

Supplementary Table S3. Genomic associations with post-cryopreservation sperm tail and neck abnormalities with regard to previously known candidate genes.

SNP	BTA ¹	SNP position (bp)	<i>p</i> -value	Alleles	SNP location	Candidate genes ²
ARS-BFGL-NGS-113327	18	12,295,233	3.50E-20	C/T	intergenic variant	<i>FOXF1</i> (84.6 Kb)
ARS-BFGL-NGS-116330	2	131,016,477	3.50E-20	A/G	intergenic variant	<i>ZBTB40</i> (76.4 Kb), <i>WNT4</i> (28.6 Kb)
ARS-BFGL-NGS-83728	11	94,227,167	3.50E-20	C/T	intron variant	<i>RABGAP1</i>
ARS-BFGL-NGS-98094	2	47,782,292	3.50E-20	C/T	intergenic variant	<i>EPC2</i> (132.3 Kb), <i>MBD5</i> (18.4 Kb)
ARS-BFGL-NGS-98828	9	20,117,983	3.50E-20	C/T	intergenic variant	<i>TTK</i> (42.3 Kb), <i>BCKDHB</i> (12.3 Kb)
BOVINEHD0600006887	6	25,017,431	3.50E-20	G/T	intron variant	<i>PPP3CA</i>
BOVINEHD1000004800	10	14,392,278	3.50E-20	A/G	intron variant	<i>MAP2K5</i>
BOVINEHD1500025946	15	65,145,149	3.50E-20	G/A	synonymous variant	<i>CD59</i>
BTA-73210-NO-RS	5	29,544,481	3.50E-20	G/A	intron variant	<i>DIP2B</i>
BTB-00401428	9	81,924,104	3.50E-20	A/G	intergenic variant	<i>AIG1</i> (90 Kb), <i>ADAT2</i> (16.4 Kb)
BTB-00671456	17	11,751,720	3.50E-20	T/G	3' UTR variant	<i>TTC29</i> , <i>POU4F2</i> (71 Kb)
BTB-01435781	17	11,466,582	3.50E-20	C/T	intergenic variant	<i>TTC29</i> (13.6 Kb)
BTB-01560502	1	5,880,498	3.50E-20	G/A	intron variant	<i>GRIK1</i>
HAPMAP38976-BTA- 71247	10	54,582,753	3.50E-20	G/T	intron variant	<i>NEDD4</i> (<i>esv4011968</i>)
HAPMAP39869-BTA- 78346	10	14,327,969	3.50E-20	T/C	upstream gene variant	<i>C10H15orf61</i>
HAPMAP41900-BTA- 54636	22	46,309,192	3.50E-20	C/T	intergenic variant	<i>WNT5A</i> (195.1 Kb)
HAPMAP45875-BTA- 37931	10	80,331,159	3.50E-20	A/T	intron variant	<i>RAD51B</i>
HAPMAP52726- RS29018162	12	44,326,840	3.50E-20	G/T	intron variant	<i>KLHL1</i>
HAPMAP54751- RS29013947	6	19,307,772	3.50E-20	C/T	intergenic variant	<i>DKK2</i> (73.7 Kb)
BTB-00403297	9	91,346,194	1.67E-07	A/C	intron variant	<i>RGS17</i>
HAPMAP44674-BTA- 84638	9	91,158,204	1.67E-07	G/T	intron variant	<i>RGS17</i>
BTA-122302-NO-RS	23	48,444,673	3.34E-07	T/G	intergenic variant	<i>LY86</i> (11.6 Kb), <i>F13A1</i> (186.9 Kb) <i>CLSPN</i> (10.9 Kb), <i>C3H1orf216</i> (8.2 Kb)
ARS-BFGL-NGS-107194	3	110,642,401	6.88E-07	T/C	intergenic variant	<i>PTPRQ</i>
BTB-00222372	5	10,278,129	7.95E-07	C/T	intron variant	<i>SLC2A10</i> (96.2 Kb), <i>U6</i> (16.4 Kb)
BTB-00894494	13	76,201,517	7.95E-07	A/C	intergenic variant	<i>ORC4</i>
ARS-BFGL-NGS-114697	2	48,356,704	9.56E-07	G/A	intron variant	
HAPMAP40994-BTA- 46361	19	61,630,610	9.56E-07	T/C	intergenic variant	<i>MAP2K6</i> (78.4 Kb)
BTA-74596-NO-RS	5	96,166,308	1.11E-06	G/A	intergenic variant	<i>ATF7IP</i> (25.1 Kb)
BTB-00389188	9	35,109,955	1.11E-06	C/T	intron variant	<i>FRK</i>
BTB-00880226	4	89,299,743	1.11E-06	G/A	intergenic variant	<i>TMEM229A</i> (62.8 Kb)

ARS-BFGL-NGS-104332	7	26,829,547	1.33E-06	A/G	intron variant	<i>FBN2</i>
ARS-BFGL-NGS-46105	9	90,247,980	1.39E-06	A/T	intron variant	<i>ESR1</i>
BTA-107369-NO-RS	8	101,683,774	1.39E-06	A/G	intron variant	<i>SVEP1</i>
ARS-BFGL-BAC-6557	1	1,234,172	1.44E-06	C/A	3' UTR variant	<i>SON</i>
ARS-BFGL-NGS-108850	26	42,896,381	1.44E-06	CTG/-	intergenic variant	<i>SPADH2</i> (9.5 Kb), <i>SPADH1</i> (17 Kb)
ARS-BFGL-BAC-12931	1	1,288,510	1.51E-06	A/G	intron variant	<i>GART</i>
ARS-BFGL-NGS-19833	4	113,416,523	2.37E-06	T/C	intergenic variant	<i>KRBA1</i> (20.4 Kb), <i>SSPO</i> (8.8 Kb)
HAPMAP24713-BTA-61641	26	42,033,314	3.33E-06	A/G	intergenic variant	<i>FGFR2</i> (102.3 Kb), <i>ATE1</i> (7.5 Kb)
ARS-BFGL-NGS-20623	26	43,687,318	4.52E-06	T/C	intergenic variant	<i>GPR26</i> (63.4 Kb)
ARS-BFGL-NGS-48262	26	33,191,302	4.52E-06	C/G	intron variant	<i>ACSL5</i>
BTA-61502-NO-RS	26	38,585,670	4.52E-06	G/A	intergenic variant	<i>RAB11FIP2</i> (27.3 Kb)
ARS-BFGL-NGS-96337	10	80,223,217	5.15E-06	C/A	intron variant	<i>ZFYVE26</i>
HAPMAP42436-BTA-114985	24	25,895,037	6.27E-06	T/C	intergenic variant	<i>TTR</i> (30.7 Kb), <i>DSG2</i> (19.1 Kb)
BTA-35174-NO-RS	14	63917588	8.14E-06	A/G	intergenic variant	<i>KLF10</i> (34.8 Kb)
BTA-50305-NO-RS	1	127568464	8.15E-06	G/A	intron variant	<i>ATR</i>
HAPMAP52436-RS29009653	6	99732094	8.15E-06	G/T	intron variant	<i>PLAC8A-202</i>
BOVINEHD0200036990	2	127435919	8.19E-06	T/C	intron variant	<i>CEP85</i>
BTB-01632102	9	32171013	9.78E-06	T/C	intron variant	<i>MAN1A1</i>

¹ BTA, *Bos taurus* chromosome. ² Distance from a significant SNP to the respective gene is given in parentheses.