Supplementary Table 1. Panel of HS2 sgRNA protospacer target sequences.

Cr#	Protospacer	PAM	Strand
1	gagacacacagaaatgtaac	AGG	+
2	ggactatgggaggtcactaa	TGG	+
3	ggtggggcactgaccccgac	AGG	-
4	gaaggttacacagaaccaga	AGG	+
5	ctagagtgatgactcctatc	TGG	-
6	gactaaaactccacctcaaa	CGG	-
7	gccctgtaagcatcctgctg	GGG	+
8	gctcatgcttggactatggg	AGG	+
9	gttctggccaggcccctgtc	GGG	-
10	aatatgtcacattctgtctc	AGG	+
11	agtgccccacccccgccttc	TGG	+
12	gtggggcactgaccccgaca	GGG	+
13	aaccttctaagcaaaccttc	TGG	-
14	gttacacagaaccagaaggc	GGG	+
15	agtcatgatgagtcatgctg	AGG	-
16	gatgagtcatgctgaggctt	AGG	-
17	actctaggctgagaacatct	GGG	+
18	gtccccagcaggatgcttac	AGG	-
19	cagggcagatggcaaaaaaa	AGG	-
20	gaggtggagttttagtcagg	TGG	+
21	aaacggcatcataaagaaaa	TGG	-

Supplementary Table 2. Significant genomic windows for RNA-seq of dCas9-KRAB + Cr4 compared to un-transduced (No LV) control cells.

id	**Gene**	**foldChange**	**log2FoldChange**	**pval**	**padj**
NM_005330	***HBE1***	0.09	-3.51	4.32E-41	1.76E-36
NM_000184	***HBG2***	0.25	-2.03	1.20E-16	2.43E-12
NM_000559	***HBG1***	0.29	-1.81	9.57E-14	1.30E-09
NM_013271	***proprotein convertase subtilisin/kexin type 1 inhibitor (PCSK1N)***	22.17	4.47	3.81E-12	3.88E-08
NM_006169	***NNMT (methyltransferase)***	0.23	-2.15	1.01E-11	8.19E-08
NM_002166	***inhibitor of DNA binding 2 (ID2)***	0.30	-1.75	4.28E-09	2.90E-05
NM_002167	***inhibitor of DNA binding 3 (ID3)***	0.26	-1.96	5.29E-09	3.08E-05
NM_001099456	***neuropeptide W (NPW)***	4.57	2.19	1.59E-08	8.11E-05
NM_138618	***Rh blood group, CcEe antigens (RHCE)***	0.38	-1.39	1.81E-06	0.00817
NM_020485	***Rh blood group, CcEe antigens (RHCE)***	0.40	-1.32	2.14E-06	0.00872
NM_015150	***raftlin, lipid raft linker 1 (RFTN1)***	7.79	2.96	2.63E-06	0.00974

Supplementary Table 3. Significant genomic windows for RNA-seq of dCas9-KRAB + Cr10 compared to un-transduced (No LV) control cells.

id	Gene	foldChange	log2FoldChange	pval	padj
NM_005330	***HBE1***	0.13	-2.97	2.70E-31	1.10E-26
NM_013271	***proprotein convertase subtilisin/kexin type 1 inhibitor (PCSK1N)***	24.00	4.58	1.11E-12	2.26E-08
NM_006169	***NNMT (methyltransferase)***	0.26	-1.96	2.61E-10	3.54E-06
NM_002167	***inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3)***	0.26	-1.95	5.83E-09	4.75E-05
NM_000184	***HBG2***	0.38	-1.40	5.84E-09	4.75E-05
NM_001099456	***neuropeptide W (NPW)***	4.69	2.23	1.04E-08	7.08E-05
NM_000559	***HBG1***	0.42	-1.26	1.56E-07	0.00091
NR_027349	***miR-17-92 cluster host gene (MIR17HG)***	3.82	1.94	2.35E-07	0.0012
NM_001124758	***spinster homolog 2 (Drosophila) (SPNS2)***	2.61	1.39	4.25E-07	0.00192
NR_027350	***miR-17-92 cluster host gene (MIR17HG)***	2.43	1.28	6.07E-07	0.00247
NM_005354	***jun D proto-oncogene (JUND)***	2.25	1.17	1.70E-06	0.0063
NM_078467	***cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A)***	0.37	-1.43	2.12E-06	0.00721
NM_000927	***ATP-binding cassette, sub-family B (MDR/TAP)***	0.23	-2.11	2.78E-06	0.0087

Supplementary Table 4. Significant genomic windows for RNA-seq of dCas9 + Cr4 compared to un-transduced (No LV) control cells.

id	**Gene**	**foldChange**	**log2FoldChange**	**pval**	**padj**
NM_006169	***NNMT (methyltransferase)***	0.249052867	-2.00548	9.26E-11	3.77E-06
NM_005354	***jun D proto-oncogene (JUND)***	2.615147754	1.386892	1.37E-08	0.000279
NM_002167	***inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3)***	0.288029008	-1.79571	6.94E-08	0.000799
NM_001099456	***neuropeptide W (NPW)***	4.209558093	2.073669	7.85E-08	0.000799
NM_001124758	***spinster homolog 2 (Drosophila) (SPNS2)***	2.687743739	1.426396	1.85E-07	0.001504
NM_003378	***VGF nerve growth factor inducible (VGF)***	3.470490126	1.795139	3.21E-07	0.002177
NM_000479	***anti-Mullerian hormone (AMH)***	3.748840994	1.906445	1.23E-06	0.006271
NM_206833	***cortexin 1 (CTXN1)***	2.313638379	1.210163	1.16E-06	0.006271

Supplementary Table 5. Significant genomic windows for RNA-seq of dCas9 + Cr10 compared to un-transduced (No LV) control cells.

id	Gene	foldChange	log2FoldChange	pval	padj
NM_002167	***inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3)***	0.2144	-2.221	3.97E-11	1.62E-06
NM_006169	***NNMT (methyltransferase)***	0.3079	-1.700	2.82E-08	0.0005745
NR_027349	***miR-17-92 cluster host gene (MIR17HG)***	4.0907	2.032	4.76E-08	0.0006454
NM_017521	***FEV (ETS oncogene family) (FEV)***	3.4844	1.801	5.32E-07	0.005417
NM_005354	***jun D proto-oncogene (JUND)***	2.2737	1.185	8.84E-07	0.007197
NM_001099456	***neuropeptide W (NPW)***	3.6778	1.879	1.44E-06	0.009782

Supplementary Table 6. Significant genomic windows for RNA-seq of dCas9-KRAB compared to un-transduced (No LV) control cells.

id	Gene	foldChange	log2FoldChange	pval	padj
NM_006169	***NNMT (methyltransferase)***	0.223744062	-2.1600787	5.85E-12	2.38E-07
NM_002167	***inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3)***	0.229528919	-2.123252163	2.86E-10	5.82E-06
NM_001099456	***neuropeptide W (NPW)***	5.214784095	2.382607523	7.70E-10	1.04E-05
NM_000032	***5'-aminolevulinate synthase 2 (ALAS2)***	0.353630952	-1.499683543	8.85E-09	9.01E-05
NM_024807	***triggering receptor expressed on myeloid cells-like 2 (TREML2)***	0.317645973	-1.654508363	1.60E-08	0.000108
NM_001037968	***5'-aminolevulinate synthase 2 (ALAS2)***	0.356363009	-1.488580505	1.45E-08	0.000108
NM_020485	***Rh blood group, CcEe antigens (RHCE)***	0.335709582	-1.574714381	1.99E-08	0.000115
NR_027349	***miR-17-92 cluster host gene (MIR17HG)***	4.20562831	2.072321352	2.87E-08	0.000146
NM_001037967	***5'-aminolevulinate synthase 2 (ALAS2)***	0.364621296	-1.455529269	3.36E-08	0.000152
NM_001114138	***dematin actin binding protein (DMTN)***	0.341936239	-1.548200763	4.82E-08	0.000196
NM_005354	***jun D proto-oncogene (JUND)***	2.458625102	1.297851766	1.04E-07	0.000383
NM_001018007	***tropomyosin 1 (alpha) (TPM1)***	0.371349353	-1.429151031	5.05E-07	0.001714
NM_004163	***RAB27B, member RAS oncogene family (RAB27B)***	0.350906617	-1.510840942	6.08E-07	0.001904
NM_001114137	***dematin actin binding protein (DMTN)***	0.36437456	-1.456505859	7.69E-07	0.002237
NM_001124758	***spinster homolog 2 (Drosophila) (SPNS2)***	2.545444408	1.347917558	8.80E-07	0.002389
NM_013271	***proprotein convertase subtilisin/kexin type 1 inhibitor (PCSK1N)***	9.346196033	3.224379298	1.11E-06	0.002816
NM_001978	***dematin actin binding protein (DMTN),***	0.407601694	-1.294768049	1.86E-06	0.004452
NM_001256008	***patatin-like phospholipase domain containing 8 (PNPLA8)***	0.401853137	-1.315259749	1.99E-06	0.004507
NM_002166	***NA binding 2, dominant negative helix-loop-helix protein (ID2)***	0.385590691	-1.374857871	2.56E-06	0.004998
NM_001114135	***dematin actin binding protein (DMTN)***	0.410773745	-1.28358412	2.58E-06	0.004998
NM_001114136	***dematin actin binding protein (DMTN)***	0.412356004	-1.278037682	2.52E-06	0.004998
NM_003378	***VGF nerve growth factor inducible (VGF)***	3.145288414	1.653192314	3.11E-06	0.005497
NM_006848	***coiled-coil domain containing 85B (CCDC85B)***	2.347641144	1.231211898	3.02E-06	0.005497
NM_213652	***hemochromatosis type 2 (juvenile) (HFE2)***	0.302825541	-1.723441206	3.38E-06	0.005741
NM_016124	***Rh blood group, D antigen (RHD)***	0.429779759	-1.218330557	3.66E-06	0.005966
NM_001114139	***dematin actin binding protein (DMTN)***	0.412855951	-1.276289595	4.20E-06	0.006483
NM_138618	***Rh blood group, CcEe antigens (RHCE)***	0.398450828	-1.327526399	4.30E-06	0.006483
NM_002587	***protocadherin 1 (PCDH1)***	0.39896065	-1.325681635	5.81E-06	0.008445
NM_001184797	***trimethyllysine hydroxylase, epsilon (TMLHE)***	0.414557265	-1.270356692	6.58E-06	0.009233

Supplementary Table 7. Significant genomic windows for anti-FLAG ChIP-seq of dCas9-KRAB + Cr4 compared to with dCas9-KRAB with no sgRNA. Cr4 protospacer sequence is located at chr11:5302033-5302052. * indicates that genomic window contains the full Cr4 target sequence.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains Seed Sequence: 5' CCAGANGG 3'**	**Located within gene?**	**Gene**
chr11: 5301749-5302337*	2.81	2.94E-24	9.22E-20	Yes	No	-
chr19: 50163899-50164161	1.54	5.01E-06	.0785	Yes	Yes	*IRF3*

Supplementary Table 8. Significant genomic windows for anti-FLAG ChIP-seq of dCas9-KRAB + Cr10 compared to dCas9-KRAB with no sgRNA. Cr10 protospacer sequence is located at chr11: 5301800-5301819. * indicates that genomic window contains the full Cr10 target sequence.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains Seed Sequence: 5' GTCTCNGG 3'**	**Located within gene?**	**Gene**
chr11: 5301749-5302337*	1.79	1.23E-10	3.86E-06	Yes	No	-

Supplementary Table 9. Significant genomic windows for anti-FLAG ChIP-seq of dCas9-KRAB + Cr4 compared to dCas9 + Cr4. Cr4 protospacer sequence is located at chr11:5302033-5302052.

Location	$\log_2$(Fold Change)	p-value	FDR	Contains seed sequence: 5' CCAGANGG 3'	Located within gene?	Gene
chr2: 3005381-3005638	-1.89	1.32E-08	4.14E-04	Yes	No	-

Supplementary Table 10. Significant genomic windows for H3K9 tri-methylation ChIP-seq of dCas9-KRAB + Cr4 compared to dCas9-KRAB without sgRNA. Cr4 protospacer sequence is located at chr11:5302033-5302052. * indicates that genomic window contains the full Cr4 target sequence.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains Seed Sequence: 5' CCAGANGG 3'**	**Located within gene?**	**Gene**
chr11: 5299712-5300301	2.34	2.57E-27	1.62E-21	No	No	-
chr11: 5301862-5302715*	2.55	2.01E-26	6.30E-21	Yes	No	-
chr10: 104593626-104593861	1.89	9.70E-15	2.03E-09	No	Yes	*CYP17A1*
chr1: 212292343-212293213	1.69	1.60E-12	2.51E-07	Yes	No	-
chr19: 50162440-50164657	1.17	2.92E-12	3.67E-07	Yes	Yes	*IRF3*
chr11: 5305857-5306185	1.62	2.56E-11	2.68E-06	Yes	No	-
chr11: 5304696-5305089	1.46	1.64E-09	0.000148	No	No	-
chr15: 63335520-63336583	1.22	3.28E-09	0.000258	Yes	Yes	*TPM1*
chrX: 71498037-71498803	1.35	1.75E-08	0.001219	Yes	No	-
chr6: 3090860-3094479	-0.74	1.22E-07	0.007662	No	Yes	*RIPK1*
chr8: 15483400-15485560	-0.83	1.78E-07	0.010144	Yes	Yes	*TUSC3*
chr16: 71971752-71973376	-0.80	1.96E-07	0.010284	No	Yes	*PKD1L3*
chr14: 73674302-73676117	-0.87	2.68E-07	0.012955	Yes	Yes	*PSEN1*
chr11: 76688558-76690234	-0.84	9.25E-07	0.04151	Yes	Yes	*ACER3*
chr8: 10872937-10874459	0.92	1.08E-06	0.04525	Yes	Yes	*XKR6*

Supplementary Table 11. Top significant genomic windows for H3K9 tri-methylation ChIP-seq of dCas9-KRAB + Cr10 compared to dCas9-KRAB without sgRNA. Cr10 protospacer sequence is located at chr11:5301800-5301819.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains Seed Sequence: 5' GTCTCNGG 3'**	**Located within gene?**	**Gene**
chr11:5299712-5300301	2.52	2.00E-32	1.26E-26	No	No	-
chr11:5301862-5302715	2.40	1.15E-23	3.60E-18	No	No	-
chr10:104593626-104593861	1.5299391	3.53E-10	0.000074	No	Yes	*CYP17A1*

Supplementary Table 12. Top significant genomic windows for H3K9 tri-methylation ChIP-seq of dCas9-KRAB +Cr4 compared to dCas9 + Cr4. Cr4 protospacer sequence is located at chr11:5302033-5302052. * indicates that genomic window contains the full Cr4 target sequence.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains Seed Sequence 5'CCAGANGG3'**	**Located within gene?**	**Gene**
chr11: 5301862-5302715	2.459	9.25E-25	5.81E-19	Yes	No	-
chr11: 5299712-5300301	2.041	3.46E-22	1.09E-16	No	No	-
chr10: 104593626-104593861	1.681	5.46E-12	1.14E-06	No	Yes	*CYP17A1*
chr8: 15483400-15485560	-1.005	2.31E-10	3.62E-05	Yes	Yes	*TUSC3*
chr11: 5304696-5305089	1.517	3.73E-10	4.03E-05	Yes	No	-
chr11: 5305857-5306185	1.518	3.85E-10	4.03E-05	No	No	-
chr19: 50162440-50164657	1.022	8.92E-10	8.01E-05	Yes	Yes	*IRF3*
chr1: 212292343-212293213	1.389	5.07E-09	3.98E-04	Yes	Yes	*DTL*
chr15: 63335520-63336583	1.195	7.24E-09	5.05E-04	Yes	Yes	*TPM1*
chr17: 25827626-25828098	-1.160	1.59E-08	9.97E-04	No	No	-
chr6: 3090860-3094479	-0.7661	3.77E-08	2.15E-03	Yes	No	-
chr5: 34727454-34728284	-0.9300	5.96E-08	3.10E-03	Yes	Yes	*RAI14*
chr2: 170612855-170613645	-1.148	6.42E-08	3.10E-03	Yes	No	-
chr11: 76688558-76690234	-0.9194	7.90E-08	3.54E-03	Yes	Yes	*ACER3*
chr14: 73674302-73676117	-0.9017	9.45E-08	3.96E-03	Yes	Yes	*PSEN1*
chr3: 195999724-196001313	-0.9045	1.25E-07	4.92E-03	Yes	Yes	*PCYT1A*
chr1: 155660498-155661143	-0.9290	1.41E-07	5.21E-03	Yes	Yes	*DAP3*
chr5: 171350838-171352308	-0.9185	1.54E-07	5.36E-03	Yes	Yes	*FBXW11*
chr6: 126273775-126275090	-0.9191	1.81E-07	5.97E-03	No	No	-
chr19:10409016-10410198	-0.9645	2.16E-07	6.60E-03	No	No	-
chr15: 78595790-78597261	-0.9210	2.21E-07	6.60E-03	Yes	No	-
chr9: 140440257-140441548	-0.8757	2.44E-07	6.98E-03	No	Yes	*PNPLA7*
chr1: 16295182-16296434	-0.8780	2.67E-07	7.30E-03	No	Yes	*ZBTB17*
chr4: 83301473-83302766	-0.8206	3.24E-07	8.47E-03	Yes	No	-
chr10:72381898-72383107	-0.9214	4.30E-07	1.08E-02	No	No	-

Supplementary Table 13. Top significant genomic windows for H3K9 tri-methylation ChIP-seq of dCas9-KRAB + Cr10 compared to dCas9 + Cr10. Cr10 protospacer sequence is located at chr11:5301800-5301819.

Location	log2(Fold Change)	p-value	FDR	Contains seed sequence: 5' GTCTCNGG 3'	Located within gene?	Gene
chr11: 5299712-5300301	2.55	1.34E-32	8.45E-27	No	No	-
chr11: 5301862-5302715	2.42	5.42E-24	1.70E-18	No	No	-

Supplementary Table 14. Top 20 significant genomic windows by p-value for DNase-seq of dCas9-KRAB + Cr4 compared to dCas9-KRAB without sgRNA. Cr4 protospacer sequence is located at chr11:5302033-5302052. * indicates that genomic window contains the full Cr4 target sequence.

Location	**$\log_2$(Fold Change)**	**p-value**	**FDR**	**Contains seed sequence: 5' CCAGANGG 3'**	**Located within gene?**	**Gene**
chr11: 5305806-5306106	-0.79	2.37E-07	1.48E-02	Yes	No	-
chr11: 5305943-5306243	-0.76	5.69E-07	1.78E-02	Yes	No	-
chr11: 5301772-5302072*	-0.71	4.33E-06	9.04E-02	Yes	No	-
chr11: 5275809-5276109	-0.68	8.52E-06	1.33E-01	No	No	-
chr11: 5276005-5276305	-0.60	6.19E-05	7.75E-01	No	No	-
chr11: 5301930-5302230*	-0.60	1.57E-04	1.00E+00	Yes	No	-
chr11: 5271045-5271345	-0.54	3.08E-04	1.00E+00	Yes	No	-
chr11: 5270905-5271205	-0.55	3.15E-04	1.00E+00	No	No	-
chr15: 68132343-68132643	0.49	8.00E-04	1.00E+00	No	No	-
chr12: 125399026-125399326	0.48	8.79E-04	1.00E+00	Yes	Yes	*UBC*
chr5: 64558528-64558828	-0.53	9.47E-04	NA	No	Yes	*ADAMTS6*
chr9: 77735162-77735463	0.51	1.03E-03	NA	No	Yes	*OSTF1*
chr1: 145437591-145437891	0.51	1.58E-03	NA	No	Yes	*NBPF10*
chr5: 64558418-64558718	-0.48	2.73E-03	NA	No	Yes	*ADAMTS6*
chr18: 27967477-27967777	-0.46	3.03E-03	NA	No	No	-
chr7: 3038570-3038871	0.39	3.80E-03	NA	No	Yes	*CARD11*
chr1: 218477714-218478014	-0.46	4.28E-03	NA	No	Yes	*RRP15*
chr12: 132933359-132933659	0.46	4.54E-03	NA	Yes	No	-
chrX: 119115698-119115998	-0.46	4.62E-03	NA	No	No	-
chr5: 148186052-148186352	-0.44	4.79E-03	1.00E+00	Yes	No	-

Supplementary Table 15. Top 20 significant genomic windows by p-value for DNase-seq of dCas9-KRAB + Cr10 compared to dCas9-KRAB without sgRNA. Cr10 protospacer sequence is located at chr11:5301800-5301819. * indicates that genomic window contains the full Cr10 target sequence.

Location	**log2(Fold Change)**	**p-value**	**FDR**	**Contains seed sequence 5' GTCTCNGG 3'**	**Located within gene?**	**Gene**
chr11: 5301930-5302230	-0.96	3.37E-10	5.06E-05	No	No	-
chr11: 5301764-5302064*	-0.85	3.52E-08	2.64E-03	Yes	No	-
chr12: 125399122-125399422	0.48	5.23E-04	1.00E+00	No	Yes	*UBC*
chr11: 5305806-5306106	-0.52	6.42E-04	1.00E+00	No	No	-
chr12: 133727528-133727829	0.50	7.07E-04	1.00E+00	No	Yes	*ZNF268*
chr11: 5305943-5306243	-0.50	1.08E-03	1.00E+00	No	No	-
chr15: 68132314-68132614	0.50	1.34E-03	1.00E+00	No	No	-
chr12: 125398922-125399222	0.43	1.98E-03	1.00E+00	No	Yes	*UBC*
chr21: 40959332-40959633	0.44	2.37E-03	1.00E+00	No	No	-
chr19: 9846791-9847091	0.46	2.61E-03	1.00E+00	No	No	-
chr1: 15666787-15667087	0.45	3.24E-03	1.00E+00	No	Yes	*FHAD1*
chr11: 5275809-5276109	-0.44	3.63E-03	1.00E+00	No	Yes	*HBG2*
chr19: 9846695-9846995	0.44	4.50E-03	1.00E+00	No	No	-
chr6: 151162841-151163141	-0.40	4.77E-03	1.00E+00	No	Yes	*PLEKHG1*
chr11: 5279828-5280129	-0.44	5.03E-03	1.00E+00	No	Yes	*HBG2*
chr19: 58873265-58873565	0.43	5.58E-03	1.00E+00	No	Yes	*ZNF497*
chr18: 60125997-60126297	0.33	6.78E-03	1.00E+00	No	Yes	*ZCCHC2*
chr1: 1830655-1830955	0.41	7.27E-03	1.00E+00	No	Yes	*GNB1*
chr8: 102075041-102075341	-0.38	7.48E-03	1.00E+00	No	Yes	*YWHAZ*
chr2: 197188902-197189202	-0.37	7.67E-03	1.00E+00	No	Yes	*HECW2*

Supplementary Table 16. Primer sequences used for qPCR

Target	**Primer**
qPCR *GAPDH* Fwd	CAATGACCCCTTCATTGACC
qPCR *GAPDH* Rev	TTGATTTTGGAGGGATCTCG
qPCR *HBE1* Fwd	TCACTAGCAAGCTCTCAGGC
qPCR *HBE1* Rev	AACAACGAGGAGTCTGCCC
qPCR *HBG1/2* Fwd	GCTGAGTGAACTGCACTGTGA
qPCR *HBG1/2* Rev	GAATTCTTTGCCGAAATGGA
qPCR *HBB* Fwd	GCACGTGGATCCTGAGAACT
qPCR *HBB* Rev	ATTGGACAGCAAGAAAGCGAG
ChIP-qPCR GAPDH Fwd	ACAGTCCAGTCCTGGGAACC
ChIP-qPCR GAPDH Rev	CAGCCGCCTGGTTCAACTG
ChIP-qPCR HS2 GATA-2 Fwd	CTGGCTCAAGCACAGCAATG
ChIP-qPCR HS2 GATA-2 Rev	GTCAGGTGGTCAGCTTCTCC
ChIP-qPCR HS2 FOSL-1 Fwd	CCCATAGTCCAAGCATGAGCAGTTC
ChIP-qPCR HS2 FOSL-1 Rev	CTCTAGGCTGAGAACATCTGGGCAC