Two independent modes of chromatin organization revealed by cohesin removal

Wibke Schwarzer, Nezar Abdennur, Anton Goloborodko, et al.

Supplementary Tables.

Supplementary Table 1 – Summary statistics of read pairs for TCC (Hi-C) libraries in this study.
Supplementary Table 2 – Statistics of Hi-C libraries in Schmitt et.al, 2016²⁷, an example of a contemporary study on primary tissues.
Supplementary Table 3 – Statistics of Hi-C libraries in other cohesin depletion studies.
Supplementary Table 4 - The list of enriched GO terms for differentially expressed genes, with a Benjamini-Hochberg p-value < 0.05.
Supplementary Table 5 – Public data sources

Supplementary Data 1.

Original scans of western blots. The selected regions for the different panels shown on Fig.1b are boxed in red. Additional biological replicates of the two conditions can be seen (samples 1 and 4)

Supplementary Data 2.

Experimental Hi-C maps show extensive similarities between replicates. (a) The curves of contact frequency P(s) vs genomic distance s. (b) Pearson correlation coefficients between *cis* eigenvectors at 100kb. (c) The average Hi-C maps around 102 500kb-600kb peaks. (d) Compartmentalization saddle plots.

Supplementary Data 3.

Consistent differences in compartment eigenvector upon Nipbl deletion (a) The genome-wide *cis* eigenvectors at 100kb: WT (green), TAM (blue), Δ Nipbl (red) are shown. (b) Zoom-in of the region shaded in grey in (a) using 20kb eigenvectors. In (a-b), the curves are shown for each of two replicates of each condition.









Supplementary Data 2



Supplementary Data 3

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Supplementary Table 1 – Summary statistics of read pairs for TCC (Hi-C) libraries in this study.

Replicate	codename	Raw read pairs	Mapped read pairs	Filtered read pairs	Cis read pairs, separation >10kb
					35,529,637
WT-R1	014637Untr	139,343,707	75,465,383	51,745,705	
		114,258,179			28,704,961
WT-R2	019440Untr		60,638,254	43,097,410	
		94,032,309			9,870,917
TAM-R1	014199TAMcontr		53,285,208	14,530,511	
		134,045,253			34,490,881
TAM-R2	014399TAMcontr		72,789,581	51,281,408	
		131,409,162			26,633,610
∆Nipbl-R1	014200Nipbl		66,635,374	42,405,784	
·		133,914,046			31,561,513
∆Nipbl-R2	016350Nipbl		69,894,091	50,527,104	

Supplementary Table 2 – Statistics of Hi-C libraries in Schmitt et.al, 2016, an example of a contemporary study on primary tissues.

Study	Raw read pairs	Filtered pairs	Cis read pairs, separation >10kb
Bladder, R1	233,041,838	52,456,550	24,121,444
Bladder, R2	236,250,557	43,395,294	19,659,511
Adrenal Gland, R1	181,680,303	48,951,415	22,449,886
Psoas Muscle, R1	196,863,028	36,856,215	13,566,008
Psoas Muscle, R2	95,110,351	25,776,091	10,410,829
Pancreas, R1	160,416,883	49,627,891	21,200,091
Pancreas, R2	12,147,138	3,538,979	1,367,214
Pancreas, R3	128,745,528	15,683,831	7,787,867
Lung, R1	308,335,703	85,597,004	24,417,652
Hippocampus, R1	187,658,680	64,151,770	29,220,961
Right Ventricle, R1	672,319,838	179,219,920	63,091,486
Small Bowel, R1	177,864,628	58,017,249	21,073,296
Spleen, R1	378,529,216	107,599,392	33,032,593
Ovary, R1	201,215,217	70,283,904	20,909,766
Dorsolateral Prefrontal Cortex, R1	165,728,687	52,713,868	25,426,433

Supplementary	Table 3 _	- Statistics	of Hi_C li	hraries in	other co	hesin de	nletion	studies
Supplementaly	Table 5 -	- Statistics		DI al les m	other to	Juesin de	piction	studies.

Study	Filtered read pairs	Cis read pairs, separation >10kb
Seitan et al, 2013, WT, R1	51,337,902	12,676,930
Seitan et al, 2013, WT, R2	96,784,574	28,679,223
Seitan et al, 2013, ∆Rad21, R1	57,060,666	14,219,809
Seitan et al, 2013, ΔRad21, R2	96,784,574	22,594,749
Zuin et.al, 2014, Control, R1	120,366,592	48,221,154
Zuin et.al, 2014, Control, R2	134,277,024	46,378,835
Zuin et.al, 2014, Rad 21 cleaved, R1	113,394,855	41,623,810
Zuin et.al, 2014, Rad 21 cleaved, R2	159,090,030	51,870,950
Sofueva et.al, 2012, Control NSC, R1	16,886,965	12,761,787
Sofueva et.al, 2012, ΔRad21 NSC Lox, R1	69,788,779	52,087,400
Sofueva et.al, 2012, ΔRad21 NSC Lox, R2	63,347,539	47,760,318
Sofueva et.al, 2012, Control AST, R1	29,246,903	21,885,386
Sofueva et.al, 2012, ΔRad21 AST Lox, R1	24,710,993	15,866,342
Sofueva et.al, 2012, ΔRad21 AST Lox, R2	20,287,207	13,980,244

Supplementary Table 4 - The list of enriched GO terms for differentially expressed genes, with a Benjamini-Hochberg p-value < 0.05.

Term	Category	Name	Regulated	Count	%
GO:0060271	BP	cilium morphogenesis	up	16	3.6
GO:0070062	CC	extracellular exosome	up	107	23.8
GO:0042995	CC	cell projection	up	36	8.0
GO:0005929	CC	cilium	up	18	4.0
GO:0005930	CC	axoneme	up	10	2.2
GO:0032869	BP	cellular response to insulin stimulus	down	14	2.4
GO:0006629	BP	lipid metabolic process	down	35	6.0
GO:0005615	CC	extracellular space	down	83	14.0
GO:0016021	CC	integral component of membrane	down	231	39.1
GO:0005783	CC	endoplasmic reticulum	down	88	14.9
GO:0005576	CC	extracellular region	down	84	14.2
GO:0005789	CC	endoplasmic reticulum membrane	down	54	9.1
GO:0043231	CC	intracellular membrane-bounded organelle	down	48	8.1
GO:0016020	CC	membrane	down	273	46.2
GO:0016324	CC	apical plasma membrane	down	25	4.2
GO:0005887	CC	integral component of plasma membrane	down	51	8.6
GO:0020037	MF	heme binding	down	21	3.6
GO:0016491	MF	oxidoreductase activity	down	47	8.0
GO:0052689	MF	carboxylic ester hydrolase activity	down	11	1.9

Supplementary Table 5 – Public data sources

Data type	Description	Cell-type	Ref.	URL
Hi-C data	Hi-C raw reads	Mouse ESC,	18	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?
		NSC, AST		acc=GSE49018
	Hi-C raw reads	Mouse	19	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?
		Developing		acc=GSE48763
		Thymocytes		
	Hi-C raw reads	Human	17	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?
		HEK293T	-	acc=GSE44267
Peaks	Annotations from Hi-C	Mouse	8	ttp://ttp.ncbi.nlm.nih.gov/geo/series/GSE63nnn/G
		CH12-LX		SE63525/suppl/GSE63525_CH12-
CTCE M1	DWM for moure		EC	LX_HICCUPS_IOOPIISt.txt.gz
motif	P WIVE FOR THOUSE		50	mics/FQG03/calls/CTCF_canonical_species
Lamin-B1	Normalized signal	Mouse ESCs	37	http://hgdownload.cse.ucsc.edu/goldenPath/mm9
DamID				/database/laminB1_AC.txt.gz
	Normalized signal	NPCs		http://hgdownload.cse.ucsc.edu/goldenPath/mm9
				/database/laminB1_EF.txt.gz
	Normalized signal	Astrocytes		http://hgdownload.cse.ucsc.edu/goldenPath/mm9
				/database/laminB1_ES.txt.gz
	Normalized signal	MEFs		http://hgdownload.cse.ucsc.edu/goldenPath/mm9
				<u>/database/laminB1_NP.txt.gz</u>
	HMM state calls		38	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?
				acc=GSE17051
ChromH	Chromatin state	Mouse	55	https://github.com/gireeshkbogu/chromatin_state
ММ	segmentation trained on	Liver,		s_chromHMM_mm9
	ENCODE mouse ChIP-seq	Adult8wks		
			45 and	http://badawalaad.aca.waaa.adw/aaldanBath/mm0
Histopo	chip-seq,			/oncodeDCC/wgEncodeLicrHistone/
ChIP-seg	peak and bigwig mes		LINCODE	<u>/encodebcc/wgEncodeLicHistone/</u>
chin Seq	Input	Mouse		
		Liver,		
	H3K2/me3	Adult8wks		
	H3K4me3			
	H3K79mez		45 and	http://badawalaad.aca.waaa.adw/aaldanBath/mm0
	ChiP-seq,	Mouro	45 and	nttp://ngdownload.cse.ucsc.edu/goldenPath/mm9
ChIP-sea		liver	ENCODE	/encodeDcc/wgEncodeLicrTbs/
chill seq	Poll	Adult8wks		
	CTCE	, lucito milo		
ENCODE	DNAse I HS	Mouse	45 and	http://bgdownload.cse.ucsc.edu/goldenPath/mm0
DNase-	bigwig	Liver.	FNCODE	/encodeDCC/wgEncodeUwDnase/
seq	~`o''''''''''''''''''''''''''''''''''''	Adult8wks		
ENCODE	Poly-A RNA-seg,	Mouse	45 and	http://hgdownload.cse.ucsc.edu/goldenPath/mm9
RNA-seq	bigwig	Liver,	ENCODE	/encodeDCC/wgEncodeUwRnaSeq/
		Adult8wks		<u> </u>
	Poly-A RNA-seq,	Mouse		http://hgdownload.cse.ucsc.edu/goldenPath/mm9
	bigwig	Liver,		/encodeDCC/wgEncodeCshlLongRnaSeq/
		Adult8wks		