Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA3 QTL in males

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
53642047	T	C	0,872	0,14111	-0,7880366	7,9465E-12	EFF=INTERGENIC(MODIFIER||||||||)
53642233	A	G	0,874	0,140913	-0,7890053	8,1742E-12	EFF=INTERGENIC(MODIFIER||||||||)
53644767	G	A	0,904	0,137347	-0,7785415	2,9081E-11	EFF=INTERGENIC(MODIFIER||||||||)
53643984	T	C	0,905	0,137255	-0,7777605	3,0784E-11	EFF=INTERGENIC(MODIFIER||||||||)
53641388	C	T	0,913	0,137459	-0,7740791	3,378E-11	EFF=INTERGENIC(MODIFIER||||||||)
53642816	A	C	0,909	0,13736	-0,775255	3,42E-11	EFF=INTERGENIC(MODIFIER||||||||)
53642173	G	T	0,917	0,137687	-0,7751592	3,433E-11	EFF=INTERGENIC(MODIFIER||||||||)
53639333	T	C	0,94	0,1364	-0,7641587	6,5587E-11	EFF=INTERGENIC(MODIFIER||||||||)
53639087	C	T	0,921	0,138535	-0,7483931	1,0565E-10	EFF=INTERGENIC(MODIFIER||||||||)
53631012	G	A	0,986	0,134583	-0,7381945	2,3741E-10	EFF=INTERGENIC(MODIFIER||||||||)
53638851	C	T	0,951	0,134431	-0,7462741	2,8782E-10	EFF=INTERGENIC(MODIFIER||||||||)
53646068	C	T	0,919	0,133313	-0,7406969	4,5111E-10	EFF=INTERGENIC(MODIFIER||||||||)
53635665	T	G	0,987	0,134378	-0,7069511	1,189E-09	EFF=INTERGENIC(MODIFIER||||||||)
53636311	A	G	0,988	0,134425	-0,7057608	1,2553E-09	EFF=INTERGENIC(MODIFIER||||||||)
53637010	G	A	0,977	0,134118	-0,7068752	1,2984E-09	EFF=INTERGENIC(MODIFIER||||||||)
53637846	G	A	0,963	0,132825	-0,7119708	1,3056E-09	EFF=INTERGENIC(MODIFIER||||||||)
53641464	A	G	0,936	0,127337	-0,7142502	5,4331E-09	EFF=INTERGENIC(MODIFIER||||||||)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA3 QTL in females

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
52179921	A	C	0,88	0,18	-0,40	2,05E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|18)
52179777	G	A	0,88	0,18	-0,40	2,05E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|18)
52200042	A	C	0,88	0,18	-0,40	2,06E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|24)
52214908	C	T	0,88	0,18	-0,40	2,06E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|29)
52227983	C	T	0,88	0,18	-0,40	2,12E-07	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tCa/tTa|S1189L|HFM1|protein_coding|CODING|ENSBTAT00000027789|31)
52221343	G	A	0,89	0,18	-0,40	2,12E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|29)
52222317	G	A	0,89	0,18	-0,40	2,12E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|29)
52169462	T	A	0,85	0,18	-0,40	2,35E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|10)
52164943	C	G	0,86	0,18	-0,40	2,72E-07	EFF=INTRON(MODIFIER||||HFM1|protein_coding|CODING|ENSBTAT00000027789|5)
52129098	G	C	0,84	0,18	-0,40	3,93E-07	EFF=INTERGENIC(MODIFIER||||||||)

Note: these two signals are linked
The variants capture the same haplotype effect
In males from INRA population, r^2 > 0,90 between the two sets and similar significance is achieved
Using the best imputed genotypes only (doses close to 0, 1 or 2), the r^2 > 0.90 between the two sets

Credible set of variants (r^2 > 0.90 with the lead variant) associated with second BTA3 QTL in females

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
69238413	T	A	0,83	0,20	-0,52	2,5386E-10	EFF=INTRON(MODIFIER|||MSH4|protein_coding|CODING|ENSBTAT00000024552|16|WARNING_TRANSCRIPT_NO_START_CODON)
69200566	C	T	0,87	0,20	-0,50	4,4661E-10	EFF=INTRON(MODIFIER|||ASB17|protein_coding|CODING|ENSBTAT00000007708|1)
69186209	G	A	0,85	0,20	-0,51	4,4674E-10	EFF=INTERGENIC(MODIFIER|||||||)
69179842	C	G	0,86	0,20	-0,50	4,6883E-10	EFF=UPSTREAM(MODIFIER||401||U6|snRNA|NON_CODING|ENSBTAT00000060003|)
69165586	C	A	0,87	0,20	-0,50	4,9443E-10	EFF=INTERGENIC(MODIFIER|||||||)
69225396	C	T	0,84	0,20	-0,51	5,2499E-10	EFF=INTRON(MODIFIER|||MSH4|protein_coding|CODING|ENSBTAT00000024552|17|WARNING_TRANSCRIPT_NO_START_CODON)
69130931	G	T	0,88	0,20	-0,50	6,267E-10	EFF=INTERGENIC(MODIFIER|||||||)
69136214	T	C	0,87	0,20	-0,50	6,4178E-10	EFF=INTERGENIC(MODIFIER|||||||)
69133518	C	T	0,87	0,20	-0,50	6,4395E-10	EFF=INTERGENIC(MODIFIER|||||||)
69162292	GAT	GATAT,GATA	0,55	0,21	-0,50	1,1621E-09	EFF=INTERGENIC(MODIFIER|||||||)
69262712	T	G	0,83	0,20	-0,50	1,2373E-09	EFF=INTRON(MODIFIER|||MSH4|protein_coding|CODING|ENSBTAT00000024552|9|WARNING_TRANSCRIPT_NO_START_CODON)
69264727	A	G	0,84	0,20	-0,49	1,273E-09	EFF=INTRON(MODIFIER|||MSH4|protein_coding|CODING|ENSBTAT00000024552|8|WARNING_TRANSCRIPT_NO_START_CODON)
69267679	A	T	0,84	0,20	-0,49	1,6241E-09	EFF=INTRON(MODIFIER|||MSH4|protein_coding|CODING|ENSBTAT00000024552|8|WARNING_TRANSCRIPT_NO_START_CODON)

Information on the *MSH4* NS variant presenting high association with female GRR but outside the credible set of variants (it does not account for all the QTL signal)

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
69267975	C	T	0,65	0,23	-0,37	1,8438E-06	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tGc/tAc|C342Y|MSH4|protein_coding|CODING|ENSBTAT00000024552|8|WARNING_TRANSCRIPT_NO_START_CODON)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA6 QTL in males

Position (Bos Tau7)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF	Position (UMD3.1)	Manual annotation (UMD3.1)
118147157	G	A	0,87	0,24	0,88	2,63E-25	EFF=INTERGENIC(MODIFIER|||||||)	109130457	intronic FGFRL1
118147156	T	C	0,85	0,25	0,88	2,73E-25	EFF=INTERGENIC(MODIFIER|||||||)	109130456	intronic FGFRL1
118134513	G	A	0,87	0,24	0,88	5,77E-25	EFF=INTERGENIC(MODIFIER|||||||)	109113935	intronic FGFRL1 / intronic CPLX1
118137317	G	A	0,83	0,23	0,89	5,94E-25	EFF=INTERGENIC(MODIFIER|||||||)	109116743	intronic FGFRL1 / intronic CPLX1
118169324	C	T	0,93	0,24	0,87	6,20E-25	EFF=INTERGENIC(MODIFIER|||||||)	109152624	downstream JZ078754 (RNF212)
118165256	C	T	0,92	0,24	0,87	7,32E-25	EFF=INTERGENIC(MODIFIER|||||||)	109148556	intergenic
118173534	G	A	0,93	0,23	0,87	8,03E-25	EFF=INTERGENIC(MODIFIER|||||||)	109156773	NS P259S RNF212 (JZ078754)
118128593	G	A	0,88	0,24	0,87	8,11E-25	EFF=INTERGENIC(MODIFIER|||||||)	109108015	intronic FGFRL1 / intronic CPLX1
118176701	G	A	0,93	0,23	0,86	1,91E-24	EFF=INTERGENIC(MODIFIER|||||||)	109159940	intronic JZ078754 (RNF212)
118137607	G	A	0,67	0,22	0,84	2,37E-21	EFF=DOWNSTREAM(MODIFIER||4736||ENSBTAG00000046933|pseudogene|NON_CODING|ENSBTAT000000	109117033	intronic FGFRL1 / intronic CPLX1

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA6 QTL in females

Position (Bos Tau7)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF	Position (UMD3.1)	Manual annotation (UMD3.1)
118137317	G	A	0,83	0,21	0,63	1,56E-16	EFF=INTERGENIC(MODIFIER|||||||)	109116743	intronic FGFRL1 / intronic CPLX1
118147157	G	A	0,87	0,22	0,61	1,78E-16	EFF=INTERGENIC(MODIFIER|||||||)	109130457	intronic FGFRL1
118134513	G	A	0,87	0,22	0,61	2,36E-16	EFF=INTERGENIC(MODIFIER|||||||)	109113935	intronic FGFRL1 / intronic CPLX1
118128593	G	A	0,88	0,22	0,61	2,67E-16	EFF=INTERGENIC(MODIFIER|||||||)	109108015	intronic FGFRL1 / intronic CPLX1
118176701	G	A	0,93	0,22	0,60	3,11E-16	EFF=INTERGENIC(MODIFIER|||||||)	109159940	intronic JZ078754 (RNF212)
118173534	G	A	0,93	0,22	0,60	3,16E-16	EFF=INTERGENIC(MODIFIER|||||||)	109156773	NS P259S RNF212 (JZ078754)
118169324	C	T	0,93	0,22	0,59	3,39E-16	EFF=INTERGENIC(MODIFIER|||||||)	109152624	downstream JZ078754 (RNF212)
118137607	G	A	0,67	0,20	0,68	3,96E-16	EFF=DOWNSTREAM(MODIFIER||4736||ENSBTAG00000046933|pseudogene|NON_CODING|ENSBTAT000000	109117033	intronic FGFRL1 / intronic CPLX1
118165256	C	T	0,92	0,22	0,59	4,96E-16	EFF=INTERGENIC(MODIFIER|||||||)	109148556	intergenic
118147156	T	C	0,85	0,23	0,59	1,27E-15	EFF=INTERGENIC(MODIFIER|||||||)	109130456	intronic FGFRL1

Credible set of variants (r^2 > 0.90 with the focal variant) associated with secondary BTA6 signal in males from New-Zealand population

Position (Bos Tau7)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF	Position (UMD3.1)	Manual annotation UMD3.1
119117260	C	A	0,69	0,04	-1,96	3,80E-16	EFF=INTRON(MODIFIER||||POLN|protein_coding|CODING|ENSBTAT00000023023|17)	108653486	intronic POLN
118987973	C	A	0,76	0,04	-1,90	4,94E-16	EFF=INTERGENIC(MODIFIER||||||||)	109854107	intergenic
118988834	C	T	0,76	0,04	-1,90	4,99E-16	EFF=INTERGENIC(MODIFIER||||||||)	109854968	intergenic
118987643	T	A	0,76	0,04	-1,90	5,26E-16	EFF=INTERGENIC(MODIFIER||||||||)	109853777	intergenic
118987651	A	AC	0,76	0,04	-1,90	5,32E-16	EFF=INTERGENIC(MODIFIER||||||||)	109853785	intergenic
118987780	G	T	0,77	0,04	-1,90	5,35E-16	EFF=INTERGENIC(MODIFIER||||||||)	109853914	intergenic
118987645	C	A	0,76	0,04	-1,90	5,36E-16	EFF=INTERGENIC(MODIFIER||||||||)	109853779	intergenic
118993083	G	A	0,76	0,04	-1,89	5,58E-16	EFF=INTERGENIC(MODIFIER||||||||)	109859218	intergenic
118984693	G	A	0,75	0,04	-1,91	6,03E-16	EFF=INTERGENIC(MODIFIER||||||||)	109850828	intergenic
118989475	A	G	0,76	0,04	-1,89	6,91E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855609	intergenic
118989180	T	C	0,76	0,04	-1,89	6,94E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855314	intergenic
118989186	G	A	0,76	0,04	-1,89	6,98E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855320	intergenic
118989185	T	C	0,76	0,04	-1,89	7,01E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855319	intergenic
118989123	A	G	0,76	0,04	-1,89	7,01E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855257	intergenic
118983781	G	A	0,76	0,04	-1,91	7,06E-16	EFF=UPSTREAM(MODIFIER||3575||WHSC2|protein_coding|CODING|ENSBTAT0000002	109849112	intergenic + NELFA (less than 5 kb)
118989315	C	T	0,76	0,04	-1,89	7,07E-16	EFF=INTERGENIC(MODIFIER||||||||)	109855449	intergenic
118990969	C	G	0,76	0,04	-1,89	7,17E-16	EFF=INTERGENIC(MODIFIER||||||||)	109857103	intergenic
119149263	A	G	0,59	0,05	-1,73	6,21E-15	EFF=INTRON(MODIFIER||||POLN|protein_coding|CODING|ENSBTAT00000023023|11)	108623237	intronic POLN
119095352	T	G	0,79	0,04	-1,59	2,38E-14	EFF=INTRON(MODIFIER||||POLN|protein_coding|CODING|ENSBTAT00000023023|17)	108676667	intronic POLN
119099134	G	T	0,79	0,04	-1,59	2,42E-14	EFF=INTRON(MODIFIER||||POLN|protein_coding|CODING|ENSBTAT00000023023|17)	108672891	intronic POLN
118193274	C	T	0,603	0,0649482	-1,43506	5,26E-17	EFF=INTERGENIC(MODIFIER||||||||)	109176513	NS A77T RNF212 5JZ078754

*The mapping of the last variant is described in supplementary materials

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in males

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
21434967	C	A	0,97	0,14	1,26	4,21E-35	EFF=UPSTREAM(MODIFIER||951||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21447979	C	T	0,90	0,14	1,31	6,67E-35	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgc/Tgc|R142C|PPP1R3E|protein_coding|CODING|ENSBTAT00000052538|2)
21437447	T	C	1,00	0,15	1,22	1,16E-34	EFF=UPSTREAM(MODIFIER||3431||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21435508	C	A	0,97	0,15	1,25	1,49E-34	EFF=UPSTREAM(MODIFIER||1492||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21433130	C	CT	0,94	0,15	1,25	1,94E-34	EFF=UTR_5_PRIME(MODIFIER||1210||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21433368	T	C	0,94	0,15	1,25	1,95E-34	EFF=UTR_5_PRIME(MODIFIER||1447||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21432767	GTTC	G	0,94	0,15	1,25	2,19E-34	EFF=UTR_5_PRIME(MODIFIER||847||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21433509	A	G	0,94	0,14	1,26	2,41E-34	EFF=UTR_5_PRIME(MODIFIER||1588||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21439886	T	C	0,96	0,15	1,23	3,11E-34	EFF=UTR_3_PRIME(MODIFIER||1595||BCL2L2|protein_coding|CODING|ENSBTAT00000026248|4)
21469710	G	A	0,90	0,14	1,30	5,55E-34	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21461898	C	CA	0,91	0,14	1,28	5,66E-34	EFF=DOWNSTREAM(MODIFIER||4438||RNF212B|protein_coding|CODING|ENSBTAT00000036401|)
21470293	C	T	0,90	0,14	1,30	7,52E-34	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21464136	A	AGAGGAG	0,91	0,14	1,31	7,61E-34	EFF=DOWNSTREAM(MODIFIER||2200||RNF212B|protein_coding|CODING|ENSBTAT00000036401|)
21470834	A	G	0,90	0,14	1,29	8,18E-34	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21469776	C	T	0,90	0,14	1,30	8,40E-34	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21471661	C	T	0,90	0,14	1,30	1,04E-33	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21456962	C	A	0,91	0,14	1,30	1,07E-33	EFF=INTERGENIC(MODIFIER||||||||)
21433559	CAA	C	0,94	0,14	1,25	2,53E-33	EFF=UTR_5_PRIME(MODIFIER||1639||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21472225	C	CA,CAAA,CA	0,79	0,13	1,38	5,50E-33	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21446789	C	G	0,99	0,15	1,09	1,01E-28	EFF=UPSTREAM(MODIFIER||3215||BCL2L2|protein_coding|CODING|ENSBTAT00000026248|)
21446724	T	G	1,00	0,15	1,08	2,15E-28	EFF=UPSTREAM(MODIFIER||3150||BCL2L2|protein_coding|CODING|ENSBTAT00000026248|)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in females

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
21461898	C	CA	0,91	0,12	0,94	9,47E-25	EFF=DOWNSTREAM(MODIFIER||4438||RNF212B|protein_coding|CODING|ENSBTAT00000036401|)
21471661	C	T	0,90	0,12	0,96	9,84E-25	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21470834	A	G	0,90	0,12	0,95	1,09E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21469776	C	T	0,90	0,12	0,95	1,12E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21469710	G	A	0,90	0,12	0,95	1,17E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21470293	C	T	0,90	0,12	0,95	1,20E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21456962	C	A	0,91	0,11	0,96	1,91E-24	EFF=INTERGENIC(MODIFIER||||||||)
21478929	T	A	0,90	0,11	0,97	2,18E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|6)
21472613	G	A	0,90	0,11	0,96	2,93E-24	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21464136	A	AGAGGAG	0,91	0,11	0,97	3,95E-24	EFF=DOWNSTREAM(MODIFIER||2200||RNF212B|protein_coding|CODING|ENSBTAT00000036401|)
21447979	C	T	0,90	0,12	0,93	1,11E-23	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|Cgc/Tgc|R142C|PPP1R3E|protein_coding|CODING|ENSBTAT00000052538|2)
21434967	C	A	0,97	0,12	0,90	2,96E-23	EFF=UPSTREAM(MODIFIER||951||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21439886	T	C	0,96	0,12	0,87	1,02E-22	EFF=UTR_3_PRIME(MODIFIER||1595||BCL2L2|protein_coding|CODING|ENSBTAT00000026248|4)
21472225	C	CA,CAAA,CA	0,79	0,10	1,02	1,02E-22	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21476907	C	G,A	0,91	0,12	0,91	1,38E-22	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|10)
21435508	C	A	0,97	0,12	0,88	1,48E-22	EFF=UPSTREAM(MODIFIER||1492||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21478867	A	G	0,90	0,12	0,91	1,55E-22	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|6)
21478701	GA	G	0,90	0,12	0,91	1,64E-22	EFF=INTRON(MODIFIER||||RNF212B|protein_coding|CODING|ENSBTAT00000036401|6)
21437447	T	C	1,00	0,12	0,86	1,87E-22	EFF=UPSTREAM(MODIFIER||3431||PABPN1|protein_coding|CODING|ENSBTAT00000021887|)
21433509	A	G	0,94	0,12	0,88	1,93E-22	EFF=UTR_5_PRIME(MODIFIER||1588||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21433130	C	CT	0,94	0,12	0,87	2,34E-22	EFF=UTR_5_PRIME(MODIFIER||1210||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21433368	T	C	0,94	0,12	0,87	2,35E-22	EFF=UTR_5_PRIME(MODIFIER||1447||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21432767	GTTC	G	0,94	0,12	0,87	2,50E-22	EFF=UTR_5_PRIME(MODIFIER||847||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)
21433559	CAA	C	0,94	0,12	0,89	4,15E-22	EFF=UTR_5_PRIME(MODIFIER||1639||PABPN1|protein_coding|CODING|ENSBTAT00000021887|1)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in males

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
21493479	A	T	0,931	0,533018	-0,6475834	4,6558E-24	EFF=INTRON(MODIFIER|||RNF212B|protein_coding|CODING|ENSBTAT00000036401|1)
21494816	T	C	0,978	0,499326	-0,6077077	3,5898E-22	EFF=UPSTREAM(MODIFIER||120||RNF212B|protein_coding|CODING|ENSBTAT00000036401|)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in females from New-Zealand population

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
21494628	G	A	0,867	0,123488	-1,1601585	9,2748E-14	EFF=SYNONYMOUS_CODING(LOW|SILENT|ggC/ggT|G23|RNF212B|protein_coding|CODING|ENSBTAT00000036401|1)

Note: these two signals are independent (low LD)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in females

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
86631169	C	T	0,95	0,40	0,79	1,84E-24	EFF=INTERGENIC(MODIFIER||||||||)
86664489	CT	C,CTT	0,66	0,38	0,88	1,65E-24	EFF=DOWNSTREAM(MODIFIER||3148||EIF2B2|protein_coding|CODING|ENSBTAT00000011424|)
86673101	A	G	0,93	0,37	0,73	3,88E-19	EFF=INTRON(MODIFIER||||MLH3|protein_coding|CODING|ENSBTAT00000061421|10)
86680485	T	C	0,96	0,39	0,79	7,47E-25	EFF=INTRON(MODIFIER||||MLH3|protein_coding|CODING|ENSBTAT00000061421|6)
86693617	T	C	0,97	0,40	0,77	1,43E-24	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAt/aGt|N408S|MLH3|protein_coding|CODING|ENSBTAT00000061421|1)
86702295	G	C	0,98	0,40	0,77	1,49E-24	EFF=UTR_3_PRIME(MODIFIER||5||ACYP1|protein_coding|CODING|ENSBTAT00000018595|3)
86706386	C	T	0,97	0,40	0,77	1,52E-24	EFF=INTRON(MODIFIER||||ACYP1|protein_coding|CODING|ENSBTAT00000018595|2)
86706846	C	T	0,98	0,40	0,77	1,54E-24	EFF=INTRON(MODIFIER||||ACYP1|protein_coding|CODING|ENSBTAT00000018595|2)
86709241	T	C,G	0,98	0,59	-0,73	4,78E-22	EFF=UPSTREAM(MODIFIER||863||ACYP1|protein_coding|CODING|ENSBTAT00000018595|)
86709874	C	A	0,98	0,40	0,76	3,41E-24	EFF=UPSTREAM(MODIFIER||1496||ACYP1|protein_coding|CODING|ENSBTAT00000018595|)
86711494	C	T	0,99	0,40	0,77	1,68E-24	EFF=UPSTREAM(MODIFIER||3116||ACYP1|protein_coding|CODING|ENSBTAT00000018595|)
86713312	G	A	0,92	0,38	0,79	1,10E-24	EFF=UPSTREAM(MODIFIER||4934||ACYP1|protein_coding|CODING|ENSBTAT00000018595|)
86717378	T	C	1,00	0,41	0,71	1,10E-21	EFF=INTRON(MODIFIER|||ZC2HC1C|protein_coding|CODING|ENSBTAT00000018587|1)
86720487	C	T	0,98	0,41	0,72	1,03E-21	EFF=INTRON(MODIFIER|||ZC2HC1C|protein_coding|CODING|ENSBTAT00000018587|1)
86720872	G	T	0,99	0,41	0,72	9,93E-22	EFF=INTRON(MODIFIER|||ZC2HC1C|protein_coding|CODING|ENSBTAT00000018587|1)
86723060	C	T	0,97	0,39	0,79	8,31E-25	EFF=DOWNSTREAM(MODIFIER||813||ZC2HC1C|protein_coding|CODING|ENSBTAT00000018587|)
86728875	AT	A	0,98	0,41	0,72	1,07E-21	EFF=INTRON(MODIFIER|||NEK9|protein_coding|CODING|ENSBTAT00000022098|21|WARNING_TRANSCRIPT_NO_START_CODON)
86729453	T	C	0,98	0,41	0,72	1,07E-21	EFF=INTRON(MODIFIER|||NEK9|protein_coding|CODING|ENSBTAT00000022098|21|WARNING_TRANSCRIPT_NO_START_CODON)
86732671	ATTTC	A	0,98	0,40	0,77	1,74E-24	EFF=INTRON(MODIFIER|||NEK9|protein_coding|CODING|ENSBTAT00000022098|19|WARNING_TRANSCRIPT_NO_START_CODON)
86732855	G	C	0,97	0,42	0,72	1,20E-21	EFF=INTRON(MODIFIER|||NEK9|protein_coding|CODING|ENSBTAT00000022098|19|WARNING_TRANSCRIPT_NO_START_CODON)
86738051	C	T	0,98	0,40	0,77	1,53E-24	EFF=INTRON(MODIFIER|||NEK9|protein_coding|CODING|ENSBTAT00000022098|16|WARNING_TRANSCRIPT_NO_START_CODON)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA10 QTL in females

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
86673101	A	G	0,93	0,41	0,52	3,56E-15	EFF=INTRON(MODIFIER||||MLH3|protein_coding|CODING|ENSBTAT00000061421|10)
86751935	C	T	0,91	0,41	0,52	3,57E-15	EFF=INTRON(MODIFIER||||NEK9|protein_coding|CODING|ENSBTAT00000022098|7|WARNING_TRANSCRIPT_NO_START_CODON)
86755249	G	T	0,95	0,41	0,51	3,57E-15	EFF=INTRON(MODIFIER||||NEK9|protein_coding|CODING|ENSBTAT00000022098|5|WARNING_TRANSCRIPT_NO_START_CODON)
86768372	T	G	0,98	0,42	0,48	2,46E-14	EFF=DOWNSTREAM(MODIFIER||1749||TMED10|protein_coding|CODING|ENSBTAT00000007481|)
86766231	CAT	C	0,98	0,41	0,49	2,49E-14	EFF=DOWNSTREAM(MODIFIER||3889||TMED10|protein_coding|CODING|ENSBTAT00000007481|)
86766800	G	A	0,98	0,42	0,48	2,60E-14	EFF=DOWNSTREAM(MODIFIER||3321||TMED10|protein_coding|CODING|ENSBTAT00000007481|)
86763787	ATATT	A	0,97	0,41	0,49	2,85E-14	EFF=INTERGENIC(MODIFIER||||||||)
86772070	A	G	1,00	0,41	0,48	3,20E-14	EFF=INTRON(MODIFIER|||TMED10|protein_coding|CODING|ENSBTAT00000007481|5)
86764892	AGG	A	0,98	0,42	0,49	3,29E-14	EFF=INTERGENIC(MODIFIER||||||||)
86764891	G	T	0,98	0,42	0,49	3,30E-14	EFF=INTERGENIC(MODIFIER||||||||)
86768306	G	A	0,98	0,42	0,48	3,98E-14	EFF=DOWNSTREAM(MODIFIER||1815||TMED10|protein_coding|CODING|ENSBTAT00000007481|)
86680485	T	C	0,96	0,43	0,49	5,34E-14	EFF=INTRON(MODIFIER||||MLH3|protein_coding|CODING|ENSBTAT00000061421|6)
86693617	T	C	0,97	0,43	0,48	6,72E-14	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aAt/aGt|N408S|MLH3|protein_coding|CODING|ENSBTAT00000061421|1)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA18 QTL in males from New-Zealand population

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
54529525	A	G	0,65	0,62	-0,54	8,98E-09	EFF=DOWNSTREAM(MODIFIER||3426||TMEM160|protein_coding|CODING|ENSBTAT00000020695|)
54531020	T	A	0,95	0,74	-0,42	2,36E-06	EFF=DOWNSTREAM(MODIFIER||1931||TMEM160|protein_coding|CODING|ENSBTAT00000020695|)
54531573	T	C	0,95	0,74	-0,42	2,39E-06	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|gTg/gCg|V420A|NPAS1|protein_coding|CODING|ENSBTAT00000020691|10)

Credible set of variants (r^2 > 0.90 with the lead variant) associated with BTA23 QTL in males

Position (Bos Tau6)	Reference allele	Alternative allele	Imputation Accuracy	Frequency	Effect	P-value	Annotation with snpEFF
27552408	T	C	0,94	0,05	-1,18	1,90E-13	EFF=INTRON(MODIFIER||||NFKBIL1|protein_coding|CODING|ENSBTAT00000019268|2)
27556583	T	C	0,97	0,05	-1,17	1,99E-13	EFF=UPSTREAM(MODIFIER||4997||ATP6V1G2|protein_coding|CODING|ENSBTAT00000019267|)
27555428	G	A	0,97	0,05	-1,17	2,01E-13	EFF=INTRON(MODIFIER||||NFKBIL1|protein_coding|CODING|ENSBTAT00000019268|2)
27555785	A	G	0,97	0,05	-1,17	2,01E-13	EFF=INTRON(MODIFIER||||NFKBIL1|protein_coding|CODING|ENSBTAT00000019268|2)
27377717	C	T	0,70	0,05	-1,23	2,67E-13	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|cGa/cAa|R631Q|MSH5|protein_coding|CODING|ENSBTAT00000026367|20)
27561840	G	C	0,92	0,05	-1,17	2,75E-13	EFF=UPSTREAM(MODIFIER||1212||NFKBIL1|protein_coding|CODING|ENSBTAT00000035817|)
27551876	T	C	0,96	0,05	-1,16	2,77E-13	EFF=INTRON(MODIFIER||||NFKBIL1|protein_coding|CODING|ENSBTAT00000019268|2)
27551895	A	G	0,96	0,05	-1,16	2,77E-13	EFF=INTRON(MODIFIER||||NFKBIL1|protein_coding|CODING|ENSBTAT00000019268|2)
27435921	T	A	0,99	0,05	-1,15	3,44E-13	EFF=DOWNSTREAM(MODIFIER||203||ABHD16A|protein_coding|CODING|ENSBTAT00000000755|)
27431131	C	G	0,99	0,05	-1,14	4,49E-13	EFF=INTRON(MODIFIER|||ABHD16A|protein_coding|CODING|ENSBTAT00000000755|7)
27573659	C	T	0,88	0,05	-1,21	4,69E-13	EFF=DOWNSTREAM(MODIFIER||2271||SNORD83|snoRNA|NON_CODING|ENSBTAT00000060475|)
27529226	G	A	0,69	0,05	-1,23	9,15E-13	EFF=UPSTREAM(MODIFIER||630||LTB|protein_coding|CODING|ENSBTAT00000027554|)
27244422	G	A	0,79	0,05	-1,20	1,20E-12	EFF=UPSTREAM(MODIFIER||1072||C2|protein_coding|CODING|ENSBTAT00000045436|)
27243216	G	T,A	0,92	0,05	-1,11	1,30E-12	EFF=INTRON(MODIFIER|||C2|protein_coding|CODING|ENSBTAT00000009798|1)
27252191	G	A	0,94	0,05	-1,14	1,44E-12	EFF=INTERGENIC(MODIFIER||||||||)
27241591	A	G	0,93	0,05	-1,14	1,45E-12	EFF=INTRON(MODIFIER|||C2|protein_coding|CODING|ENSBTAT00000009798|3)
27298179	CCTT	C	0,95	0,05	-1,12	1,48E-12	EFF=INTRON(MODIFIER|||SLC44A4|protein_coding|CODING|ENSBTAT00000045367|9)
27256840	A	T	0,95	0,05	-1,13	1,53E-12	EFF=INTERGENIC(MODIFIER||||||||)
27240172	T	A	0,79	0,05	-1,18	1,55E-12	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|tAc/tTc|Y210F|C2|protein_coding|CODING|ENSBTAT00000009798|5)
27242073	A	G	0,93	0,05	-1,14	1,56E-12	EFF=INTRON(MODIFIER|||C2|protein_coding|CODING|ENSBTAT00000009798|3)
27262046	G	A	0,96	0,05	-1,13	1,57E-12	EFF=INTERGENIC(MODIFIER||||||||)
27268266	C	T	0,96	0,05	-1,13	1,60E-12	EFF=INTERGENIC(MODIFIER||||||||)
27293140	C	T	0,94	0,05	-1,12	1,60E-12	EFF=INTRON(MODIFIER|||SLC44A4|protein_coding|CODING|ENSBTAT00000045367|1)
27293082	A	C	0,91	0,05	-1,13	1,61E-12	EFF=INTRON(MODIFIER|||SLC44A4|protein_coding|CODING|ENSBTAT00000045367|1)
27242318	A	G	0,93	0,05	-1,14	1,63E-12	EFF=SYNONYMOUS_CODING(LOW|SILENT|ccT/ccC|P92|C2|protein_coding|CODING|ENSBTAT00000009798|3)
27244332	C	T	0,95	0,05	-1,13	1,63E-12	EFF=UPSTREAM(MODIFIER||982||C2|protein_coding|CODING|ENSBTAT00000045436|)
27270434	A	G	0,97	0,05	-1,13	1,69E-12	EFF=UPSTREAM(MODIFIER||3600||ZBTB12|protein_coding|CODING|ENSBTAT00000045434|)
27510065	C	T	0,67	0,05	-1,20	1,71E-12	EFF=UPSTREAM(MODIFIER||4608||AIF1|protein_coding|CODING|ENSBTAT00000027388|)
27292772	C	T	0,89	0,05	-1,14	1,71E-12	EFF=INTRON(MODIFIER|||SLC44A4|protein_coding|CODING|ENSBTAT00000045367|1)
27508554	Q	G	0,66	0,05	-1,20	1,76E-12	EFF=UPSTREAM(MODIFIER||3098||AIF1|protein_coding|CODING|ENSBTAT00000027388|)
27264559	C	T	0,98	0,05	-1,13	1,90E-12	EFF=INTERGENIC(MODIFIER||||||||)
27315855	T	C	0,95	0,05	-1,10	2,14E-12	EFF=INTERGENIC(MODIFIER||||||||)
27243583	C	T	0,93	0,05	-1,12	2,15E-12	EFF=UPSTREAM(MODIFIER||233||C2|protein_coding|CODING|ENSBTAT00000045436|)
27500660	A	G	0,58	0,05	-1,23	2,20E-12	EFF=UPSTREAM(MODIFIER||891||ENSBTAG00000037350|miRNA|NON_CODING|ENSBTAT00000051850|)
27306012	C	T	0,97	0,05	-1,09	2,39E-12	EFF=DOWNSTREAM(MODIFIER||675||SLC44A4|protein_coding|CODING|ENSBTAT00000045367|)
27323325	C	T	0,95	0,05	-1,10	2,86E-12	EFF=DOWNSTREAM(MODIFIER||1911||SNORD52|snoRNA|NON_CODING|ENSBTAT00000059981|)
27327955	A	G	0,88	0,05	-1,10	6,65E-12	EFF=UPSTREAM(MODIFIER||2653||SNORD52|snoRNA|NON_CODING|ENSBTAT00000059981|)
27212490	G	A	0,66	0,06	-1,13	1,53E-11	EFF=NON_SYNONYMOUS_CODING(MODERATE|MISSENSE|aCg/aTg|T714M|SKIV2L|protein_coding|CODING|ENSBTAT00000007339|18)
27234192	C	G	0,82	0,06	-1,08	2,18E-11	EFF=UPSTREAM(MODIFIER||2900||CFB|protein_coding|CODING|ENSBTAT00000009800|)