STable 3. IPA analysis of significant canonical pathways in the GWAS dataset[a]

Pathways	***P* value**[b]	**q value**[c]	**Ratio**[d]
G beta-gamma signaling	0.0000177	0.012	7/88
CXCR4 signaling	0.0000882	0.03	8/152
CREB signaling in neurons	0.000199	0.07	8/171
CCR5 signaling in macrophages	0.000451	0.08	5/69
Agrin interactions at neuromuscularjunctior	0.000447	0.08	5/69

[a] IPA was conducted on genes with the tagged SNPs that had $P < 0.0005$ in Cox regressi

[b] Calculated using Fisher exact test (right-tailed).

[c] q value method to correct multiple comparisons.

[d] No. of genes in current study included in a pathway/no. of all genes making up the corr

Molecules
GNG4, GNAO1, GNB5, PRKCE ,GNAL, PRKCA, EGFR
GNG4, DOCK1, GNAO1, GNB5, PRKCE, MAPK9, GNAL, PRKCA
GNG4, GNAO1, GNB5, PRKCE, GRIK2, GRIA4, GNAL, PRKCA
GNG4, GNB5, PRKCE, MAPK9, PRKCA
NRG3, LAMA2, MAPK9, ITGAL, EGFR

on of the GWAS data.

esponding pathway.