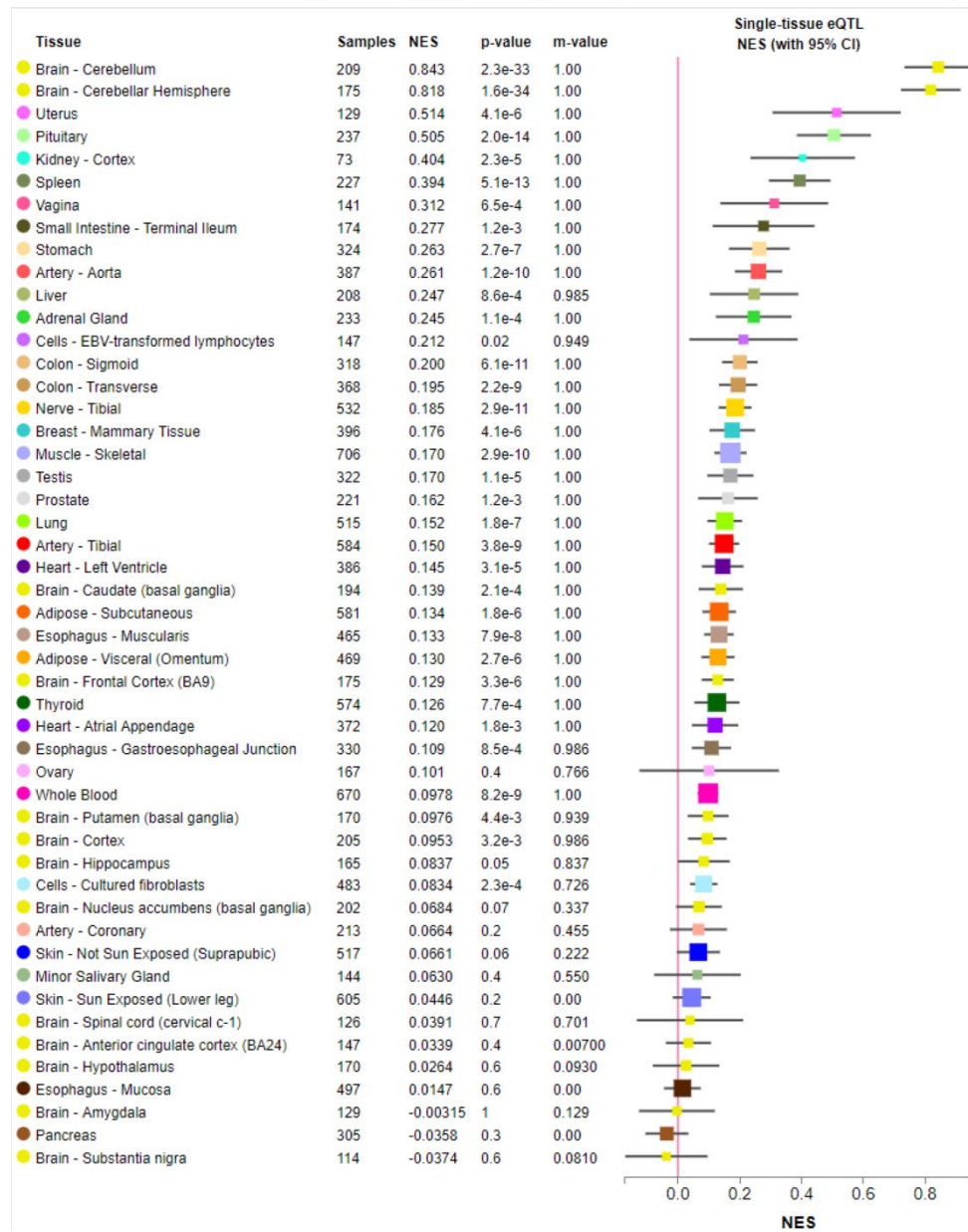# SUPPLEMENTARY FIGURES

Multi-tissue eQTL Comparison ⓘ
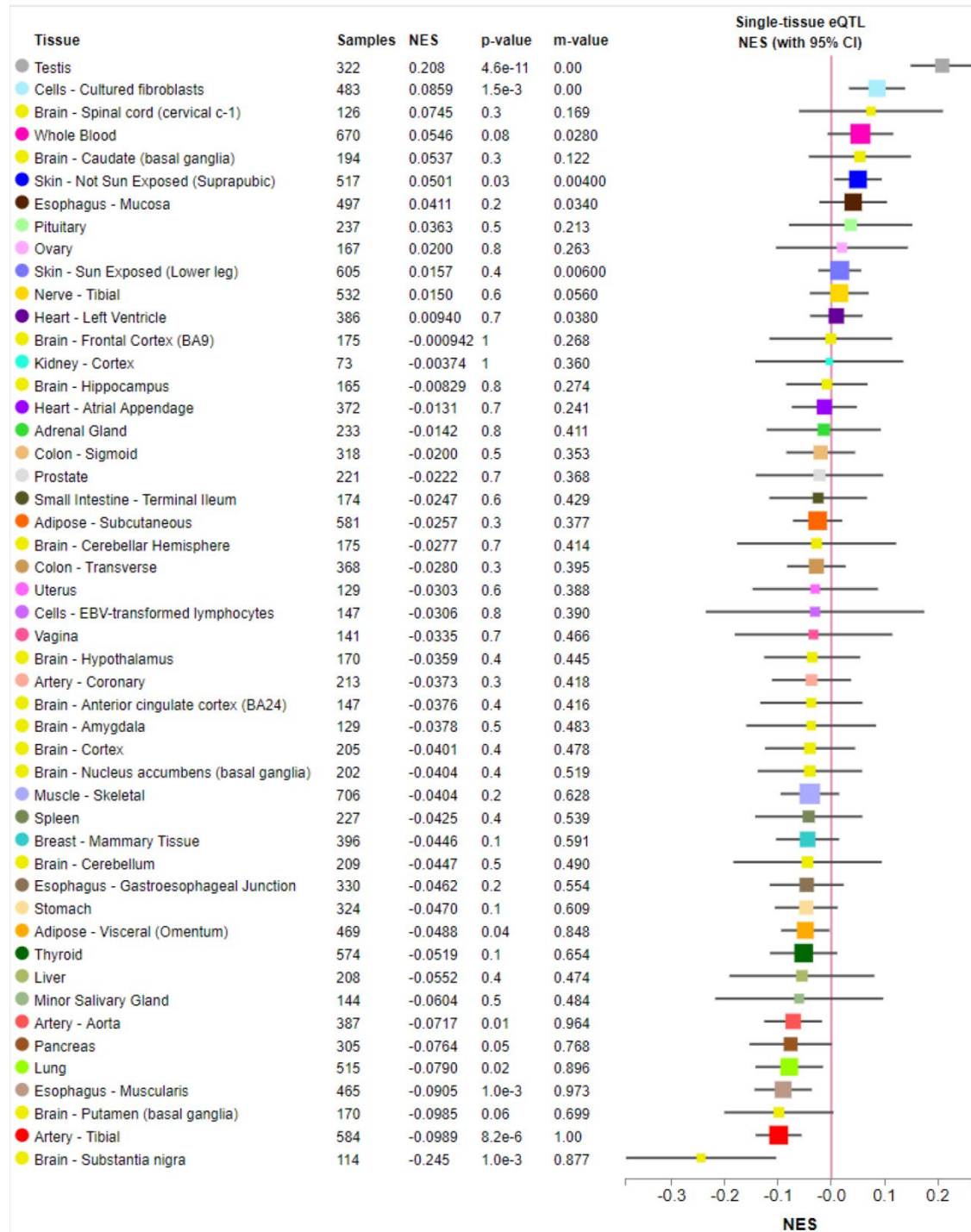
ENSG00000148700.14 ADD3 and chr10_109975992_C_T_b38 eQTL (Meta Analysis RE2 P-Value: 3.668709999999998e-253)

Tissue	Samples	NES	p-value	m-value	Single-tissue eQTL NES (with 95% CI)
Brain - Cerebellum	209	0.843	2.3e-33	1.00	
Brain - Cerebellar Hemisphere	175	0.818	1.6e-34	1.00	
Uterus	129	0.514	4.1e-6	1.00	
Pituitary	237	0.505	2.0e-14	1.00	
Kidney - Cortex	73	0.404	2.3e-5	1.00	
Spleen	227	0.394	5.1e-13	1.00	
Vagina	141	0.312	6.5e-4	1.00	
Small Intestine - Terminal Ileum	174	0.277	1.2e-3	1.00	
Stomach	324	0.263	2.7e-7	1.00	
Artery - Aorta	387	0.261	1.2e-10	1.00	
Liver	208	0.247	8.6e-4	0.985	
Adrenal Gland	233	0.245	1.1e-4	1.00	
Cells - EBV-transformed lymphocytes	147	0.212	0.02	0.949	
Colon - Sigmoid	318	0.200	6.1e-11	1.00	
Colon - Transverse	368	0.195	2.2e-9	1.00	
Nerve - Tibial	532	0.185	2.9e-11	1.00	
Breast - Mammary Tissue	396	0.176	4.1e-6	1.00	
Muscle - Skeletal	706	0.170	2.9e-10	1.00	
Testis	322	0.170	1.1e-5	1.00	
Prostate	221	0.162	1.2e-3	1.00	
Lung	515	0.152	1.8e-7	1.00	
Artery - Tibial	584	0.150	3.8e-9	1.00	
Heart - Left Ventricle	386	0.145	3.1e-5	1.00	
Brain - Caudate (basal ganglia)	194	0.139	2.1e-4	1.00	
Adipose - Subcutaneous	581	0.134	1.8e-6	1.00	
Esophagus - Muscularis	465	0.133	7.9e-8	1.00	
Adipose - Visceral (Omentum)	469	0.130	2.7e-6	1.00	
Brain - Frontal Cortex (BA9)	175	0.129	3.3e-6	1.00	
Thyroid	574	0.126	7.7e-4	1.00	
Heart - Atrial Appendage	372	0.120	1.8e-3	1.00	
Esophagus - Gastroesophageal Junction	330	0.109	8.5e-4	0.986	
Ovary	167	0.101	0.4	0.766	
Whole Blood	670	0.0978	8.2e-9	1.00	
Brain - Putamen (basal ganglia)	170	0.0976	4.4e-3	0.939	
Brain - Cortex	205	0.0953	3.2e-3	0.986	
Brain - Hippocampus	165	0.0837	0.05	0.837	
Cells - Cultured fibroblasts	483	0.0834	2.3e-4	0.726	
Brain - Nucleus accumbens (basal ganglia)	202	0.0684	0.07	0.337	
Artery - Coronary	213	0.0664	0.2	0.455	
Skin - Not Sun Exposed (Suprapubic)	517	0.0661	0.06	0.222	
Minor Salivary Gland	144	0.0630	0.4	0.550	
Skin - Sun Exposed (Lower leg)	605	0.0446	0.2	0.00	
Brain - Spinal cord (cervical c-1)	126	0.0391	0.7	0.701	
Brain - Anterior cingulate cortex (BA24)	147	0.0339	0.4	0.00700	
Brain - Hypothalamus	170	0.0264	0.6	0.0930	
Esophagus - Mucosa	497	0.0147	0.6	0.00	
Brain - Amygdala	129	-0.00315	1	0.129	
Pancreas	305	-0.0358	0.3	0.00	
Brain - Substantia nigra	114	-0.0374	0.6	0.0810	

NES scale: 0.0 0.2 0.4 0.6 0.8

NES

Supplementary Figure 1. Multi-tissue eQTL plot for rs17095355 on *ADD3* expression. The plot was based on genotype and transcriptome data from the GTEx Analysis Release V8 (dbGaP Accession phs000424.v8.p2). The modeled allele is rs17095355 risk allele T.
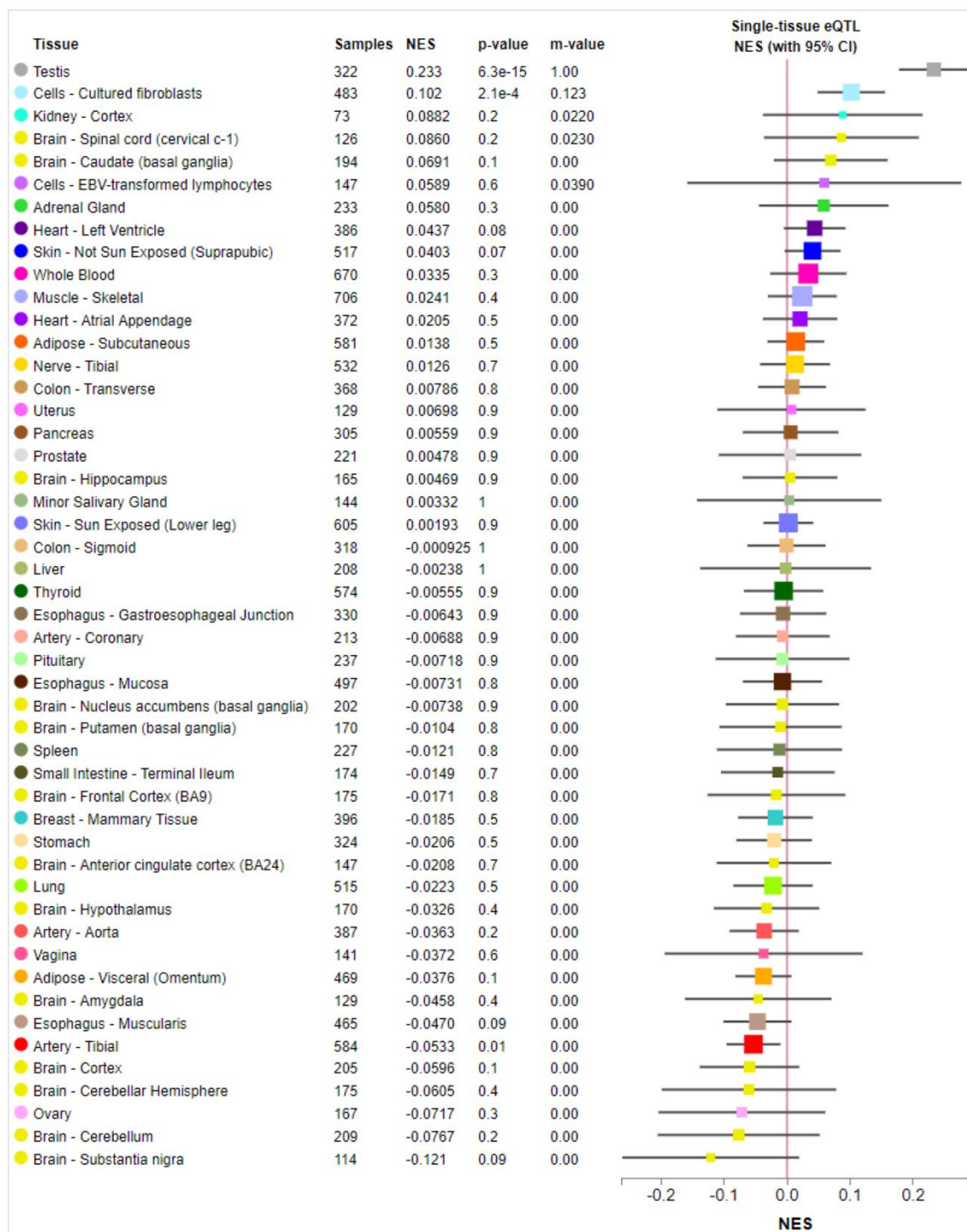
Multi-tissue eQTL Comparison ⓘ

ENSG00000063660.8 GPC1 and chr2_240431648_T_C_b38 eQTL (Meta Analysis RE2 P-Value: 5.589559999999999e-16)

Tissue	Samples	NES	p-value	m-value	Single-tissue eQTL NES (with 95% CI)
Testis	322	0.208	4.6e-11	0.00	
Cells - Cultured fibroblasts	483	0.0859	1.5e-3	0.00	
Brain - Spinal cord (cervical c-1)	126	0.0745	0.3	0.169	
Whole Blood	670	0.0546	0.08	0.0280	
Brain - Caudate (basal ganglia)	194	0.0537	0.3	0.122	
Skin - Not Sun Exposed (Suprapubic)	517	0.0501	0.03	0.00400	
Esophagus - Mucosa	497	0.0411	0.2	0.0340	
Pituitary	237	0.0363	0.5	0.213	
Ovary	167	0.0200	0.8	0.263	
Skin - Sun Exposed (Lower leg)	605	0.0157	0.4	0.00600	
Nerve - Tibial	532	0.0150	0.6	0.0560	
Heart - Left Ventricle	386	0.00940	0.7	0.0380	
Brain - Frontal Cortex (BA9)	175	-0.000942	1	0.268	
Kidney - Cortex	73	-0.00374	1	0.360	
Brain - Hippocampus	165	-0.00829	0.8	0.274	
Heart - Atrial Appendage	372	-0.0131	0.7	0.241	
Adrenal Gland	233	-0.0142	0.8	0.411	
Colon - Sigmoid	318	-0.0200	0.5	0.353	
Prostate	221	-0.0222	0.7	0.368	
Small Intestine - Terminal Ileum	174	-0.0247	0.6	0.429	
Adipose - Subcutaneous	581	-0.0257	0.3	0.377	
Brain - Cerebellar Hemisphere	175	-0.0277	0.7	0.414	
Colon - Transverse	368	-0.0280	0.3	0.395	
Uterus	129	-0.0303	0.6	0.388	
Cells - EBV-transformed lymphocytes	147	-0.0306	0.8	0.390	
Vagina	141	-0.0335	0.7	0.466	
Brain - Hypothalamus	170	-0.0359	0.4	0.445	
Artery - Coronary	213	-0.0373	0.3	0.418	
Brain - Anterior cingulate cortex (BA24)	147	-0.0376	0.4	0.416	
Brain - Amygdala	129	-0.0378	0.5	0.483	
Brain - Cortex	205	-0.0401	0.4	0.478	
Brain - Nucleus accumbens (basal ganglia)	202	-0.0404	0.4	0.519	
Muscle - Skeletal	706	-0.0404	0.2	0.628	
Spleen	227	-0.0425	0.4	0.539	
Breast - Mammary Tissue	396	-0.0446	0.1	0.591	
Brain - Cerebellum	209	-0.0447	0.5	0.490	
Esophagus - Gastroesophageal Junction	330	-0.0462	0.2	0.554	
Stomach	324	-0.0470	0.1	0.609	
Adipose - Visceral (Omentum)	469	-0.0488	0.04	0.848	
Thyroid	574	-0.0519	0.1	0.654	
Liver	208	-0.0552	0.4	0.474	
Minor Salivary Gland	144	-0.0604	0.5	0.484	
Artery - Aorta	387	-0.0717	0.01	0.964	
Pancreas	305	-0.0764	0.05	0.768	
Lung	515	-0.0790	0.02	0.896	
Esophagus - Muscularis	465	-0.0905	1.0e-3	0.973	
Brain - Putamen (basal ganglia)	170	-0.0985	0.06	0.699	
Artery - Tibial	584	-0.0989	8.2e-6	1.00	
Brain - Substantia nigra	114	-0.245	1.0e-3	0.877	

NES axis: -0.3   -0.2   -0.1   -0.0   0.1   0.2

NES

Supplementary Figure 2. Multi-tissue eQTL plot for rs6707262 on *GPC1* expression. The plot was based on genotype and transcriptome data from the GTEx Analysis Release V8 (dbGaP Accession phs000424.v8.p2). The modeled allele is rs6707262 risk allele G.
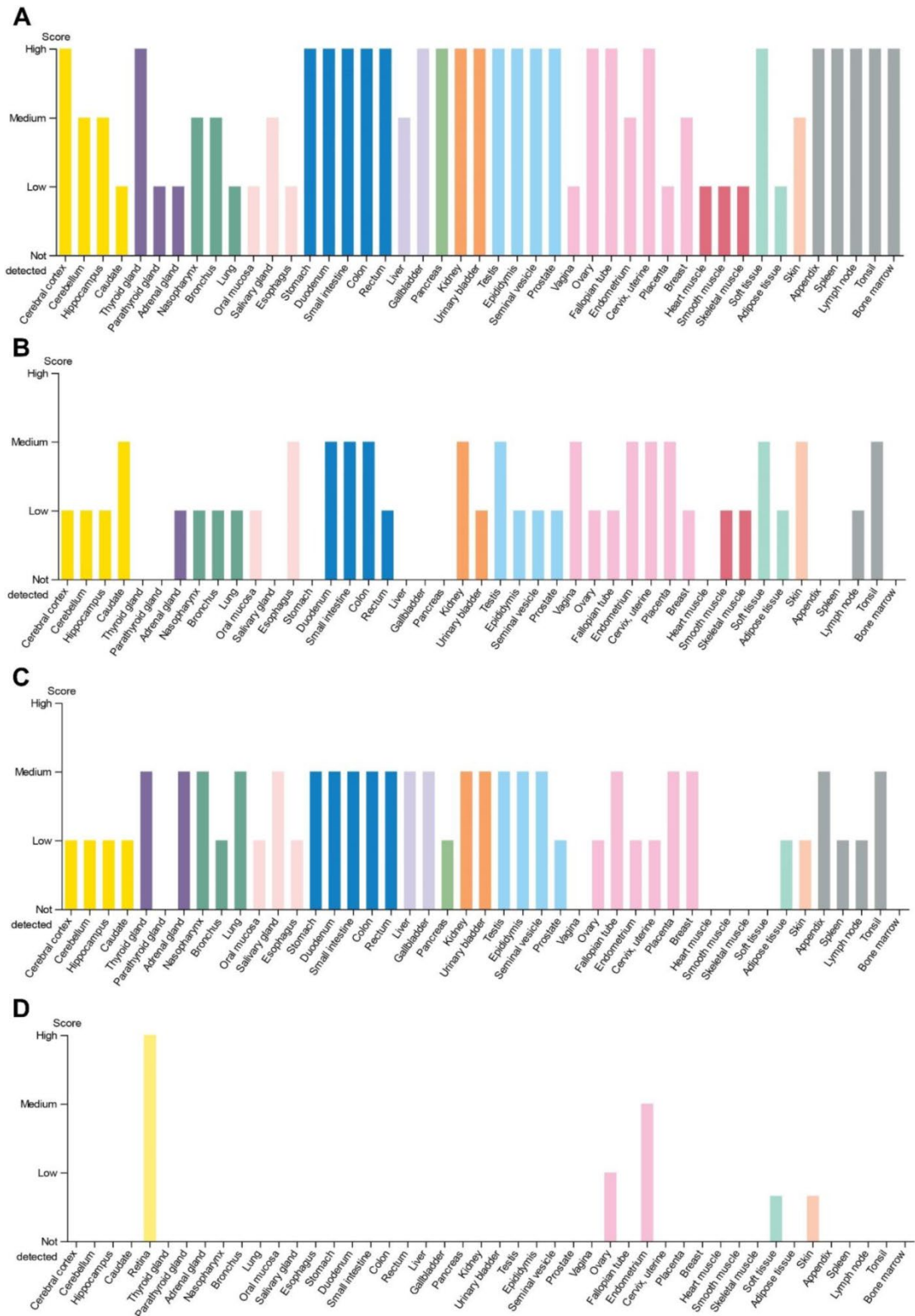
Multi-tissue eQTL Comparison ⓘ

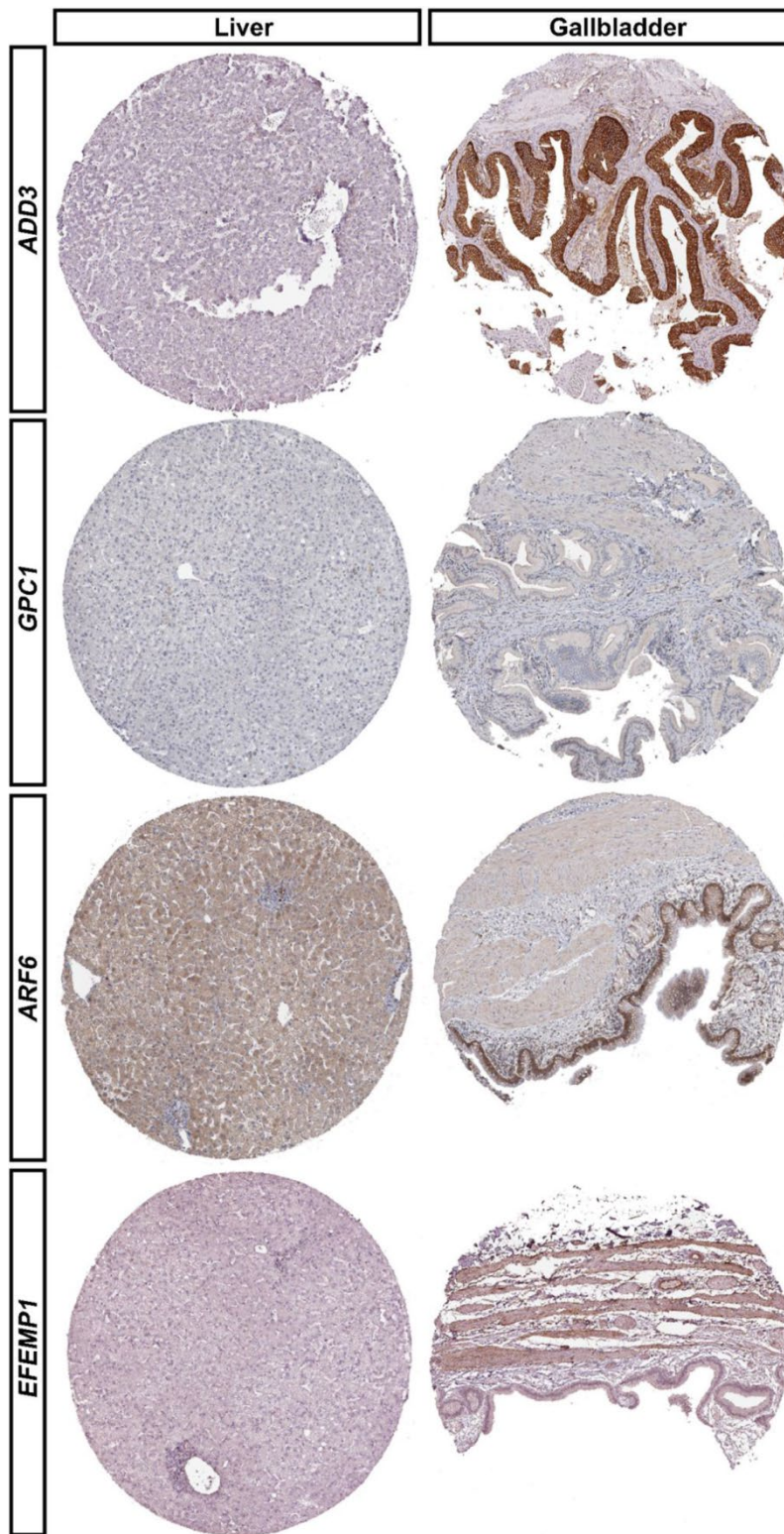ENSG00000063660.8 GPC1 and chr2_240423252_T_C_b38 eQTL (Meta Analysis RE2 P-Value: 2.61716e-10)

Tissue	Samples	NES	p-value	m-value
Testis	322	0.233	6.3e-15	1.00
Cells - Cultured fibroblasts	483	0.102	2.1e-4	0.123
Kidney - Cortex	73	0.0882	0.2	0.0220
Brain - Spinal cord (cervical c-1)	126	0.0860	0.2	0.0230
Brain - Caudate (basal ganglia)	194	0.0691	0.1	0.00
Cells - EBV-transformed lymphocytes	147	0.0589	0.6	0.0390
Adrenal Gland	233	0.0580	0.3	0.00
Heart - Left Ventricle	386	0.0437	0.08	0.00
Skin - Not Sun Exposed (Suprapubic)	517	0.0403	0.07	0.00
Whole Blood	670	0.0335	0.3	0.00
Muscle - Skeletal	706	0.0241	0.4	0.00
Heart - Atrial Appendage	372	0.0205	0.5	0.00
Adipose - Subcutaneous	581	0.0138	0.5	0.00
Nerve - Tibial	532	0.0126	0.7	0.00
Colon - Transverse	368	0.00786	0.8	0.00
Uterus	129	0.00698	0.9	0.00
Pancreas	305	0.00559	0.9	0.00
Prostate	221	0.00478	0.9	0.00
Brain - Hippocampus	165	0.00469	0.9	0.00
Minor Salivary Gland	144	0.00332	1	0.00
Skin - Sun Exposed (Lower leg)	605	0.00193	0.9	0.00
Colon - Sigmoid	318	-0.000925	1	0.00
Liver	208	-0.00238	1	0.00
Thyroid	574	-0.00555	0.9	0.00
Esophagus - Gastroesophageal Junction	330	-0.00643	0.9	0.00
Artery - Coronary	213	-0.00688	0.9	0.00
Pituitary	237	-0.00718	0.9	0.00
Esophagus - Mucosa	497	-0.00731	0.8	0.00
Brain - Nucleus accumbens (basal ganglia)	202	-0.00738	0.9	0.00
Brain - Putamen (basal ganglia)	170	-0.0104	0.8	0.00
Spleen	227	-0.0121	0.8	0.00
Small Intestine - Terminal Ileum	174	-0.0149	0.7	0.00
Brain - Frontal Cortex (BA9)	175	-0.0171	0.8	0.00
Breast - Mammary Tissue	396	-0.0185	0.5	0.00
Stomach	324	-0.0206	0.5	0.00
Brain - Anterior cingulate cortex (BA24)	147	-0.0208	0.7	0.00
Lung	515	-0.0223	0.5	0.00
Brain - Hypothalamus	170	-0.0326	0.4	0.00
Artery - Aorta	387	-0.0363	0.2	0.00
Vagina	141	-0.0372	0.6	0.00
Adipose - Visceral (Omentum)	469	-0.0376	0.1	0.00
Brain - Amygdala	129	-0.0458	0.4	0.00
Esophagus - Muscularis	465	-0.0470	0.09	0.00
Artery - Tibial	584	-0.0533	0.01	0.00
Brain - Cortex	205	-0.0596	0.1	0.00
Brain - Cerebellar Hemisphere	175	-0.0605	0.4	0.00
Ovary	167	-0.0717	0.3	0.00
Brain - Cerebellum	209	-0.0767	0.2	0.00
Brain - Substantia nigra	114	-0.121	0.09	0.00

Supplementary Figure 3. Multi-tissue eQTL plot for rs6750380 on *GPC1* expression. The plot was based on genotype and transcriptome data from the GTEx Analysis Release V8 (dbGaP Accession phs000424.v8.p2). The modeled allele is rs6750380 risk allele G.

Supplementary Figure 4. The expression of *ADD3*, *GPC1*, *ARF6* and *EFEMP1* in human tissues. (**A–D**) stand for *ADD3*, *GPC1*, *ARF6* and *EFEMP1* expression respectively in human tissues from THE HUMAN PROTEIN ATLAS (https://www.proteinatlas.org/). The vertical axis indicates the expression level of the gene in each tissue.

Supplementary Figure 5. Immunohistochemistry analysis of *ADD3*, *GPC1*, *ARF6* **and** *EFEMP1* **in adult human liver and gallbladder tissues from THE HUMAN PROTEIN ATLAS database (https://www.proteinatlas.org/).**