Supplementary material

**Table S1: The GTEx [1] database (v7) used in this study,** indicating the number of samples within each tissue.

Tissue	Number of Samples	Tissue	Number of Samples
Adipose, subcutaneous	442	Colon, sigmoid	233
Adipose, visceral Omentum	355	Colon, transverse	274
Adrenal gland	190	Esophagus, gastroesophageal junction	244
Artery, aorta	299	Esophagus, mucosa	407
Artery, coronary	173	Esophagus, muscularis	370
Artery, tibial	441	Fallopian tube	7
Bladder	11	Heart, atrial appendage	297
Brain, amygdala	100	Heart, left ventricle	303
Brain, anterior cingulate cortex BA24	121	Kidney, cortex	45
Brain, caudate basal ganglia	160	Liver	175
Brain, cerebellar Hemisphere	136	Lung	427
Brain, cerebellum	173	Minor salivary gland	97
Brain, cortex	158	Muscle, skeletal	564
Brain, frontal Cortex BA9	129	Nerve, tibial	414
Brain, hippocampus	123	Ovary	133
Brain, hypothalamus	121	Pancreas	248
Brain, nucleus accumbens basal ganglia	147	Pituitary	183
Brain, putamen basal ganglia	124	Prostate	152
Brain, spinal cord cervical c1	91	Skin, not sun-exposed, suprapubic	387
Brain, substantia nigra	88	Skin, sun-exposed, lower leg	473
Breast, mammary tissue	290	Small intestine, terminal Ileum	137
Cells, EBV-transformed lymphocytes	130	Spleen	162
Cells, transformed fibroblasts	343	Stomach	262
Cervix, ectocervix	6	Testis	259
Cervix, endocervix	5	Thyroid	446
Vagina	115	Uterus	111

	407	
Whole blood	407	

|		Group A			Group B	
	Cell A	Cell B	Cell C	Cell A	Cell B	Cell C
Gene 1		Gene-Centered			Gene-Centered	
Gene 2	Cell-			Cell-		
Gene 3	Centered			Centered		

Figure S1: Gene- and cell-centered MAE calculations.
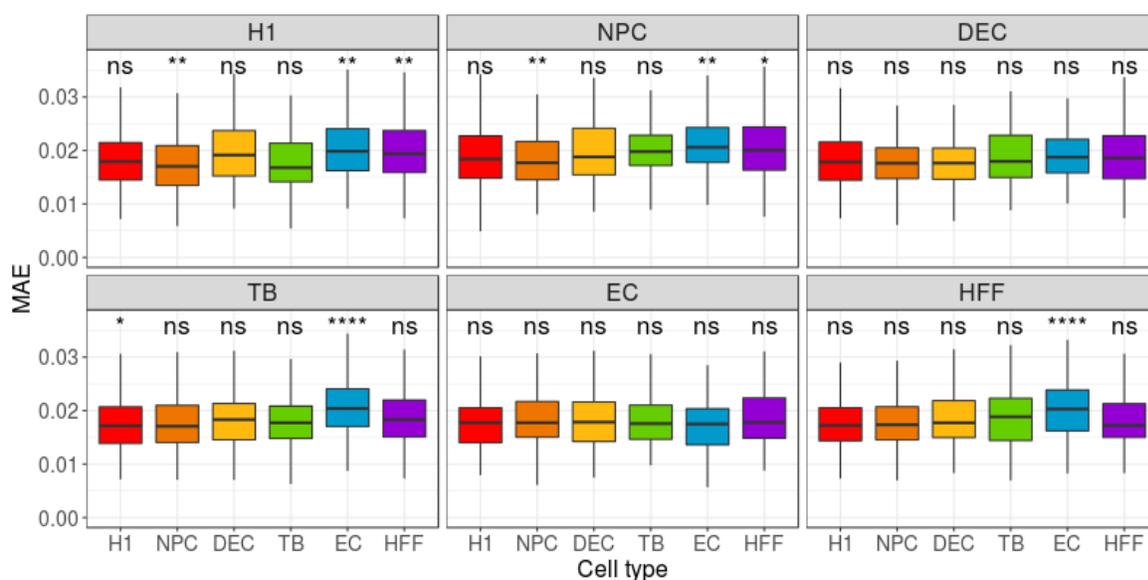
Figure S2: Distribution of group-based, cell-centered MAE scores calculated across the 200 genes that were found to have the lowest gene-centered MAE scores. The 200 genes with the lowest MAE scores were detected separately for each cell type, and then cell-centered MAE scores were calculated based on these genes. Panel titles represent the focus group (e.g., the "H1" panel indicates the cell-centered MAE score distribution calculated for each cell type, based on the 200 genes that have the lowest gene-centered MAE scores within the H1 group). H1: human embryonic stem cells (n = 375 cells), NPC: neural progenitor cells (n = 173 cells), DEP: definitive endoderm progenitors (n = 138 cells), EC: endothelial cells (n = 105 cells), TB: trophoblasts (n = 69 cells), HFF: human foreskin fibroblasts (n = 159 cells). Each group was compared with each of the other groups using a Wilcoxon test. Ns: non-significant (p > 0.05), *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, ****p ≤ 0.0001.
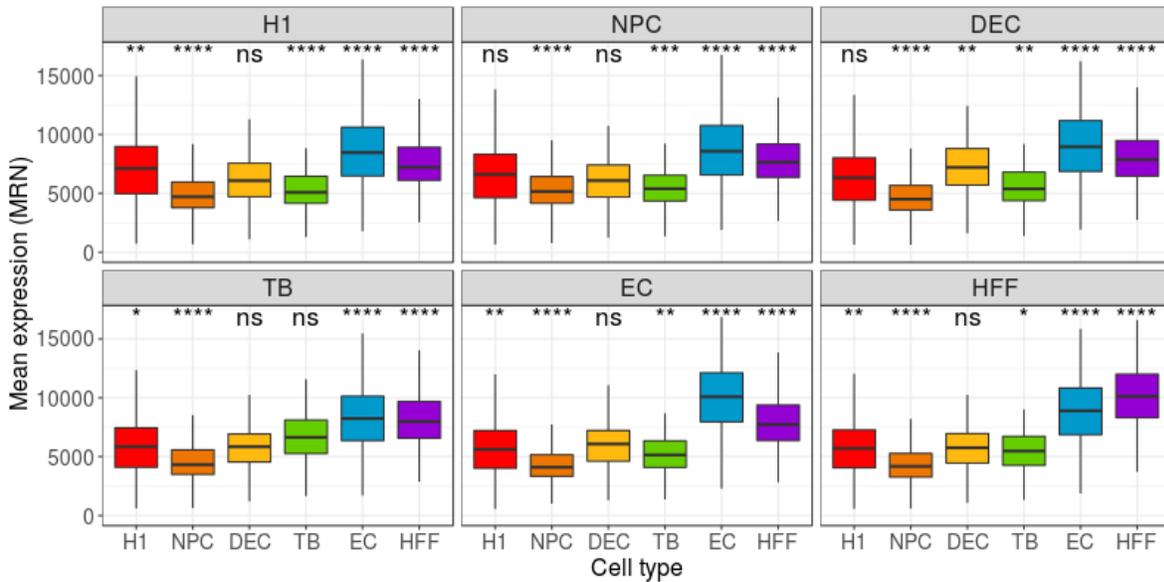
Figure S3: Distribution of group-based, cell-centered mean-expression (mean-EXP) scores, calculated across the 200 genes that were found to have the highest gene-centered mean-EXP scores. The 200 genes with the highest mean-EXP scores were detected separately for each cell type, and then cell-centered mean-EXP scores were calculated, based on these genes. Panel titles indicate the focus group. H1: human embryonic stem cells (n = 375 cells), NPC: neural progenitor cells (n = 173 cells), DEP: definitive endoderm progenitors (n = 138 cells), EC: endothelial cells (n = 105 cells), TB: trophoblasts (n = 69 cells), HFF: human foreskin fibroblasts (n = 159 cells). Each group was compared with each of the other groups using a Wilcoxon test. Ns: non-significant (p > 0.05), *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, ****p ≤ 0.0001.

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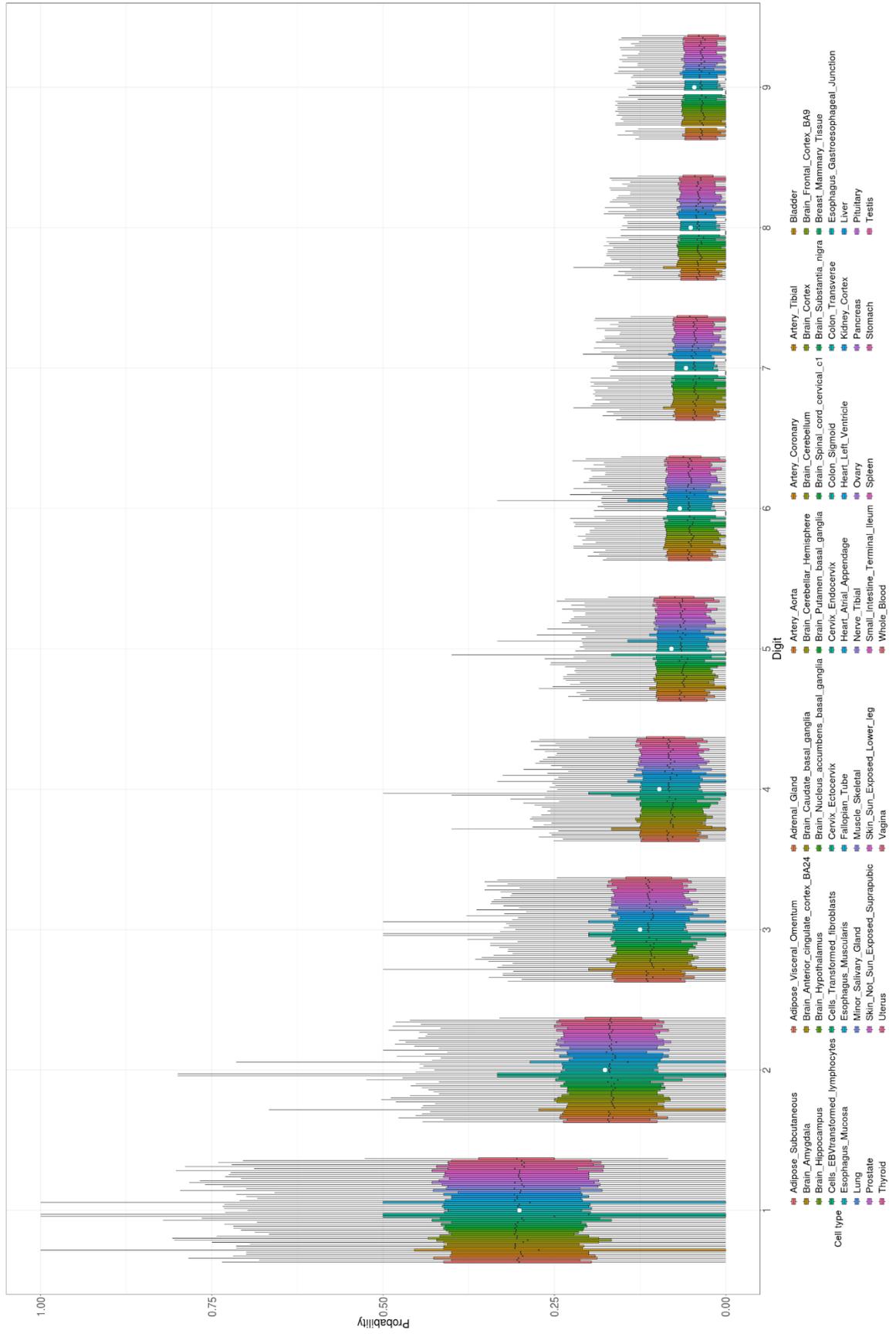
Figure S4: First-digit distribution of gene-centered expression data for 53 tissues included in the GTEx dataset [1]**.** White circles represent the Benford first-digit distribution. See **Table S2** for further details.

References

1.   GTEx Portal Available online: https://gtexportal.org/home/.