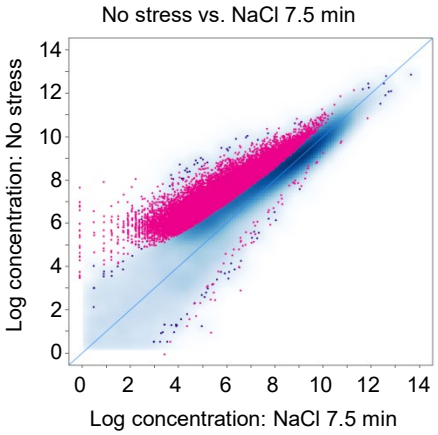
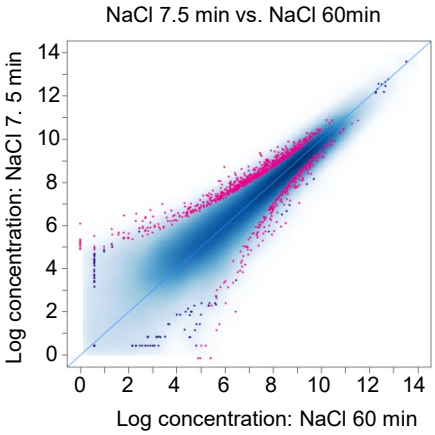
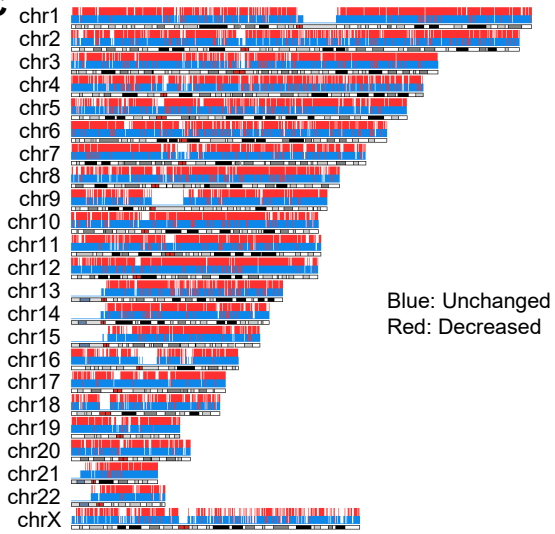
A



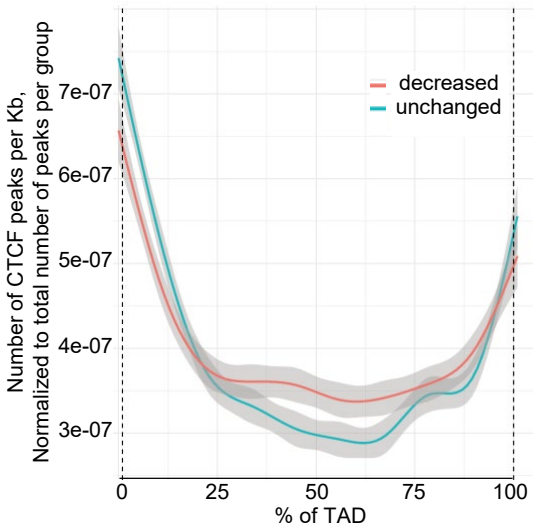
B



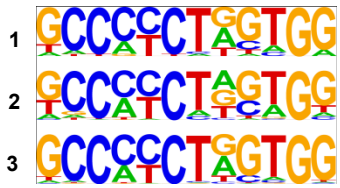
C



D



E



F

CTCF motifs	Information content per bp	% target sequences with motif
1	1,731	44,34%
2	1,668	49,20%
3	1,784	58,18%

G

1

Co-occupancy CTCF sites	decreased	increased	unchanged
decreased_vs_unchanged	4,54E-249	0,5025688	0.4825084-0.5234212
increased_vs_unchanged	2,27E-112	3,9403509	3.4682874-4.4836796
RAD21	5258	866	9140
No RAD21	16853	354	14723

2

Co-occupancy CTCF sites	decreased	increased	unchanged
ENCODE constitutive	3398	66	7504
Not ENCODE constitutive	17515	224	18487
Fisher-test results	**P-value**	**Odds-ratio**	**95% CI**
decreased vs. unchanged	1,50E-232	0,48	0.4566-0.5003
increased vs. unchanged	2,24E-002	0,73	0.5423-0.9605

H

P-value	Odds-ratio	95% CI
0	6,274386	5.772209-6.820943
	CTCF decreased	**CTCF unchanged**
RAD21 decreased	2459	1121
RAD21 unchanged	2816	8055

Figure S4. Chromatin binding of architectural proteins is strongly affected by osmostress. A and B) Scatterplots of global CTCF binding assessed using ChIP-seq, comparing control with 7.5 min NaCl-stressed (110 mM NaCl) cells (16394 peaks FDR<0.05), and 7.5 min NaCl- with 60 min NaCl-stressed cells (481 peaks FDR<0.05). Each dot corresponds to one peak. A red color indicates a significant change. C) Genome-wide distribution of CTCF sites showing no change (blue) or a significant signal decrease (red) due to NaCl treatment (110mM). D) Distribution of unchanged CTCF binding sites and of CTCF binding sites with a decreasing signal following osmostress throughout TAD bodies in % (normalized by size); dotted lines indicate adjacent borders. E) *De novo* motifs for CTCF binding sites identified by HOMER that show 1) decreased, 2) increased and 3) unchanged CTCF binding following osmostress. F) Information content of and percent of target sites with identified *de novo* motifs for CTCF groups shown in E). G) Contingency tables for the overlap of different classes of CTCF sites and 1) basal RAD21 peaks or 2) constitutive CTCF sites based on ENCODE data, as well as corresponding results for the indicated comparisons (Fisher's exact test; CI - confidence interval). H) Co-occupancy of RAD21 and CTCF depending on their respective behavior after hyper-osmotic shock (decreasing signal vs. unchanged signal), results of Fisher's exact test are presented as in G).