

Ray-Jones et al., Genetic Coupling of Enhancer Activity and Connectivity in Gene Expression Control

Description of Supplementary Data

Supplementary Data 1. Monocyte meta-analysis eQTLs used for eQTL Capture Hi-C design.

Supplementary Data 2. eQTL CHi-C QC summary statistics

Supplementary Data 3. ATAC-seq QC summary statistics

Supplementary Data 4. RNA-seq QC summary statistics

Supplementary Data 5. The locations of TADs in primary monocytes detected from Hi-C data

Supplementary Data 6. CHi-C ABC analysis results

Supplementary Data 7. BaseQTL results for CHi-C data (Tab A: Significant contact eQTL; Tab B: Contact eQTL summary statistics; Tab C: Contact non eQTL summary statistics)

Supplementary Data 8. BaseQTL results for ATAC-seq data

Supplementary Data 9. BaseQTL results for RNA-seq data

Supplementary Data 10. Trimodal QTL detection by GUESS analysis results

Supplementary Data 11. Causal mediation analysis results

Supplementary Data 12. TF enrichment analysis results (Tab A: Enrichment for known and predicted binding sites of monocyte TFs; Tab B: Enrichment for known binding sites of all TFs contained in the Remap database)

Supplementary Data 13. Prediction of cQTL effects on TF binding (Tab A: consensus predictions; Tab B: Enformer predictions; Tab C: DeepSea predictions, Tab D: Known and predicted TF binding sites overlapping cQTLs)

Supplementary Data 14. cQTL integration with GWAS SNPs (Tab A: Intersection of cQTLs with GWAS SNPs accounting for LD; Tab B: Additional information on white blood cell GWAS SNPs overlapping cQTLs).

Supplementary Data 15. Monocyte sample information