

Description of Additional Supplementary Files

File name: Supplementary Data 1.

Description: Summary statistics of steady-state cis-pQTL mapping in each context using linear regression model with TensorQTL, reporting top cis-pqtls per context.

File name: Supplementary Data 2. Annotation of all independent cis-pQTLs across contexts ($k = 1,629$) with RegulomeDB. (pre-calculated score file for dbSNP v153 <https://www.regulomedb.org/regulome-search/>).

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File Name: Supplementary Data 3. Variance explained by the top cis-pQTLs across all contexts for each of the 630 proteins associated with at least one cis-pQTL (pGenes) based on linear regression model using TensorQTL.

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File Name: Supplementary Data 4. PheWAS query results for differential cis-pQTLs and their proxy variants ($r^2 > 0.8$), using “phewas” function of “ieugwasr” package.

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File Name: Supplementary Data 5.

Description: Genetic association analysis of the LBR-associated differential cis-pQTL (rs74148404) with selected plasma metabolites; using the same linear regression model as in cis-pQTL mapping (TensorQTL) adjusting for age, sex, BMI, medication use and the first three genotype PCs.

File Name: Supplementary Data 6.

Description: Colocalization results of differential cis-pQTLs and PheWAS selected traits, using the “coloc” R package.