in H. sapiens Search

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- *C. familiaris*
- *G. gallus*
- *D. melanogaster*
- *A. mellifera*
- *D. rerio*
- *C. elegans*
- *A. thaliana*
- *Z. mays*
- *S. cerevisiae*
- *S. pombe*
- *P. falciparum*
- *H. vulgare*

Format: 'genome'. Click here to to display this entry in format 'text'.

General Information

Promoter ID:	**TP53_1**
Promoter type:	region
Organism:	Homo sapiens (Human)
Gene Symbol:	TP53
Description of the gene:	tumor protein p53
Sequence:	tttcccctcccatgtgctcaagactggcgctaaaagttttgagcttctcAAAAGTCTAGA
Position in the genome:	Chromosome [NC_000017.11]; Strand [-]; Position [7687487]
Ensembl:	ENSG00000141510
RefSeq:	NM_001276696
NCBI Gene:	TP53
GeneCards:	TP53

Promoter Image [View it at UCSC]

- MGA FTP site

Documents

Other Resources

References

What is new

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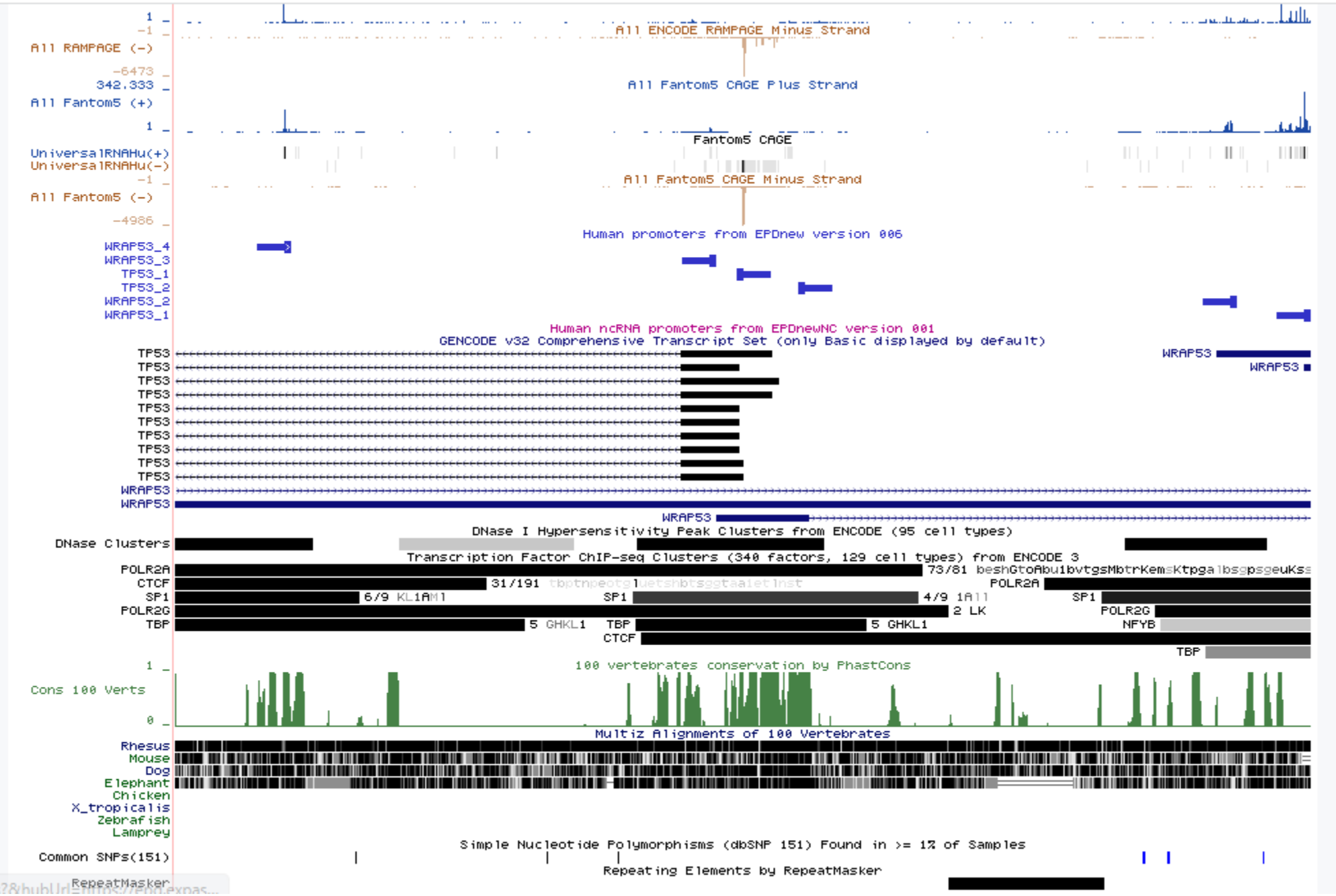

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Published base frequency tables and weight matrices:

- Inr-DPE motif found in *D. melanogaster*
- Bucher, P (1990). *Weight matrix descriptions of four eukaryotic RNA polymerase II promoter elements derived from 502 unrelated promoters.* *J. Mol. Biol. 212, 563-578*.
  - TATA-box
  - Initiatior
  - CCAAT-box
  - GC-box

Promoter element HMMs derived from EPD release 68 (September 2001):

- TATA-box HMM trained from 900 unrelated general promoter sequences:

Position	1	2	3	4	5	6	7	8	9	10	11	12
% A	21.4	15.9	3.7	91.1	0.0	94.5	67.3	97.3	52.1	40.7	16.5	23.6
% C	22.7	39.3	9.8	0.0	0.0	0.0	0.0	0.0	0.0	9.1	34.8	37.1
% G	28.2	35.2	2.9	0.0	0.0	0.0	0.0	2.7	12.0	40.2	38.0	30.4
% T	27.7	9.6	83.6	8.9	100.0	5.5	32.7	0.0	35.9	10.0	10.7	8.9
Consensus			T	A	T	A	W	A	W	R		

- TATA-box HMM trained from 600 unrelated vertebrate promoter sequences:

Position	1	2	3	4	5	6	7	8	9	10	11	12
% A	17.7	19.3	6.6	83.4	0.0	95.0	72.3	94.2	53.3	29.3	17.7	22.7
% C	21.1	36.1	14.8	0.0	0.0	0.0	0.0	0.0	0.0	9.0	32.5	33.0

in All databases Search

GC-box base frequency table and weigth matrix

(from Bucher 1990, J. Mol. Biol. 212, 563-578, Table 6)

Position	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7
# A	102	97	50	67	0	2	54	46	1	79	23	0	20	40
# C	40	31	6	1	0	0	170	1	3	0	17	166	86	24
# G	50	112	154	206	274	272	0	224	222	171	192	35	52	109
# T	82	34	64	0	0	0	50	3	48	24	42	73	116	101
W(A)	0.00	0.00	-0.52	-0.39	-4.07	-3.42	-1.05	-1.09	-3.57	-0.03	-1.35	-3.98	-1.56	-0.72
W(C)	-0.95	-1.12	-2.26	-3.25	-3.80	-4.23	0.00	-3.67	-3.05	-3.52	-1.90	0.00	-0.42	-1.45
W(G)	-1.16	-0.38	0.00	0.00	0.00	0.00	-4.58	0.00	0.00	0.00	0.00	-1.83	-1.09	-0.27
W(T)	-0.10	-1.00	-0.15	-3.75	-3.93	-4.02	-0.98	-3.34	-0.69	-1.14	-0.83	-0.56	0.00	0.00
Consensus	a/t	a/g	g/t/a	G/a	G	G	C/t/a	G/a	G/t	g/a/t	g/t	c/t	t/c	t/g
Preferred region: Position 0 between -164 and +1 relative to transcription start site.										Optimizid cut-off value: -4.90 (88.0%)				