

TLR2 RE#4

This RE is located -656 bp from TSS

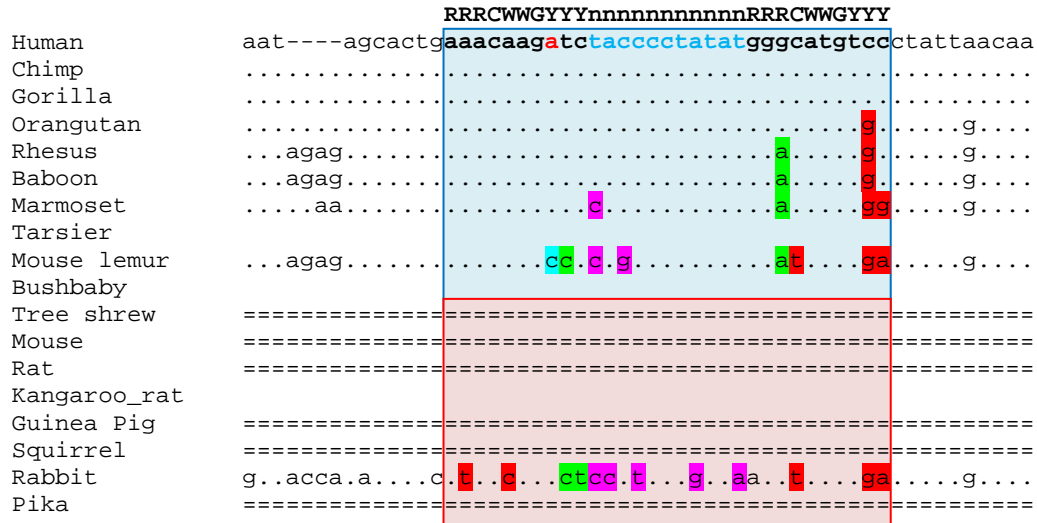
```

RRRCWWGYYYnnnnnnnnnnRRRCWWGYYY
AATAGCACTGAAACAAGaTctaccctatatGGGCATGTCCCTATTAACAA    Positive strand
n=11
TTGTTAATAGGGACATGCCCatataggggtaGAtCTTGTTTCAGTGCTATT    Negative strand
    
```

Chromosome coordinates: Ensembl Genome Browser: 4: 154621975-154622005

154621940 GATAGAMAAATGAACATTGGATCAGAATAGCACTGAAACAAGATCTACCCCTATATGGGCATGTCCCTATTAACA 154622014

Sequence alignment and conservation in primates and rodents



TLR3 RE#4

This RE is located -1929 from TSS

RRRCWWGYYYRRRCWWGYYY
 CTGAGACTATAGGCATGCACCAACATGCCAGCTAATTTT Positive strand Full RE Sp:0 2MM(1:1)
 AAAATTAGCTGGGCATGTTGGTGCATGCCTATAGTCTCAG Negative strand

Chromosome coordinates: Ensembl Genome Browser: 4: 186988380-186988399

186988309 TCAATGCAAACCTTGAATTTGCCTGGACTCAAGTGATCCTCCCACCTCAGCCTCCCAAGTAGCTGAGACTATAGGC 186988383
 186988384 ATGCACCAACATGCCAGCTAATTTTGTAAATTTTGTAGAGATGGAGTTTTACCACGTTGCCAGGTTGGTCTT 186988458

Sequence alignment and conservation in primates and rodents

	RRRCWWGYYYRRRCWWGYYY
Human	ctgagactatag ^g catgc ^a c ^c aacatgcccagc ^t aatttt
Chimpt.....
Gorillat.....
Orangutant.....
Rhesusc.....t.....t.....ct.ca.....c.....
Baboonc.....t.....t.....ct.ca.....
Marmoset	...g.....c.....g.....ct.....
Tarsier	.c.ga....c.....catg....c..c.t.tg.....
Mouse lemur	=====
Bushbaby	=====
Tree shrew	=====
Mouse	=====
Rat	=====
Kangaroo rat	=====
Guinea Pig	-----
Squirrel	=====
Rabbit	=====
Pika	-----

TLR4 RE#2

This RE is located -2354 from TSS

RRRCWWGYYYnnRRRCWWGYYY
 AGTGTGCATAAGGCATGCTCcaGAGCAAgtCTTTTGCTATTT Positive strand Full RE Sp:2 1MM (0:1)
 AAATAGCAAAAAGAtTTGCTCtgGAGCATGCCTTATGCACACT Negative strand

Chromosome coordinates: Ensembl Genome Browser: 9: 120464256-120464277
 120464235 CTGGATTGCYTAGTGTGCATAAGGCATGCTCcaGAGCAAATCTTTTGCTATTTTTAGAACTAACTAGCCCTGGT 120464309

Sequence alignment and conservation in primates and rodents

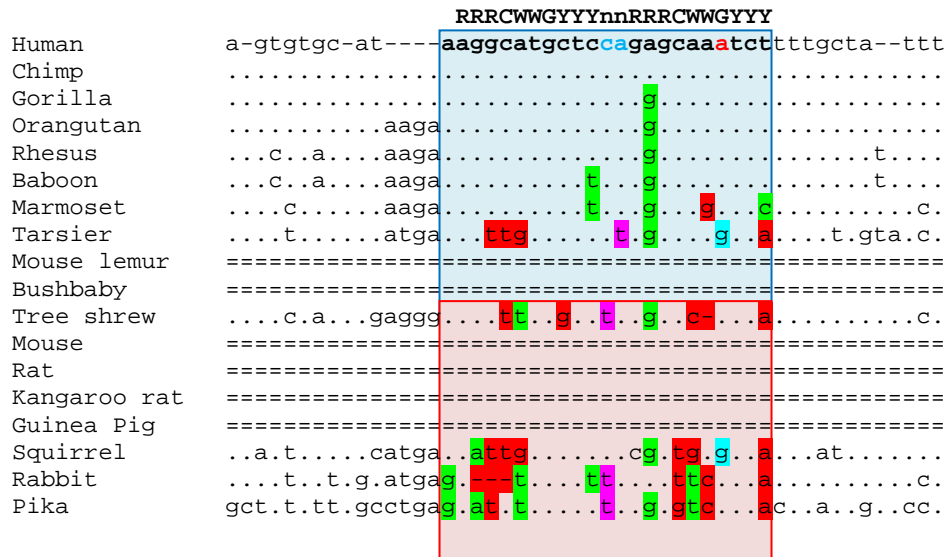


Figure S8 (continuation)

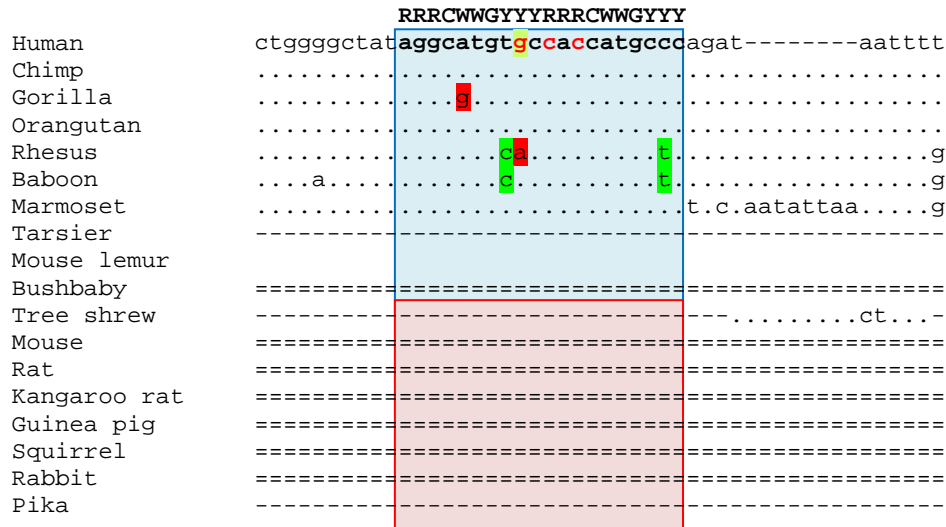
TLR5 RE#3

This RE is located -832 from TSS*

*(originally two different transcription sites were reported, those TSS are separated by 5995bp, the coordinates of this p53RE is relative to the second TSS (Chr 1: 223310629). The first TSS is located at Chr 1: 223316624.

RRRCWWGYYYYRRRCWWGYYY
 AAAATATCTGGGCATGgTgGcACATGCCTATAGCCCCAG Positive strand Full RE Sp:0 2/3MMs (2:1/0) *SNP
 CTGGGGCTATAGGCATGTgCcAcCATGCCAGATAATTTT Negative strand

Chromosome coordinates: Ensembl Genome Browser: 1: 223311442 -223311461
 223311499 GACCCCTCCACCCCCACCCCCACACACAAAAATTATCTGGGCATGGTGGYACATGCCTATAGCCCCAGCTACTCC 223311425



TLR5 RE#3 more information

SNP: 223311450: rs2192617 C/T (source dbSNP 130)

For population diversity and detailed information of this SNP click the following link [dbSNP 130: rs2192617](http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs2192617)
 (http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs2192617)

TLR5 reported transcripts(source Ensembl, currently release 57 - Mar 2010):

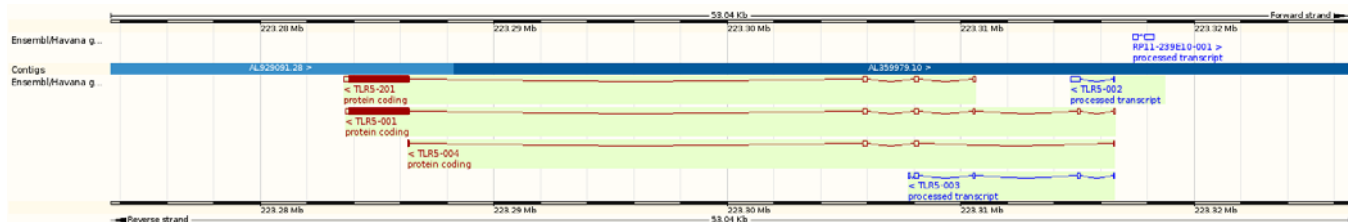


Figure S8 (continuation)

TLR6 RE#6

This RE is located -1332 from TSS*

*(originally two different transcription sites were reported, those TSS are separated by 27278bp, the coordinates of this p53RE is relative to the second TSS (Chr 4: 38831160). The first TSS is localted at Chr 4: 38858438.

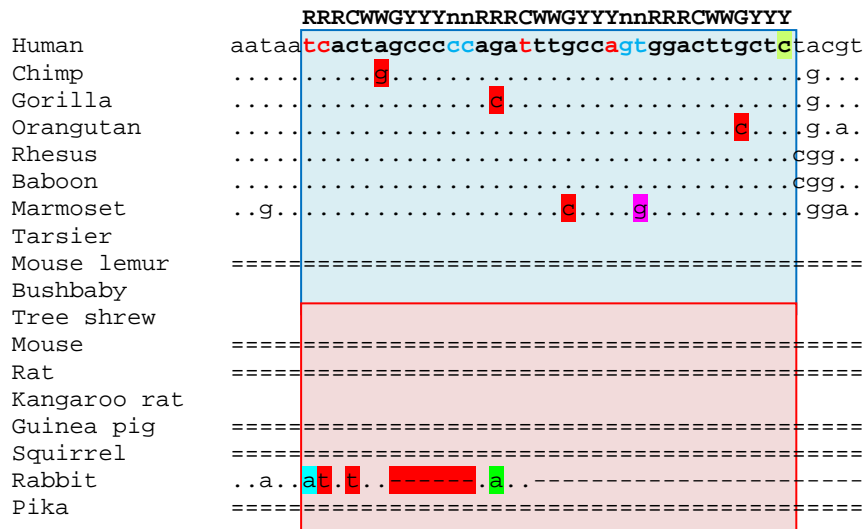
```

RRRCWGWYYYnnRRRCWGWYYYnnRRRCWGWYYY
ACGTAGAGCAAGTCCactGGCAAaTCTggGGCTAGTgaTTATT      Positive strand
AATAAtcACTAGCCCccAGAtTTGCCagtGGACTTGCTCTACGT      Negative strand
    
```

Chromosome coordinates: Ensembl Genome Browser: 4: 38832459 -38832492

```

38832538 TCCATTGCTTTTTTGCAAGGTTTGTGTTATTTTCAGGGCAAACRTARAGCAAGTCCACTGGCAAATCTGGGGGCT 38832464
38832463 AGTGAATTATTTGTTTTGATTTTTATTTTTTAAATCAGACATTTTAAACACTACAATGAGGTAMCTCTARAAAT 38832389
    
```



TLR6 RE#6 more information

SNP: 38832492: rs167251 G/A (source dbSNP 130)

For population diversity and detailed information of this SNP click the following link [dbSNP 130: rs167251](http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs167251) (http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs167251)

TLR6 reported transcripts (source Ensembl, currently release 57 - Mar 2010):



TLR8 RE#6

This RE is located -1074 from TSS

RRRCWWGYYYRRRCWWGYYY
 CTGGGGTGTAAGGCAAGaTgAAACATaTCaCATCCCGTTC Positive strand Full RE Sp:0 3/4MM (2:1/2)*SNP
 GAACGGGATgtGATATGTTTcaTCTGCCTTACACCCAG Negative strand

Chromosome coordinates: Ensembl Genome Browser: X: 12923665 -12923684

12923639 TGGTTTTCTCCCACTCCTGGGGTGTAAGGCAAGATGAAACATaTCaCATCCCGTTCTAAACTTTATTCTTGTGGC 12923713

	RRRCWWGYYYRRRCWWGYYY
Human	ctgggg---tgtaaggcaagatgaaacatatacatcccgttc
Chimp
Gorilla	
Orangutana...
Rhesusa...
Baboona...
Marmoseta...
Tarsier	=====
Mouse lemur	ga...a...a-.tt.c.tca...-----
Bushbaby	ta.....g.t.....a.....c.t....t.tc..
Tree shrew	aat.....c.t.g.g...a...
Mouse	ag.a..ctc.a..gaa..gag-----c.t.ac..
Rat	=====
Kangaroo rat	
Guinea pig	=====
Squirrel	ag.....a..aa...tg.....c..t.t...t.a...
Rabbit	
Pika	=====

TLR8 RE#6 more information

SNP: 12923681: rs3761624 A/G (source dbSNP 130)

For population diversity and detailed information of this SNP click the following link [dbSNP 130: rs3761624](http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs3761624) (http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs3761624)

Figure S8 (continuation)

TLR9 RE#14

This RE is located -720 from TSS*

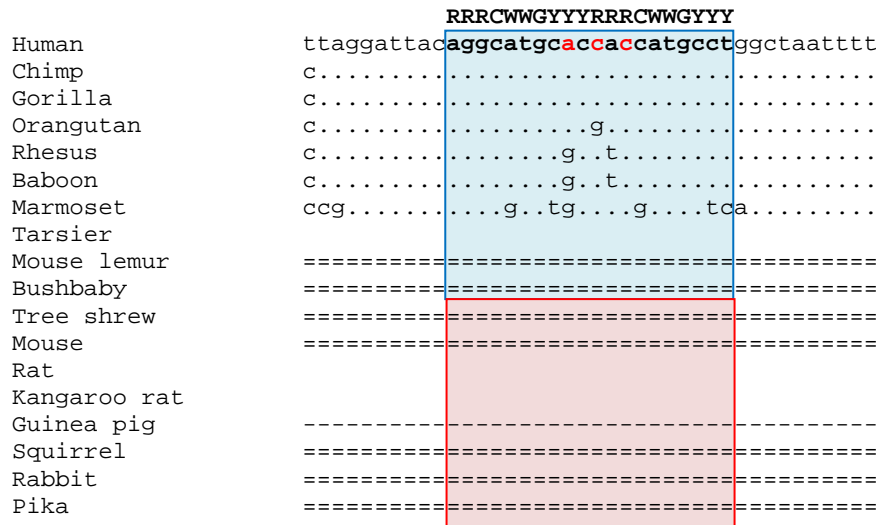
*(originally two different transcription sites were reported, those TSS are separated by 13004bp, the coordinates of this p53RE is relative to the first TSS (Chr 3: 52273183 now assigned for TWF2 gene). The second TSS is located at Chr 3: 52260179.

The distance between the two regions (each region 10kb) analyzed is 2956bp

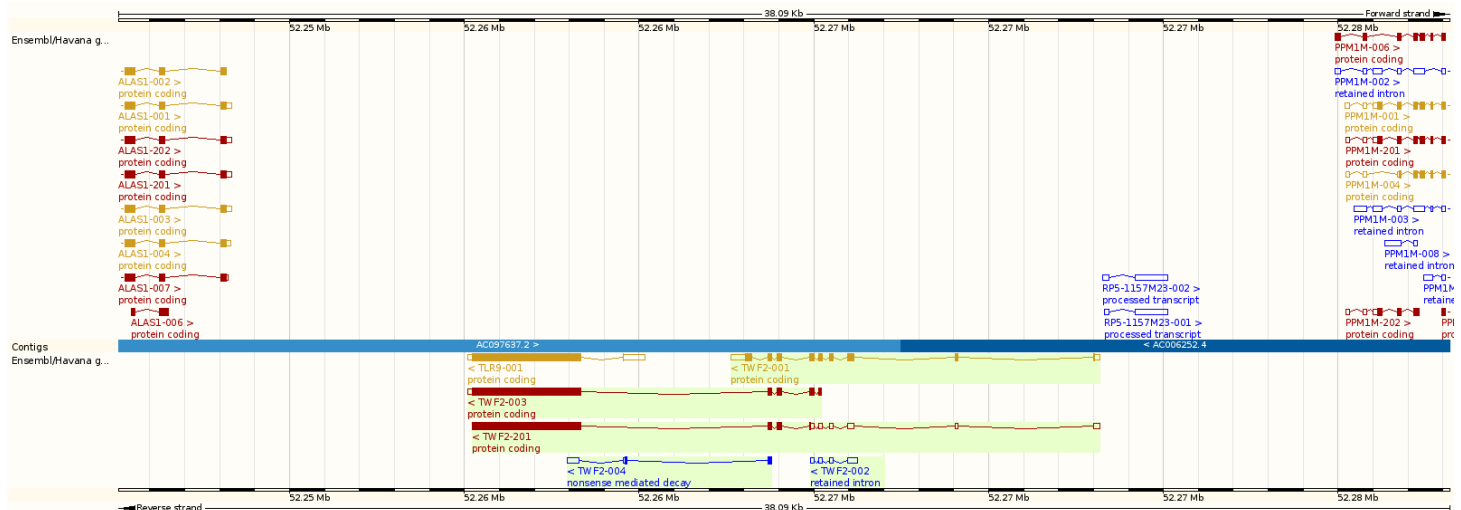
RRRCWWGYYRRRCWWGYYY
 AAAATTAGCCAGGCATGgTggtGCATGCCTGTAATCCTAA Positive strand Full RE Sp:0 3MM (2:1)
 TTAGGATTACAGGCATGCaCaAcCATGCCTGGCTAATTTT Negative strand

Chromosome coordinates: Ensembl Genome Browser: 3: 52273914-52273933

52273983 ACTGACCAACATAGAGAAACCCCGTCTCTACTAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGTAATCCTAA 52273909



TLR9 reported transcripts (source Ensembl, currently release 57 - Mar 2010):



TLR10 RE#4

This RE is located -2226 from TSS

RRRCWWGYYYRRRCWWGYYY
 TGTGTAATATAGACATGTTTGTAtATGTTTAGGTTGAGGAG Positive strand Full RE Sp:0 2MM (0:2)
 CTCCTCACCTAAACATaTaaAACATGTCTATATTACACA Negative strand

Chromosome coordinates: Ensembl Genome Browser: 4: 38786796-38786815
 38786889 TCATCCAACAAGCTGGGAATMCCCTCTCCAACGTTCCCTGACGGGTGTTCCCTGTCTTCCCTACGTTTGTGTAATATA 38786815
 38786814 GACATGTTTGTATATGTTTAGGTTGAGGAGCAGAGCTGGTTTTGTTTTGCTGTTGTTTTTCTTTTACAGTTATTT 38786740

Sequence alignment and conservation in primates and rodents

