

## SUPPLEMENTARY FIGURE LEGENDS

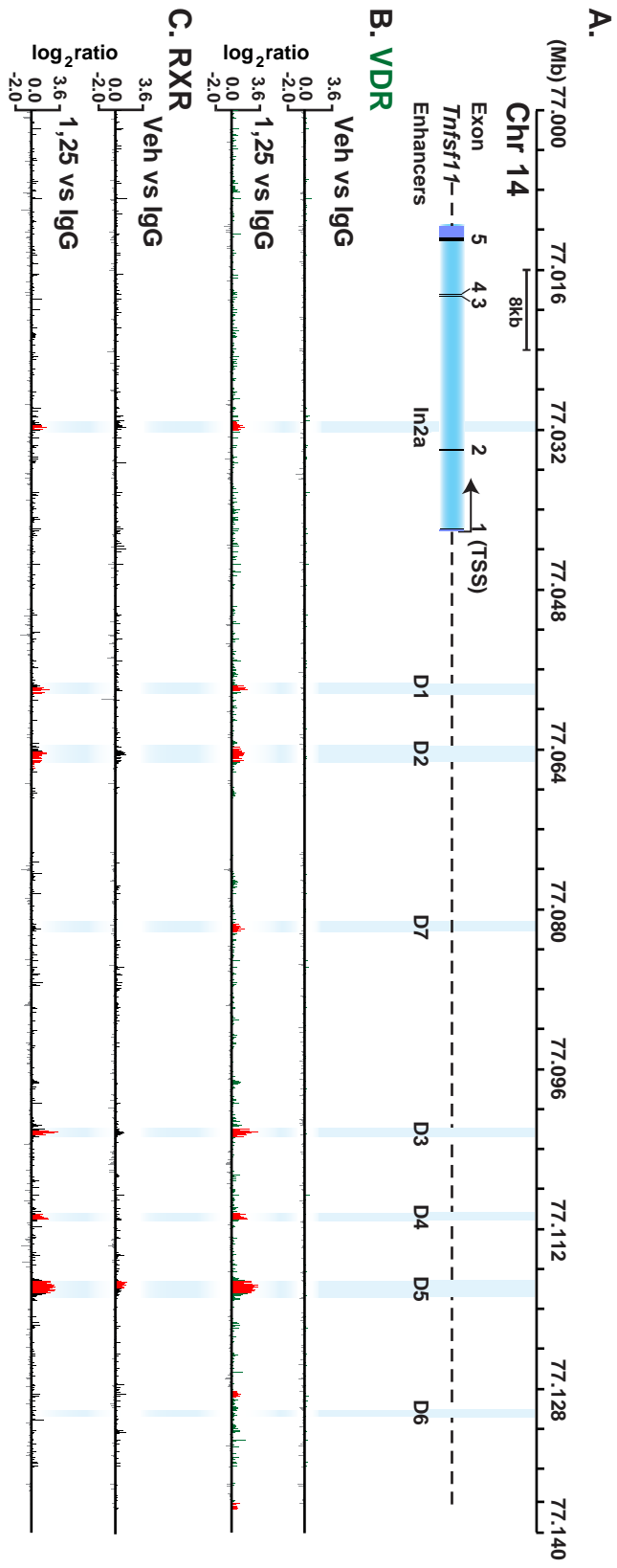
**S. Fig. 1. ChIP-chip analysis reveals localization of VDR and RXR to the *Rankl* gene locus in response to 1,25(OH)<sub>2</sub>D<sub>3</sub>.** ST2 cells were treated with either vehicle or 1,25(OH)<sub>2</sub>D<sub>3</sub> for 6 hours and then subjected to ChIP-chip analysis using antibodies to VDR, RXR or IgG. Immunoprecipitated DNA was amplified by ligation-mediated PCR, labeled with Cy3 or Cy5, and co-hybridized to custom DNA microarrays as described in Experimental Procedures. *A*, The upper track depicts the *Rankl* gene locus. Nucleotide positions (Mb) are shown on chromosome 14 (February 2006 assembly). The *Rankl* gene is depicted by the horizontal blue bar and the positions of the distal enhancer regions are indicated below the chromosomal position and designated by descending blue bands. *B*, Interaction of VDR with the *Rankl* gene locus in response to 1,25(OH)<sub>2</sub>D<sub>3</sub>. Data tracks represent the log<sub>2</sub> ratios of fluorescence obtained from 1) a vehicle-treated sample precipitated with antibodies to either VDR or IgG (VDR<sub>veh</sub> vs IgG) (basal) and 2) an 1,25(OH)<sub>2</sub>D<sub>3</sub>-treated sample precipitated with antibodies to either VDR or IgG (VDR<sub>1,25</sub> vs IgG) (total inducible VDR). *C*, Interaction of RXR with the *Rankl* gene locus in response to 1,25(OH)<sub>2</sub>D<sub>3</sub> as described in (*B*). All peaks highlighted in red are statistically significant (FDR<0.05).

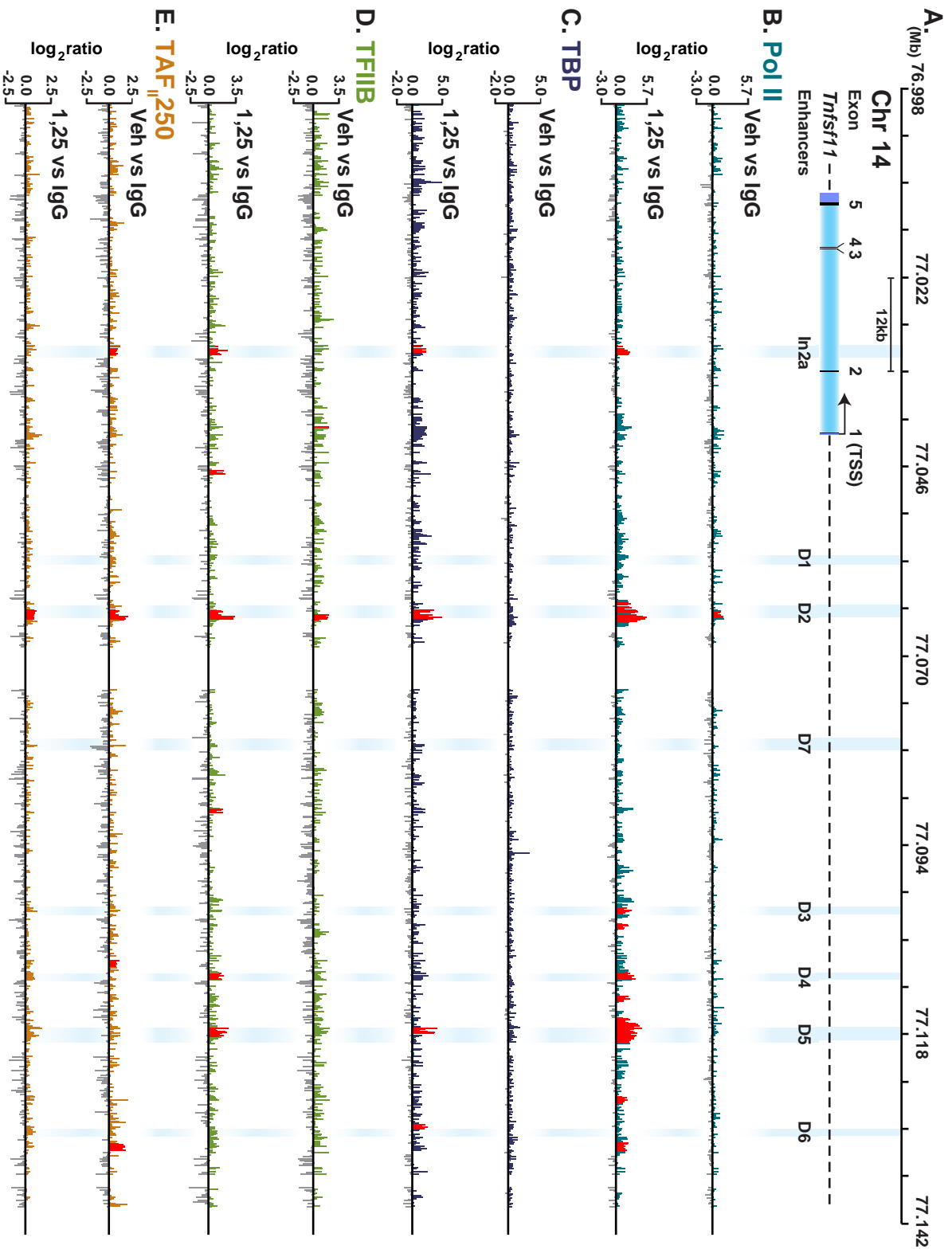
**S. Fig. 2. ChIP-chip analysis reveals recruitment of RNA pol II and components of the pre-initiation complex at mRLD2 and mRLD5 in response to 1,25(OH)<sub>2</sub>D<sub>3</sub>.** ST2 cells were treated as in Figure 1 and then subjected to ChIP analysis using antibodies to RNA pol II, TBP, TFIIB, TAF<sub>II</sub>250 or IgG. Immunoprecipitated DNA was amplified by ligation-mediated PCR, labeled with Cy3 or Cy5, and co-hybridized to custom DNA microarrays as described in Materials and Methods. *A*, Schematic of the *Rankl* locus as in Fig. 1A. *B*, Recruitment of RNA pol II to the *Rankl* gene locus in response to 1,25(OH)<sub>2</sub>D<sub>3</sub>. Data tracks represent the log<sub>2</sub> ratios of fluorescence obtained from 1) a vehicle-treated sample precipitated with antibodies to either RNA pol II or IgG (RNA pol II<sub>veh</sub> vs IgG) (basal) and 2) a 1,25(OH)<sub>2</sub>D<sub>3</sub>-treated sample precipitated with antibodies to either RNA pol II or IgG (RNA pol II<sub>1,25</sub> vs

IgG) (inducible). C, D, and E, Recruitment of TBP, TFIIB, TAF<sub>II</sub>250 under treatment conditions as described in (B). All peaks highlighted in red are statistically significant peaks (FDR<0.05).

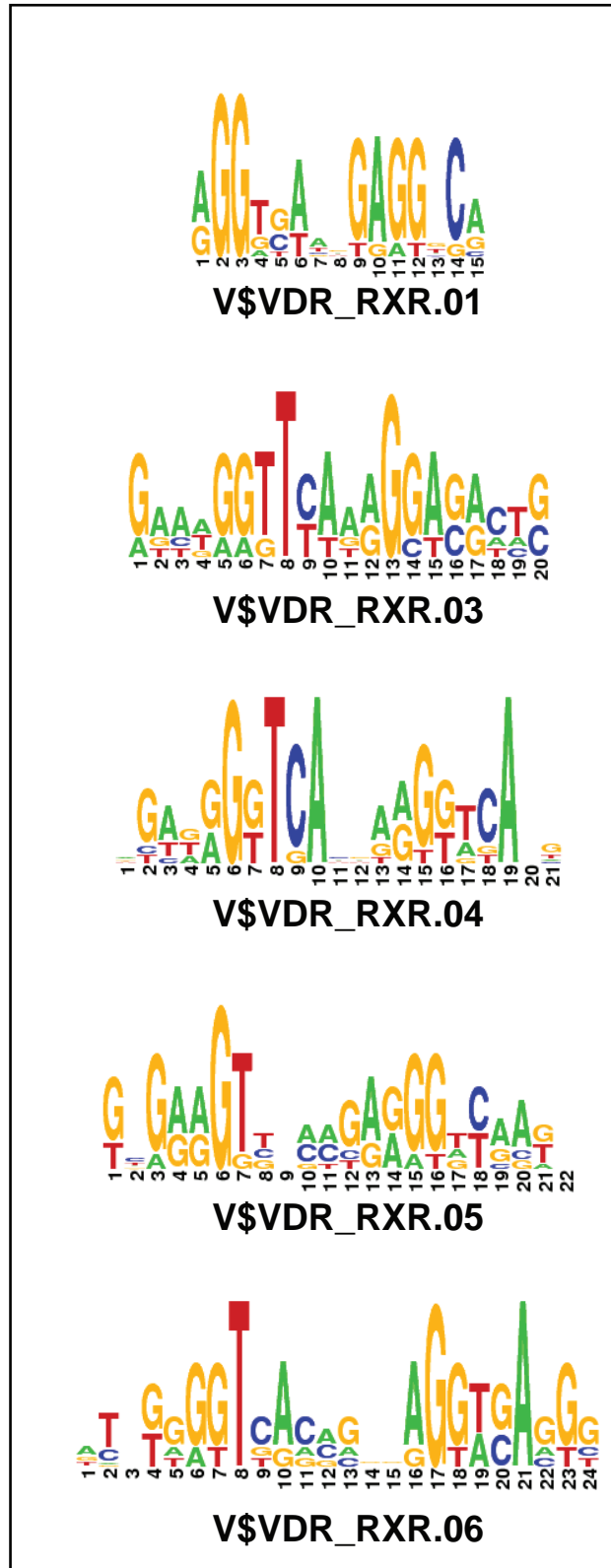
**S. Fig. 3 VDR, C/EBP $\beta$  and CTCF DNA binding motifs.** A. Logos generated from Genomatix for VDR (A), C/EBP $\beta$ (B) and CTCF (C).

**S. TABLE 1. VDR, C/EBP $\beta$  and CTCF DNA binding motifs at the regulatory regions of the mouse *Rankl* gene locus.**

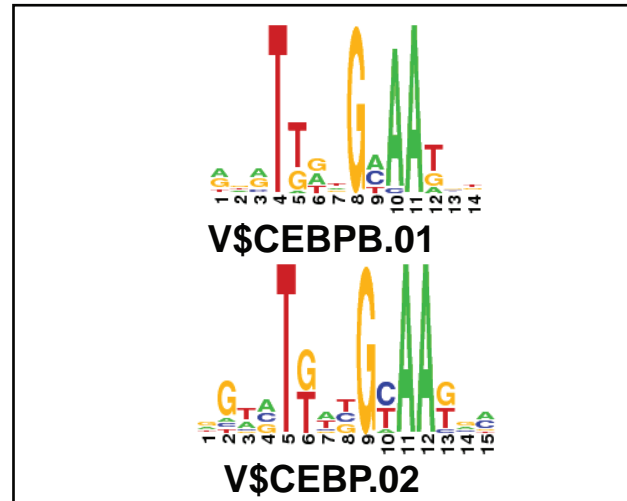




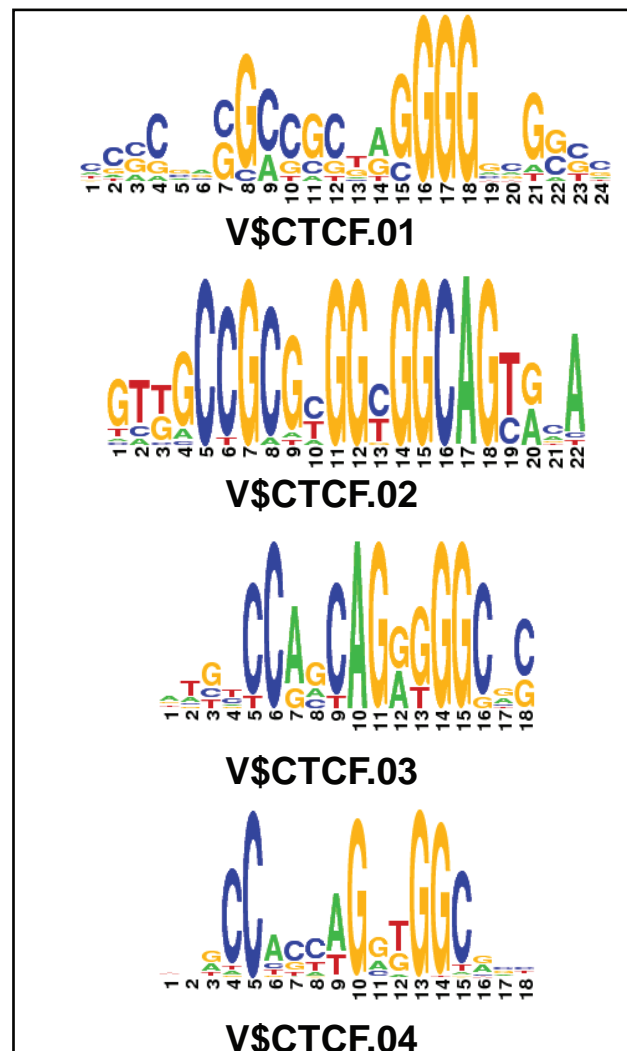
A.



B.



C.



Supp.Table 1  
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	motif start	motif end	Matrix	Opt	strand	core sim	matrix sim	Sequence
CTCF binding Sites								
CTCF-1	77007886	77007912	V\$CTCF.04	0.85	-	0.949	0.904	ctaccagacaccaggGGGCgcatgt
CTCF-1	77007929	77007955	V\$CTCF.04	0.85	-	0.949	0.862	ctaccagacaacagaGGGCgcatgt
D5a	77118035	77118061	V\$CTCF.01	0.8	+	1	0.847	gaaccagcactaGGGAagcatgaa
CTCF-2	77217206	77217232	V\$CTCF.02	0.69	+	1	0.708	cagggtgtctgtggaaGGCAGtgtgt
C/EBP beta binding sites								
D1	77057096	77057110	V\$CEBP.02	0.92	-	0.885	0.929	agagttagGAAAttc
D1	77057452	77057466	V\$CEBPB.01	0.94	+	1	0.953	actgtttGAAAttc
D1	77057708	77057722	V\$CEBP.02	0.92	-	1	0.931	agaatgtgCAAagt
D1	77057739	77057753	V\$CEBPB.01	0.94	+	1	0.94	acagttagGAAAgag
D2	77063484	77063498	V\$CEBP.02	0.92	+	1	0.954	ggaatttGCAAcca
D2	77063627	77063641	V\$CEBP.02	0.92	+	0.971	0.925	tgacttagGTAActa
D2	77064675	77064689	V\$CEBPB.01	0.94	+	1	0.953	aatcttaGCAAttc
D7	77082129	77082143	V\$CEBP.02	0.92	-	0.971	0.93	ggtctattGTAAGca
D7	77082202	77082216	V\$CEBP.02	0.92	+	0.971	0.959	tggatgatGTAAGca
D3	77100460	77100474	V\$CEBPB.01	0.94	+	1	0.942	attgtatGCAAaag
D3	77100497	77100511	V\$CEBP.02	0.92	-	1	0.923	ttcatgtGCAAtgc
D3	77101213	77101227	V\$CEBP.02	0.92	-	1	0.924	ttcttagGCAAggt
D3	77101307	77101321	V\$CEBPB.01	0.94	+	1	0.947	cagcttgGAAAgat
D3	77102156	77102170	V\$CEBPB.01	0.94	+	0.88	0.96	agggttatGGAAtgc
D3	77102367	77102381	V\$CEBPB.01	0.94	-	1	0.945	ttactttaGAAAtag
D4	77110762	77110776	V\$CEBPB.01	0.94	+	1	0.953	tgctttgGAAAtgg
D5	77117172	77117186	V\$CEBP.02	0.92	+	0.885	0.954	agtgtttGAAAgcc
D5	77117212	77117226	V\$CEBP.02	0.92	+	1	0.926	ggagtgtGCAAAtt
D5	77117466	77117480	V\$CEBPB.01	0.94	-	1	0.967	ctcattgtGCAAttg
D5	77118697	77118711	V\$CEBPB.01	0.94	+	1	0.949	tgggttaaGAAAcaca
D5	77118826	77118840	V\$CEBPB.01	0.94	+	1	0.96	aatctttGAAAtgc
D6	77135279	77129693	V\$CEBPB.01	0.94	-	1	0.981	gaaattggGCAAtag
D6	77129687	77129701	V\$CEBPB.01	0.94	-	1	0.945	gaagtgaGAAAttg
D6	77130517	77130531	V\$CEBPB.01	0.94	-	1	0.972	agtgttaGCAAttg
D6	77130596	77130610	V\$CEBPB.01	0.94	-	0.94	0.941	aaagttgaGTAAGta
D6	77130633	77130647	V\$CEBPB.01	0.94	-	1	0.981	tggcttGAAAtat
D6	77130645	77130659	V\$CEBPB.01	0.94	+	1	0.951	ccacttaGCAAtgg
D6	77130679	77130694	V\$CEBPB.01	0.94	-	1	0.951	actttggGAAAtgg
CTCF2	77217002	77217016	V\$CEBP.02	0.92	+	0.971	0.93	ggtgtattGTAAGcc
CTCF2	77217211	77217225	V\$CEBP.02	0.92	+	0.857	0.945	tgtctgtGGAAggc
VDR binding sites								
D1	77057876	77057900	V\$VDR_RXR.04	0.79	+	0.714	0.806	acaactGTGTCaagaaggtcacttt
D1	77057902	77057926	V\$VDR_RXR.04	0.79	-	0.821	0.778	gatgtggGCTCagctaggtcccaga
D2	77064338	77064362	V\$VDR_RXR.05	0.79	-	0.809	0.79	ctgaGCAGttggcaggccatctc
D7	77081781	77081805	V\$RXR_RXR.01	0.78	-	0.833	0.806	tggggaaaagagcagaGCTCaggcc
D7	77081908	77081932	V\$VDR_RXR.04	0.79	+	0.928	0.793	tttgagaGTTCAcacaactgacaag
D3	77102300	77102324	V\$VDR_RXR.01	0.85	+	0.785	0.754	gttcatgggctcttGGGgacaattc
D4	77110375	77111104	V\$VDR_RXR.05	0.79	-	1	0.802	aaatGAAGtagatgggggggaggc
D5	77117973	77117997	V\$VDR_RXR.04	0.79	-	1	0.816	taacaagGTCaagaggggctgac
D6	77130060	77130084	V\$VDR_RXR.06	0.75	-	1	0.779	atgtaggaaccgggAGGTgaatgt