

Supplementary Table 2. Putative 6 finger protein target sites in the human genome. The number of matching residues and DNA strand are indicated. Unmatching positions are in uppercase letters, or represented by an X. Cdh5 gene is located on the NT_010546 genome contig (mRNA region 1212630..1247537). Ets1 gene locus is on chromosome 11 contig NT_033899 (mRNA region 9225151..9285056). erg is on chromosome 21 contig NT_011512 (mRNA region 25332729..25525028). Flil1 is on chromosome 17 contig NT_030843 (mRNA region 11820022..1187246)

Protein	target site/sequence	Chr.	genome contig	Pos.	DNA strand	Match/18
CD144-3	GTAGGTTGGGAAAGAGGA					
	gtaggttgggaaagaggX	6	NT_007299.10	4464476	+	17
	Xtaggttgggaaagagga	2	NT_022135.10	4595471	+	17
	gtaggGtgggaaagagga	20	NT_011333.5	1301936	+	17
	gtaggGtgggaaagagga	12	NT_024397.12	348174	+	17
	gtaggttgggGaagagga	11	NT_009307.11	1418071	-	17
	gtaggtGgggaaagagga	10	NT_008902.12	3207156	+	17
	gtaggttgggGagagga	8	NT_028251.7	1586418	-	17
	gtaggGtgggaaagagga	8	NT_023666.12	286197	-	17
	gtaggttgggCagagga	8	NT_023666.12	1741512	+	17
	gtaggtGgggaaagagga	7	NT_007933.10	10671166	-	17
	gtaggttggAaaagagga	6	NT_007592.10	3870959	+	17
	gtGggttgggaaagagga	3	NT_005986.12	2163357	+	17
	gtagCttgggaaagagga	3	NT_022594.7	334592	+	17
	gtaggttggAaaagaggX	16	NT_024797.10	3671835	-	16
	XXaggttgggaaagaAga	16	NT_024797.10	4013883	+	15
	XXagCttgggaaagagga	16	NT_024797.10	3695670	-	15
	XXaggttgggaaagaggX	16	NT_010604.10	216067	+	15
	XXaggttGtaaagagga	16	NT_010604.10	2522008	+	15
	XXXXgttgggaaagagga	16	NT_010604.10	2399376	-	14
	gtaggAtgggaaagaggX	16	NT_010478.10	4318036	+	16
CD144-4	TGAGCGGCTTGAGGGGTC					
	tgagcCgcttgaggggtc	20	NT_030871.1	885453	+	17
	tgagGggcttgaggggtc	10	NT_030059.7	10686449	+	17
	tgagcggcttgaggggXX	16	NT_010422.1	2416153	+	16
	tgagGggcttgaggggtX	X	NT_025323.5	290796	-	16
	XgagcggcttgagAggtc	17	NT_033299.2	116456	-	16
	XgagcggcttgagAggtc	14	NT_026437.8	33697112	+	16
	tgTgcggcttgaggggtX	9	NT_019501.10	1139745	-	16
	tgTgcggcttgaggggtX	9	NT_017539.12	66222	-	16
	tgagcTgcttgaggggtX	5	NT_006547.10	3039604	-	16
	XgagcggctCgaggggtc	2	NT_005472.7	19765	-	16
	XXXgcggcttgaggggtc	2	NT_034484.1	1333820	+	15
	tgagTggcttgaggggXX	16	NT_033288.2	1451945	+	15
	tgagGggcttgaggggXX	16	NT_010478.10	3972014	-	15
	tgagcTgcttgaggggXX	16	NT_010463.10	193638	+	15

CD144-5	GCTAGAGCAGTTGACTAA					
	gctagagcagttAactaa	22	NT_011520.8	13062356	+	17
	gctagagcagttgactXX	17	NT_035424.1	538509	+	16
	gctagagcaCttgactaa	10	NT_033896.2	142573	+	17
	gctagagcagttgactXX	4	NT_034703.1	15435	-	16
	XXtagagcagttgactaa	3	NT_022481.12	409397	+	16
	gctagagcagttgactXX	2	NT_005204.10	5077923	-	16
	gctagagcagGtgacAaa	2	NT_005204.10	6742791	-	16
	XctagagcagttAactaX	16	NT_033283.2	193229	+	15
	XctagagcagCtgactaX	16	NT_019609.8	168950	+	15
	gcCagagcaAttgactaa	16	NT_010478.10	504882	+	16
	XXXXgagcagttgactaa	16	NT_010441.10	691170	-	14
CD144-13	GCAGACGGTTAGGACGCC					
	XcagaTggttaggacgcc	14	NT_026437.8	39284183	+	16
	XcagacggttaggacgXX	2	NT_022171.10	1659667	-	15
	XcagacggttaggaGgcX	20	NT_011362.7	9602229	-	15
	XXagacggtGaggacgcc	19	NT_011104.12	2400119	-	15
	XXagacggttaggaGgcc	12	NT_009540.12	1153869	+	15
	gcagCcAgttaggacgcc	10	NT_035039.1	268184	+	16
	gcagacagtttaggaGgcc	10	NT_030059.7	14112143	-	16
	XXagacggttaggacAcc	9	NT_033215.2	135229	+	15
	gcaCacggttaggaTgcc	7	NT_007819.10	26691943	+	16
	XXagaAggttaggacgcc	7	NT_007819.10	21279600	+	15
	gcagacggAtaggaGgcc	6	NT_007592.10	6082039	-	16
	gcaCacggttaggacAcc	6	NT_025741.9	16594488	+	16
	XcagacggttaggaGgcX	5	NT_023132.9	1824513	+	15
	gcagaGggttaggacTcc	4	NT_006204.12	7343495	-	16
	XXXgacggttaggacgcX	4	NT_022760.11	1102170	+	14
	gcagacggttGggaGgcc	2	NT_005334.10	3807742	+	16
	gcagaAggtAaggacgcc	2	NT_034487.1	2632363	+	16
	XXagacggttaggacTcc	2	NT_025652.9	1402742	+	15
	gcagaAggttaggacTcc	2	NT_022173.10	907471	-	16
	gcagaAggttaggacgXX	1	NT_004982.12	1850235	+	15
	gcagaTggttaggaGgcc	1	NT_004525.12	1143579	-	16
CD144-23	GTCAGAGGAGTAGGCGTA					
	gtcagaggagtaggcTta	4	NT_022836.11	2301799	-	17
	gtcagaggagtaggcXXX	X	NT_025319.10	1492665	+	15
	gtcagaggagtaggcXXX	20	NT_011362.7	4471243	+	15
	gtcagaggagtaggcXXX	17	NT_010718.10	7820772	+	15
	gtcagaggagtaggcXXX	17	NT_010718.10	4139157	+	15
	gtcagaggagGaggcgtX	12	NT_009759.12	2318917	-	16
	gtcagaggagtaggcXXX	8	NT_008048.11	656001	-	15
	XXcagaggagtaggcgtX	7	NT_007914.10	1926014	-	15
	gtcagaggagtaggcXXX	5	NT_023195.10	4124654	-	15
	XxcagaggagtaggcgtX	4	NT_006316.12	4168530	+	15
	gtcagaggagtaggcXXX	1	NT_030577.5	278460	-	15
	XXcagaggagtagGcgta	16	NT_035396.1	107719	+	15
	XXcagaggagGaggcgtta	16	NT_024826.5	186387	+	15
	XxcagaggagtagCcgta	16	NT_010542.10	511498	-	15

CD144-29	TGATGAGGTGTAGGCAAA					
	tgatgaggtgtaggcaaa	7	NT_007933.10	12719628	-	18
	tgatgaCgtgtaggcTaa	7	NT_007933.10	15148065	-	16
	tgatgaggtgtaggcaaX	11	NT_035088.1	2058992	+	17
	tgatgaggtgtaggTaaa	X	NT_035616.1	799279	+	17
	XXatgaggtgtaggcaaa	13	NT_024524.10	22415346	-	16
	XgatgaggtgtaggGaaa	13	NT_024524.10	8890703	+	16
	XgatgaggtgtaggcaaX	10	NT_008818.12	110747	-	16
	tgatgGggtgtaggcaaa	8	NT_008046.10	691384	-	17
	tgatgagAtgtaggcaaa	2	NT_005332.10	3865780	-	17
	tgatgaggAgttaggcaaa	1	NT_021979.12	19669	+	17
	tgatgaggtgtTggcaaX	X	NT_035625.1	140921	-	16
	tgatgaggtgGaggcaaX	17	NT_024901.10	1394367	+	16
	tgatgaggtgAaggAaaa	17	NT_024901.10	445219	-	16
	XgatgaggtgtTggcaaa	17	NT_024897.10	434168	+	16
	XgatgaggGtaggcaaa	15	NT_010344.10	1945507	-	16
	tgatgaggtgtaggAaaX	10	NT_008705.12	21375980	-	16
	tgatgaggtgGaggcaaX	10	NT_008705.12	4565047	-	16
	tgatgaggtgtaggcXXX	9	NT_023974.12	1000807	-	15
	XXatgaggtgtaggcaaX	7	NT_007914.10	6468245	+	15
	tgatgaggtgtaggcXXX	7	NT_007914.10	11154470	+	15
	XgatgaggtgAaggcaaa	5	NT_029973.5	211611	-	16
	XgatgaggtgtaggcaXX	5	NT_023133.8	1107799	-	15
	XXXtgaggtgtaggcaaa	4	NT_006383.12	4504327	-	15
	XgatgaggtgtaggGaaa	4	NT_022846.9	1019880	+	16
	XgatgaggtCtaggcaaa	3	NT_022401.11	204396	-	16
	tgatgaggtgCaggcaaX	2	NT_005403.10	9820931	+	16
	XgatgaggtgtTggcaaa	2	NT_005403.10	11972844	-	16
	XgatgagAtgtaggcaaa	2	NT_005370.10	270288	+	16
	tgatgaggtgtaCTcaaa	16	NT_034001.2	1061484	+	16
	tgatgagCtgtGggcaaa	16	NT_031902.2	98	-	16
	tgatgaggtgAGggcaaa	16	NT_024797.10	1597215	-	16
	tgatgGAgtaggcaaa	16	NT_010498.10	3434029	-	16
	tgatgaggGgCaggcaaa	16	NT_010422.10	678299	+	16