Legends to Supplementary Tables and Figures.

Supplementary Table 1. LD measures, D', for the ten *GAB2* SNPs in each sample set. The upper-right half shows controls and the lower-left half LOAD.

Supplementary Table 2. Case-control haplotype analysis in the three sample sets, *All*, *Negative-ε4* and *Positive-ε4*. Significant permutaion *P*-values are highlighted in bold.

Supplementary Figure 1. Overview of an extended LD pattern including *GAB2* in JPT (A) and CEU (B). The genomic positions are according to NCBI build 35. The vertical arrow in Fig. A indicates a break point in the LD block including *GAB2*.

Supplementary Figure 2. Examples of TaqMan genotyping for ten *GAB2* SNPs.

Supplementary Figure 3. HapMap genotype data concerning the ten SNPs of *GAB2* in CEU, CHB, JPT and YRI.

Supplementary Table 1.

Sample set	dbSNP	rs901104	rs1385600	rs1007837	rs2510038	rs4945261	rs7101429	rs10793294	rs4291702	rs7115850	rs2373115
Overall set											
All	rs901104	*	0.9987	0.996	0.9974	0.9934	0.9921	-0.9725	0.9843	0.9831	0.9788
	rs1385600	0.9974	*	0.9975	1	0.9949	0.98	-0.948	0.9949	0.985	0.9813
	rs1007837	0.9974	0.9962	*	0.9987	0.991	0.9772	-0.948	0.991	0.9822	0.9786
	rs2510038	0.9987	0.9975	0.9975	*	0.9962	0.9962	-0.9738	0.9924	0.9875	0.9822
	rs4945261	0.9935	0.9962	0.9923	0.9937	*	0.9987	-0.9735	1	0.99	0.9847
	rs7101429	0.9921	0.9798	0.977	0.9936	1	*	-0.9845	0.9987	0.9887	0.9699
	rs10793294	-0.9875	-0.9526	-0.9526	-0.982	-1	-1	*	-1	-0.974	-0.9485
	rs4291702	0.987	0.9949	0.9897	0.9911	0.9975	1	-1	*	0.9899	0.9846
	rs7115850	0.9832	0.98	0.9798	0.9862	0.9886	0.9872	-0.9762	0.9898	*	0.9937
	rs2373115	0.9828	0.9861	0.9847	0.9859	0.9897	0.9782	-0.9461	0.9884	0.9937	*
Subsets											
Negative- ε 4	rs901104	*	0.9984	0.9952	0.9969	0.9936	0.9936	-0.9668	0.9826	0.9858	0.9808
	rs1385600	0.9946	*	0.997	1	0.9939	0.979	-0.9378	0.9939	0.985	0.9836
	rs1007837	0.9973	0.9974	*	0.9985	0.9892	0.9787	-0.9379	0.9892	0.9817	0.9818
	rs2510038	0.9973	0.9974	1	*	0.997	0.9985	-0.9685	0.9909	0.991	0.9848
	rs4945261	0.9892	0.9947	0.9947	0.9947	*	1	-0.9684	1	0.9925	0.9863
	rs7101429	0.9861	0.9761	0.9732	0.9893	1	*	-0.9815	1	0.991	0.9715
	rs10793294	-0.9862	-0.9477	-0.9482	-0.9738	-1	-1	*	-1	-0.9689	-0.9384
	rs4291702	0.9809	0.9894	0.9892	0.9894	0.9973	1	-1	*	0.9924	0.9862
	rs7115850	0.9757	0.9714	0.9789	0.9816	0.9895	0.9867	-0.974	0.9894	*	0.9925
	rs2373115	0.9779	0.9841	0.9839	0.9838	0.9919	0.9784	-0.9472	0.9919	0.9921	*
Positive- ε 4	rs901104	*	1	1	1	0.9923	0.9847	-1	0.9923	0.9698	0.9689
	rs1385600	1	*	1	1	1	1	-1	1	0.9848	0.9772
	rs1007837	0.9975	0.9976	*	1	1	1	-1	1	0.9846	0.9769
	rs2510038	1	0.9976	0.9951	*	1	1	-1	1	0.9849	0.9695
	rs4945261	0.9975	0.9976	0.9902	0.9951	*	1	-1	1	0.9848	0.9767
	rs7101429	0.9975	0.9831	0.9804	0.9975	1	*	-1	1	0.9774	0.9767
	rs10793294	-0.9885	-0.9565	-0.9562	-0.9889	-1	-1	*	-1	-1	-1
	rs4291702	0.9925	1	0.9902	0.9927	1	1	-1	*	0.9848	0.9767
	rs7115850	0.9901	0.9879	0.9805	0.9903	0.9879	0.9877	-0.9779	0.9903	*	1
	rs2373115	0.9874	0.988	0.9853	0.9878	0.9877	0.9779	-0.9451	0.9852	0.9951	*

Supplementary Table 2.

Sample set	Haplotype	Frequency		Permutation P	OR (95% CIs)
		LOAD	Control	(10,000)	
Overall set					
All	[H1] A-G-C-A-A-G-C-A-C-A	0.4147	0.4145	1	1.00 (0.91 - 1.10)
	[H2] G-A-T-G-G-A-C-G-G-C	0.3681	0.35	0.1254	1.08 (0.99 - 1.20)
	[H3] G-A-T-G-G-A-A-G-G-C	0.1868	0.1988	0.2441	0.93 (0.82 - 1.05)
	Others	0.0304	0.0367	-	-
	Global	-	-	**0.0017**	-
Subsets					
Negative- ε 4	[H1] A-G-C-A-A-G-C-A-C-A	0.4183	0.4161	0.9237	0.99 (0.88 - 1.13)
	[H2] G-A-T-G-G-A-C-G-G-C	0.3739	0.3503	0.1196	0.90 (0.79 - 1.03)
	[H3] G-A-T-G-G-A-A-G-G-C	0.1741	0.195	0.0974	1.15 (0.98 - 1.35)
	Others	0.0337	0.0386	-	-
	Global	-	-	0.0595	-
Positive- ε 4	[H1] A-G-C-A-A-G-C-A-C-A	0.4114	0.4064	0.8432	1.02 (0.84 - 1.24)
	[H2] G-A-T-G-G-A-C-G-G-C	0.3632	0.3509	0.6096	1.06 (0.86 - 1.29)
	[H3] G-A-T-G-G-A-A-G-G-C	0.198	0.2156	0.3599	0.90 (0.71 - 1.13)
	Others	0.0274	0.0271	-	-
	Global	-	-	0.3255	-

Supplementary Figure 1.

A

JPT

B

CEU
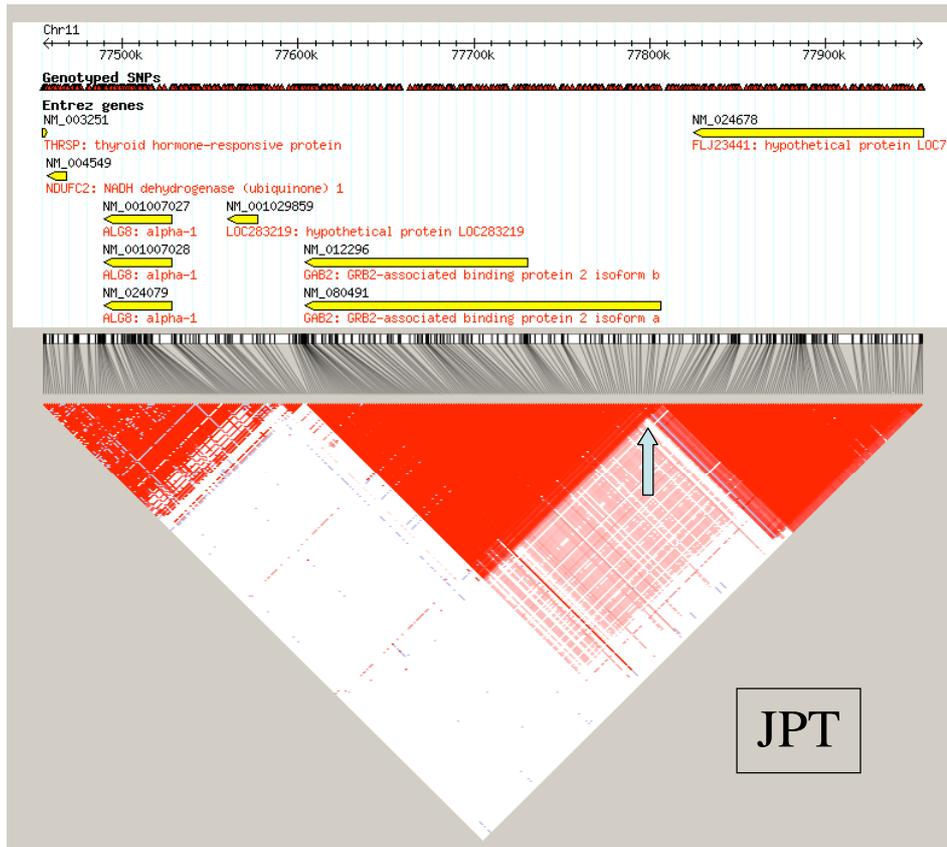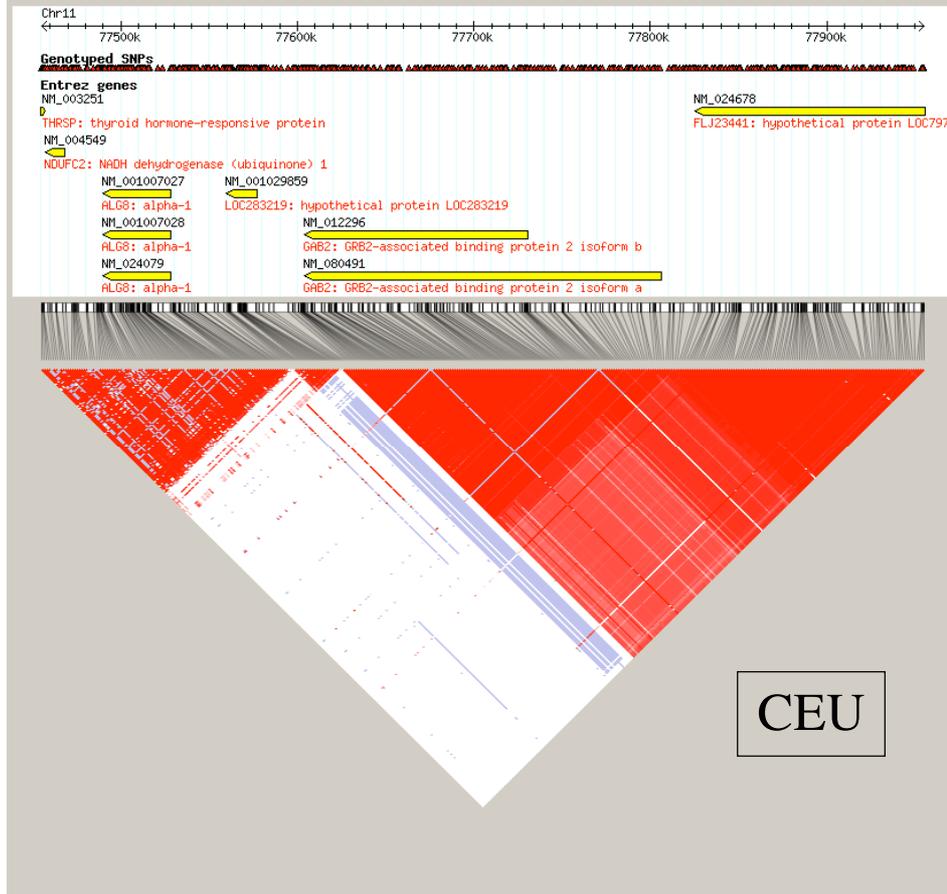
Supplementary Figure 2.

rs901104
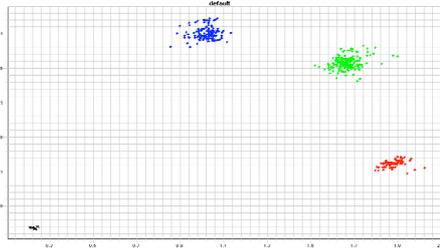
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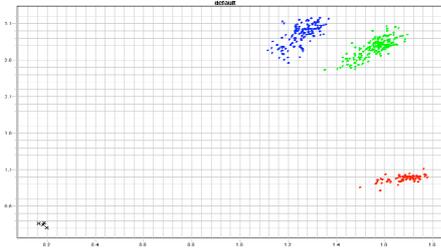
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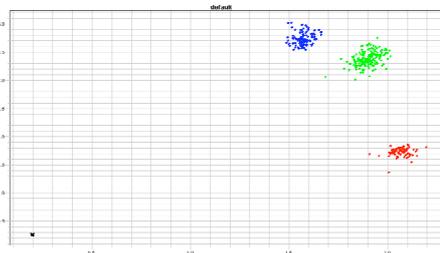
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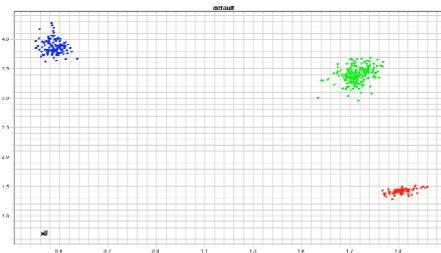

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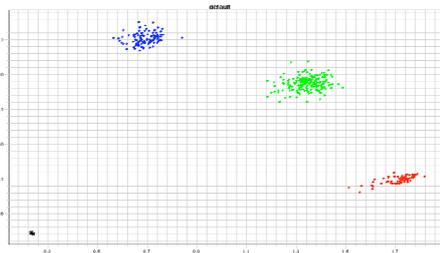
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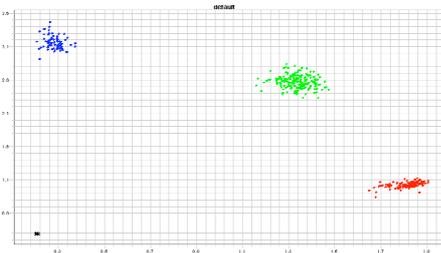
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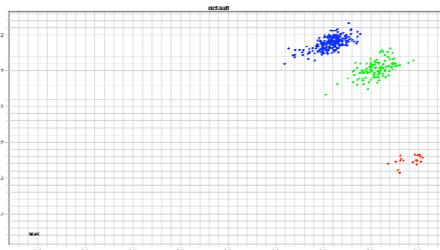
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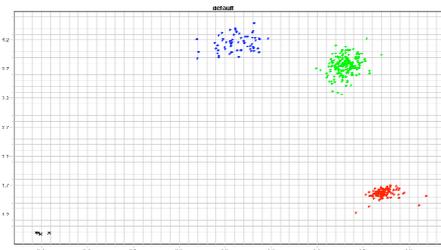
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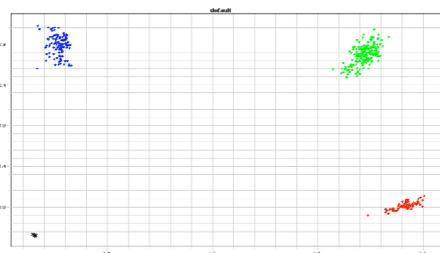
rs2373115

Supplementary Figure 3.