

Supplemental Table 5. Differentially regulated genes with statistically identified octamer sequences -500 to +100

Symbol	Position ⁺	Sequence	Strand	Opt.	Matrix	
					Sim.	Weight Matrix [†]
<i>No radiation (supplemental Table I)</i>						
Gpx3	-298	TCTATGTTAAGTCTCT	pos	0.80	0.875	V\$OCT1.06
Atm	-292	AGCATGGTAATCTAT	neg	0.80	0.941	V\$OCT1.04
Rgs4 [‡]	-248	CAAATGCAAAACTTG	neg	0.84	0.961	V\$OCT1.02
Fyxd6	-420	TTCATGCTAATTCGG	pos	0.80	0.924	V\$OCT1.06
Dcn	-31	CATATGGTAATGATA	neg	0.80	0.901	V\$OCT1.04
Dcn	-111	CATATGCAAAAGGGAT	pos	0.84	0.956	V\$OCT1.02
Col10a1	-383	TTAATGTAATTTCA	pos	0.80	0.879	V\$OCT1.06
Edil3	-301	AAGATGCAAACTCTA	neg	0.84	0.955	V\$OCT1.02
Smoc2	+5	AATGTGATAATTTGT	neg	0.80	0.855	V\$OCT1.06
Smoc2	-485	TTTATGCTAAGGAGG	neg	0.77	0.895	V\$OCT1.01
Bcl11b	-288	AAAATGCAAAACAAT	neg	0.84	0.956	V\$OCT1.02
Mitc1	-486	TAAATGCAAAACAGAT	neg	0.84	0.956	V\$OCT1.02
Atp10d	-434	AATATGTTTATTTTA	neg	0.80	0.864	V\$OCT1.06
Ampd3	-173	CTTAAGCTAATTTGTG	pos	0.80	0.864	V\$OCT1.06
Olr1	-469	GGAAATGCAAACTCCTA	neg	0.80	0.881	V\$OCT1.04
Khsrp	+24	ACCATGCAAAAGCAGC	pos	0.84	0.962	V\$OCT1.02
Elav12	-187	TGCATGCAAACTTGC	pos	0.84	0.958	V\$OCT1.02
Ghitm	-496	CATATATTAATTTTAC	neg	0.80	0.880	V\$OCT1.06
Hist2h2aa1	-131	CTTATGTAATGAGA	pos	0.77	0.925	V\$OCT1.01
Centd2	-185	GATATGAGAAGCAGC	neg	0.77	0.832	V\$OCT1.01
<i>After radiation (supplemental Table II)</i>						
Sesn2	-230	TTCATGCAAAAGTTT	pos	0.84	0.957	V\$OCT1.02
Sdfr2 [‡]	-20	TGTATGTGAATTTATA	pos	0.80	0.903	V\$OCT1.06
Ccng1	-279	ACAATGCAAAACAAA	pos	0.84	0.961	V\$OCT1.02
Prkaa2	-164	ATTATGTAACAAGT	pos	0.77	0.851	V\$OCT1.01
Ptges [‡]	-319	TTTATGCTAATGTGT	neg	0.77	0.945	V\$OCT1.01
Inpp5f	-102	CAAATGAAAAATGAAA	neg	0.80	0.879	V\$OCT1.04
Calmbp1	-226	TTTATGCAAAAGTATT	pos	0.77	0.857	V\$OCT1.01
Sfmbt1	-77	TGTTTGTTAATTTTT	pos	0.80	0.875	V\$OCT1.06
Zfp423	+17	GTATGCAAAAAAAA	neg	0.84	0.964	V\$OCT1.02
Prrx1	-224	TTTATGCAAAATCTA	neg	0.84	0.967	V\$OCT1.02
Zfh4	+69	ATTCGCTAATTTATT	neg	0.80	0.868	V\$OCT1.06
Abcb1	-183	TCTATGTAATGTCT	pos	0.77	0.885	V\$OCT1.01
Oxct1	-264	AGTATGATAATAGCA	pos	0.80	0.856	V\$OCT1.06
Sgol1	+73	ATAATGTCAATTTCC	neg	0.80	0.851	V\$OCT1.06
Sgol2 [‡]	-233	AATATGTTAATGGAG	pos	0.80	0.864	V\$OCT1.06
Bsc12	-217	GGGATGCAAAACAGCA	neg	0.84	0.951	V\$OCT1.02

position relative to the octamer sequence (bold) and the first annotated transcription initiation site

[†]references and Re- (random expectation) values for matrices using optimal threshold cutoffs:

V\$OCT1.01: Verrijzer et al. (1992); 3 matches per 100,000 bp

V\$OCT1.02: Sturm, et al. (1988); 1.3 matches per 10,000 bp

V\$OCT1.04: Groenen et al. (1992); 1 match per 1,000 bp

V\$OCT1.06: van Leeuwen et al. (1995); 4 matches per 100,000 bp

[‡]also contains a perfect octamer (Table 4)