

Supplementary Table 1 - ChIP-seq experiments

	GEO accession ID	Experiment ID	# of peaks	Single ChIP-specific (#)	Common (#)	Common (%)	Merged replica ChIPs
Stag1 ChIP in wild-type	GSM1979724	14549	27168	7595	19560	72%	27072
	GSM1979725	14954	20741	790		96%	
Stag1 ChIP in <i>Ctcf</i> KO	GSM1979726	14551	31487	6927	12533	64%	39292
	GSM1979727	19587	23380	1584		89%	
	GSM1979728	26233	39320	16001		44%	
Stag1 ChIP in <i>Smc3</i> KO	GSM1979729	19588	1487	116	1143	91%	5898
	GSM1979730	26234	6007	3200		26%	
	GSM1979731	27235	2956	349		77%	
Stag1 ChIP in <i>Wapl</i> KO	GSM1979732	19589	18659	1111	14775	93%	29418
	GSM1979733	20318	19938	738		95%	
	GSM1979734	26235	31193	10270		59%	
Stag1 ChIP in <i>Ctcf Wapl</i> DKO	GSM1979735	26236	n.a.	---	---	---	---
	GSM1979736	27237	n.a.	---	---	---	---
Scc1 ChIP in wild-type	GSM1979737	20093	19125	2463	16547	87%	22702
	GSM1979738	20105	19581	2883		85%	
Scc1 ChIP in <i>Ctcf</i> KO	GSM1979739	20094	26670	16572	7777	32%	39433
	GSM1979740	20106	37649	29818		21%	
	GSM2221806	27715	11790	3501		69%	
	GSM1979741	20095	1265	61		91%	
Scc1 ChIP in <i>Smc3</i> KO	GSM1979742	20319	4917	3208	635	17%	5003
	GSM1979743	27716	1577	442		59%	
	GSM1979744	20096	16112	313		98%	
Scc1 ChIP in <i>Wapl</i> KO	GSM1979745	20320	18728	534	13227	96%	28162
	GSM1979746	27717	31547	12746		51%	
	GSM1979747	26238	n.a.	---		---	
Scc1 ChIP in <i>Ctcf Wapl</i> KO	GSM1979748	27718	n.a.	---	---	---	---
Cohesin sites in wild-type	---	Scc1 (wt)	22702	1293	20889	94%	28335
	---	Stag1 (wt)	27072	6156		77%	
Cohesin sites in <i>Ctcf</i> KO	---	Scc1 (<i>Ctcf</i> KO)	39433	7911	30181	79%	46915
	---	Stag1 (<i>Ctcf</i> KO)	39292	8785		77%	
Cohesin sites in <i>Smc3</i> KO	---	Scc1 (<i>Smc3</i> KO)	5003	986	4006	80%	6883
	---	Stag1 (<i>Smc3</i> KO)	5898	1881		68%	
Cohesin sites in <i>Wapl</i> KO	---	Scc1 (<i>Wapl</i> KO)	29418	2823	25093	90%	31602
	---	Stag1 (<i>Wapl</i> KO)	28162	3688		87%	
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + 6h serum	GSM1979749	29071	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + 2.5h ActD	GSM1979750	29072	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + 5h ActD	GSM1979751	29073	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 0	GSM1979752	29074	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 2	GSM1979753	29075	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 4	GSM1979754	29076	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 6	GSM1979755	29077	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 8	GSM1979756	29078	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - day 10	GSM1979757	29079	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO - DRB	GSM1979758	32721	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + DRB	GSM1979759	32722	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + DRB + 30 min washout	GSM1979760	32723	n.a.	---	---	---	---
Scc1 ChIP in <i>Ctcf Wapl</i> DKO + DRB + 1 day washout	GSM1979761	32724	n.a.	---	---	---	---
H3K4me2 in wild-type	GSM1979762	16816	39536	4409	34701	89%	58221
	GSM1979763	18867	57332	19761		64%	
H3K4me2 in <i>Ctcf</i> KO	GSM1979764	16820	37290	1124	33671	97%	56011
	GSM1979765	18868	53818	19996		63%	
H3K4me2 in <i>Smc3</i> KO	GSM1979766	16826	33271	1444	30671	96%	57386
	GSM1979767	18869	61807	30207		50%	
H3K4me2 in <i>Wapl</i> KO	GSM1979768	16828	44824	513	42295	99%	72240
	GSM1979769	18870	73665	30944		58%	
H3K9ac in wild-type	GSM1979770	16818	24765	4066	20387	83%	35234
	GSM1979771	18871	27110	5247		80%	
H3K9ac in <i>Ctcf</i> KO	GSM1979772	16822	23822	6561	16663	72%	26880
	GSM1979773	18872	17565	609		96%	
H3K9ac in <i>Smc3</i> KO	GSM1979774	16824	20112	2827	17038	86%	28371
	GSM1979775	18873	21099	3327		84%	
H3K9ac in <i>Wapl</i> KO	GSM1979776	16830	21242	4254	16765	80%	32714
	GSM1979777	18874	19967	2558		87%	
open chromatin in wild-type	---	H3K4me2 (wt)	58221	31495	26064	45%	65405
	---	H3K9ac (wt)	35234	7848		77%	
open chromatin ChIP in <i>Ctcf</i> KO	---	H3K4me2 (<i>Ctcf</i> KO)	56011	32293	23556	42%	57243
	---	H3K9ac (<i>Ctcf</i> KO)	26880	1395		94%	
open chromatin ChIP in <i>Smc3</i> KO	---	H3K4me2 (<i>Smc3</i> KO)	57386	34830	22229	39%	61797
	---	H3K9ac (<i>Smc3</i> KO)	28371	4739		82%	
open chromatin ChIP in <i>Wapl</i> KO	---	H3K4me2 (<i>Wapl</i> KO)	72240	50218	21823	30%	75441
	---	H3K9ac (<i>Wapl</i> KO)	26893	3400		87%	
CTCF ChIP in wild-type	GSM1979778	9147	31648	1232	30297	96%	51694
	GSM1979779	27719	52193	21695		58%	
CTCF ChIP in <i>Ctcf</i> KO	GSM1979780	19593	11245	---	---	---	---
CTCF ChIP in <i>Smc3</i> KO	GSM1979781	12156	49609	6870	42731	86%	49609
	GSM1979782	27721	44803	1518		97%	
CTCF ChIP in <i>Wapl</i> KO	GSM1979783	9149	35841	989	34633	97%	57866
	GSM1979784	27722	58211	23062		60%	
Nipbl ChIP in 3T3 cells	GSM1979785	22603	28830	---	---	---	---
Wapl ChIP in 3T3 cells	GSM2430399	22604	12463	---	---	---	---

Supplementary Table 2 - RNA-seq and GRO-seq experiments

I. RNA-seq experiments

GEO accession number	Experiment ID	Abb	Genotype	Active Cre	Culturing
GSM1979794	12525	Wild-type	C57BL/6	---	10 d
GSM1979795	12526			Adeno-Cre	
GSM1979796	12527			---	
GSM1979797	12528			Adeno-Cre	
GSM1979798	12529	Wild-type	R26 (CreER/+)	---	10 d
GSM1979799	12530			OHT	
GSM1979800	12531			---	
GSM1979801	12532			OHT	
GSM1979802	11647	Ctcf KO	Ctcf (fl/fl)	---	10 d
GSM1979803	11649			Adeno-Cre	
GSM1979804	12535			---	
GSM1979805	12536			Adeno-Cre	
GSM1979806	9611	Smc3 KO	R26 (CreER/+) Smc3 (fl/fl)	---	10 d
GSM1979807	9612			OHT	
GSM1979808	10502		---		
GSM1979809	10503		OHT		
GSM1979810	9930		R26 (CreER/+) Smc3 (fl/-)	---	15 d
GSM1979811	9931			OHT	
GSM1979812	10504			---	
GSM1979813	10505			OHT	
GSM1979814	9934	Wapl KO	R26 (CreER/+) Wapl (fl/-)	---	10 d
GSM1979815	9935			OHT	
GSM1979816	10506			---	
GSM1979817	10507			OHT	
GSM1979818	28013	Ctcf Wapl KO	Ctcf (fl/fl) Wapl (fl/fl)	---	10 d
GSM1979819	28014			Adeno-Cre	
GSM1979820	30255			---	
GSM1979821	30256			Adeno-Cre	
GSM1979822	28018			Adeno-Cre	
					10 d; +6 h serum

II. GRO-seq experiments

GEO accession number	Experiment ID	Abb	Genotype	Active Cre	Culturing
GSM1979786	17593	Wild-type	R26 (CreER/+)	---	10 d
GSM1979787	17594			OHT	
GSM1979788	20107		C57BL/6	---	10 d
GSM1979789	20108			Adeno-Cre	
GSM1979790	30250	Ctcf Wapl KO	Ctcf (fl/fl) Wapl (fl/fl)	---	10 d
GSM1979791	30251			Adeno-Cre	
GSM1979792	30252			---	
GSM1979793	30253			Adeno-Cre	10 d; +3.5 h DRB
GSM2196441	32718			Adeno-Cre	
GSM2196442	32720			Adeno-Cre	
					10 d; +3.5 h DRB; +1 d no DRB

Supplementary Table 3 - Oligonucleotides

I. Genotyping oligonucleotides

	oligonucleotide sequence	PCR size
<i>Ctcf</i> (wild-type, floxed and deleted allele)	5'- CTAGGAGTGTAGTTCAGTGAGGCC	-3'
	5'- GCTCTAAAGAAGGTTGTGAGTTC	-3'
	5'- GCTTCCTCTTGAAAACACAC	-3'
	5'- TGCTACTAATCTCCACCTCACAG	-3'
<i>Smc3</i> (wild-type, floxed and deleted allele)	5'- CAGCCATCTTCGTCCAGAGCAGCGATTGGC	-3'
	5'- TGTGTCTATAAACACATGTATGC	-3'
	5'- AAGGCGCATAACGATACCAC	-3'
<i>Wapl</i> (wild-type, floxed and deleted allele)	5'- ACTGTTCCAGATAGCCCTGC	-3'
	5'- CCACTGCGGTTTCTGCATTG	-3'
	5'- AACAGTTGTGAGCCACTACC	-3'
CreER insertion in <i>Rosa26</i> locus	5'- GCGAAGAGTTTGTCCCTCAACC	-3'
	5'- GGAGCGGAGAAATGGATATG	-3'
	5'- AAAGTCGCTCTGAGTTGTTAT	-3'
Actin-Flipase	5'- GGTCCAACCTGCAGCCCAAGCTTCC	-3'
	5'- GTGGATCGATCTACCCCTTGCG	-3'

II. ChIP-qPCR oligonucleotides

Chr6 negative site	5'- TGCAGGTGGGATTAAGTGTG	-3'
	5'- CTACCCACCCCTATTCTCC	-3'
<i>Runx1</i>	5'- AGGCCTTGTCTGAAGTTTGG	-3'
	5'- CCTCCAGGTGAGACTGATCC	-3'
<i>Myc</i>	5'- GGGATCCTGAGTCGAGTATAA	-3'
	5'- CACTCCAGAGCTGCCTTCTTAG	-3'
Cohesin island-1	5'- TGGCCCTGGTAAGTTTTGAC	-3'
	5'- TCCAGCTTGCAACAGAATTG	-3'
Cohesin island-2	5'- TGCATCTCTTGTCTCACGG	-3'
	5'- GCCACAAGAAAAGCTCTGG	-3'
<i>Bzw1</i>	5'- TTTAGGGTGGGACAGAGACG	-3'
	5'- GCGAAGAGAAAAGAGCCAGA	-3'
<i>Pabpc1</i>	5'- AAAGAGCGTTAACCCGTCAG	-3'
	5'- GGTAGGAGAACGAGGCAGTT	-3'
CTCF site 1	5'- TCCATCAAGTTCAGAGCAGGTA	-3'
	5'- GCAGCATACGCTTACGTTACAG	-3'
TTS	5'- GGTTAGGAACGGGTTAACTTT	-3'
	5'- GTCTTGACTGTTCCATCTTCC	-3'

III. GRO-seq oligonucleotides

RT_oligonucleotide	5'- AGACGTGTGCTCTTCCGATCT	-3'
M_fw	5'- AATGATACGGCGACCCAGATCTACACTCTTCCCTACACGACGCTCTTCCGATCT	-3'
M1_rev	5'- CAAGCAGAAGACGGCATAACGAGATATCACGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M2_rev	5'- CAAGCAGAAGACGGCATAACGAGATCGATGTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M3_rev	5'- CAAGCAGAAGACGGCATAACGAGATTTAGGCCTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M4_rev	5'- CAAGCAGAAGACGGCATAACGAGATTGACCAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M5_rev	5'- CAAGCAGAAGACGGCATAACGAGATACAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M6_rev	5'- CAAGCAGAAGACGGCATAACGAGATGCCAATGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M7_rev	5'- CAAGCAGAAGACGGCATAACGAGATACTTGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M8_rev	5'- CAAGCAGAAGACGGCATAACGAGATTAGCTTGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M9_rev	5'- CAAGCAGAAGACGGCATAACGAGATGGCTACGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'
M10_rev	5'- CAAGCAGAAGACGGCATAACGAGATCTTGTAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT	-3'