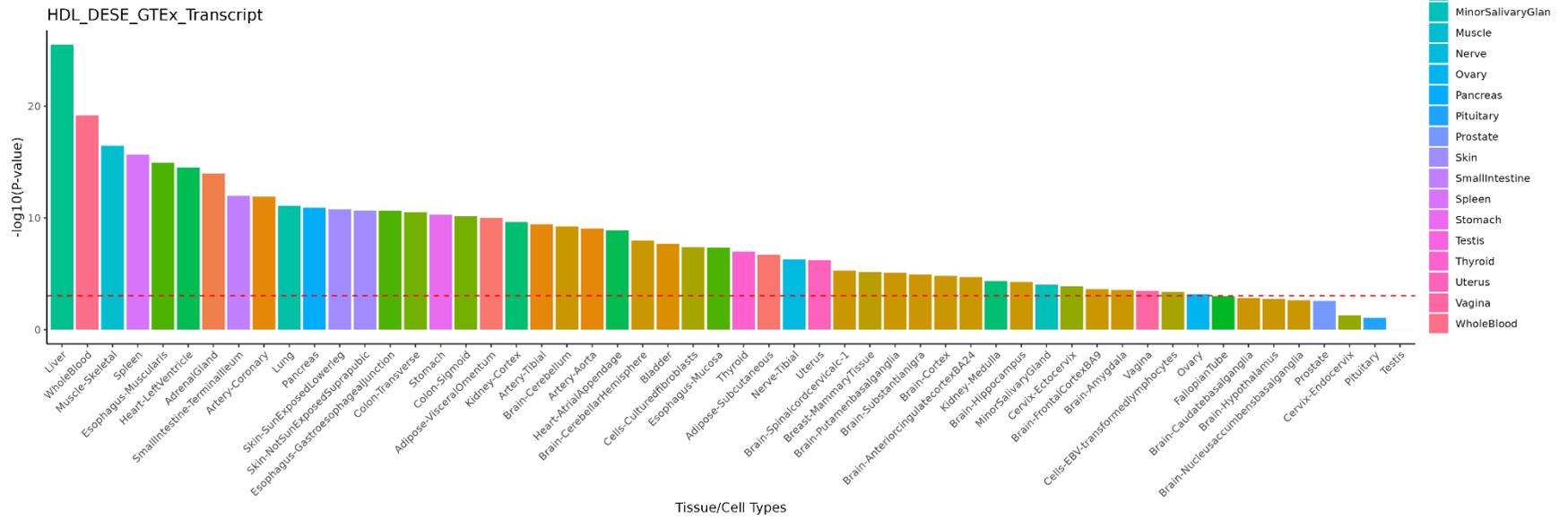
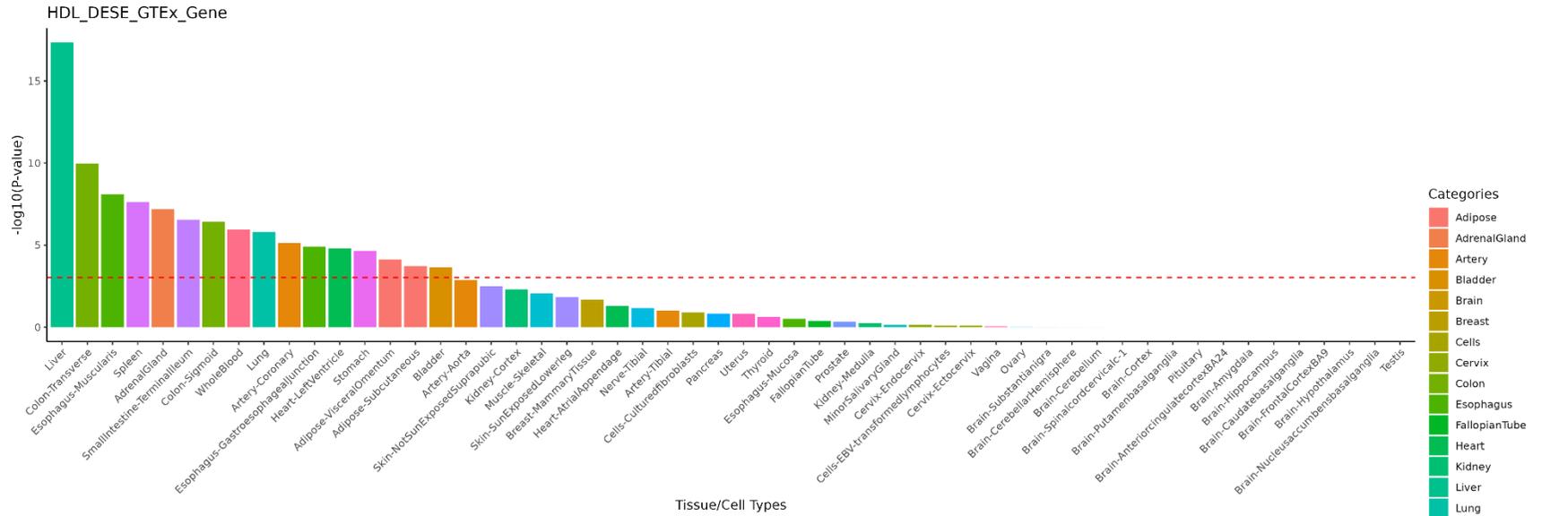
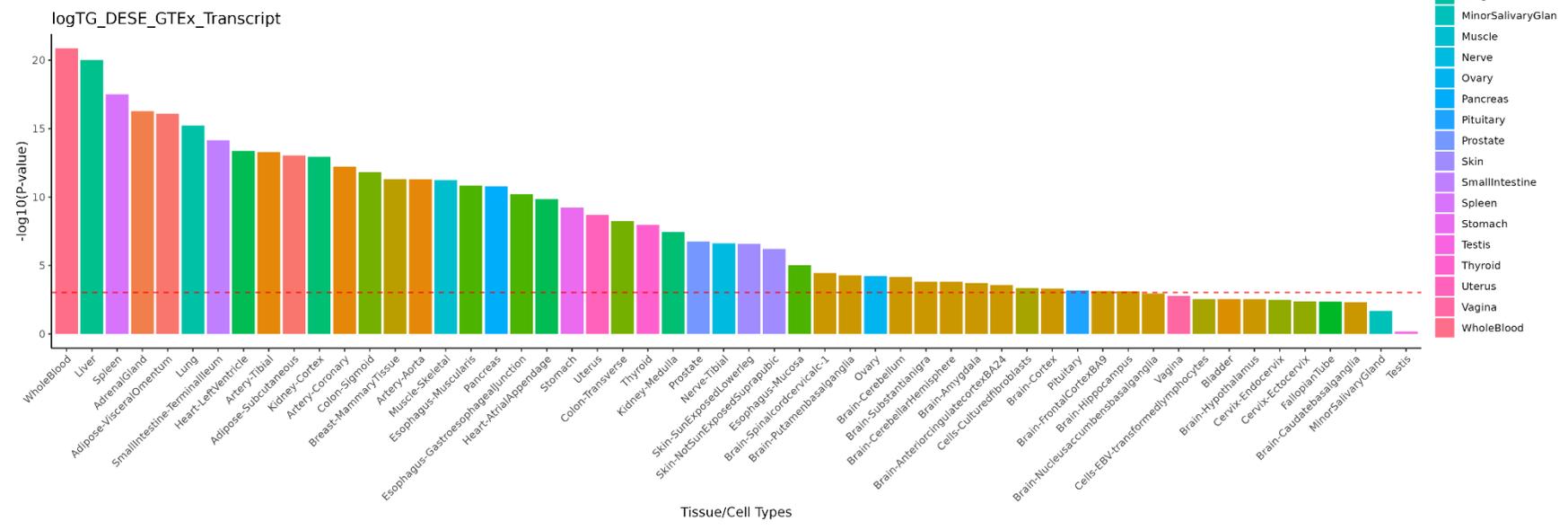
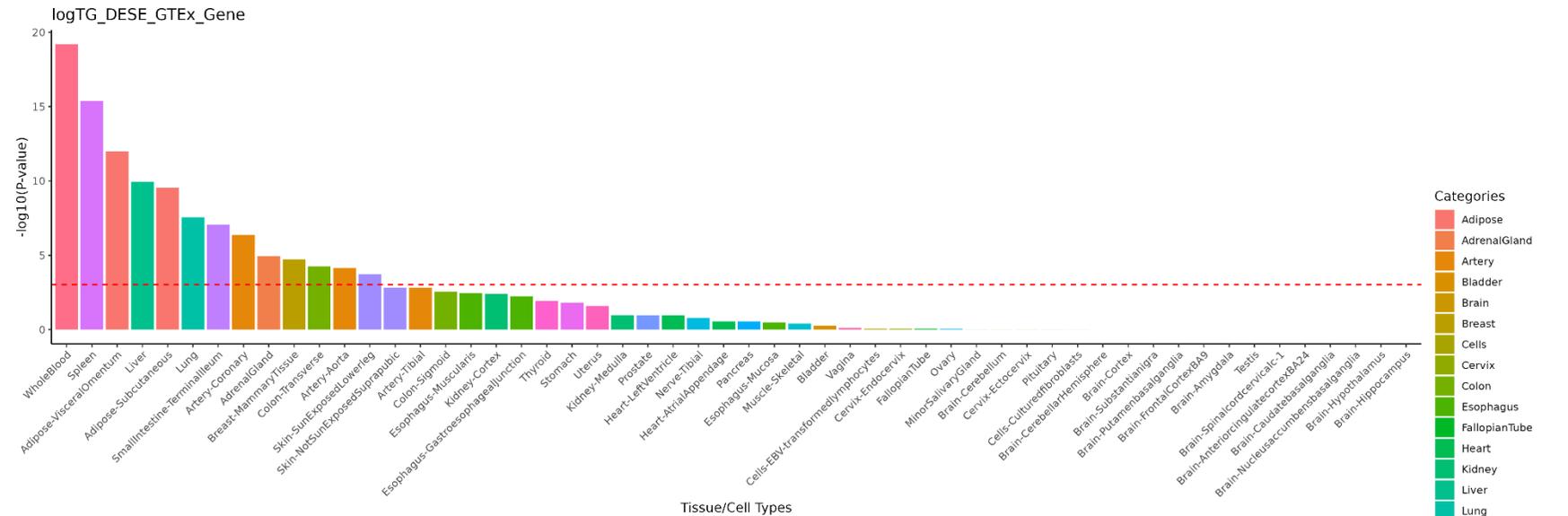


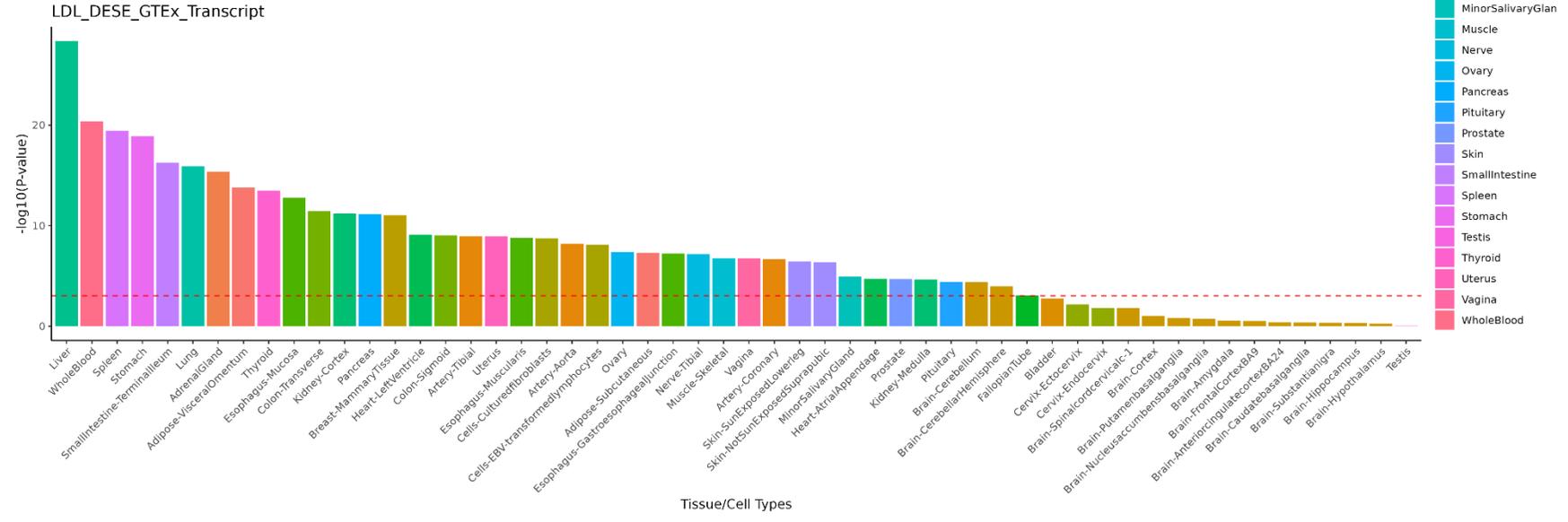
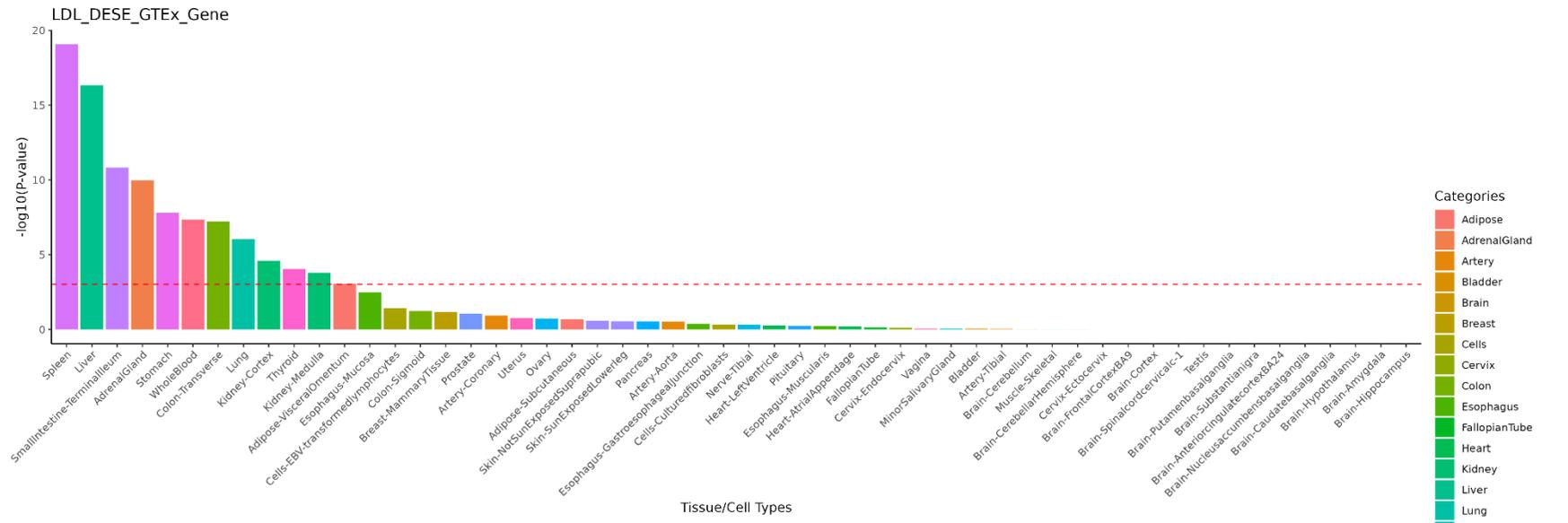
A



B

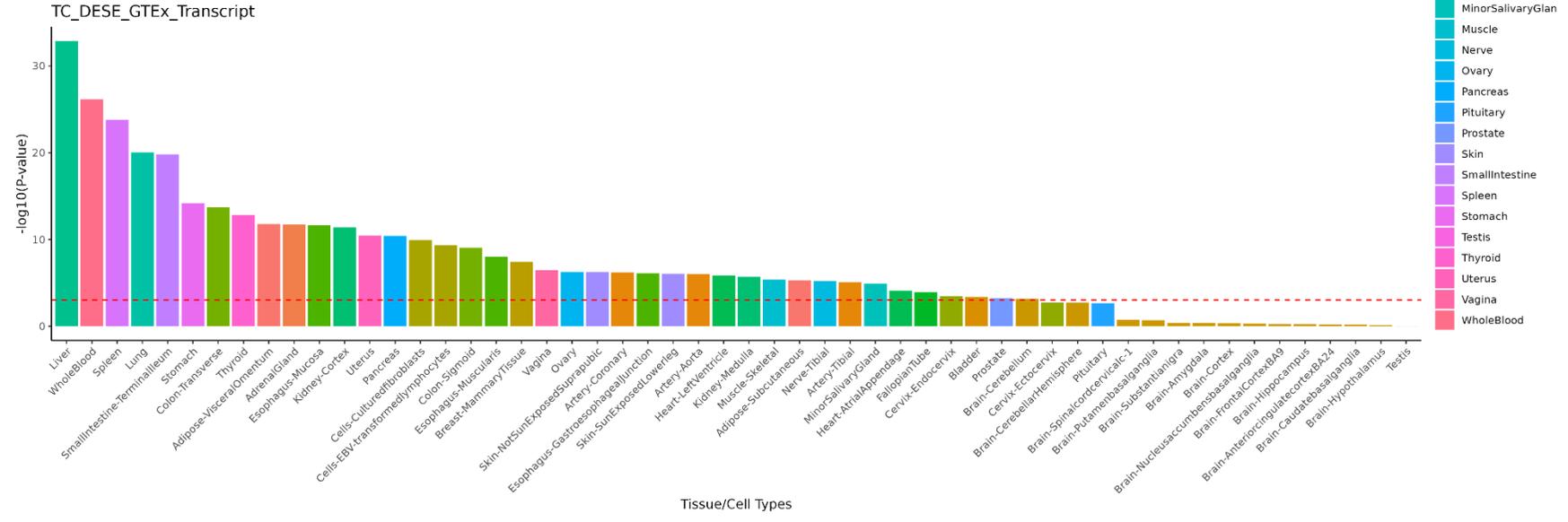
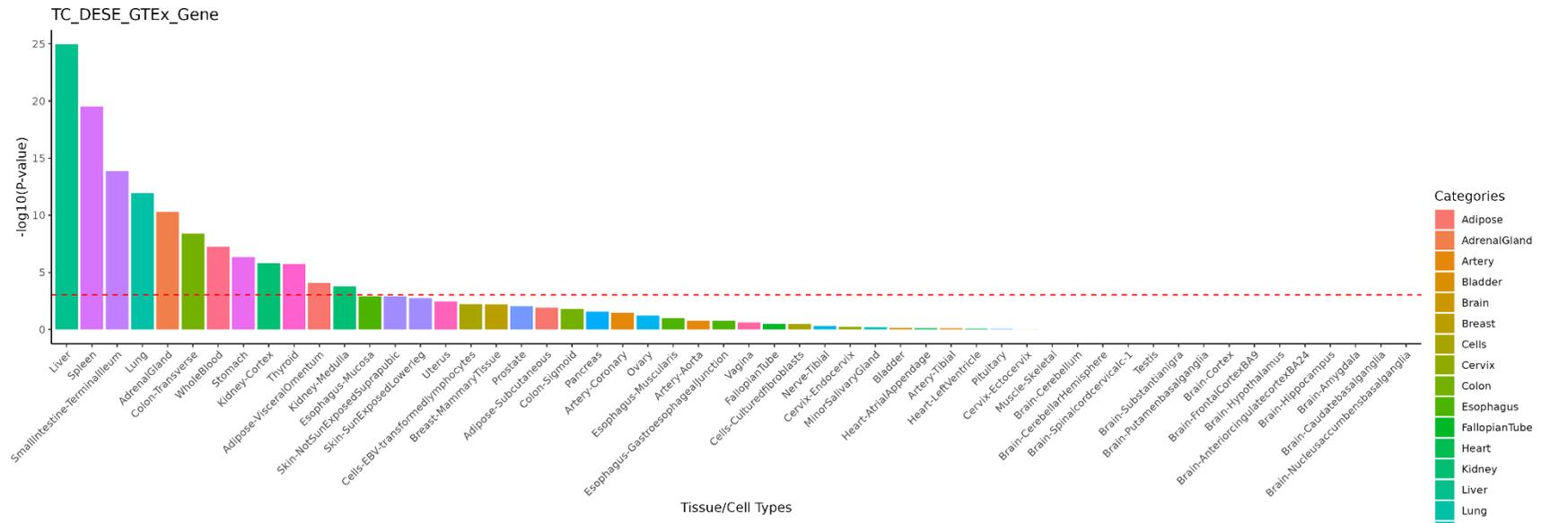


C



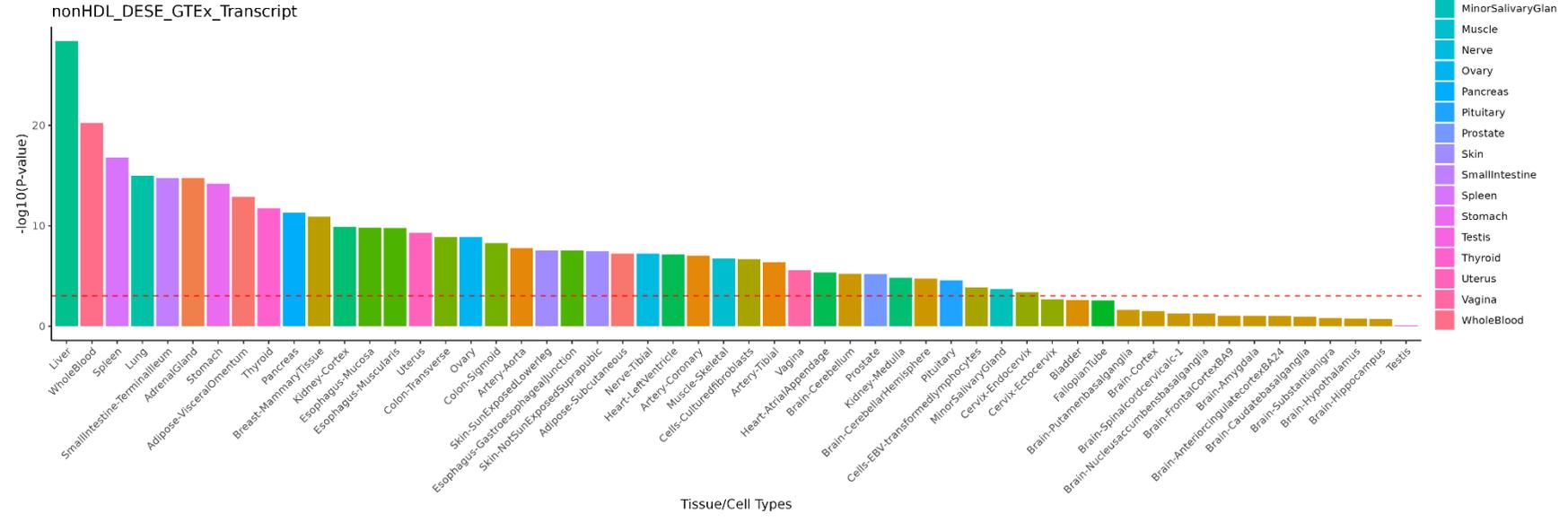
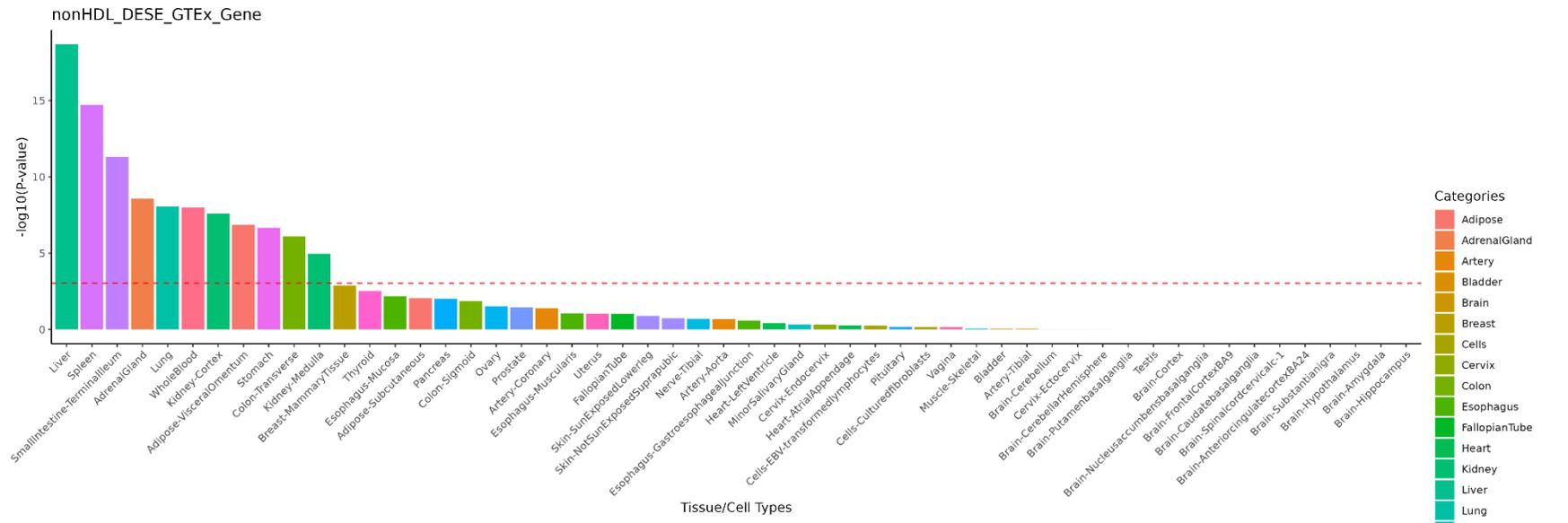
- Categories
- Adipose
  - AdrenalGland
  - Artery
  - Bladder
  - Brain
  - Breast
  - Cells
  - Cervix
  - Colon
  - Esophagus
  - FallopianTube
  - Heart
  - Kidney
  - Liver
  - Lung
  - MinorSalivaryGland
  - Muscle
  - Nerve
  - Ovary
  - Pancreas
  - Pituitary
  - Prostate
  - Skin
  - SmallIntestine
  - Spleen
  - Stomach
  - Testis
  - Thyroid
  - Uterus
  - Vagina
  - WholeBlood

D



- Categories
- Adipose
  - AdrenalGland
  - Artery
  - Bladder
  - Brain
  - Breast
  - Cells
  - Cervix
  - Colon
  - Esophagus
  - FallopianTube
  - Heart
  - Kidney
  - Liver
  - Lung
  - MinorSalivaryGlan
  - Muscle
  - Nerve
  - Ovary
  - Pancreas
  - Pituitary
  - Prostate
  - Skin
  - SmallIntestine
  - Spleen
  - Stomach
  - Testis
  - Thyroid
  - Uterus
  - Vagina
  - WholeBlood

E



**Figure S3. Lipid traits – tissue/cell type associations estimated by DESE according to GTEx gene-level and GTEx transcript-level selective expression.**

We performed phenotype-tissue association tests in five lipid traits: **(A)** HDL-C, **(B)** TG, **(C)** LDL-C, **(D)** TC, and **(E)** nonHDL-C with 54 GTEx tissues. For each lipid traits, the upper panel showed the estimated driver tissues according to GTEx gene-level selective expression and the bottom panel showed estimated driver tissues according to GTEx transcript-level selective expression. The tissues were ranked by their association significance ( $-\log_{10}(\text{P-value})$ ) with each lipid traits. The red horizontal line denoted the significance threshold using a Bonferroni correction.