

Additional file 14: TFBS modules occurring in at least three of the seven promoter regions of the human 8q24.3 ZNF genes

Gene	TFBS module	1st TFBS	Start	End	Strand	Sequence	Core similarity	Matrix similarity	2nd TFBS	Start	End	Strand	Sequence	Core similarity	Matrix similarity
ZNF7	EGRF SP1F 01	V\$EGRF/EGR1.02	262	278	(-)	CAGGGGCGGGGCGGGGC	1.000	0.907	V\$SP1F/SP1.01	259	273	(-)	GCGGGGCGGGGCGGGC	1.000	1.000
ZNF7	ETSF SP1F 03	V\$ETSF/PEA3.01	301	321	(-)	GAGGGAGAGGAGGGCCAGAG	1.000	0.836	V\$SP1F/SP1.03	281	295	(-)	AGTGGGCGGTGCTGCT	1.000	0.932
ZNF7	SP1F AP2F 01	V\$SP1F/GC.01	322	336	(-)	AGGGGGCGGAGCCGC	1.000	0.965	V\$AP2F/AP2.02	297	311	(-)	AGGGCCGAGAGCCGC	0.905	0.795
ZNF7	EGRF SP1F 01	V\$EGRF/EGR1.02	325	341	(-)	CGGGCACGGGCGCGAGC	1.000	0.924	V\$SP1F/GC.01	322	336	(-)	AGGGGGCGGAGCCGC	1.000	0.965
ZNF7	EGRF SP1F 01	V\$EGRF/EGR1.02	353	369	(-)	GCGCGTGGGGGCGGGGT	1.000	0.903	V\$SP1F/SP1.01	350	364	(-)	TGGGGGCGGGGTACA	1.000	0.997
ZNF7	KLFS SP1F 01	V\$KLFS/KLF6.01	364	380	(-)	AGGCGGGGCTGGCGCCT	1.000	0.932	V\$SP1F/SP1.01	350	364	(-)	TGGGGGCGGGGTACA	1.000	0.997
ZNF7	IKRS AP2F 01	V\$IKRS/IK2.01	390	402	(-)	GGGCGGGACACAGA	1.000	0.919	V\$AP2F/AP2.02	410	424	(-)	GGGGCCGAGGGACA	0.905	0.910
ZNF7	SP1F ETSF 04	V\$SP1F/GC.01	471	485	(+)	GGGAGGCGGGGCTGA	1.000	0.930	V\$ETSF/CETS1P54.01	451	471	(-)	CAGGCTCCGGAGAAGGGGTGG	1.000	0.843
ZNF7	ETSF SP1F 03	V\$ETSF/ELK1.02	521	541	(+)	GGGCGGCGCGGAAGTTTGC	1.000	0.980	V\$SP1F/SP1.03	542	556	(+)	GCGGGGCGGACGCGG	1.000	0.924
ZNF16	ETSF SP1F 05	V\$ETSF/ELK1.02	491	511	(+)	GGCGGGCGGGAATTCGGGGC	1.000	0.961	V\$SP1F/GC.01	487	501	(+)	GAGCGGCGGGCCGGA	1.000	0.835
ZNF16	SP1F ETSF 01	V\$SP1F/SP1.01	504	518	(+)	TCGGGGCGGGACTTC	1.000	0.976	V\$ETSF/ELK1.02	491	511	(+)	GGCGGGCGGGAATTCGGGGC	1.000	0.961
ZNF16	ETSF ETSF 02	V\$ETSF/ELK1.02	507	527	(-)	TGACCCCGGGAAGTCCGCC	1.000	0.977	V\$ETSF/ELK1.02	491	511	(+)	GGCGGGCGGGAATTCGGGGC	1.000	0.961
ZNF34	ETSF ETSF 06	V\$ETSF/PEA3.01	154	174	(+)	GGCCCTAAGGAAGGGTCCGGT	1.000	0.930	V\$ETSF/SP1 PU1.02	165	185	(-)	GAGAAACGGGAACCGACCCT	1.000	0.918
ZNF34	EGRF SP1F 01	V\$EGRF/EGR1.02	578	594	(+)	CCCGGGCGGGGCGGGCG	1.000	0.969	V\$SP1F/SP1.01	583	597	(+)	CGGGGGCGGGCGCGC	1.000	0.976
ZNF250	ETSF SP1F 04	V\$ETSF/SP1 PU1.02	53	73	(+)	CAGCAGCGGGAACCGCAAGG	1.000	0.912	V\$SP1F/SP1.03	145	159	(+)	GCGGGGCGGACAGGG	1.000	0.885
ZNF250	ETSF SP1F 03	V\$ETSF/PDEF.01	411	431	(+)	GCCTCCAGGATTGGCGAAT	1.000	0.888	V\$SP1F/SP1.01	438	452	(+)	TGGGGGCGGGAATCTG	1.000	0.973
ZNF250	EGRF SP1F 01	V\$EGRF/EGR1.02	433	449	(+)	GGCTGTGGGGGCGGGAA	1.000	0.987	V\$SP1F/SP1.01	438	452	(+)	TGGGGGCGGGAATCTG	1.000	0.973
ZNF250	SP1F AP2F 01	V\$SP1F/SP1.01	438	452	(+)	TGGGGGCGGGAATCTG	1.000	0.973	V\$AP2F/AP2.02	460	474	(+)	GGAGCCCGGGAATCTG	0.905	0.808
ZNF250	SP1F ETSF 01	V\$SP1F/SP1.03	452	466	(+)	GAGGGGCGGGAAGCC	1.000	0.897	V\$ETSF/SP1 PU1.02	438	458	(+)	TGGGGGCGGGAATCTG	1.000	0.941
ZNF250	NFKB SP1F 04	V\$NFKB/NFKAPPAB.01	468	480	(+)	CAGGGATTGGCGG	1.000	0.810	V\$SP1F/SP1.03	494	508	(-)	AAAGGGCTGCCCGC	1.000	0.828
ZNF250	EGRF SP1F 01	V\$EGRF/EGR1.02	484	500	(+)	CGCAGACGGGCGGGGC	1.000	0.909	V\$SP1F/SP1.01	489	503	(+)	ACGGGGCGGGCAGC	1.000	1.000
ZNF251	IKRS AP2F 01	V\$IKRS/IK2.01	69	81	(+)	AAAAGGGATTAC	1.000	0.928	V\$AP2F/AP2.02	44	58	(+)	CTGGCTCTGGGACT	1.000	0.894
ZNF251	ETSF ETSF 04	V\$ETSF/ELK1.02	460	480	(-)	CGGGAACCGGAAGCCAGCCG	1.000	0.987	V\$ETSF/SP1 PU1.02	511	531	(+)	GGGGGCGGGGAAGCCTCGCTG	1.000	0.956
ZNF251	SP1F ETSF 01	V\$SP1F/SP1.03	447	461	(+)	TCCGGGCGGAACCCG	1.000	0.901	V\$ETSF/ELK1.02	432	452	(+)	GCGGCCCGGGAAGATCCGGG	1.000	0.948
ZNF251	ETSF ETSF 02	V\$ETSF/ELK1.02	460	480	(-)	CGGGAACCGGAAGCCAGCCG	1.000	0.987	V\$ETSF/SP1 PU1.02	446	466	(+)	ATCCGGGCGGAACCGCGCTG	1.000	0.946
ZNF251	EGRF SP1F 01	V\$EGRF/EGR1.02	505	521	(+)	CCCGCAGGGGCGGGGA	1.000	0.919	V\$SP1F/SP1.01	510	524	(+)	AGGGGGCGGGGAAGC	1.000	0.997
ZNF251	NFKB SP1F 04	V\$NFKB/NFKAPPAB50.01	515	527	(+)	GCGGGGAAGCCTG	1.000	0.809	V\$SP1F/SP1.03	540	554	(-)	GGCGGGCGGGCCGA	1.000	0.903
ZNF251	EGRF SP1F 01	V\$EGRF/EGR1.02	566	582	(-)	CGGGGAGGGGCGGGCT	1.000	0.966	V\$SP1F/SP1.01	563	577	(-)	AGGGGGCGGGCTAGG	1.000	0.977
ZNF251	KLFS SP1F 01	V\$KLFS/KLF.01	572	588	(-)	CAGAGCGGGGAGGGGG	1.000	0.950	V\$SP1F/SP1.01	563	577	(-)	AGGGGGCGGGCTAGG	1.000	0.977
ZNF251	ETSF ETSF 04	V\$ETSF/ETS1.01	640	660	(-)	GCCACCGAGGAAGCCGAGG	1.000	0.963	V\$ETSF/ELF2.01	693	713	(+)	TCCGACCGAGGAAGGAGGCCA	1.000	0.941
ZNF251	ETSF SP1F 05	V\$ETSF/ELF2.01	693	713	(+)	TCGGACCGAGGAAGGAGCCCA	1.000	0.941	V\$SP1F/SP1.03	682	696	(+)	GTGGGCGAGTGTCCG	1.000	0.872
ZNF252	SP1F ETSF 01	V\$SP1F/SP1.03	223	237	(+)	GAAGGGCGGGGTCCA	1.000	0.885	V\$ETSF/SP1 PU1.02	214	234	(+)	CTAGGTGAGGAAGGGCCGGGT	1.000	0.958
ZNF252	IKRS AP2F 01	V\$IKRS/IK2.01	384	396	(+)	AACCGGAAGGAG	1.000	0.947	V\$AP2F/AP2.02	360	374	(+)	TCCGCCAAGGGCTGG	0.823	0.866
ZNF252	ETSF ETSF 02	V\$ETSF/SP1 PU1.02	480	500	(+)	GGCAGGGCGGAAGTTTCAGATT	1.000	0.991	V\$ETSF/ELK1.02	498	518	(-)	CCTGGGCGGGAATGCCTAAT	1.000	0.984
ZNF252	ETSF SP1F 05	V\$ETSF/SP1 PU1.02	480	500	(+)	GGCAGGGCGGAAGTTTCAGATT	1.000	0.991	V\$SP1F/SP1.03	476	490	(+)	GAAGGGCAGGGCGGGA	1.000	0.896
ZNF252	ETSF SP1F 03	V\$ETSF/GABPB1.01	604	624	(+)	CCTGGTGCAGGAGTGCAGGAG	1.000	0.812	V\$SP1F/SP1.01	630	644	(+)	CTGGGGCGGGCAGGG	1.000	0.955
ZNF252	ETSF SP1F 03	V\$ETSF/CETS1P54.01	613	633	(+)	GAGGTGCGGAGTGGCGCTGG	1.000	0.817	V\$SP1F/SP1.03	634	648	(+)	GGCGGGCAGGGCGG	1.000	0.900
ZNF252	KLFS SP1F 01	V\$KLFS/KLF.03	617	633	(+)	TGCCGAGATTGGCGCTGG	1.000	0.892	V\$SP1F/SP1.01	630	644	(+)	CTGGGGCGGGCAGGG	1.000	0.955
ZNF252	EGRF SP1F 01	V\$EGRF/EGR1.02	625	641	(+)	TGGCGCTGGGGCGGGCA	1.000	0.879	V\$SP1F/SP1.01	630	644	(+)	CTGGGGCGGGCAGGG	1.000	0.955
ZNF517	ETSF SP1F 04	V\$ETSF/CETS1P54.01	146	166	(+)	CCCTGGCCGGACGCCCCGCT	1.000	0.924	V\$SP1F/SP1.03	230	244	(+)	CGGGGGCAGAGATG	1.000	0.883
ZNF517	SP1F ETSF 01	V\$SP1F/SP1.02	161	175	(-)	GAAGGGCGGAGCGGG	1.000	0.938	V\$ETSF/ETS1.01	164	184	(-)	GACCCGAGGAAGGGCGGAGC	1.000	0.967
ZNF517	IKRS AP2F 01	V\$IKRS/IK2.01	203	215	(-)	GTTGGGAGCAGC	1.000	0.906	V\$AP2F/AP2.02	225	239	(-)	TCTGCCCGGGGTGG	0.905	0.894
ZNF517	NFKB SP1F 02	V\$NFKB/CREL.01	354	366	(-)	CTGGGGGTTCCG	1.000	0.942	V\$SP1F/TIEG.01	352	366	(-)	CTGGGGGTTCCGGG	1.000	0.728
ZNF517	EGRF SP1F 01	V\$EGRF/EGR1.02	483	499	(+)	GTTTCCGGGGCGGGGA	1.000	0.886	V\$SP1F/SP1.01	488	502	(+)	CGGGGGCGGGGAAGG	1.000	0.997
ZNF517	SP1F AP2F 01	V\$SP1F/SP1.01	488	502	(+)	CGGGGGCGGGGAAGG	1.000	0.997	V\$AP2F/AP2.02	507	521	(+)	GGAGCCTGAGAGCCG	1.000	0.793
ZNF517	ETSF SP1F 04	V\$ETSF/SP1 PU1.02	489	509	(+)	GGGGGGCGGGGAAGAACCGGA	1.000	0.956	V\$SP1F/SP1.01	580	594	(+)	GCGGGGCGGGGACTG	1.000	0.997

Individual colors denote different module families

Start / End Position within promoter region relative to first nucleotide of the sequence
strand orientation:
(+) Sense strand with respect to transcript
(-) Antisense strand with respect to transcript

Genomatix Matrix Family Library Version 8.1
Genomatix Module Library Version 5.2, Vertebrate Modules (June 2009)
Prediction by Genomatix ModelInspector 5.6.5