

Supplementary Table 6. Effect of sequence variants associated with RA overall or its seropositive/seronegative subsets on mRNA expression (cis-eQTL) in various tissues.

Lead variant	eQTL variant	R ²	Gene	P	effect (SD)	tissue	EA	effect unit	hgnc	geneid	Source (Suppl. T.7)
chr1:2800059	chr1:2569783	0.84	PRXL2B	1.26E-10	-0.14	Cells_Cultured_fibroblasts	T	beta	28390	127281	GTEEx v8
chr1:2800059	chr1:2575976	0.90	TTC34	3.32E-18	0.26	Artery_Tibial	T	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2591773	0.95	TTC34	1.82E-13	0.42	Brain_Cerebellum	C	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2593018	0.89	MMEL1	3.74E-24	-0.71	Brain_Nucleus_accumbens_basal_ganglia	C	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2593018	0.89	PRXL2B	2.10E-16	-0.27	Lung	C	beta	28390	127281	GTEEx v8
chr1:2800059	chr1:2593476	0.95	MMEL1	1.88E-243	-33.32	blood	T	zscore	14668	79258	Vosa et al.
chr1:2800059	chr1:2594221	0.95	MMEL1	<E-310	-0.69	blood	A	beta	14668	79258	deCODE genetics
chr1:2800059	chr1:2594221	0.95	MMEL1	1.32E-27	-0.52	Whole_Blood	A	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2596694	0.96	MMEL1	3.50E-27	0.78	Spleen	C	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2601185	0.96	MMEL1	8.15E-69	0.75	Lung	T	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2602113	0.96	MMEL1	2.49E-54	na	MO	na	na	14668	79258	Zeller et al. (2010)
chr1:2800059	chr1:2606399	0.99	TTC34	1.39E-15	0.20	Nerve_Tibial	T	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2607567	0.92	MMEL1	1.29E-26	-0.46	Artery_Tibial	C	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2607961	0.92	MMEL1	2.17E-17	-0.71	Liver	C	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2608357	0.98	TTC34	2.45E-12	0.26	Esophagus_Muscularis	T	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2608357	0.98	TTC34	5.58E-15	0.33	Esophagus_Gastroesophageal_Junction	T	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2623124	0.99	TTC34	2.21E-13	0.35	Pancreas	G	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2636061	0.99	MMEL1	1.86E-16	0.42	Small_Intestine_Terminal_Ileum	G	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2636061	0.99	TTC34	6.90E-11	-0.47	Cells_EBV-transformed_lymphocytes	G	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2636061	0.99	TTC34	7.24E-15	-0.27	Whole_Blood	G	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2642639	0.97	TTC34	6.72E-16	-0.55	Pituitary	C	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2642639	0.97	TTC34	7.64E-12	-0.26	Artery_Aorta	C	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2791865	0.99	TTC34	2.54E-14	0.30	Heart_Atrial_Appendage	A	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2791865	0.99	TTC34	2.89E-17	0.20	Thyroid	A	beta	34297	100287898	GTEEx v8
chr1:2800059	chr1:2803608	1.00	MMEL1	2.88E-10	-0.25	Colon_Transverse	G	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2804584	1.00	MMEL1	8.42E-35	-0.47	Thyroid	A	beta	14668	79258	GTEEx v8
chr1:2800059	chr1:2804584	1.00	TTC34	6.16E-18	0.28	Skin_Sun_Exposed_Lower_leg	A	beta	34297	100287898	GTEEx v8
chr2:60881694	chr2:60856371	0.93	REL	1.12E-15	-0.02	whole_blood	T	fx	9954	5966	Yao et al. (2017)
chr2:60881694	chr2:60881694	1.00	REL	1.27E-09	-0.38	STARNET_Blood	G	beta	9954	5966	Hauberg et al. (2017)
chr2:60881694	chr2:60937196	0.96	PUS10	1.23E-14	-0.03	whole_blood	G	fx	26505	150962	Yao et al. (2017)
chr2:111119036	chr2:111119036	1.00	BCL2L11	1.77E-141	0.58	blood	C	beta	994	10018	deCODE genetics
chr2:191094763	chr2:191105153	0.98	GLS	5.88E-09	-0.01	whole_blood	C	fx	4331	2744	Yao et al. (2017)
chr2:203874196*	chr2:203829540	0.92	CTLA4	2.30E-70	17.73	blood	A	zscore	2505	1493	Vosa et al.
chr2:203874196*	chr2:203878211	0.89	CTLA4	2.11E-15	0.42	Testis	T	beta	2505	1493	GTEEx v8
chr2:203880280**	chr2:203829540	0.80	CTLA4	2.30E-70	17.73	blood	A	zscore	2505	1493	Vosa et al.
chr2:203880280**	chr2:203878211	0.98	CTLA4	2.11E-15	0.42	Testis	T	beta	2505	1493	GTEEx v8
chr5:56148856	chr5:56148856	1.00	ANKRD55	<E-310	-0.81	blood	A	beta	25681	79722	deCODE genetics
chr5:56148856	chr5:56148856	1.00	ANKRD55	3.27E-310	-73.83	blood	A	zscore	25681	79722	Vosa et al.
chr5:56148856	chr5:56148856	1.00	ANKRD55	4.62E-43	0.84	white_blood_cells	G	beta	25681	79722	Pala et al. (2017)
chr5:56148856	chr5:56148856	1.00	IL6ST	1.90E-44	-0.18	blood	A	beta	6021	3572	deCODE genetics
chr5:56148856	chr5:56148856	1.00	IL6ST	2.00E-36	-12.60	blood	A	zscore	6021	3572	Vosa et al.

Lead variant	eQTL variant	R ²	Gene	P	effect (SD)	tissue	EA	effect unit	hgnc	geneid	Source (Suppl. T.7)
chr6:167127770	chr6:167119243	0.97	CCR6	4.92E-11	0.34	adipose	A	beta	1607	1235	deCODE genetics
chr6:167127770	chr6:167119243	0.97	CCR6	4.98E-148	25.91	blood	A	zscore	1607	1235	Vosa et al.
chr6:167127770	chr6:167119305	0.97	CCR6	6.04E-15	-0.04	whole_blood	G	fx	1607	1235	Yao et al. (2017)
chr6:167127770	chr6:167125409	0.97	CCR6	1.45E-205	0.38	blood	T	beta	1607	1235	deCODE genetics
chr7:128938247	chr7:128932712	0.86	IRF5	4.13E-43	0.42	Esophagus_Mucosa	A	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128932712	0.86	IRF5	5.06E-18	0.37	Adrenal_Gland	A	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128932712	0.86	IRF5	9.68E-11	0.22	Heart_Left_Ventricle	A	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128935498	0.81	IRF5	1.11E-86	0.40	Whole_Blood	G	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128935498	0.81	IRF5	1.88E-30	0.34	Skin_Not_Sun_Exposed_Suprapubic	G	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128935498	0.81	IRF5	2.74E-27	0.44	Stomach	G	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128935498	0.81	IRF5	2.81E-38	0.32	Skin_Sun_Exposed_Lower_leg	G	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128935498	0.81	IRF5	3.58E-18	0.32	Colon_Sigmoid	G	beta	6120	3663	GTEEx v8
chr7:128938247	chr7:128938247	1.00	IRF5	2.36E-26	0.64	white_blood_cells	T	beta	6120	3663	Pala et al. (2017)
chr8:11480078	chr8:11486464	0.98	BLK	2.08E-23	na	MO	na	na	1057	640	Zeller et al. (2010)
chr8:11480078	chr8:11493510	0.93	FAM167A	3.27E-310	86.83	blood	A	zscore	15549	83648	Vosa et al.
chr8:11480078	chr8:11495032	0.91	BLK	1.33E-40	0.86	white_blood_cells	T	beta	1057	640	Pala et al. (2017)
chr8:11480078	chr8:11482373	1.00	BLK	4.84E-16	0.60	STARNET_Blood	T	beta	1057	640	Hauberg et al. (2017)
chr8:11480078	chr8:11493510	0.93	BLK	3.55E-27	0.44	LCL	G	beta	1057	640	Grundberg et al. (2016)
chr8:11480078	chr8:11482373	1.00	FAM167A	5.39E-27	0.30	Cells_Cultured_fibroblasts	C	beta	15549	83648	GTEEx v8
chr8:11480078	chr8:11482373	1.00	BLK	9.41E-54	0.04	whole_blood	T	fx	1057	640	Yao et al. (2017)
chr8:11480078	chr8:11480078	1.00	BLK	5.14E-28	-0.24	Whole_Blood	C	beta	1057	640	GTEEx v8
chr8:11480078	chr8:11491677	0.99	FAM167A	6.15E-44	-0.42	LCL	G	beta	15549	83648	Grundberg et al. (2016)
chr8:11480078	chr8:11493510	0.93	FAM167A	1.12E-89	-1.15	STARNET_Blood	G	beta	15549	83648	Hauberg et al. (2017)
chr8:11480078	chr8:11486464	0.98	FAM167A	2.37E-74	-1.24	white_blood_cells	C	beta	15549	83648	Pala et al. (2017)
chr8:11480078	chr8:11493510	0.93	BLK	3.27E-310	-52.05	blood	A	zscore	1057	640	Vosa et al.
chr9:120873843*	chr9:120877952	0.95	TRAF1	4.42E-23	na	MO	na	na	12031	7185	Zeller et al. (2010)
chr9:120873843*	chr9:120881577	0.95	PSMD5	3.19E-12	0.02	whole_blood	T	fx	9563	5711	Yao et al. (2017)
chr9:120873843*	chr9:120896705	0.94	PHF19	7.85E-11	0.31	Esophagus_Gastroesophageal_Junction	A	beta	24566	26147	GTEEx v8
chr9:120873843*	chr9:120902741	0.95	TRAF1	6.85E-15	-0.30	dendritic_flu	na	beta	12031	7185	Lee et al. (2014)
chr9:120873843*	chr9:120906929	0.95	PHF19	6.33E-201	-30.24	blood	C	zscore	24566	26147	Vosa et al.
chr9:120873843*	chr9:120914118	0.93	PHF19	1.34E-15	0.29	Esophagus_Muscularis	C	beta	24566	26147	GTEEx v8
chr9:120873843*	chr9:120928959	0.91	PHF19	1.83E-10	-0.40	STARNET_Blood	T	beta	24566	26147	Hauberg et al. (2017)
chr9:120873843*	chr9:120928959	0.91	TRAF1	2.62E-170	0.35	blood	T	beta	12031	7185	deCODE genetics
chr9:120873843*	chr9:120928959	0.91	TRAF1	4.40E-14	-0.24	Artery_Tibial	G	beta	12031	7185	GTEEx v8
chr9:120873843*	chr9:120928959	0.91	TRAF1	5.10E-32	-0.36	Skin_Not_Sun_Exposed_Suprapubic	G	beta	12031	7185	GTEEx v8
chr9:120873843*	chr9:120928959	0.91	TRAF1	5.54E-21	-0.24	Skin_Sun_Exposed_Lower_leg	G	beta	12031	7185	GTEEx v8
chr9:120873843*	chr9:120928959	0.91	TRAF1	5.90E-12	-0.14	Whole_Blood	G	beta	12031	7185	GTEEx v8
chr9:120873843*	chr9:120930801	0.95	TRAF1	6.22E-08	0.34	STARNET_Blood	C	beta	12031	7185	Hauberg et al. (2017)
chr9:120873843*	chr9:120930801	0.92	TRAF1	6.22E-08	0.34	STARNET_Blood	C	beta	12031	7185	Hauberg et al. (2017)
chr9:120933192**	chr9:120929191	1.00	TRAF1	1.40E-25	0.72	Brain_Cerebellum	G	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120929191	1.00	TRAF1	1.24E-16	0.68	Brain_Spinal_cord_cervical_c-1	G	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120906048	1.00	TRAF1	1.26E-21	0.66	Brain_Cerebellar_Hemisphere	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120878222	1.00	TRAF1	9.87E-15	0.52	Brain_Amygdala	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120920828	1.00	TRAF1	1.18E-24	0.48	Brain_Putamen_basal_ganglia	T	beta	12031	7185	GTEEx v8

Lead variant	eQTL variant	R ²	Gene	P	effect (SD)	tissue	EA	effect unit	hgnc	geneid	Source (Suppl. T.7)
chr9:120933192**	chr9:120920828	1.00	TRAF1	2.35E-13	0.47	Brain_Substantia_nigra	T	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120928863	1.00	TRAF1	1.78E-18	0.47	Brain_Hypothalamus	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120924933	1.00	TRAF1	2.19E-21	0.46	Brain_Hippocampus	A	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120929191	1.00	TRAF1	2.30E-34	0.46	Testis	G	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120929191	1.00	TRAF1	1.34E-10	0.44	Ovary	G	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120909559	1.00	TRAF1	4.55E-24	0.44	Brain_Caudate_basal_ganglia	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120929191	1.00	TRAF1	3.31E-23	0.42	Brain_Nucleus_accumbens_basal_ganglia	G	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120915851	0.98	TRAF1	2.14E-15	0.37	Brain_Cortex	A	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120946008	0.91	TRAF1	4.34E-12	0.30	Brain_Frontal_Cortex_BA9	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120930590	1.00	TRAF1	2.40E-34	0.27	Muscle_Skeletal	T	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120930590	1.00	TRAF1	2.59E-10	0.23	Heart_Left_Ventricle	T	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120899028	1.00	TRAF1	5.93E-23	-0.16	CMC_Brain_DLPFC	A	beta	12031	7185	Hauberg et al. (2017)
chr9:120933192**	chr9:120904499	0.90	TRAF1	8.92E-11	-0.24	Artery_Aorta	C	beta	12031	7185	GTEEx v8
chr9:120933192**	chr9:120888049	0.99	TRAF1	1.64E-39	-0.73	STARNET_Muscle_skeletal	T	beta	12031	7185	Hauberg et al. (2017)
chr10:31122426	chr10:31122426	1.00	ZEB1	3.71E-15	-0.15	Cells_Cultured_fibroblasts	T	beta	11642	6935	GTEEx v8
chr13:28029870	chr13:28029870	1.00	FLT3	1.30E-10	0.82	Lung	C	beta	3765	2322	GTEEx v8
chr17:39908216	chr17:39756124	0.83	GSDMA	<E-310	0.47	lung	T	beta	13311	284110	Hao et al. (2012)
chr17:39908216	chr17:39869782	0.94	ZBP2	5.46E-24	-0.22	Testis	A	beta	20678	124626	GTEEx v8
chr17:39908216	chr17:39900944	0.98	GSDMB	1.70E-19	-0.20	Colon_Transverse	A	beta	23690	55876	GTEEx v8
chr17:39908216	chr17:39909987	0.80	ORMDL3	6.66E-24	-0.25	Lung	C	beta	16038	94103	GTEEx v8
chr17:39908216	chr17:39910014	0.80	ORMDL3	1.74E-16	0.50	STARNET_Artery_aortic_root_(AS)	G	beta	16038	94103	Hauberg et al. (2017)
chr17:39908216	chr17:39910119	0.80	GSDMB	3.39E-83	1.11	white_blood_cells	T	beta	23690	55876	Pala et al. (2017)
chr17:39908216	chr17:39910119	0.80	ORMDL3	6.08E-92	1.16	white_blood_cells	T	beta	16038	94103	Pala et al. (2017)
chr17:39908216	chr17:39916474	0.92	GSDMB	2.02E-16	0.31	Small_Intestine_Terminal_ileum	T	beta	23690	55876	GTEEx v8
chr17:39908216	chr17:39916474	0.92	ORMDL3	5.95E-11	-0.13	Adipose_Subcutaneous	T	beta	16038	94103	GTEEx v8
chr19:10359299	chr19:10310306	0.91	FDX2	6.53E-14	-0.31	Thyroid	C	beta	30546	112812	GTEEx v8
chr19:10359299	chr19:10310306	0.91	ZGLP1	<E-310	0.97	blood	C	beta	37245	100125288	deCODE genetics
chr19:10359299	chr19:10310306	0.91	ZGLP1	1.53E-10	-0.27	Brain_Nucleus_accumbens_basal_ganglia	C	beta	37245	100125288	GTEEx v8
chr19:10359299	chr19:10310306	0.91	ZGLP1	1.55E-11	-0.24	Nerve_Tibial	C	beta	37245	100125288	GTEEx v8
chr19:10359299	chr19:10310306	0.91	ZGLP1	1.65E-21	-0.32	Thyroid	C	beta	37245	100125288	GTEEx v8
chr19:10359299	chr19:10310306	0.91	ZGLP1	3.69E-11	-0.45	Brain_Cerebellum	C	beta	37245	100125288	GTEEx v8
chr19:10359299	chr19:10310306	0.91	ZGLP1	5.73E-12	-0.35	Testis	C	beta	37245	100125288	GTEEx v8
chr19:10359299	chr19:10359300	1.00	FDX2	4.25E-08	-0.13	LCL	C	beta	30546	112812	Grundberg et al. (2016)

Different lead signals in RA overall (*) and seropositive RA (**) at the same locus pointing to same candidate causal genes.

***Sequence variants associated both with RA overall and its seropositive and seronegative subsets.