

Supporting Information

Guénard et al. 10.1073/pnas.1216959110

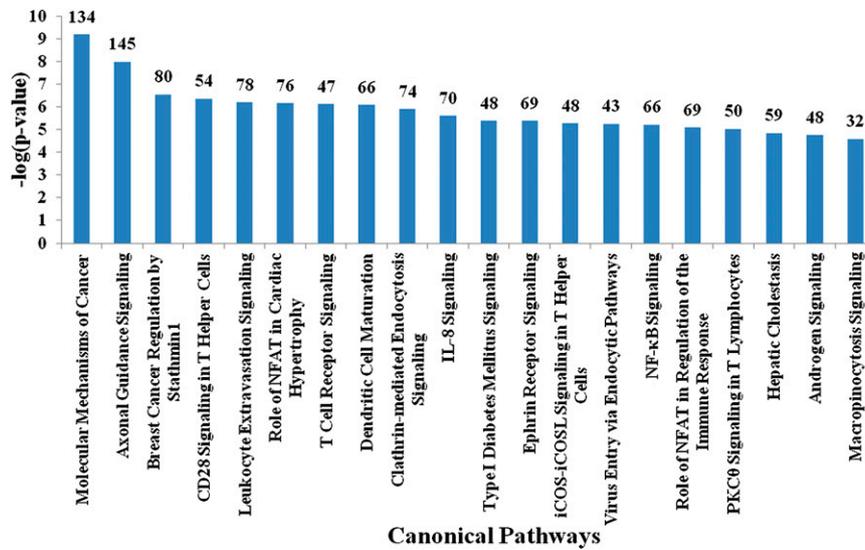


Fig. S1. Top 20 pathways identified from differential methylation and IPA analysis. The number of differentially methylated genes in each pathway is reported over histogram bars.

Other Supporting Information Files

- [Table S1 \(DOCX\)](#)
- [Table S2 \(DOCX\)](#)
- [Table S3 \(DOCX\)](#)
- [Table S4 \(DOCX\)](#)
- [Table S5 \(DOCX\)](#)
- [Table S6 \(DOCX\)](#)
- [Table S7 \(DOCX\)](#)
- [Table S8 \(DOCX\)](#)
- [Table S9 \(DOCX\)](#)