Cell_type	num_fQTls	min_bonf_corrected_p_val	max_bonf_corrected_p_val
Microg	2735	1.48E-18	0.049895352
Ex8	1027	8.84E-36	0.04994986
Ex3	329	4.73E-20	0.046433697
Ex4	202	1.72E-16	0.048801323
Ex7	521	2.36E-19	0.048236537
Astro	61	3.14E-06	0.046176513
In6	23	7.97E-09	0.049550722
In8	21	0.000119951	0.043654396
Ex5	3	2.33E-06	0.006690033
Endoth	43	0.002804026	0.045040673

Original merged gene expression dataset
- # genes:
  - prior to filtering lowly-expressed genes: 57820
  - after filtering out lowly-expressed genes: 43885
- # samples: 1931
- # samples for which genotype data is avail: 1452

Expression matrix for all adults:
- # genes:
  - prior to filtering lowly-expressed genes: 57820
  - after filtering out lowly-expressed genes: 42524
- # samples: 1387
- # samples for which genotype data is avail: **1387**

Expression matrix for all European adults:
- # genes:
  - prior to filtering lowly-expressed genes: 57820
  - after filtering out lowly-expressed genes: 41353
- # samples: 938
- # samples for which genotype data is avail: **938**

Re-calculate fQTLs based on a revised gene expression matrix (biomarkers)

Means of calculating eQTLs

cis/trans

use all genes in the genome to calculate eQTLs

use only the ~440 biomarker genes to calculate eQTLs

pull out those eQTLs that match the 440 biomarker genes, and find matches between their associated SNVs and those SNVs that correspond to fQTLs

find matches between ALL of the SNVs in this set of eQTLs and those SNVs that correspond to fQTLs

simply extract gene expression values for these genes from the original normzlized expression matrix (which contains all genes)

re-normalize the gene expression matrix (from scratch) using only the 440 biomarker genes

Additional variables:
    Use only adult samples?

    Use only adult European samples? If so, then should we:
        - include or exclude genotype principal components (not an option for trans-eQTLs)?
        - include or exclude PEER factors (not an option for trans-eQTLs)?