

**Supplementary Table S4.** Genomic associations with post-cryopreservation sperm tail and neck abnormalities with regard to previously unknown candidate genes.

SNP	BTA <sup>1</sup>	SNP position (bp)	<i>p</i> -value	Alleles	SNP location	Candidate genes <sup>2</sup>
ARS-BFGL-NGS-113327	18	12,295,233	3.50E-20	C/T	intergenic variant	<i>ENSBTAG00000054270</i> (113.9 Kb)
BOVINEHD2400014613	24	51,876,107	3.50E-20	C/T	intergenic variant	<i>ENSBTAG00000051721</i> (105 Kb), <i>ENSBTAG00000049503</i> (54.6 Kb)
BTB-01402723	10	94,482,815	3.50E-20	A/G	intron variant	<i>ENSBTAG00000050021</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>ENSBTAG00000049764</i> (47.7 Kb)
HAPMAP39377-BTA-113470	21	36,623,599	4.84E-07	A/C	intergenic variant	<i>ENSBTAG00000054263</i> (66.2 Kb)
ARS-BFGL-NGS-107194	3	110,642,401	6.88E-07	T/C	intergenic variant	<i>C3H1orf216</i> (8.2 Kb)
HAPMAP40994-BTA-46361	19	61,630,610	9.56E-07	T/C	intergenic variant	<i>ENSBTAG00000049077</i> (34.1 Kb)
BTA-74596-NO-RS	5	96,166,308	1.11E-06	G/A	intergenic variant	<i>ENSBTAG00000051346</i> (93.4 Kb)
HAPMAP48384-BTA-54234	22	35,354,500	1.44E-06	G/A	intergenic variant	<i>ENSBTAG00000051801</i> (17.7 Kb)
BTA-61502-NO-RS	26	38,585,670	4.52E-06	G/A	intergenic variant	<i>ENSBTAG00000049634</i> (199.2 Kb)
BTA-35174-NO-RS	14	63,917,588	8.14E-06	A/G	intergenic variant	<i>ENSBTAG00000052148</i> (58.7 Kb)
ARS-BFGL-NGS-18962	1	130,517,998	8.15E-06	T/C	synonymous variant	<i>ENSBTAG00000051936</i>
ARS-BFGL-NGS-73903	23	49,725,139	8.19E-06	A/G	intergenic variant	<i>ENSBTAG000000513166</i> (115.3 Kb), <i>ENSBTAG00000052017</i>

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