Supplemental Information

Movie S1. TSEA plots for each of the 57 traits from the GWAS catalog that had a significant result in at least one tissue.

Table S1. Summarized RPKM values of 18,056 genes across 25 tissues from GTEx.

Table S3. pSI values for all genes across 25 tissues available from GTEx. Derived by pSI analysis of GTEx data release dated 1/31/13. Genes in rows, tissues in columns. Sub-dissections of the same tissue were aggregated into a single tissue. First row contains tissue names, first column contains HUGO approved gene names. NA = pSI > 0.1.

Table S2. Key for which sub tissues were summarized into whole tissue.

Sub tissue	Whole tissue
Adipose Subcutaneous	Adipose Tissue
Adipose Visceral Omentum	Adipose Tissue
Adrenal Gland	Adrenal Gland
Artery Aorta	Blood Vessel
Artery Coronary	Blood Vessel
Artery Tibial	Blood Vessel
Brain Amygdala	Brain
Brain Anterior cingulate cortex BA24	Brain
Brain Caudate basal ganglia	Brain
Brain Cerebellar Hemisphere	Brain
Brain Cerebellum	Brain
Brain Cortex	Brain
Brain Frontal Cortex BA9	Brain
Brain Hippocampus	Brain
Brain Hypothalamus	Brain
Brain Nucleus accumbens basal ganglia	Brain
Brain Putamen basal ganglia	Brain
Brain Spinal cord cervical	Brain
Brain Substantia nigra	Brain
Breast Mammary Tissue	Breast
Cells EBV transformed lymphocytes	NA
Cells Transformed fibroblasts	NA
Colon Transverse	Colon
Esophagus Mucosa	Esophagus
Esophagus Muscularis	Esophagus
Fallopian Tube	Fallopian Tube
Heart Atrial Appendage	Heart
Heart Left Ventricle	Heart
Kidney Cortex	Kidney
Liver	Liver
Lung	Lung
Muscle Skeletal	Muscle
Nerve Tibial	Nerve
Ovary	Ovary
Pancreas	Pancreas
Pituitary	Pituitary
Prostate	Prostate
Skin Not Sun Exposed Suprapubic	Skin
Skin Sun Exposed Lower leg	Skin
Stomach	Stomach
Testis	Testis
Thyroid	Thyroid
Uterus	Uterus
Vagina	Vagina
Whole Blood	Blood

Table S4: Validation of tissue specific transcript enrichment by systematic GO analysis. Results of enrichment analyses using the TSEA tool for gene lists derived for each tissue at multiple pSI thresholds compared to a GO term selected to represent the development of that tissue ('On Target Results' columns). Note that several tissues had no unique GO term (Colon, Esophagus, and Stomach all utilized the same 119 genes associated with 'GO:0048565, digestive track development'). Also included, a matrix of the highest TSEA p value for analysis of random gene lists of identical length ("Random gene list" columns). No significant overlap was seen at any threshold using randomly selected genes.

				On Target results for each tissue, by pSI				Random gene list			
	GO.ID	GO.term	# of genes in GO term	pSI_.05	pSI_.01	pSI_.001	pSI_.0001	pSI_.05	pSI_.01	pSI_.001	pSI_.0001
Adipose Tissue	GO:0060612	adipose tissue development	27	0.2245283	0.6447261	1	0.4994756	0.7767606	0.9425186	1	1
Adrenal Gland	GO:0030325	adrenal gland development	26	0.0516088	0.0502182	0.0024848	0.0158593	1	1	1	1
Blood	GO:0002520	immune system development	664	9.61E-33	1.80E-24	9.55E-06	1	0.7529454	0.7157377	1	1
Blood Vessel	GO:0001568	blood vessel development	535	8.51E-18	1.28E-13	0.1609899	1	0.8526613	0.9797447	1	1
Brain	GO:0007420	brain development	568	5.74E-21	1.94E-22	1.37E-17	7.02E-18	0.9912776	0.9985581	1	1
Breast	GO:0030879	mammary gland development	140	4.74E-07	0.0027594	0.0470135	0.0822336	0.8979868	1	0.9067467	0.8962612
Colon	GO:0048565	digestive tract development	119	0.0012155	0.2698233	1	1	0.9632348	1	1	1
Esophagus	GO:0048565	digestive tract development	119	0.0582282	0.6190532	1	1	0.9665582	1	1	1
Fallopian Tube	GO:0060066	oviduct development	3	1	1	1	1	1	1	1	1
Heart	GO:0007507	heart development	424	5.54E-16	1.00E-20	7.21E-18	2.59E-11	0.9998406	0.9644155	1	1
Kidney	GO:0001822	kidney development	221	5.02E-08	2.90E-09	1.53E-07	5.85E-06	0.8168252	0.9675896	1	1
Liver	GO:0001889	liver development	105	3.75E-09	8.00E-06	0.1509639	0.6523775	0.9900871	1	1	1
Lung	GO:0030324	lung development	171	0.0007387	0.0146273	0.9612879	0.5134674	0.9998393	1	1	1
Muscle	GO:0060537	muscle development	320	2.33E-21	1.79E-21	2.49E-14	0.0004612	0.8205008	0.9747358	0.7229468	0.9832756
Nerve	GO:0021675	nerve development	73	0.011859	0.0133223	0.0162835	0.6620925	0.6590795	0.8963201	1	1
Ovary	GO:0008585	female gonad development	96	0.0001898	8.27E-07	0.2545461	0.0645636	0.8615195	1	0.9632877	0.578157
Pancreas	GO:0031016	pancreas development	82	2.31E-13	3.47E-11	0.0189874	1	1	0.8824443	1	1
Pituitary	GO:0021983	pituitary gland development	45	0.0002955	6.84E-05	0.0001013	0.0001724	0.8987947	1	1	1
Prostate	GO:0030850	prostate gland development	50	7.98E-05	0.0016398	0.090186	0.7277544	1	1	1	1
Skin	GO:0043588	skin development	313	5.68E-82	6.36E-77	1.13E-56	2.47E-38	0.9972169	0.9952375	1	1
Stomach	GO:0048565	digestive tract development	119	0.000109	0.19514	1	1	0.9212691	0.9703533	1	1
Testis	GO:0008584	male gonad development	122	0.000186	0.0055787	0.0039445	0.0385807	0.6120688	0.7348369	1	1
Thyroid	GO:0030878	thyroid gland development	19	0.0250885	0.0019105	0.0008738	5.60E-05	1	1	1	1
Uterus	GO:0060065	uterus development	14	0.1065938	0.1341815	0.3577264	1	1	1	1	1
Vagina	GO:0060068	vagina development	12	0.3888183	0.3004131	1	1	1	1	1	1

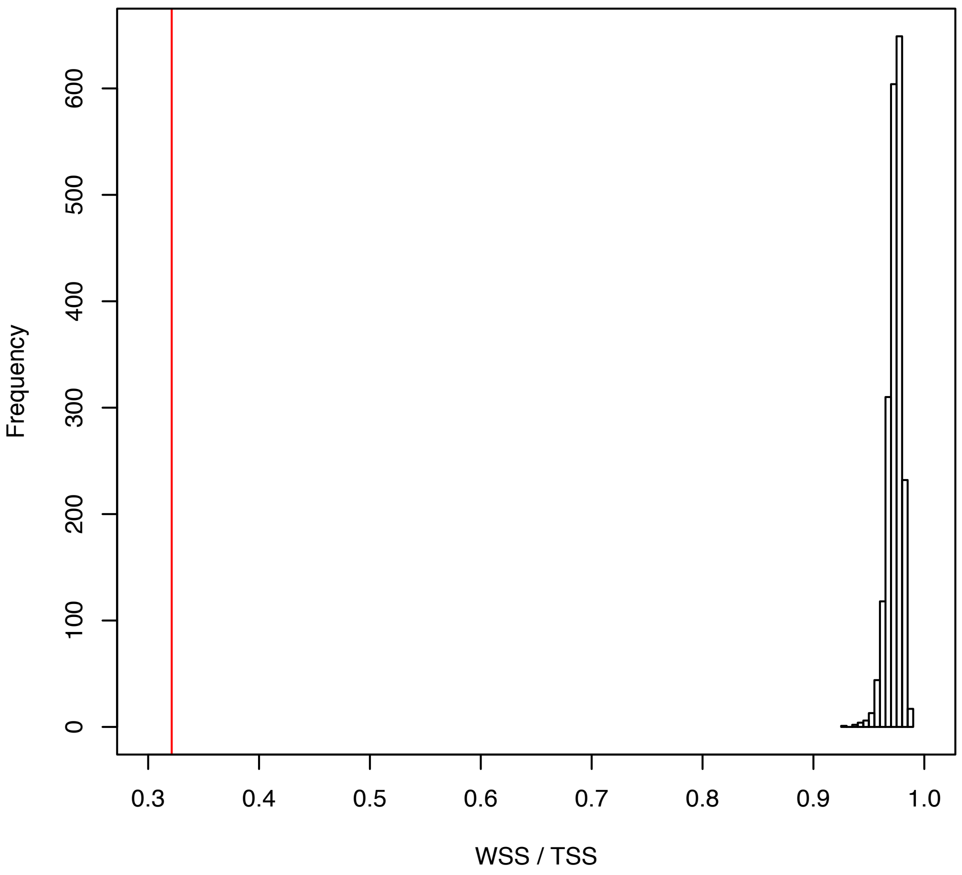

Figure S1. Within tissue variation of gene expression is less than expected by chance. The observed within tissue variation across all genes within a tissue is 0.321 (red line) which is always less than the within tissue variance calculated by permuting the tissue group 2000 times (histogram) ($p < 1/2000$).

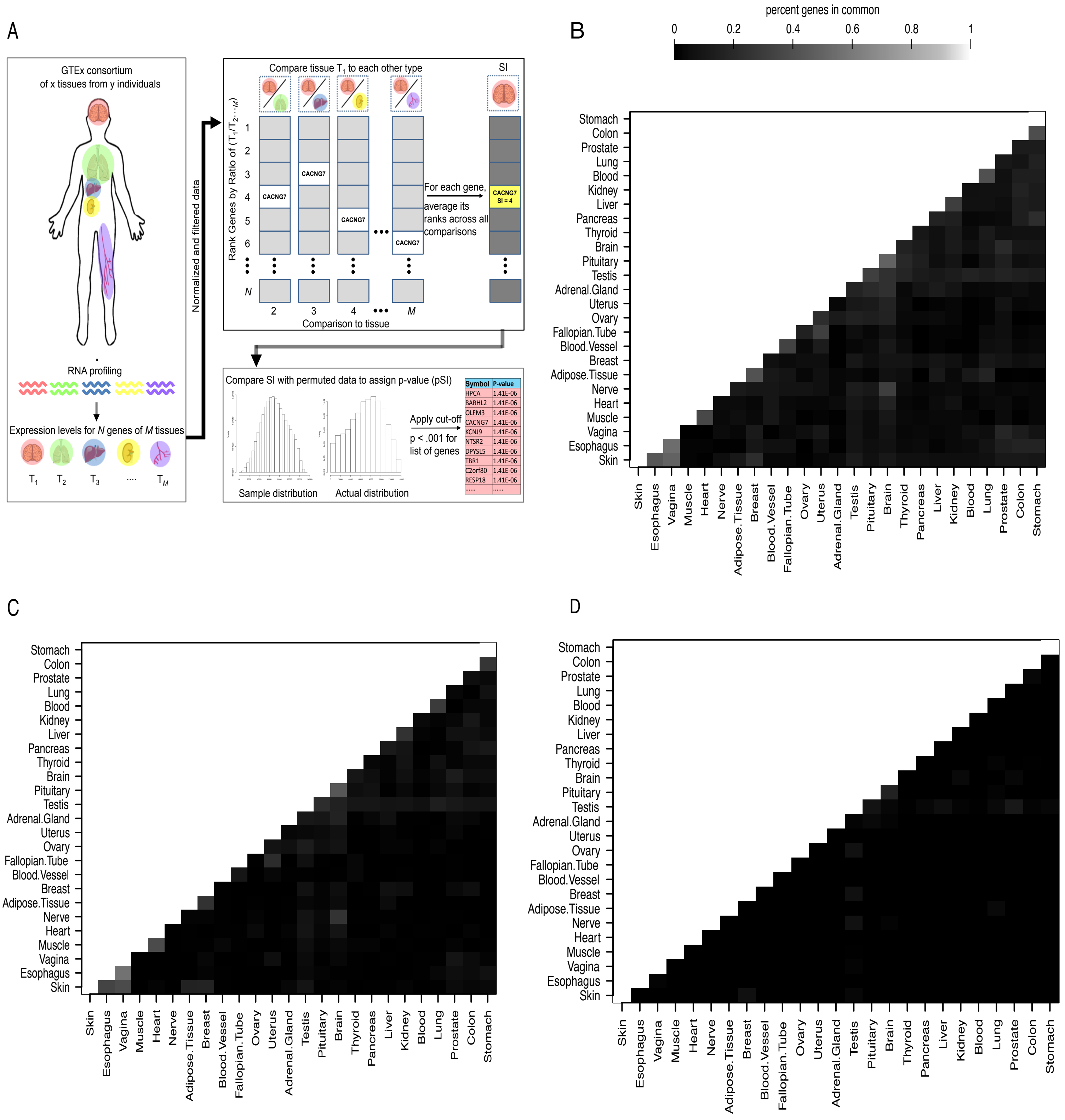

Figure S2. Fraction of tissue enriched transcript lists that overlap at moderate and stringent thresholds. A) Cartoon of the pSI method used to define tissue specific gene lists. B) moderately enriched transcript lists (pSI<0.05) are large and show substantial overlap between related tissues; C) an intermediate threshold (pSI <0.01) identifies a smaller number of transcripts with less overlap between tissue; D) a more stringent threshold (pSI < 0.001) shows the least amount of overlap. Data from pSI <0.0001 not shown.

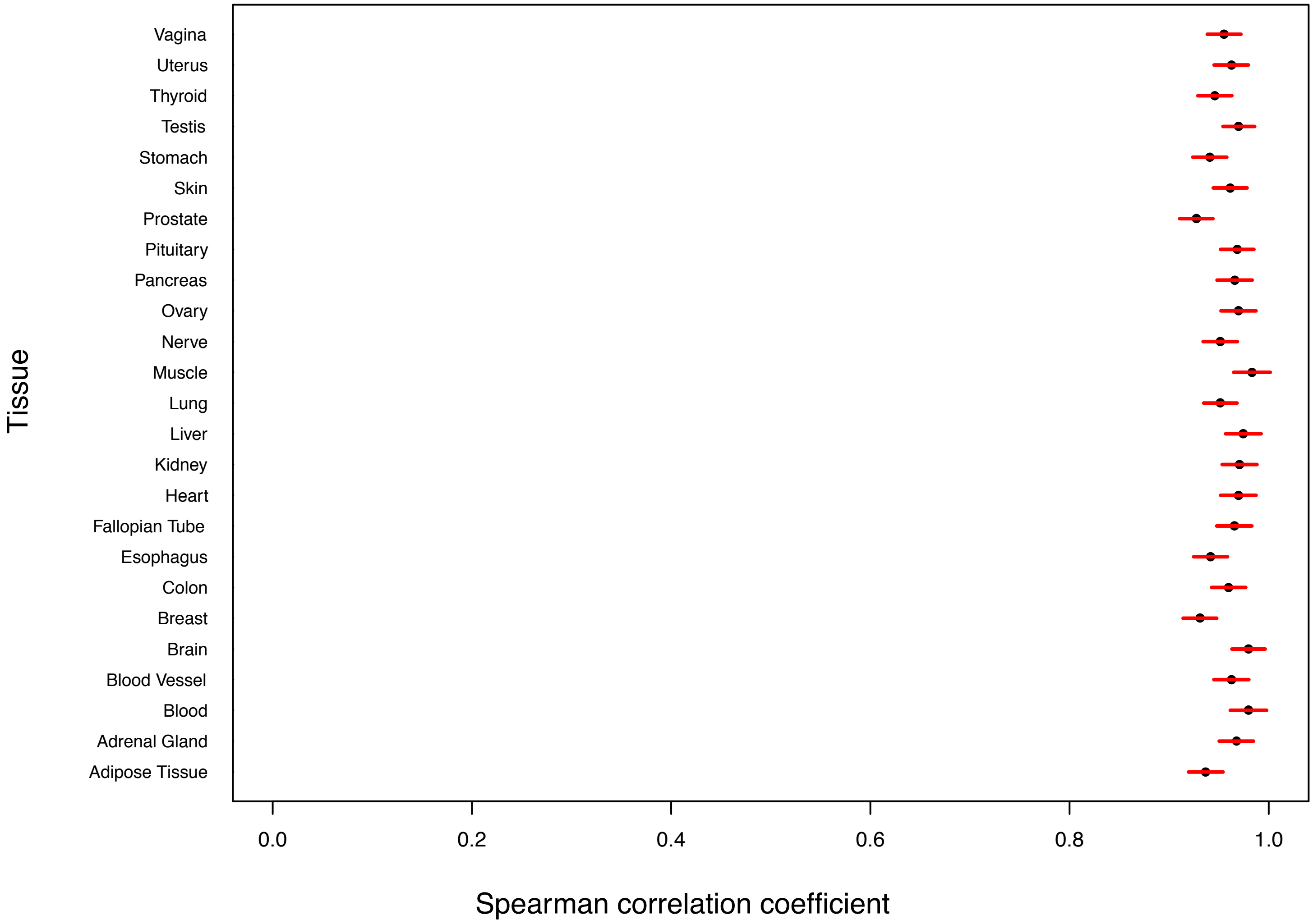

Figure S3. Shannon entropy and SI values of genes in tissues are correlated. Spearman's correlation between Shannon entropy and SI values for genes within tissues. Displayed as point estimate ± 2 S.E.

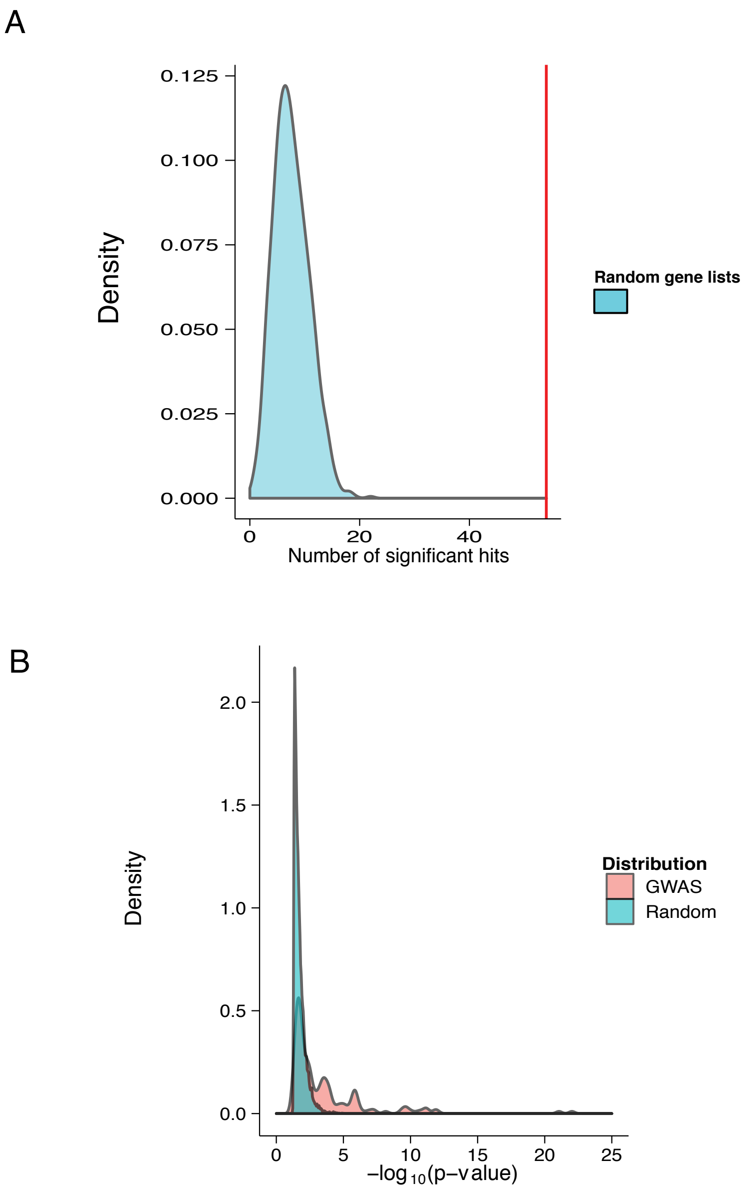

Figure S4. Selective expression results are robust to how SNPs are assigned to genes. A) Of the 87 quantitative and disease trait associated gene lists examined, 54 (red line), showed enrichment in at least one tissue. 1000 randomizations of 87 equivalently sized random gene lists resulted in a mean of 8.81 (+/– 3.53 s.d.) gene lists showing enrichment (blue distribution). B) Median statistical enrichment of those random gene lists showing signal was p-value=0.026 (1.58 as plotted in –log10 scale, blue distribution, range: 0.05 to 2.83E-6), while those from disease and trait associated lists was p-value=0.0027 (2.57, pink distribution, range: 0.05 to 8.50E-28).

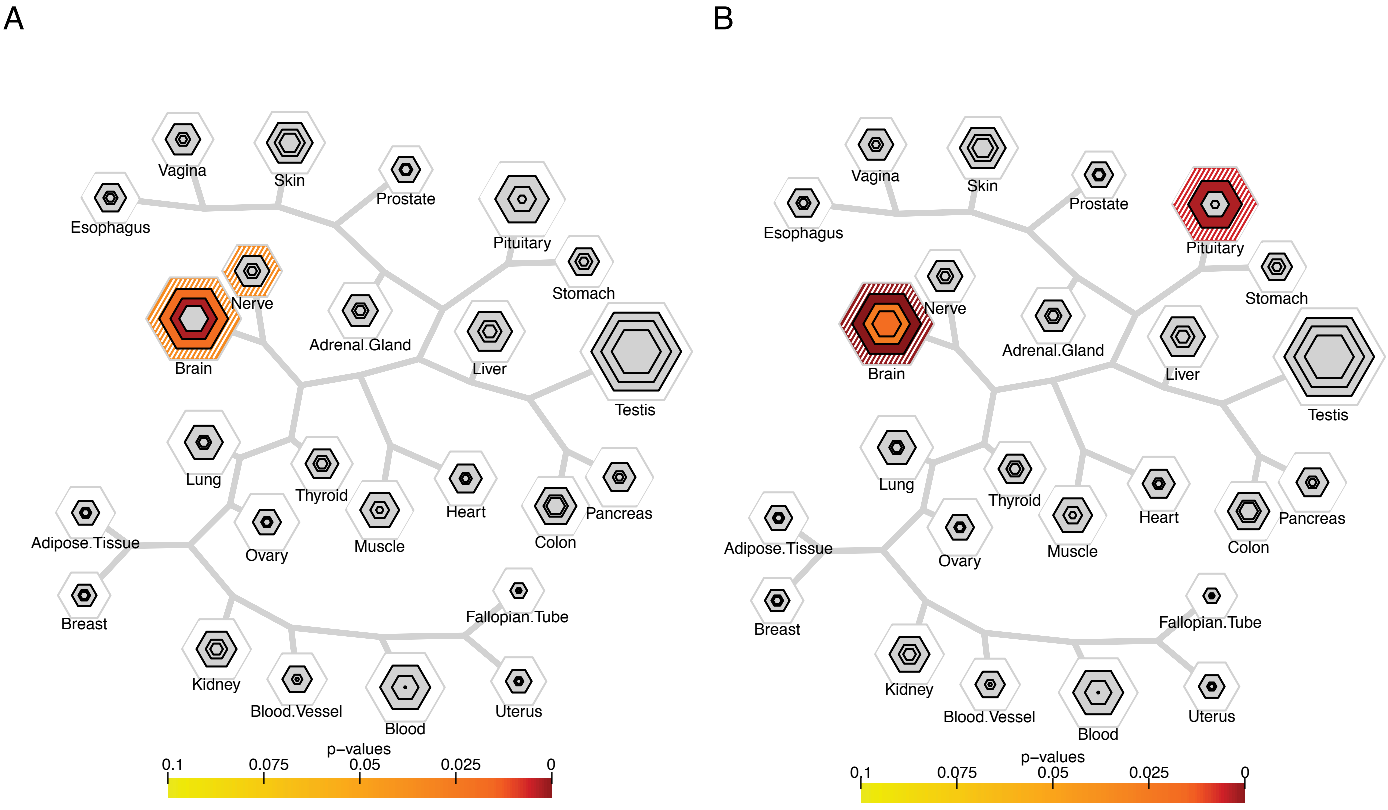

Figure S5. TSEA results using exome data. A) 49 genes with multiple observed de novo mutations in exomes from children with autism are enriched in the brain and nerve. B) 18 genes with multiple observed de novo mutations in exomes from children with epilepsy are erniched in the brain and pituitary.