Supplementary Figure 1: LD plot around the BDNF-AS locus. Highlighted in red are the 4 key SNPs used in the HYST analysis of the BDNF-AS locus. The remaining ones (along with the rs6484320) are the eight SNPs significantly associated with ever smoking in the combined TAG-ENGAGE- Oxford-GlaxoSmithKline consortia sample, and are located on chromosome 11, overlapping the BDNF gene and the BDNF-AS locus (see Figure 3b in 2 for a zoom plot around the region). In our gene-based analysis of ever smoking the noncoding antisense RNA transcript BDNF-AS locus yielded the lowest p-value ($P=6.25E-07$), yet the BDNF gene did not reach genome-wide significance ($P=0.00013$). This result combined with the observed high LD among the 11 SNPs suggest that the eight significant SNPs reported in the combined TAG analysis were tagging better the non-coding RNA BDNF-AS locus.
Supplementary Figure 2: Top pathways in the quantity smoked and in the ever smoking analyses. The pathways were manually curated by experts in the field and originate from the Reactome database (www.reactome.org). The nodes represent the pathways, the edges represent interactions between pathways. The size of the node indicates the strength of association, and it is based on the \(-\log_{10}\) values of the p-values, i.e., smaller p-values (more significant) are displayed as larger nodes.

(a) The Neuronal system pathway
(b) The Cell-Cycle pathways

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REFERENCES

