

Supplementary table S4 Regulatory effects of the ten BC-associated SNPs of the *M*
(HaploReg, v4.1, <http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>)

Query SNP: **rs1940475** and variants with $r^2 \geq 0.8$

		LD	LD					AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter histone marks
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons		
11	102721214	0.85	1	rs2186602	T	C	0.81	0.59	0.60	0.57				
11	102722311	0.85	1	rs948218	T	A	0.81	0.59	0.60	0.57				
11	102722322		1	rs1940474	G	T	0.65	0.54	0.59	0.53				
11	102722517		1	rs1940475	T	C	0.72	0.54	0.59	0.53				
11	102723248	0.85	1	rs7123658	A	T	0.81	0.59	0.60	0.57				
11	102723645	0.85		rs6590983	A	C	0.81	0.59	0.60	0.57				
11	102724404		1	rs1939012	T	C	0.76	0.54	0.59	0.53				
11	102724761	0.85	1	rs3765620	G	A	0.81	0.59	0.60	0.57				
11	102725749	0.84	1	rs11225395	A	G	0.81	0.59	0.60	0.57				
11	102726340	0.84	1	rs33952053	TG	T	0.82	0.59	0.60	0.57				
11	102727079	0.84	1	rs1939013	T	C	0.83	0.59	0.60	0.57				
11	102727181	0.84	1	rs1939014	A	T	0.81	0.59	0.60	0.57				
11	102727628	0.84	1	rs3758857	T	C	0.81	0.59	0.60	0.57				
11	102727726	0.84	1	rs3758858	G	A	0.81	0.59	0.60	0.57				BLD, MUS
11	102727749	0.99	1	rs3758859	C	A	0.65	0.54	0.59	0.53				BLD, MUS
11	102727924	0.84	1	rs6590985	T	C	0.81	0.59	0.60	0.57				BLD, MUS
11	102728128	0.84	1	rs6590986	C	T	0.81	0.59	0.60	0.57				
11	102729275	0.84	1	rs10750653	A	G	0.82	0.59	0.60	0.57				

Query SNP: **rs1799750** and variants with $r^2 \geq 0.8$

		LD	LD					AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter histone marks
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons		
11	102799764		1	rs1799750	TC	T	0.55	0.44	0.33	0.49				

Query SNP: **rs679620** and variants with $r^2 \geq 0.8$

		LD	LD					AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter histone marks
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons		
11	102807707	0.82	-0.92	rs526215	C	T	0.04	0.34	0.15	0.45				ESC, iPSC, LNG

11	102808321	0.81	-0.92	rs1144396	C	A	0.51	0.37	0.33	0.45
11	102808927	0.82	-0.92	rs565082	T	C	0.41	0.37	0.33	0.45
11	102811772	0.81	-0.91	rs502174	A	C	0.42	0.37	0.32	0.45
11	102816687	0.83	-0.93	rs10791596	T	C	0.41	0.36	0.33	0.45
11	102819770	0.89	-0.96	rs2097248	C	T	0.41	0.37	0.33	0.47
11	102819867	0.84	-0.92	rs200587503	T	TG	0.42	0.36	0.33	0.46
11	102820431	0.9	-0.96	rs756544	G	C	0.34	0.37	0.33	0.46
11	102820659	0.91	-0.97	rs12804136	G	A	0.41	0.37	0.33	0.47
11	102820751	0.9	-0.97	rs11225434	T	C	0.39	0.37	0.33	0.47
11	102821493	0.91	-0.97	rs7117013	A	G	0.43	0.38	0.33	0.47
11	102822132	0.91	-0.97	rs10895364	C	T	0.43	0.39	0.33	0.47
11	102822879	0.92	-0.98	rs12801529	T	A	0.40	0.38	0.33	0.47
11	102823462	0.92	-0.98	rs10895365	C	T	0.39	0.37	0.33	0.47
11	102825487	0.89	-0.96	rs6590993	G	T	0.39	0.37	0.33	0.47
11	102825901	0.92	-0.98	rs6590994	C	T	0.34	0.37	0.33	0.47
11	102826358	0.96	-0.98	rs10895366	G	A	0.03	0.34	0.15	0.46
11	102826390	0.96	-0.98	rs7126392	G	A	0.38	0.36	0.32	0.46
11	102826825	0.94	-0.97	rs2212637	C	T	0.41	0.37	0.33	0.46
11	102827605	0.96	-0.98	rs12792871	C	G	0.03	0.35	0.15	0.46
11	102827993	0.95	-0.98	rs7926920	G	A	0.40	0.37	0.33	0.46
11	102828729	0.92	-0.96	rs7946057	A	T	0.40	0.37	0.33	0.46
11	102830290	0.98	-1	rs1010698	G	T	0.40	0.37	0.33	0.46
11	102831127	0.98	-1	rs2155013	T	C	0.40	0.37	0.33	0.46
11	102831532	0.98	-1	rs4754884	G	A	0.40	0.37	0.33	0.46
11	102832897	0.99	1	rs635746	A	G	0.58	0.62	0.67	0.54
11	102833340	0.99	1	rs633962	C	T	0.56	0.62	0.68	0.54
11	102833449	0.99	1	rs666734	G	C	0.58	0.62	0.67	0.54
11	102834166	0.99	1	rs595840	A	G	0.71	0.64	0.67	0.54
11	102836608	0.99	1	rs639752	C	A	0.56	0.62	0.67	0.54
11	102837183	0.98	0.99	rs575027	A	G	0.58	0.62	0.67	0.54
11	102838694	0.98	0.99	rs520540	A	G	0.58	0.62	0.68	0.54
11	102840607	1	1	rs591058	T	C	0.69	0.63	0.67	0.54
11	102842734	1	1	rs602128	A	G	0.57	0.62	0.67	0.54
11	102842889	1	1	rs679620	T	C	0.71	0.64	0.67	0.54

4 tissues

FAT, GI

22 tissues

GI

GI

GI







GI

11	102843046	1	1	rs678815	G	C	0.69	0.63	0.67	0.54			
11	102843985	0.99	0.99	rs617819	C	G	0.71	0.64	0.67	0.54			
11	102844950	0.99	0.99	rs632478	T	G	0.69	0.63	0.67	0.54			
11	102845590	0.99	0.99	rs645419	A	G	0.69	0.63	0.67	0.54			
11	102846249	0.95	0.99	rs573521	A	G	0.68	0.63	0.66	0.53			CRVX

Query SNP: **rs243865** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	histone marks
16	55477625	0.99	1	rs243866	G	A	0.01	0.19	0.09	0.28			5 tissues
16	55477894		1	rs243865	C	T	0.02	0.19	0.09	0.27			4 tissues
16	55478410	0.99	1	rs243864	T	G	0.02	0.19	0.09	0.28			5 tissues
16	55479711	0.92	1	rs243862	C	T	0.02	0.18	0.09	0.26			24 tissues

Query SNP: **rs3918242** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	histone marks
20	45986352	0.89	0.95	rs142450006	TTTTC	T	0.07	0.10	0.17	0.17			
20	45986358	0.86	0.95	rs201501785	T	TTC	0.07	0.10	0.17	0.17			
20	45995328	0.95	0.98	rs1888235	C	T	0.13	0.09	0.18	0.17			
20	46002014	0.95	0.98	rs6073984	A	G	0.13	0.09	0.17	0.17			
20	46003728	0.86	0.98	rs6065912	G	A	0.11	0.09	0.08	0.16			
20	46007096		1	rs3918241	T	A	0.13	0.09	0.17	0.17			
20	46007337		1	rs3918242	C	T	0.12	0.09	0.17	0.17			
20	46011053	0.99	1	rs2274755	G	T	0.16	0.10	0.16	0.18			15 tissues
20	46011936	0.99	1	rs2236416	A	G	0.12	0.09	0.16	0.18			15 tissues
20	46014472	0.98	1	rs17577	G	A,C	0.17	0.10	0.18	0.18			21 tissues
20	46014953	0.98	1	rs3918261	A	G	0.21	0.10	0.18	0.18			5 tissues
20	46016326	0.98	1	rs13925	G	A	0.15	0.10	0.18	0.18			
20	46016700	0.96	1	rs3918270	G	A	0.17	0.10	0.18	0.18			
20	46016954	0.93	0.97	rs3918271	G	A	0.17	0.10	0.18	0.18			

20	46020003	0.82	1	rs66553311	C	G	0.50	0.27	0.41	0.20			
20	46021679	0.89	0.98	rs10432735	A	T	0.18	0.11	0.18	0.19			

Query SNP: **rs3918249** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	histone marks
20	45987758	0.83	0.94	rs6017721	A	G	0.71	0.34	0.75	0.41			SKIN
20	46005037	0.94	0.99	rs3848721	C	T	0.49	0.29	0.72	0.40			9 tissues
20	46005181	0.94	0.99	rs3848722	A	G	0.72	0.32	0.72	0.40			11 tissues
20	46005911	0.9	0.96	rs4810482	T	C	0.72	0.32	0.72	0.39			BRN, GI, ADRL
20	46006273	0.85	0.99	rs3761158	G	A	0.73	0.43	0.76	0.42			
20	46006318	0.95	0.99	rs3761159	C	T	0.43	0.29	0.72	0.40			
20	46006464	0.99	0.99	rs6065913	C	T	0.34	0.28	0.72	0.39			BLD
20	46006977	0.99	0.99	rs3918240	C	T	0.34	0.28	0.72	0.39			
20	46009497	1	1	rs3918249	T	C	0.56	0.31	0.72	0.39			4 tissues
20	46010142	0.83	0.92	rs3918251	A	G	0.52	0.30	0.64	0.40			4 tissues
20	46011586	0.99	0.99	rs17576	A	G	0.35	0.28	0.72	0.39			17 tissues
20	46014194	0.82	-0.98	rs13969	A	C	0.38	0.49	0.24	0.57			23 tissues

Query SNP: **rs17576** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	histone marks
20	45987758	0.82	0.94	rs6017721	A	G	0.71	0.34	0.75	0.41			SKIN
20	46005037	0.92	0.99	rs3848721	C	T	0.49	0.29	0.72	0.40			9 tissues
20	46005181	0.92	0.99	rs3848722	A	G	0.72	0.32	0.72	0.40			11 tissues
20	46005911	0.89	0.96	rs4810482	T	C	0.72	0.32	0.72	0.39			BRN, GI, ADRL
20	46006273	0.84	0.99	rs3761158	G	A	0.73	0.43	0.76	0.42			
20	46006318	0.94	0.99	rs3761159	C	T	0.43	0.29	0.72	0.40			
20	46006464	0.98	0.99	rs6065913	C	T	0.34	0.28	0.72	0.39			BLD

20	46006977	0.98	0.99	rs3918240	C	T	0.34	0.28	0.72	0.39			
20	46009497	0.99	0.99	rs3918249	T	C	0.56	0.31	0.72	0.39			4 tissues
20	46010142	0.84	0.93	rs3918251	A	G	0.52	0.30	0.64	0.40			4 tissues
20	46011586	1	1	rs17576	A	G	0.35	0.28	0.72	0.39			17 tissues
20	46014194	0.83	-0.98	rs13969	A	C	0.38	0.49	0.24	0.57			23 tissues

Query SNP: **rs3787268** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter histone marks
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	
20	45991015	0.87	0.94	rs35610751	C	G	0.10	0.17	0.35	0.21			
20	45991065	0.86	0.94	rs6073980	G	A	0.13	0.17	0.35	0.22			
20	46001252	0.89	0.98	rs6073983	A	T	0.09	0.16	0.36	0.22			FAT, BLD
20	46006183	0.98	0.99	rs3761157	C	T	0.09	0.16	0.36	0.21			
20	46013092	1	1	rs3787268	G	A	0.09	0.16	0.36	0.21			BLD, SKIN
20	46015131	1	1	rs3918262	A	G	0.09	0.16	0.36	0.21			LIV
20	46022571	0.95	0.98	rs6073989	G	T	0.09	0.16	0.36	0.21			24 tissues
20	46023675	0.95	0.98	rs16991010	A	C	0.09	0.16	0.36	0.21			
20	46024480	0.95	0.98	rs6130998	C	T	0.09	0.16	0.37	0.21			
20	46026853	0.95	0.98	rs6130999	G	A	0.09	0.16	0.37	0.21			
20	46027473	0.95	0.98	rs6073991	A	G	0.09	0.16	0.37	0.21			
20	46031067	0.91	0.97	rs13039389	G	C	0.08	0.16	0.37	0.22			ESDR, IPSC, BRN
20	46032717	0.94	0.98	rs6131001	C	T	0.08	0.16	0.37	0.21			BRN

Query SNP: **rs2250889** and variants with $r^2 \geq 0.8$

		LD	LD				AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter histone marks
chr	pos (hg38)	(r^2)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	
20	46013767	1	1	rs2250889	G	C	0.82	0.80	0.76	0.95			24 tissues
20	46024910	0.92	0.97	rs6094239	G	A	0.82	0.80	0.77	0.95			

Query SNP: **rs17577** and variants with $r^2 \geq 0.8$

		LD	LD			AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter	
chr	pos (hg38)	(r ²)	(D')	variant	Ref	Alt	freq	freq	freq	freq	cons	cons	histone marks
20	45986352	0.88	0.95	rs142450006	TTTTC	T	0.07	0.10	0.17	0.17			
20	45986358	0.84	0.95	rs201501785	T	TTC	0.07	0.10	0.17	0.17			
20	45995328	0.94	0.98	rs1888235	C	T	0.13	0.09	0.18	0.17			
20	46002014	0.94	0.98	rs6073984	A	G	0.13	0.09	0.17	0.17			
20	46003728	0.84	0.98	rs6065912	G	A	0.11	0.09	0.08	0.16			
20	46007096	0.98	1	rs3918241	T	A	0.13	0.09	0.17	0.17			
20	46007337	0.98	1	rs3918242	C	T	0.12	0.09	0.17	0.17			
20	46011053	0.99	1	rs2274755	G	T	0.16	0.10	0.16	0.18	<div></div>	<div></div>	15 tissues
20	46011936	0.99	1	rs2236416	A	G	0.12	0.09	0.16	0.18			15 tissues
20	46014472	1	1	rs17577	G	A,C	0.17	0.10	0.18	0.18	<div></div>	<div></div>	21 tissues
20	46014953	1	1	rs3918261	A	G	0.21	0.10	0.18	0.18			5 tissues
20	46016326	1	1	rs13925	G	A	0.15	0.10	0.18	0.18	<div></div>	<div></div>	
20	46016700	0.98	1	rs3918270	G	A	0.17	0.10	0.18	0.18			
20	46016954	0.95	0.97	rs3918271	G	A	0.17	0.10	0.18	0.18			
20	46020003	0.84	1	rs66553311	C	G	0.50	0.27	0.41	0.20			
20	46021679	0.91	0.98	rs10432735	A	T	0.18	0.11	0.18	0.19	<div></div>		

MMP gene and SNPs in high LD ($r^2 \geq 0.80$)

Enhancer histone marks	Proteins	Motifs	NHGRI/EBI	GRASP QTL	Selected eQTL	GENCODE	RefSeq
DNAse	bound	changed	GWAS hits	hits	hits	genes	genes
BLD		5 altered motifs			3 hits	MMP8	MMP8
BLD		TCF4			3 hits	MMP8	MMP8
BLD		Fox,Foxi1,Foxj2			2 hits	MMP8	MMP8
BLD	BLD,BLD	CIZ,Myc,NF-AT1		1 hit	2 hits	MMP8	MMP8
BLD					3 hits	MMP8	MMP8
BLD		27 altered motifs			3 hits	MMP8	MMP8
BLD		HNF1	1 hit		2 hits	MMP8	MMP8
BLD, SKIN	SKIN	Foxp1,Sox		1 hit	3 hits	MMP8	MMP8
10 tissues	SKIN				3 hits	MMP8	794bp 5' of MMP8
BLD, SKIN		Pax-4				MMP8	1.4kb 5' of MMP8
BLD, SPLN	KID	Foxa			3 hits	28bp 5' of MMP8	2.1kb 5' of MMP8
BLD, SPLN		4 altered motifs			3 hits	130bp 5' of MMP8	2.2kb 5' of MMP8
7 tissues	BLD	EWSR1-FLI1,Pax-5,STAT			3 hits	577bp 5' of MMP8	2.7kb 5' of MMP8
7 tissues	SKIN,BLD	4 altered motifs			3 hits	675bp 5' of MMP8	2.8kb 5' of MMP8
7 tissues	SKIN,BLD	HNF4,Ncx			2 hits	698bp 5' of MMP8	2.8kb 5' of MMP8
6 tissues	8 tissues	GR,NRSF			3 hits	873bp 5' of MMP8	3kb 5' of MMP8
6 tissues	20 tissues	4 bound proteins			3 hits	1.1kb 5' of MMP8	3.2kb 5' of MMP8
	ESDR				2 hits	2.2kb 5' of MMP8	4.3kb 5' of MMP8

Enhancer histone marks	Proteins	Motifs	NHGRI/EBI	GRASP QTL	Selected eQTL	GENCODE	RefSeq
DNAse	bound	changed	GWAS hits	hits	hits	genes	genes
6 tissues	5 tissues	CFOS,GATA2			8 hits	1.6kb 5' of MMP1	LOC100288077

Enhancer histone marks	Proteins	Motifs	NHGRI/EBI	GRASP QTL	Selected eQTL	GENCODE	RefSeq
DNAse	bound	changed	GWAS hits	hits	hits	genes	genes
ESC, iPSC					3 hits	9.5kb 5' of MMP1	LOC100288077

ESC, ESDR, IPSC	5 tissues	CTCF	NRSF, Sin3A k-20	3 hits	10kb 5' of MMP1	LOC100288077
				3 hits	11kb 5' of MMP1	LOC100288077
GI			HDAC2, Irf, p300	3 hits	14kb 5' of MMP1	LOC100288077
	OVRY, GI, LIV	FOXA1, FOXA2	4 altered motifs	3 hits	19kb 5' of MMP1	LOC100288077
			4 altered motifs	3 hits	16kb 3' of MMP3	LOC100288077
	BLD		Ets, HNF4, NF-kappaB	3 hits	16kb 3' of MMP3	LOC100288077
			HNF1	3 hits	15kb 3' of MMP3	LOC100288077
			7 altered motifs	3 hits	15kb 3' of MMP3	LOC100288077
			Foxp3, Obox 6	3 hits	15kb 3' of MMP3	LOC100288077
			4 altered motifs	3 hits	14kb 3' of MMP3	LOC100288077
			EWSR1-FLI1	3 hits	14kb 3' of MMP3	LOC100288077
				3 hits	13kb 3' of MMP3	LOC100288077
	LNG		4 altered motifs	3 hits	12kb 3' of MMP3	LOC100288077
			5 altered motifs	3 hits	10kb 3' of MMP3	LOC100288077
				3 hits	9.9kb 3' of MMP3	LOC100288077
			Sin3Ak-20	3 hits	9.4kb 3' of MMP3	LOC100288077
			Glis2, MAZR, Zic	3 hits	9.4kb 3' of MMP3	LOC100288077
			ZBRK1, Zfx	3 hits	9kb 3' of MMP3	LOC100288077
			ATF3	3 hits	8.2kb 3' of MMP3	LOC100288077
			4 altered motifs	3 hits	7.8kb 3' of MMP3	LOC100288077
			7 altered motifs	3 hits	7.1kb 3' of MMP3	LOC100288077
	SKIN, BRST		4 altered motifs	3 hits	5.5kb 3' of MMP3	LOC100288077
FAT	KID		TCF4	3 hits	4.7kb 3' of MMP3	LOC100288077
ESC, IPSC, SKIN	31 tissues	CTCF, RAD21, SMC3	NF-kappaB	3 hits	4.3kb 3' of MMP3	LOC100288077
	GI		4 altered motifs	3 hits	2.9kb 3' of MMP3	LOC100288077
				3 hits	2.5kb 3' of MMP3	LOC100288077
			Gfi1, SIX5	3 hits	2.4kb 3' of MMP3	LOC100288077
			5 altered motifs	3 hits	1.6kb 3' of MMP3	LOC100288077
13 tissues	11 tissues	P300, TBP, S TAT3		3 hits	MMP3	MMP3
10 tissues			Maf, PRDM1, Spz1	3 hits	MMP3	MMP3
				3 hits	MMP3	MMP3
			4 altered motifs	3 hits	MMP3	MMP3
			ATF3, PU.1	3 hits	MMP3	MMP3
			p300	3 hits	MMP3	MMP3

	LNG,SKIN,S KIN		Hoxd10,Pou 3f2		3 hits	MMP3	MMP3
FAT, SKIN	SKIN		Mef2		3 hits	181bp 5' of MMP3	373bp 5' of MMP3
			ZEB1		3 hits	1.1kb 5' of MMP3	1.3kb 5' of MMP3
			Hsf,STAT		3 hits	1.8kb 5' of MMP3	2kb 5' of MMP3
BRST, SKIN		ZNF263	8 altered motifs	1 hit	3 hits	2.4kb 5' of MMP3	2.6kb 5' of MMP3

Enhancer histone marks	Proteins	Motifs	NHGR/EBI	GRASP QTL	Selected eQTL	GENCODE	RefSeq
	DNAse	bound	changed	GWAS hits	hits	hits	genes
18 tissues	MUS,MUS,S KIN		5 altered motifs		1 hit	1 hit	MMP2
15 tissues	ESDR,IPSC, MUS		Myf		1 hit	1 hit	MMP2
14 tissues	4 tissues		5 altered motifs		1 hit	1 hit	MMP2
	19 tissues		14 altered motifs				MMP2

Enhancer histone marks	Proteins	Motifs	NHGR/EBI	GRASP QTL	Selected eQTL	GENCODE	RefSeq
	DNAse	bound	changed	GWAS hits	hits	hits	genes
			8 altered motifs			6 hits	14kb 5' of ZNF335
			9 altered motifs			5 hits	14kb 5' of ZNF335
10 tissues	CRVX	MAFK	8 altered motifs		4 hits	10 hits	14kb 5' of MMP9
BLD, THYM	ESDR				2 hits	6 hits	6.9kb 5' of MMP9
6 tissues	ESDR,BLD		Pax-5		1 hit	9 hits	5.2kb 5' of MMP9
BLD, THYM, SPLN			24 altered motifs		1 hit	9 hits	1.8kb 5' of MMP9
BLD, THYM, SPLN	IPSC		4 altered motifs		1 hit	6 hits	1.6kb 5' of MMP9
	7 tissues				2 hits	9 hits	MMP9
BLD	33 tissues	6 bound proteins	NF-Y		1 hit	9 hits	MMP9
SKIN	22 tissues	4 bound proteins			1 hit	6 hits	MMP9
BLD	BLD,BRST		Foxo,GR		6 hits	9 hits	MMP9
			4 altered motifs		1 hit	6 hits	MMP9
			5 altered motifs		1 hit	9 hits	RP11-465L10.10
			8 altered motifs			6 hits	RP11-465L10.10

			HNF4,Zbtb3		7 hits	RP11-465L10.10	1.7kb 5' of SLC12A5	
21 tissues	7 bound proteins		Pax-4,ZNF219,Zfp281		1 hit	5 hits	RP11-465L10.10	9bp 5' of SLC12A5

Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	RefSeq genes
7 tissues	4 tissues		4 altered motifs		2 hits	20 hits	16kb 5' of ZNF335	16kb 5' of ZNF335
15 tissues	20 tissues		SP1,STAT,Zfp281			9 hits	3.9kb 5' of MMP9	3.9kb 5' of MMP9
14 tissues	19 tissues		4 altered motifs			9 hits	3.7kb 5' of MMP9	3.7kb 5' of MMP9
11 tissues	ESC,BLD		AP-1		2 hits	10 hits	3kb 5' of MMP9	3kb 5' of MMP9
6 tissues	BLD		11 altered motifs			11 hits	2.6kb 5' of MMP9	2.6kb 5' of MMP9
6 tissues	4 tissues					9 hits	2.6kb 5' of MMP9	2.6kb 5' of MMP9
4 tissues	BLD,BLD,BLD					11 hits	2.4kb 5' of MMP9	2.4kb 5' of MMP9
BLD, THYM, SPLN	BLD		6 altered motifs			11 hits	1.9kb 5' of MMP9	1.9kb 5' of MMP9
BLD	BLD,BLD		4 altered motifs			9 hits	MMP9	MMP9
	BLD,LIV		5 altered motifs			8 hits	MMP9	MMP9
4 tissues	ESC		Pax-4			12 hits	MMP9	MMP9
SKIN	24 tissues	7 bound proteins	4 altered motifs			7 hits	MMP9	MMP9

Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	RefSeq genes
7 tissues	4 tissues		4 altered motifs		2 hits	20 hits	16kb 5' of ZNF335	16kb 5' of ZNF335
15 tissues	20 tissues		SP1,STAT,Zfp281			9 hits	3.9kb 5' of MMP9	3.9kb 5' of MMP9
14 tissues	19 tissues		4 altered motifs			9 hits	3.7kb 5' of MMP9	3.7kb 5' of MMP9
11 tissues	ESC,BLD		AP-1		2 hits	10 hits	3kb 5' of MMP9	3kb 5' of MMP9
6 tissues	BLD		11 altered motifs			11 hits	2.6kb 5' of MMP9	2.6kb 5' of MMP9
6 tissues	4 tissues					9 hits	2.6kb 5' of MMP9	2.6kb 5' of MMP9
4 tissues	BLD,BLD,BLD					11 hits	2.4kb 5' of MMP9	2.4kb 5' of MMP9

BLD, THYM, SPLN	BLD		6 altered motifs		11 hits	1.9kb 5' of MMP9	1.9kb 5' of MMP9
BLD	BLD,BLD		4 altered motifs		9 hits	MMP9	MMP9
	BLD,LIV		5 altered motifs		8 hits	MMP9	MMP9
4 tissues	ESC		Pax-4		12 hits	MMP9	MMP9
SKIN	24 tissues	7 bound proteins	4 altered motifs		7 hits	MMP9	MMP9

Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	RefSeq genes
			Nkx3			2 hits	18kb 5' of MMP9	18kb 5' of MMP9
			BDP1,LUN-1			2 hits	18kb 5' of MMP9	18kb 5' of MMP9
9 tissues	BLD,BRN		Arid5b			4 hits	7.7kb 5' of MMP9	7.7kb 5' of MMP9
6 tissues	4 tissues		9 altered motifs			3 hits	2.7kb 5' of MMP9	2.7kb 5' of MMP9
BLD	BLD,BLD		6 altered motifs			4 hits	MMP9	MMP9
BLD	BLD,LIV	9 bound proteins	9 altered motifs			3 hits	MMP9	MMP9
	16 tissues		5 altered motifs			3 hits	RP11-465L10.7	SLC12A5
			Mrg			3 hits	RP11-465L10.7	SLC12A5
	BLD,BLD,LNG		CDP			3 hits	RP11-465L10.7	SLC12A5
		NRSF	EBF,SZF1-1			2 hits	RP11-465L10.7	SLC12A5
	49 tissues	NRSF,ZNF143,BCL3	SZF1-1,T3R		2 hits	3 hits	RP11-465L10.7	SLC12A5
			BAF155,TFIIA			2 hits	SLC12A5	SLC12A5
			4 altered motifs			2 hits	SLC12A5	SLC12A5

Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	RefSeq genes
	15 tissues	CTCF	NRSF				MMP9	MMP9
			7 altered motifs				RP11-465L10.7	SLC12A5

Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	RefSeq genes
			8 altered motifs			6 hits	14kb 5' of ZNF335	14kb 5' of ZNF335
			9 altered motifs			5 hits	14kb 5' of ZNF335	14kb 5' of ZNF335
10 tissues	CRVX	MAFK	8 altered motifs		4 hits	10 hits	14kb 5' of MMP9	14kb 5' of MMP9
BLD, THYM	ESDR				2 hits	6 hits	6.9kb 5' of MMP9	6.9kb 5' of MMP9
6 tissues	ESDR,BLD		Pax-5		1 hit	9 hits	5.2kb 5' of MMP9	5.2kb 5' of MMP9
BLD, THYM, SPLN			24 altered motifs		1 hit	9 hits	1.8kb 5' of MMP9	1.8kb 5' of MMP9
BLD, THYM, SPLN	IPSC		4 altered motifs		1 hit	6 hits	1.6kb 5' of MMP9	1.6kb 5' of MMP9
	7 tissues				2 hits	9 hits	MMP9	MMP9
BLD	33 tissues	6 bound proteins	NF-Y		1 hit	9 hits	MMP9	MMP9
SKIN	22 tissues	4 bound proteins			1 hit	6 hits	MMP9	MMP9
BLD	BLD,BRST		Foxo,GR		6 hits	9 hits	MMP9	MMP9
			4 altered motifs		1 hit	6 hits	MMP9	MMP9
			5 altered motifs		1 hit	9 hits	RP11-465L10.10	138bp 3' of MMP9
			8 altered motifs			6 hits	RP11-465L10.10	392bp 3' of MMP9
			HNF4,Zbtb3			7 hits	RP11-465L10.10	1.7kb 5' of SLC12A5
	21 tissues	7 bound proteins	Pax-4,ZNF219,Zfp281		1 hit	5 hits	RP11-465L10.10	9bp 5' of SLC12A5

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