A CTCF-independent role for cohesin in tissue-specific transcription

SUPPLEMENTAL FIGURES

Figure S1. Overlap of STAG1 and RAD21 binding events in MCF7 cells.
Figure S2. SWEmbl and MACS peak calls are almost identical.
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Figure S5. ER dependence of ER-Cohesin binding events.

SUPPLEMENTAL REFERENCE

DATA ACCESSION NUMBERS - ARRAYEXPRESS

Data deposited under ArrayExpress accession numbers

E-TABM-828 and E-MTAB-158.

SUPPLEMENTAL FIGURES

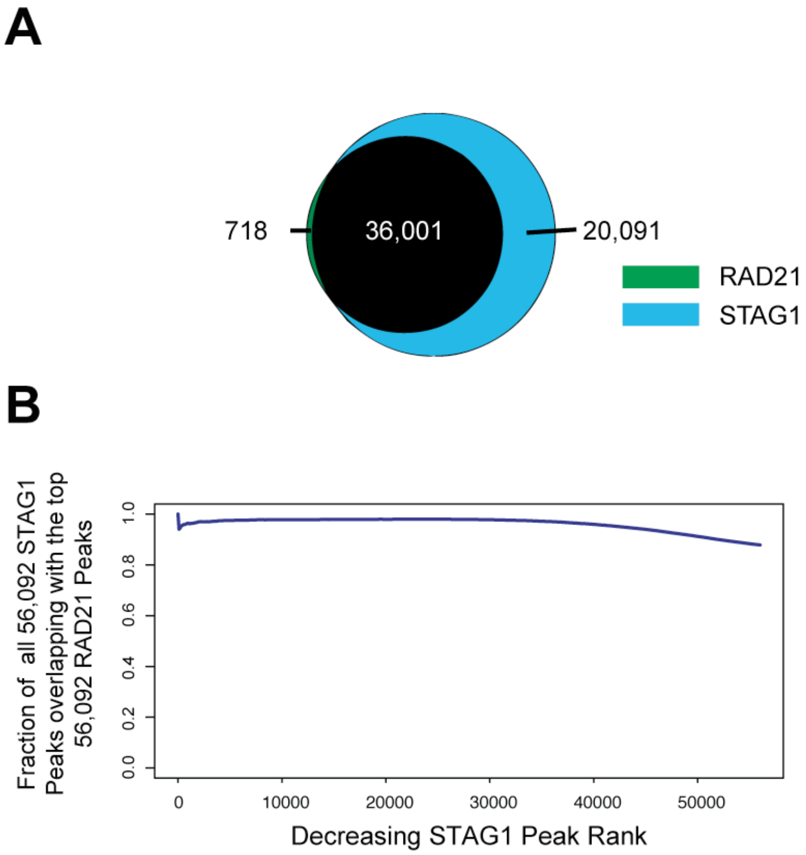

Figure S1. Overlap of STAG1 and RAD21 binding events in MCF7 cells.
(A) Overlap of RAD21 and STAG1 binding in MCF7 cells. **(B)** We determined the top 56,092 RAD21 binding events and overlapped these with the ranked STAG1 peak set. Both sets overlap almost perfect demonstrating, that the presence of RAD21 negative STAG1 binding events appears to be the result of modestly lower enrichment by the RAD21 antibody.

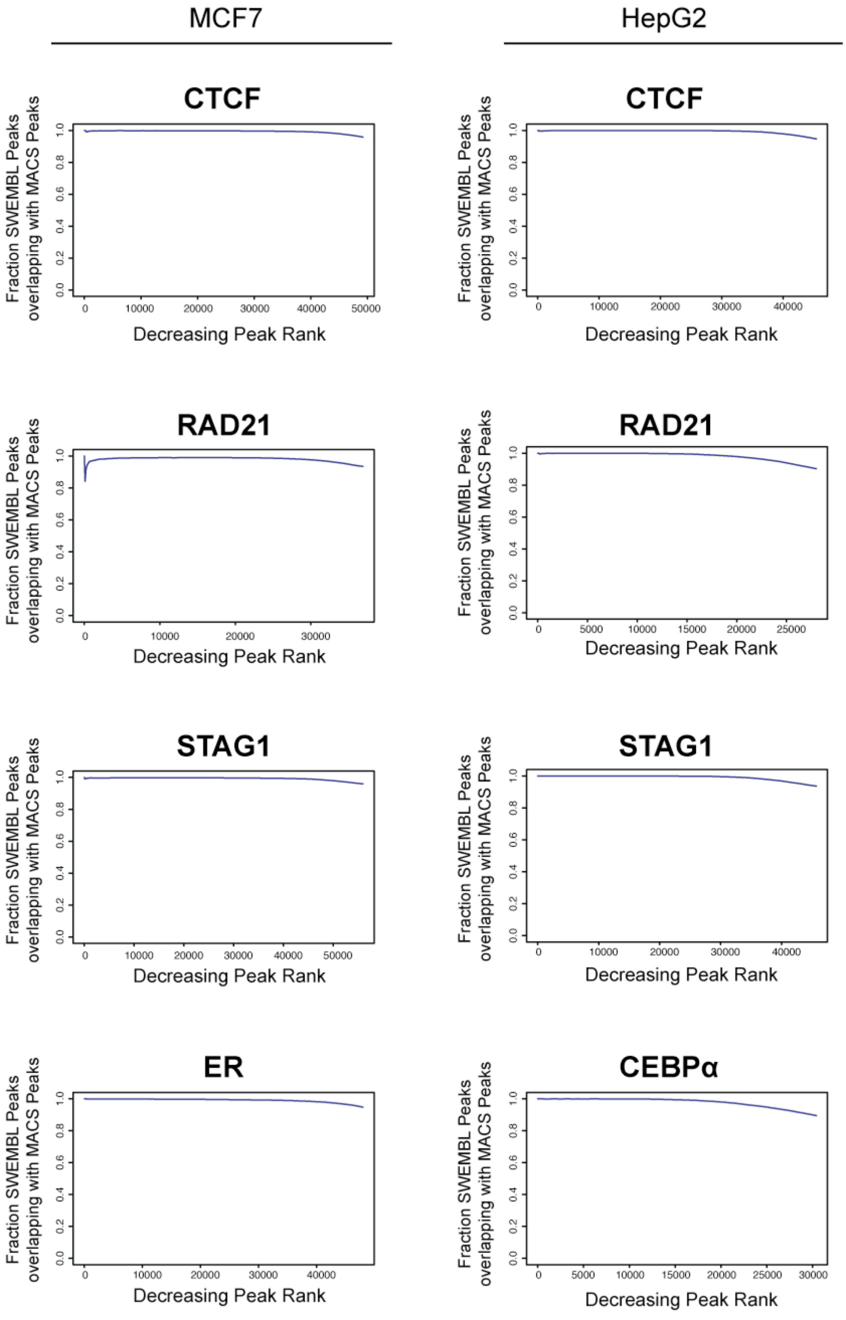

Figure S2. SWEmbl and MACS peak calls are almost identical.
In order to validate our SWEmbl peak calls using an independent method, we determined the binding events using MACS (Zhang et al. 2008). Based on MACS p-value we determined the same number of binding events for each factor as found by SWEmbl. We ranked the SWEmbl peak sets based on enrichment and calculated the fraction of SWEmbl peaks that overlap with the MACS data set for each rank. On average the overlap between the complete peak-sets determined by both methodologies is greater than 90%.

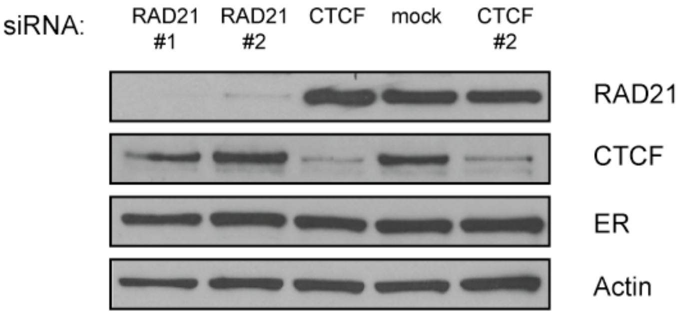

Figure S3. Western blot confirming efficient knockdown in MCF7 nuclear extracts.

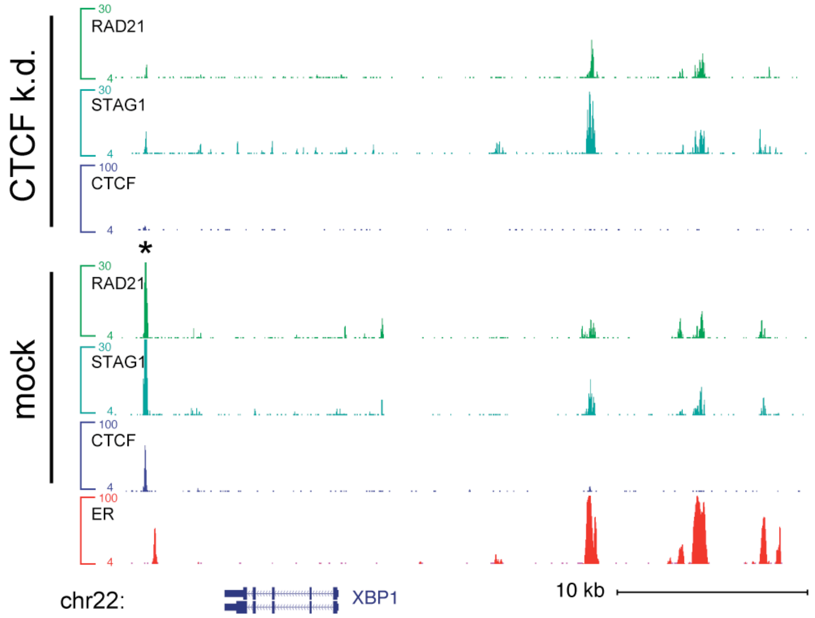

Figure S4. CTCF independence of ER-Cohesin binding events confirmed by RNAi-ChIP-seq. Genomic binding tracks of CTCF, STAG1 and RAD21 before and after CTCF knockdown (CTCF k.d.). A CTCF dependent cohesin binding event is shown on the left (*) as well as several CTCF independent cohesin binding events overlapping with ER upstream of the XBP1 gene.

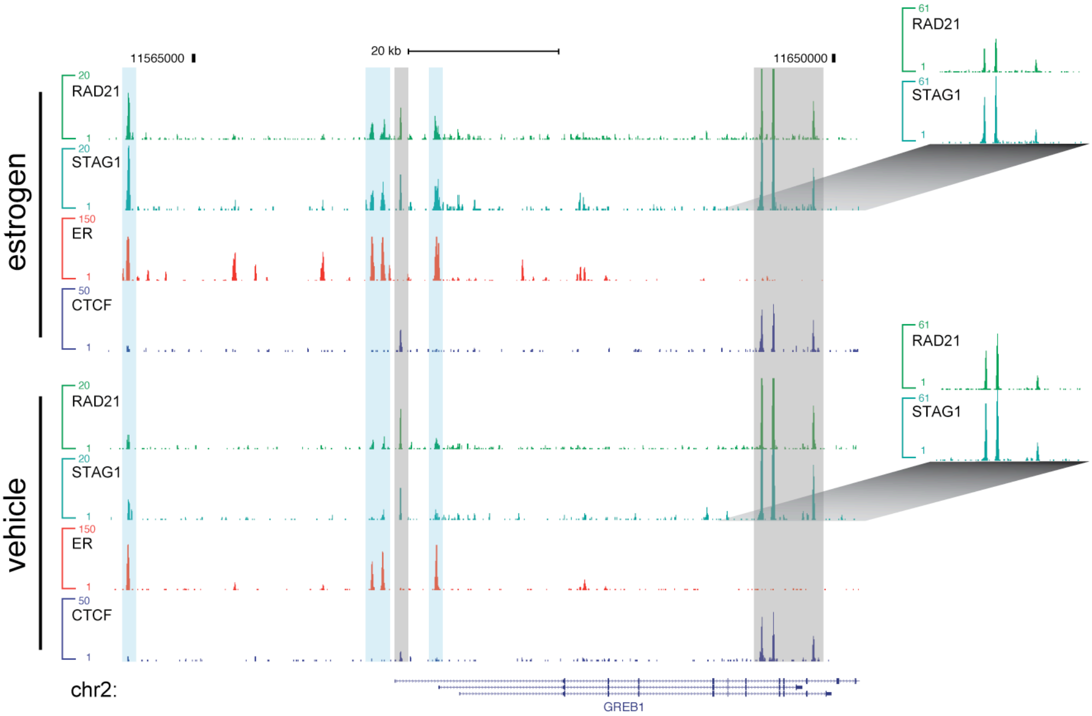

Figure S5. ER dependence of ER-Cohesin binding events. Genomic binding tracks of CTCF, ER, STAG1 and RAD21 after 45 minutes of vehicle or estrogen treatment. Genomic regions more enriched for cohesin after estrogen treatment are highlighted in blue. CTCF binding events are highlighted in grey. The inset on the right shows the cohesin track using a different scale to fully display the two strong cohesin binding events that overlap with CTCF.

SUPPLEMENTAL REFERENCE

Zhang, Y., Liu, T., Meyer, C.A., Eeckhoute, J., Johnson, D.S., Bernstein, B.E., Nussbaum, C., Myers, R.M., Brown, M., Li, W. et al. 2008. Model-based analysis of ChIP-Seq (MACS). *Genome Biol* **9**(9): R137.