To compute fQTLs:

     + cell fractions file used as is

     + sheared up genome into 250 pieces (rapid calc)

     + computed fQTLs in a 'cis' manner in order to include covariates (next slide)

     + ran a 'hacked' version of the cis search (w/covariates) to identify fQTLs
          - sanity checks in QTLtools – effects of varying window sizes
          - cell types added as "genes" to each chromosome
          - set cis-window length to exceed the length of the chromosome
          - merge results for each cell type across chromosomes

     + Bonferroni correction after nominal pass

Filter input files to include only adult samples w/genotype data and genotype PCs: 1362 samples

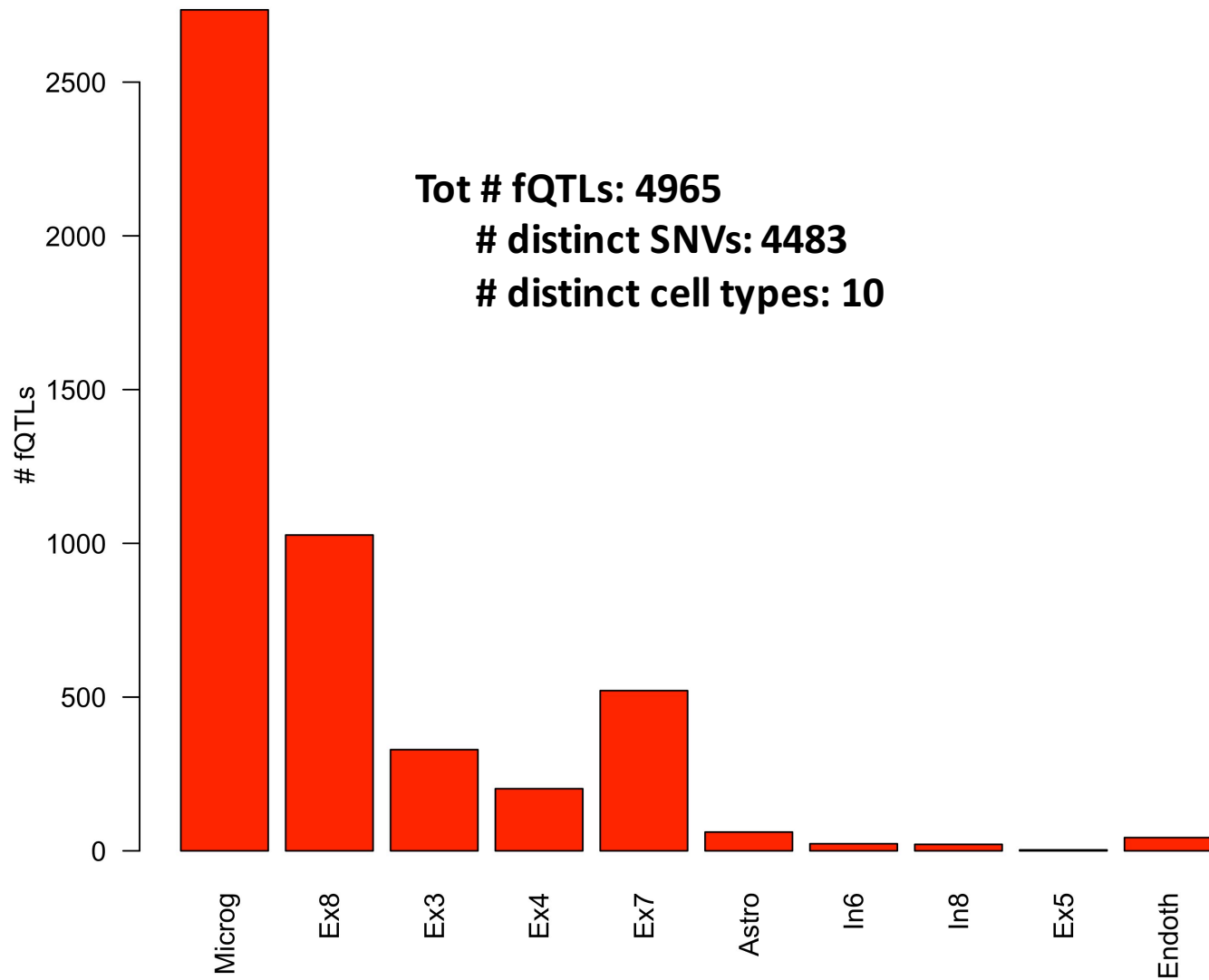1) **Genotype file**

2) **Covariates file**
   - 3 genotype PCs
   - gender
   - disease status
   - study (GTEx, Brainspan, Bipseq, etc)
   - NOT included as covariates:
     + age
     + PEER factors (not appropriate for cell fractions)
     + genotype PCs for 25 GTEx samples

3) **Cell fractions** (ie, the phenotype file)
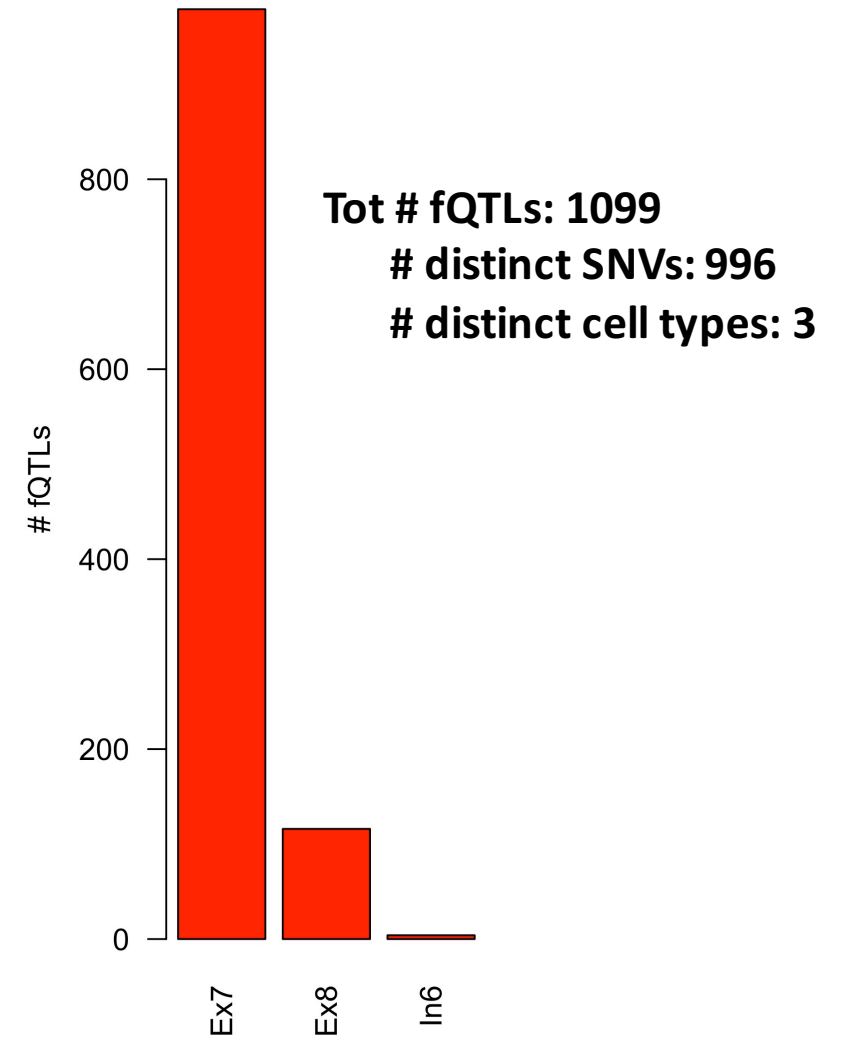   includes only the 10 selected cell types on which we've previously decided
   - Ex3
   - Ex4
   - Ex5
   - Ex7
   - Ex8
   - In6
   - In8
   - Astrocytes
   - Endothelial
   - Microglia

fQTLs without covariates

Tot # fQTLs: 4965
    # distinct SNVs: 4483
    # distinct cell types: 10

fQTLs w/covariates

Tot # fQTLs: 1099
    # distinct SNVs: 996
    # distinct cell types: 3

Pending (in order)

+ if necessary: improvements to current fQTLs identification pipeline (w/covariates)

+ re-calc (based on updated fQTLs): residual-QTLs on 440 biomarker genes (first trans, then cis)

+ SNV overlaps accr. QTL types

+ adaptive thresholding

+ could we do the fQTL like height?