

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: List of 59,972 significantly independent cis-eQTLs.

File Name: Supplementary Data 2

Description: List of 1,592 significantly independent cis-pQTLs.

File Name: Supplementary Data 3

Description: List of 3,978 significantly independent splicing-QTLs.

File Name: Supplementary Data 4

Description: Functional enrichment results.

File Name: Supplementary Data 5

Description: List of all SNPs significantly associated with two phenotypes in cis and/or trans (n=69,532 trios).

File Name: Supplementary Data 6

Description: List of annotates genes to topologically associated domains (TADs) called in 8 different blood cell types.

File Name: Supplementary Data 7

Description: List of 2,320 significantly independent trans-eQTLs.

File Name: Supplementary Data 8

Description: List of 533 significantly independent trans-pQTLs.

File Name: Supplementary Data 9

Description: List of 301 significantly independent metabolites-QTLs.

File Name: Supplementary Data 10

Description: List of pQTLs and the matching eQTLs.

File Name: Supplementary Data 11

Description: List of replicated QTLs in various studies.

File Name: Supplementary Data 12

Description: Causal model that passed evaluation criteria.

File Name: Supplementary Data 13

Description: List of 3,652 QTLs with a GWAS SNPs.

File Name: Supplementary Data 14

Description: Summary of GWAS SNPs identified as QTLs in this study.

File Name: Supplementary Data 15

Description: List of 16 GWAS studies used in the co-localization analysis.

File Name: Supplementary Data 16

Description: Results from the co-localization analysis (COLOC).

File Name: Supplementary Data 17

Description: STRING enrichment analysis output from the big cluster network from Cytoscape.

File Name: Supplementary Data 18

Description: List of excluded GWAS for enrichment analysis.

File Name: Supplementary Data 19

Description: DIRECT consortium full list.