

Supplementary Table. 1 Q-PCR primer of genes

Gene Name	Forward Sequence (5'to3')	Reverse Sequence (5'to3')
<i>P30</i>	TGTTTCATGCGGGTAGCCTG	GGGCTCTTGCTCAAACAACG
<i>18L</i>	ATGGGAGGCTCTACAAGCAA	GATGCCGTTGTGGTGTCTA
<i>PE296R</i>	TTTACACCTAGGCGCTGTGG	TGTGGCGGCATCATTTAGGT
<i>P72</i>	CTGCTCATGGTATCAATCTTATCGA	GATACCACAAGATCAGCCGTA
<i>ARL4C</i>	TGCTGGTCATCGCCAACAAG	TTGAGGGACTTCCTGCGTTT
<i>CD163</i>	CAGAAGCGAAGACAGAGGCA	ACCAGGAGACAGAGGACTGTA
<i>CD244</i>	TCCTGAAGAAGGGACCACCA	ATGCTCTCTGTCCAACCTCTTG
<i>CD84</i>	ATCCCAGGCTAGACAGCAGA	GGCTATGCTAGCTCATGCCA
<i>MRC1</i>	CGGCTAGTAACGGCTAGTGG	GGCTCAGGCTTTGGTGTGTTG
<i>PTPRCAP</i>	CTGCTTGGAGAGCCTCAGAC	CAGGGCTGGAGGGGTTTTATT
<i>CD93</i>	GAGGGGTACAGGCCTCACTA	TCTCATCTCTATTCTTCACTCCGA
<i>CD69</i>	GAAATGTGTGTGGCGAGTGC	TCCTGGAATTTTTCCCCCTTTT
<i>KLRB1</i>	AACCCACATGTTGAAGTGCG	CTTTCAAGGCCGGAATCCCT
<i>CLEC12A</i>	TCTTGTAACCACACGATGGCA	CAGGCACTCAGCAAATGAGG
<i>NCR1</i>	GCTGGGTTCCGGCTAAGTAT	G TTCACGCTTCCAGGTGACT
<i>MSR1</i>	TGTCAAGTTCGATGCTCGCT	CCAGCACGACAAACACAAGG
<i>GAPDH</i>	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Supplementary Table. 2 sgRNA sequences targeting the *ARL4C* regulatory elements

sgRNA ID	sgRNA sequences	Target elements location
<i>ARL4C</i> -E1-sgRNA1	TTAGGAGGAGGAGGGAATCTTGG	chr15:134,350,054-134,350,252
<i>ARL4C</i> -E2-sgRNA2	AAAAGATTCATTCTCTGGAGAGG	chr15:134,366,607-134,366,805
<i>ARL4C</i> -E3-sgRNA3	TCTTCATCTGCAGGGGCACATGG	chr15:134,468,572-134,468,770
<i>ARL4C</i> -E4-sgRNA4	TGTGTTCCAAAGGCAGGCACTGG	chr15:134,481,487-134,481,685
<i>ARL4C</i> -P-sgRNA5	TTCAAAGTAGCTTCCTTGGCTGG	chr15:121,520,893-121,521,109

Supplementary Table. 3 Number of chromatin interactions identified by BL-HiCHIP data

Samples	Trim linker	Valid pairs	Cis reads	Trans reads	Loops
0 hip_rep1	393,585,897	126,915,894	96,806,817	30,109,077	73,106
0 hip_rep2	171,361,939	74,205,681	60,725,031	13,480,650	108,694
6 hip_rep1	207,265,323	73,170,013	60,392,975	12,777,038	86,543
6 hip_rep2	179,170,908	75,900,099	62,077,986	13,822,113	109,263

Supplementary Table. 4 Enrichment statistics for CUT&Tag and ATAC-seq reads

Sample name	Total_reads	Mapping_reads	Peak_number	Filter peaks	Merge Peak
H3K4me3_0 hpi_rep1	88,290,458	85,069,416	28,223	23,635	18,535
H3K4me3_0 hpi_rep2	138,169,466	133,676,431	26,714	21,582	
H3K4me3_6 hpi_rep1	128,380,366	124,496,653	22,699	18,711	16,694
H3K4me3_6 hpi_rep2	112,006,394	108,512,775	22,717	19,082	
H3K27ac_0 hpi_rep1	112,052,342	109,229,506	95,555	67,137	49,329
H3K27ac_0 hpi_rep2	83,904,536	81,626,977	101,390	73,092	
H3K27ac_6 hpi_rep1	106,639,284	104,219,713	100,322	67,728	50,544
H3K27ac_6 hpi_rep2	93,307,058	91,090,734	99,652	67,670	
H3K27me3_0 hpi_rep1	121,515,906	109,801,989	75,846	22,177	20,969
H3K27me3_0 hpi_rep2	109,961,884	100,365,059	78,601	25,029	
H3K27me3_6 hpi_rep1	85,715,944	78,030,980	59,495	14,445	12,495
H3K27me3_6 hpi_rep2	108,335,506	97,967,656	52,924	13,134	
Pol2_0 hpi_rep1	106,017,388	100,043,781	89,255	51,262	40,112
Pol2_0 hpi_rep2	72,575,692	68,081,286	84,377	54,300	
Pol2_6 hpi_rep1	97,496,094	92,567,599	97,815	55,764	46,293
Pol2_6 hpi_rep2	125,031,676	118,402,082	98,523	57,650	
0 hpi_IgG_rep1	67,862,722	62,054,757	-	-	-
0 hpi_IgG_rep2	69,902,124	64,161,364	-	-	
6 hpi_IgG_rep1	103,668,940	92,048,333	-	-	-
6 hpi_IgG_rep2	83,526,564	74,020,673	-	-	
0 hpi_PAM_ATAC_rep1	375,118,144	356,385,182	270,779	145,205	126,702
0 hpi_PAM_ATAC_rep2	394,134,862	372,742,893	273,585	147,035	
6 hpi_PAM_ATAC_rep1	399,122,804	383,681,215	270,772	157,620	144,422
6 hpi_PAM_ATAC_rep2	406,757,268	390,625,164	264,795	161,831	