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Supplemental information

Transcriptome-wide association study of the plasma proteome reveals *cis* and *trans* regulatory mechanisms underlying complex traits

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Supplemental Figures

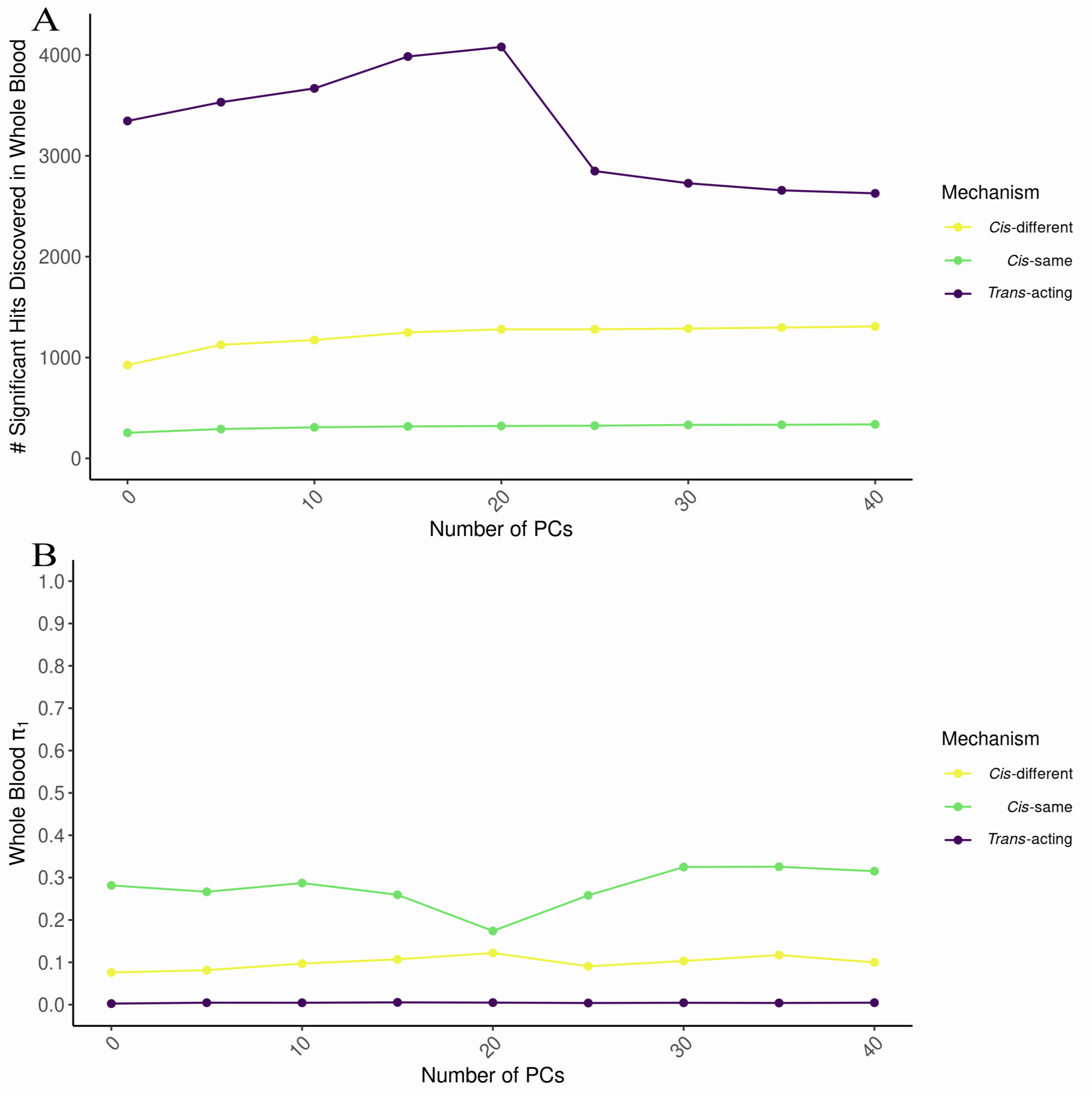

Figure S1. TWAS results in INTERVAL using GTEx whole blood transcriptome models across protein principal components (PCs). (A) Counts of transcript-protein pairs that associate in each mechanism category with FDR<0.05. The protein matrix was adjusted for 0-40 PCs in 5 PC increments, taking the residuals as the adjusted protein levels in the association tests. (B) Expected true positive rates (π_1) across protein PCs.

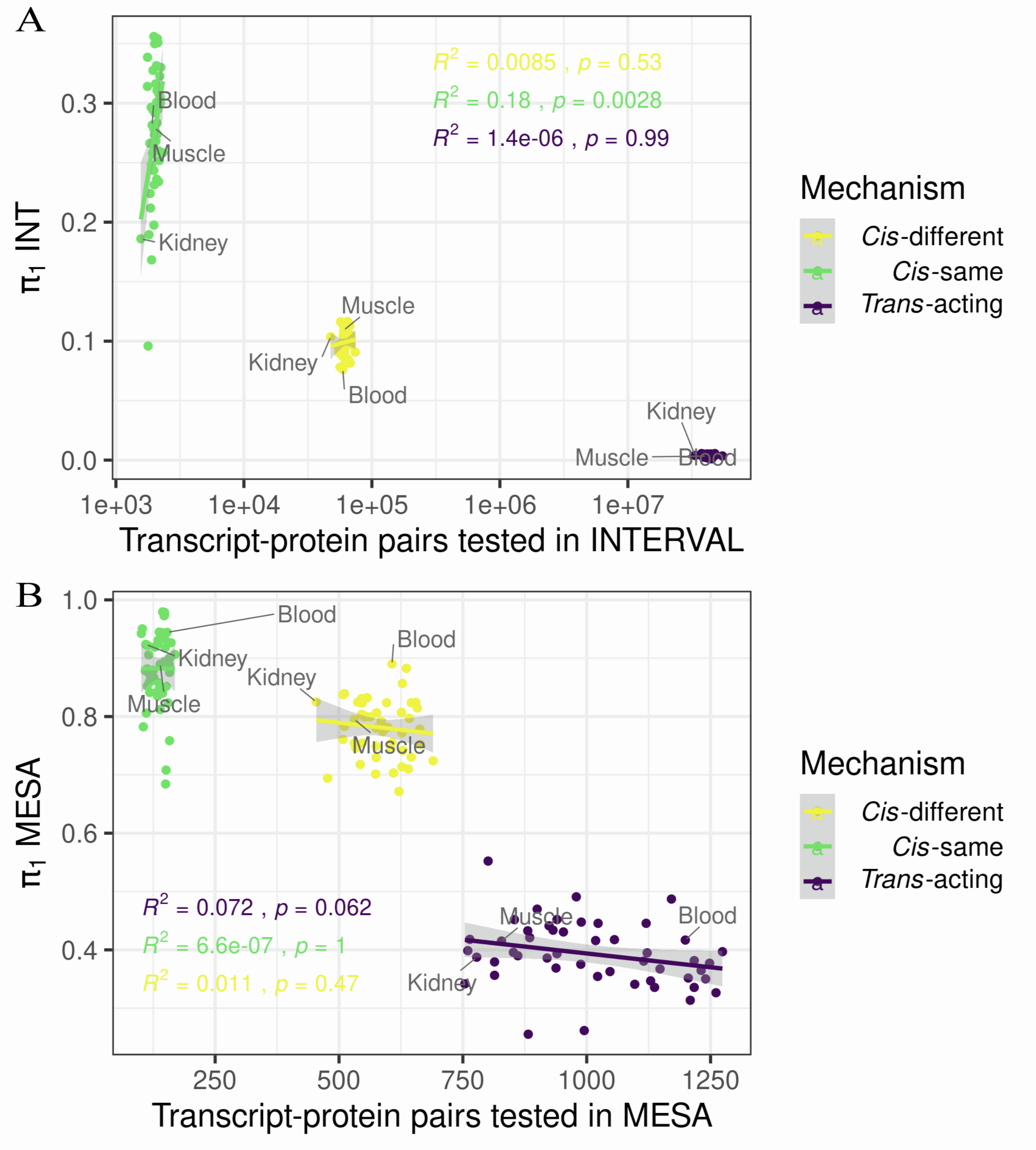

Figure S2. Comparison of π_1 expected true positive rates to the number of predicted transcript-protein pairs tested in each GTEx tissue trascriptome prediction model. (A) Linear regression results in INTERVAL colored by each mechanism class. (B) Linear regression results in MESA colored by each mechanism class. Note only transcript-protein pairs with FDR<0.05 in INTERVAL were tested in TOPMed MESA. Tissues with the most samples in GTEx (Muscle – Skeletal, n=706 and Whole Blood, n=670) and the least samples in GTEx (Kidney – Cortex, n=73) are labeled.

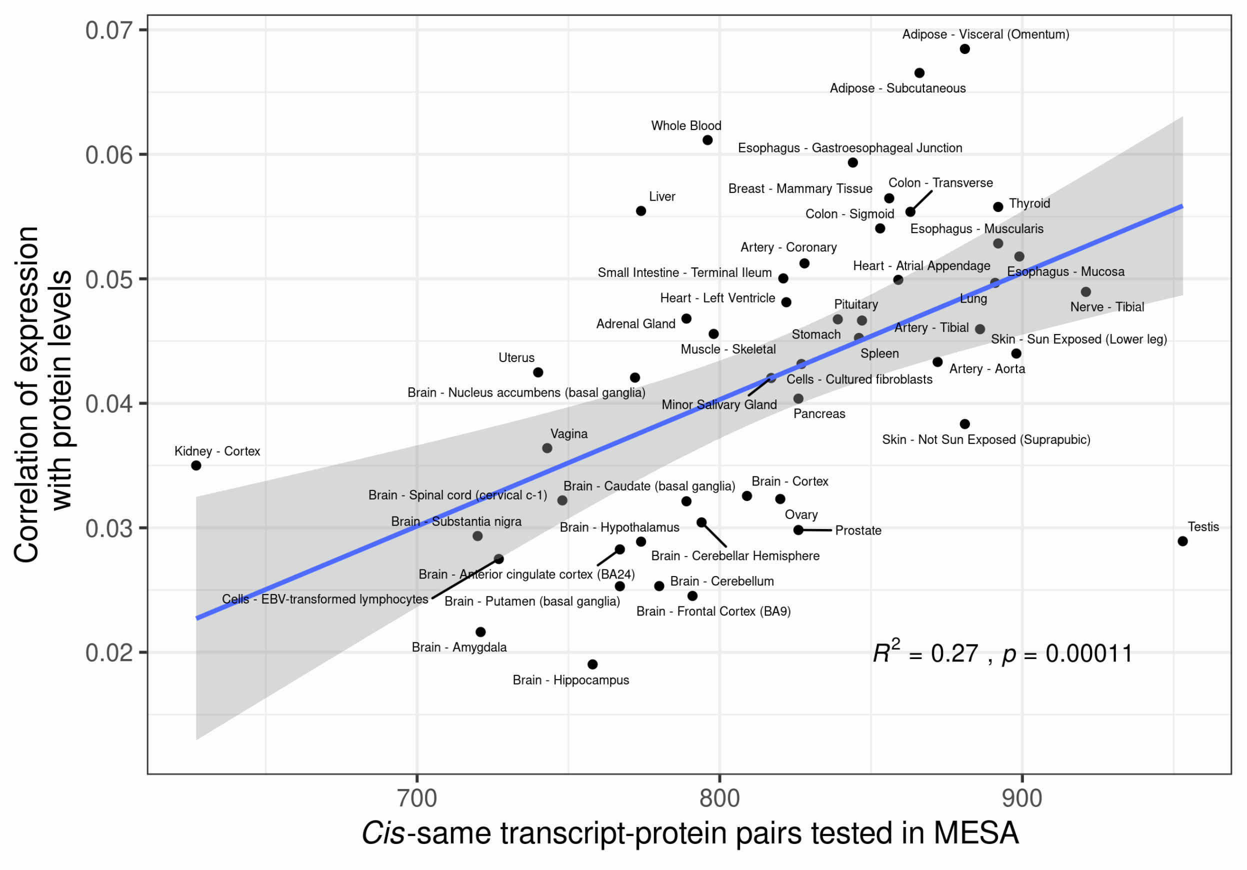

Figure S3. Comparison of median Pearson correlation between predicted expression and protein levels with the number of cis-same transcript-protein pairs tested. Points are labeled by GTEx transcriptome prediction model tissue. The blue line is the linear regression line and 95% confidence interval in gray.

Supplemental Tables

Table S1. Number of genes in the transcriptome prediction model per tissue.

Tissue	# of Genes	Tissue	# of Genes
Adipose Subcutaneous	14,732	Esophagus Mucosa	14,589
Adipose Visceral Omentum	14640	Esophagus Mucularis	14,603
Adrenal Gland	13,622	Heart Atrial Appendage	14,035
Artery Aorta	14,396	Heart Left Ventricle	13,200
Artery Coronary	13,878	Kidney Cortex	11,164
Artery Tibial	14,493	Liver	12,714
Brain Amygdala	12,814	Lung	15,058
Brain Anterior Cingulate Cortex BA24	13,528	Minor Salivary Gland	13,884
Brain Caudate Basal Ganglia	14,118	Muscle Skeletal	13,381
Brain Cerebellar Hemisphere	13,771	Nerve Tibial	15,373
Brain Cerebellum	13,992	Ovary	13,738
Brain Cortex	14,284	Pancreas	13,695
Brain Frontal Cortex BA9	14,091	Pituitary	14,647
Brain Hippocampus	13,526	Prostate	14,450
Brain Hypothalamus	13,741	Skin Not Sun Exposed Subrapubic	14,932
Brain Nucleus Accumbens Basal Ganglia	14,062	Skin Sun Exposed Lower Leg	15,204
Brain Putamen Basal Ganglia	13,694	Small Intestine Terminal Ileum	14,065
Brain Spinal Cord Cervical C-1	13,096	Spleen	14,073
Brain Substantia Nigra	12,637	Stomach	14,102
Breast Mammary Tissue	14,654	Testis	17,867
Cells Cultered Fibroblasts	13,976	Thyroid	15,308
Cells EBV-Transformed Lymphocytes	12,398	Uterus	13,199
Colon Sigmoid	14,363	Vagina	12,969
Colon Transverse	14,582	Whole Blood	12,623
Esophagus Gastroesophageal Junction	14,285		

Table S2. Genes with either predicted or observed expression and protein measurements for every tissue.

Tissue	Genes Tested	Tissue	Genes Tested
Adipose Subcutaneous	866	Esophagus Mucularis	892
Adipose Visceral Omentum	881	Heart Atrial Appendage	859
Adrenal Gland	789	Heart Left Ventricle	822
Artery Aorta	872	Kidney Cortex	627
Artery Coronary	828	Liver	774
Artery Tibial	886	Lung	891
Brain Amygdala	721	Minor Salivary Gland	817
Brain Anterior Cingulate Cortex BA24	767	Muscle Skeletal	798
Brain Caudate Basal Ganglia	789	Nerve Tibial	921
Brain Cerebellar Hemisphere	794	Ovary	820
Brain Cerebellum	780	Pancreas	826
Brain Cortex	809	Pituitary	847
Brain Frontal Cortex BA9	791	Prostate	826
Brain Hippocampus	758	Skin Not Sun Exposed Subrapubic	881
Brain Hypothalamus	774	Skin Sun Exposed Lower Leg	898
Brain Nucleus Accumbens Basal Ganglia	772	Small Intestine Terminal Ileum	821
Brain Putamen Basal Ganglia	767	Spleen	846
Brain Spinal Cord Cervical C-1	748	Stomach	839
Brain Substantia Nigra	720	Testis	953
Breast Mammary Tissue	856	Thyroid	892
Cells Cultered Fibroblasts	827	Uterus	740
Cells EBV-Transformed Lymphocytes	727	Vagina	743
Colon Sigmoid	853	Whole Blood	796
Colon Transverse	863	Monocytes – observed[a]	862
Esophagus Gastroesophageal Junction	844	PBMC – observed[a]	862
Esophagus Mucosa	899	T-cells – observed[a]	862

[a] Observed expression tissues are marked, the rest are predicted expression levels.

Table S3. INTERVAL TWAS for protein results for every tissue. π_1 is the expected true positive rate and the number of transcript-protein pairs tested is indicated for each mechanism class.

Tissue	*Trans-acting* π_1	*Pairs tested*	*Cis-acting* π_1	*Pairs tested*	*Cis-different* π_1	*Pairs tested*	*Cis-same* π_1	*Pairs tested*
Adipose Subcutaneous	0.0047	45519311	0.0905	68056	0.0839	65927	0.2950	2129
Adipose Visceral Omentum	0.0038	45112261	0.1214	67748	0.1154	65655	0.3107	2093
Adrenal Gland	0.0052	41622061	0.1056	62015	0.0995	60067	0.2943	1948
Artery Aorta	0.0052	44459436	0.1092	66129	0.1012	64000	0.3510	2129
Artery Coronary	0.0041	42425522	0.1185	63253	0.1133	61242	0.2743	2011
Artery Tibial	0.0040	45006116	0.1029	67045	0.0985	64890	0.2341	2155
Brain Amygdala	0.0043	38985756	0.0905	57171	0.0903	55386	0.0959	1785
Brain Anterior Cingulate Cortex BA24	0.0020	41159402	0.0977	60553	0.0954	58653	0.1683	1900
Brain Caudate Basal Ganglia	0.0015	43159564	0.1122	63791	0.1075	61796	0.2598	1995
Brain Cerebellar Hemisphere	0.0030	42161917	0.0953	63077	0.0920	61097	0.1975	1980
Brain Cerebellum	0.0033	42799470	0.1012	63273	0.0967	61296	0.2435	1977
Brain Cortex	0.0023	43762809	0.1091	64905	0.1030	62865	0.2958	2040
Brain Frontal Cortex BA9	0.0027	43036320	0.1023	63492	0.0970	61517	0.2653	1975
Brain Hippocampus	0.0036	41085591	0.0986	60906	0.0923	59018	0.2965	1888
Brain Hypothalamus	0.0026	41705870	0.1177	61681	0.1135	59784	0.2479	1897
Brain Nucleus Accumbens Basal Ganglia	0.0035	42906136	0.0906	63455	0.0853	61514	0.2580	1941
Brain Putamen Basal Ganglia	0.0036	41939367	0.1120	61914	0.1050	59964	0.3276	1950
Brain Spinal Cord Cervical C-1	0.0047	39565605	0.0825	58308	0.0782	56443	0.2119	1865
Brain Substantia Nigra	0.0032	38209132	0.1034	55808	0.0958	54041	0.3386	1767
Breast Mammary Tissue	0.0050	44906127	0.1239	66864	0.1165	64758	0.3543	2106
Cells Cultered Fibroblasts	0.0049	43559973	0.0872	64062	0.0812	62005	0.2683	2057
Cells EBV-Transformed Lymphocytes	0.0055	37649767	0.1021	57560	0.0954	55796	0.3141	1764
Colon Sigmoid	0.0035	44292598	0.1106	66017	0.1052	63910	0.2739	2107
Colon Transverse	0.0044	44792441	0.1154	66774	0.1115	64690	0.2361	2084

Esophagus Gastroesophageal Junction	0.0034	43875442	0.1134	65798	0.1072	63714	0.3008	2084
Esophagus Mucosa	0.0034	45175253	0.1093	68197	0.1046	66016	0.2518	2181
Esophagus Mucularis	0.0011	45189402	0.1100	67404	0.1034	65233	0.3076	2171
Heart Atrial Appendage	0.0035	43208691	0.1127	64749	0.1054	62675	0.3316	2074
Heart Left Ventricle	0.0026	40714721	0.0961	61147	0.0874	59168	0.3561	1979
Kidney Cortex	0.0039	33484277	0.1064	49300	0.1037	47733	0.1860	1567
Liver	0.0051	38860581	0.1210	58803	0.1163	56962	0.2663	1841
Lung	0.0031	46342757	0.1173	69343	0.1127	67168	0.2598	2175
Minor Salivary Gland	0.0048	42192031	0.1140	63014	0.1087	61039	0.2784	1975
Muscle Skeletal	0.0034	41571704	0.1147	62287	0.1092	60284	0.2792	2003
Nerve Tibial	0.0055	47830487	0.1102	70807	0.1030	68561	0.3301	2246
Ovary	0.0033	41915015	0.0972	62893	0.0914	60894	0.2737	1999
Pancreas	0.0044	42078288	0.1127	63231	0.1049	61220	0.3500	2011
Pituitary	0.0050	44752909	0.0916	66488	0.0854	64391	0.2833	2097
Prostate	0.0030	43999548	0.1039	65235	0.0984	63189	0.2759	2046
Skin Not Sun Exposed Subrapubic	0.0038	46342210	0.0891	69890	0.0815	67687	0.3227	2203
Skin Sun Exposed Lower Leg	0.0041	47192423	0.1037	71122	0.0972	68903	0.3051	2219
Small Intestine Terminal Ileum	0.0023	42745652	0.0995	63667	0.0952	61672	0.2314	1995
Spleen	0.0033	43155273	0.1053	64743	0.0993	62727	0.2919	2016
Stomach	0.0041	43048735	0.1069	64433	0.1000	62388	0.3163	2045
Testis	0.0035	54800000	0.0958	76465	0.0907	74134	0.2583	2331
Thyroid	0.0037	47563494	0.1112	70680	0.1051	68446	0.3000	2234
Uterus	0.0041	40141495	0.0998	60065	0.0959	58216	0.2241	1849
Vagina	0.0026	39167972	0.1004	58600	0.0975	56788	0.1895	1812
Whole Blood	0.0026	39095230	0.0825	61223	0.0761	59306	0.2816	1917

Table S4. TOPMed MESA TWAS for protein results for every tissue. π_1 is the expected true positive rate and the number of transcript-protein pairs tested is indicated for each mechanism class.

Tissue	*Trans-*Acting π_1	*Pairs tested*	*Cis-*acting π_1	*Pairs tested*	*Cis-*different π_1	*Pairs tested*	*Cis-*same π_1	*Pairs tested*
Adipose Subcutaneous	0.3517	1205	0.7811	790	0.7418	629	0.9264	161
Adipose Visceral Omentum	0.3265	1261	0.7529	784	0.7138	627	0.8893	157
Adrenal Gland	0.4307	953	0.8616	690	0.8309	546	0.9794	144
Artery Aorta	0.3410	1097	0.7311	769	0.6716	621	0.9786	148
Artery Coronary	0.2554	882	0.7736	745	0.7555	607	0.8493	138
Artery Tibial	0.3544	1022	0.8095	774	0.7720	627	0.9727	147
Brain Amygdala	0.4180	764	0.7772	621	0.7607	508	0.8522	113
Brain Anterior Cingulate Cortex BA24	0.4518	854	0.7556	657	0.7179	543	0.9218	114
Brain Caudate Basal Ganglia	0.4476	989	0.8169	712	0.8065	576	0.8575	136
Brain Cerebellar Hemisphere	0.3417	754	0.7715	649	0.7545	531	0.8412	118
Brain Cerebellum	0.4520	940	0.8446	617	0.8376	508	0.8787	109
Brain Cortex	0.3934	940	0.7664	692	0.7493	575	0.8585	117
Brain Frontal Cortex BA9	0.3860	920	0.8247	674	0.8037	546	0.9190	128
Brain Hippocampus	0.4210	885	0.8350	672	0.8267	546	0.8668	126
Brain Hypothalamus	0.5522	801	0.8129	670	0.8011	552	0.8714	118
Brain Nucleus Accumbens Basal Ganglia	0.4337	932	0.8005	674	0.7995	563	0.8059	111
Brain Putamen Basal Ganglia	0.4909	979	0.8254	687	0.7991	552	0.9309	135
Brain Spinal Cord Cervical C-1	0.3899	861	0.8511	627	0.8393	511	0.9059	116
Brain Substantia Nigra	0.3986	760	0.7339	578	0.6943	477	0.9424	101
Breast Mammary Tissue	0.3469	1129	0.7406	722	0.7014	574	0.8935	148
Cells Cultered Fibroblasts	0.2617	995	0.8408	682	0.8322	557	0.8793	125
Cells EBV-Transformed Lymphocytes	0.3793	814	0.7590	652	0.7545	547	0.7824	105
Colon Sigmoid	0.3949	1122	0.7361	733	0.7297	575	0.7586	158
Colon Transverse	0.4455	1120	0.7872	737	0.7816	598	0.8119	139

Esophagus Gastroesophageal Junction	0.3673	1148	0.8216	784	0.8071	626	0.8831	158
Esophagus Mucosa	0.3807	1115	0.8939	779	0.8826	636	0.9436	143
Esophagus Mucularis	0.3357	1137	0.8678	797	0.8566	628	0.9063	169
Heart Atrial Appendage	0.3969	1274	0.8026	797	0.7969	642	0.8235	155
Heart Left Ventricle	0.4327	881	0.7376	685	0.7459	534	0.7082	151
Kidney Cortex	0.3874	778	0.8443	564	0.8251	454	0.9237	110
Liver	0.4455	1023	0.7877	732	0.7741	588	0.8401	144
Lung	0.3502	1240	0.7596	804	0.7305	646	0.8757	158
Minor Salivary Gland	0.3688	938	0.8299	773	0.8237	646	0.8622	127
Muscle Skeletal	0.4151	828	0.8153	670	0.7949	531	0.8896	139
Nerve Tibial	0.3771	1248	0.7853	810	0.7520	664	0.9333	146
Ovary	0.3564	814	0.7627	739	0.7462	605	0.8350	134
Pancreas	0.4871	1171	0.8268	727	0.8238	596	0.8408	131
Pituitary	0.3628	1047	0.7373	755	0.7033	610	0.8881	145
Prostate	0.3753	988	0.8194	722	0.7918	585	0.9448	137
Skin Not Sun Exposed Subrapubic	0.3136	1209	0.8065	811	0.7784	663	0.9332	148
Skin Sun Exposed Lower Leg	0.3816	1217	0.8387	813	0.8243	655	0.9001	158
Small Intestine Terminal Ileum	0.4412	924	0.8430	681	0.8232	547	0.9246	134
Spleen	0.3356	1217	0.8058	724	0.7800	575	0.9175	149
Stomach	0.4160	1018	0.7056	790	0.7101	640	0.6843	150
Testis	0.4175	1056	0.7689	838	0.7241	690	0.9738	148
Thyroid	0.3648	1231	0.8217	809	0.8147	658	0.8516	151
Uterus	0.3957	852	0.8009	624	0.7831	511	0.8815	113
Vagina	0.4698	900	0.8451	641	0.8246	538	0.9504	103
Whole Blood	0.4168	1199	0.9013	760	0.8902	607	0.9443	153

Table S5. *Trans*-targets are enriched for transcription factor binding motifs.

Transcription Factor Gene	MSigDB Accession	# of Targets in Gene Set	# of Sig. Targets in Gene Set	Significant Target Genes	P-value	Adjusted P-value
NFKB	NFKB_C	66	16	*VCAM1, TNFSF18, BDNF, PTHLH, IL23A, CDH5, ICAM1, IL27RA, SIRT2, SNAP25, BCL2L1, IL2, TSLP, IRF1, TNFSF15, PAPPA*	2.6e-4	3.04e-2
NFKB	NFKB_Q6	54	16	*VCAM1, TNFSF18, BDNF, STIP1, CADM1, PTHLH, IL23A, GREM1, MED1, RNF43, ICAM1, TSLP, TNFSF15, PAPPA*	2.99e-4	3.04e-2
NFKB	NFKB_Q6_01	61	19	*VCAM1, TNFSF18, BDNF, CADM1, PTHLH, IL23A, GREM1, TP53, RNF43, EBI3, ICAM1, IL27RA, SIRT2, SNAP25, MMP9, IL6ST, TSLP, TNFSF15, PAPPA*	1.25e-6	5.43e-4
RELA	NFKAPPAB_01	61	16	*VCAM1, TNFSF18, BDNF, IL23A, GREM1, CXCL16, TP53, MED1, LAMA1, EBI3, ICAM1, IL27RA, MMP9, TSLP, IRF1, TNFSF15*	9.51e-5	1.93e-2
RELA	NFKAPPAB65_01	52	14	*TNFSF18, BDNF, PTHLH, GREM1, CXCL16, TP53, RNF43, LAMA1, ICAM1, SIRT2, MMP9, IL6ST, TSLP, TNFSF15*	1.94e-4	2.95e-2
NFAT1C	TGGAAA_NFAT_Q4_01	351	59	*ISG15, TNFRSF8, BCAR3, TSHB, NTRK1, FASLG, FGF8, ADM, BDNF, FTH1, STIP1, CADM1, ERBB3, IL23A, IGF1, TNFSF11, IL25, GREM1, SPINT1, CDH5, TP53, MAP2K3, RNF43, COLEC12, RETN, ICAM1,*	1.78e-6	5.43e-4

				POMC, LRP1B, SNAP25, JAG1, JAG1, USP25, PDGFB, CHL1, LTF, LSAMP, FSTL1, APOD, PDGFRA, IBSP, IL2, CCL28, IL6ST, PDE4D, CAST, SEMA6A, IL5, IL12B, APOM, EHMT2, IL17F, SYNCRIP, SMPDL3A, INHBA, HGF, SEMA3A, ANGPT1, TNFRSF11B, TPM2, PAK3		
FOXF2	FREAC2_01	44	12	*TXNDC12, BDNF, CADM1, IGF1, IL25, GREM1, AKT2, IL6ST, CD109, CGA, INHBA, PAPPA*	4.9e-4	3.4e-2
AR	AR_Q2	17	7	*BDNF, MSTN, SNAP25, AGER, SYNCRIP, INHBA, CD36*	5.02e-4	3.4e-2
GATA1	GATA1_04	51	13	*TSHB, ADM, IGF1, IL34, CEBPB, PDGFRA, CAST, IL5, EPO, MSR1, PRSS3, CCL27, PAPPA*	5.87e-4	3.40e-2
STAT1	STAT_01	55	14	*BDNF, TNFSF11, GZMB, MAP2K3, VTN, LPO, ICAM1, USP25, OSM, THPO, IL6ST, RASA1, IRF1, EHMT2*	3.68e-4	3.21e-2

Table S6. ***Cis*- and *Trans*-targets are enriched for mapped GWAS catalog associations (FDR < 0.05).**

Mechanism	Gene Set	# of Targets in Gene Set	# of Significant Targets in Gene Set	P-value	Adjusted P-value
Trans-acting	Blood Protein Levels	862	122	2.26e-8	4.10e-5
Trans-acting	Inflammatory Bowel Disease	190	38	2.64e-6	2.39e-3
Cis-acting	Blood Protein Levels	862	229	4.73e-125	8.58e-122
Cis-acting	Ankylosing Spondylitis	22	11	1.89e-7	1.62e-4
Cis-acting	Inflammatory Bowel Disease	190	36	2.68e-7	1.62e-4
Cis-acting	Chronic Inflammatory Diseases	48	13	5.21e-5	2.36e-2

Table S7. Pleiotropic regulatory loci discovered in INTERVAL.

Locus	Genes in Locus	Chromosome	Location (bp)	Unique Targets	Replicated Targets (significant / tested)
1	*CFHR3, CFHR1, CFHR4*	1	196,774,813 – 196,888,014	134	5/56
2	*BCHE*	3	165,772,904	56	3/12
3	*C7*	5	40,909,497	280	51/103
4	*C6*	5	41,142,116	81	9/42
5	*HLA-DQB2, HLA-DQA1*	6	32,628,179 – 32,756,098	82	10/31
6	*SKIV2L, CYP21A2, C4B*	6	31,959,117 – 32,038,327	86	18/34
7	*GSDMD*	8	143,553,207	54	2/20
8	*ABO*	9	133,233,278	55	27/33
9	*SARM1, TMEM199, POLDIP2, SUPT6H, TNFAIP1, TMEM97, IFT20, SLC46A1, ERVE-1, SLC13A2*	17	28,232,590 – 28,662,198	290	37/86
10	*MYADM, NLRP12, AC008753.3*	19	53,787,597 – 53,864,763	555	1/218
11	*APOE*	19	44,905,791	78	1/17

Table S8. Pleiotropic regulatory genes are enriched for mapped GWAS catalog associations (FDR < 0.05).

Locus	Genes in Locus	Associated GWAS Catalog Traits
1	*CFHR3, CFHR1, CFHR4*	Nephropathy, Age-related macular degeneration, Matrix metalloproteinase-8 levels, Complement C3 and C4 levels, IgA nephropathy, Advanced age-related macular degeneration
5	*HLA-DQB2, HLA-DQA1*	Immunoglobulin A vasculitis, Strep throat, Childhood steroid-sensitive nephrotic syndrome, Neuromyelitis optica, Pneumonia, Neuromyelitis optica (AQP4-IgG-positive), Chronic hepatitis C infection, Drug-induced liver injury (flucloxacillin), Plantar warts, Shingles, Myositis, Multiple sclerosis (OCB status), Late-onset myasthenia gravis, Lymphoma, PEG-asparaginase hypersensitivity without enzyme activity in childhood acute lymphoblastic leukemia, Peanut allergy, Response to hepatitis B vaccine, Nephropathy, Cervical cancer, Asthma (moderate or severe), Sarcoidosis (non-Lofgren's syndrome without extrapulmonary manifestations), IgA nephropathy, Allergy, Self-reported allergy, Allergic sensitization, Childhood ear infection, Sjögren's syndrome, Primary biliary cirrhosis, Tuberculosis, Systemic sclerosis, Tonsillectomy, Hypothyroidism, Takayasu arteritis, Chronic lymphocytic leukemia, Squamous cell lung carcinoma, Allergic rhinitis, Itch intensity from mosquito bite adjusted by bite size, Celiac disease, Asthma or allergic disease (pleiotropy), Lung cancer, Rheumatoid arthritis, Red blood cell count, Allergic disease (asthma, hay fever or eczema), Asthma, Prostate cancer, Systemic lupus erythematosus, Ulcerative colitis, Type 2 diabetes, Autism spectrum disorder or schizophrenia, Crohn's disease, Schizophrenia, Inflammatory bowel disease
6	*SKIV2L, CYP21A2, C4B*	Prostate cancer, Ulcerative colitis, Autism spectrum disorder or Schizophrenia, Inflammatory bowel disease
9	*SARM1, TMEM199, POLDIP2, SUPT6H, TNFAIP1, TMEM97, IFT20, SLC46A1, ERVE-1, SLC13A2*	Osteoprotegerin levels, Blood protein levels
10	*MYADM, NLRP12, AC008753.3*	None

Table S9. TOPMed MESA *cis*-same π_1 values for every predicted and observed tissue.

Tissue	*Cis*-same π_1	# Transcript-protein pairs tested
Brain Putamen basal ganglia	0.4912	767
Skin Sun Exposed Lower leg	0.4662	898
Small Intestine Terminal Ileum	0.4610	821
Kidney Cortex	0.4480	627
Esophagus Muscularis	0.4473	892
Uterus	0.4406	740
Liver	0.4317	774
Cells Cultured fibroblasts	0.4195	827
Adrenal Gland	0.4193	789
Minor Salivary Gland	0.4040	817
Esophagus Mucosa	0.3960	899
Testis	0.3945	953
Muscle Skeletal	0.3910	798
Brain Caudate basal ganglia	0.3896	789
Heart Atrial Appendage	0.3850	859
Pituitary	0.3845	847
Brain Hypothalamus	0.3726	774
Colon Transverse	0.3708	863
Thyroid	0.3651	892
Brain Frontal Cortex BA9	0.3633	791
Adipose Subcutaneous	0.3530	866
Brain Spinal cord cervical c-1	0.3472	748
Ovary	0.3440	820
Adipose Visceral Omentum	0.3427	881
Brain Anterior cingulate cortex BA24	0.3408	767
Heart Left Ventricle	0.3408	822
Brain Hippocampus	0.3366	758
Brain Substantia nigra	0.3319	720
Whole Blood	**0.3311**	796
Breast Mammary Tissue	0.3239	856
Prostate	0.3223	826
Skin Not Sun Exposed Suprapubic	0.3222	881
Artery Aorta	0.3183	872
Brain Cerebellum	0.3168	780
Cells EBV-transformed lymphocytes	0.3129	727
Brain Cortex	0.3048	809
Lung	0.3031	891

Vagina	0.3028	743
Esophagus Gastroesophageal Junction	0.2962	844
Brain Nucleus accumbens basal ganglia	0.2905	772
Colon Sigmoid	0.2872	853
Brain Amygdala	0.2848	721
Nerve Tibial	0.2764	921
Spleen	0.2747	846
Artery Coronary	0.2684	828
Artery Tibial	0.2678	886
Stomach	0.2662	839
Pancreas	0.2418	826
PBMC – observed	0.2393	862
Monocytes – observed	0.1928	862
Brain Cerebellar Hemisphere	0.1819	794
T-cells – observed	0.0768	862

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