

**Supplementary Table 3** Logistic regression analysis in discovery cohort, using gender as covariate.

CHR	MARKER	F_A	F_U	ALT	OR(95% CI)	P value
6	DQA1:160:D	0.36	0.19	DQA1:160:D	2.36(1.94-2.87)	1.04E-17
6	DQA1:160:A	0.38	0.21	DQA1:160:A	2.27(1.87-2.75)	6.25E-17
6	chr6_32602137_C_G	0.41	0.24	G	2.23(1.84-2.69)	1.14E-16
6	chr6_32431785_A_C	0.33	0.18	C	2.25(1.84-2.76)	2.61E-15
6	chr6_32440743_C_T	0.33	0.18	T	2.25(1.84-2.75)	3.45E-15
6	DQA1*03:03	0.16	0.06	DQA1*03:03	3.16(2.37-4.22)	5.25E-15
6	chr6_32510392_C_T	0.35	0.19	T	2.09(1.73-2.51)	8.19E-15
6	DQA1:187:A	0.4	0.25	DQA1:187:A	2.08(1.73-2.51)	1.46E-14
6	DQA1:187:T	0.4	0.25	DQA1:187:T	2.08(1.73-2.51)	1.46E-14
6	DQA1:47:Q	0.4	0.25	DQA1:47:Q	2.08(1.73-2.51)	1.46E-14
6	DQA1:56:R	0.4	0.25	DQA1:56:R	2.08(1.73-2.51)	1.46E-14
6	DQA1:26:S	0.4	0.25	DQA1:26:S	2.08(1.73-2.51)	1.46E-14
6	DQA1:26:T	0.4	0.25	DQA1:26:T	2.08(1.73-2.51)	1.46E-14
6	DQA1:76:V	0.4	0.25	DQA1:76:V	2.08(1.73-2.51)	1.46E-14
6	chr6_32403963_C_G	0.12	0.04	G	3.65(2.61-5.11)	4.85E-14
6	chr6_32449188_G_A	0.58	0.42	A	2.05(1.70-2.47)	5.39E-14
6	DRB1*04:05	0.12	0.04	DRB1*04:05	3.45(2.49-4.78)	7.94E-14
6	chr6_32453286_C_G	0.37	0.53	C	0.49(0.41-0.60)	1.04E-13
6	chr6_32680928_T_G	0.18	0.07	G	2.74(2.10-3.57)	1.13E-13
6	chr6_32681339_C_T	0.18	0.07	T	2.74(2.10-3.57)	1.13E-13
6	chr6_32660051_T_C	0.33	0.5	T	0.51(0.42-0.61)	2.27E-13
6	chr6_32663999_G_C	0.33	0.5	G	0.51(0.42-0.61)	2.80E-13

6	chr6_32659158_G_A	0.33	0.5	G	0.51(0.42-0.61)	2.80E-13
6	chr6_32663851_C_T	0.34	0.5	C	0.51(0.42-0.61)	3.15E-13
6	chr6_32198847_G_A	0.13	0.05	A	3.23(2.35-4.43)	3.52E-13
6	chr6_32205980_T_C	0.13	0.05	C	3.23(2.35-4.43)	3.52E-13
6	chr6_32205174_T_G	0.13	0.05	G	3.23(2.35-4.43)	3.52E-13
6	chr6_32204850_C_T	0.13	0.05	T	3.23(2.35-4.43)	3.52E-13
6	chr6_32453318_T_C	0.6	0.45	C	1.93(1.61-2.31)	9.20E-13
6	chr6_32446853_A_T	0.56	0.41	T	1.93(1.61-2.31)	1.26E-12
6	chr6_32671103_T_C	0.21	0.1	C	2.36(1.86-2.99)	1.31E-12
6	chr6_32665311_T_C	0.21	0.1	C	2.36(1.86-2.99)	1.31E-12
6	chr6_32670368_A_G	0.21	0.1	G	2.36(1.86-2.99)	1.31E-12
6	chr6_32672903_G_A	0.21	0.1	A	2.36(1.86-2.99)	1.31E-12
6	chr6_32670495_C_T	0.21	0.1	T	2.36(1.86-2.99)	1.31E-12
6	chr6_32670414_C_T	0.21	0.1	T	2.36(1.86-2.99)	1.31E-12
6	chr6_32672361_A_G	0.21	0.1	G	2.36(1.86-2.99)	1.31E-12
6	chr6_32671601_G_T	0.21	0.1	T	2.36(1.86-2.99)	1.31E-12
6	chr6_32669137_T_C	0.21	0.1	C	2.36(1.86-2.99)	1.31E-12
6	chr6_32672135_C_T	0.21	0.1	T	2.36(1.86-2.99)	1.31E-12
6	chr6_32443432_C_G	0.56	0.41	G	1.93(1.61-2.31)	1.36E-12
6	chr6_32446922_T_C	0.56	0.41	C	1.93(1.61-2.31)	1.53E-12
6	chr6_32447518_T_A	0.56	0.41	A	1.92(1.60-2.31)	1.56E-12
6	chr6_32444096_C_T	0.56	0.41	T	1.92(1.60-2.31)	1.61E-12
6	chr6_32428772_A_G	0.56	0.41	G	1.92(1.60-2.31)	1.61E-12
6	chr6_32443666_G_C	0.56	0.41	C	1.92(1.60-2.30)	2.01E-12
6	chr6_32447216_A_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12
6	chr6_32445691_C_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12

6	chr6_32444330_A_C	0.56	0.41	C	1.92(1.60-2.30)	2.01E-12
6	chr6_32447219_G_A	0.56	0.41	A	1.92(1.60-2.30)	2.01E-12
6	chr6_32445079_C_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12
6	chr6_32447111_A_G	0.56	0.41	G	1.92(1.60-2.30)	2.01E-12
6	chr6_32447162_G_A	0.56	0.41	A	1.92(1.60-2.30)	2.01E-12
6	chr6_32452361_C_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12
6	chr6_32447341_G_A	0.56	0.41	A	1.92(1.60-2.30)	2.01E-12
6	chr6_32443172_C_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12
6	chr6_32447014_G_A	0.56	0.41	A	1.92(1.60-2.30)	2.01E-12
6	chr6_32444198_G_T	0.56	0.41	T	1.92(1.60-2.30)	2.01E-12
6	chr6_32188909_C_T	0.1	0.03	T	3.78(2.60-5.49)	3.27E-12
6	chr6_32444078_G_A	0.56	0.41	A	1.91(1.59-2.29)	3.38E-12
6	chr6_32453372_A_G	0.32	0.47	A	0.51(0.42-0.62)	3.99E-12
6	chr6_32188996_G_A	0.1	0.03	A	3.73(2.57-5.41)	4.66E-12
6	chr6_32188943_G_A	0.1	0.03	A	3.73(2.57-5.41)	4.66E-12
6	chr6_32443665_T_C	0.56	0.41	C	1.90(1.58-2.27)	5.16E-12
6	chr6_32636289_T_C	0.4	0.26	C	1.91(1.59-2.30)	5.23E-12
6	DQB1:185:I	0.4	0.26	DQB1:185:I	1.91(1.59-2.30)	5.23E-12
6	DQB1:185:T	0.4	0.26	DQB1:185:T	1.91(1.59-2.30)	5.23E-12
6	DQB1:23:L	0.11	0.04	DQB1:23:L	3.20(2.30-4.45)	5.64E-12
6	DQB1:23:R	0.11	0.04	DQB1:23:R	3.20(2.30-4.45)	5.64E-12
6	DQB1*04:01	0.11	0.04	DQB1*04:01	3.20(2.30-4.45)	5.64E-12
6	chr6_32663579_C_G	0.12	0.04	G	3.12(2.26-4.31)	5.77E-12
6	chr6_32189262_G_C	0.1	0.03	C	3.67(2.53-5.32)	6.63E-12
6	chr6_32681385_G_A	0.11	0.04	A	3.14(2.26-4.36)	7.73E-12
6	chr6_32633498_G_DEL:T	0.4	0.26	DEL:T	1.90(1.58-2.28)	7.99E-12

6	chr6_32402552_G_A	0.16	0.07	A	2.58(1.96-3.38)	8.95E-12
6	chr6_32400811_C_A	0.16	0.07	A	2.58(1.96-3.38)	8.95E-12
6	chr6_32188727_C_T	0.09	0.03	T	3.66(2.52-5.32)	9.97E-12
6	chr6_32447085_T_C	0.34	0.48	T	0.52(0.43-0.63)	1.11E-11
6	chr6_32305814_C_A	0.1	0.03	A	3.42(2.40-4.88)	1.16E-11
6	chr6_32312458_T_C	0.1	0.03	C	3.42(2.40-4.88)	1.16E-11
6	chr6_32450378_A_DEL: CTT	0.54	0.4	DEL:CTT	1.90(1.58-2.29)	1.22E-11
6	chr6_32600101_G_C	0.21	0.11	C	2.28(1.80-2.90)	1.22E-11
6	DRB1:120:N	0.23	0.13	DRB1:120:N	2.17(1.73-2.72)	1.25E-11
6	chr6_32674737_C_A	0.12	0.04	A	2.96(2.16-4.06)	1.36E-11
6	chr6_32504267_G_DEL: TTTT	0.56	0.41	DEL:TTTT	1.76(1.49-2.07)	1.39E-11
6	DRB1:11:V	0.23	0.13	DRB1:11:V	2.16(1.73-2.71)	1.59E-11
6	chr6_32395956_C_T	0.16	0.07	T	2.55(1.94-3.34)	1.67E-11
6	chr6_32377284_C_T	0.26	0.15	T	2.14(1.71-2.67)	2.07E-11
6	chr6_32380909_A_C	0.26	0.15	C	2.14(1.71-2.67)	2.07E-11
6	chr6_32591588_A_G	0.21	0.11	G	2.26(1.78-2.87)	2.13E-11
6	chr6_32382201_A_G	0.16	0.07	G	2.53(1.93-3.32)	2.14E-11
6	chr6_32660104_C_T	0.13	0.05	T	2.84(2.09-3.85)	2.19E-11
6	chr6_32191445_G_A	0.09	0.03	A	3.54(2.44-5.13)	2.28E-11
6	DRB1:120:S	0.23	0.13	DRB1:120:S	2.15(1.71-2.69)	2.39E-11
6	chr6_32452626_C_G	0.54	0.4	G	1.88(1.56-2.26)	2.57E-11
6	chr6_32450270_C_DEL: CTT	0.54	0.4	DEL:CTT	1.88(1.56-2.26)	2.59E-11
6	chr6_32660115_G_C	0.13	0.05	C	2.81(2.07-3.81)	3.16E-11

6	chr6_32665270_C_A	0.13	0.05	A	2.81(2.07-3.81)	3.16E-11
6	chr6_32665001_T_A	0.13	0.05	A	2.81(2.07-3.81)	3.16E-11
6	chr6_32664154_C_A	0.13	0.05	A	2.81(2.07-3.81)	3.16E-11
6	chr6_32664119_A_T	0.13	0.05	T	2.81(2.07-3.81)	3.16E-11
6	chr6_32664373_G_T	0.13	0.05	T	2.81(2.07-3.81)	3.16E-11
6	chr6_32666559_C_T	0.13	0.05	T	2.81(2.07-3.81)	3.16E-11
6	chr6_32671391_C_T	0.13	0.05	T	2.81(2.07-3.81)	3.16E-11
6	chr6_32664356_G_C	0.13	0.05	C	2.81(2.07-3.81)	3.16E-11
6	chr6_32657916_T_C	0.13	0.05	C	2.81(2.07-3.81)	3.16E-11
6	chr6_32658360_T_C	0.13	0.05	C	2.81(2.07-3.81)	3.16E-11
6	chr6_32667199_T_C	0.13	0.05	C	2.81(2.07-3.81)	3.16E-11
6	chr6_32650101_C_A	0.13	0.05	A	2.81(2.07-3.81)	3.16E-11
6	chr6_32666235_G_A	0.13	0.05	A	2.80(2.07-3.80)	3.31E-11
6	chr6_32452028_A_DEL: CCCGGCCAGCGGCAAGGCCGCTC T	0.53	0.4	DEL:CCCGGCCAGCGGCAAGGCCGCTC T	1.89(1.56-2.28)	3.34E-11
6	chr6_32215654_G_A	0.11	0.04	A	3.12(2.23-4.37)	3.47E-11
6	chr6_32359833_C_T	0.16	0.07	T	2.54(1.93-3.35)	3.48E-11
6	chr6_32442836_T_G	0.53	0.39	G	1.90(1.57-2.30)	3.50E-11
6	chr6_32379736_G_A	0.25	0.15	A	2.12(1.70-2.65)	3.50E-11
6	chr6_32359331_T_C	0.15	0.07	C	2.55(1.93-3.36)	3.70E-11
6	chr6_32197528_C_A	0.1	0.03	A	3.33(2.33-4.75)	3.74E-11
6	chr6_32202630_G_T	0.1	0.03	T	3.33(2.33-4.75)	3.74E-11
6	chr6_32196904_A_G	0.1	0.03	G	3.33(2.33-4.75)	3.74E-11
6	chr6_32599163_C_T	0.21	0.11	T	2.21(1.75-2.80)	3.88E-11
6	chr6_32668633_G_T	0.27	0.16	T	2.04(1.65-2.52)	4.05E-11

6	chr6_32668667_A_G	0.27	0.16	G	2.04(1.65-2.52)	4.05E-11
6	chr6_32672556_A_G	0.27	0.16	G	2.04(1.65-2.52)	4.05E-11
6	chr6_32672654_G_T	0.27	0.16	T	2.04(1.65-2.52)	4.05E-11
6	chr6_32672659_C_T	0.27	0.16	T	2.04(1.65-2.52)	4.05E-11
6	chr6_32672913_T_A	0.27	0.16	A	2.04(1.65-2.52)	4.05E-11
6	chr6_32668729_C_G	0.27	0.16	G	2.04(1.65-2.52)	4.05E-11
6	chr6_32669712_A_G	0.27	0.16	G	2.04(1.65-2.52)	4.05E-11
6	chr6_32672491_G_A	0.27	0.16	A	2.04(1.65-2.52)	4.05E-11
6	chr6_32672523_C_T	0.27	0.16	T	2.04(1.65-2.52)	4.05E-11
6	chr6_32672529_C_T	0.27	0.16	T	2.04(1.65-2.52)	4.05E-11
6	chr6_32672494_G_A	0.27	0.16	A	2.04(1.65-2.52)	4.05E-11
6	chr6_32672412_G_A	0.27	0.16	A	2.04(1.65-2.52)	4.05E-11
6	chr6_32672668_G_A	0.27	0.16	A	2.04(1.65-2.52)	4.05E-11
6	chr6_32675470_G_A	0.12	0.05	A	2.82(2.07-3.83)	4.56E-11
6	chr6_32160153_C_A	0.09	0.03	A	3.58(2.45-5.25)	4.84E-11
6	chr6_32501816_G_DEL:A	0.58	0.44	DEL:A	1.77(1.50-2.11)	5.16E-11
6	chr6_32500848_T_DEL:C	0.58	0.44	DEL:C	1.77(1.50-2.11)	5.16E-11
6	chr6_32364964_A_G	0.15	0.07	G	2.54(1.92-3.36)	5.66E-11
6	DQB1:71:D	0.13	0.05	DQB1:71:D	2.77(2.04-3.76)	6.07E-11
6	chr6_32658355_A_G	0.13	0.05	G	2.77(2.04-3.76)	6.07E-11
6	DQB1:56:P	0.13	0.05	DQB1:56:P	2.77(2.04-3.76)	6.07E-11
6	DQB1:56:L	0.13	0.05	DQB1:56:L	2.77(2.04-3.76)	6.07E-11
6	chr6_32659582_A_G	0.13	0.05	G	2.77(2.04-3.76)	6.07E-11
6	DQB1:70:E	0.13	0.05	DQB1:70:E	2.77(2.04-3.76)	6.07E-11
6	chr6_32658610_G_T	0.13	0.05	T	2.77(2.04-3.76)	6.07E-11
6	chr6_32363017_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11

6	chr6_32373903_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32363391_C_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363351_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32369249_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32367477_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32368016_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32355745_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32362785_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32371253_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32362967_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32366182_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32374105_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32367353_G_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32358432_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32368352_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32368355_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32356265_C_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32369466_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32357411_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32355908_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32357493_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32364194_A_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32363387_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32365955_A_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32366569_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32363786_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11

6	chr6_32363212_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363186_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32366556_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363772_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363649_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32369439_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32367971_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32369428_T_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32373866_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32367897_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32373907_A_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363790_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32374135_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32363888_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32362521_C_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363100_C_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32366342_G_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32355803_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32362920_G_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32356019_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32368134_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32363147_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32370927_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32373904_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363256_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363219_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11

6	chr6_32358162_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363558_A_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32363712_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32364011_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32367902_T_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32366488_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32367412_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32358666_A_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32369258_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32369454_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363493_T_C	0.15	0.07	C	2.51(1.91-3.31)	6.47E-11
6	chr6_32367239_C_G	0.15	0.07	G	2.51(1.91-3.31)	6.47E-11
6	chr6_32357974_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32363084_C_T	0.15	0.07	T	2.51(1.91-3.31)	6.47E-11
6	chr6_32374185_G_A	0.15	0.07	A	2.51(1.91-3.31)	6.47E-11
6	chr6_32672430_A_G	0.26	0.16	G	2.02(1.64-2.50)	6.63E-11
6	chr6_32584693_C_G	0.21	0.12	G	2.17(1.72-2.73)	7.46E-11
6	chr6_32598854_G_A	0.22	0.12	A	2.07(1.66-2.57)	7.99E-11
6	chr6_32358202_G_A	0.15	0.07	A	2.50(1.90-3.29)	8.17E-11
6	chr6_32328380_A_G	0.1	0.04	G	3.17(2.23-4.49)	9.44E-11
6	chr6_32289495_C_T	0.1	0.04	T	3.17(2.23-4.49)	9.44E-11
6	chr6_32295296_T_A	0.1	0.04	A	3.17(2.23-4.49)	9.44E-11
6	chr6_32297839_G_A	0.1	0.04	A	3.17(2.23-4.49)	9.44E-11
6	chr6_32318384_A_G	0.1	0.04	G	3.17(2.23-4.49)	9.44E-11
6	chr6_32184894_C_T	0.09	0.03	T	3.52(2.40-5.16)	1.03E-10
6	chr6_32183158_C_T	0.09	0.03	T	3.52(2.40-5.16)	1.03E-10

6	chr6_32186115_C_G	0.09	0.03	G	3.52(2.40-5.16)	1.03E-10
6	chr6_32179780_A_G	0.09	0.03	G	3.52(2.40-5.16)	1.03E-10
6	chr6_32182002_C_T	0.09	0.03	T	3.52(2.40-5.16)	1.03E-10
6	chr6_32185892_A_T	0.09	0.03	T	3.52(2.40-5.16)	1.03E-10
6	chr6_32186641_C_T	0.09	0.03	T	3.52(2.40-5.16)	1.03E-10
6	chr6_32180120_T_G	0.09	0.03	G	3.52(2.40-5.16)	1.03E-10
6	chr6_32658911_C_T	0.18	0.31	C	0.49(0.39-0.61)	1.09E-10
6	chr6_32376654_G_T	0.15	0.07	T	2.47(1.88-3.25)	1.12E-10
6	chr6_32380322_T_G	0.15	0.07	G	2.47(1.88-3.25)	1.12E-10
6	chr6_32156904_C_G	0.09	0.03	G	3.54(2.41-5.21)	1.18E-10
6	chr6_32369316_A_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32366097_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32360464_C_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32359700_T_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32369173_T_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32364057_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32354531_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32355682_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32355536_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32366132_C_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32363491_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32357782_G_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32370112_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32369312_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32359699_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32369517_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10

6	chr6_32359769_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32369238_C_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32369381_C_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32363973_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32366070_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32369336_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32369554_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32367401_C_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32366141_A_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32360440_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32359724_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32355557_C_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32369293_A_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32366039_T_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32373774_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32354240_A_G	0.15	0.07	G	2.48(1.88-3.28)	1.20E-10
6	chr6_32359756_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32366022_C_T	0.15	0.07	T	2.48(1.88-3.28)	1.20E-10
6	chr6_32364214_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32369681_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32363448_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32370860_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32360363_T_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32360472_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10
6	chr6_32365016_G_C	0.15	0.07	C	2.48(1.88-3.28)	1.20E-10
6	chr6_32367009_G_A	0.15	0.07	A	2.48(1.88-3.28)	1.20E-10

6	chr6_32590916_A_G	0.39	0.53	A	0.55(0.46-0.66)	1.31E-10
6	chr6_32590953_T_C	0.39	0.53	T	0.55(0.46-0.66)	1.31E-10
6	chr6_32273836_A_G	0.1	0.04	G	3.12(2.20-4.42)	1.45E-10
6	chr6_32680640_T_A	0.36	0.24	A	1.85(1.53-2.24)	1.51E-10
6	chr6_32660023_T_C	0.3	0.44	T	0.54(0.45-0.65)	1.58E-10
6	chr6_32159860_G_A	0.09	0.03	A	3.45(2.36-5.05)	1.67E-10
6	chr6_32341516_G_A	0.15	0.07	A	2.47(1.87-3.26)	1.75E-10
6	chr6_32341576_C_T	0.15	0.07	T	2.47(1.87-3.26)	1.75E-10
6	chr6_32280736_A_G	0.1	0.04	G	3.12(2.20-4.42)	1.92E-10
6	chr6_32299563_T_C	0.1	0.04	C	3.12(2.20-4.42)	1.92E-10
6	chr6_32280435_C_T	0.1	0.04	T	3.12(2.20-4.42)	1.92E-10
6	chr6_32289642_T_C	0.1	0.04	C	3.12(2.20-4.42)	1.92E-10
6	chr6_32216166_G_A	0.11	0.04	A	2.92(2.10-4.06)	2.02E-10
6	chr6_32219663_A_T	0.11	0.04	T	2.92(2.10-4.06)	2.02E-10
6	chr6_32217508_T_G	0.11	0.04	G	2.92(2.10-4.06)	2.02E-10
6	chr6_32216355_T_C	0.11	0.04	C	2.92(2.10-4.06)	2.02E-10
6	chr6_32220741_A_C	0.11	0.04	C	2.92(2.10-4.06)	2.02E-10
6	chr6_32329582_A_G	0.1	0.04	G	3.10(2.19-4.40)	2.16E-10
6	chr6_32179589_C_G	0.09	0.03	G	3.46(2.36-5.07)	2.18E-10
6	chr6_32171181_A_G	0.09	0.03	G	3.46(2.36-5.07)	2.18E-10
6	chr6_32354341_T_C	0.15	0.07	C	2.45(1.86-3.24)	2.20E-10
6	chr6_32370791_G_A	0.15	0.07	A	2.45(1.86-3.23)	2.39E-10
6	chr6_32663610_C_A	0.3	0.44	C	0.55(0.45-0.66)	2.41E-10
6	chr6_32663289_C_A	0.3	0.44	C	0.55(0.45-0.66)	2.59E-10
6	chr6_32659743_G_C	0.3	0.44	G	0.55(0.45-0.66)	2.59E-10
6	chr6_32664722_A_T	0.3	0.44	A	0.55(0.45-0.66)	2.59E-10

6	chr6_32659994_C_T	0.3	0.44	C	0.55(0.45-0.66)	2.59E-10
6	chr6_32659878_A_G	0.3	0.44	A	0.55(0.45-0.66)	2.59E-10
6	chr6_32663391_A_G	0.3	0.44	A	0.55(0.45-0.66)	2.59E-10
6	chr6_32451693_T_C	0.5	0.36	C	1.80(1.50-2.16)	2.63E-10
6	DRB1:33:H	0.2	0.11	DRB1:33:H	2.17(1.70-2.75)	2.86E-10
6	DRB1:96:Y	0.2	0.11	DRB1:96:Y	2.17(1.70-2.75)	2.86E-10
6	DRB1:180:L	0.2	0.11	DRB1:180:L	2.17(1.70-2.75)	2.86E-10
6	DRB1:33:N	0.2	0.11	DRB1:33:N	2.17(1.70-2.75)	2.86E-10
6	chr6_32234981_T_A	0.1	0.04	A	3.07(2.17-4.35)	2.93E-10
6	chr6_32271755_G_T	0.1	0.04	T	3.07(2.17-4.35)	2.93E-10
6	chr6_32220270_G_T	0.1	0.04	T	3.07(2.17-4.35)	2.93E-10
6	chr6_32230927_T_C	0.1	0.04	C	3.07(2.17-4.35)	2.93E-10
6	chr6_32233915_C_A	0.1	0.04	A	3.07(2.17-4.35)	2.93E-10
6	chr6_32223143_G_A	0.1	0.04	A	3.07(2.17-4.35)	2.93E-10
6	chr6_32267284_G_A	0.1	0.04	A	3.07(2.17-4.35)	2.93E-10
6	chr6_32231297_C_T	0.1	0.04	T	3.07(2.17-4.35)	2.93E-10
6	DRB1:70:D	0.29	0.43	DRB1:70:D	0.55(0.45-0.66)	3.50E-10
6	DRB1:13:H	0.2	0.11	DRB1:13:H	2.15(1.69-2.74)	3.67E-10
6	chr6_32217614_T_C	0.11	0.04	C	2.88(2.06-4.00)	3.98E-10
6	chr6_32664117_A_G	0.39	0.54	A	0.59(0.50-0.69)	4.23E-10
6	chr6_32211210_C_G	0.1	0.04	G	3.05(2.15-4.33)	4.36E-10
6	chr6_32256688_A_G	0.09	0.03	G	3.35(2.29-4.90)	5.07E-10
6	chr6_32212735_T_A	0.1	0.04	A	3.00(2.12-4.25)	5.32E-10
6	chr6_32212727_A_G	0.1	0.04	G	3.00(2.12-4.25)	5.32E-10
6	DRB1:180:V	0.2	0.11	DRB1:180:V	2.13(1.68-2.71)	5.61E-10
6	chr6_32254701_G_C	0.1	0.04	C	3.02(2.13-4.28)	5.88E-10

6	chr6_32238436_T_A	0.1	0.04	A	3.02(2.13-4.28)	5.88E-10
6	chr6_32428715_G_A	0.47	0.35	A	1.77(1.47-2.12)	7.31E-10
6	chr6_32428062_C_T	0.47	0.34	T	1.75(1.46-2.09)	1.51E-09
6	chr6_32428079_C_A	0.47	0.34	A	1.75(1.46-2.09)	1.66E-09
6	chr6_31766751_G_T	0.07	0.02	T	3.77(2.45-5.81)	1.79E-09
6	chr6_32588970_A_INS: AAC	0.49	0.36	INS:AAC	1.75(1.46-2.09)	1.79E-09
6	chr6_32587628_G_C	0.49	0.36	C	1.75(1.46-2.09)	1.79E-09
6	chr6_32587117_C_G	0.49	0.36	G	1.74(1.45-2.09)	1.90E-09
6	chr6_32663446_G_A	0.58	0.45	A	1.71(1.44-2.04)	1.92E-09
6	chr6_32663564_A_G	0.58	0.45	G	1.71(1.44-2.04)	1.92E-09
6	chr6_32664163_A_C	0.58	0.45	C	1.71(1.44-2.04)	1.92E-09
6	chr6_32321833_A_G	0.1	0.04	G	2.78(1.99-3.89)	2.00E-09
6	chr6_32060557_A_G	0.07	0.02	G	3.75(2.43-5.77)	2.06E-09
6	chr6_32025058_C_A	0.07	0.02	A	3.75(2.43-5.77)	2.06E-09
6	chr6_32664332_T_C	0.58	0.45	C	1.71(1.43-2.03)	2.38E-09
6	chr6_32663986_C_G	0.58	0.45	G	1.71(1.43-2.03)	2.38E-09
6	chr6_32428115_G_A	0.47	0.35	A	1.73(1.45-2.08)	2.43E-09
6	chr6_32660347_G_A	0.3	0.43	G	0.57(0.47-0.68)	2.57E-09
6	chr6_32591597_T_C	0.49	0.36	C	1.73(1.45-2.08)	2.68E-09
6	chr6_32588193_A_G	0.49	0.36	G	1.73(1.45-2.08)	2.68E-09
6	chr6_32608392_C_INS:T	0.49	0.36	INS:T	1.73(1.45-2.08)	2.68E-09
6	chr6_32590120_C_A	0.49	0.36	A	1.73(1.45-2.08)	2.68E-09
6	chr6_32587613_C_T	0.49	0.36	T	1.73(1.45-2.08)	2.68E-09
6	chr6_32591566_A_G	0.49	0.36	G	1.73(1.45-2.08)	2.68E-09
6	chr6_32663260_G_A	0.58	0.45	A	1.70(1.43-2.02)	2.84E-09

6	chr6_32664675_A_G	0.58	0.45	G	1.70(1.43-2.02)	2.84E-09
6	chr6_32626475_G_A	0.41	0.29	A	1.72(1.44-2.06)	2.91E-09
6	chr6_32668336_A_C	0.14	0.25	A	0.48(0.38-0.62)	3.52E-09
6	chr6_32658310_G_A	0.24	0.36	G	0.55(0.45-0.67)	3.67E-09
6	chr6_32592027_A_DEL:ATCT	0.48	0.36	DEL:ATCT	1.73(1.44-2.07)	3.79E-09
6	chr6_31774859_A_T	0.07	0.02	T	3.69(2.39-5.69)	3.81E-09
6	chr6_32668323_G_A	0.14	0.24	G	0.48(0.38-0.62)	4.19E-09
6	chr6_32668705_A_T	0.14	0.24	A	0.48(0.38-0.62)	4.19E-09
6	chr6_32329731_T_C	0.1	0.04	C	2.73(1.95-3.81)	4.30E-09
6	chr6_32626302_T_G	0.41	0.29	G	1.71(1.43-2.05)	4.31E-09
6	chr6_32626272_C_A	0.41	0.29	A	1.71(1.43-2.05)	4.31E-09
6	chr6_32670464_G_T	0.14	0.25	G	0.49(0.38-0.62)	5.49E-09
6	chr6_32446100_C_T	0.29	0.41	C	0.55(0.45-0.68)	5.71E-09
6	chr6_32669132_C_T	0.14	0.24	C	0.49(0.38-0.62)	6.52E-09
6	chr6_32670897_T_C	0.14	0.24	T	0.49(0.38-0.62)	6.52E-09
6	chr6_32668713_C_G	0.14	0.24	C	0.49(0.38-0.62)	6.52E-09
6	chr6_32670308_A_G	0.14	0.24	A	0.49(0.38-0.62)	6.52E-09
6	chr6_32674952_T_C	0.14	0.24	T	0.49(0.38-0.62)	6.52E-09
6	chr6_32438867_G_T	0.48	0.36	T	1.70(1.42-2.04)	6.72E-09
6	chr6_32359611_A_G	0.22	0.13	G	1.94(1.55-2.43)	6.83E-09
6	chr6_32451834_A_G	0.52	0.4	G	1.72(1.43-2.07)	7.14E-09
6	DQA1:34:E	0.4	0.52	DQA1:34:E	0.59(0.50-0.71)	7.46E-09
6	DQA1:34:Q	0.4	0.52	DQA1:34:Q	0.59(0.50-0.71)	7.46E-09
6	chr6_32362389_G_A	0.22	0.13	A	1.94(1.55-2.43)	7.61E-09

6	chr6_32589721_T_DEL: AATTCTC	0.48	0.36	DEL:AATTCTC	1.72(1.43-2.07)	7.62E-09
6	chr6_32433167_G_T	0.48	0.36	T	1.70(1.42-2.03)	8.72E-09
6	chr6_32667958_A_G	0.14	0.25	A	0.49(0.39-0.63)	8.77E-09
6	chr6_32360341_C_A	0.22	0.13	A	1.93(1.54-2.42)	8.85E-09
6	chr6_32431124_G_A	0.48	0.36	A	1.69(1.42-2.03)	8.99E-09
6	chr6_32434240_G_A	0.48	0.36	A	1.70(1.42-2.03)	9.07E-09
6	chr6_32430326_T_A	0.48	0.36	A	1.70(1.42-2.03)	9.07E-09
6	DRB1:104:A	0.48	0.36	DRB1:104:A	1.70(1.42-2.03)	9.36E-09
6	DRB1:98:E	0.48	0.36	DRB1:98:E	1.70(1.42-2.03)	9.36E-09
6	DRB1:149:Q	0.26	0.38	DRB1:149:Q	0.56(0.46-0.69)	9.44E-09
6	chr6_32431640_T_A	0.48	0.36	A	1.69(1.42-2.03)	9.58E-09
6	chr6_32355003_C_T	0.22	0.13	T	1.93(1.54-2.42)	9.84E-09
6	DRB1:10:Y	0.26	0.38	DRB1:10:Y	0.56(0.46-0.69)	1.05E-08
6	DRB1:11:S	0.26	0.38	DRB1:11:S	0.56(0.46-0.69)	1.05E-08
6	DRB1:12:T	0.26	0.38	DRB1:12:T	0.56(0.46-0.69)	1.05E-08
6	DRB1:12:K	0.26	0.38	DRB1:12:K	0.56(0.46-0.69)	1.05E-08
6	chr6_32066447_G_A	0.1	0.04	A	2.63(1.89-3.67)	1.08E-08
6	chr6_32355858_T_C	0.22	0.13	C	1.92(1.54-2.41)	1.09E-08
6	chr6_32362433_C_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32358533_A_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32362703_G_T	0.22	0.13	T	1.92(1.54-2.41)	1.09E-08
6	chr6_32358008_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32360532_A_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32362741_C_T	0.22	0.13	T	1.92(1.54-2.41)	1.09E-08

6	chr6_32360443_C_T	0.22	0.13	T	1.92(1.54-2.41)	1.09E-08
6	chr6_32362408_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32362832_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32362669_T_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32362745_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32358163_A_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32358213_T_C	0.22	0.13	C	1.92(1.54-2.41)	1.09E-08
6	chr6_32358144_T_C	0.22	0.13	C	1.92(1.54-2.41)	1.09E-08
6	chr6_32362702_T_C	0.22	0.13	C	1.92(1.54-2.41)	1.09E-08
6	chr6_32362453_A_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32355677_T_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32357344_T_G	0.22	0.13	G	1.92(1.54-2.41)	1.09E-08
6	chr6_32358459_G_T	0.22	0.13	T	1.92(1.54-2.41)	1.09E-08
6	chr6_32356307_C_T	0.22	0.13	T	1.92(1.54-2.41)	1.09E-08
6	chr6_32362639_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32358011_G_A	0.22	0.13	A	1.92(1.54-2.41)	1.09E-08
6	chr6_32432992_A_INS:T	0.48	0.36	INS:T	1.69(1.41-2.02)	1.09E-08
6	chr6_32429758_T_C	0.48	0.36	C	1.69(1.41-2.02)	1.09E-08
6	chr6_32432835_C_T	0.48	0.36	T	1.69(1.41-2.02)	1.09E-08
6	chr6_32433192_C_G	0.48	0.36	G	1.69(1.41-2.02)	1.09E-08
6	chr6_32432181_A_G	0.48	0.36	G	1.69(1.41-2.02)	1.09E-08
6	chr6_32429643_T_C	0.48	0.36	C	1.69(1.41-2.02)	1.09E-08
6	chr6_32451963_G_A	0.48	0.36	A	1.69(1.41-2.02)	1.09E-08
6	chr6_31792890_C_T	0.08	0.02	T	3.23(2.16-4.83)	1.14E-08
6	DRB1:98:K	0.48	0.36	DRB1:98:K	1.69(1.41-2.02)	1.33E-08
6	DRB1:104:S	0.48	0.36	DRB1:104:S	1.69(1.41-2.02)	1.33E-08

6	DRB1:149:H	0.26	0.38	DRB1:149:H	0.57(0.47-0.69)	1.38E-08
6	chr6_32438542_T_C	0.48	0.36	C	1.68(1.41-2.02)	1.40E-08
6	chr6_32434850_G_C	0.48	0.36	C	1.68(1.41-2.02)	1.40E-08
6	chr6_32445600_G_A	0.48	0.36	A	1.68(1.41-2.01)	1.41E-08
6	chr6_32604008_A_INS: TTC	0.52	0.39	INS:TTC	1.62(1.37-1.92)	1.44E-08
6	chr6_32429825_C_T	0.48	0.36	T	1.68(1.41-2.01)	1.47E-08
6	chr6_32663256_T_C	0.15	0.25	T	0.50(0.40-0.64)	1.47E-08
6	chr6_32663606_G_C	0.15	0.25	G	0.50(0.40-0.64)	1.47E-08
6	chr6_32664880_T_G	0.15	0.25	T	0.50(0.40-0.64)	1.47E-08
6	chr6_32666738_C_T	0.15	0.25	C	0.50(0.40-0.64)	1.47E-08
6	chr6_32658327_G_T	0.15	0.25	G	0.50(0.40-0.64)	1.47E-08
6	chr6_32604047_A_INS: TTT	0.52	0.39	INS:TTT	1.63(1.37-1.92)	1.49E-08
6	chr6_32355285_A_G	0.22	0.13	G	1.92(1.53-2.40)	1.57E-08
6	chr6_32354629_A_G	0.22	0.13	G	1.92(1.53-2.40)	1.57E-08
6	chr6_32354834_G_A	0.22	0.13	A	1.92(1.53-2.40)	1.57E-08
6	chr6_32360551_C_G	0.22	0.13	G	1.92(1.53-2.40)	1.57E-08
6	DRB1:57:S	0.17	0.09	DRB1:57:S	2.09(1.62-2.70)	1.59E-08
6	chr6_32663447_T_C	0.15	0.25	T	0.50(0.40-0.64)	1.60E-08
6	chr6_32432077_G_C	0.48	0.36	C	1.68(1.40-2.01)	1.60E-08
6	chr6_32434349_C_T	0.48	0.36	T	1.68(1.40-2.01)	1.60E-08
6	chr6_32434361_C_A	0.48	0.36	A	1.68(1.40-2.01)	1.60E-08
6	chr6_32439029_T_C	0.48	0.36	C	1.68(1.40-2.01)	1.60E-08
6	chr6_32663925_C_A	0.15	0.25	C	0.50(0.40-0.64)	1.61E-08
6	chr6_32188642_T_C	0.29	0.19	C	1.81(1.47-2.22)	1.65E-08

6	chr6_32358728_G_A	0.22	0.13	A	1.91(1.52-2.39)	1.73E-08
6	chr6_32188297_G_C	0.29	0.19	C	1.80(1.47-2.21)	1.87E-08
6	chr6_32664458_T_C	0.15	0.25	T	0.51(0.40-0.64)	1.90E-08
6	chr6_32667280_A_G	0.15	0.25	A	0.51(0.40-0.64)	1.90E-08
6	chr6_32664284_C_G	0.15	0.25	C	0.51(0.40-0.64)	1.90E-08
6	chr6_32514219_A_G	0.5	0.38	G	1.63(1.38-1.94)	1.91E-08
6	chr6_32438648_C_T	0.48	0.36	T	1.68(1.40-2.01)	1.95E-08
6	DRB1:47:Y	0.32	0.44	DRB1:47:Y	0.59(0.49-0.71)	2.03E-08
6	DRB1:47:F	0.32	0.44	DRB1:47:F	0.59(0.49-0.71)	2.03E-08
6	chr6_32189032_T_C	0.29	0.19	C	1.80(1.46-2.21)	2.12E-08
6	chr6_32665086_C_T	0.15	0.25	C	0.51(0.40-0.64)	2.25E-08
6	chr6_32665367_T_G	0.15	0.25	T	0.51(0.40-0.64)	2.25E-08
6	chr6_32666054_G_A	0.18	0.1	A	1.94(1.54-2.45)	2.50E-08
6	chr6_32343743_A_C	0.22	0.13	C	1.90(1.51-2.37)	2.63E-08
6	DQB1:182:N	0.58	0.46	DQB1:182:N	1.65(1.38-1.96)	3.08E-08
6	DQB1:140:A	0.58	0.46	DQB1:140:A	1.65(1.38-1.96)	3.08E-08
6	DQB1:182:S	0.58	0.46	DQB1:182:S	1.65(1.38-1.96)	3.08E-08
6	DQB1:140:T	0.58	0.46	DQB1:140:T	1.65(1.38-1.96)	3.08E-08
6	chr6_32674130_G_A	0.31	0.21	A	1.74(1.43-2.12)	3.20E-08
6	chr6_32674159_C_G	0.31	0.21	G	1.74(1.43-2.12)	3.20E-08
6	chr6_32665285_G_T	0.15	0.25	G	0.52(0.41-0.65)	4.01E-08
6	chr6_32063793_T_C	0.08	0.03	C	3.03(2.04-4.50)	4.02E-08
6	chr6_32520387_A_DEL: TG	0.5	0.38	DEL:TG	1.60(1.35-1.90)	4.72E-08
6	chr6_32072395_A_G	0.08	0.03	G	3.02(2.03-4.49)	4.85E-08
6	chr6_32514162_A_T	0.5	0.38	T	1.60(1.35-1.90)	4.94E-08

6	chr6_32513840_T_A	0.23	0.35	A	0.59(0.48-0.71)	6.29E-08
6	chr6_32513885_G_T	0.5	0.38	T	1.59(1.35-1.89)	6.54E-08
6	chr6_32032756_A_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32040484_T_C	0.08	0.03	C	2.97(2.00-4.42)	6.63E-08
6	chr6_32021776_G_C	0.08	0.03	C	2.97(2.00-4.42)	6.63E-08
6	chr6_32039872_C_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32058948_C_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32036450_G_A	0.08	0.03	A	2.97(2.00-4.42)	6.63E-08
6	chr6_32017035_C_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32035469_G_A	0.08	0.03	A	2.97(2.00-4.42)	6.63E-08
6	chr6_32017161_C_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32036135_C_T	0.08	0.03	T	2.97(2.00-4.42)	6.63E-08
6	chr6_32017540_A_G	0.08	0.03	G	2.97(2.00-4.42)	6.63E-08
6	chr6_32513942_G_T	0.5	0.38	T	1.59(1.35-1.89)	6.65E-08
6	chr6_32428285_C_T	0.29	0.4	C	0.59(0.48-0.71)	6.73E-08
6	chr6_32513938_T_C	0.23	0.35	C	0.59(0.48-0.71)	7.61E-08
6	chr6_32584739_T_C	0.14	0.24	C	0.52(0.41-0.66)	8.33E-08
6	DQA1:215:L	0.47	0.36	DQA1:215:L	1.63(1.36-1.95)	8.50E-08
6	DQA1:50:L	0.47	0.36	DQA1:50:L	1.63(1.36-1.95)	8.50E-08
6	DQA1:53:R	0.47	0.36	DQA1:53:R	1.63(1.36-1.95)	8.50E-08
6	DQA1:215:F	0.47	0.36	DQA1:215:F	1.63(1.36-1.95)	8.50E-08
6	chr6_32671248_G_A	0.24	0.15	A	1.81(1.46-2.25)	8.71E-08
6	DRB1:31:F	0.29	0.19	DRB1:31:F	1.73(1.41-2.11)	8.77E-08
6	DRB1:13:F	0.29	0.19	DRB1:13:F	1.73(1.41-2.11)	8.77E-08
6	chr6_32510438_C_T	0.5	0.38	T	1.59(1.34-1.88)	8.83E-08
6	chr6_32513862_G_T	0.23	0.35	T	0.59(0.49-0.72)	8.84E-08

6	chr6_32513915_C_T	0.23	0.35	T	0.59(0.49-0.72)	8.84E-08
6	chr6_32062252_C_T	0.08	0.03	T	2.92(1.97-4.32)	1.01E-07
6	chr6_32587588_A_G	0.4	0.51	A	0.61(0.51-0.73)	1.03E-07
6	chr6_32446833_A_G	0.29	0.39	A	0.59(0.48-0.72)	1.08E-07
6	chr6_32144530_C_T	0.08	0.03	T	2.86(1.94-4.22)	1.13E-07
6	chr6_32140302_T_C	0.08	0.03	C	2.86(1.94-4.22)	1.13E-07
6	chr6_32445519_A_G	0.29	0.4	A	0.59(0.49-0.72)	1.16E-07
6	chr6_32085599_C_A	0.08	0.03	A	2.83(1.93-4.15)	1.16E-07
6	chr6_32676251_C_A	0.11	0.2	C	0.50(0.38-0.64)	1.25E-07
6	chr6_32428186_G_C	0.29	0.39	G	0.59(0.49-0.72)	1.29E-07
6	chr6_32445727_T_C	0.29	0.4	T	0.59(0.49-0.72)	1.30E-07
6	chr6_31936630_C_T	0.07	0.03	T	2.91(1.96-4.33)	1.32E-07
6	chr6_32044316_C_T	0.07	0.03	T	2.91(1.96-4.33)	1.32E-07
6	chr6_31934494_G_A	0.07	0.03	A	2.91(1.96-4.33)	1.32E-07
6	chr6_32042200_C_T	0.07	0.03	T	2.91(1.96-4.33)	1.32E-07
6	chr6_32030200_G_T	0.07	0.03	T	2.91(1.96-4.33)	1.32E-07
6	chr6_32404377_A_C	0.17	0.09	A	1.98(1.54-2.55)	1.33E-07
6	chr6_32429011_C_T	0.29	0.39	C	0.59(0.49-0.72)	1.33E-07
6	chr6_32404048_G_C	0.17	0.09	G	1.98(1.54-2.55)	1.33E-07
6	chr6_32401079_A_G	0.17	0.09	A	1.98(1.54-2.55)	1.33E-07
6	chr6_32386619_T_C	0.25	0.16	T	1.77(1.43-2.19)	1.50E-07
6	chr6_32383256_A_C	0.25	0.16	A	1.77(1.43-2.19)	1.50E-07
6	chr6_32388275_C_T	0.25	0.16	C	1.77(1.43-2.19)	1.50E-07
6	chr6_32443269_A_C	0.29	0.39	A	0.59(0.49-0.72)	1.61E-07
6	chr6_32431623_T_C	0.29	0.39	T	0.59(0.49-0.72)	1.61E-07
6	chr6_32447154_C_G	0.29	0.39	C	0.59(0.49-0.72)	1.61E-07

6	chr6_32446843_A_G	0.29	0.39	A	0.59(0.49-0.72)	1.61E-07
6	chr6_32447545_T_G	0.29	0.39	T	0.59(0.49-0.72)	1.61E-07
6	chr6_32443641_G_A	0.29	0.39	G	0.59(0.49-0.72)	1.61E-07
6	chr6_32431358_T_G	0.29	0.39	T	0.59(0.49-0.72)	1.61E-07
6	chr6_32447364_T_C	0.29	0.39	T	0.59(0.49-0.72)	1.61E-07
6	chr6_31909200_A_G	0.07	0.03	G	2.95(1.97-4.43)	1.65E-07
6	chr6_32087260_G_A	0.08	0.03	A	2.78(1.89-4.07)	1.74E-07
6	chr6_32015864_C_T	0.07	0.03	T	2.90(1.94-4.32)	1.93E-07
6	chr6_32660375_A_G	0.15	0.24	A	0.53(0.42-0.67)	2.00E-07
6	chr6_32444475_T_C	0.27	0.37	T	0.59(0.49-0.72)	2.06E-07
6	DRB1:233:T	0.22	0.33	DRB1:233:T	0.58(0.47-0.71)	2.15E-07
6	chr6_32311193_A_G	0.07	0.03	G	2.85(1.92-4.23)	2.36E-07
6	chr6_32520538_G_DEL: TGTT	0.49	0.38	DEL:TGTT	1.57(1.32-1.86)	2.38E-07
6	chr6_32675902_T_G	0.11	0.2	T	0.50(0.39-0.65)	2.39E-07
6	chr6_32139638_C_T	0.07	0.03	T	2.83(1.91-4.19)	2.41E-07
6	chr6_31948022_C_G	0.07	0.03	G	2.89(1.93-4.33)	2.51E-07
6	chr6_31937511_T_C	0.07	0.03	C	2.89(1.93-4.33)	2.51E-07
6	chr6_32587090_C_T	0.49	0.38	T	1.60(1.34-1.92)	2.60E-07
6	chr6_31920219_T_C	0.07	0.03	C	2.84(1.91-4.23)	2.90E-07
6	chr6_32606217_G_A	0.5	0.39	A	1.56(1.31-1.84)	3.02E-07
6	DRB1:233:R	0.22	0.32	DRB1:233:R	0.58(0.48-0.72)	3.33E-07
6	chr6_32100210_G_C	0.08	0.03	C	2.72(1.85-4.00)	3.37E-07
6	chr6_32339511_C_T	0.11	0.05	T	2.23(1.64-3.04)	3.70E-07
6	chr6_32669018_C_A	0.12	0.2	C	0.51(0.39-0.66)	3.98E-07
6	chr6_32681631_C_T	0.12	0.2	C	0.51(0.39-0.66)	3.98E-07

6	chr6_32406843_C_T	0.17	0.1	C	1.90(1.48-2.44)	4.06E-07
6	DRB1:13:S	0.13	0.22	DRB1:13:S	0.54(0.42-0.68)	4.10E-07
6	chr6_32218989_G_A	0.34	0.24	A	1.64(1.35-1.98)	4.19E-07
6	chr6_32443266_T_C	0.34	0.44	T	0.62(0.51-0.74)	4.28E-07
6	chr6_32439077_T_C	0.27	0.37	T	0.60(0.50-0.73)	4.48E-07
6	chr6_32441100_A_C	0.27	0.37	A	0.60(0.50-0.73)	4.48E-07
6	chr6_32626139_C_G	0.29	0.4	G	0.62(0.51-0.75)	4.74E-07
6	DRB1:86:V	0.31	0.42	DRB1:86:V	0.62(0.51-0.75)	4.88E-07
6	DRB1:86:G	0.31	0.42	DRB1:86:G	0.62(0.51-0.75)	4.88E-07
6	chr6_32218299_T_C	0.33	0.24	C	1.63(1.35-1.98)	4.96E-07
6	DRB1:67:I	0.32	0.43	DRB1:67:I	0.63(0.52-0.75)	5.19E-07
6	chr6_32585504_G_C	0.41	0.52	G	0.64(0.54-0.76)	5.37E-07
6	chr6_32543450_A_INS: AGTT	0.31	0.41	INS:AGTT	0.62(0.51-0.74)	5.71E-07
6	chr6_32218666_T_G	0.33	0.24	G	1.63(1.34-1.97)	5.72E-07
6	chr6_32219725_A_G	0.33	0.24	G	1.63(1.34-1.97)	5.72E-07
6	chr6_32219962_G_A	0.33	0.24	A	1.63(1.34-1.97)	5.72E-07
6	chr6_32218681_A_G	0.33	0.24	G	1.63(1.34-1.97)	5.72E-07
6	chr6_32220037_A_C	0.33	0.24	C	1.63(1.34-1.97)	5.72E-07
6	chr6_32219010_T_A	0.33	0.24	A	1.63(1.34-1.97)	5.72E-07
6	chr6_32566288_G_A	0.48	0.38	A	1.58(1.32-1.89)	5.93E-07
6	chr6_32566287_G_C	0.48	0.38	C	1.58(1.32-1.89)	5.93E-07
6	chr6_32684935_C_T	0.16	0.25	T	0.56(0.45-0.71)	6.98E-07
6	chr6_32114833_T_C	0.07	0.03	C	2.70(1.82-4.01)	7.74E-07
6	DQA1:76:L	0.25	0.35	DQA1:76:L	0.61(0.50-0.74)	8.02E-07
6	chr6_32590154_T_C	0.35	0.46	T	0.63(0.53-0.76)	8.74E-07

6	chr6_32590159_C_A	0.35	0.46	C	0.63(0.53-0.76)	8.74E-07
6	chr6_32649676_G_T	0.12	0.2	G	0.53(0.41-0.68)	8.84E-07
6	DRB1:10:Q	0.3	0.4	DRB1:10:Q	0.62(0.52-0.75)	9.14E-07
6	chr6_32555855_C_DEL: TTT	0.3	0.41	DEL:TTT	0.62(0.52-0.75)	9.27E-07
6	chr6_32367017_G_A	0.16	0.09	G	1.91(1.47-2.47)	9.48E-07

A P-value less than  $1.0 \times 10^{-6}$  was used as the cut-off for significance.

ALT: Minor allele name (based on whole sample)

F\_A: Frequency of alt allele in cases

F\_U: Frequency of alt allele in controls

CI: confidence interval