

Target ID	position	correlation coefficient	p value	q value	exp mean	meth mean	H3k27Ac	transcription factors	location
cg27120934	129480619						no	polr2a	intronic
cg02645710	85430085	-0.1881684	0.01877	0.005184	3.3067569	0.267062	no	polr2a,sin3a,yy1	promoter
cg25697769	39097335						high	polr2a,atf2,phf8	promoter
cg04868078	197898229						moderate	gabpa,elf1	exoniccoding
cg23680282	85430336	-0.2844	0.02063	0.002832	0.8488	0.117552	high	polr2a,sin3a,yy1	first intron
cg24132989	88050339						no	none	intronic
cg21364560	95242555	-0.2940194	0.01687	0.002729	10.6345684	0.21759	no	polr2a,e2h2,ctcf,egr1	promoter
cg08821669	120875978	-0.1948	0.000799	0.0003744	11.521848	0.021354	high	polr,ctcf	1stexoncoding
cg14905634	73057369						no	none	1stexonicnoncoding
cg17030055	24645065	-0.1965188	0.01375	0.003963	5.1615058	0.069254	no	polr2a	1stexonicnoncoding
cg11641791	38821429	-0.3949692	0.001122	0.0003591	4.4024256	0.135569	no	no	promoter
cg17728974	105403577						high	polr2a,sin3a	promoter
cg11792281	26443366						no	none	intronic
cg12414181	75287860						no	polr2a,mx11,znf143	promoter
cg02062326	75643727	-0.3113	5.606E-08	1.263E-08	12.6038617	0.06726	high	polr2a,max,gabpa	promoter
cg23274377	220263237	-0.3465128	0.00858	0.0024	9.3818711	0.038806	high	polr,ctcf	promoter
cg18803079	64014643	-0.2201	7.707E-07	5.486E-08	6.7982044	0.74987	no	none	promoter
cg13114458	75905515	-0.3169	7.249E-11	1.306E-11	9.6442085	0.04388	high	polr2a,gabpa,e2f1	promoter
cg01311718	214015137	-0.1869449	0.00000945	0.000000594	7.7274229	0.04322	high	polr2a,znf263	promoter
cg02609279	182325952	-0.4569764	0	0	8.189539	0.692826	high	polr2a,gata1	intronic
cg02071276	224303989	-0.2753	5.283E-10	5.051E-11	10.0044862	0.068616	no	ctcf,Rad21	intronic
cg18295068	166060400	-0.4428	5.466E-07	1.759E-07	6.2330279	0.101475	no	ctcf,Rad21,smc3	1stexonicnoncoding
cg15946310	159436034	-0.483	6.689E-07	5.514E-07	9.945	0.018556	high	polr2a,jun,gabpa,elf1	promoter
cg09365677	240061611	-0.2185	0.000001373	1.464E-07	4.808942	0.035882	no	ctcf,Rad21,smc3	1stexonicnoncoding
ch.11.319992F	319992						high	none	exonic
cg12092090	13617584	-0.2332	0.0001631	0.00001583	6.380564	0.062255	no	none	promoter
cg19533977	57719682	-0.2762	6.976E-08	8.195E-09	13.3620395	0.150087	no	runx3	intronic
cg01400516	47175936	-0.4589059	0.0003817	0.0001314	8.5733169	0.019579	moderate	polr2a,ctcf,gata2	1stintron
cg20101489	224467074	-0.1794531	0.000003681	2.008E-07	5.077037	0.088753	moderate	polr2aq,ctcf,sp2	1stexonicnoncoding
cg23134869	77593233	-0.4681	0	0	5.5618344	0.25591	high	polr2a,yy1	promoter
cg25477497	87228808	-0.6991858	0	0	9.461778	0.367254	no	foxa1,foxa2	exonic
cg25947619	86233220						moderate	polr2a,spi1	intronic
cg14534336	65028980						high	polr2a,stat3,taf1	1stexonicnoncoding
cg07002382	44116782						high	polr2a,cebpb,taf1	1stexonicnoncoding

cg08264335	44116782	-0.3934405	0.002639	0.0009381	9.6083289	0.052874	moderate	none	exonic
cg12273284	12490844	-0.4832	3.467E-08	1.327E-08	7.6487782	0.126881	no	none	intronic
cg26345971	85430215	-0.3811535	5.775E-10	8.988E-11	1.9994466	0.268673	no	polr2a,sin3a	intronic
cg10225640	121790611						high	polr2a,taf1	promoter
ch.1.3587792F	3587792						no	none	intronic
cg00719685	220263698						moderate	polr,ctcf	promoter
cg03814610	89744940						high	polr2a,znf263	promoter
cg17616217	89744940	-0.3216	0.00001986	0.000005823	9.5973308	0.1142	no	none	intergenic
cg19579903	30583082						high	polr2a,yy1,taf1	intronic
cg18469624	53459998	-0.1918	0.00003889	0.000003701	9.505816	0.11861	high	polr2a,etf1,max	promoter
cg10558887	36919409	-0.5807849	0	0	9.162	0.139128	high	none	1stintronic
cg16951385	65029115	-0.1848534	0.01334	0.003867	10.1485358	0.058096	high	polr2a,stat3,taf1	promoter
cg23404012	71066865	-0.2523	1.261E-09	1.281E-10	8.09469	0.046598	high	none	intronic
cg03547245	55335015	-0.3859	1.371E-14	4.337E-15	6.716429	0.08912	moderate	max,ctcf	intronic
cg12129209	102276033	-0.4256	0	0	11.248696	0.059091	high	polr2a,txf1	promoter
cg03846926	21807211						moderate	taf1,cebpb	1stexonicnoncoding
cg26800788	63649371						no	none	promoter5
cg04254487	134304883	-0.5187	2.031E-09	9.363E-10	8.3824493	0.212056	moderate	ctcf,tebbp	intronic
cg08757862	38807382	-0.3392271	1.85E-19	2.194E-20	7.227838	0.612254	moderate	polr2a,ctcf,ikzf1	promoter
cg10944144	64777807	-0.2851448	1.317E-13	1.141E-14	2.971848	0.021102	high	polr2a,myc,atf2	promoter
cg02981003	134965914						no	none	promoter
cg26401673	43431343	-0.3162	2.53E-13	3.317E-14	8.9418901	0.846658	high	polr2a,gata2,fos	intronic
ch.2.800013F	800013						no	none	intronic
cg19781109	91244526						no	none	intronic
cg06237608	91244584						no	none	promoter5
cg25510609	86233236						high	polr2a,spi1,max	intronic
cg02558537	107328586	-0.4164131	0	0	8.177458	0.027635	high	polr2a,yy1,e2f1	promoter
cg11378242	244999800	-0.2903	1.73E-16	1.529E-17	10.08	0.017718	high	polr2a	1stintronic
cg17485454	87,281,281						no	polr2a,yy1,spi1	1stexonicnoncoding
cg04838988	70984437						no	e2h2,rbbp5	promoter
cg27509202	35484972						high	polr2a,jun,fos	1stexonicnoncoding
cg19021985	22398190	-0.2973	5.944E-09	7.885E-10	7.7477895	0.779761	moderate	polr2a,SPI1	1stexonicnoncoding
cg00994804	36259383						high	polr2a,rbb5	exoniccoding
ch.1.659794R	659794						moderate	none	promoter
cg22664298	29680347						no	none	intergenic