Table S1. SNPs associated with motion sickness ($p < 1.0E-05$). Alleles are reported in alphabetical order with respect to the positive strand of build 37 of the human genome. The effect is the change per copy of the second allele on a four-point scale of increasing motion sickness. Frequency is the frequency of the alphabetically second allele in the cohort. Frequency is for imputed SNPs unless the genotyped SNP was used in the analysis (those marked with a *). Quality is imputation r2 for imputed SNPs, call rate for genotyped SNPs (those marked with a *).

Table S2. Associations between 35 motion sickness-associated SNPs and six correlated and clinically important phenotypes. N is the number of people with data for motion sickness and PONV, altitude sickness, morning sickness, hay fever, vertigo, or migraines.

Table S3: Sex-specific effects for significant SNPs. Estimated effect sizes for females, males, and their ratio. P-values are for a non-zero interaction term between sex and genotype. SNPs are sorted by increasing p-value.

Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes, and glucose homeostasis — Supplement

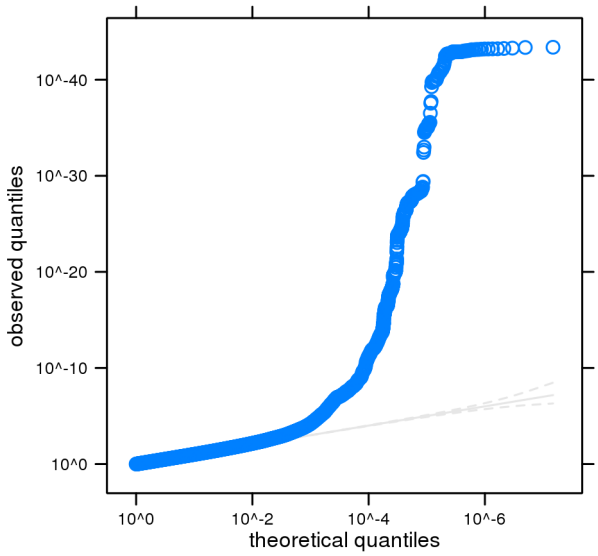
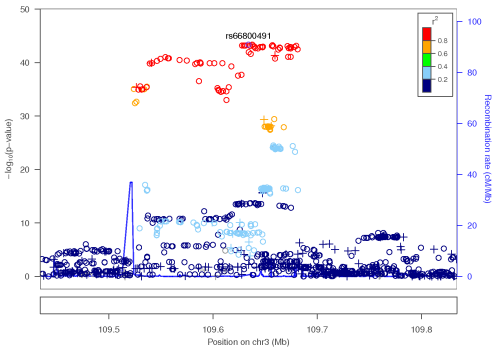


Figure S1: **Quantile-quantile plot.** Observed versus expected p-values under the null.

Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes, and glucose homeostasis — Supplement



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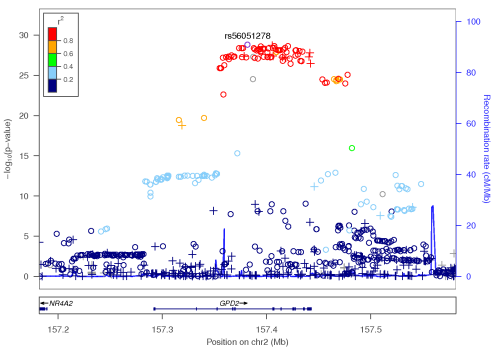

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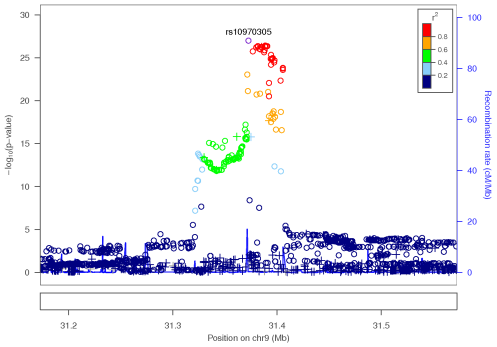

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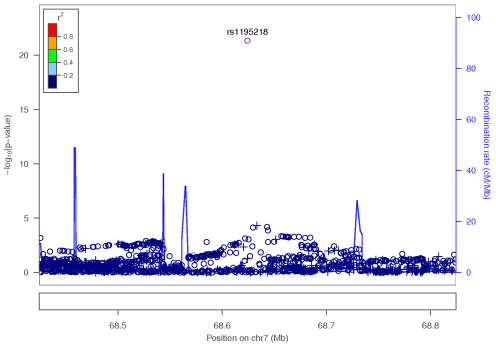

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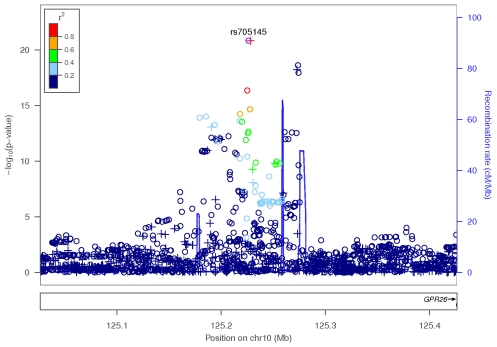

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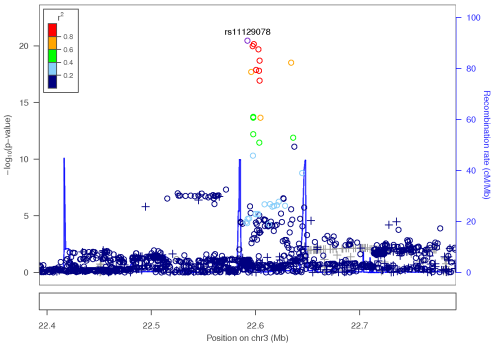

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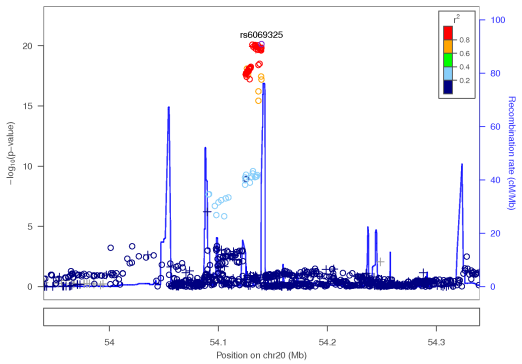
Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.



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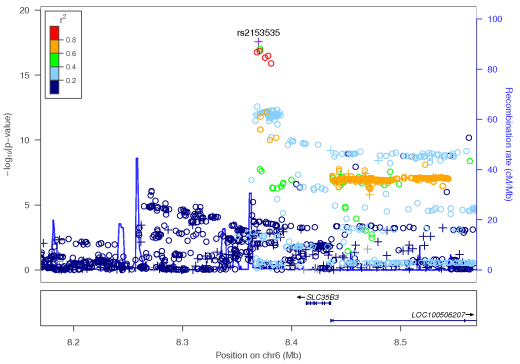

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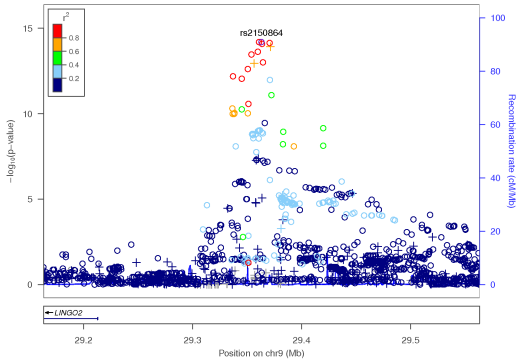

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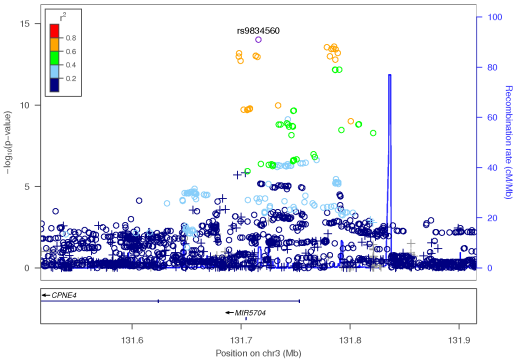

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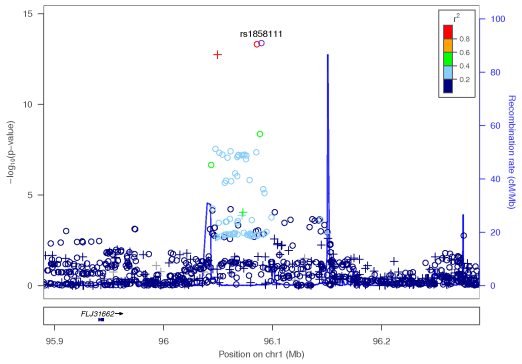

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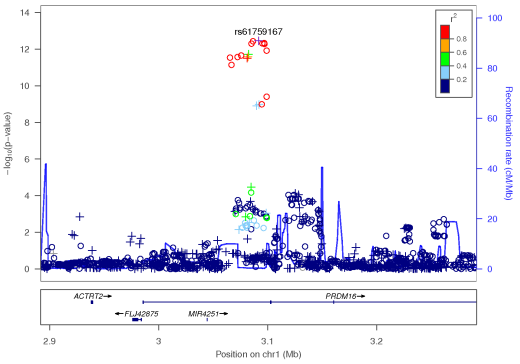

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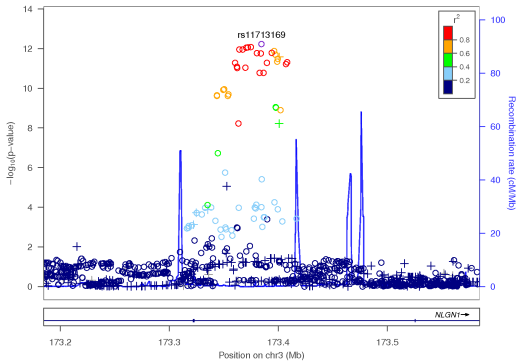
Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.



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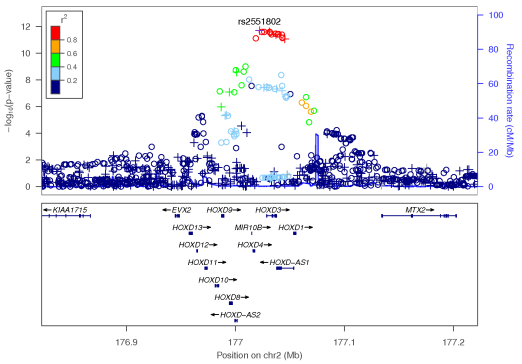

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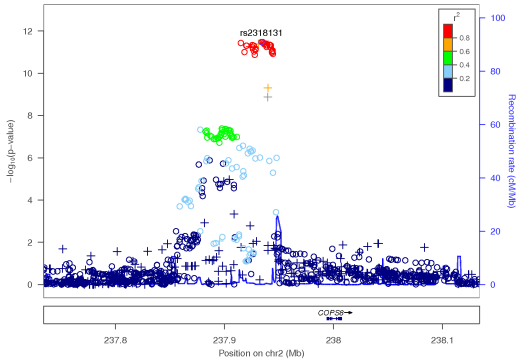

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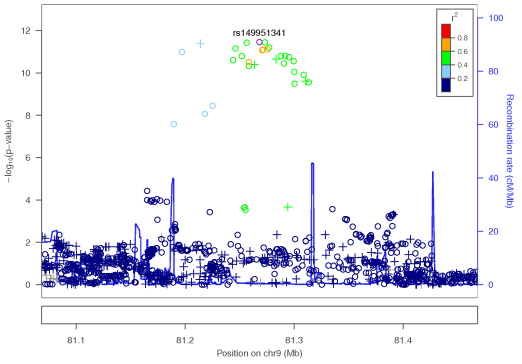

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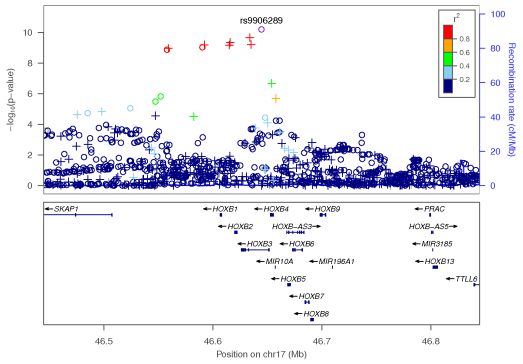

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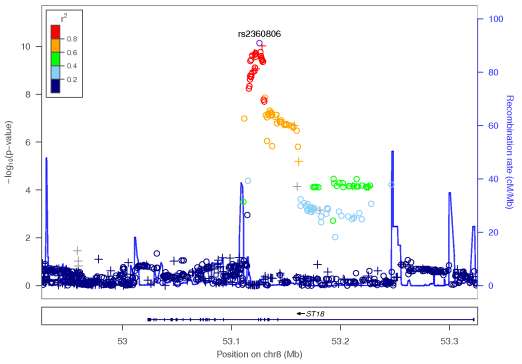

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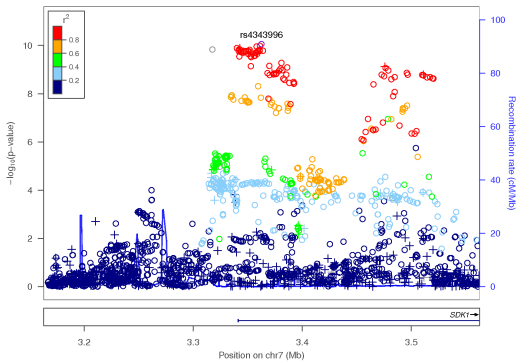
Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.



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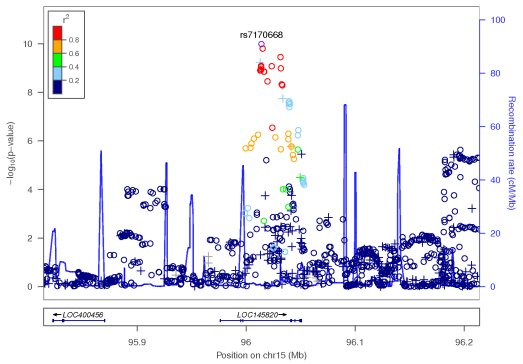

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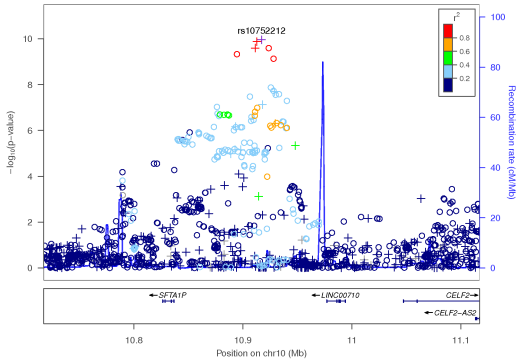

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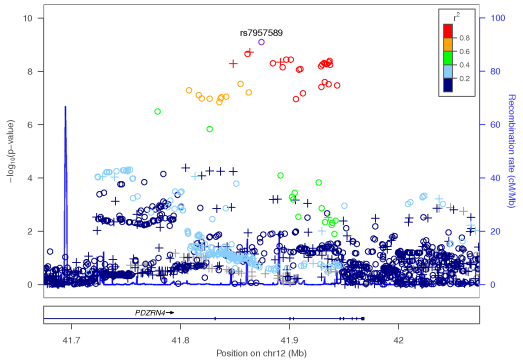

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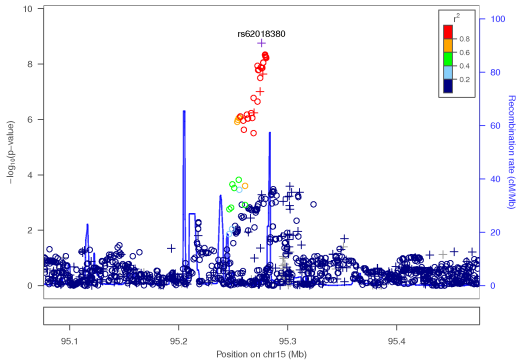

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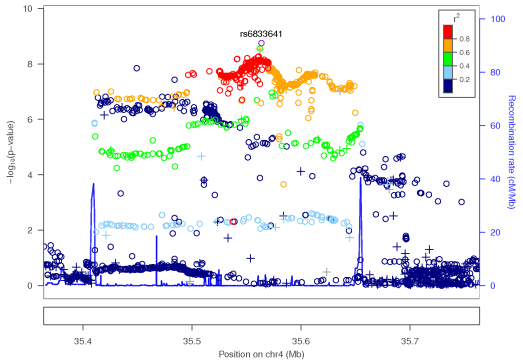

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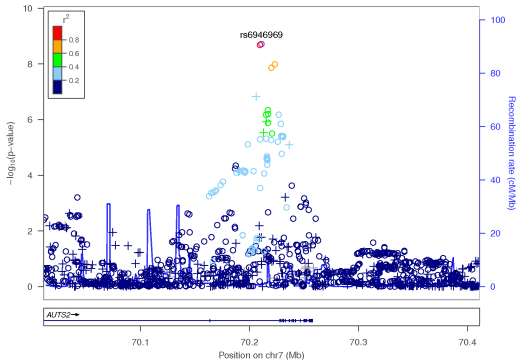
Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.



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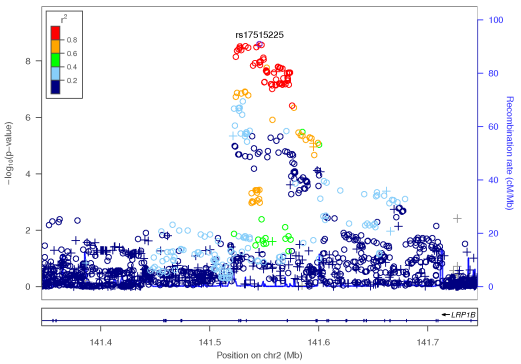

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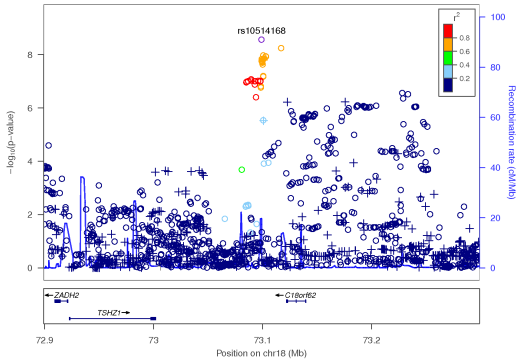

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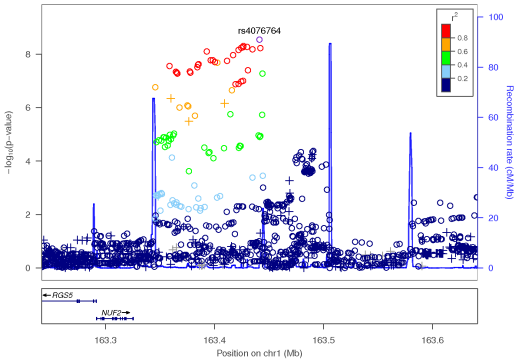

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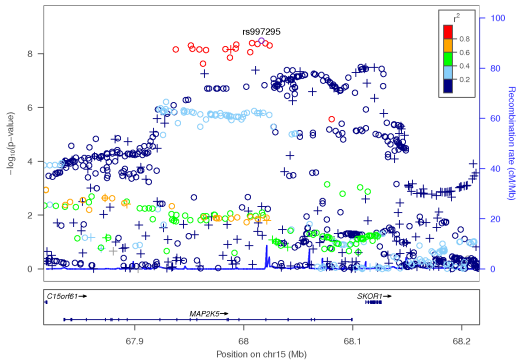

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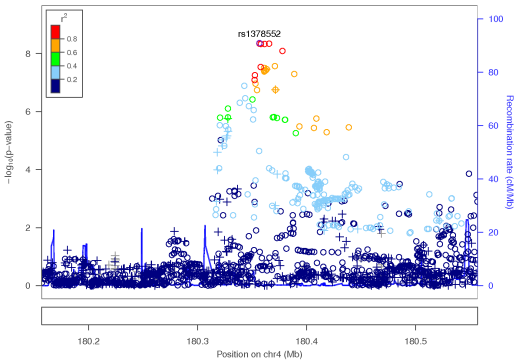

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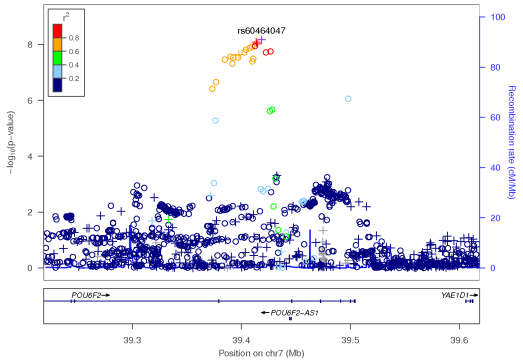
Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.



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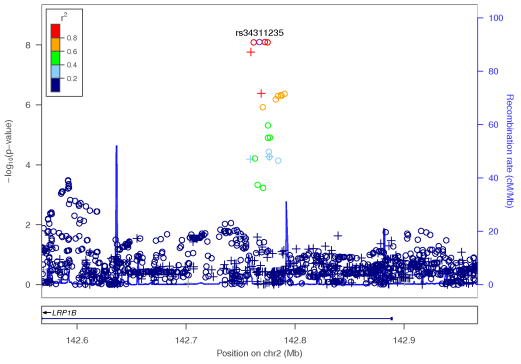

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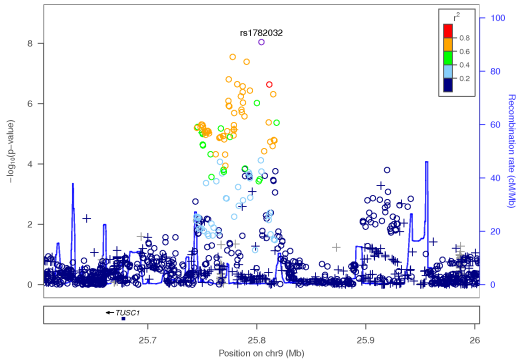

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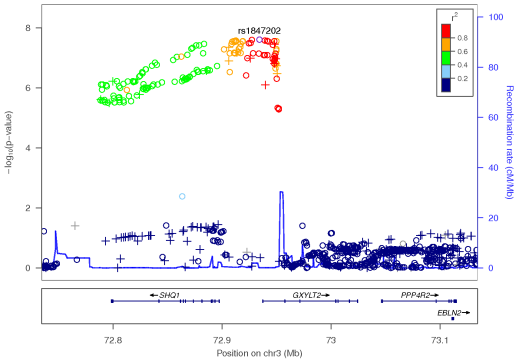

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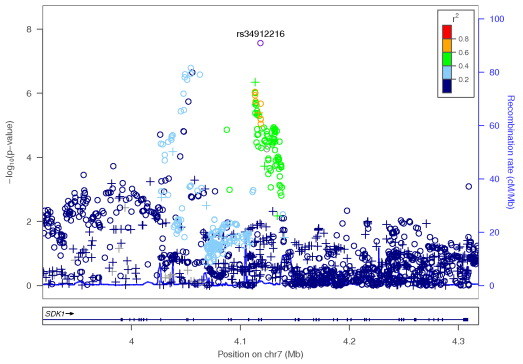

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Figure S2: **Region plots for genome-wide significant regions.** SNPs are colored by r^2 with the index SNP (which is labeled). Circles are imputed SNPs, plus signs are genotyped SNPs.