Supplementary Table 1. Association of EHOA GWS variants in the individual study populations

											Iceland (N = 918 cases / 109,249 controls)				UK Biobank (N = 63 cases / 430,875 controls)				The Netherlands (N = 139 cases / 5,102 controls)				Spain (N = 218 cases / 164 controls)				USA (N = 145 cases / 5,308 controls)			
rsName	Chr	Pos_build38	Effect Allele	Other Allele	Freq (%) EA	P_value	OR	P_value_GWS_threshold	P_bonferroni	P_{het}	I2	P value	OR	Freq (%) EA	Info	P value	OR	Freq (%) EA	Info	P value	OR	Freq (%) EA	Info	P value	OR	Freq (%) EA	Info	P value	OR	Freq (%) EA	Info
rs17013495	chr4	87885460	C	T	42.7	8.4E-14	0.72	1.2E-09	3.5E-06	0.18	36.9	2.5E-11	0.70	38.7	1.000	0.71	1.07	43.5	0.999	0.042	0.76	43.0	0.995	5.2E-03	0.60	45.9	0.987	0.020	0.71	42.3	0.990
rs11243284	chr6	8945086	C	T	29.8	4.2E-11	1.35	4.0E-10	5.2E-03	0.67	0	2.9E-08	1.35	29.5	1.000	0.33	1.20	30.3	1.000	0.15	1.22	29.7	0.987	0.011	1.71	29.7	0.817	0.018	1.47	30.0	0.867
rs1800801	chr12	14885854	T	C	39.0	3.6E-13	1.37	2.4E-09	7.5E-06	0.17	38.0	5.0E-07	1.30	37.2	1.000	8.3E-04	1.84	37.8	0.999	7.1E-05	1.70	37.4	1.000	0.14	1.29	45.1	0.989	0.026	1.38	37.3	0.988
rs11631127	chr15	57977811	G	C	47.8	7.1E-18	0.69	4.0E-10	8.9E-10	0.59	0	2.3E-11	0.70	42.4	1.000	0.25	0.81	46.5	1.000	8.4E-05	0.60	47.3	0.998	0.058	0.70	55.8	0.995	5.6E-04	0.61	47.1	0.994

Supplementary Table 2. Association of EHOA variants with EHOA under additive, recessive and full genotype models

		Additive model			Recessive model			Genotype specific model						
								Heterozygotes			Homozygotes			
Variant[allele]	Chr	OR (95% CI)	P value	P_{het}	OR (95% CI)	P value	P_{het}	OR (95% CI)	P value	P_{het}	OR (95% CI)	P value	P_{het}	P model
rs17013495[T]	chr4	1.395 (1.279-1.522)	8.77E-14	0.17	1.600 (1.346-1.901)	9.64E-08	0.16	1.342 (1.098-1.641)	0.0041	0.48	2.011 (1.630-2.481)	7.07E-11	0.63	0.289
rs11243284[C]	chr6	1.354 (1.237-1.482)	4.22E-11	0.67	1.674 (1.387-2.022)	8.47E-08	0.41	1.307 (1.147-1.491)	6.27E-05	0.77	1.773 (1.457-2.157)	1.07E-08	0.66	0.446
rs1800801[T]	chr12	1.368 (1.257-1.488)	3.55E-13	0.17	1.848 (1.594-2.143)	3.86E-16	0.14	1.151 (1.002-1.323)	0.047	0.87	2.012 (1.705-2.373)	1.09E-16	0.34	0.0011
rs11631127[C]	chr15	1.456 (1.337-1.587)	7.15E-18	0.59	1.608 (1.376-1.880)	2.68E-09	0.45	1.320 (1.095-1.591)	0.0036	0.42	2.089 (1.726-2.528)	3.69E-14	0.48	0.241

Association of the four EHOA variants with EHOA is shown for the additive model, the recessive model, and for the full model evaluating risk at the heterozygous genotypes and homozygous genotypes. The effect allele of each variant is shown within square brackets, with the odds ratio (OR) with 95% confidence interval (CI), the P value, and the heterogeneity P value (P_{het}) for each model, and the P value (P model) for deviation from the additive model.

Supplementary Table 3. Association of rs1800801 in 5'UTR of MGP with hand osteoarthritis subtypes under additive, recessive and full genotype model

		Additive model			Recessive model			Genotype specific model						
								Heterozygotes			Homozygotes			
Phenotype	N cases / N controls	OR (95% CI)	P value	Phet	OR (95% CI)	P value	Phet	OR (95% CI)	P value	Phet	OR (95% CI)	P value	Phet	P model
Erosive hand OA	1,484 / 550,680	1.368 (1.257-1.488)	3.6E-13	0.17	1.848 (1.594-2.143)	3.9E-16	0.14	1.151 (1.002-1.323)	0.047	0.87	2.012 (1.705-2.373)	1.1E-16	0.34	0.0011
Finger OA	7,871 / 608,869	1.143 (1.099-1.188)	1.5E-11	0.026	1.258 (1.173-1.349)	1.1E-10	0.035	1.103 (1.037-1.173)	0.0017	0.60	1.349 (1.242-1.464)	1.0E-12	0.031	0.12
Thumb OA	9,865 / 623,814	1.066 (1.031-1.103)	1.6E-04	0.28	1.064 (0.999-1.133)	0.055	0.22	1.108 (1.052-1.166)	1.0E-04	0.44	1.129 (1.050-1.214)	0.0010	0.19	0.056
Hand OA	14,841 / 626,618	1.080 (1.050-1.111)	8.4E-08	0.081	1.132 (1.074-1.193)	3.31E-06	0.059	1.073 (1.027-1.120)	0.0016	0.34	1.181 (1.112-1.254)	6.8E-08	0.08	0.19

Association of the rs180081[T] with hand osteoarthritis subtypes is shown for the additive model, the recessive model, and for the full model evaluating risk at the heterozygous genotypes and homozygous genotypes. The odds ratio (OR) with 95% confidence interval (CI), the P value, and the heterogeneity P value (Phet) is shown for each model, and the P value (P model) for deviation from the additive model. The finger, thumb and hand OA analysis included data from Iceland, US, UK, and The Netherlands, whereas all datasets were included in the erosive hand OA analysis.

Supplementary Table 4. EHOA variants, or their correlated variants, are located in regions defined as candidate cis-regulatory elements by ENCODE project (screen.encodeproject.org).

	GWAS association, lead sequence variant for each signal			
cCRE annotation:	**rs17013495** (chr4:87885460) LD class = 68	**rs11243284** (chr6:8945086) LD class = 17	**rs1800801** (chr12:14885854) LD class = 107	**rs11631127** (chr15:57977811) LD class =155
DNase-H3K4me3				chr15:58008570:SG
Promoter-like sequence (PLS)				chr15:58065219:IG
Promoter-like sequence (PLS)-CTCF-bound			chr12:14885854:SG	
Enhancer-like sequence, distal (dELS)	chr4:87868563:SG, chr4:87868643:SG	chr6:8948008:SG, chr6:8948226:SG	chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14851053:SG, chr12:14851097:IG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58040343:SG, chr15:58040385:SG
Enhancer-like sequence, distal (dELS)-CTCF-bound	chr4:87863666:SG, chr4:87885460:SG	chr6:8949691:SG	chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14901082:SG	chr15:57923529:SG
Enhancer-like sequence, proximal (pELS)			chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14883768:SG	chr15:58063976:IG, chr15:58064657:SG
Enhancer-like sequence, proximal (pELS)-CTCF bound				chr15:58064164:SG

The variants are shown by their position in Build38, with SG ending for SNPs and IG for indels

Supplementary Table 5. Location of EHOA variants, or their correlated variants, in candidate cis-regulatory elements (cCRE) by tissue or cell type (encodeproject.org)

Tissue/cell type	UBERON/CL	rs17013495 (chr4:87885460)	rs11243284 (chr6:8945086)	rs1800801 (chr12:14885854)	rs11631127 (chr15:57977811)
activated CD4-positive, alpha-beta T cell	CL_0000896			chr12:14910656:SG	chr15:58065219:IG
activated CD8-positive, alpha-beta T cell	CL_0000906			chr12:14910656:SG	
adipose tissue	UBERON_0001013			chr12:14885854:SG	
				chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
adrenal gland	UBERON_0002369			chr12:14836364:SG, chr12:14885854:SG	chr15:58065219:IG
amnion	UBERON_0000305			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14885854:SG	
amniotic stem cell	CL_0002639			chr12:14836364:SG, chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG
aorta	UBERON_0000947			chr12:14885854:SG	
ascending aorta	UBERON_0001496			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG, chr12:14910656:SG	
astrocyte	CL_0000127	chr4:87885460:SG		chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
astrocyte of the cerebellum	CL_0002603			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
astrocyte of the hippocampus	CL_0002604			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
astrocyte of the spinal cord	CL_0002606			chr12:14836364:SG, chr12:14885854:SG	
B cell	CL_0000236				chr15:58065219:IG
bipolar neuron	CL_0000103		chr6:8948008:SG, chr6:8948226:SG, chr6:8949691:SG		chr15:58065219:IG
body of pancreas	UBERON_0001150			chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	chr15:57923529:SG
brain	UBERON_0000955			chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
brain microvascular endothelial cell	CL_2000044	chr4:87868563:SG, chr4:87868643:SG		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14885854:SG	
brain pericyte	CL_2000043			chr12:14836364:SG	chr15:57923529:SG
breast epithelium	UBERON_0008367			chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
bronchial epithelial cell	CL_0002328			chr12:14836364:SG, chr12:14910656:SG	chr15:58040343:SG, chr15:58040385:SG
cardiac muscle cell	CL_0000746			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58065219:IG
cardiac myoblast	CL_0010021			chr12:14851053:SG, chr12:14851097:IG	chr15:58065219:IG
cardiovascular progenitor cell	CL_0002664				chr15:58064164:SG, chr15:58064657:SG
caudate nucleus	UBERON_0001873			chr12:14885854:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	
CD14-positive monocyte	CL_0001054	chr4:87885460:SG		chr12:14836364:SG	chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
CD1c-positive myeloid dendritic cell	CL_0002399				chr15:58065219:IG
CD4-positive, alpha-beta memory T cell	CL_0000897				chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
CD4-positive, alpha-beta T cell	CL_0000624			chr12:14839301:SG, chr12:14910656:SG	chr15:58065219:IG
CD4-positive, CD25-positive, alpha-beta regulatory T cell	CL_0000792				chr15:58065219:IG
CD8-positive, alpha-beta memory T cell	CL_0000909				chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
CD8-positive, alpha-beta T cell	CL_0000625			chr12:14836364:SG	
cell of skeletal muscle	CL_0000188			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG
cerebellar cortex	UBERON_0002129			chr12:14883768:SG, chr12:14885854:SG	
cerebellum	UBERON_0002037			chr12:14883768:SG	
chorion	UBERON_0003124			chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG	chr15:58065219:IG
chorionic villus	UBERON_0007106			chr12:14836364:SG, chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG	
choroid plexus epithelial cell	CL_0000706			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14910656:SG	chr15:57923529:SG
cingulate gyrus	UBERON_0002967			chr12:14885854:SG	
colonic mucosa	UBERON_0000317			chr12:14885854:SG	chr15:57923529:SG
common myeloid progenitor, CD34-positive	CL_0001059	chr4:87885460:SG		chr12:14885854:SG	chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
coronary artery	UBERON_0001621			chr12:14885854:SG	
dermis blood vessel endothelial cell	CL_2000010			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58065219:IG
dermis microvascular lymphatic vessel endothelial cell	CL_2000041			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG
duodenal mucosa	UBERON_0000320			chr12:14885854:SG	
ectodermal cell	CL_0000221				chr15:58065219:IG
effector memory CD4-positive, alpha-beta T cell	CL_0000905				chr15:58065219:IG
embryonic facial prominence	UBERON_0012314			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064657:SG
endocrine pancreas	UBERON_0000016			chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:58064657:SG, chr15:58065219:IG
endodermal cell	CL_0000223				chr15:58065219:IG
endothelial cell of umbilical vein	CL_0002618			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
epithelial cell of amnion	CL_0002536			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14885854:SG	chr15:58040343:SG, chr15:58040385:SG
epithelial cell of esophagus	CL_0002252			chr12:14836364:SG, chr12:14910656:SG	chr15:58040343:SG, chr15:58040385:SG
epithelial cell of prostate	CL_0002231			chr12:14836364:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58040343:SG, chr15:58040385:SG
epithelial cell of proximal tubule	CL_0002306			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
esophagus	UBERON_0001043				chr15:58065219:IG
esophagus muscularis mucosa	UBERON_0004648			chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
esophagus squamous epithelium	UBERON_0006920			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
eye	UBERON_0000970				chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
fat cell	CL_0000136			chr12:14836364:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG
femur	UBERON_0000981			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG
fibroblast of cardiac tissue	CL_0002548			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
fibroblast of dermis	CL_0002551			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG
fibroblast of gingiva	CL_0002552			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14885854:SG	chr15:57923529:SG
fibroblast of lung	CL_0002553	chr4:87885460:SG		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58064657:SG
fibroblast of mammary gland	CL_0002555			chr12:14836364:SG, chr12:14885854:SG	chr15:57923529:SG
fibroblast of periodontal ligament	CL_2000017			chr12:14836364:SG, chr12:14885854:SG	
fibroblast of pulmonary artery	CL_0002557			chr12:14836364:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58065219:IG
fibroblast of skin of abdomen	CL_2000013			chr12:14836364:SG, chr12:14885854:SG	
fibroblast of skin of back	CL_0011022			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
fibroblast of the aortic adventitia	CL_0002547			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	chr15:57923529:SG
fibroblast of the conjunctiva	CL_0002550			chr12:14836364:SG, chr12:14885854:SG	
fibroblast of upper back skin	CL_0011021			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14854918:IG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG
fibroblast of villous mesenchyme	CL_0002558			chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG
forelimb muscle	UBERON_0003662			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG
foreskin fibroblast	CL_1001608			chr12:14836364:SG, chr12:14910656:SG	chr15:58040343:SG, chr15:58040385:SG, chr15:58065219:IG
foreskin keratinocyte	CL_1001606			chr12:14836364:SG, chr12:14901082:SG	
foreskin melanocyte	CL_2000045	chr4:87885460:SG		chr12:14836364:SG, chr12:14885854:SG	chr15:57923529:SG
gastrocnemius medialis	UBERON_0011907				

gastroesophageal sphincter	UBERON_0004550	chr4:87863666:SG		chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
germinal center	UBERON_0010754	chr4:87885460:SG		chr12:14854918:IG	
glomerular endothelial cell	CL_0002188			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG
glutamatergic neuron	CL_0000679		chr6:8949691:SG		
heart	UBERON_0000948			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
heart left ventricle	UBERON_0002084			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
heart right ventricle	UBERON_0002080			chr12:14834162:SG, chr12:14834298:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
hematopoietic multipotent progenitor cell	CL_0000837	chr4:87885460:SG		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
hepatocyte	CL_0000182			chr12:14836364:SG, chr12:14885854:SG	chr15:58065219:IG
hindlimb muscle	UBERON_0003663			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
immature natural killer cell	CL_0000823				chr15:58065219:IG
inferior parietal cortex	UBERON_0006088			chr12:14883768:SG	
inflammatory macrophage	CL_0000863			chr12:14836364:SG	chr15:58065219:IG
iris pigment epithelial cell	CL_0002565			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14910656:SG	
keratinocyte	CL_0000312			chr12:14836364:SG	
kidney	UBERON_0002113	chr4:87863666:SG		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
kidney capillary endothelial cell	CL_1000892			chr12:14836364:SG, chr12:14910656:SG	
kidney epithelial cell	CL_0002518			chr12:14836364:SG	
kidney glomerular epithelial cell	CL_1000510			chr12:14836364:SG	chr15:58065219:IG
kidney tubule cell	CL_1000507			chr12:14836364:SG	
large intestine	UBERON_0000059	chr4:87868563:SG, chr4:87868643:SG		chr12:14836364:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:57923529:SG, chr15:58040343:SG, chr15:58040385:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
layer of hippocampus	UBERON_0002305			chr12:14885854:SG	chr15:58065219:IG
left cardiac atrium	UBERON_0002079			chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
left colon	UBERON_0008971			chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	
left forelimb	UBERON_8300002			chr12:14885854:SG	chr15:58065219:IG
left hindlimb	UBERON_8300004			chr12:14883768:SG, chr12:14885854:SG	chr15:58065219:IG
left kidney	UBERON_0004538			chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
left lobe of liver	UBERON_0001115				chr15:57923529:SG
left lung	UBERON_0002168			chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
left renal cortex interstitium	UBERON_0018117			chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
left renal pelvis	UBERON_0018115			chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
limb	UBERON_0002101			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
liver	UBERON_0002107			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
lower leg skin	UBERON_0004264				
lower lobe of left lung	UBERON_0008953	chr4:87863666:SG			chr15:58065219:IG
lung	UBERON_0002048			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58040343:SG, chr15:58040385:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
lung microvascular endothelial cell	CL_2000016			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
mammary gland epithelial cell	CL_0002327			chr12:14836364:SG, chr12:14885854:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58040343:SG, chr15:58040385:SG
medulla oblongata	UBERON_0001896			chr12:14885854:SG	chr15:57923529:SG
mesenchymal stem cell	CL_0000134			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14854918:IG, chr12:14885854:SG	
mesodermal cell	CL_0000222			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
middle frontal area -8	UBERON_0006483			chr12:14883768:SG, chr12:14885854:SG	chr15:58065219:IG
middle frontal gyrus	UBERON_0002702			chr12:14883768:SG	
mucosa of descending colon	UBERON_0004992			chr12:14885854:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:57923529:SG
mucosa of gallbladder	UBERON_0005033			chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
mucosa of rectum	UBERON_0003346			chr12:14883768:SG, chr12:14885854:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:57923529:SG, chr15:58065219:IG
mucosa of stomach	UBERON_0001199			chr12:14885854:SG	chr15:57923529:SG
muscle cell	CL_0000187			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG	chr15:57923529:SG
muscle layer of colon	UBERON_0012489			chr12:14883768:SG, chr12:14885854:SG	chr15:58065219:IG
muscle layer of duodenum	UBERON_0012488			chr12:14883768:SG, chr12:14885854:SG	chr15:58064657:SG, chr15:58065219:IG
muscle of arm	UBERON_0001499			chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
muscle of back	UBERON_0002324			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
muscle of leg	UBERON_0001383			chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
myoepithelial cell of mammary gland	CL_0002324			chr12:14885854:SG	chr15:58065219:IG
myotube	CL_0002372			chr12:14836364:SG	chr15:57923529:SG
naive thymus-derived CD4-positive, alpha-beta T cell	CL_0000895			chr12:14910656:SG	chr15:58065219:IG
natural killer cell	CL_0000623			chr12:14885854:SG	chr15:58064657:SG
nephron	UBERON_0001285			chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
neural cell	CL_0002319				chr15:58065219:IG
neural crest cell	CL_0011012			chr12:14851053:SG, chr12:14851097:IG	chr15:58065219:IG
neural progenitor cell	CL_0011020				chr15:58064164:SG, chr15:58065219:IG
neuroepithelial stem cell	CL_0002259				chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
neuronal stem cell	CL_0000047				chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
neutrophil	CL_0000775				chr15:58065219:IG
non-pigmented ciliary epithelial cell	CL_0002304			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14910656:SG	
omental fat pad	UBERON_0010414				chr15:58065219:IG
ovary	UBERON_0000992			chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064657:SG, chr15:58065219:IG
pancreas	UBERON_0001264			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	chr15:57923529:SG
peripheral blood mononuclear cell	CL_2000001				chr15:58065219:IG
Peyers patch	UBERON_0001211				chr15:58040343:SG, chr15:58040385:SG
placenta	UBERON_0001987			chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG, chr12:14885854:SG	chr15:58064657:SG, chr15:58065219:IG
podocyte	CL_0000653			chr12:14836364:SG	
posterior cingulate gyrus	UBERON_0002740	chr4:87863666:SG			
prostate gland	UBERON_0002367			chr12:14883768:SG, chr12:14885854:SG	chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
psoas muscle	UBERON_0008450			chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14839301:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
pulmonary artery endothelial cell	CL_1001568			chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	chr15:57923529:SG
radial glial cell	CL_0000681				chr15:58065219:IG
rectal smooth muscle tissue	UBERON_0018112			chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	

renal cortex interstitium	UBERON_0005270		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
renal cortical epithelial cell	CL_0002584		chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG	
renal pelvis	UBERON_0001224		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
retina	UBERON_0000966			chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
retinal pigment epithelial cell	CL_0002586		chr12:14836364:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14885854:SG	
right atrium auricular region	UBERON_0006631		chr12:14885854:SG	
right cardiac atrium	UBERON_0002078		chr12:14836364:SG, chr12:14839301:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
right forelimb	UBERON_8300001		chr12:14883768:SG, chr12:14885854:SG	chr15:58065219:IG
right hindlimb	UBERON_8300003		chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
right kidney	UBERON_0004539		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
right lobe of liver	UBERON_0001114			chr15:57923529:SG
right lung	UBERON_0002167		chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
right renal cortex interstitium	UBERON_0018118		chr12:14854918:IG, chr12:14883768:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
right renal pelvis	UBERON_0018116		chr12:14854918:IG, chr12:14883768:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
sciatic nerve	UBERON_0001322		chr12:14885854:SG	
sigmoid colon	UBERON_0001159		chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
skeletal muscle myoblast	CL_0000515		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14901082:SG	chr15:57923529:SG
skeletal muscle of trunk	UBERON_0001774		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
skeletal muscle tissue	UBERON_0001134		chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
skin epidermis	UBERON_0001003		chr12:14851053:SG, chr12:14851097:IG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG, chr12:14910656:SG	chr15:58065219:IG
skin of body	UBERON_0002097		chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG	chr15:57923529:SG, chr15:58063976:IG
small intestine	UBERON_0002108	chr4:87868563:SG, chr4:87868643:SG	chr12:14836364:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58040343:SG, chr15:58040385:SG, chr15:58064657:SG, chr15:58065219:IG
smooth muscle cell	CL_0000192		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	chr15:58064657:SG, chr15:58065219:IG
smooth muscle cell of the brain vasculature	CL_0002590		chr12:14836364:SG	chr15:57923529:SG
spinal cord	UBERON_0002240		chr12:14834162:SG, chr12:14834298:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
spleen	UBERON_0002106		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14847226:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
stomach	UBERON_0000945	chr4:87885460:SG	chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58040343:SG, chr15:58040385:SG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
stomach smooth muscle	UBERON_0004222		chr12:14883768:SG, chr12:14885854:SG	chr15:58065219:IG
stromal cell of bone marrow	CL_0010001		chr12:14836364:SG, chr12:14854918:IG, chr12:14885854:SG	chr15:57923529:SG
subcutaneous abdominal adipose tissue	UBERON_0014455		chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
substantia nigra	UBERON_0002038		chr12:14885854:SG	
superior temporal gyrus	UBERON_0002769		chr12:14883768:SG	
suppressor macrophage	CL_0000862		chr12:14836364:SG	chr15:58065219:IG
suprapubic skin	UBERON_0036149		chr12:14847029:SG, chr12:14847226:SG, chr12:14851053:SG, chr12:14851097:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG, chr12:14910656:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
testis	UBERON_0000473		chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
T-helper 1 cell	CL_0000545		chr12:14910656:SG	
T-helper 17 cell	CL_0000899			chr15:58065219:IG
T-helper 2 cell	CL_0000546		chr12:14910656:SG	
thoracic aorta	UBERON_0001515		chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58065219:IG
thymus	UBERON_0002370			chr15:58064657:SG, chr15:58065219:IG
thyroid gland	UBERON_0002046		chr12:14847029:SG, chr12:14847226:SG, chr12:14851053:SG, chr12:14851097:IG, chr12:14854918:IG, chr12:14885854:SG	chr15:57923529:SG
tibial artery	UBERON_0007610		chr12:14885854:SG	
tibial nerve	UBERON_0001323		chr12:14836364:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG
tongue	UBERON_0001723		chr12:14883768:SG, chr12:14885854:SG	chr15:57923529:SG, chr15:58064657:SG, chr15:58065219:IG
transverse colon	UBERON_0001157		chr12:14885854:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG	
trophoblast	UBERON_0000088	chr4:87868563:SG, chr4:87868643:SG, chr4:87885460:SG	chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG, chr12:14910656:SG, chr12:14911149:IG, chr12:14911328:SG, chr12:14911429:SG, chr12:14836364:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG	
trophoblast cell	CL_0000351		chr12:14834162:SG, chr12:14834298:SG, chr12:14836364:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG	chr15:57923529:SG
umbilical cord	UBERON_0002331		chr12:14885854:SG	chr15:58065219:IG
upper lobe of left lung	UBERON_0008952		chr12:14885854:SG	
ureter	UBERON_0000056		chr12:14847029:SG, chr12:14847226:SG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
urinary bladder	UBERON_0001255	chr4:87885460:SG	chr12:14847029:SG, chr12:14847226:SG, chr12:14854918:IG, chr12:14883768:SG, chr12:14885854:SG, chr12:14901082:SG	chr15:57923529:SG, chr15:58063976:IG, chr15:58064164:SG, chr15:58064657:SG, chr15:58065219:IG
uterus	UBERON_0000995		chr12:14885854:SG	
vagina	UBERON_0000996			

The variants are shown by their position in Build38, with SG ending for SNPs and IG for indels

Supplementary Table 6. Co-localisation of EHOA variants and expression of genes at the EHOA loci (eQTL)

EHOA variants	chr:pos(hg38)	EA / OA	Freq% EA	OR	Gene	Tissue	eQTL variant	r^2	EA / OA	Freq% EA	Effect	*P value*	Source	# individuals/tissue	COLOC PP3	COLOC PP4
rs17013495	chr4:87885460	T/C	59.6	1.4	SPP1	Spleen	rs4693198	0.91	C/T	59.6	-0.48	1.1E-09	GTEx v8	227	0.12	0.88
					"	Esophagus – Mucosa	rs4693897	0.91	G/T	59.5	-0.32	1.4E-08	GTEx v8	497	1.00	0.00
					"	Whole blood	rs12644436	0.91	G/A	59.4	-0.18	9.0E-09	GTEx v8	670	1.00	0.00
rs1800801	chr12:14885854	T/C	37.2	1.37	MGP	Lung	rs11614330	0.98	T/C	36.9	-0.19	5.9E-13	GTEx v8	515	0.09	0.91
					"	Thyroid	rs4581512	0.95	T/G	37.4	-0.17	3.1E-08	GTEx v8	574	0.05	0.95
					"	Adipose	rs9668569	0.91	T/C	37.2	-0.53	2.8E-22	deCODE	770	0.08	0.92
					"	Blood*	rs11056199	0.89	C/A	39.9	0.40	6.9E-226	deCODE	17,940	1.00	0.00
rs11631127	chr15:57977811	C/G	57.6	1.46	ALDH1A2	Cultured fibroblasts	rs3742961	0.93	C/T	60.2	-0.30	9.0E-11	GTEx v8	483	0.14	0.86

Data is shown for datasets in GTEx and deCODE genetics. For each variant the gene whose expression is correlated with the erosive variants is shown (Gene), the tissue (Tissue), the top expression variant (eQTL variant), the correlation between the top expression variant and the erosive variant (r2), the effect allele (EA) and the other allele (OA) of the variants, the frequency of their effect allele (Freq% EA), the effect on transcription in standard deviation (Effect), the P value of the expression correlation, the source of data (Source), and the number of individuals in each analysis (# individuals/tissue). The position of the erosive variants are shown in build 38, and the OR af the association with erosive osteoarthritis. PP3 is the posterior probability for two independent signals, and PP4 is the posterior probability for one shared signals using COLOC (Giambartolomei et al, PLoS genetics. 2014;10(5):e1004383)

* The expression of MGP in blood is very low but the direction of effect is consistent with that reported by den Hollander, W. et al, 2017.

Supplementary Table 7. Co-localisation of the EHOA associated variants and levels of proteins in plasma (cis-pQTL)

Erosive variants	chr:pos(hg38)	EA / OA	Freq% EA	OR	Gene	Protein	pQTL variant	r^2	EA / OA	Freq% EA	Effect	P value	COLOC PP3	COLOC PP4	Comment
rs17013495	chr4:87885460	T/C	59.6	1.396	SPP1	Osteopontin	rs990862	0.80	T/C	65.9	-0.063	1.8E-13	1.00	0.00	Five independent cis-signals for SPP1, and 2 independent trans signals. Rs990862 explains 5% of the variance explained by the pQTLs
rs1800801	chr12:14885854	T/C	37.2	1.37	MGP	Matrix Gla Protein	rs7294636	0.99	A/G	37.4	-0.250	8.3E-111	0.12	0.88	Two independent cis-signals for the MGP protein (in opposite directions), and 6 trans signals. Rs12307494 explains 72% of the variance explained by the pQTLs.

Data is based on proteins measured in plasma from 35,339 in Iceland (deCODE genetics) using the Somalogic platform. The top variant that correlates with the levels of the protein (Protein) and its encoding gene (Gene) in plasma (pQTL variant) is shown, and the correlation between the top pQTL variant and the erosive variant (r2), the effect allele (EA) and the other allele (OA) of the variants, the frequency of their effect allele (Freq% EA), the effect on protein levels in standard deviation (Effect), and the P value of the protein level-variant correlation. The position of the erosive variants are shown in build 38 (chr:pos(hg38)), and the odds ratio (OR) af the association with erosive osteoarthritis. PP3 is the posterior probability for two independent signals, and PP4 is the posterior probability for one shared signals using COLOC (Giambartolomei et al, PLoS genetics. 2014;10(5):e1004383)

Supplementary Table 8. Lead sequence variants for two of the four EHOA signals, or their correlated variants, reside within enhancer elements that are predicted to affect nearby genes in different tissue/cell types based on EpiMap (http://compbio.mit.edu/epimap/).

Tissue / cell type	rs1800801 (chr12:14885854)	rs11631127 (chr15:57977811)
ACUTE_LYMPHOBLASTIC_LEUKEMIA	MGP (chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14901082:SG)	
ACUTE_PROMYELOCYTIC_LEUKEMIA	MGP (chr12:14854918:IG)	
ADENOID_CYSTIC_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)	
ADIPOCYTE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)	
ADIPOCYTE_FROM_MSC	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)	
ADIPOSE_TISSUE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG, chr12:14901082:SG)	
ADRENAL_GLAND	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), WBP11 (chr12:14847029:SG, chr12:14894016:SG)	ALDH1A2 (chr15:58061348:SG)
AMMONS_HORN	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
AMNION	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), WBP11 (chr12:14844512:SG)	
AMNION_EPITHELIAL_CELL	ART4 (chr12:14835521:SG)	
AMNION_STEM_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
AMNIOTIC_FLUID_FROM_MSC	MGP (chr12:14854918:IG)	
ANGULAR_GYRUS	ART4 (chr12:14835521:SG), MGP (chr12:14894016:SG)	
AORTA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG, chr12:14901082:SG)	
AORTA_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG)	
ARM_MUSCLE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), WBP11 (chr12:14894016:SG)	
ASCENDING_AORTA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG), WBP11 (chr12:14844512:SG, chr12:14890950:SG, chr12:14890963:SG), MGP (chr12:14844512:SG, chr12:14847029:SG, chr12:14854918:IG, chr12:14878220:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)	
ASTROCYTE	ART4 (chr12:14835521:SG, chr12:14847029:SG), MGP (chr12:14847029:SG)	
ASTROCYTE_HIPPOCAMPUS	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG)	
ASTROCYTE_SPINAL_CORD	MGP (chr12:14854918:IG)	
B_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG)	ALDH1A2 (chr15:58061348:SG)
B_CELL_LYMPHOMA	ART4 (chr12:14835521:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14854918:IG, chr12:14878220:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG)	
BACK_MUSCLE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), WBP11 (chr12:14894016:SG)	
BODY_OF_PANCREAS	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), WBP11 (chr12:14847029:SG, chr12:14894016:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)	
BONE_ARM	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
BONE_FEMUR	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
BONE_LEG	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
BONE_MARROW_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
BONE_MARROW_STROMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
BONE_MARROW_STROMAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)	
BRAIN	MGP (chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)	
BRAIN_MICROVASCULAR_ENDOTHELIAL_CELL	MGP (chr12:14854918:IG)	
BRAIN_VASCULATURE_SMOOTH_MUSCLE_CELL	MGP (chr12:14894016:SG)	
BREAST_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), GUCY2C (chr12:14911328:SG)	
BREAST_EPITHELIUM	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG), H2AJ (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14894016:SG)	
BREAST_FIBROBLAST	ART4 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)	
BRONCHIAL_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
BURKITT_LYMPHOMA	MGP (chr12:14854918:IG), WBP11 (chr12:14854918:IG)	
CARDIAC_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)	
CARDIAC_MUSCLE_DERIV	ART4 (chr12:14835521:SG)	
CARDIAC_MYOCYTE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG)	
CAUDATE_NUCLEUS	ART4 (chr12:14835521:SG), MGP (chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)	
CD34_CMP	ART4 (chr12:14835521:SG), MGP (chr12:14854918:IG), GUCY2C (chr12:14911328:SG)	
CD4_T_CELL	ERP27 (chr12:14911328:SG)	ALDH1A2 (chr15:58061348:SG)
CD8_T_CELL		CGNL1 (chr15:58061348:SG), ALDH1A2 (chr15:58061348:SG), GCOM1 (chr15:58061348:SG), LIPC (chr15:58061348:SG)
CEREBELLAR_CORTEX	MGP (chr12:14897475:SG, chr12:14897803:SG)	
CEREBELLUM	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
CERVIX_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	

CHORION	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14854918:IG, chr12:14901082:SG), ERP27 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), H2AJ (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14847029:SG)
CHORIONIC_VILLUS	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), ERP27 (chr12:14840920:SG)
CHOROID_PLEXUS_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
CINGULATE_GYRUS	ART4 (chr12:14835521:SG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)
COLON_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
COLON_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
COLON_MUCOSA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14894016:SG), MGP (chr12:14894016:SG)
COLON_MUSCLE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
COLORECTAL_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
CONJUNCTIVA_FIBROBLAST	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG)
CORONARY_ARTERY	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), WBP11 (chr12:14844512:SG), MGP (chr12:14844512:SG, chr12:14847029:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG)
DERMIS_BLOOD_VESSEL_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14894016:SG), WBP11 (chr12:14894016:SG), GUCY2C (chr12:14911328:SG)
DERMIS_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14901082:SG)
DERMIS_LYMPHATIC_VESSEL_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
DESMOPLASTIC_MEDULLOBLASTOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
DUODENUM_MUCOSA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)
DUODENUM_MUSCLE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)
EMBRYONIC_FACIAL_PROMINENCE	MGP (chr12:14854918:IG, chr12:14894016:SG)
ENDOCRINE_PANCREAS	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)
ENDODERMAL_DERIV	MGP (chr12:14894016:SG)
ENDOMETRIAL_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), WBP11 (chr12:14844512:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)
EPIDERMAL_MELANOCYTE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
ESC	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14854918:IG)
ESOPHAGUS	WBP11 (chr12:14894016:SG), MGP (chr12:14894016:SG)
ESOPHAGUS_MUSCULARIS_MUCOSA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG, chr12:14901082:SG)
ESOPHAGUS_SQUAMOUS_EPITHELIUM	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG)
EYE_RETINOBLASTOMA	ART4 (chr12:14835521:SG)
FIBROSARCOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
FORESKIN_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
FORESKIN_KERATINOCYTE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
FORESKIN_MELANOCYTE	ART4 (chr12:14835521:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14854918:IG, chr12:14894016:SG)
FRONTAL_CORTEX	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
GASTROCNEMIUS_MEDIALIS	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG)
GASTROESOPHAGEAL_SPHINCTER	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG, chr12:14901082:SG)
GERMINAL_CENTER	MGP (chr12:14854918:IG)
GERMINAL_MATRIX	ART4 (chr12:14835521:SG)
GINGIVAL_FIBROBLAST	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
GLIOBLASTOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
GLOBUS_PALLIDUS	MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)
GLOMERULUS_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG)
GLOMERULUS_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
GLOMERULUS_VISCERAL_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
HEART	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14878220:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG)
HEART_LEFT_ATRIUM	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14844512:SG), MGP (chr12:14878220:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)
HEART_LEFT_VENTRICLE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG, chr12:14901082:SG)
HEART_RIGHT_ATRIUM	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG), WBP11 (chr12:14844512:SG), MGP (chr12:14847029:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG, chr12:14901082:SG)

HEART_RIGHT_VENTRICLE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG, chr12:14901082:SG)	
HEPATIC_STELLATE_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
HEPATOCELLULAR_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14847029:SG)	
HEPATOCYTE_DERIV	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG)	
HIPPOCAMPUS	ART4 (chr12:14835521:SG), MGP (chr12:14894016:SG)	
INFERIOR_PARIETAL_CORTEX	MGP (chr12:14894016:SG)	
iPSC	MGP (chr12:14854918:IG)	
IRIS_PIGMENT_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)	
ISLET_PRECURSOR_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
KERATINOCYTE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14897475:SG, chr12:14897803:SG)	
KIDNEY	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG)	
KIDNEY_CAPILLARY_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
KIDNEY_CELL	WBP11 (chr12:14835521:SG), ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
KIDNEY_CLEAR_CELL_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
KIDNEY_EPITHELIAL_CELL	ART4 (chr12:14835521:SG)	
KIDNEY_RHABOID_TUMOR	MGP (chr12:14897475:SG, chr12:14897803:SG)	
LARGE_CELL_LUNG_CANCER	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
LARGE_INTESTINE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG), H2AJ (chr12:14836364:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG, chr12:14894016:SG), WBP11 (chr12:14844512:SG, chr12:14894016:SG)	
LEG_MUSCLE	ART4 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), WBP11 (chr12:14894016:SG)	
LIMB_EMBRYO	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), WBP11 (chr12:14894016:SG)	
LIVER	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), H2AJ (chr12:14836364:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG, chr12:14894016:SG, chr12:14901082:SG), GUCY2C (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14844512:SG)	
LUNG	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), WBP11 (chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG)	
LUNG_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
LUNG_EPITHELIAL_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), ERP27 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14844512:SG, chr12:14847029:SG)	CGNL1 (chr15:57923529:SG), ALDH1A2 (chr15:57923529:SG), RNF111 (chr15:57923529:SG)
LUNG_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG)	
LUNG_MICROVASCULAR_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
LYMPHOBLASTOID_CELL_LINE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14854918:IG)	
LYMPHOCYTE	MGP (chr12:14854918:IG)	
MAMMARY_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
MAMMARY_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14901082:SG)	
MAMMARY_GLAND_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840920:SG, chr12:14854918:IG, chr12:14901082:SG)	
MAMMARY_GLAND_DUCTAL_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14840920:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14901082:SG)	
MAMMARY_LUMINAL_EPITHELIAL_CELL	ART4 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)	
MAMMARY_MYOEPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), GUCY2C (chr12:14911328:SG)	
MAMMARY_STEM_CELL	ART4 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)	
MEDULLA_OBLONGATA	MGP (chr12:14894016:SG)	
MEDULLOBLASTOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), ERP27 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
MELANOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG), GUCY2C (chr12:14911328:SG)	
MESENCHYMAL_STEM_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), H2AJ (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)	
MESODERMAL_DERIV	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG)	
MIDBRAIN	MGP (chr12:14894016:SG)	
MIDDLE_FRONTAL_AREA	MGP (chr12:14894016:SG)	
MIDDLE_FRONTAL_GYRUS	MGP (chr12:14894016:SG)	
MPP	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), ATF7IP (chr12:14836364:SG), WBP11 (chr12:14844512:SG, chr12:14901082:SG), MGP (chr12:14844512:SG, chr12:14847029:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)	
MUSCLE_EWING_SARCOMA	MGP (chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)	
MYELOGENOUS_LEUKEMIA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
MYELOMA	ART4 (chr12:14851053:SG, chr12:14851097:IG)	

MYOCYTE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
NEURAL_PROGENITOR_DERIV	ART4 (chr12:14835521:SG), MGP (chr12:14854918:IG, chr12:14894016:SG)
NEUROBLASTOMA	ART4 (chr12:14835521:SG)
NEUROEPITHELIOMA	MGP (chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)
NEUROGLIOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
NEURON_DERIV	ART4 (chr12:14835521:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14901082:SG), WBP11 (chr12:14901082:SG)
NEUROSPHERE	ART4 (chr12:14835521:SG)
NON-PIGMENTED_CILIARY_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
OCCIPITAL_LOBE	MGP (chr12:14894016:SG)
OLFACTORY_NEUROSPHERE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)
OMENTAL_FAT_PAD	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)
OSTEOBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
OSTEOSARCOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14897475:SG, chr12:14897803:SG)
OVARY	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG), STRAP (chr12:14890950:SG, chr12:14890963:SG), WBP11 (chr12:14894016:SG)
PANCREAS	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14901082:SG)
PANCREATIC_DUCT_EPITHELIAL_CELL	WBP11 (chr12:14835521:SG), ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
PARATHYROID_ADENOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)
PERICYTE	MGP (chr12:14854918:IG)
PERIDONTAL_LIGAMENT_FIBROBLAST	MGP (chr12:14854918:IG)
PEYERS_PATCH	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG, chr12:14901082:SG)
PLACENTA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14844512:SG, chr12:14894016:SG, chr12:14901082:SG), WBP11 (chr12:14901082:SG)
PLASMA_CELL_MYELOMA	ART4 (chr12:14851053:SG, chr12:14851097:IG)
PONS	MGP (chr12:14894016:SG)
PROSTATE_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
PROSTATE_EPITHELIAL_CARCINOMA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), SMCO3 (chr12:14840920:SG)
PROSTATE_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
PROSTATE_GLAND	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)
PROXIMAL_TUBULE_EPITHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
PSOAS_MUSCLE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG, chr12:14901082:SG)
PULMONARY_ARTERY_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
PULMONARY_ARTERY_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
PUTAMEN	MGP (chr12:14894016:SG)
RECTUM_MUCOSA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG), GUCY2C (chr12:14911328:SG)
RECTUM_MUSCLE	MGP (chr12:14894016:SG, chr12:14901082:SG)
RENAL_CELL_ADENOCARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
RENAL_CELL_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
RENAL_CORTEX_INTERSTITIUM	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
RENAL_CORTICAL_EPITHELIAL_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), GUCY2C (chr12:14911328:SG)
RENAL_PELVIS	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
SIGMOID_COLON	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG), GUCY2C (chr12:14911328:SG)
SKELETAL_MUSCLE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)
SKELETAL_MUSCLE_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
SKELETAL_MUSCLE_MYOBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
SKELETAL_MUSCLE_SATELLITE_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG)
SKIN_FIBROBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), WBP11 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14897475:SG, chr12:14897803:SG)
SKIN_LEG	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)
SKIN_OF_BODY	MGP (chr12:14847029:SG, chr12:14894016:SG)
SMALL_INTESTINE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)
SMOOTH_MUSCLE_DERIV	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14899824:SG, chr12:14899901:SG, chr12:14900018:SG)
SPINAL_CORD	ART4 (chr12:14835521:SG), MGP (chr12:14854918:IG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)
SPLEEN	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG, chr12:14894016:SG), ERP27 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), H2AJ (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), WBP11 (chr12:14844512:SG)
SQUAMOUS_CELL_CARCINOMA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)
STOMACH	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), WBP11 (chr12:14894016:SG)

STOMACH_MUSCLE	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)	
SUBSTANTIA_NIGRA	ART4 (chr12:14835521:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG)	
SUPERIOR_TEMPORAL_GYRUS	MGP (chr12:14894016:SG)	
T17_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
TEMPORAL_LOBE	ART4 (chr12:14835521:SG), MGP (chr12:14894016:SG)	
TESTIS	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14847029:SG, chr12:14894016:SG), WBP11 (chr12:14894016:SG)	
THORACIC_AORTA	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14844512:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG, chr12:14901082:SG)	
THYROID_GLAND	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), H2AJ (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14844512:SG, chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG)	
TIBIAL_ARTERY	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG)	
TIBIAL_NERVE	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG), WBP11 (chr12:14901082:SG)	
TONGUE	MGP (chr12:14854918:IG, chr12:14894016:SG)	
TRANSVERSE_COLON	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG), WBP11 (chr12:14894016:SG)	
TROPHOBLAST	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14854918:IG, chr12:14901082:SG)	
TROPHOBLAST_DERIV	ART4 (chr12:14835521:SG, chr12:14851053:SG, chr12:14851097:IG)	
TRUNK_MUSCLE	MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG), ART4 (chr12:14847029:SG)	
TUBULE_CELL	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
UMBILICAL_CORD	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG), MGP (chr12:14894016:SG, chr12:14897475:SG, chr12:14897803:SG)	
UMBILICAL_VEIN_ENDOTHELIAL_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14854918:IG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14894016:SG), WBP11 (chr12:14847029:SG, chr12:14894016:SG)	
URINARY_BLADDER	ART4 (chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14901082:SG), WBP11 (chr12:14894016:SG)	
UROTHELIUM_CELL	ART4 (chr12:14835521:SG, chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG)	
UTERUS	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14847029:SG), MGP (chr12:14847029:SG, chr12:14894016:SG, chr12:14901082:SG)	ALDH1A2 (chr15:58061348:SG)
VAGINA	ART4 (chr12:14840136:SG, chr12:14840214:SG, chr12:14840505:SG, chr12:14840674:SG, chr12:14840920:SG, chr12:14851053:SG, chr12:14851097:IG), MGP (chr12:14847029:SG, chr12:14879684:SG, chr12:14879827:SG, chr12:14879925:IG, chr12:14879926:SG, chr12:14890950:SG, chr12:14890963:SG, chr12:14894016:SG, chr12:14901082:SG)	
VILLOUS_MESENCHYME_FIBROBLAST	MGP (chr12:14854918:IG)	

The variants are shown by their position in Build38, with SG ending for SNPs and IG for indels

Supplementary Table 9. Enrichment-Analysis: EHOA association signals are nominally enriched within regulatory regions specific for vascular/endothelial cell types.

Annotation	Number of overlapping GWAS loci	*P* -value	Expected intersection (95%CI)	Observed intersection (95%CI)	Enrichment (95%CI)
Vascular-endothelial	4	0.011	0.35 (0-0.75)	1 (1.00-1.00)	2.84 (2.84-2.84)
Pulmonary development	3	0.06	0.31 (0-0.75)	0.75 (0.25-1)	2.44 (0.813-3.25)
Musculoskeletal	3	0.27	0.50 (0-1)	0.75 (0.25-1)	1.52 (0.505-2.02)
Digestive	3	0.29	0.51 (0.25-1)	0.75 (0.369-1)	1.47 (0.723-1.96)
Myeloid-erythroid	3	0.41	0.57 (0-1)	0.75 (0.369-1)	1.32 (0.65-1.76)
StromalA	1	0.59	0.21 (0-0.5)	0.25 (0-0.75)	1.21 (0-3.61)
Renal-cancer	2	0.69	0.47 (0-0.75)	0.5 (0-1)	1.06 (0-2.12)
Organ development-renal	2	0.72	0.50 (0-1)	0.5 (0-1)	0.99 (0-1.99)
StromalB	3	0.76	0.73 (0.25-1)	0.75 (0.25-1)	1.03 (0.342-1.37)
Lymphoid	2	0.52	0.60 (0.25-1)	0.5 (0-1)	0.83 (0-1.66)
Primitive-embryonic	3	0.55	0.82 (0.5-1)	0.75 (0.25-1)	0.91 (0.304-1.22)
Placental-trophoblast	2	0.48	0.63 (0.25-1)	0.5 (0-1)	0.80 (0-1.6)
Cardiac	1	0.51	0.38 (0-0.75)	0.25 (0-0.75)	0.66 (0-1.99)
Cancer-epithelial	1	0.47	0.43 (0-1)	0.25 (0-0.75)	0.58 (0-1.75)
Neural	2	0.30	0.71 (0.25-1)	0.5 (0-1)	0.70 (0-1.41)
Tissue-invariant	0	0.034	0.52 (0-1)	0 (0-0)	0 (0-0)

Supplementary Table 10. Association of EHOA variants and correlated GWS variants in public datasets

Locus	Variant	EHOA / Correlated GWS	EA	NEA	LD (r2)	P-value	Beta	Odds Ratio	Trait	PMID	N Cases	N Overall	Study ID
4q22.1-MEPE	rs17013495	EHOA	T	C		8.5E-21	0.018		Urate			411,640	UKBio_deCODE
4q22.1-MEPE	rs17013495	EHOA	T	C		1.7E-07		1.06	Gout		16,353	431,047	UKBio_deCODE
4q22.1-MEPE	rs17013495	EHOA	T	C		1.8E-07		0.93	Plantar_fascial_fibromatosis		12,959	431,047	UKBio_deCODE
4q22.1-MEPE	rs17013495	EHOA	T	C		4.8E-07	0.038		Pelvis_DXA_BMD			35,596	UKBio_deCODE
4q22.1-MEPE	rs17013495	EHOA	T	C		5.2E-07	-0.013		Alkaline phosphatase			412,141	UKBio_deCODE
4q22.1-MEPE	rs17013495	EHOA	T	C		5.3E-07	-0.090		Hand grip strength (left)			359,704	NEALE2_46_raw
4q22.1-MEPE	rs17013495	EHOA	T	C		8.1E-07	0.037		Trunk_DXA_BMD			35,596	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		5.0E-35	-0.029		Mean_grip_strength			427,745	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		8.6E-33	-0.219		Hand grip strength (left)			359,704	NEALE2_46_raw
12p12.3-MGP	rs1800801	EHOA	T	C		8.2E-27	-0.197		Hand grip strength (right)			359,729	NEALE2_47_raw
12p12.3-MGP	rs1800801	EHOA	T	C		1.1E-14	-0.015		Heel bone mineral density	PMID:30598549		426,824	GCST006979
12p12.3-MGP	rs1800801	EHOA	T	C		6.4E-11		1.05	Any fracture over 40 years		55,982	431,047	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		2.2E-10	-0.016		Speed_of_sound_through_heel_SOS			399,133	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		1.4E-09	-0.015		Heel bone mineral density			398,823	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		2.9E-09		1.03	Any fracture		103,590	431,047	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		4.5E-09	-0.015		Heel_bone_ultrasound_T_score			401,039	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		1.5E-08		1.04	Low hand grip strength (60 years and older) (EWGSOP)	PMID:33510174	48,596	256,523	GCST90007526
12p12.3-MGP	rs1800801	EHOA	T	C		7.2E-08	-0.041		DXA_Arms_BMD			35,597	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		1.7E-07	-0.013		Heel_broadband_ultrasound_attenuation_BUA			398,131	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		1.9E-07	-0.010		Appendicular lean mass	PMID:33097823		450,243	GCST90000025
12p12.3-MGP	rs1800801	EHOA	T	C		2.3E-07		1.04	Arthrosis_unspecified		46,615	431,047	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		4.8E-07		1.04	Fractured/broken bones in last 5 years		34,780	359,241	NEALE2_2463
12p12.3-MGP	rs1800801	EHOA	T	C		8.9E-07	-0.012		Creatinine			411,927	UKBio_deCODE
12p12.3-MGP	rs1800801	EHOA	T	C		9.3E-07		1.04	Fracture low trauma		35,439	431,047	UKBio_deCODE
12p12.3-MGP	rs3887182*	Correlated GWS	A	G	0.92	3.0E-213	0.721		Blood protein levels [ART4, 6576_1_3]	PMID:30072576		3,200	GCST006585_131
12p12.3-MGP	rs67482087*	Correlated GWS	G	T	0.98	8.0E-182	0.690		Blood protein levels [ART4, 6576_1_3]	PMID:30072576		3,200	GCST006585_131
12p12.3-MGP	rs2287226	Correlated GWS	G	A	0.91	5.3E-33	-0.220		Hand grip strength (left)			359,704	NEALE2_46_raw
12p12.3-MGP	rs11056198	Correlated GWS	A	G	0.91	7.7E-28	-0.201		Hand grip strength (right)			359,729	NEALE2_47_raw
12p12.3-MGP	rs2430689	Correlated GWS	G	C	0.87	3.0E-16	-0.016		Heel bone mineral density	PMID:30598549		426,824	GCST006979
12p12.3-MGP	rs67482087	Correlated GWS	G	T	0.98	2.0E-15	-0.199		Blood protein levels [MGP, 6520_87_3]	PMID:30072576		3,200	GCST006585_1144
12p12.3-MGP	rs4764133	Correlated GWS	T	C	0.97	2.0E-15	0.830		Osteoarthritis of the hand	PMID:28855172		12,754	GCST009596
12p12.3-MGP	rs2430690	Correlated GWS	C	T	0.84	3.0E-15			Heel bone mineral density	PMID:30595370		446,000	GCST007066
12p12.3-MGP	rs2430689	Correlated GWS	G	C	0.87	5.0E-14			Heel bone mineral density	PMID:30048462		394,929	GCST006433
12p12.3-MGP	rs4764133	Correlated GWS	T	C	0.97	5.0E-14	0.650		Finger osteoarthritis severity (hand Klsum)	PMID:33055079		2,994	GCST90010717
12p12.3-MGP	rs2287226	Correlated GWS	G	A	0.91	1.0E-12	-0.002		Hand grip strength	PMID:29691431		334,825	GCST005830
12p12.3-MGP	rs3887182	Correlated GWS	A	G	0.92	2.0E-12	-0.172		Blood protein levels [MGP, 6520_87_3]	PMID:30072576		3,200	GCST006585_1144
12p12.3-MGP	rs11614333	Correlated GWS	T	C	0.91	2.0E-12	-0.160		Hand grip strength	PMID:29313844		195,180	GCST005235
12p12.3-MGP	rs4764133	Correlated GWS	T	C	0.97	3.0E-12	0.810		Hand osteoarthritis severity (hand Klsum)	PMID:33055079		6,032	GCST90010716
12p12.3-MGP	rs10846071	Correlated GWS	T	C	0.92	4.0E-12	-0.002		Hand grip strength	PMID:29691431		334,825	GCST005830
12p12.3-MGP	rs10630224	Correlated GWS	TGC	T	0.76	1.4E-10		1.06	Low hand grip strength (60 years and older) (EWGSOP)	PMID:33510174		256,523	GCST90007526
12p12.3-MGP	rs10630224	Correlated GWS	TGC	T	0.76	3.2E-09		1.07	Low hand grip strength (60 years and older) (EWGSOP)	PMID:33510174		135,468	GCST90007527
12p12.3-MGP	rs11419786	Correlated GWS	TG	T	0.63	1.3E-08		1.05	Fractured/broken bones in last 5 years			359,241	NEALE2_2463
12p12.3-MGP	rs11056244	Correlated GWS	A	T	0.73	3.7E-08	0.524		Impedance of arm (left)			354,807	NEALE2_23110_raw
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		1.2E-07		1.17	Polyarthrosis		2,610	149,831	FINNGEN_R5_M13_ARTHROSIS_POLY
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		1.5E-07	-0.094		Hand grip strength (right)			359,729	NEALE2_47_raw
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		1.9E-07		1.05	Low hand grip strength (60 years and older) (EWGSOP)	PMID:33510174	34,589	135,468	GCST90007527
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		2.1E-07		0.97	Knee pain | pain type(s) experienced in last month		76,628	360,391	NEALE2_6159_7
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		2.2E-07		0.96	Knee_joint_operation		28,317	431,047	UKBio_deCODE
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		2.3E-07		1.04	Low hand grip strength (60 years and older) (EWGSOP)	PMID:33510174	48,596	256,523	GCST90007526
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		3.8E-07		0.96	Knee osteoarthritis		37,270	430,938	UKBio_deCODE
15q21.3-ALDH1A2	rs11631127	EHOA	C	G		3.3E-07	-0.091		Hand grip strength (left)			359,704	NEALE2_46_raw

15q21.3-ALDH1A2	rs11631127	EHOA	C	G		4.7E-07	0.95	Knee osteoarthritis	PMID:30664745	24,955	403,124	GCST007090
15q21.3-ALDH1A2	rs4775006	Correlated GWS	A	C	0.74	3.0E-22		Brain region volumes [X4th ventricle]	PMID:31676860		19,629	GCST009518_4
15q21.3-ALDH1A2	rs4775006	Correlated GWS	A	C	0.74	1.0E-18		Subcortical volume (min-P)	PMID:32665545		26,502	GCST010698
15q21.3-ALDH1A2	rs4775006	Correlated GWS	A	C	0.74	2.0E-18		Brain morphology (min-P)	PMID:32665545		26,502	GCST010699
15q21.3-ALDH1A2	rs3204689	Correlated GWS	C	G	0.65	1.0E-11		Osteoarthritis (hand, severe)	PMID:24728293		78,162	GCST002410
15q21.3-ALDH1A2	rs66725070	Correlated GWS	G	GACAT	0.73	3.0E-10	0.87	Barrett's esophagus	PMID:27527254		23,326	GCST003738
15q21.3-ALDH1A2	rs4775006	Correlated GWS	A	C	0.74	8.4E-10	1.06	Knee osteoarthritis	PMID:30664745		403,124	GCST007090
15q21.3-ALDH1A2	rs8033270	Correlated GWS	C	G	0.64	9.0E-10	0.84	Polyarhtrosis			149,831	FINNGEN_R5_M13_ARTHROSIS_POLY
15q21.3-ALDH1A2	rs4775006	Correlated GWS	A	C	0.74	7.1E-09	1.03	Knee pain | pain type(s) experienced in last month			360,391	NEALE2_6159_7

Association results assessed by UKBiobank associations at deCODE genetics, and by Open Targets Genetics (https://genetics.opentargets.org/) which summarizes association data for the variants in public datasets (UK Biobank, FinnGen, and GWAS Catalog). The site was accessed on Febuary, 23rd, 2022. The look-up results for the EHOA variants are shown directly, and for correlated variants ($r^2 > 0.60$) that have been reported to associate with a given trait at a GWS level in the Open Targets Genetics database. The effect allele, the other allele, r^2 with EHOA variant at the locus, P value and beta or odds ratio (OR) are shown for each trait, along with publication ID, number of cases and/or overal study sample, and the Study ID. Associations with P < 1e-6 are shown.

*We note that this association is most likely due to a missense variant in ART4 which changes the binding of the Somalogic probe to the plasma protein

Supplementary Table 11. Association of EHOA variants with bone density, grip strength and urate levels

				FN_BMD (N = 107,310)		LS_BMD (N = 106,228)		eBMD (N = 398,823)		Grip strength (N = 427,745)		Urate (N = 411,640)	
Variant	**Chr**	**EA**	**NEA**	**P value**	**Effect**	**P value**	**Effect**	**P value**	**Effect**	**P value**	**Effect**	**P value**	**Effect**
rs17013495	chr4	T	C	4.9E-04	0.015	1.6E-09	0.028	0.89	0	1.9E-05	-0.010	8.5E-21	0.018
rs11243284	chr6	C	T	0.082	-0.008	0.0035	-0.015	0.78	-0.001	2.7E-03	-0.007	0.76	0.001
rs1800801	chr12	T	C	1.4E-05	-0.019	8.9E-08	-0.025	1.4E-09	-0.015	5.0E-35	-0.029	0.036	-0.004
rs11631127	chr15	C	G	0.59	-0.002	8.3E-07	0.023	0.21	-0.003	9.8E-10	-0.014	0.95	0

Results for eBMD, grip strength and urate levels are from the UK Biobank resource, run at deCODE genetics. Results for FN (femoral neck) and LS (lumbar spine) BMD are derived from our unpublished meta-analysis of BMD in Iceland, UK Biobank, and the publicly available GEFOS consortium (Zheng et al, Nature, 2015).

Supplementary Table 12. Significant association of EHOA polygenic risk score with phenotypes in UK biobank

Phenotype	P value	Effect /OR	N cases	N controls	N overall	nR2
Grip strength (mean, age, sex, height adj.)	6.0E-41	-0.022			427,745	0.00048
Other arthrosis (ICD10:M19)	4.8E-29	1.05	73,440	357,607		0.00048
Any OA	2.1E-19	1.04	103,173	327,874		0.00029
Polyarthrosis (ICD10:M15)	4.9E-17	1.08	12,326	418,612		0.00072
Hand OA	4.7E-16	1.15	3,416	427,631		0.00175
Pain due to OA	7.5E-14	1.05	44,262	98,258		0.00053
Pain in hands in last three months	2.8E-13	1.11	5,766	64,039		0.00174
Heberden nodes with arthropathy	1.1E-12	1.30	758	428,428		0.00464
Finger OA	1.3E-13	1.29	834	428,352		0.00407
Other arthritis (ICD10:M13)	6.3E-10	1.04	33,303	397,744		0.00021
Operation of joint of finger (OPCS:Z83)	1.3E-09	1.10	4,289	426,758		0.00082

A PRS for EHOA was generated from the Icelandic, the Dutch, the US and Spanish EHOA datasets. The MHC region was excluded from the EHOA PRS. The results are shown from a scan of diverse phenotypes derived from the UK Biobank. Significance was set as $P < 1.0 \times 10^{-5}$, accounting for 5,000 main phenotypes. nR2 is the Nagelkerke's correlation coefficient.

Supplementary Table 13. Association of finger, hand, thumb, knee, hip, spine, and all OA GWS variants from the GO consortium in EHOA meta-analysis

							GO consortium results		EHOA_meta	
OA phenotype	Variant	EA	NEA	EA_freq%	GO_locus_number	Associated GWS OA phenotypes	OR	P	OR	P
FingerOA	rs7294636	A	G	37.3	21	finger	1.16	3.0E-16	1.36	6.8E-13
FingerOA	rs9396861	A	C	61.0	77	hand,finger	1.13	9.3E-11	1.23	3.2E-06
FingerOA	rs11588154	T	G	16.6	7	finger	0.83	6.1E-10	0.86	0.01
FingerOA	rs8031133	T	G	54.5	30	hand, finger, thumb, knee	1.11	1.1E-09	1.40	2.4E-14
FingerOA	rs11550348	A	G	11.0	45	hand,finger	0.84	6.2E-09	0.76	1.9E-04
HandOA	rs11071366	A	T	61.4	30	hand, finger, thumb, knee	0.90	4.9E-17	0.71	7.1E-15
HandOA	rs3993110	A	C	60.8	10	hand	1.09	3.8E-11	1.14	0.0028
HandOA	rs3771498	T	C	52.1	52	hand, thumb, hip, all	0.92	6.8E-11	0.86	2.8E-04
HandOA	rs8112559	C	G	88.6	45	hand,finger	1.13	7.3E-11	1.32	1.8E-04
HandOA	rs10062749	T	G	26.9	73	hand,thumb	1.08	2.0E-09	1.15	0.0029
HandOA	rs7748189	A	G	73.2	77	hand,finger	1.08	6.1E-09	1.24	1.2E-05
HandOA	rs1560080	A	G	82.5	71	hand	0.91	9.6E-09	0.84	0.0011
ThumbOA	rs4238326	T	C	60.7	30	hand, finger, thumb, knee	0.89	7.3E-12	0.71	7.4E-15
ThumbOA	rs2862851	T	C	46.5	52	hand, thumb, hip, all	1.11	3.2E-10	1.16	4.4E-04
ThumbOA	rs11588850	A	G	82.0	6	thumb	0.87	3.5E-10	1.06	0.34
ThumbOA	rs10062749	T	G	26.9	73	hand,thumb	1.11	1.3E-08	1.15	0.0029
SpineOA	rs201194999	T	C	30.1	69	all,spine	0.85	1.2E-08	0.57	0.27
KneeOA	rs143384	A	G	59.1	53	knee,all	1.07	1.0E-23	1.08	0.09
KneeOA	rs9940278	T	C	43.5	35	knee,hip	1.06	3.2E-16	0.97	0.56
KneeOA	rs34195470	A	G	44.5	36	knee	0.95	3.1E-13	0.99	0.85
KneeOA	rs4548913	A	G	62.8	37	knee, all	0.95	3.2E-12	0.92	0.04
KneeOA	rs72760655	A	C	33.1	92	knee,all	1.05	7.3E-11	1.05	0.29
KneeOA	rs7581446	T	C	48.3	50	knee	0.95	1.7E-10	0.98	0.62
KneeOA	rs753350451	D	I	20.2	19	knee	0.93	3.4E-10	0.98	0.77
KneeOA	rs58973023	A	T	48.9	27	knee	1.06	4.7E-10	1.04	0.41
KneeOA	rs4775006	A	C	41.6	30	hand, finger, thumb, knee	1.05	8.5E-10	0.69	3.0E-16
KneeOA	rs4380013	A	G	18.8	29	knee	1.06	8.7E-10	1.05	0.36
KneeOA	rs1426371	A	G	27.1	18	knee	0.95	8.9E-10	1.03	0.51
KneeOA	rs66906321	T	C	17.5	51	knee	0.95	1.7E-09	0.97	0.64
KneeOA	rs7967762	T	C	15.6	24	knee	1.06	2.1E-09	1.08	0.19
KneeOA	rs72979233	A	G	75.3	15	knee	0.95	2.5E-09	0.92	0.07
KneeOA	rs2163832	T	C	32.1	43	knee,all	1.05	2.7E-09	1.23	6.2E-06
KneeOA	rs11705555	A	C	76.4	56	knee	1.05	3.0E-09	1.00	0.97
KneeOA	rs2791549	A	C	29.6	5	knee, hip	1.05	3.1E-09	1.05	0.26
KneeOA	rs10842226	A	G	42.0	22	knee	1.05	3.6E-09	0.91	0.03
KneeOA	rs10974438	A	C	64.6	99	knee	1.04	4.9E-09	1.07	0.14
KneeOA	rs6500609	C	G	11.0	34	knee	0.94	5.2E-09	0.97	0.67
KneeOA	rs10038860	A	G	27.4	73	knee	1.05	5.6E-09	1.16	0.0013
KneeOA	rs12914479	C	G	66.0	33	knee	1.04	7.1E-09	1.07	0.13
KneeOA	rs2066928	A	G	48.3	75	knee	0.96	1.2E-08	0.97	0.47
KneeOA	rs7680647	T	C	63.1	68	knee,hip,all	0.96	1.2E-08	0.85	3.2E-04
HipOA	rs10843013	A	C	78.4	23	hip	0.90	2.9E-24	0.96	0.46
HipOA	rs12209223	A	C	11.1	83	hip	1.15	1.9E-22	1.16	0.03
HipOA	rs11164653	T	C	41.3	1	hip,all	0.92	2.8E-18	1.01	0.84
HipOA	rs12908498	C	G	53.8	32	hip	1.08	1.9E-16	1.06	0.18
HipOA	rs2416564	T	C	59.8	95	hip	0.93	1.0E-15	1.06	0.18
HipOA	rs765002298	D	I	19.7	90	hip	0.90	1.8E-15	1.03	0.58
HipOA	rs4252548	T	C	2.4	46	hip	1.25	2.2E-15	1.36	0.03
HipOA	rs1046934	A	C	64.9	4	hip	1.07	3.8E-14	0.99	0.80
HipOA	rs79895530	T	C	13.0	91	hip	0.90	7.0E-14	1.05	0.42
HipOA	rs2268023	A	T	41.1	63	hip	1.07	1.6E-13	0.95	0.21
HipOA	rs1913707	A	G	60.5	66	hip,all	1.07	1.8E-13	1.06	0.16
HipOA	rs2862851	T	C	46.5	52	hand, thumb, hip, all	1.07	3.9E-13	1.16	4.4E-04
HipOA	rs9475400	T	C	9.8	82	hip	1.11	8.0E-13	1.04	0.56
HipOA	rs111844273	A	G	2.1	89	hip	1.26	1.0E-12	1.10	0.49
HipOA	rs6908606	A	G	71.1	81	hip	0.93	3.9E-12	0.91	0.06
HipOA	rs2605098	A	G	33.2	5	hip	1.07	6.8E-12	1.09	0.05
HipOA	rs1330349	C	G	58.9	93	hip	1.06	6.9E-12	1.02	0.59
HipOA	rs4411121	T	C	31.4	2	hip	1.07	2.2E-11	1.06	0.22
HipOA	rs12377624	C	G	36.2	97	hip	0.94	4.6E-11	1.02	0.66
HipOA	rs143083812	T	C	0.11	86	hip	2.90	8.2E-11	3.48	0.0087
HipOA	rs1401796	A	C	51.3	39	hip,all	0.94	1.4E-10	0.97	0.52
HipOA	rs746239049	D	I	20.5	31	hip	0.92	3.3E-10	0.89	0.05
HipOA	rs12160491	A	G	71.1	57	hip	0.94	4.4E-10	1.01	0.81
HipOA	rs67924081	A	G	73.9	13	hip	1.07	7.8E-10	1.02	0.71
HipOA	rs10831477	T	G	81.1	17	hip,all	1.07	1.2E-09	1.01	0.81
HipOA	rs9835230	A	G	24.3	61	hip	1.07	1.3E-09	1.11	0.04
HipOA	rs2521348	T	C	38.7	41	hip	1.06	1.6E-09	0.94	0.14
HipOA	rs34560402	T	C	6.5	14	hip	0.89	1.6E-09	0.96	0.63
HipOA	rs9940278	T	C	43.5	35	knee,hip	1.06	1.8E-09	0.97	0.56
HipOA	rs3740129	A	G	45.9	8	hip	1.06	1.8E-09	1.05	0.25
HipOA	rs79056043	A	G	93.7	25	hip	0.89	2.0E-09	0.84	0.05
HipOA	rs79220007	T	C	92.7	78	hip	0.90	2.2E-09	1.01	0.91

HipOA	rs798756	T	C	19.4	68	knee,hip,all	0.93	2.2E-09	0.85	0.0044
HipOA	rs4073717	T	G	20.1	74	hip	0.94	2.5E-09	0.90	0.05
HipOA	rs17677724	T	C	16.1	72	hip,all	1.07	3.5E-09	1.12	0.05
HipOA	rs1809889	T	C	28.0	20	hip	1.06	3.6E-09	1.07	0.17
HipOA	rs10983775	T	C	54.2	96	hip	0.95	4.7E-09	0.99	0.80
HipOA	rs66989638	A	G	12.7	48	hip	1.08	4.8E-09	1.00	0.97
HipOA	rs7862601	A	G	62.4	94	hip	0.94	6.2E-09	0.94	0.15
HipOA	rs7222178	A	T	19.5	40	hip	1.07	7.4E-09	1.01	0.82
HipOA	rs10940168	A	G	39.4	76	hip	0.95	7.7E-09	1.01	0.76
HipOA	rs6855246	A	G	92.8	64	hip,all	0.90	7.9E-09	1.08	0.53
HipOA	rs10465114	A	G	22.0	98	hip	1.06	9.0E-09	1.01	0.89
AllOA	rs13107325	T	C	7.1	64	hip,all	1.08	3.2E-17	0.94	0.65
AllOA	rs3771501	A	G	46.8	52	hand, thumb, hip, all	1.04	4.0E-15	1.16	6.4E-04
AllOA	rs1913707	A	G	60.5	66	hip,all	1.03	1.4E-12	1.06	0.16
AllOA	rs2425061	A	G	62.8	53	knee,all	1.03	2.1E-12	0.94	0.14
AllOA	rs216175	A	C	82.8	37	all	1.04	2.7E-12	1.09	0.11
AllOA	rs2622873	T	C	88.0	1	hip,all	1.05	4.2E-11	1.03	0.66
AllOA	rs10405617	A	G	31.9	43	knee,all	1.03	9.3E-11	1.22	1.5E-05
AllOA	rs12901372	C	G	52.7	32	all	1.03	1.0E-10	1.07	0.10
AllOA	rs11731421	A	G	34.6	68	knee,hip,all	1.03	1.9E-10	1.19	1.0E-04
AllOA	rs75621460	A	G	2.6	44	all	1.10	1.1E-09	1.06	0.65
AllOA	rs4979341	T	C	27.5	92	knee,all	1.03	1.4E-09	1.04	0.41
AllOA	rs12667224	A	G	52.0	85	all	0.97	1.7E-09	0.96	0.30
AllOA	rs62242105	A	G	33.1	62	hip	0.97	2.9E-09	1.01	0.79
AllOA	rs201194999	T	C	30.1	69	all,spine	0.88	3.1E-09	0.57	0.27
AllOA	rs62182810	A	G	54.4	49	all	1.03	3.8E-09	1.07	0.15
AllOA	rs11729628	T	G	23.9	65	all	0.97	4.7E-09	0.91	0.05
AllOA	rs1401795	A	G	50.0	39	all	1.03	6.2E-09	1.03	0.47
AllOA	rs10831476	A	C	81.1	17	hip,all	1.03	7.8E-09	1.01	0.82
AllOA	rs17677555	C	G	25.6	72	hip,all	1.03	1.1E-08	1.08	0.13

The Genetics of Osteoarthritis (GO) consortium data is from Boer et al, Cell, 2021. OR (odds ratio) and P values and ORs are shown for the respective osteoarthritis (OA) phenotypes in the GO consortium data. The OA phenotypes that are significantly associated with the respective signal in GO are listed under the column "Associated GWS OA phenotypes" (often represented by a different, but highly correlated, variant).