Supplementary Table 3 *In silico* functional look-up in HaploReg v3 and RegulomeDB v1.1

chr	pos(hg19)	LD(r^2)*	LD(D')*	variant	Ref	Alt	Alternative allele frequency				Conservation		Histone marks		DNase	Proteins bound	Motifs changed	Drivers disrupted	GENCODE genes	RefSeq genes	dbSNP func annot	RegulomeDB score†
							AFR	AMR	ASN	EUR	GERP	SiPhy	Promoter	Enhancer								
6	4.1E+07	0.84	-0.95	rs2496644	A	C	0.69	0.82	0.66	0.97				IPSC, LIV			DMRT2,Evi-1		RP11-328M4.2	31kb 5' of FOXP4		No Data
6	4.1E+07	0.83	0.94	rs181350472	A	G	0.11	0.17	0.34	0.03							10 altered motifs		RP11-328M4.2	31kb 5' of FOXP4		6
6	4.1E+07	0.86	0.95	rs9367107	G	A	0.12	0.17	0.34	0.03							6 altered motifs		RP11-328M4.2	31kb 5' of FOXP4		6
6	4.1E+07	0.95	0.98	rs12660421	G	A	0.06	0.17	0.33	0.03			LIV	6 organs	GI				RP11-328M4.2	26kb 5' of FOXP4		No Data
6	4.1E+07	0.89	-0.96	rs1977358	T	C	0.75	0.82	0.66	0.97				GI, LIV			Maf		RP11-328M4.2	24kb 5' of FOXP4		No Data
6	4.1E+07	0.95	-0.98	rs1977357	G	A	0.75	0.82	0.67	0.97				GI, LIV					RP11-328M4.2	24kb 5' of FOXP4		5
6	4.1E+07	0.95	0.98	rs41435745	G	C	0.06	0.17	0.33	0.03				4 organs			Pax-6,Sp100		RP11-328M4.2	24kb 5' of FOXP4		5
6	4.1E+07	1	1	**rs7741164**	G	A	0.06	0.17	0.33	0.03				ESDR, GI, LIV			8 altered motifs		RP11-328M4.2	21kb 5' of FOXP4	intronic	6
6	4.1E+07	0.94	0.99	rs1853837	C	A	0.19	0.21	0.32	0.11				6 organs	SKIN,GI		VDR		RP11-328M4.2	17kb 5' of FOXP4	intronic	5
9	2.2E+07	1	1	**rs72658409**	C	T	0.16	0.05	0.09	0.07			BLD	9 organs	BLD		Foxm1,Foxp1,YY1		39kb 3' of CDKN2B-AS1	39kb 3' of CDKN2B-AS1		No Data
9	2.2E+07	1	1	rs10965267	T	G	0.19	0.05	0.09	0.08							Obox6,Spdef		41kb 3' of CDKN2B-AS1	41kb 3' of CDKN2B-AS1		No Data
9	2.2E+07	1	1	rs10965270	G	A,C	0.01	0.02	0.09	0.06									41kb 3' of RP11-408N14.1	42kb 3' of CDKN2B-AS1		No Data
9	2.2E+07	0.94	-0.98	rs861190	G	A	0.8	0.95	0.91	0.93				BLD, STRM			CDP		37kb 3' of RP11-408N14.1	46kb 3' of CDKN2B-AS1		6
12	5.2E+07	0.93	0.98	rs61914027	C	A	0.06	0.49	0.3	0.21				5 organs			Smad		2.2kb 5' of ACVR1B	2.2kb 5' of ACVR1B		5
12	5.2E+07	0.9	0.96	rs58617820	T	C	0.35	0.54	0.3	0.24				5 organs			7 altered motifs		2.1kb 5' of ACVR1B	2.1kb 5' of ACVR1B		5
12	5.2E+07	0.92	0.97	rs61914028	G	A	0.11	0.5	0.3	0.23				5 organs	4 organs		Foxa,STAT		2kb 5' of ACVR1B	2kb 5' of ACVR1B		5
12	5.2E+07	0.98	0.99	rs4761839	G	A	0.04	0.49	0.31	0.2			20 organs	11 organs	8 organs		GR,HDAC2		ACVR1B	ACVR1B	intronic	5
12	5.2E+07	0.85	-1	rs7962469	A	G	0.22	0.38	0.66	0.65	🟦		10 organs	18 organs	12 organs		NF-I		ACVR1B	ACVR1B	intronic	4
12	5.2E+07	1	1	**rs11610143**	C	G	0.04	0.49	0.31	0.2	🟦	🟪	8 organs	18 organs	12 organs				ACVR1B	ACVR1B	intronic	4
12	5.2E+07	1	1	rs11612312	T	C	0.04	0.49	0.31	0.2	🟦	🟪	8 organs	18 organs	12 organs		Pou5f1		ACVR1B	ACVR1B	intronic	4
12	5.2E+07	1	1	rs79583832	CA	C	0.04	0.49	0.31	0.2				8 organs			5 altered motifs		ACVR1B	ACVR1B	intronic	No Data
12	5.2E+07	1	1	rs61914045	G	A	0.04	0.49	0.31	0.2				8 organs			E2F		ACVR1B	ACVR1B	intronic	No Data
12	5.2E+07	0.82	0.98	rs813469	G	A	0.6	0.56	0.34	0.27			ESDR	11 organs			10 altered motifs		ACVR1B	ACVR1B	intronic	6
12	5.2E+07	0.85	1	rs813470	G	A	0.6	0.57	0.34	0.27			ESDR	13 organs			4 altered motifs		ACVR1B	ACVR1B	intronic	5
12	5.2E+07	0.84	0.93	rs11169970	G	A	0.11	0.51	0.31	0.22			ESDR, BLD, BONE	20 organs	THYM		TFII-I		ACVR1B	ACVR1B	intronic	4
12	5.2E+07	0.83	0.92	rs34437092	A	G	0.12	0.51	0.31	0.22				PANC	GI		10 altered motifs		ACVR1B	ACVR1B	intronic	5
12	5.2E+07	0.86	-0.94	rs4761841	G	C	0.92	0.51	0.7	0.79			BLD	BLD					ACVR1B	ACVR1B	intronic	No Data
12	5.2E+07	0.8	-0.92	rs4761842	G	C	0.92	0.51	0.68	0.79			BLD	BLD			ELF1,Foxa		ACVR1B	ACVR1B	intronic	No Data
17	7.6E+07	0.9	0.98	rs9908045	G	A	0.65	0.73	0.55	0.52	🟦		22 organs	4 organs	31 organs	9 bound proteins	7 altered motifs		SYNGR2	SYNGR2	intronic	2a
17	7.6E+07	0.98	1	rs9908349	C	T	0.58	0.57	0.53	0.41			22 organs	6 organs	7 organs	ELF1,POL2	10 altered motifs	PATZ1_1,Pro_c50;SP1_2,Pro_c50	SYNGR2	SYNGR2	intronic	2b
17	7.6E+07	1	1	**rs3794742**	G	A	0.59	0.58	0.53	0.41			22 organs	8 organs	25 organs	EBF1,POL2,ZNF263	E2A,Gfi1		SYNGR2	SYNGR2	intronic	3a
17	7.6E+07	0.98	1	rs3829575	C	T	0.6	0.59	0.53	0.41			19 organs	14 organs	21 organs		Roaz		SYNGR2	SYNGR2	intronic	4
17	7.6E+07	0.97	1	rs870355	A	G	0.6	0.59	0.54	0.41			15 organs	15 organs	26 organs	POL2,POL24H8	Evi-1		SYNGR2	SYNGR2	intronic	4
17	7.6E+07	0.98	1	rs1810063	G	A	0.59	0.59	0.53	0.41			BLD, SKIN, GI	13 organs	BLD,BLD		4 altered motifs		SYNGR2	SYNGR2	intronic	4
17	7.6E+07	0.97	1	rs4583318	C	A	0.51	0.57	0.54	0.41			SKIN, GI, BLD	13 organs			5 altered motifs		SYNGR2	SYNGR2	intronic	5

*LD calculation was limited to the 1000G phase 1 ASN population and the threshold was set to r2>=0.8

†RegulomeDB scores: 1a, eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak;1b, eQTL + TF binding + any motif + DNase Footprint + DNase peak;1c, eQTL + TF binding + matched TF motif + DNase peak;binding + matched TF motif;
1d, eQTL + TF binding + any motif + DNase peak;1e, eQTL + TF;1f, eQTL + TF binding / DNase peak;2a, TF binding + matched TF motif + matched DNase Footprint + DNase peak;2b,TF binding + any motif + DNase Footprint + DNase peak;+ any motif + DNase peak;
2c, TF binding + matched TF motif + DNase peak;3a, TF binding; 3b, TF binding + matched TF motif;4, TF binding + DNase peak;5, TF binding or DNase peak;6, other