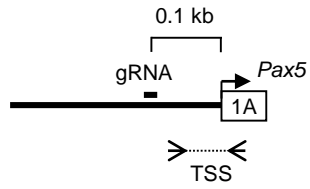


Supplementary Figure S1

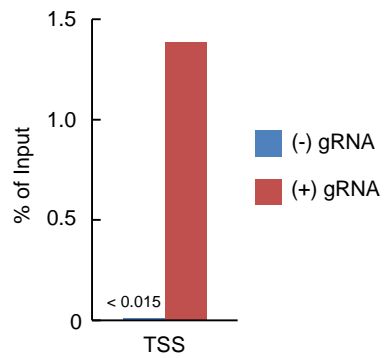
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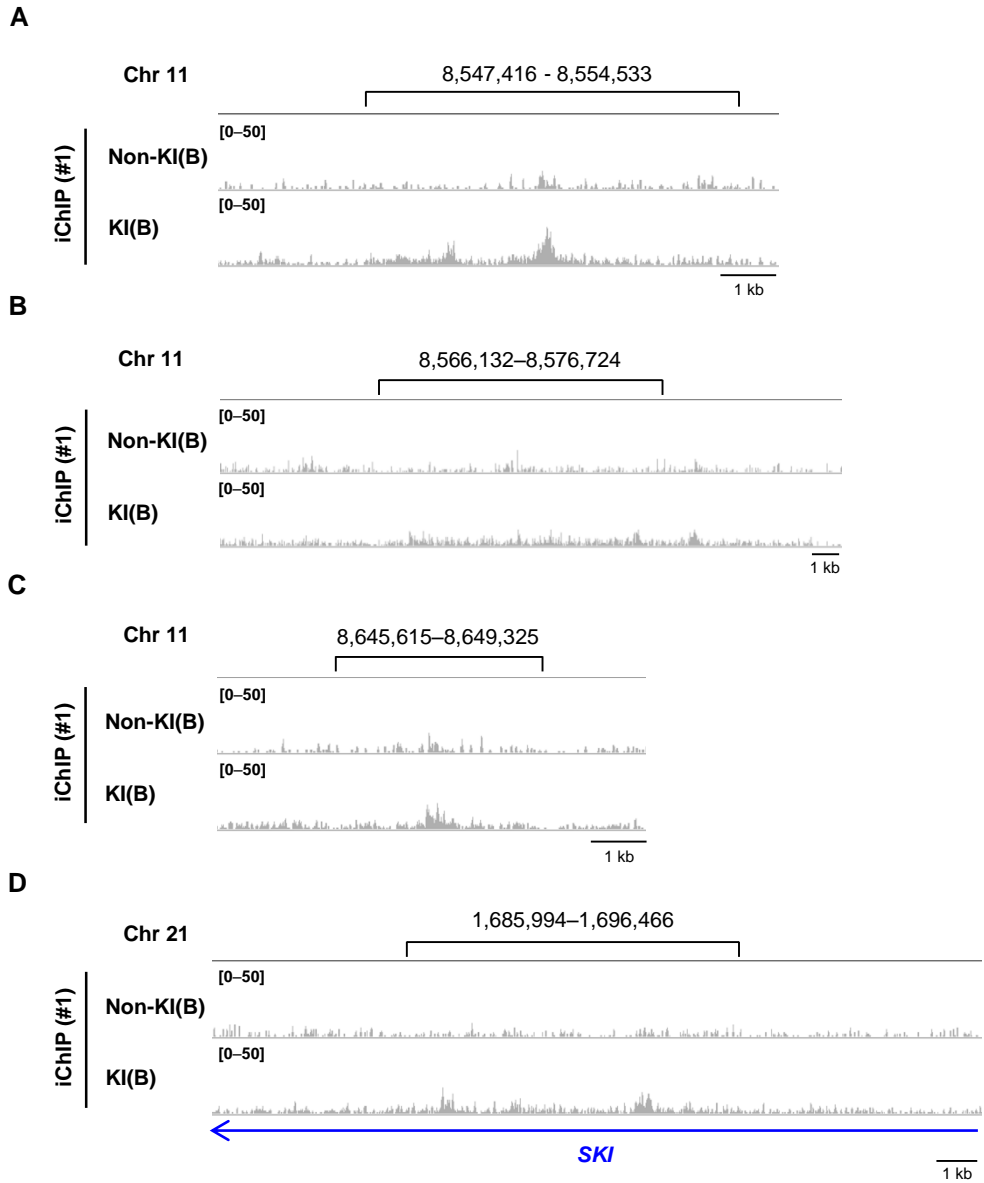
B

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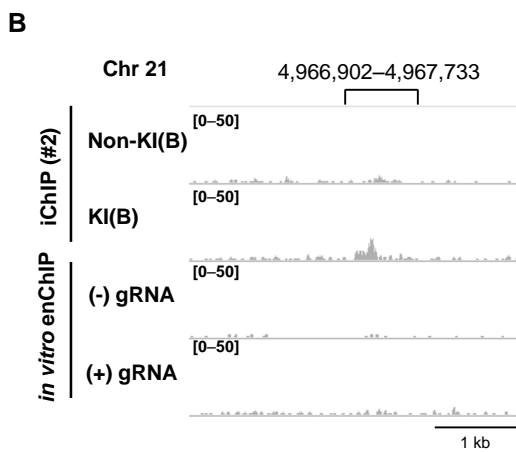
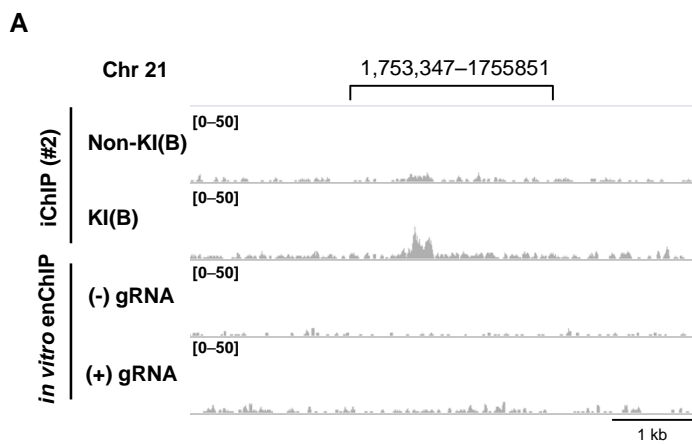
C



Supplementary Figure S2



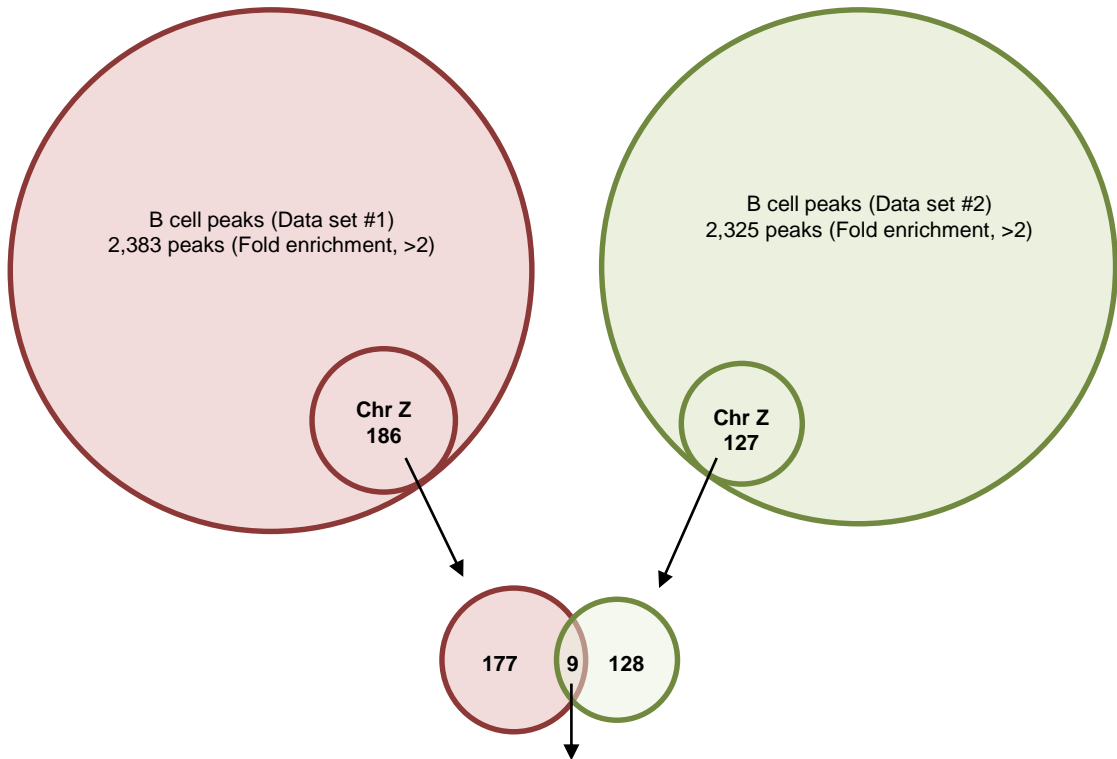
Supplementary Figure S3



Supplementary Figure S4

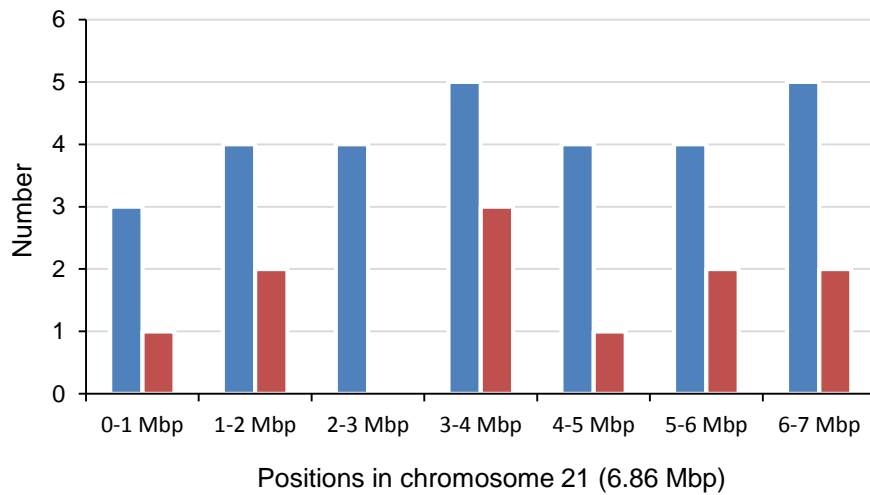
sequence	score	mismatches	locus
CGTCAGGCTCTGCTGGCCTCGG	0.6	3MMs [3:11:13]	chr3:-99566330
CGGGGGCCCTGGTGGCCTGGG	0.5	4MMs [4:5:9:11]	chr15:-11125782
TTGCAGGCCCGGCTGGCCTGGG	0.4	4MMs [1:2:9:13]	chr12:+11477384
TGTCAGGCTCTGCTGGCCTGGG	0.3	4MMs [1:3:11:13]	chr3:+99518274
CGGCAGCCACGGGTCCGCCTCGG	0.3	3MMs [7:9:15]	chr9:-908349
GGGCAGGATCGCGTGGCATTGG	0.3	4MMs [1:8:12:19]	chr4:+3876999
GGGCTGTCTCGGGTGGGCCTGGG	0.2	4MMs [1:5:7:16]	chr5:+57943847
CTGCAGGCTCCCGTGTCTCCTGAG	0.2	4MMs [2:11:12:17]	chr3:-17761948
GGGCAGGCCCGGGTGGCCTCAG	0.2	4MMs [1:8:9:16]	chr8:+7479787
AGGCAGGACCCGGTGTGCCTTGG	0.2	4MMs [1:8:9:16]	chr1:-34513890
CCGGAGGCTCCGGTGGCCTCAG	0.1	4MMs [2:4:11:16]	chrZ:+19851342
CTGCAGGCACGGCTGCACCTCGG	0.1	4MMs [2:9:13:17]	chr24:-1742686
CGGCGGGCGGGGTGTGCCTAGG	0.1	4MMs [5:9:10:16]	chr2:+85697950
AGGGAGGCTCGGGTGGGCCCGGG	0.1	4MMs [1:4:16:20]	chr2:+115166870
CGGCGTGTGGGGCGGCCTAGG	0.1	4MMs [5:6:10:14]	chr21:+671425
CTGCAGGCTGGGGTGCAGCTTGG	0.1	4MMs [2:10:17:18]	chr7:+29178289
CAGCAGGCTCTGGTGCACATGGG	0.1	4MMs [2:11:17:19]	chr9:-22780280
CTGCAGCCTCGAGTGGCCTCAG	0.1	4MMs [2:7:12:16]	chr5:+44604323
CGGCAGGCAGGGAGGCCTCGG	0.1	4MMs [9:10:11:14]	chr18:+5449056
CTGCAGGCTCAGGAGCCCTTGG	0.1	4MMs [2:11:14:17]	chr23:-3037645
GGGCAGGCTTGGGAGAGCCTGGG	0.0	4MMs [1:10:14:16]	chr27:+1435846
CTGCAGTCTCGGGTGGGACTTAG	0.0	4MMs [2:7:16:18]	chr4:+86154512
CGGCATCCTCGGGCCCGCCTGGG	0.0	4MMs [6:7:14:15]	chr4:-1601108
CGCCAGGCCCGGGAGAGCCTGAG	0.0	4MMs [3:9:14:16]	chr1:-34110060
CGGCAGGCTGGGGTGTGACCAAG	0.0	4MMs [10:16:18:20]	chr8:-21181895
CGGCATGCTCAGGTGTGTCTGAG	0.0	4MMs [6:11:16:18]	chrZ:+55687786
CGGCAGGCTCGGCTGTCCGTGGG	0.0	4MMs [13:16:17:19]	chr11:-1192610
CGGCAGGCTCGGATTAGCTCGG	0.0	4MMs [13:15:17:18]	chr23:+5009064
CGGCAGGCCCGGGAGCGGGTAAG	0.0	4MMs [9:14:18:19]	chrZ:+9069818

Supplementary Figure S5



Data set #1							Data set #2									
chr	start	end	length	summit	tags	$-\log_{10}(pvalue)$	fold_enrichment	start	end	length	summit	tags	$-\log_{10}(pvalue)$	fold_enrichment	fwd	rev
chrZ	331146	332935	1790	1495	103	85.73	4.17	331283	333044	1762	1431	110	55.55	2.77		
chrZ	8943565	8944403	839	303	46	54.81	5.41	8943522	8944983	1462	363	73	52.17	3.77		
chrZ	40367218	40367928	711	517	117	221.15	9.5	40367267	40368168	902	468	162	64.4	6.21		
chrZ	52573289	52574274	986	470	48	106.46	8.9	52573401	52573979	579	332	27	62.3	6.85		
chrZ	65614805	65616234	1430	559	142	69.47	6.07	65614834	65615956	1123	566	105	95.88	5.16		
chrZ	66066227	66070713	4487	1678	289	63.26	3.98	66066776	66070524	3749	1112	286	71.04	3.41		
chrZ	73039200	73040445	1246	503	138	60.37	4.84	73039175	73040354	1180	521	151	57.02	3.68		
chrZ	73405844	73406350	507	315	25	50.95	4.91	73405854	73406498	645	305	25	55.74	7.19		
chrZ	81611786	81613470	1685	1108	597	3100	115.99	81611754	81613591	1838	1161	526	3100	74.37	2090:PAX5:NM_204424,	

Supplementary Figure S6



- 29 peaks in chromosome 21, which were identified by iChIP-Seq (Step 3 in Figure 2)
- 11 peaks in chromosome 21, which were confirmed by *in vitro* enChIP-Seq (Figure 3D)

Supplementary Figure S7

LexA BE



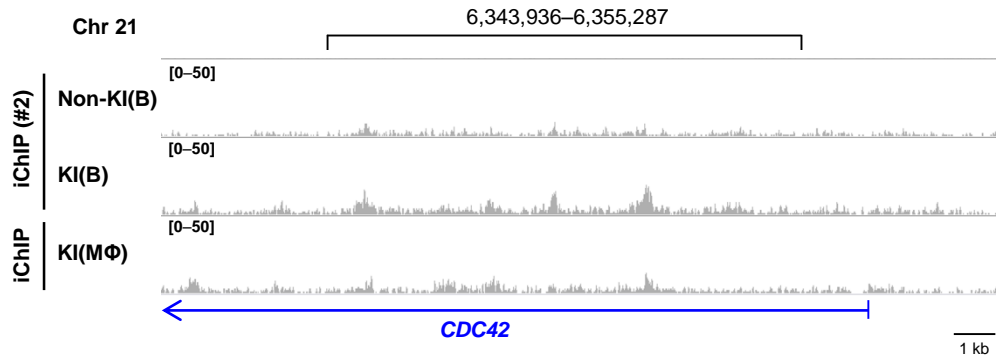
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-1

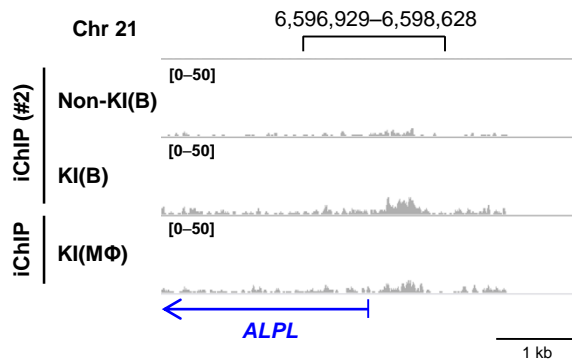
Pax5 gRNA

Supplementary Figure S8

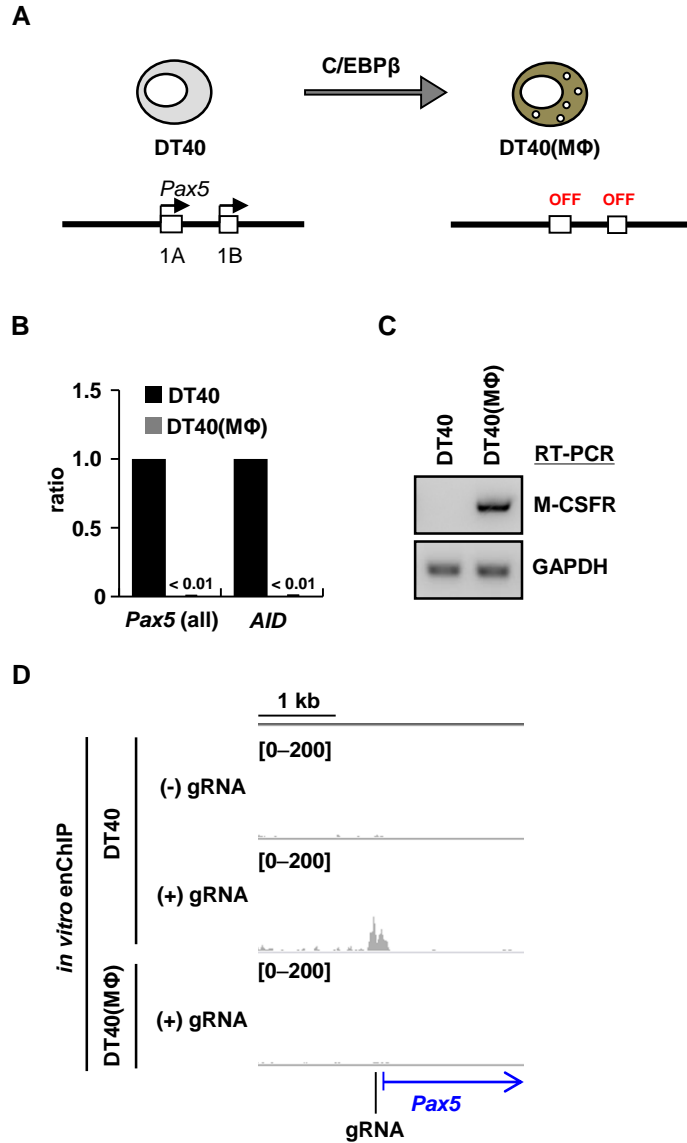
A



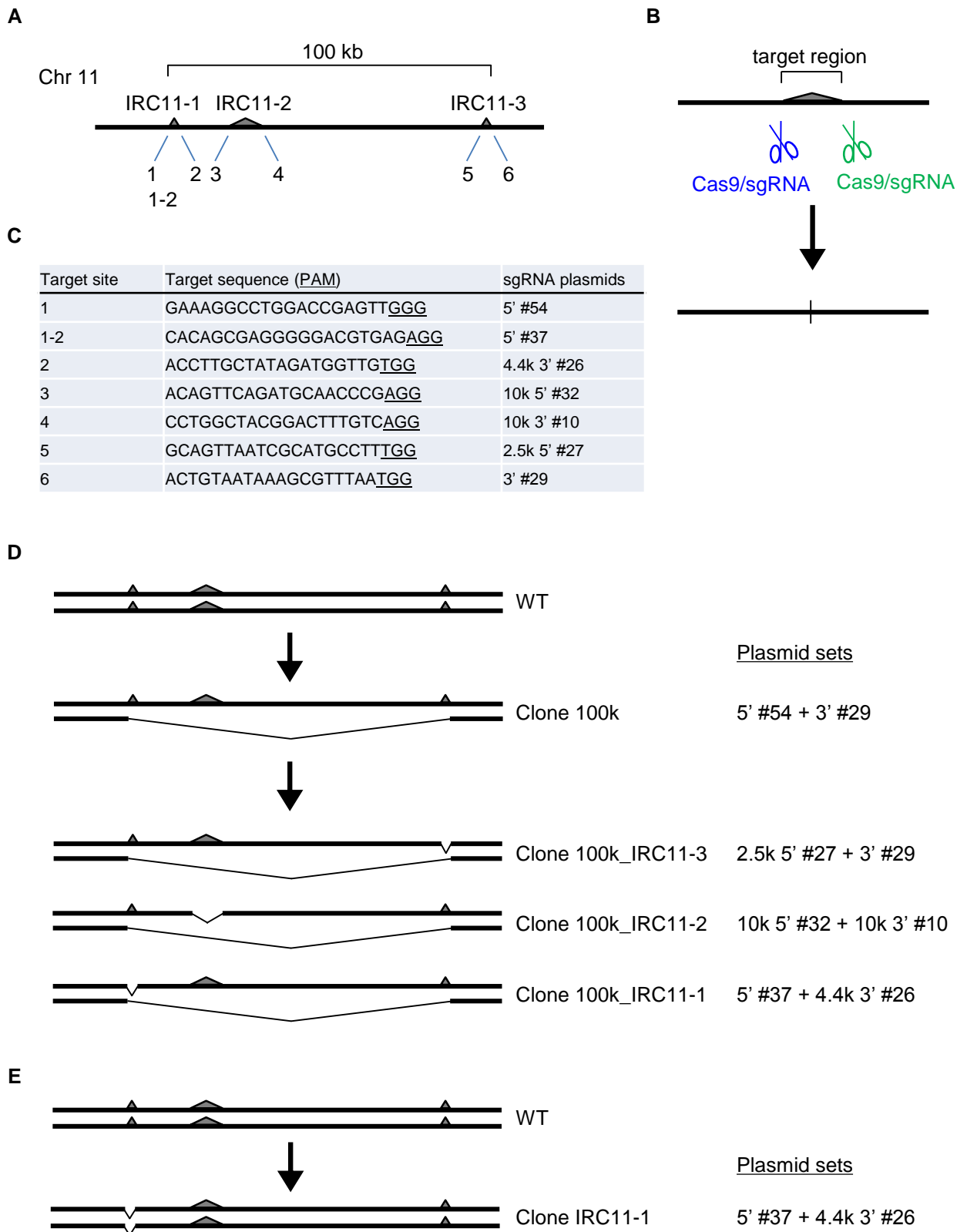
B



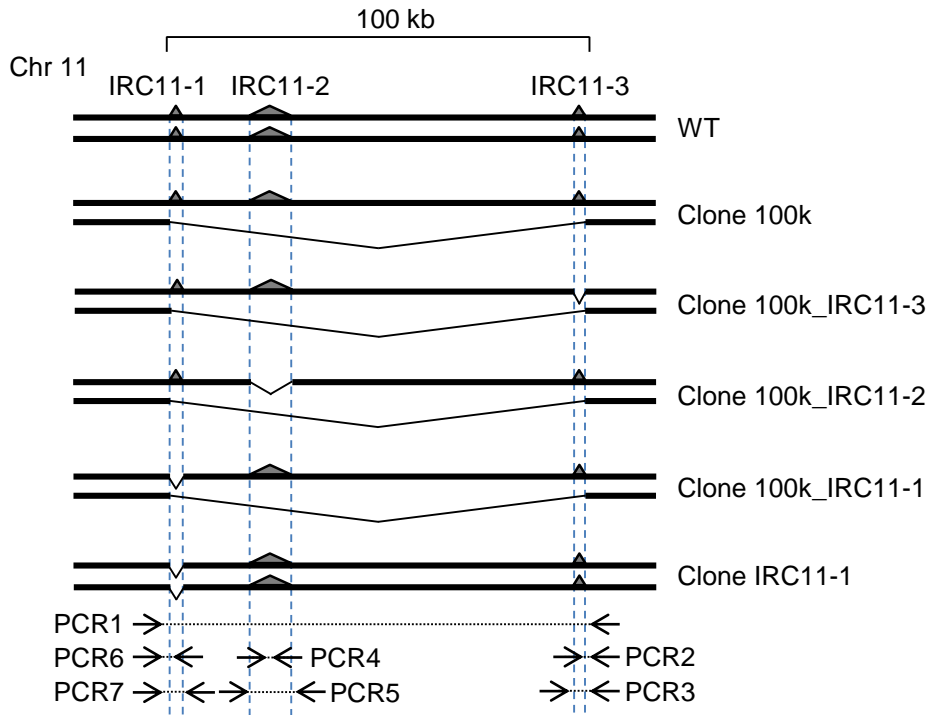
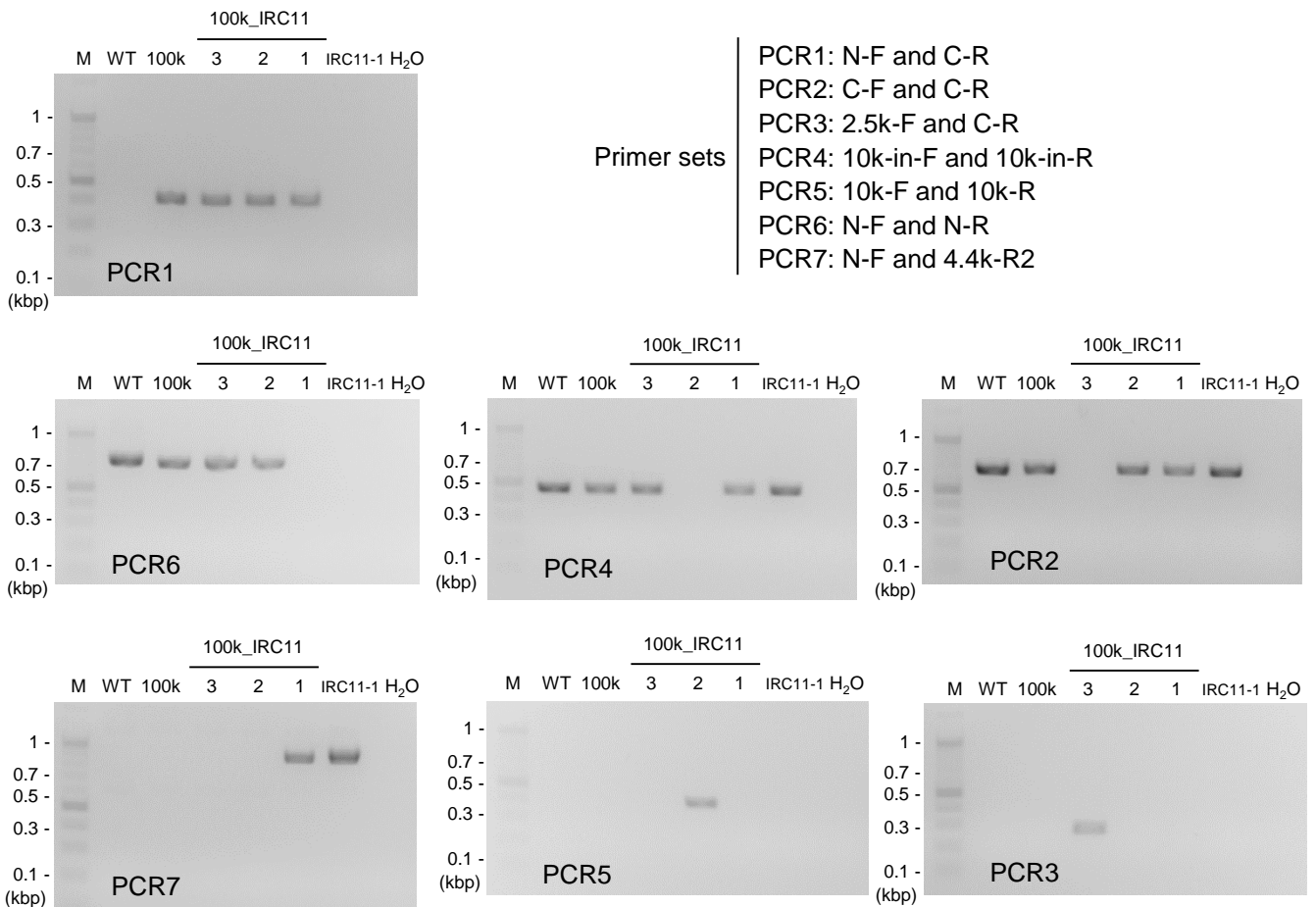
Supplementary Figure S9



Supplementary Figure S10



Supplementary Figure S11

A**B**

M: DNA ladder marker