

Top SNPs in PGX EMMA III

October 2008

Phenotype

VWI

p-values of EMMA III : top hits in each locus are highlighted in yellow

p-values of "marker" SNP matching SDP of top hit position, but comprising a full allele set in EMMA (22 alleles in total) are highlighted in light brown

Locus	chr	approx. range of locus (Mb)	chr position of top hit in build mm9	# allele 1	# allele 2	candidate gene (if matching SNP SDP at indicated position)	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT	
1	3	81-85	82'991'172	14	8	no gene	2.593-06	3.681-05	5.989-05	6.698E-03	4.695-05	2.193E-04	2.921E-04	8.247E-03	
			82'995'959	12	10	no gene	1.260-05	5.428-05	1.342-05	5.130E-04	1.222-04	2.838E-04	1.233E-04	1.268E-03	
			82'998'875	9	10	no gene	1.899-04	3.829E-04	5.936-05	5.249E-04	7.180E-04	1.095E-03	3.465E-04	1.373E-03	
			82'600'039	16	5	no gene	7.888-05	2.325-04	1.302E-03	1.712E-02	3.156E-04	6.616E-04	2.232E-03	1.787E-02	
			82'933'861	15	6	EG627094	1.722-04	4.042E-04	2.698E-03	4.557E-02	5.903E-04	1.055E-03	4.086E-03	4.355E-02	
			82'359'090	15	7	downstream of Npyr2	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'538'880	15	7	no gene	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'565'497	15	7	no gene	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'915'534	15	7	no gene	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'940'809	15	7	no gene	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'952'757	15	7	no gene	1.917-04	2.639E-04	2.582E-03	6.638E-02	6.093E-04	7.629E-04	3.894E-03	6.225E-02	
			82'348'468	15	6	Npy2r (neuropeptide Y receptor 2)	2.305-04	5.424E-04	2.922E-03	7.199E-02	7.235E-04	1.299E-03	4.367E-03	6.712E-02	
83'572'000	14	6	Sfrp2 (secreted frizzled-related protein 2)	2.376-04	5.039E-04	3.867E-03	5.388E-02	7.634E-04	1.276E-03	5.492E-03	5.079E-02				
2	3	86-90	87'719'795	13	7	Hdgf (maybe Arhgef11)	4.236-06	9.464-05	1.159E-04	3.615E-03	7.343-05	4.413E-04	4.919E-04	1.000E+00	
			for hit 1	87'720'406	14	8	Hdgf	3.219E-04	1.719E-03	3.639E-03	1.736E-02	9.004E-04	2.992E-03	5.267E-03	1.859E-02
			87'487'048	10	10	Arhgef11	1.031-05	3.737-05	1.302E-04	4.658E-04	1.196-04	2.542E-04	5.339E-04	1.228E-03	
			87'651'865	12	9	Sh2d2a	2.281E-03	5.943E-03	1.918E-03	9.467E-03	3.631E-03	7.578E-03	3.645-05	1.095E-02	
			89'441'864	13	6	Kcnn3 (intron 3)	4.050-05	2.526-05	6.046-05	3.800-05	2.479-04	1.961E-04	3.337E-04	2.551E-04	
			89'367'928	15	6	Kcnn3 (intron 1)	1.530-04	1.674-04	2.781E-04	6.709E-04	3.631E-03	5.497E-04	7.744E-04	1.405E-03	
3	4	single position	94'807'400	17	4	no gene (close to Jun)	4.458-06	3.345-06	3.351-06	5.094-05	7.167-05	6.006-05	5.655-05	2.634E-04	
4	7	75-77	75'814'117	17	5	upstream of Arrdc4; lgf1r?	8.610-06	3.038-06	8.642-06	3.525E-04	9.462-05	5.191-05	1.625-05	9.137E-04	
			75'824'602	17	5	upstream of Arrdc4	8.610-06	3.038-06	8.642-06	3.525E-04	9.462-05	5.191-05	1.625-05	9.137E-04	
5	1	11.5-12.5	11'899'477	14	7	Rik	5.356E-03	1.211E-03	9.609E-03	1.393E-03	7.185E-03	1.351-06	1.140E-02	2.657E-03	
			11'871'998	13	7	Rik	9.446-05	1.211-05	6.068-05	2.680-06	4.387E-04	1.300E-04	3.198E-04	6.280-05	
			11'902'481	14	8	Rik	1.985E-03	7.631E-04	2.933E-03	2.056E-04	3.290E-03	1.645E-03	4.406E-03	7.017E-04	

Locus	chr	approx. range of locus (Mb)	chr position of top hit in build mm9	# allele 1	# allele 2	candidate gene (if matching SNP SDP at indicated position)	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
6	1	38.5-39.5	38'947'935	14	5	Chst10 (carbohydrate sulfo-transferase)	3.200E-04	5.804-04	1.454E-03	9.333E-04	9.458E-04	8.232-07	2.627E-03	1.852E-03
7	2	130.5-132	131'352'413	16	6	Pank2; Rnf24; Smox; Adra1d; Adam33 ??	2.305E-03	2.930E-04	2.658-03	6.748E-04	3.625E-03	2.584-06	3.936E-03	1.441E-03
			130'881'869	15	5	Adam33	2.325-04	5.101-05	4.673E-04	8.330E-03	7.430E-04	2.852E-04	1.154E-03	9.832E-03
			130'952'456	17	4	upstream of Hspa12b (see AWI, L2)	6.072-05	1.439-05	8.115-05	1.134E-03	2.630-04	1.094-04	3.110E-04	1.938E-03
8	2	117-118	117'682'002	15	4	no gene	1.207-05	4.120-05	1.174-06	3.131-06	1.147-04	2.381E-04	3.157-05	4.706-05
			117'696'873	12	9	no gene	6.487E-03	2.854E-03	1.973E-03	4.515-06	8.073E-03	4.202E-03	3.137E-03	5.630-05
			118'088'072	15	5		1.931-04	8.831-05	7.352-05	4.225E-04	6.543E-04	3.951E-04	3.345E-04	9.796E-04
			117'677'222	15	7		2.929E-03	9.549E-04	1.751E-04	6.703E-05	4.239E-03	1.805E-03	5.396E-04	2.562E-04
9	4	151-153	151'355'820	16	5	close to Dnajc11 and Thap3 (Kcnab2)	2.058-05	7.615-05	3.346-07	5.804-06	1.285-04	3.058E-04	1.386-05	6.049-05
			152'394'133	17	4	no gene	3.127-05	2.481E-04	3.999-07	2.307-07	1.664-04	6.750E-04	1.521-05	9.927-06
			151'352'086	16	6	Dnajc11	7.306-05	2.852E-04	2.866-06	6.664-05	3.017-04	7.650E-04	4.565-05	2.741E-04
			151'390'225	16	6	Klhl21	7.306-05	2.852E-04	2.866-06	6.664-05	3.017-04	7.650E-04	4.565-05	2.741E-04
			152'310'182	16	6	no gene	7.306-05	2.852E-04	2.866-06	6.664-05	3.017-04	7.650E-04	4.565-05	2.741E-04
			152'328'074	14	5	no gene	2.521E-04	1.567E-03	4.042-06	3.019-06	8.068E-04	2.822E-03	7.218-05	5.996-05
			152'341'831	17	5	no gene	1.169-04	8.581E-04	4.147-06	8.025-06	4.094E-04	1.672E-03	5.587-05	6.998-05
			152'394'171	17	5	no gene	1.169-04	8.581E-04	4.147-06	8.025-06	4.094E-04	1.672E-03	5.587-05	6.998-05
			152'430'021	17	5	no gene	1.169-04	8.581E-04	4.147-06	8.025-06	4.094E-04	1.672E-03	5.587-05	6.998-05
			152'465'351	17	5	no gene	1.169-04	8.581E-04	4.147-06	8.025-06	4.094E-04	1.672E-03	5.587-05	6.998-05
10	10	110-110.5	110'702'509	16	4	Osbpl8 (oxysterol binding protein-like 8)	7.548-06	2.377-05	1.588-06	4.203-06	1.008-04	1.901E-04	4.156-05	6.966-05
			110'780'652	18	4	downstream of Osbpl8	2.060-05	6.222-05	1.141-05	3.756E-04	1.583-04	3.023E-04	1.050E-04	9.530E-04
			110'607'856	18	4	Osbpl8	2.060-05	6.222-05	1.141-05	3.756E-04	1.583-04	3.023E-04	1.050E-04	9.530E-04
			110'636'818	18	4	Osbpl8	2.060-05	6.222-05	1.141-05	3.756E-04	1.583-04	3.023E-04	1.050E-04	9.530E-04
			110'755'023	18	4	downstream of Osbpl8 (Bbs10 ?)	2.060-05	6.222-05	1.141-05	3.756E-04	1.583-04	3.023E-04	1.050E-04	9.530E-04

Locus	chr	approx. range of locus (Mb)	chr position of top hit in build mm9	# allele 1	# allele 2	candidate gene (if matching SNP SDP at indicated position)	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
11	1	94.5-95.5	94'914'398	10	5	Kif1A (kinesin family member); Aqp12 ?	4.472E-04	2.617E-03	2.766E-04	6.643-07	1.343E-03	4.373E-03	9.884E-04	5.212-05
			94'893'324	16	6	upstream of Kif1A	4.639E-02	2.751E-02	3.666E-03	4.684-05	4.486E-02	2.779E-02	5.106E-03	2.609E-04
			94'953'664	16	6	Kif1A (intron 19)	4.639E-02	2.751E-02	3.666E-03	4.684-05	4.486E-02	2.779E-02	5.106E-03	2.609E-04
12	2	119-121	119'637'990	12	8	Tyro3 (protein tyrosine kinase); gene-rich	5.652E-03	1.421E-03	3.507E-04	3.255-07	7.155E-03	2.443E-03	8.888E-04	1.487-05
			120'869'441	13	7	between Epb4.2 and Tgm5	3.170E-03	9.289E-04	1.437E-04	1.921-06	4.656E-03	1.872E-03	3.770E-04	3.575-05
13	5	104-105	104'572'764	15	5	Sparcl1	3.647E-04	5.519E-04	1.638-05	8.030-07	1.087E-03	1.378E-03	1.564E-04	4.076-05
			104'515'280	17	4	Sparcl1 (intron 8)	1.299E-03	1.140E-03	9.770-05	5.597-06	2.521E-03	2.213E-03	4.125E-04	9.503E-05
14	6	76-77	76'524'788	12	10	no gene	1.911E-01	1.694E-01	1.933E-01	1.095-01	1.766E-01	1.563E-01	1.785E-01	1.463-06
15	5	127.5-128.5	128'006'028	18	4	Tmem132c (transmembrane protein 132C; intron 5)	2.416-05	8.338-06	1.817-05	1.994-05	1.580-04	8.573-05	1.302E-04	1.286E-04
			128'006'079	18	4	Tmem132c (intron 5)	2.416-05	8.338-06	1.817-05	1.994-05	1.580-04	8.573-05	1.302E-04	1.286E-04
16	9	65.5-66	65'899'904	18	4	between Csnk1g1 and Snx22	1.967-04	8.396-06	4.523E-04	1.075E-02	6.374E-04	2.147E-04	1.070E-03	1.224E-02
			64'463'047	13	7	Megf11	3.649E-03	6.218E-03	7.215E-03	1.743-05	5.344E-03	8.061E-03	8.987E-03	1.647E-04
17	7	16-17	16'488'107	14	5	Crxos1 (intron 3)	9.400-05	3.369-05	3.162-06	7.346E-05	1.024-04	3.262-05	4.312-06	1.390E-04
			15'194'001	13	5	Rik	1.137-04	1.424-04	2.790E-04	6.614-06	1.059-04	1.431E-04	2.879E-04	1.639-05
18	6	125-126	125'528'422	17	5	Vwf (intron 6)	6.201-05	3.695-05	4.072-06	2.661-05	2.769-04	2.041E-04	5.622-05	1.629E-04
19	7	24.5-25.5	25'140'278	18	4	downstream of Lypd5	1.177-05	1.703-05	8.226-06	3.775-05	1.135-04	1.384E-04	8.625-05	2.045E-04
20	4	72-73.5	73'016'585	13	7	upstream of LOC gene	2.074E-03	1.771E-03	1.511E-03	2.659-06	3.544E-03	3.103E-03	2.714E-03	7.346-05
			73'202'146	13	7	between LOC and Rik genes	2.074E-03	1.771E-03	1.511E-03	2.659-06	3.544E-03	3.103E-03	2.714E-03	7.346-05
			72'313'856	15	7	no gene	4.352E-03	5.743E-03	2.588E-03	2.840-06	6.018E-03	7.411E-03	3.904E-03	6.197-05
21	4	82.5-83.5	82'834'365	9	11	LOC gene	1.494E-02	4.302E-03	5.896E-03	3.179-06	1.630E-02	5.884E-03	7.506E-03	5.747-05
22	6	145-146	145'091'729	16	6	Lrmp (lymphoid-restricted membrane protein; intron 3)	6.089E-03	6.128E-03	1.103-04	4.025-06	7.410E-03	7.493E-03	3.843E-04	3.913-05

Locus	chr	approx. range of locus (Mb)	chr position of top hit in build mm9	# allele 1	# allele 2	candidate gene (if matching SNP SDP at indicated position)	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
23	6	5-6	5'476'010	13	5	Slc25a13?	6.685E-03	3.182E-03	1.486E-03	4.607-06	8.612E-03	4.845E-03	2.756E-03	8.981E-05
			5'519'967	16	6		9.983E-01	9.586E-01	9.901E-01	7.487E-01	9.918E-01	9.516E-01	9.946E-01	7.266E-01
24	18	60.5-61.5	60'889'758	12	7	Ndst1 (N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1)	1.936-05	7.420-05	1.017-04	9.014-06	6.509-05	6.806-05	7.154-05	2.488-06
25	4	135-136	135'298'806	16	5	Il22ra1 (intron 4)	4.968-03	6.292E-03	5.991E-04	9.645E-04	7.542-06	7.939E-03	1.360E-03	2.052E-03
26	5	45-46	45'736'224	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
			45'776'195	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
			45'792'376	10	12	no gene (upstream of Lap3, leucine aminopeptidase 3)	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
27	5	47-48	47'619'864	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
			47'638'996	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
			47'704'974	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
			47'729'042	10	12	no gene	1.785E-02	9.025E-03	5.524-03	2.176E-02	1.906E-02	1.064E-02	6.138-06	2.263E-02
28	12	101.5-102.5	102'095'964	12	8	Rik	5.362E-01	7.143E-01	5.761E-01	5.346-01	5.128E-01	6.969E-01	1.360E-03	2.973-06
			102'085'056	12	10	Rik	6.521E-01	8.098E-01	7.234E-01	6.491E-01	6.334E-01	7.981E-01	7.076E-01	6.294E-01
29	12	113.5-114	113'701'753	12	9	no gene	4.428E-01	4.849E-01	3.410E-01	5.843-01	4.210E-01	4.636E-01	3.202E-01	3.884-06
			113'701'290	12	9	no gene	4.428E-01	4.849E-01	3.410E-01	5.843-01	4.210E-01	4.636E-01	3.202E-01	3.884-06
30	6	110-110.5	110'232'069	13	9	no gene	9.533E-01	7.441E-01	9.462E-01	9.977-01	9.495E-01	7.315E-01	9.421E-01	6.407-06
31	1	3-3.5	3'125'499	8	14	no gene	8.794E-01	9.741E-01	9.534E-01	6.049-01	8.704E-01	9.704E-01	9.538E-01	7.007-06
32	17	12-13	12'465'938	13	9	Map3k4 (intron 2)	6.140E-01	7.056E-01	6.285E-01	2.801-01	5.978E-01	2.482E-01	6.124E-01	8.838-06
			12'503'901	13	9	Map3k4 (intron 1)	6.140E-01	7.056E-01	6.285E-01	2.801-01	5.978E-01	2.482E-01	6.124E-01	8.838-06
			12'539'636	13	9	no gene	6.140E-01	7.056E-01	6.285E-01	2.801-01	5.978E-01	2.482E-01	6.124E-01	8.838-06

In summary

1 correct
2 inflated
3 correct
4 correct
5 inflated
6 inflated
7 correct
8 inflated
9 inflated
10 inflated
11 inflated
12 inflated
13 inflated
14 correct
15 correct
16 correct
17 inflated
18 correct
19 correct
20 inflated
21 inflated
22 correct
23 inflated
24 inflated
25 correct
26 *false positive*
27 *false positive*
28 inflated
29 inflated
30 *false positive*
31 *false positive*
32 *false positive*

Top SNPs in PGX EMMA III

October 2008

Phenotype **AWI**

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 hits of each association scan

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	15	96'776'527	8	12	close to Slc38a4	9.963-07	4.929-08	3.478-05	9.70E-03	2.255-05	5.653-06	1.837-04	1.09E-02
1	15	96'941'901	7	13	close to Slc38a4	1.394-06	7.152-08	8.323-06	2.54E-02	3.025-05	5.274-06	7.585-05	2.54E-02
1	15	96'621'748	8	12	close to Slc38a4	1.597-06	2.960-06	5.236-07	7.44E-03	3.354-05	4.574-05	1.911-05	9.09E-03
1	15	96'783'680	9	13	close to Slc38a4	3.995-05	3.099-05	5.752-06	2.69E-03	1.855-04	1.469-04	5.729-05	3.84E-03
1	15	96'783'801	9	13	close to Slc38a4	3.995-05	3.099-05	5.752-06	2.69E-03	1.855-04	1.469-04	5.729-05	3.84E-03
1	15	96'757'796	7	15	close to Slc38a4	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	96'757'900	7	15	close to Slc38a4	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	97'487'753	7	15	close to Rpap3	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	97'488'188	7	15	close to Rpap3	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	97'488'250	7	15	close to Rpap3	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	97'508'231	7	15	close to Rpap3	5.068-05	1.891-06	1.271-05	2.76E-02	2.313-04	2.818-05	8.537-05	2.73E-02
1	15	96'603'063	7	14	close to Slc38a2	4.314-05	3.388-06	2.650-06	1.70E-02	2.240-04	4.373-05	3.993-05	1.79E-02
2	2	130'881'869	15	5	Adam33	2.050-06	1.480-04	8.82E-03	3.72E-02	4.546-06	5.001-04	9.96E-03	3.57E-02
2	2	130'952'456	17	4	Hspa12b	4.781-06	3.70E-04	5.05E-03	2.17E-02	6.358-06	8.49E-04	6.11E-03	2.18E-02
3	12	106'809'584	10	8	Bdkrb2 (bradykinin receptor, beta 2)	5.297-07	9.974-05	3.39E-02	4.52E-02	2.572-05	4.342-04	3.26E-02	4.31E-02
3	12	106'753'156	14	6	close to Bdkrb2	4.735-06	1.759-04	2.09E-02	6.66E-02	7.355-05	5.445-04	2.14E-02	6.20E-02
4	3	104'093'148	8	10	close to Magi3	1.30E-03	2.096-06	1.16E-02	4.69E-02	2.54E-03	5.233-05	1.29E-02	4.37E-02
5	10	120'899'587	13	9	Rassf3	1.93E-03	7.569-06	2.14E-03	2.76E-02	3.07E-03	7.348-05	3.07E-03	2.72E-02
5	10	121'065'248	13	9	Xpot (exportin)	1.93E-03	7.569-06	2.14E-03	2.76E-02	3.07E-03	7.348-05	3.07E-03	2.72E-02
6	17	9'251'653	14	5	no gene	2.548-04	1.396-06	1.37E-04	2.618-05	7.337-04	2.827-05	4.83E-04	1.895-04
7	6	50'294'528	9	5	Osbpl3	9.92E-03	1.60E-03	8.334-07	4.42E-03	1.17E-02	2.91E-03	2.755-05	6.42E-03
8	3	134'132'525	17	4	no gene	2.37E-03	5.23E-04	1.45E-03	8.951-06	3.57E-03	1.15E-03	2.52E-03	9.391-05
8	3	134'083'634	16	4	no gene	2.37E-03	5.23E-04	1.45E-03	1.369-05	3.57E-03	1.15E-03	2.52E-03	1.309-04

Top SNPs in PGX EMMA III

October 2008

Phenotype BWS

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 hits of each association scan

loci are numbered as for BWE

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	1	157'724'450	7	11	Qscn6, Cep350	1.530-06	1.570-06	5.798-06	1.010-04	3.923-05	4.084-05	8.010-05	4.109-04
2	1	160'090'318	9	11	no gene	4.344-06	5.835-06	6.269-06	1.373-05	6.521-05	7.978-05	8.466-05	1.142-04
3a	5	77'895'444	10	9	downstream of Rest, Polr2b and Igfbp7	3.597-06	2.534-06	4.270-06	5.307-07	5.476-05	4.603-05	6.104-05	1.917-05
3b	5	79'189'684	7	8	no gene	8.034-06	4.436-05	1.509-05	2.682-05	1.271-04	3.172-04	1.77E-04	2.316-04
3b	5	79'213'585	11	8		2.824-05	3.311-06	7.381-07	1.689-05	1.738-04	5.047-05	2.140-05	1.160-04
3c	5	80'076'361	10	8	no gene	1.458-05	5.555-05	1.673-05	6.078-05	1.483-04	3.270-04	1.700-04	3.070-04
4	5	91'238'566	8	13	no gene; between Cxcl1 and Cxcl5	2.530-07	4.55-06	5.458-06	1.319-05	1.285-05	6.401-05	7.303-05	1.016-04
4	5	91'288'973	7	13	no gene; between Cxcl1 and Cxcl5	1.178-06	6.465-06	8.605-06	2.072-05	3.207-05	8.669-05	1.071-04	1.453-04
5a	5	97'762'858	10	12	predicted gene	1.277-06	8.610-06	7.381-07	4.026-07	2.715-05	8.378-05	2.200-05	1.371-05
5b	5	98'791'983	9	6	Rik; close to Fgf5	1.718-06	1.412-05	1.45E-04	4.664-05	5.884-05	1.707-04	6.32E-04	3.30E-04
5b	5	98'799'267	9	13	Rik; close to Fgf5	9.562-06	1.19E-04	3.259-05	1.141-05	8.624-05	4.88E-04	1.97E-04	8.911-05
6	3	119'716'225	11	9	no gene	1.704-05	4.488-07	2.835-06	1.237-05	1.349-04	1.984-05	5.164-05	1.140-04

how come that significance is lower in iso 10 group ?

the groups should be homogeneous for this trait!

Top SNPs in PGX EMMA III

October 2008

Phenotype **BWE**

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 (?) hits of each association scan

loci are numbered as for BWS

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	1	157'724'450	7	11	Qscn6, Cep350	5.117-06	5.304-05	6.519-05	5.86E-04	7.233-05	2.92E-04	3.235-04	1.34E-03
1	1	157'714'026	7	11		4.82E-05	5.97E-06	2.87E-04	3.16E-03	2.62E-04	8.059-05	8.27E-04	4.54E-03
2	1	160'090'318	9	11	no gene	1.569-06	3.078-07	4.834-06	3.938-06	3.984-05	1.943-05	7.413-05	5.832-05
2	1	160'101'381	10	12	no gene	1.61-06	1.487-07	1.014-06	2.706-06	3.192-05	1.016-05	2.629-05	4.006-05
3a	5	77'895'444	10	9	downstream of Rest, Polr2b and Igfbp7	4.368-07	8.083-06	1.225-06	5.402-06	1.767-05	8.791-05	3.163-05	7.005-05
3b	5	79'189'684	7	8	no gene	2.604-06	4.188-06	6.971-06	3.788-05	7.037-05	9.362-05	1.201-04	2.775-04
3b	5	79'213'585	11	8		5.335-05	2.778-05	2.390-06	8.990-05	2.583-04	1.79E-04	4.360-05	3.587-04
3c	5	80'076'361	10	8	no gene	2.576-05	1.96E-04	4.565-06	1.659-04	1.921-04	7.43E-04	8.256-05	5.95E-04
4	5	91'238'566	8	13	no gene; between Cxcl1 and Cxcl5	3.650-07	1.125-04	6.679-05	1.26E-03	1.588-05	4.73E-04	3.209-04	2.20E-03
4	5	91'288'973	7	13	no gene; between Cxcl1 and Cxcl5	2.936-06	3.19E-04	1.268-04	1.95E-03	5.301-05	9.81E-04	5.181-04	3.12E-03
5a	5	97'762'858	10	12	predicted gene	1.226-07	4.761-07	3.814-08	1.788-07	8.199-06	1.844-05	4.952-06	9.413-06
5a	5	97'755'919	9	12	predicted gene	1.57E-06	4.50E-06	5.593-07	2.108-06	3.249-05	5.076-05	2.009-05	3.715-05
5b	5	98'791'983	9	6	Rik; close to Fgf5	7.054-08	1.794-05	3.667-05	1.782-04	1.445-05	2.04E-04	2.921-04	6.454-04
5b	5	98'799'267	9	13	Rik; close to Fgf5	7.709-06	1.845-05	7.274-06	5.692-05	7.883-05	1.47E-04	8.025-05	2.492-04
6	3	119'716'225	11	9	no gene	1.386-05	8.398-05	2.176-05	1.321-04	1.201-04	3.77E-04	1.601-04	4.77E-04
7	4	136'024'312	8	14	between Htr1d (5-hydroxytryptamine-(serotonin)-receptor 1d) and Luzp1 (leucine zipper protein 1)	2.977-06	6.462-07	2.657-06	1.727-07	4.535-05	2.105-05	4.514-05	9.570-06
8	1	94'970'423	10	6	Kif1A, exon 8, coding SNP	6.858-05	2.139-05	6.928-07	4.131-06	3.96E-04	1.98E-04	3.640-05	8.735-05
8	1	94'893'324	16	6	close to Kif1A	3.88E-04	5.539-05	1.886-05	9.762-07	9.57E-04	2.66E-04	1.377-04	2.489-05
8	1	94'953'664	16	6	Kif1A intron 19	3.88E-04	5.539-05	1.886-05	9.762-07	9.57E-04	2.66E-04	1.377-04	2.489-05
9	15	48'564'653	14	4	close to Csmc3	8.800-05	3.924-05	1.401-05	1.904-06	4.11E-04	2.76E-04	1.488-04	4.837-05
10	4	57'810'855	14	8	between Palm2(paralemmmin 2) and Akap2 (A kinase (PRKA) anchor protein 2)	6.76E-03	8.57E-03	2.23E-02	3.42E-02	8.42E-03	1.210-06	1.50E-02	3.37E-02

Top SNPs in PGX EMMA III

October 2008

Phenotype **BWG**

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 hits of each association scan

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	4	24'590'164	9	11	Klhl32 (kelch-like 32)	1.407-07	2.26E-02	>1.169E-01	>1.189E-01	6.709-07	2.23E-02	>1.064E-01	>1.071E-01
1	4	25'165'243	9	12	Fhl5 (four and a half LIM domains 5)	1.813-07	4.41E-02	>1.169E-01	>1.189E-01	2.717-06	4.13E-02	>1.064E-01	>1.071E-01
2	4	27'083'237	9	11	no gene	2.73-06	1.78E-02	>1.169E-01	>1.189E-01	2.742-06	1.78E-02	>1.064E-01	>1.071E-01
2	4	27'385'037	9	11	no gene	2.73-06	1.78E-02	>1.169E-01	>1.189E-01	2.742-06	1.78E-02	>1.064E-01	>1.071E-01
3	4	148'955'499	8	10	between Ctnnbip1 (catenin beta interacting protein 1) and Clstn1 (calsyntenin 1)	1.244-06	9.06E-02	5.57E-02	>1.189E-01	6.031-06	8.19E-02	5.08E-02	>1.071E-01
4	14	49'018'445	5	16	no gene	4.639-06	1.97E-02	1.12E-01	>1.189E-01	9.036-06	2.00E-02	1.02E-01	>1.071E-01
5	7	131'996'982	6	11	no gene	4.943-06	7.58E-02	>1.169E-01	>1.189E-01	7.017-06	6.80E-02	>1.064E-01	>1.071E-01
5	7	132'034'869	9	11	no gene	5.878-06	3.88E-02	>1.169E-01	>1.189E-01	7.677-06	3.65E-02	>1.064E-01	>1.071E-01
6	9	38'271'612	5	15	Olfr genes (Olfr 904)	5.419-06	2.33E-02	>1.169E-01	>1.189E-01	1.149-05	2.32E-02	>1.064E-01	>1.071E-01
7	10	21'801'164	12	7	downstream of Sgk	6.298-06	4.52E-02	>1.169E-01	>1.189E-01	6.030-05	4.25E-02	>1.064E-01	>1.071E-01
8	2	45'584'470	8	14	no gene	6.452-06	8.55E-04	7.03E-02	>1.189E-01	1.769-05	1.53E-03	4.33E-02	>1.071E-01
8	2	46'412'280	8	14	no gene	6.452-06	8.55E-04	7.03E-02	>1.189E-01	1.769-05	1.53E-03	4.33E-02	>1.071E-01
9	18	73'152'735	7	8	no gene	6.746-06	8.55E-04	7.03E-02	>1.189E-01	8.61E-05	>1.09E-01	4.33E-02	>1.071E-01
10	8	66'485'305	9	13	close to Tll1 (tolloid-like)	9.62E-05	9.499-08	2.17E-03	>1.189E-01	1.49E-04	5.188-06	2.77E-03	>1.071E-01
10	8	66'497'864	9	13	Tll1 (tolloid-like)	9.62E-05	9.499-08	2.17E-03	>1.189E-01	1.49E-04	5.188-06	2.77E-03	>1.071E-01
10	8	66'434'356	9	12	close to Tll1 (tolloid-like)	2.81E-04	3.440-07	2.01E-03	>1.189E-01	3.23E-04	1.273-05	2.67E-03	>1.071E-01
10	8	66'492'658	7	13	close to Tll1 (tolloid-like)	4.28E-03	4.939-06	1.11E-02	>1.189E-01	4.61E-03	5.988-05	1.15E-02	>1.071E-01
11	2	64'515'925	11	7	no gene	2.26E-04	3.501-07	>1.169E-01	>1.189E-01	3.35E-04	7.243-06	>1.064E-01	>1.071E-01
12	18	29'864'982	18	4	no gene	3.82E-01	2.908-06	>1.169E-01	>1.189E-01	>8.907E-02	2.805-05	>1.064E-01	6.94E-02
12	18	28'455'187	16	4	no gene	4.65E-01	6.584-06	>1.169E-01	>1.189E-01	>8.907E-02	5.329-05	>1.064E-01	9.70E-02
13	2	142 hits at p<10 ⁻⁹ from 18'754'798 to 26'103'095 (3 hits wi				3.11E-01	8.06E-02	1.37E-02	5.816-12	>8.907E-02	7.42E-02	1.35E-02	1.922-07

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
14	3	75'870'702	18	4	close to Fstl5 (follistatin like 5)	3.11E-01	8.06E-02	1.37E-02	6.136-10	>8.907E-02	7.42E-02	1.35E-02	8.666-07
14	3	75'906'491	18	4	Fstl5 (intron 1)	3.11E-01	8.06E-02	1.37E-02	6.136-10	>8.907E-02	7.42E-02	1.35E-02	8.666-07
14	3	75'943'844	18	4	Fstl5 (intron 1)	3.11E-01	8.06E-02	1.37E-02	6.136-10	>8.907E-02	7.42E-02	1.35E-02	8.666-07
14	3	75'944'070	18	4	Fstl5 (intron 1)	3.11E-01	8.06E-02	1.37E-02	6.136-10	>8.907E-02	7.42E-02	1.35E-02	8.666-07
14	3	75'977'304	18	4	Fstl5 (intron 2)	3.11E-01	8.06E-02	1.37E-02	6.136-10	>8.907E-02	7.42E-02	1.35E-02	8.666-07
14	3	75'927'523	17	4	Fstl5 (intron 1)	>1.087E-01	1.06E-01	1.47E-02	3.531-09	>8.907E-02	9.66E-02	1.46E-02	2.082-06
14	3	76'047'990	17	5	Fstl5 (intron 3)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'074'186	17	5	Fstl5 (intron 3)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'112'536	17	5	Fstl5 (intron 3)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'117'549	17	5	Fstl5 (intron 3)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'125'838	17	5	Fstl5 (intron 3)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'134'607	17	5	Fstl5 (intron 4)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'143'621	17	5	Fstl5 (intron 4)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
14	3	76'143'821	17	5	Fstl5 (intron 4)	>1.087E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
15	15	100'275'534	5	14	between Slc11a2 and Tcfcp2	3.63E-01	7.27E-02	1.80E-02	4.453-07	>8.907E-02	6.70E-02	1.85E-02	2.623-05
16	11	31'161'304	16	6	between Asb3 (ankyrin repeat and SOCS box- containing protein 3) and Stc2 (stanniocalcin 2)	2.96E-01	1.05E-01	2.25E-02	2.403-06	>8.907E-02	9.59E-02	2.20E-02	4.022-05
16	11	32'138'996	17	5	Mare (alpha globin regulatory element containing gene)	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
16	11	32'150'068	17	5	Mare	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
16	11	32'150'099	17	5	Mare	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
16	11	32'155'673	17	5	Mare	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
16	11	32'157'203	17	5	Mare	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05
16	11	32'168'022	17	5	Mare	3.50E-01	>1.184E-01	1.47E-02	3.830-06	>8.907E-02	>1.09E-01	1.45E-02	5.120-05

Top SNPs in PGX EMMA III

October 2008

Phenotype **SBP**

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 hits of each association scan

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	1	40'082'962	16	5	between Map4k4 and Il1r2	4.333-08	4.314-06	3.667-09	7.73E-05	4.820-06	3.949-05	7.536-07	2.48E-04
1	1	39'355'826	12	8	Npas2	9.372-06	1.73E-03	2.86E-03	6.35E-04	8.756-05	2.68E-03	3.89E-03	1.23E-03
1	1	40'586'235	14	8	Il18rap	9.812-06	1.84E-04	2.56E-04	9.99E-05	7.695-05	4.70E-04	5.51E-04	3.05E-04
2	1	174'496'479	16	6	downstream of Ccdc19	9.648-07	2.807-08	7.51E-04	2.537-06	2.362-05	4.13-06	1.35E-03	3.114-05
3	15	10'502'419	12	4	Rai14 (retinoic acid induced 14)	6.409-06	3.39E-02	1.54E-02	7.79E-03	9.927-05	3.14E-02	1.77E-02	1.02E-02
4	16	69'832'723	8	13	no gene	1.57E-04	2.189-07	1.035-06	7.44E-05	4.74E-04	9.315-06	1.395-05	2.51E-04
4	16	69'809'658	7	13	no gene	2.09E-05	2.374-07	8.604-07	3.44E-04	1.39E-04	1.097-05	1.455-05	7.75E-04
4	16	69'801'520	8	14	no gene	1.23E-04	4.271-07	4.099-06	1.10E-04	3.81E-04	1.165-05	3.052-05	3.10E-04
4	16	69'829'859	8	14	no gene	1.23E-04	4.271-07	4.099-06	1.10E-04	3.81E-04	1.165-05	3.052-05	3.10E-04
4	16	69'844'121	8	14	no gene	1.23E-04	4.271-07	4.099-06	1.10E-04	3.81E-04	1.165-05	3.052-05	3.10E-04
4	16	69'844'264	8	12	no gene	3.27E-04	1.230-06	7.640-06	3.14E-04	7.81E-04	2.357-05	5.038-05	6.92E-04
4	16	69'803'212	7	12	no gene	3.76E-05	1.549-06	3.056-06	7.00E-04	2.16E-04	3.225-05	3.345-05	1.35E-03
5	12	17'462'872	8	9	downstream of Nol10	4.56E-04	3.602-06	7.96E-03	1.07E-04	1.09E-03	6.604-05	8.79E-03	2.85E-04
6	14	121'290'632	18	4	upstream of Ranbp5	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
6	14	121'580'882	18	4	Farp1	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
6	14	121'808'558	18	4	downstream of Stk24	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
6	14	121'851'153	18	4	between Stk24 and Slc15a1	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
6	14	121'870'684	18	4	Slc15a1	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
7	18	58'794'451	18	4	upstream of Isoc1	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04
7	18	58'838'764	18	4	Isoc1 (isochorismatase domain containing 1)	2.114-05	4.057-06	9.835-05	6.96E-05	1.137-04	4.230-05	2.703-04	1.985-04

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
8	1	80'948'509	14	8	upstream of Rik gene	1.23E-04	4.074-06	4.626-05	6.181-05	3.97E-04	4.100-05	1.640-04	2.33E-04
8	1	80'948'680	14	8	upstream of Rik gene	1.23E-04	4.074-06	4.626-05	6.181-05	3.97E-04	4.100-05	1.640-04	2.33E-04
8	1	80'954'974	14	8	upstream of Rik gene	1.23E-04	4.074-06	4.626-05	6.181-05	3.97E-04	4.100-05	1.640-04	2.33E-04
8	1	81'140'853	14	8	Rik gene	1.23E-04	4.074-06	4.626-05	6.181-05	3.97E-04	4.100-05	1.640-04	2.33E-04
8	1	80'948'250	12	8	upstream of Rik gene	2.38E-04	8.852-06	1.28E-04	3.32E-05	6.89E-04	7.861-05	3.64E-04	1.807-04
8	1	80'927'568	13	8	upstream of Rik gene	1.80E-04	9.040-06	6.751-05	6.423-05	5.41E-04	7.111-05	2.272-04	2.57E-04
9	8	97'521'342	15	7	Gpr56	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'536'095	15	7	Gpr56	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'567'351	15	7	Gpr56	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'570'684	15	7	no gene	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'574'815	15	7	no gene	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'616'392	15	7	Katnb1	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'675'182	15	7	no gene	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'752'335	15	7	no gene	3.31E-04	1.14E-03	3.815-07	3.57E-03	7.44E-04	1.76E-03	7.700-06	4.29E-03
9	8	97'610'163	14	7	Katnb1	4.59E-04	1.75E-03	6.348-07	3.82E-03	9.81E-04	2.50E-03	1.185-05	4.61E-03
9	8	97'734'320	14	7	no gene	6.40E-04	2.08E-03	1.001-06	6.06E-03	1.23E-03	2.83E-03	1.414-05	6.65E-03
9	8	97'466'278	10	12	Gpr114	6.49E-04	6.92E-04	6.407-06	1.72E-02	1.19E-03	1.21E-03	3.946-05	1.68E-02
10	11	117'417'319	7	15	upstream of Tnrc6c	4.28E-03	2.54E-03	1.64E-03	5.010-08	5.34E-03	3.45E-03	2.34E-03	4.179-06
10	11	117'547'031	7	15	Tnrc6c (trinucleotide repeat containing 6C)	4.28E-03	2.54E-03	1.64E-03	5.010-08	5.34E-03	3.45E-03	2.34E-03	4.179-06
10	11	117'559'860	7	15	Tnrc6c	4.28E-03	2.54E-03	1.64E-03	5.010-08	5.34E-03	3.45E-03	2.34E-03	4.179-06
10	11	117'755'403	7	15	end of chromosome	4.28E-03	2.54E-03	1.64E-03	5.010-08	5.34E-03	3.45E-03	2.34E-03	4.179-06
10	11	117'410'377	6	14	upstream of Tnrc6c	1.78E-03	2.63E-03	1.07E-03	4.359-07	2.76E-03	3.67E-03	1.77E-03	1.870-05
10	11	117'749'722	7	13	end of chromosome	3.36E-02	1.77E-02	6.37E-03	6.301-07	3.26E-02	1.82E-02	7.83E-03	3.241-05
10	11	117'749'606	7	14	end of chromosome	3.66E-02	2.38E-02	1.27E-02	8.154-07	3.53E-02	2.36E-02	1.37E-02	3.241-05
11	1	75'525'204	9	11	Stk11ip (serine/threonine kinase 11 interacting protein)	1.61E-03	3.31E-04	8.84E-03	4.359-07	2.61E-03	7.76E-04	9.59E-03	1.578-05
12	19	26'002'150	5	14	no gene	3.51E-03	5.64E-03	1.33E-03	1.097-06	4.71E-03	6.77E-03	2.12E-03	2.570-05

Top SNPs in PGX EMMA III

October 2008

Phenotype HR

top hits are highlighted in yellow

p-values are indicated in blue when found in top 58 hits of each association scan

Locus	chr	chr position of top hit in build mm9	# allele 1	# allele 2	gene	con REMLt	ate REMLt	iso 1 REMLt	iso 10 REMLt	con LRT	ate LRT	iso 1 LRT	iso 10 LRT
1	3	12'488'632	6	10	no gene	1.650-05	2.37E-03	>9.788E-02	>9.854E-02	1.832-04	4.51E-03	>9.017E-02	>8.794E-02
2	17	33'222'672	12	10	upstream of Zfp563	3.445-05	1.885-08	5.30E-03	8.60E-02	1.972-04	3.868-06	6.74E-03	8.01E-02
3	3	136'275'789	6	9	upstream of Ppp3ca	>7.548E-02	2.671-07	4.77E-02	>9.854E-02	1.73E-02	2.126-05	4.41E-02	>8.794E-02
4	5	46'647'683	11	9	no gene	5.479-05	1.804-06	2.62E-02	>9.854E-02	2.996-04	4.766-05	2.63E-02	>8.794E-02
5	11	110'383'615	7	11	downstream of Map2k6	1.13E-03	1.037-06	1.17E-03	1.87E-03	2.15E-03	3.291-05	2.31E-03	3.13E-03
6	12	89'722'471	7	14	downstream of Adck1	3.69E-04	4.873-07	2.63E-02	>9.854E-02	9.77E-04	1.773-05	2.68E-02	>8.794E-02
6	12	89'980'833	6	12	LOC gene	3.16E-04	1.434-06	6.71E-02	>9.854E-02	1.00E-03	4.263-05	6.20E-02	>8.794E-02
7	7	19'995'563	8	8	downstream of Fosb	>7.548E-02	>9.098E-02	1.10E-02	5.638-08	>7.080E-02	>8.44E-02	1.23E-02	1.003-05
7	7	19'899'774	11	8	between Klcl3 and Mark4	>7.548E-02	>9.098E-02	2.70E-03	3.609-07	>7.080E-02	>8.44E-02	4.07E-03	1.945-05
8	16	45'072'305	11	11	upstream of Ccdc80	>7.548E-02	>9.098E-02	6.85E-03	1.029-07	>7.080E-02	>8.44E-02	8.09E-03	7.545-06
8	16	45'221'826	11	11	upstream of Btla	>7.548E-02	>9.098E-02	6.85E-03	1.029-07	>7.080E-02	>8.44E-02	8.09E-03	7.545-06
8	16	44'618'442	8	14	no gene	>7.548E-02	>9.098E-02	8.81E-03	2.363-07	>7.080E-02	>8.44E-02	1.03E-02	1.254-05
8	16	44'657'090	8	14	no gene	>7.548E-02	>9.098E-02	8.81E-03	2.363-07	>7.080E-02	>8.44E-02	1.03E-02	1.254-05
8	16	45'072'153	11	10	upstream of Ccdc80	>7.548E-02	>9.098E-02	8.52E-03	3.786-07	>7.080E-02	>8.44E-02	9.77E-03	1.532-05
9	19	46'331'705	7	9	Gbf1 (golgi-specific brefeldin A-resistance factor 1)	>7.548E-02	>9.098E-02	6.53E-04	1.508-06	>7.080E-02	>8.44E-02	1.62E-03	6.236-05
10	14	75'635'507	15	7	between Lcp1 (lymphocyte cytosolic protein 1) and Cpb2 (carboxypeptidase B2 (plasma))	>7.548E-02	>9.098E-02	4.78E-03	3.545-06	>7.080E-02	>8.44E-02	5.99E-03	4.627-05
10	14	73'598'556	7	11	Rb1	>7.548E-02	>9.098E-02	8.36E-03	7.539-06	>7.080E-02	>8.44E-02	9.93E-03	1.218-04

