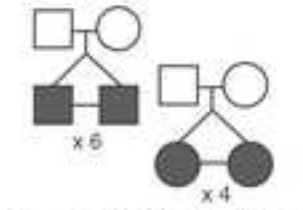
Supplemental Figure 1



10 quad families, monozygotic twins concordant for autism diagnosis

high-coverage (~40x), paired-end whole genome sequencing with Illumina

alignment + variant calling

alignment with BWA and variant calling with GATK

forestDNM

DNM calling with forestDNM, a custom machine learning tool

putative germline mutations

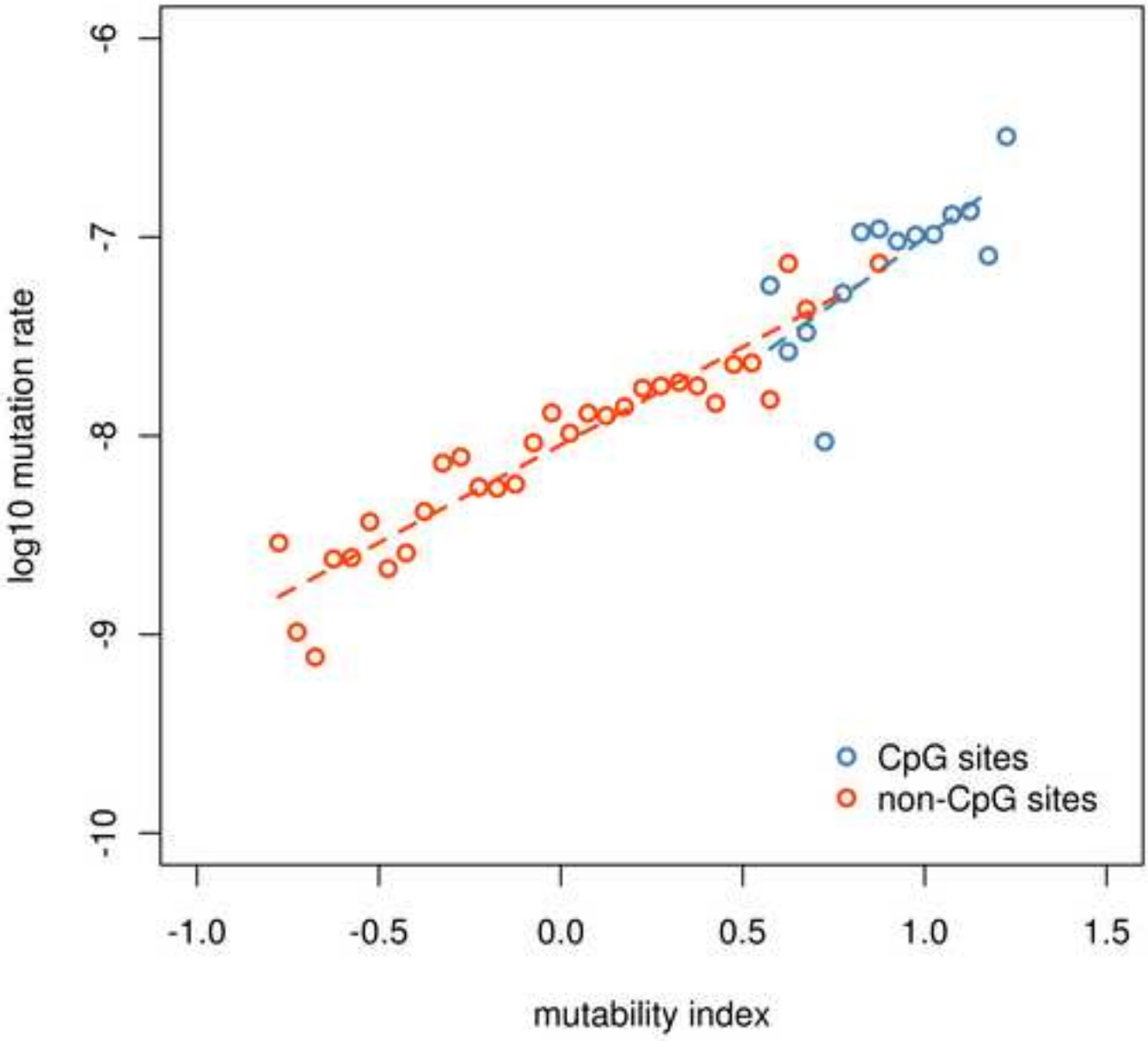
668 germline DNMs in 10 families

DNM validation with Sanger sequencing and Sequenom genotyping

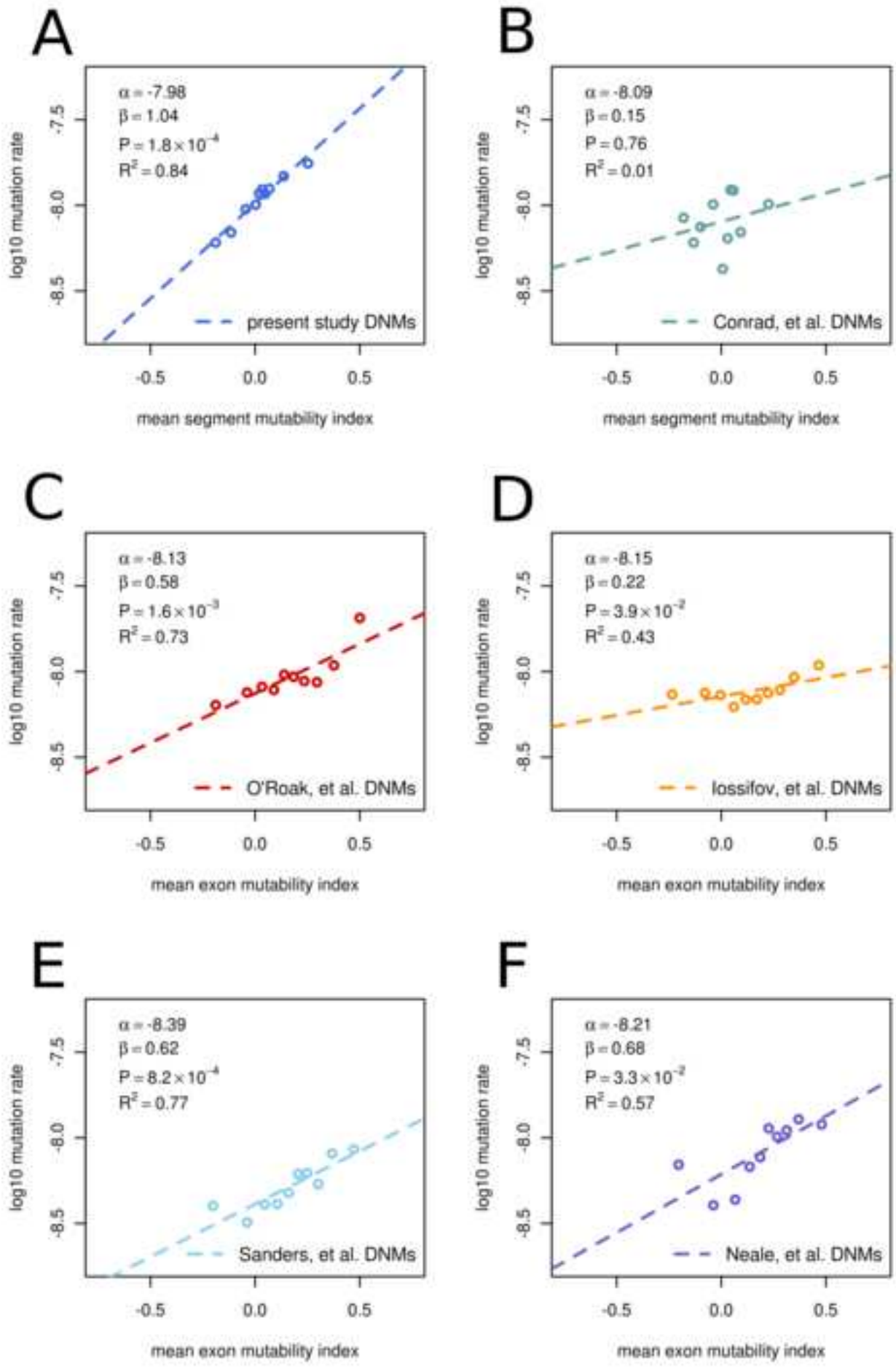
validated germline mutations

581 germline DNMs in 10 families

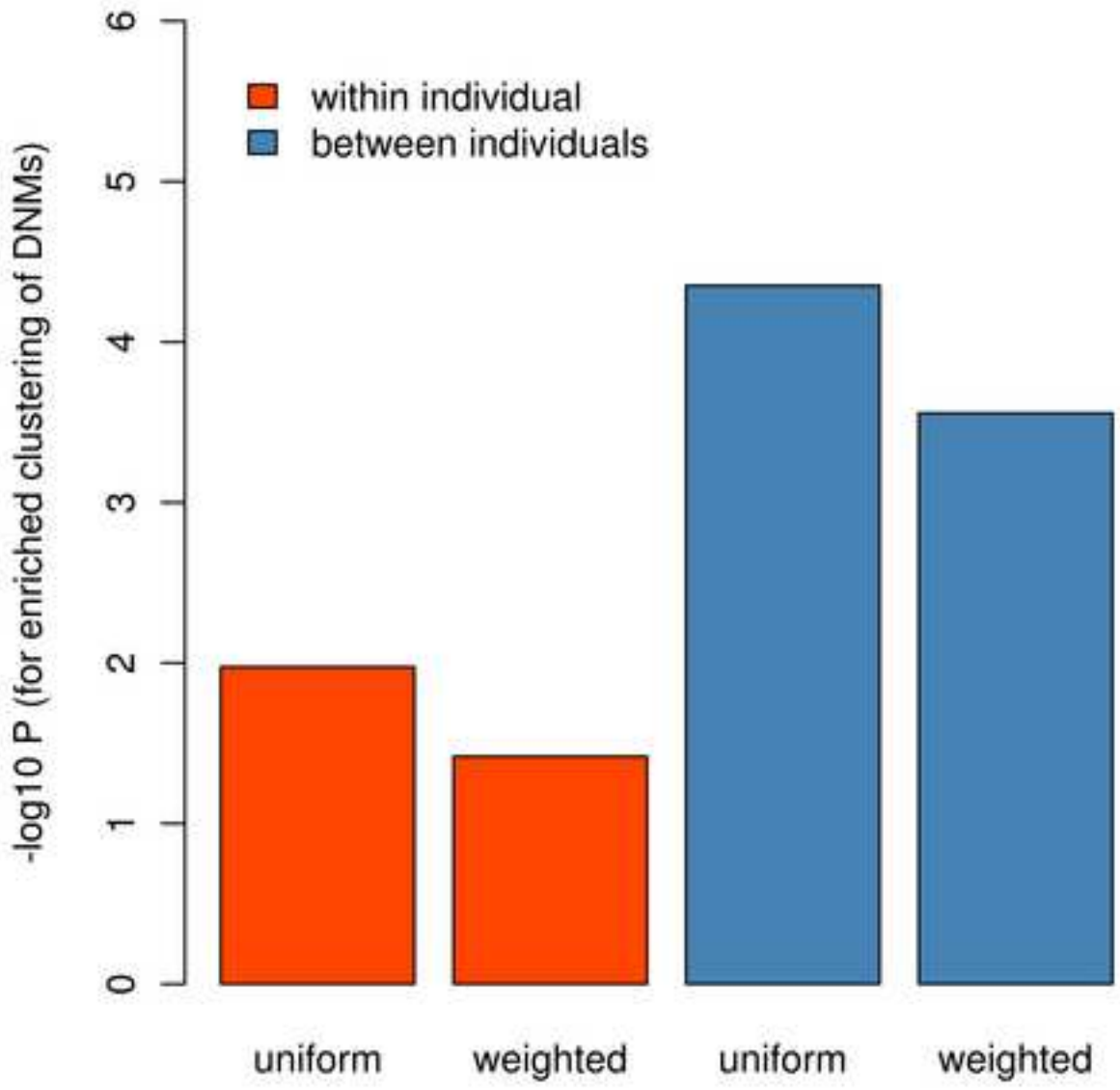
Supplemental Figure 2



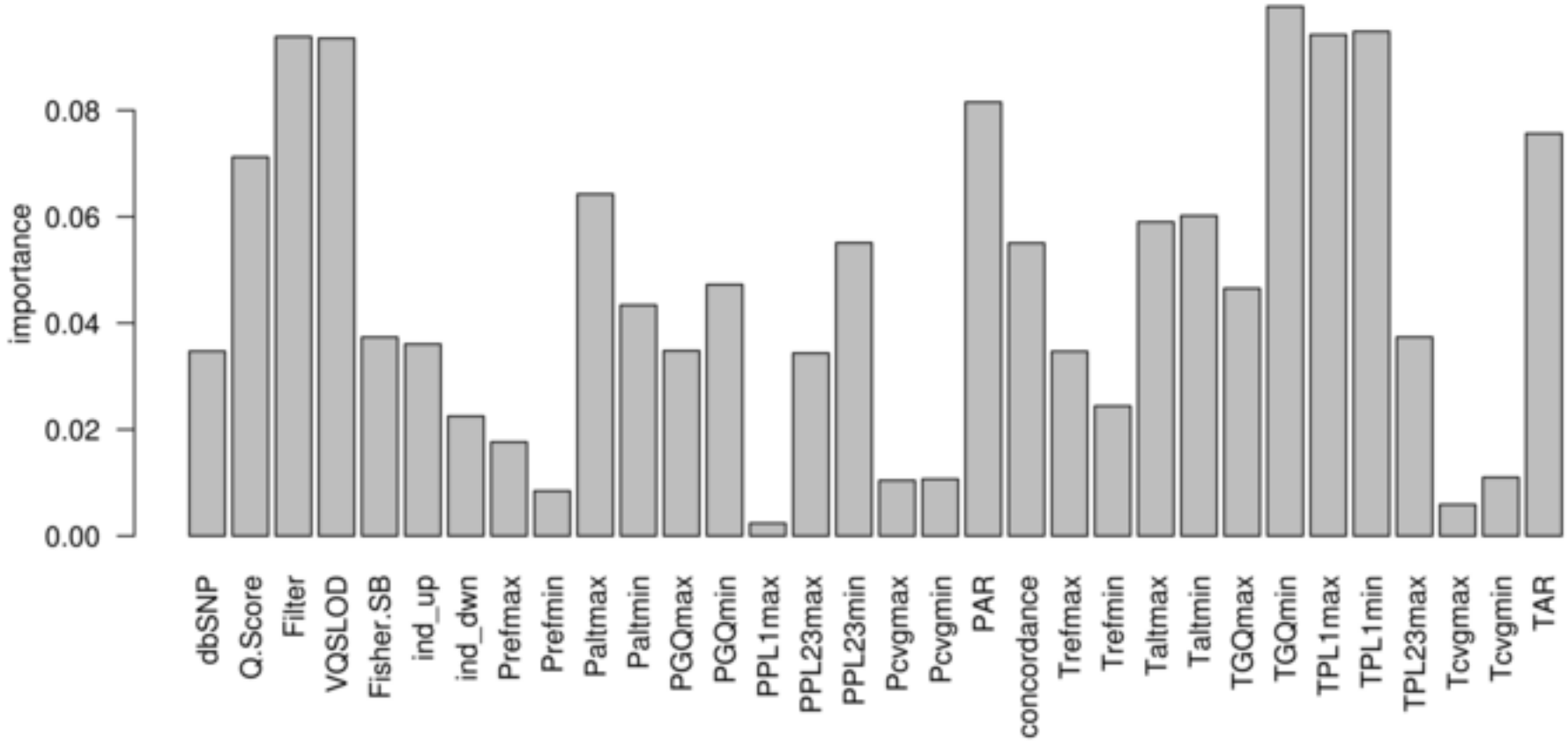
Supplemental Figure 3



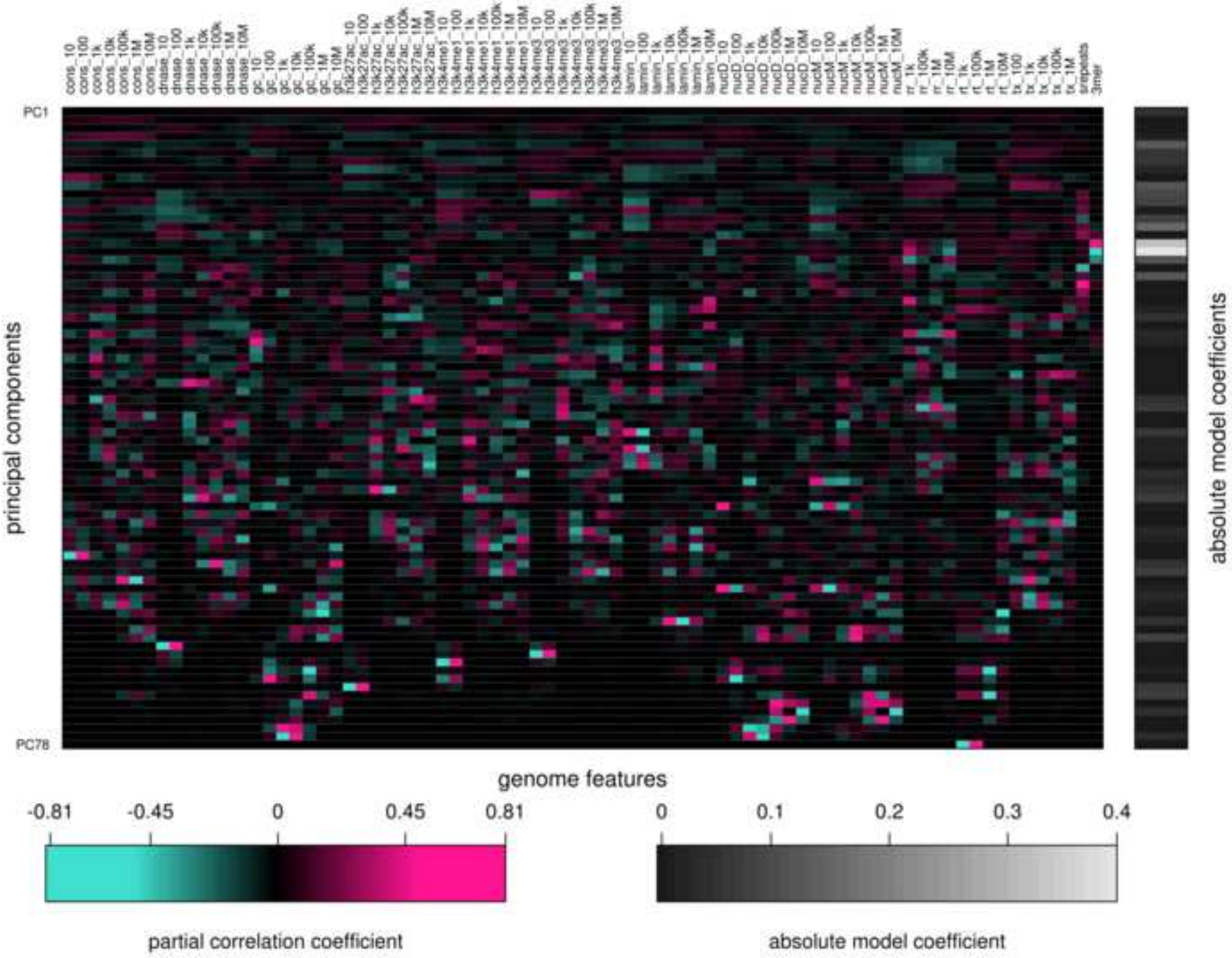
Supplemental Figure 4



Supplemental Figure 5



Supplemental Figure 6



Supplemental Figure 7