCAGCAACAGG	130
<i>Ndufb8</i>	Forward: TTCGGCTTTGTGGCTTTC Reverse: CGCTCCAGGTACAGATTATTG	110
<i>Atp5g1</i>	Forward: ATGCCAGGAACCCATCTC Reverse: GGAAGGCGACCATCAAAC	102

<i>Mbd2</i>	Forward: GGAGTCGGTCCAGGTAGCA Reverse: AAGCCAAACAGCAGGGTTC	126
<i>Hagh</i>	Forward: GAAGGTTTATGGAGGTGATG Reverse: AGTATGGCAGGGTGTTGA	115
<i>Atp5o</i>	Forward: TTCAGGTCTACGGCATCG Reverse: GCAGCAGCTCCTTCTCCA	96
<i>Tfam</i>	Forward: GGAATGTGGAGCGTGCTA Reverse: GCTACCCATGCTGGAAAA	126
<i>β-actin</i>	Forward: ACTCGCTGCGCTCGGTCGTT Reverse: CCTTTTGCTGGCCTTTTGCTCAC	125