

Supporting Information

Lymphoma case	1q12 anomaly (aHCF)	FISH probe set	Interprobe genomic distance	Maximum expected 3D interphase FISH distance	Measured 3D interphase FISH distance
B593	(-)	RP11-7707-cen2	23 Mb	-	2.00 μm
CH1	(+)	1q12-cen2	67 Mb	5.83 μm	1.04 μm
GAR	(+)	1q12-cen2	135.5 Mb	11.78 μm	1.26 μm
BL136	(+)	1q12-cen1	82 Mb	7.13 μm	2.71 μm

Table SI Expected and measured interphase FISH distances for the 1q12-cen probe sets in lymphoma B cells presenting aHCF compared to a control normal region in 2p13 (FISH probe set RP11-7707 – cen2) in control lymphoma B cells (not presenting aHCF)

Antibody	Reference	Type
H3K9me3	Millipore (07-523)	Polyclonal
H3K27me3	Millipore (07-449)	Polyclonal
H4K20me3	Millipore (07-749)	Polyclonal
H4ac	Millipore (06-598)	Polyclonal
HP1 α	Euromedex (2HP-2G9-AS)	Monoclonal
HP1 β	Euromedex (1MOD-1A9-AS)	Monoclonal
HP1 γ	Euromedex (2MOD-1G6-AS)	Monoclonal

Table SII Antibodies used for ChIP analyses (see text for details).

Gene/Sequence	Forward primer	Reverse primer
ChIP		
<i>EXOC6B</i> _1	ATCTCCTTCCTGGTGGACCT	TGTGGCTCGCTAAACATTTG
<i>EXOC6B</i> _2	ATTTGGGTCCAAAGCATCAC	TACCAAAAACCCCGAGAACA
<i>EXOC6B</i> _3	GCCTGGCCTGTGTTTTCTAA	TAAGATCCCCTGACGCAGTT
<i>EXOC6B</i> _4	CAAAGGATGGGATGCAAAGG	TCCAGAGGAGGATGGTTTG
<i>CYP26B1</i> _5	TCTTTTCTCCTTCCCAGGT	CCCTAAGGCACAGTTTCGAG
<i>CYP26B1</i> _6	CAGACGGACGAGATGAGACA	GAAGCCAAGCAGGCACCTAAG
<i>CYP26B1</i> _7	GACTGGGGTGCAACTTTGTT	AACCCACCAGCTTGACTCAC
<i>CYP26B1</i> _8	GTTCAAGACGCATTTGTTGG	GAATTGGACACCGTGTGG
<i>ZNF638</i> _9	ACGTCTGTCTATCCCAAGGTT	CCCTATGGCAATGATGTGTG
<i>ZNF638</i> _10	TTGCCATAGGATCAAAGG	AGTGAGGGAAGATTGCACCA
<i>ZNF638</i> _11	TGAAGGCACAAATGATCAGG	GGTTCTGTGCCTGTCTCTC
<i>ZNF638</i> _12	AGTCTTTGGAGGCGGTA	TATGCCTACCCGACTAACAGC
<i>GMCL1</i> _13	CTGGCACTTGAGAGGAAAGG	CCTGGGCTTCCTTAACATGA
<i>GMCL1</i> _14	ATCCAGCATATCGCCTCATC	TGGGCCTGTGCTAAGCTAGT
<i>GMCL1</i> _15	TTGACAGGGTGAATGTGGAA	GTTGAAAATGCGGAACACCT
<i>GMCL1</i> _16	CCCCAAGATGAGGATGAGAA	TACTCTGCGGCTACCCACTT
<i>Iq1</i>	CTCTCCCTGCAGTGACCTTC	TCAGGGACAGCCTGAACTCT
<i>Iq2</i>	CTTAGGGGTGCTTGCTTCTG	GCTCCTCCTGTCTGTTCTGG
Satellite II	TGAATGGAATCGTCATCGAA	CCATTCGATAATTCCGCTTG
<i>GAPDH</i>	GCTCTCTGCTCCTCCTGTTC	CTTCAGGCCGTCCCTAGC
RT-Q-PCR		
<i>EXOC6B</i>	TCTTGCAGAGATCGAGAGC	GTCGTGATTACGGATACGAGTTT
<i>CYP26B1</i>	AGTTTGTGGACAATGTCTTCTCC	CCTTGCTGCTCTCAATGAGGA
<i>ZNF638</i>	ATGTCGAGACCCAGGTTTAATCC	GTAGGTGCTCGTGGCCTTT
<i>GMCL1</i>	ACTGGAGATTCCTGACCAGAAC	CCAAAATGGCAACAACCTCGACT
<i>U6</i>	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT

Table SIII Primer pairs used for ChIP analyses or RT-Q-PCR, as indicated (see text for details).

Figure S1 Genetic characterisation of the der(2)t(1;2)(q12;p13) in CH1 lymphoma B cells. (A) Agilent 244K CGH-array profile of the 2p breakpoint region. Genomic coordinates and BAC clones mapping to the region are indicated. The t(1;2) breakpoint (bk) is represented by the dashed horizontal line. 2p regions in 2 (2N) or 3 (3N) copies are indicated. (B) Confirmation of the breakpoint region by dual colour FISH and identification of a 'mirror image' 2p duplication on the der(2) chromosome, using 2p BAC probes, as indicated.

A

Figure S2 3D-FISH characterisation of aHCF positive and negative human lymphoma B cells. (A) 3D immuno-FISH showing colocalisation between 1q12 satellite DNA (red) and foci enriched in H3K9me3 (green) (white arrows), in CH1 cells; DNA is counterstained with DAPI (blue). (B) 3D FISH analyses in human lymphoma B cells that do not harbour 1q12 pericentric heterochromatin ; 1q12 (green signals), chromosome 2 centromere (red signals). Note the absence of aHCF.

Figure S3 Model showing how aberrant heterochromatic foci might form as a consequence of long range intrachromosomal interactions between translocated 1q12 and chromosome 2 centromeric regions, in CH1 lymphoma B cell interphase nuclei. The nuclear organisation of the 2p arm is not known but for simplicity is presented as a single large loop displaced away from the aHCF.

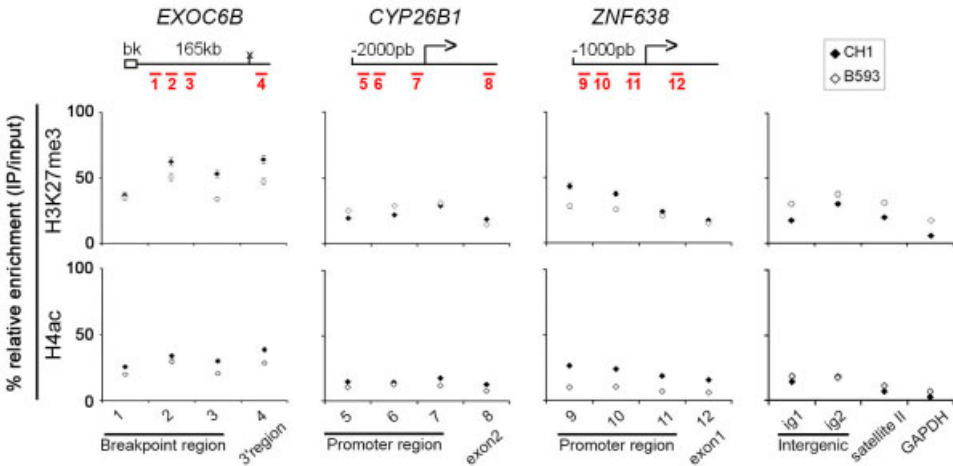


Figure S4 Q-ChIP analysis of H3K27me3, H4ac (A) and HP1 β (B) enrichment across the indicated 2p, satellite II and control sequences. Details as in the legend of Figure 3A. Bk indicates breakpoint.