

Supplementary materials.

I. Primers used in the study

All are listed 5' to 3':

TAP2-1-5' GAGAATCACTTGAACCTGGGAG
TAP2-1-3' AAGGAAACCCCAGGAAGAAATA
TAP2-2-5' TTGTCCACAGTGTACCACATGA
TAP2-2-3' ATCTTGCAATTCAGCATGACAC
TAP2-3-5' TATTTCTTCCTGGGGTTTCCTT
TAP2-3-3' ACCACCTCCCAAATAAAAACA
TAP2-4-5' CATGATGTGTCATGCTGAATTG
TAP2-4-3' CGGGCTCTCCTAAATAGAAGGT
TAP2-5-5' ATAGAACAAGAACCAAAGCCCA
TAP2-5-3' GGCGGTTACTCTGGGATATAAA
TAP2-6-5' GGACAACAGATAAAGTTGCCCT
TAP2-6-3' CTGTCAACGGATACGAGATGAG
TAP2-7-5' AAGTGACTIONCCACTCCACGCT
TAP2-7-3' AGTAAAGCCGCGTCCACCAGC
TAP2-8-5' CATCTCGTATCCGTTGACAGAG
TAP2-8-3' AGGGCCTAGAAATGGAGTTAGG
TAP2-9-5' CCTCACTATTCTGGTCGTGTGA
TAP2-9-3' TGAAATGGTTTTTCGAGGGTACT
TAP2-10-5' GGTGAATGTAGTCACCATTCTG
TAP2-10-3' ATGACTGCACCTAACACTGTGG
TAP2-11-5' GATGGTGGACCCACCAGATTAT
TAP2-11-3' GAGGGGCAAAAGAGAAAGAAAT
TAP2-12-5' GGCAGGGAATTTATTATTGCAG
TAP2-12-3' CCTCTGAACATCCTCCTTCACT
TAP2-13-5' CATCTCCCTCCCCTCTTATTCT
TAP2-13-3' TATACCTTCTCCCCTAACGGCT
TAP2-14-5' CGGATACCACCCTGATGAGTAA
TAP2-14-3' GGTTGGGGGTAGTAGGCAGTTA
TAP2-15-5' ATAGGAAGGGGAGATGATAGGC
TAP2-15-3' TCTTTTGTAATTGCCCGATCT
TAP2-16-5' CTCCGTTGTACCTTCTGTCTCC
TAP2-16-3' CAGAAAGTGGTGTGATGAGGA
TAP2-17-5' AGATCGGGCAATTTACAAAAGA
TAP2-17-3' CTTGGATATAACACCAAACGCA
TAP2-18-5' TCTTTGCCATTTTCTGATTTT
TAP2-18-3' TGTTCAAGGGGCTCTTTATAGC
TAP2-19-5' CCTTCCTTCTGATTCAGACAC
TAP2-19-3' GAAGGCCACAAAGAAAAAGAGA
TAP2-20-5' GCTATAAAGAGGCCCTTGAACA
TAP2-20-3' CTCATACACATACACTACATGG

II. Polymorphism data used for analyses.

Labels refer to the western chimpanzees listed in Methods. The genotypes are given as pseudohaplotypes, *i.e.* the phase is unknown. Positions are given with respect to the sequence from Jeffreys *et al.* (2000), available at <http://www.le.ac.uk/ge/ajj/tap2/SEQdata.html/>.

Positions:

536 552 556 557 568 703 1114 1211 1613 1808 2090 2176 2417 2669 3271 3319 3491
3600 3804 3841 4006 4062 4075 4196 4274 4415 4451 4452 4466 4572 4613 4887 4927
5197 5503 5569 5775 5789 5854 5868 6342 6388 6796 7429 7978 8089 8113 8377 8621
8824 8974 9141 9159 9501 9649 9680 9759

> 311

ATACCCTGGAGGCAAGAATCTTCCGATAGACGCCAGTC
CCTAGTTGTCCCCGACCTC
ATACCCTGGAGGCAAAAATCTTCTGATAGACGCCAATC
CCTAGTTGTCTCGACATC

> 312

GCACCCTGGAGGCAAGAGTCTTCCGATAGACGCCAGTC
CCTAGTTGCCCCCGACCTC
ATGTCTTGAAAATAAAGATCTTTCGATAGACCTCAGTCC
CTAGTTGTACCCGATATC

> 313

GCACCCTGGAGGCAAGAGTCTTCCGATAGACGCCAGTC
CCCAGTTGTCCCCGGCCTC
ATGTCTTGAAAATAAAAATCTTCCGATAGACCCCAGTCC
CTAATTGTCCCCAACCAAT

> 314

GCACCCTGGAGGCAAGAGTCTTCCGATAGACCCCAGTC
CCCAGTTGCCCCCGGCCTC
ATGTCTTGAAAATAAAAATCTTCCGATAGACCCCAGTCC
CTAATTGTACCTAACCAT

> 317

GCACCCTGGAGGTGGGGGGCCCCCAGGAGGCCCCAGCC
CCCGGTCGTCCCCGACCAC
ATGTTTTGAAAATAAGAATTTTCCAATATATCCTAGTGT
TCAATTCTCTCCAACCAT

> 320

GCACCCTGGAGATAAGGGCCCCCAGGAGGCCCCAGCC
CCCGGTCGTCCCCGGCCAC
ATGTTTTGAAAATGAGAATCTTCCAATATATCCTAGTGT
TCAATTCTCTCCAACCAT

> 321

ATACCCTGGAGGGCAAGAATCTTCCGATAGACGCCGGTC
CCTAGTTGCCCCCGACCTC
ATACCCTAGAGGGCAAAAATCTTCCGATAGACGCCAGTC
CCTAGCTGTCCCCGACATC

> 322

GCACCCTGGAGGGCAAGGGTCTTCCGATAGACGCCGGTC
CCTAGTTGCCCCCGACCTC
ATGTCTTGAAAATAAAAATCTTCCGATAGACCCCAAGTCC
CTAGCTGTCCCCGACATC

> 325

ATACCCTGGAGGGCAAGGATCTTCCGATAGACGCCAGTC
CCTAGTTGTCCCCGGCCTC
ATACCCTAGAGGGCAAAAATCTTCTGATAGACGCCAGTC
CCTAGTTGTCCTCAACAAT

> 326

GCACCCTGGGGGGCAAGAGTCTTCCGATAGACGCCAGTC
CCCAGTTGTCCCCGGCCTC
ATGTCTTAAAATAAAGATCTTCCAATAGACCCCAAGTCC
CTAATTGTACCCAACAAT

> 328

ATACCCTGGAGGGCGAGGACCCCCCGGGAGGGCGCCAGCC
CCCGGTTGTCCCCGACCTC
ATACTCTAGAGATAAAAATCTTTCAATATATCTTAGTGT
TTAGTTCTATCCGACCAC

> 329

ATACTCCGGAGGGCAAGGACCCCCCGGGAGGGCGCCAGCC
CCCGGTCGCCCCCGACCTC
ATACTCTGGAGATAAAAATCTTCCAATATATCCTAGTGT
TTAGTTCTATCTGACCAC

> Annaclara

GCACCCTGGAGGGCAAGAGTCTTCCGATAGACGCCAGTC
CCCAGTTGTCCCCGGCCTC
ATGTCTTAAAATAAAAATCTTCCAATAGACCCCAAGTCC
CTAATTGTCCCCAACAAT

> Frits

ATACCCTGGAGGGCAAAAATCTTCCGATCGACGCCAGTC
CCTAGTTGTCCCCGACATC
ATACCCTAGAGGGCAAAAATCTTCTGATAGACGCCAGTC
CCTAGTTGTCCTCGACATC

> Hilko

GCGTCTTGAAAACAGGAGTCTTCCGATAGACCCCAAGTC
CCCAGTTGTCCCCGGCCTC
GCGTCTTGAAAACAAGAGTCTTCCAATAGACCCCAAGTC
CTAATTGTCCCCAATAAT

> Liesbetha

ATACCCTGGAGGGCAAAAATCTTCTGATAGACGCCAGTC
CCTAGTTGTCCTCGACATC
ATACCCTGGAGGGCAAAAATCTTCTGATAGACGCCAGTC
CCTAGTTGTCCTCGACATC

> Louise

ATACCCTGGAGGGCAAAAATCTTCCGATAGACGCCGGTC
CCTAGTTGTCCTCGACATC
ATACCCTAGAGGGCAAAAATCTTCCGATAGACGCCAGTC
CCTAGCTGTCCTCGACATC

> Marco

ATACCCTGGAGGGCAAAAATCTTCCGATCGACGCCAGTC
CCTAGTTGTCCTCGACCTC
ATACCCTGGAGGGCAAAAATCTTTTGATAGACGTCAGTC
CCTAGTTGTACTCGACATC

> Oscar

ATACCCTGGAGGGCAAGGACCCCCCGGGAGGGCGCCAGCC
CCCGGTCGTCCCCGACCTC
ATACTCTGGAGATGAAAATCTTCTAATATATCCTAGTGT
TTAGTTCTCTTCGACAAC

> Regina

ATACCCTGGAGGGCGAGGACCCCCCGGGAGGGCGCCAGCC
CCCGGTCGTCCCCGACCTC
ATACTCTAGAGATAAGAATCTTCCAATATATCCTAGTGT
TTAGTTCTCTCCGACAAC

> Socrates

GCACCCTGGAGGGCAAGAGTCTTCCGATAGACGCCAGTC
CCTAGTTGTCCTCGACATC
ATGTCTTAAAAATAAAAATCTTCCGATAGACCCCAGTCC
CTAGTTGTCCTCGATATC

> Sonja

ATACCCTGGAGGGCAAAAATCTTCCGATAGACGCCGGTC
CCTAGTTGTCCTCGACCTC
ATACCCTAGAGGGCAAAAATCTTCCGATAGACGCCAGTC
CCTAGCTGTCCTCGACATC

> Yoran

GTACCCTGGAGGGCAAGAGTCTTCCGATAGACGCCGGTC
CCCAGTTGTCCTCGGCCTC
ACGTCTTGAAAATAAAAATCTTCCAATAGACCCCAGTC
CCTAACTGTCCCCAACCAT

> Yvonne

GCACCCTGGAAGTAAGGGCCCCCAGGAGACCCCAGCC
CCCGGTCGTCCCCGGCCAC
ATGTTTTGAAAATGAGAATCTTCCAATATGTCCTAGTGT
TCAATTCTCTCCAACCAT

III. Search for sequence motifs previously associated with recombination hotspots.

Unless indicated otherwise, all searches used the interface available from http://bioweb.pasteur.fr/seqanal/interfaces/scan_for_matches.html and were run with the following tolerance levels: 0 for a mismatch, 0 for an indel.

The locations of the motifs are indicated by []. Positions are given with respect to the sequence from Jeffrey *et al.* (2000), available at <http://www.le.ac.uk/ge/ajj/tap2/SEQdata.html/>.

In the consensus sequences, the following equivalencies are used:

R = (A,G)
Y = (T,C)
W = (A,T)
S = (G,C)
M = (A,C)
K = (G,T)
H = (A,T,C)
B = (G,C,T)
V = (G,A,C)
D = (G,A,T)
N = (A,G,C,T)

1) Search for motifs listed in Smith *et al.* (1998).

Possible location where Pur element promotes duplex opening: ATATATTTT
>humantap2:[5330,5338]
>chimptap2:[5330,5338]

(ATTTT)_n
none

WAWTTDDWWWDHWGWHMAWTT
none

2) Search for additional motifs listed in Badge *et al.* (2000).

CHI: GCTGGTGG
>humantap2:[3527,3534]
>humantap2:[3794,3801]
>chimptap2:[3527,3534]
>chimptap2:[3794,3801]

ade6-M26 heptamer: ATGACGT
none

LTR-IS: TGGAAATCCCC

none

retrotransposon LTR: TCATACACCACGCAGGGGTAGAGGACT

none

XY32 homopurine-pyrimidine H-palindrome:

AAGGGAGAARGGGTATAGGGRAAGAGGGAA

none

human minisatellite core sequence: GGGCAGGARG

GGGCAGGAAG:

>humantap2:[5547,5556]

>chimptap2:[5547,5556]

human hypervariable minisatellite sequences:

GGAGGTGGGCAGGARG,AGAGGTGGGCAGGTGG

none

pur: GGNGAGGGAGARRRR

>humantap2:[8784,8799]

GGAAGAGGGAGAGAAA

translin: GCNC[A/T][G/C][G/C][A/T] N(0-2) GCCC[A/T][G/C][G/C][A/T] ->

GCNCWSSW N(0-2) GCCCWSSW

GCNCWSSWGCCCWSSW

GCNCWSSWNGCCCWSSW

GCNCWSSWNNGCCCWSSW

none

human replication origin consensus: WAWTTDDWWWDHWGWHMAWTT

none

S.cerevisiae ARS: WTTTATRTTTW

none

S.pombe ARS: WRTTTATTTAW

none

scaffold attachment regions:

AATAAAYAAA: none

TWWTDTTWWW or TTWTWTTWTT: TTTTTTTTTT

>humantap2:[2301,2310]

>humantap2:[3201,3246]

>humantap2:[3247,3256]

>chimplap2:[3201,3246]
>chimplap2:[8105,8114]
>chimplap2:[8278,8287]

WADAWAYAWW:
AAGAAACATT
>humantap2:[2749,2758]
>chimplap2:[2749,2758]

TAGAAACATA
>humantap2:[5323,5332]
>chimplap2:[5323,5332]

AAAATACAAA
>humantap2:[9736,9745]
>chimplap2:[9736,9745]

topoisomerase II binding site: GTNWAYATTNATNRR
none

3) Search for additional motifs listed in Petes (2001).

β hotspot:
(CCGNN)₁₂:
none

(CGGATCCG)₄:
none

GC content: human 46.8%, chimp 47.0%

(GT)_n:
none (no more than 3 repeats)

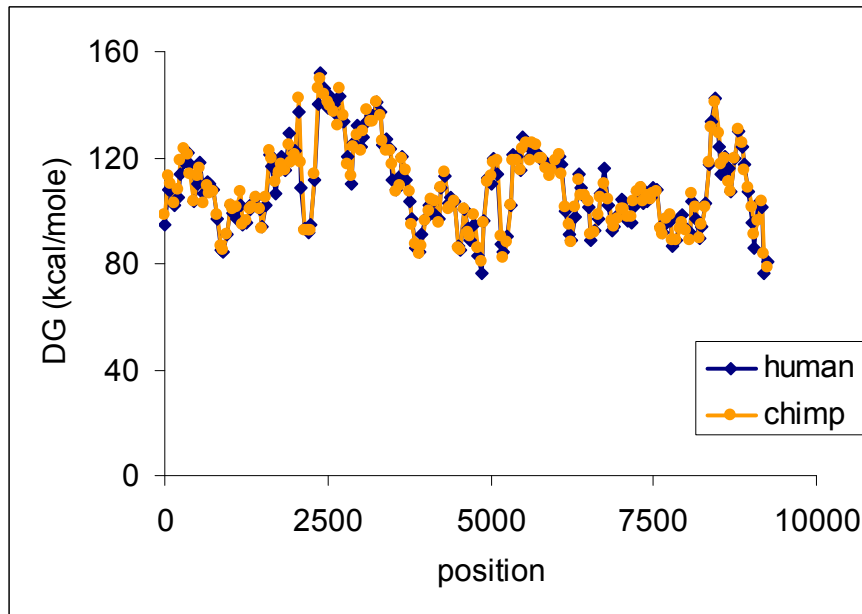
CoHR: -AG-T-GAACAA-ATAATC-AAAAAAAAAAAAACTGT--C----C-A-----
Cf. Blumental-Perry *et al.* (2000)
none

4) Search for additional motifs listed in Wall *et al.* (2003).

(RY)_n:
none (no more than 6 repeats)

WEB-THERMODYN: <http://wings.buffalo.edu/gsa/dna/dk/>
no difference

Helical stability of the DNA sequence.



References:

Badge RM, Yardley J, Jeffreys AJ, Armour JA (2000) Crossover breakpoint mapping identifies a subtelomeric hotspot for male meiotic recombination. *Hum Mol Genet* 9:1239-1244

Blumental-Perry A, Zenvirth D, Klein S, Onn I, Simchen G (2000) DNA motif associated with meiotic double-strand break regions in *Saccharomyces cerevisiae*. *EMBO Rep* 1:232-238

Jeffreys AJ, Ritchie A, Neumann R (2000) High resolution analysis of haplotype diversity and meiotic crossover in the human TAP2 recombination hotspot. *Hum Mol Genet* 9:725-733

Petes TD (2001) Meiotic recombination hot spots and cold spots. *Nat Rev Genet* 2:360-369

Smith RA, Ho PJ, Clegg JB, Kidd JR, Thein SL (1998) Recombination breakpoints in the human beta-globin gene cluster. *Blood* 92:4415-4421

Wall JD, Frisse LA, Hudson RR, Rienzo AD (2003) Comparative linkage disequilibrium analysis of the β -globin hotspot in primates. *Am J Hum Genet* 73:1330-1340.