

Suppl.Table.1. Resilience genomic loci identified at the suggestive threshold of significance ($p < 1 \times 10^{-5}$) using FUMA-GWAS.

Locus	rsID	Chr	Position	Non-Effect	Effect	Ref_MAF	Meta_p	Z-score	Nearest gene(s)	dist	Consequence	CADD	pos.Map	eQTLs
-	rs139460883	1	14426083	G	T	0.011	7.69E-07	4.943	RNU6-1265P	24644	intergenic	1.11	0	0
-	rs10912183	1	187758485	G	T	0.287	5.43E-06	-4.548	RP5-925F19.1	74618	intergenic	0.86	0	0
-	rs73176273	2	11235162	T	C	0.294	1.90E-06	4.764	AC062028.1	4814	intergenic	11.38	0	0
1	rs6763014	3	112512647	T	G	0.498	1.01E-05	-4.415	RP11-180K7.1	8677	intergenic	1.37	0	1
1	rs10804503	3	112513358	C	T	0.431	2.06E-03	3.082	RP11-180K7.1	7966	intergenic	0.52	0	1
1	rs10934187	3	112513482	G	A	0.488	1.39E-05	-4.345	RP11-180K7.1	7842	intergenic	0.48	0	1
1	rs6797028	3	112515187	G	A	0.497	9.44E-06	-4.430	RP11-180K7.1	6137	intergenic	2.40	0	1
1	rs6772960	3	112515540	T	C	0.497	1.10E-05	-4.397	RP11-180K7.1	5784	intergenic	3.27	0	1
1	rs9875150	3	112515784	C	T	0.498	1.07E-05	-4.403	RP11-180K7.1	5540	intergenic	3.51	0	1
1	rs9821278	3	112515884	A	G	0.431	2.38E-03	3.038	RP11-180K7.1	5440	intergenic	4.02	0	1
1	rs9859168	3	112515906	T	C	0.498	1.11E-05	-4.395	RP11-180K7.1	5418	intergenic	0.02	0	1
1	rs6789210	3	112516328	C	T	0.497	1.04E-05	-4.409	RP11-180K7.1	4996	intergenic	2.60	0	1
1	rs6800648	3	112516433	G	A	0.489	9.93E-06	-4.419	RP11-180K7.1	4891	intergenic	2.27	0	1
1	rs6793183	3	112517755	C	T	0.497	1.01E-05	-4.416	RP11-180K7.1	3569	intergenic	3.71	0	1
1	rs9832885	3	112518459	G	A	0.497	7.36E-05	-3.965	RP11-180K7.1	2865	intergenic	11.92	0	1
2	rs78180970	3	193598924	C	T	0.178	4.88E-06	-4.570	RP11-528A4.2	37110	intergenic	0.33	0	0
2	rs73890903	3	193613240	C	T	0.177	1.64E-04	-3.769	RP11-528A4.2	51426	intergenic	4.80	0	0
2	rs78541467	3	193618823	G	C	0.172	1.85E-04	-3.738	RP11-699L21.1	56337	intergenic	0.22	0	0
-	rs147694396	4	147509032	A	G	0.019	6.09E-06	-4.523	RNU1-44P	7669	intergenic	1.54	0	0
-	rs76273681	6	92011080	A	G	0.032	3.04E-06	4.669	RP1-177110.1	88950	intergenic	0.41	0	0
3	rs58658066	7	11554555	C	G	0.115	2.04E-05	-4.261	AC004538.3	0	ncRNA_intronic	7.44	1	0
3	rs17633522	7	11555542	G	C	0.115	8.10E-06	-4.463	AC004538.3	0	ncRNA_intronic	0.63	1	0
3	rs10486142	7	11559955	T	C	0.115	1.51E-05	-4.327	THSD7A	0	intronic	6.02	1	0
3	rs56671626	7	11561644	G	C	0.126	4.81E-05	-4.065	THSD7A	0	intronic	4.66	1	0
4	rs35299971	14	40763557	C	T	0.486	1.66E-05	-4.307	RP11-662J14.1	91898	intergenic	1.43	0	0
4	rs7153205	14	40790811	C	T	0.439	5.32E-06	4.552	RP11-662J14.1	64644	intergenic	9.38	0	1
4	rs12588094	14	40798479	G	A	0.475	5.38E-05	-4.039	RP11-662J14.1	56976	intergenic	1.24	0	0
4	rs1950241	14	40802371	C	T	0.475	5.37E-05	-4.039	RP11-662J14.1	53084	intergenic	0.56	0	1
4	rs61989120	14	40818021	T	C	0.440	2.97E-06	4.673	RP11-662J14.1	37434	intergenic	0.22	0	1
4	rs141604435	14	40849721	G	A	0.477	2.75E-02	-2.204	RP11-662J14.1	5734	intergenic	0.79	0	1
4	rs12893089	14	40851097	A	C	0.477	2.85E-02	-2.190	RP11-662J14.1	4358	intergenic	2.04	0	1
4	rs12888686	14	40857356	T	A	0.479	3.05E-02	-2.163	RP11-662J14.2	0	ncRNA_intronic	2.10	1	1
4	rs17780892	14	40858183	G	A	0.477	2.84E-02	-2.191	RP11-662J14.2	0	ncRNA_intronic	2.07	1	1
4	rs11851674	14	40858958	T	G	0.478	3.20E-02	-2.145	RP11-662J14.2	613	downstream	10.57	1	1
4	rs1952935	14	40859517	A	C	0.478	2.79E-02	-2.199	RP11-662J14.2	1172	intergenic	9.93	0	1
4	rs11851600	14	40860432	G	T	0.478	2.47E-02	-2.246	RP11-662J14.2	2087	intergenic	5.39	0	1
5	rs11649705	17	19612489	G	A	0.088	1.26E-02	2.496	SLC47A2	0	intronic	4.89	1	1
5	rs11657623	17	19612945	T	C	0.088	1.27E-02	2.493	SLC47A2	0	intronic	6.94	1	1

5	rs115685297	17	19756449	T	A	0.074	2.43E-05	4.221	ULK2	0 intronic	0.14	1	1
5	rs112155453	17	19771057	C	G	0.069	3.93E-06	4.615	ULK2	0 UTR5	10.11	1	1
5	rs72841970	17	19777031	G	A	0.058	2.05E-04	3.713	ULK2	5781 intergenic	0.56	0	1
-	rs17518744	18	6979919	A	G	0.488	9.86E-06	4.421	LAMA1	0 intronic	8.45	1	0

Ref_MAF: Minor allele frequency in the reference panel

Lead locus variant

Top variant

Suppl.Table.2. Annotated eQTL effects in brain, blood and immune cells of variants in suggestive resilience loci.

rsID	Chr	Position	Database	Tissue	eGene	FDR	eQTL allele	GWAS allele	Aligned direction
rs115685297	17	19756449	eQTLcatalogue	Alasoo_2018_ge_macrophage_IFNg	AKAP10	2.25E-04	T	A	-
rs112155453	17	19771057	eQTLcatalogue	Alasoo_2018_ge_macrophage_IFNg	AKAP10	9.57E-05	C	G	-
rs72841970	17	19777031	eQTLcatalogue	Alasoo_2018_ge_macrophage_IFNg	AKAP10	7.11E-05	G	A	-
rs6763014	3	112512647	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	G	T	-
rs10804503	3	112513358	eQTLcatalogue	BLUEPRINT_ge_monocyte	CD200R1	2.96E-03	C	T	+
rs10804503	3	112513358	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	3.21E-02	C	T	-
rs10934187	3	112513482	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.08E-03	A	G	-
rs6797028	3	112515187	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	A	G	-
rs6772960	3	112515540	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	C	T	-
rs9875150	3	112515784	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.38E-03	T	C	-
rs9821278	3	112515884	eQTLcatalogue	BLUEPRINT_ge_monocyte	CD200R1	3.00E-03	A	G	+
rs9821278	3	112515884	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	3.35E-02	A	G	-
rs9859168	3	112515906	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	C	T	-
rs6789210	3	112516328	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	T	C	-
rs6800648	3	112516433	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.08E-03	A	G	-
rs6793183	3	112517755	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.35E-03	T	C	-
rs9832885	3	112518459	eQTLcatalogue	BLUEPRINT_ge_monocyte	GTPBP8	6.34E-03	A	G	-
rs11649705	17	19612489	eQTLcatalogue	BLUEPRINT_ge_monocyte	AKAP10	1.24E-02	G	A	-
rs11657623	17	19612945	eQTLcatalogue	BLUEPRINT_ge_monocyte	AKAP10	1.19E-02	T	C	-
rs112155453	17	19771057	eQTLcatalogue	BLUEPRINT_ge_monocyte	AKAP10	2.96E-07	C	G	-
rs72841970	17	19777031	eQTLcatalogue	BLUEPRINT_ge_monocyte	AKAP10	3.79E-06	G	A	-
rs11649705	17	19612489	eQTLcatalogue	BLUEPRINT_ge_neutrophil	AKAP10	2.19E-04	G	A	-
rs11657623	17	19612945	eQTLcatalogue	BLUEPRINT_ge_neutrophil	AKAP10	2.13E-04	T	C	-
rs112155453	17	19771057	eQTLcatalogue	BLUEPRINT_ge_neutrophil	AKAP10	6.49E-10	C	G	-
rs72841970	17	19777031	eQTLcatalogue	BLUEPRINT_ge_neutrophil	AKAP10	5.06E-08	G	A	-
rs6763014	3	112512647	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	G	T	-
rs10934187	3	112513482	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.01E-03	A	G	-
rs6797028	3	112515187	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	A	G	-
rs6772960	3	112515540	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	C	T	-
rs9875150	3	112515784	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.03E-03	T	C	-
rs9859168	3	112515906	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	C	T	-
rs6789210	3	112516328	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	T	C	-
rs6800648	3	112516433	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.01E-03	A	G	-
rs6793183	3	112517755	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	T	C	-
rs9832885	3	112518459	eQTLcatalogue	BLUEPRINT_ge_T-cell	NEPRO	2.05E-03	A	G	-
rs72841970	17	19777031	eQTLcatalogue	BrainSeq_ge_brain	RP11-209D14.2	4.88E-02	G	A	-
rs11649705	17	19612489	eQTLcatalogue	CEDAR_B-cell_CD19	ALDH3A2	1.36E-06	G	A	-

rs11657623	17	19612945 eQTLcatalogue	CEDAR_B-cell_CD19	ALDH3A2	1.51E-06	T	C	-
rs115685297	17	19756449 eQTLcatalogue	CEDAR_B-cell_CD19	ALDH3A2	4.87E-04	T	A	-
rs112155453	17	19771057 eQTLcatalogue	CEDAR_B-cell_CD19	ALDH3A2	6.67E-04	C	G	-
rs72841970	17	19777031 eQTLcatalogue	CEDAR_B-cell_CD19	ALDH3A2	8.89E-04	G	A	-
rs11649705	17	19612489 eQTLcatalogue	CEDAR_monocyte_CD14	ALDH3A2	2.16E-02	G	A	+
rs11657623	17	19612945 eQTLcatalogue	CEDAR_monocyte_CD14	ALDH3A2	2.19E-02	T	C	+
rs115685297	17	19756449 eQTLcatalogue	CEDAR_neutrophil_CD15	AKAP10	8.68E-05	T	A	-
rs112155453	17	19771057 eQTLcatalogue	CEDAR_neutrophil_CD15	AKAP10	2.85E-05	C	G	-
rs72841970	17	19777031 eQTLcatalogue	CEDAR_neutrophil_CD15	AKAP10	1.49E-04	G	A	-
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2012_B-cell_CD19	ALDH3A2	1.54E-07	G	A	-
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2012_B-cell_CD19	ALDH3A2	1.63E-07	T	C	-
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2012_B-cell_CD19	ALDH3A2	6.67E-05	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2012_B-cell_CD19	ALDH3A2	7.94E-05	C	G	-
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2012_B-cell_CD19	ALDH3A2	6.80E-05	G	A	-
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_IFN24	SLC47A1	5.86E-07	G	A	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_IFN24	SLC47A1	6.04E-07	T	C	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_IFN24	SLC47A1	8.36E-04	T	A	+
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_IFN24	SLC47A1	7.38E-04	C	G	+
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_IFN24	SLC47A1	9.13E-04	G	A	+
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	5.05E-05	G	A	+
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_LPS2	SLC47A1	3.86E-07	G	A	+
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	4.04E-02	G	A	+
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	1.32E-06	G	A	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	5.17E-05	T	C	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_LPS2	SLC47A1	3.96E-07	T	C	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	4.15E-02	T	C	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	1.37E-06	T	C	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	1.27E-02	T	A	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_LPS2	SLC47A1	9.95E-06	T	A	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	4.60E-04	T	A	+
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	1.68E-02	C	G	+
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_LPS2	SLC47A1	1.02E-05	C	G	+
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	7.03E-04	C	G	+
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	1.27E-02	G	A	+
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_LPS2	SLC47A1	6.33E-06	G	A	+
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_LPS2	ALDH3A2	9.07E-04	G	A	+
rs6763014	3	112512647 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.47E-02	G	T	-
rs10804503	3	112513358 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	4.83E-02	C	T	-
rs10804503	3	112513358 eQTLcatalogue	Fairfax_2014_naive	CD200R1	5.09E-05	C	T	+
rs10934187	3	112513482 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.51E-02	A	G	-

rs6797028	3	112515187 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	2.39E-02	A	G	-
rs6772960	3	112515540 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	2.33E-02	C	T	-
rs9875150	3	112515784 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	2.34E-02	T	C	-
rs9821278	3	112515884 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	3.23E-02	A	G	-
rs9821278	3	112515884 eQTLcatalogue	Fairfax_2014_naive	CD200R1	3.81E-05	A	G	+
rs9859168	3	112515906 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.35E-02	C	T	-
rs6789210	3	112516328 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	2.26E-02	T	C	-
rs6800648	3	112516433 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.01E-02	A	G	-
rs6793183	3	112517755 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.68E-02	T	C	-
rs9832885	3	112518459 eQTLcatalogue	Fairfax_2014_naive	GTPBP8	1.54E-02	A	G	-
rs11649705	17	19612489 eQTLcatalogue	Fairfax_2014_naive	SLC47A1	3.78E-08	G	A	+
rs11657623	17	19612945 eQTLcatalogue	Fairfax_2014_naive	SLC47A1	3.84E-08	T	C	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_naive	SLC47A1	7.49E-04	T	A	+
rs115685297	17	19756449 eQTLcatalogue	Fairfax_2014_naive	AKAP10	1.52E-04	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_naive	SLC47A1	6.31E-04	C	G	+
rs112155453	17	19771057 eQTLcatalogue	Fairfax_2014_naive	AKAP10	1.22E-04	C	G	-
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_naive	SLC47A1	4.49E-04	G	A	+
rs72841970	17	19777031 eQTLcatalogue	Fairfax_2014_naive	AKAP10	8.67E-05	G	A	-
rs11649705	17	19612489 eQTLcatalogue	GENCORD_ge_LCL	ALDH3A2	3.19E-07	G	A	-
rs11657623	17	19612945 eQTLcatalogue	GENCORD_ge_LCL	ALDH3A2	3.18E-07	T	C	-
rs115685297	17	19756449 eQTLcatalogue	GENCORD_ge_LCL	ALDH3A2	1.88E-02	T	A	-
rs11649705	17	19612489 eQTLcatalogue	Lepik_2017_ge_blood	ALDH3A2	4.51E-11	G	A	-
rs11649705	17	19612489 eQTLcatalogue	Lepik_2017_ge_blood	AKAP10	1.92E-08	G	A	-
rs11657623	17	19612945 eQTLcatalogue	Lepik_2017_ge_blood	ALDH3A2	1.40E-11	T	C	-
rs11657623	17	19612945 eQTLcatalogue	Lepik_2017_ge_blood	AKAP10	6.65E-08	T	C	-
rs112155453	17	19771057 eQTLcatalogue	Lepik_2017_ge_blood	ALDH3A2	6.42E-06	C	G	-
rs112155453	17	19771057 eQTLcatalogue	Lepik_2017_ge_blood	AKAP10	1.01E-09	C	G	-
rs72841970	17	19777031 eQTLcatalogue	Lepik_2017_ge_blood	ALDH3A2	2.05E-05	G	A	-
rs72841970	17	19777031 eQTLcatalogue	Lepik_2017_ge_blood	AKAP10	1.13E-09	G	A	-
rs115685297	17	19756449 eQTLcatalogue	Quach_2016_ge_monocyte_IAV	AKAP10	1.65E-03	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Quach_2016_ge_monocyte_IAV	AKAP10	9.24E-04	C	G	-
rs72841970	17	19777031 eQTLcatalogue	Quach_2016_ge_monocyte_IAV	AKAP10	3.47E-02	G	A	-
rs115685297	17	19756449 eQTLcatalogue	Quach_2016_ge_monocyte_LPS	AKAP10	2.23E-03	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Quach_2016_ge_monocyte_LPS	AKAP10	1.32E-03	C	G	-
rs115685297	17	19756449 eQTLcatalogue	Quach_2016_ge_monocyte_naive	AKAP10	1.15E-03	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Quach_2016_ge_monocyte_naive	AKAP10	5.64E-04	C	G	-
rs72841970	17	19777031 eQTLcatalogue	Quach_2016_ge_monocyte_naive	AKAP10	3.67E-02	G	A	-
rs115685297	17	19756449 eQTLcatalogue	Quach_2016_ge_monocyte_Pam3CSK4	AKAP10	9.85E-03	T	A	-
rs112155453	17	19771057 eQTLcatalogue	Quach_2016_ge_monocyte_Pam3CSK4	AKAP10	7.97E-03	C	G	-
rs6797028	3	112515187 PsychENCODE	PsychENCODE_eQTLs	CD200R1L	3.87E-03	G	G	+

rs6797028	3	112515187 PsychENCODE PsychENCODE_eQTLs	RP11-180K7.1	1.49E-02	G	G	+
rs6797028	3	112515187 PsychENCODE PsychENCODE_eQTLs	RP11-484K9.4	7.30E-03	G	G	+
rs6772960	3	112515540 PsychENCODE PsychENCODE_eQTLs	CD200R1L	3.12E-03	T	T	+
rs6772960	3	112515540 PsychENCODE PsychENCODE_eQTLs	RP11-180K7.1	9.93E-03	T	T	+
rs6772960	3	112515540 PsychENCODE PsychENCODE_eQTLs	RP11-484K9.4	5.65E-03	T	T	+
rs9821278	3	112515884 PsychENCODE PsychENCODE_eQTLs	CD200R1L	1.39E-04	G	G	+
rs9821278	3	112515884 PsychENCODE PsychENCODE_eQTLs	RP11-180K7.1	2.83E-03	G	G	+
rs9821278	3	112515884 PsychENCODE PsychENCODE_eQTLs	RP11-484K9.4	2.00E-03	G	G	+
rs9859168	3	112515906 PsychENCODE PsychENCODE_eQTLs	CD200R1L	1.08E-03	T	T	+
rs9859168	3	112515906 PsychENCODE PsychENCODE_eQTLs	RP11-180K7.1	6.43E-03	T	T	+
rs9859168	3	112515906 PsychENCODE PsychENCODE_eQTLs	RP11-484K9.4	1.18E-02	T	T	+
rs6800648	3	112516433 PsychENCODE PsychENCODE_eQTLs	CD200R1L	7.75E-04	G	G	+
rs6800648	3	112516433 PsychENCODE PsychENCODE_eQTLs	RP11-180K7.1	9.57E-03	G	G	+
rs115685297	17	19756449 PsychENCODE PsychENCODE_eQTLs	SPECC1	4.44E-07	A	A	+
rs115685297	17	19756449 PsychENCODE PsychENCODE_eQTLs	RP11-209D14.2	1.85E-19	A	A	+
rs115685297	17	19756449 PsychENCODE PsychENCODE_eQTLs	SNORD3D	2.89E-02	A	A	+
rs115685297	17	19756449 PsychENCODE PsychENCODE_eQTLs	RP11-78O7.2	9.73E-04	A	A	-
rs112155453	17	19771057 PsychENCODE PsychENCODE_eQTLs	SPECC1	2.37E-07	G	G	+
rs112155453	17	19771057 PsychENCODE PsychENCODE_eQTLs	RP11-209D14.2	9.98E-21	G	G	+
rs112155453	17	19771057 PsychENCODE PsychENCODE_eQTLs	SNORD3D	2.16E-02	G	G	+
rs112155453	17	19771057 PsychENCODE PsychENCODE_eQTLs	RP11-78O7.2	8.05E-04	G	G	-
rs11649705	17	19612489 DICE B_cell_naive	ALDH3A2	4.90E-02	A	A	+
rs11657623	17	19612945 DICE B_cell_naive	ALDH3A2	4.90E-02	C	C	+
rs112155453	17	19771057 DICE B_cell_naive	ALDH3A2	4.90E-02	G	G	+
rs112155453	17	19771057 BRAINEAC PUTM	CCDC144A	2.47E-02	NA	G	NA
rs72841970	17	19777031 BRAINEAC PUTM	CCDC144A	2.47E-02	NA	A	NA
rs11649705	17	19612489 GTEX/v8 Whole_Blood	ALDH3A2	1.08E-10	A	A	+
rs11649705	17	19612489 GTEX/v8 Whole_Blood	AKAP10	1.08E-70	A	A	+
rs11657623	17	19612945 GTEX/v8 Whole_Blood	ALDH3A2	1.08E-10	C	C	+
rs11657623	17	19612945 GTEX/v8 Whole_Blood	AKAP10	1.08E-70	C	C	+
rs112155453	17	19771057 GTEX/v8 Whole_Blood	AKAP10	1.08E-70	G	G	+
rs72841970	17	19777031 GTEX/v8 Whole_Blood	AKAP10	1.08E-70	A	A	+
rs72841970	17	19777031 GTEX/v8 Whole_Blood	SPECC1	9.66E-05	A	A	+
rs72841970	17	19777031 GTEX/v8 Whole_Blood	LGALS9B	3.18E-34	A	A	-
rs112155453	17	19771057 GTEX/v8 Brain_Anterior_cingulate_cortex_BA24	RP11-209D14.2	3.79E-10	G	G	+
rs7153205	14	40790811 GTEX/v8 Brain_Cortex	RP11-662J14.1	7.06E-04	C	T	+
rs1950241	14	40802371 GTEX/v8 Brain_Cortex	RP11-662J14.1	7.06E-04	T	C	+
rs1950241	14	40802371 GTEX/v8 Brain_Cortex	RP11-662J14.2	1.36E-03	T	C	+
rs61989120	14	40818021 GTEX/v8 Brain_Cortex	RP11-662J14.1	7.06E-04	T	C	+
rs141604435	14	40849721 GTEX/v8 Brain_Cortex	RP11-662J14.1	7.06E-04	A	G	+

rs12893089	14	40851097 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	C	A	+
rs12888686	14	40857356 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	A	T	+
rs17780892	14	40858183 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	A	G	+
rs11851674	14	40858958 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	G	T	+
rs1952935	14	40859517 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	C	A	+
rs11851600	14	40860432 GTEX/v8	Brain_Cortex	RP11-662J14.1	7.06E-04	T	G	+
rs112155453	17	19771057 GTEX/v8	Brain_Cortex	RP11-209D14.2	4.10E-12	G	G	+
rs72841970	17	19777031 GTEX/v8	Brain_Cortex	RP11-209D14.2	4.10E-12	A	A	+
rs112155453	17	19771057 GTEX/v8	Brain_Frontal_Cortex_BA9	RP11-209D14.2	1.40E-07	G	G	+
rs72841970	17	19777031 GTEX/v8	Brain_Frontal_Cortex_BA9	RP11-209D14.2	1.40E-07	A	A	+
rs11649705	17	19612489 GTEX/v8	Brain_Hypothalamus	RP11-209D14.2	1.52E-06	A	A	+
rs11657623	17	19612945 GTEX/v8	Brain_Hypothalamus	RP11-209D14.2	1.52E-06	C	C	+
rs112155453	17	19771057 GTEX/v8	Brain_Hypothalamus	RP11-209D14.2	1.52E-06	G	G	+

Suppl.Table.3. Combined list of genes suggested by variant- and gene-based GWAS meta-analyses of resilience.

Analysis (Type)	Ensembl ID	Symbol	Chr	Start (bp)	End (bp)	Strand
Gene-meta (sugg)	ENSG00000143622	RIT1	1	155867599	155881195	-1
Gene-meta (sugg)	ENSG00000132680	KHDC4	1	155882834	155904191	-1
Gene-meta (sugg)	ENSG00000173080	RXFP4	1	155911480	155912625	1
Gene-meta (sugg)	ENSG00000116584	ARHGEF2	1	155916630	155976861	-1
Gene-meta (sugg)	ENSG00000196482	ESRRG	1	216676588	217311097	-1
Gene-meta (significant)	ENSG00000169855	ROBO1	3	78646390	79816965	-1
SNP-meta (sugg, eGene)	ENSG00000242770	RP11-180K7.1	3	112521325	112531666	1
SNP-meta (sugg, eGene)	ENSG00000206531	CD200R1L	3	112534556	112565703	-1
SNP-meta (sugg, eGene)	ENSG00000163606	CD200R1	3	112640056	112693969	-1
SNP-meta (sugg, eGene)	ENSG00000272844	RP11-484K9.4	3	112709294	112710000	-1
SNP-meta (sugg, eGene)	ENSG00000163607	GTPBP8	3	112709765	112733907	1
SNP-meta (sugg, eGene)	ENSG00000163608	NEPRO	3	112721287	112738708	-1
Gene-meta (sugg)	ENSG00000171815	PCDHB1	5	140430979	140433512	1
Gene-meta (sugg)	ENSG00000112365	ZBTB24	6	109783797	109804440	-1
Gene-meta (sugg)	ENSG00000203733	GJE1	6	142454227	142456288	1
Gene-meta (sugg)	ENSG00000176381	PRR18	6	166719168	166721936	-1
Gene-meta (sugg)	ENSG00000164877	MICALL2	7	1468101	1499138	-1
SNP-meta (sugg, mapped)	ENSG00000230333	AC004538.3	7	11221359	11559802	1
SNP-meta (sugg, mapped)	ENSG00000005108	THSD7A	7	11409984	11871824	-1
Gene-meta (sugg)	ENSG00000164532	TBX20	7	35242042	35293758	-1
Gene-meta (sugg)	ENSG00000153993	SEMA3D	7	84624869	84816171	-1
Gene-meta (sugg)	ENSG00000197150	ABCB8	7	150725510	150744869	1
Gene-meta (sugg)	ENSG00000214106	PAXIP1-AS2	7	154720208	154741618	1
Gene-meta (sugg)	ENSG00000157212	PAXIP1	7	154735397	154794794	-1
Gene-meta (sugg)	ENSG00000169071	ROR2	9	94325373	94712444	-1
Gene-meta (sugg)	ENSG00000243444	PALM2	9	112403068	112713755	1
Gene-meta (sugg)	ENSG00000167325	RRM1	11	4115937	4160106	1
Gene-meta (sugg)	ENSG00000168062	BATF2	11	64755415	64764517	-1
Gene-meta (sugg)	ENSG00000111707	SUDS3	12	118814185	118855840	1
Gene-meta (sugg)	ENSG00000100445	SDR39U1	14	24908972	24912111	-1
SNP-meta (sugg, eGene)	ENSG00000258418	RP11-662J14.1	14	40855456	40855998	1
SNP-meta (sugg, mapped, eGene)	ENSG00000258480	RP11-662J14.2	14	40856762	40858344	1
Gene-meta (sugg)	ENSG00000140157	NIPA2	15	23004684	23034427	-1
Gene-meta (sugg)	ENSG00000213918	DNASE1	16	3661729	3730144	1
Gene-meta (sugg)	ENSG00000168447	SCNN1B	16	23289552	23392620	1
Gene-meta (sugg)	ENSG00000169189	NSMCE1	16	27236312	27280115	-1
Gene-meta (sugg)	ENSG00000245888	CTD-3203P2.2	16	27279526	27301813	1
Gene-meta (sugg)	ENSG00000174939	ASPHD1	16	29911696	29931185	1
Gene-meta (sugg)	ENSG00000174943	KCTD13	16	29916333	29938356	-1
SNP-meta (sugg, eGene)	ENSG00000170160	CCDC144A	17	16592851	16707767	1
SNP-meta (sugg, eGene)	ENSG00000262202	SNORD3D	17	19015313	19015949	-1
SNP-meta (sugg, eGene)	ENSG00000142494	SLC47A1	17	19398698	19482347	1
SNP-meta (sugg, eGene)	ENSG00000072210	ALDH3A2	17	19551449	19580911	1
SNP-meta (sugg, mapped)	ENSG00000180638	SLC47A2	17	19581601	19622292	-1
SNP-meta (sugg, mapped)	ENSG00000083290	ULK2	17	19674142	19771249	-1
SNP-meta (sugg, eGene)	ENSG00000270091	RP11-78O7.2	17	19799903	19800600	-1
SNP-meta (sugg, eGene)	ENSG00000108599	AKAP10	17	19807615	19881656	-1
SNP-meta (sugg, eGene)	ENSG00000261033	RP11-209D14.2	17	19911364	19912547	-1
SNP-meta (sugg, eGene)	ENSG00000128487	SPECC1	17	19912657	20222339	1
SNP-meta (sugg, eGene)	ENSG00000170298	LGALS9B	17	20352708	20370852	-1
Gene-meta (significant)	ENSG00000141977	CIB3	19	16272179	16284336	-1
Gene-meta (sugg)	ENSG00000086548	CEACAM6	19	42254885	42276113	1
Gene-meta (significant)	ENSG00000183103	LYPD4	19	42341148	42348760	-1
Gene-meta (sugg)	ENSG00000142025	DMRTC2	19	42348806	42356401	1
Gene-meta (sugg)	ENSG00000198125	MB	22	36002811	36033998	-1
Gene-meta (sugg)	ENSG00000073150	PANX2	22	50609160	50618723	1

Suppl.Table.4. Pathway gene sets overrepresented in the network created for resilience candidate genes.

Pathway term (non-disease-specific)	N	Overlap (≥ 3)	% of N (≥ 3)	FDR (<0.05)	Genes
Activation of anterior HOX genes in hindbrain development during early embryogenesis(R)	66	6	9.1	5.68E-04	EP300,NCOR1,PAXIP1,RXRA,POLR2D,SUZ12
Transmission across Electrical Synapses (R)	5	3	60.0	6.89E-04	PANX1,PANX2,GJD2
Posttranslational regulation of adherens junction stability and disassembly(N)	48	5	10.4	6.89E-04	ROBO1,RAC1,CTNNA1,CTNNB1,PTPN6
RAC1 signaling pathway(N)	54	5	9.3	8.84E-04	RAC1,MAPK8,CTNNA1,STAT3,CTNNB1
SUMOylation(R)	175	7	4.0	1.80E-03	NR3C1,SUMO1,EP300,NSMCE1,RXRA,RAD21,SUZ12
Adherens junction(K)	71	5	7.0	1.80E-03	EP300,RAC1,CTNNA1,CTNNB1,PTPN6
N-cadherin signaling events(N)	34	4	11.8	1.80E-03	RAC1,MAPK8,CTNNA1,CTNNB1
RHO GTPases activate IQGAPs(R)	11	3	27.3	1.80E-03	RAC1,CTNNA1,CTNNB1
Nonhomologous End-Joining (NHEJ)(R)	36	4	11.1	1.89E-03	RIF1,SUMO1,PAXIP1,ATM
Glucocorticoid receptor regulatory network(N)	78	5	6.4	2.31E-03	NR3C1,PRKACG,EP300,SGK1,MAPK8
NR1H2 and NR1H3-mediated signaling(R)	45	4	8.9	3.72E-03	KDM1A,EP300,NCOR1,RXRA
Notch-mediated HES/HEY network(N)	47	4	8.5	4.04E-03	KDM1A,EP300,NCOR1,STAT3
FoxO family signaling(N)	49	4	8.2	4.43E-03	EP300,SGK1,MAPK8,CTNNB1
Regulation of Androgen receptor activity(N)	51	4	7.8	4.56E-03	NR3C1,EP300,MAPK8,RXRA
Signaling by PTK6(R)	51	4	7.8	4.56E-03	LRRK2,NR3C1,RAC1,STAT3
Wnt signaling pathway(K)	160	6	3.8	4.66E-03	PRKACG,EP300,RAC1,ROR2,MAPK8,CTNNB1
E-cadherin signaling in keratinocytes(N)	21	3	14.3	5.24E-03	RAC1,CTNNA1,CTNNB1
Tight junction(K)	169	6	3.6	5.36E-03	PRKACG,RAC1,ARHGEF2,MAPK8,MICALL2,RAB13
Signaling events mediated by HDAC Class I(N)	56	4	7.1	5.36E-03	SUMO1,EP300,NCOR1,STAT3
Beta-catenin independent WNT signaling(R)	113	5	4.4	6.83E-03	RAC1,PSMA2,ROR2,GNG2,CTNNB1
Thyroid hormone signaling pathway(K)	121	5	4.1	8.44E-03	PRKACG,EP300,NCOR1,RXRA,CTNNB1
Circadian Clock(R)	67	4	6.0	8.44E-03	NR3C1,EP300,NCOR1,RXRA
Signaling by ALK(R)	27	3	11.1	8.44E-03	EP300,STAT3,PTPN6
Adipocytokine signaling pathway(K)	69	4	5.8	8.70E-03	ADIPOQ,MAPK8,RXRA,STAT3
AP-1 transcription factor network(N)	70	4	5.7	8.70E-03	NR3C1,EP300,ACTA1,CTNNB1
CDC42 signaling events(N)	70	4	5.7	8.70E-03	RAC1,MAPK8,CTNNA1,CTNNB1
FoxO signaling pathway(K)	131	5	3.8	8.76E-03	EP300,SGK1,MAPK8,STAT3,ATM
Retinoic acid receptors-mediated signaling(N)	30	3	10.0	8.76E-03	EP300,MAPK8,RXRA
Nectin adhesion pathway(N)	30	3	10.0	8.76E-03	RAC1,CTNNA1,CTNNB1
ESR-mediated signaling(R)	137	5	3.7	9.59E-03	KDM1A,EP300,GNG2,RAD21,POLR2D
Transcriptional regulation of granulopoiesis(R)	32	3	9.4	9.59E-03	EP300,RXRA,STAT3
Noncanonical Wnt signaling pathway(N)	32	3	9.4	9.59E-03	RAC1,ROR2,MAPK8
Fluid shear stress and atherosclerosis(K)	139	5	3.6	1.02E-02	SUMO1,RAC1,ARHGEF2,MAPK8,CTNNB1
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)(N)	80	4	5.0	1.05E-02	RAC1,MAPK8,CTNNA1,CTNNB1
CXCR4-mediated signaling events(N)	81	4	4.9	1.10E-02	RAC1,GNG2,STAT3,PTPN6
E-cadherin signaling in the nascent adherens junction(N)	36	3	8.3	1.14E-02	RAC1,CTNNA1,CTNNB1
Transcriptional regulation of white adipocyte differentiation(R)	84	4	4.8	1.15E-02	EP300,ADIPOQ,NCOR1,RXRA
ErbB2/ErbB3 signaling events(N)	37	3	8.1	1.15E-02	RAC1,MAPK8,STAT3
Signaling events mediated by HDAC Class II(N)	38	3	7.9	1.24E-02	NR3C1,SUMO1,GNG2
Signaling by SCF-KIT(R)	41	3	7.3	1.43E-02	RAC1,STAT3,PTPN6
Heme signaling(R)	43	3	7.0	1.64E-02	EP300,NCOR1,RXRA

DNA Double Strand Break Response(R)	46	3	6.5	1.84E-02	SUMO1,MAPK8,ATM
Netrin-1 signaling(R)	49	3	6.1	2.20E-02	ROBO1,RAC1,MAPK8
Signaling by NTRK1 (TRKA)(R)	107	4	3.7	2.28E-02	EP300,SGK1,STAT3,RIT1
Factors involved in megakaryocyte development and platelet production(R)	107	4	3.7	2.28E-02	KDM1A,AKAP10,PRKACG,RAC1
Signaling events mediated by Stem cell factor receptor (c-Kit)(N)	52	3	5.8	2.38E-02	MAPK8,STAT3,PTPN6
Notch signaling pathway(N)	52	3	5.8	2.38E-02	KDM1A,EP300,NCOR1
Growth hormone synthesis, secretion and action(K)	119	4	3.4	2.80E-02	PRKACG,EP300,MAPK8,STAT3
p53 pathway(N)	57	3	5.3	2.80E-02	EP300,MAPK8,ATM
Cytoprotection by HMOX1(R)	121	4	3.3	2.91E-02	NCOR1,PSMA2,RXRA,STAT3
Neurotrophic factor-mediated Trk receptor signaling(N)	60	3	5.0	2.91E-02	RAC1,STAT3,RIT1
Signaling events mediated by focal adhesion kinase(N)	61	3	4.92	3.05E-02	RAC1,ACTA1,MAPK8
Relaxin signaling pathway(K)	129	4	3.1	3.24E-02	RXFP4,PRKACG,MAPK8,GNG2
Signaling events mediated by VEGFR1 and VEGFR2(N)	63	3	4.76	3.24E-02	CTNNA1,CTNNB1,PTPN6
Ras Pathway(P)	63	3	4.76	3.24E-02	RAC1,MAPK8,STAT3
BCR signaling pathway(N)	65	3	4.62	3.24E-02	RAC1,MAPK8,PTPN6
E2F transcription factor network(N)	69	3	4.35	3.82E-02	EP300,RRM1,ATM
Regulation of nuclear SMAD2/3 signaling(N)	77	3	3.9	4.39E-02	NR3C1,EP300,NCOR1
Bacterial invasion of epithelial cells(K)	77	3	3.9	4.39E-02	RAC1,CTNNA1,CTNNB1
EGF receptor signaling pathway(P)	82	3	3.66	4.60E-02	RAC1,MAPK8,STAT3
p75 NTR receptor-mediated signalling(R)	88	3	3.41	4.86E-02	RAC1,ARHGEF2,MAPK8
Post-translational modification: synthesis of GPI-anchored proteins(R)	88	3	3.41	4.86E-02	CEACAM7,GPLD1,LYPD4
MAPK6/MAPK4 signaling(R)	89	3	3.37	4.86E-02	PRKACG,RAC1,PSMA2
Integration of energy metabolism(R)	90	3	3.33	4.93E-02	PRKACG,ADIPOQ,GNG2

R: Reactome
N: NCI-Nature
K: KEGG
P: Panther