

Table S1: Primers used in this study to construct the various deletion mutants of the promoter. F stands for forward primers and R for reverse primers. The relevant restriction sites used for subcloning in the pGL3-basic vector are shown in bold.

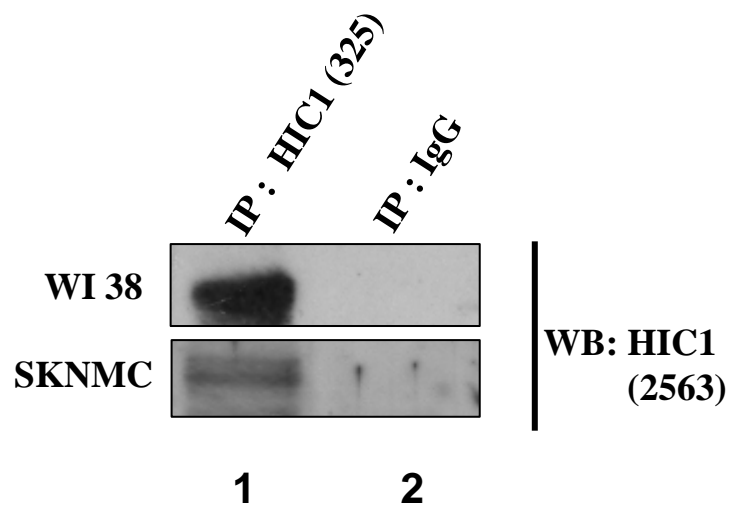
Gene	Primers	Sequence	Construct
CXCR7	F766	CGTTGGT ACC GGGATGGGCTGGCGGGTGGC	
CXCR7	R767	CGTTCT CGAG GCTGGGCTGGCTGGGCTGGC	-813/+168
CXCR7	F838	GGATCC GGTAC CTTAACAAGGAAAACCCAGGC	
CXCR7	R839	CGCAGG CTCGAG GGCTGGCTGGGCTGGCTGGG	-386/+164
CXCR7	F921	GGATCC GGTAC CTTTGTCTTTGGCTGACG	
CXCR7	R839	CGCAGG CTCGAG GGCTGGCTGGGCTGGCTGGG	-191/+164
CXCR7	F920	GGATCC GGTAC CTGGGATGGGGGTGGCACG	
CXCR7	R839	CGCAGG CTCGAG GGCTGGCTGGGCTGGCTGGG	-26/+164

Table S2: Primers used in this study for qRT-PCR. F stands for forward primers and R for reverse primers.

Gene	Species	Primers	Sequence
SIRT1	Human	F864	GCGGGAATCCAAAGGATAAT
SIRT1	Human	R865	CACCTAGGACATCGAGGAACTACC
CXCR7	Human	F814	CACAGCACAGCCAGGAAGG
CXCR7	Human	R815	GTTCCCTGGCTCTGAGTAGTCGA
GAPDH	Human	F842	AAGGTGGTGAAGCAGGCGT
GAPDH	Human	R843	GAGGTCCACCACCCTGTTGC
Actin	Human	F840	GCATCCTCACCCCTGAAGTA
Actin	Human	R841	CAGAGGCGTACAGGGATAG

Table S3: Primers used in this study for ChIP and ChIP upon ChIP experiments. F stands for forward primers and R for reverse primers. The length of the corresponding amplified PCR product is indicated.

Gene	Primers	Sequence	Length (bp)
SIRT1	F774	GATAGAAACGCTGTGCTCCA	
SIRT1	R775	CCTTCCTTTCTAGCGTGAGC	293
CXCR7	F897	GAAGAGGCATTCACAGGAGC	
CXCR7	R896	CAGAAAGGAGCCTCTAGC	348
GAPDH	R847	TCCTCCTGTTTCATCCAAGC	
GAPDH	F848	TAGTAGCCGGGCCCTACTTT	218



**Fleuriel, Rood, Touka, Pinte et al.,
Supplementary Figure 1**

CLUSTAL alignments of the 5' Promoter sequences and first non-coding exons of *CXCR7*

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Mo          AGCAGAGTGACCACCAGCCCTTTGGAGGGTGGGGGGCACTTGGGGAGGCGTTACAGTGGC 60
Rat         AGCAGAGTGACCGCCAGCTCTT-GGAGGGTGGGGGGCACTTGGGGAGGCGTTGCAGTGC 59
Chimp       -CCAGAGCATTGCACATGGGATGGGCTGGCGGGTGGCCCTTGGGTCCCTATCTTATGGAC 59
Hu          -----GGATGGGCTGGCGGGTGGCCTTTGGGTCCCTATCTTATGGAC 42
Cons                    *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

HiRE
Mo          GCGGCTTTAAAAGTAAA-GATTGGG--TCATTTGTGCTTGAGTTTACTAAATGGGGAA 117
Rat         A--GTTTTAAAAGTAAAAGATTGGG--TCATTTT-----ACTAAGTGAAGCA 102
Chimp       G-ATTTTGTAAATGGGGCAATTGGAGATGAGTCT-----CACCTGGATCACATT 107
Hu          G-ATTTTGTAAATGGGGCAATTGGAGATGAGTAT-----CACCTGGATCACATT 90
Cons                    ***  **  *  *  *  *  *  *  *  *  *  *  *  *

Mo          TTGCAAGAGACACATTTAAAAAACAAAACAGGGAATCTTAGCAATGTGCATCGCGATTAG 177
Rat         TTGCAAGGGGACACTTTTTTA-----CAGGGAATCTGAACAATGAGCATCTTGATTAG 153
Chimp       TTTAGGTTGAATTCTCCTCCGTG-----GGGGAACTTTAGCAATACGCATCCAAATAAG 160
Hu          TTTAGGTTGAATTCTCCTCCGTG-----GGGGAACTTTAGCAATACGCATCCAAATAAG 143
Cons        **      **      *  *  *  *  *  *  *  *  *  *  *  *

HiRE
Mo          AATGTAGATTTTGATAAAGATGAGGACTGCGATAAAAGTTGGCTAAGCTCACAAATGACGA 237
Rat         AATGTAGATTTTGATAAAGATGACGATAGCGAGAAAAGTCGGCTAAGCTCACCATGACGA 213
Chimp       AATGTAGATTGCAATAATTGTAGTAA-----AGTGTTTGCCAGACTCATC-TCAGAA 211
Hu          AATGTAGATTGCAATAATTGTAGTAA-----AGTGTTTGCCAGACTCATC-TCAGAA 194
Cons        *****  ****  *  *  *  *  *  *  *  *  *  *  *

HiRE
Mo          CT-----CTACCTCACCTGCGACAAGGCCTTTTCA-GTGACTGGCACTGCTCGA-CT 287
Rat         TAAAGGGCTGCTACTTCCCTGCGTCAAGACCTTTTCA-GCGACTGGCAATTGCTCAG-CC 271
Chimp       AAAGACATTATCAAAAAGCAATTATTATCTTCTTAATGCGTGTCTGGCACTGGCAGACA 271
Hu          AAAGACATTATCAAAAAGCAATTATTATCTTCTTAATGCGTGTCTGGCACTGGCAGACA 254
Cons                    *  *  *  *  *  *  *  *  *  *  *  *  *  *

Mo          CCGTGGAACACGGTCTT-AATAGGGCCTTAAGGACTTTGTG-TAAGAGTTCCA-GCAGA- 343
Rat         CTGTAGAACCGGTCTT-ACTAGGGACTCAAGGACTTTGTG-TAAGAGTTCTT-ACAGA- 327
Chimp       CTGTAGAATACTATCTTGATTAGAGTCTCAAGGATTTTGTACTTAAAGTCCTTACAAAT 331
Hu          CTGTAGAATACTATCTTGATTAGAGTCTCAAGGATTTTGTACTTAAAGTCCTTACAAAT 314
Cons        *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

Mo          -----ATCTGGATCCAACCTA-----AAGGCACTTCCCTCACTTCTGGGTGATGGCGG 392
Rat         -----ATC-----CAACCTA-----AAGGCACTTTC-----TGGGTGATGGCCG 361
Chimp       AAAAATATTCAAGTATAATCTATTATAAAGACTCTTTTCTCCACTTTGGGGATATA-CGG 390
Hu          AAAAGTATTCAAGTATAATCTATTATAAAGACTCTTTTCTCCACTTTGGGGATATA-CGG 373
Cons        **      **  **  *  *  *  *  *  *  *  *  *  *  *

HiRE
Mo          TACAGGGTCGATTAATCGTCCCCTTTCCAAAATGTGACTTCTGTCCAGGAGGCAATCGACA 452
Rat         TACAGGGTGGATTAATCGTTCCTGTCCAAAATGTGAGTTCGTTTCAGGAGGCAATCGACA 421
Chimp       TGTGGTATCGATTCAATTGGTCA-TACCAAACTGTTACTTCTGTTTTGGAGGAATTAACA 449
Hu          TGTGGCAATCGATTCAATTGGTCA-TACCAAACTGTTACTTCTGTTTTGGAGGAATTAACA 432
Cons        *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

Mo          AAGAAAGAGCAAGCTTGACAAACCAACATCGAAGTTCAGAAGTTCAGAGTAATTTGTCTT 512
Rat         AAGAAAGAGTAAGCTTGACAAATCAACAGCGAAGTTCAAAAGTTCAGAGTAATTTGTCTT 481
Chimp       AGGAAAACCCAGGCTTAGTAAATCAACATCGAAGTTCAGAAGTTCAGAGTAATTTGTCTT 509
Hu          AGGAAAACCCAGGCTTAGTAAATCAACATCGAAGTTCAGAAGTTCAGAGTAATTTGTCTT 492
Cons        *  ****  *  ****  **  *****  *****  *****  *****

HiRE
Mo          GGAACAAAGTCTTCCCTGAAGCTAC-AAGGCAATCAAAGGAACTCCCGGTGCTCATGGGA 571
Rat         GGAACAAAGTCTTCCCTGAAGCTAC-AAGGCAATCAAAGGAACTCCTGGTACTCGTGGGA 540
Chimp       GGAACAAAGTCTTCCCTAGAGCGAAGAAGCAATTCACAGGAGCTCTTGGTGTAAATGGGA 569
Hu          GGAACAAAGTCTTCCCTAGAGCGAAGAAGCAATTCACAGGAGCTCTTGGTGTAAATGGGA 552
Cons        *****  *****  ***  *  *****  *****  *****  ***  *  *****

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Legends to Supplementary Figures

Supplementary Figure S1. Detection of endogenous HIC1 proteins in the Ewings/PNET cell line, SK-N-MC.

Total lysates from SK-N-MC were immunoprecipitated using the polyclonal anti HIC1 (325) antibody (lane 1) or with normal rabbit IgG (lane 2). These samples were separated by SDS/PAGE electrophoresis followed by Western blot analyses using another polyclonal anti HIC1 (2563) antibody (bottom panel). As a positive control, a similar experiment was performed with a lysate of normal human WI38 fibroblasts known to express HIC1 (10) (top panel).

Supplementary Figure S2. CLUSTAL alignments of the *CXCR7* promoter regions.

The genomic sequences for the human (NC_000002), *Pan troglodytes* (NW_006470), rat (NW_047817) and *Mus musculus* (NC_000067) *CXCR7* genes were extracted from GenBank. These sequences were anchored on the conserved splice donor site (gt) at the 3' end of the first non-coding exon and aligned using CLUSTAL/Jalview (EMBL) and default parameters. In the consensus lane (**Cons**), identical residues are shown as *****, conserved substitutions as **:** and semi-conserved substitutions as **.** under the aligned sequences. The output file was subsequently edited manually. Putative HIC1 responsive elements (HiRE) (5) are indicated in bold letters with the GGCA (or TGCC) core motif highlighted. The sites found in the human sequence and analyzed by transient transfection assays are numbered from 1 to 11. Those conserved in the primate and rodent genomes are numbered using roman numerals. The Transcription start site (TSS) defined for the human gene (NM_020311; gi 114155149) is highlighted in grey.