

Scores	Tag	L1102	L1214	L1232	HOSE1	HOSE2	HS
1	CTGGAGGCTG	9.5	8.71	10.67	0	0	229335
1	CTGGAGGCTG	9.5	8.71	10.67	0	0	169350
1	CTGGAGGCTG	9.5	8.71	10.67	0	0	61384
1	CTGGAGGCTG	9.5	8.71	10.67	0	0	105633
1	CTGGAGGCTG	9.5	8.71	10.67	0	0	149152
1	GCAACTGTGA	7.77	8.71	6.67	0	0	169476
1	ATTTGTCCCA	14.68	7.62	5.33	0	0	57301
1	ATTTGTCCCA	14.68	7.62	5.33	0	0	356122
1	GTCGGGCCTC	71.65	39.18	22.67	1.16	0	73769
1	ATTCTCCAGT	35.39	39.18	44.01	85.74	89.13	458218
1	ATTCTCCAGT	35.39	39.18	44.01	85.74	89.13	406300
1	AGGGCTTCCA	56.98	37	69.35	134.4	141.05	458148
1	CTGCTATACG	11.22	14.15	9.34	41.71	38.94	180946
1	TTGGTGAAGG	10.36	18.5	17.34	61.41	49.32	426138
1	GCCGTGTCCG	21.58	9.79	8	54.45	58.84	356666
1	GCCGTGTCCG	21.58	9.79	8	54.45	58.84	380843
1	ACCCACGTCA	0.86	0	1.33	27.81	20.77	298184
1	ACCCACGTCA	0.86	0	1.33	27.81	20.77	400124
1	TCTCCATACC	0.86	1.09	0	23.17	25.09	
1	CCCTTGTCGG	0.86	0	0	26.65	20.77	127824
1	CTTCTTGCCC	0	0	1.33	47.5	36.34	347939
1	CTTCTTGCCC	0	0	1.33	47.5	36.34	424220
1	CTGTACTTGT	0.86	0	0	63.72	29.42	75678
1	CCCAACGCGC	0	0	0	83.42	47.59	347939
1	GCAAGAAAGT	0	0	0	26.65	39.81	36977
1	GCAAGAAAGT	0	0	0	26.65	39.81	155376
1	ACACAGCAAG	0	0	0	23.17	15.58	
1	AGCTTCCACC	0	0	0	11.59	7.79	355542
1	GAGTGGCTAC	0	0	0	9.27	6.92	
1	ATGGTGGGGG	0	0	0	8.11	22.5	343586
1	AGATCCCAAG	0	0	0	5.79	8.65	50813
1	TGGAAGGAGG	0	0	0	8.11	6.06	
1	TAGCCGGGAC	0	0	0	5.79	7.79	107740
1	TGTGGATGTG	0	0	0	4.63	12.11	180878
1	GGGTAGGGGG	0	0	0	34.76	9.52	13323
0.99	AATAAAGCAA	2.59	7.62	8	0	0	76698
0.99	AATAAAGCAA	2.59	7.62	8	0	0	126043
0.99	GGAACAAACA	8.63	3.26	18.67	0	0	375108
0.99	ACTCAATAAA	13.81	16.32	8	1.16	0.87	73149
0.99	ACTCAATAAA	13.81	16.32	8	1.16	0.87	104019
0.99	ATGACTCAAG	37.12	54.41	24.01	5.79	0.87	211595
0.99	ATGACTCAAG	37.12	54.41	24.01	5.79	0.87	239752

0.99	GAGGGAGTTT	117.41	138.21	110.7	200.44	182.58	76064
0.99	GAGGGAGTTT	117.41	138.21	110.7	200.44	182.58	356342
0.99	GGGCAGGCGT	1.73	2.18	0	18.54	11.25	737
0.99	TAGTTGGAAC	0	0	1.33	6.95	13.85	1119
0.99	GGCCCCTCAC	0	1.09	1.33	31.28	11.25	274313
0.99	GGCCCCTCAC	0	1.09	1.33	31.28	11.25	150390
0.98	GGAGCACACA	8.63	2.18	4	0	0	193490
0.98	GGAGCACACA	8.63	2.18	4	0	0	235709
0.98	CTCGCGCTGG	50.07	8.71	32.01	1.16	0	25640
0.98	TTTGTGTCAC	13.81	9.79	9.34	0	1.73	84162
0.98	TTTGTGTCAC	13.81	9.79	9.34	0	1.73	15093
0.98	TGCTGAATCA	14.68	8.71	18.67	2.32	1.73	288862
0.98	CTTGAGCAAT	13.81	10.88	16	2.32	1.73	848
0.98	TGCACGTTTT	85.47	66.39	80.02	213.19	139.32	169793
0.98	TGCACGTTTT	85.47	66.39	80.02	213.19	139.32	381037
0.98	TTGGCCAGGC	84.6	50.06	46.68	196.96	136.72	332156
0.98	TTGGCCAGGC	84.6	50.06	46.68	196.96	136.72	432714
0.98	TCTCTGATGC	4.32	3.26	2.67	24.33	14.71	167679
0.98	TCTCTGATGC	4.32	3.26	2.67	24.33	14.71	6441
0.98	GGATATGTGG	3.45	1.09	29.34	117.02	77.01	326035
0.98	TCAAGCCATC	0.86	1.09	4	49.82	17.31	326035
0.98	CAAATCCAAA	1.73	0	0	8.11	12.11	
0.98	TAGTTGGAAA	0.86	0	1.33	16.22	65.76	1119
0.98	GAGGCCAAGA	0.86	0	0	17.38	123.74	89552
0.98	GAGGCCAAGA	0.86	0	0	17.38	123.74	151536
0.97	TTAAAGGCCG	2.59	9.79	2.67	0	0	79086
0.97	CGGCACCTTA	0.86	0	0	5.79	8.65	209100
0.97	GGATGTGAAA	0	0	0	3.48	26.83	433387
0.97	GGATGTGAAA	0	0	0	3.48	26.83	458155
0.96	TAATCCTCAA	25.04	39.18	13.34	0	3.46	78409
0.96	TAATCCTCAA	25.04	39.18	13.34	0	3.46	234489
0.96	TTGGTCAGGC	21.58	19.59	18.67	41.71	44.13	54627
0.96	TTGGTCAGGC	21.58	19.59	18.67	41.71	44.13	172012
0.96	GGACCACTGA	63.02	53.33	40.01	184.22	102.11	119598
0.96	GGACCACTGA	63.02	53.33	40.01	184.22	102.11	458180
0.96	GTGTTGCACA	12.95	4.35	4	39.39	25.09	165590
0.96	GTGTTGCACA	12.95	4.35	4	39.39	25.09	381090
0.96	CCTCGGAAAA	3.45	2.18	0	12.74	11.25	343481
0.96	CCTCGGAAAA	3.45	2.18	0	12.74	11.25	425668
0.96	CGTGGGTGGG	0	1.09	2.67	15.06	6.92	8941
0.96	CGTGGGTGGG	0	1.09	2.67	15.06	6.92	202833
0.96	TAGCTGAAAA	0	0	0	2.32	13.85	13493
0.96	TAGCTGAAAA	0	0	0	2.32	13.85	1119

0.95	GCAAAACACG	6.91	17.41	1.33	0	0	350313
0.95	AGGGGATTCC	9.5	3.26	1.33	0	0	75412
0.95	GTGTGGGGGG	12.95	14.15	5.33	2.32	1.73	117484
0.95	GTGTGGGGGG	12.95	14.15	5.33	2.32	1.73	2340
0.95	GCCACCCCCT	0	0	0	3.48	49.32	32246
0.95	GCCACCCCCT	0	0	0	3.48	49.32	172510
0.94	GGGGTGGGGC	5.18	8.71	5.33	0	0.87	154868
0.94	GGGGTGGGGC	5.18	8.71	5.33	0	0.87	353831
0.94	AAAGTCTAGA	8.63	6.53	2.67	1.16	0	82932
0.94	TGGAAGTCTA	8.63	9.79	5.33	1.16	0.87	132262
0.94	TGGAAGTCTA	8.63	9.79	5.33	1.16	0.87	351929
0.94	ATGTAGTAGT	15.54	13.06	16	2.32	5.19	406404
0.94	CACCTAATTG	120.86	80.53	64.02	229.41	163.55	
0.94	CCGTCCAAGG	16.4	15.24	10.67	63.72	32.02	397609
0.94	CATCTTCACC	2.59	5.44	4	15.06	14.71	
0.94	TTCCCTATT	1.73	0	0	10.43	6.06	3132
0.93	TCCTTGCTTC	10.36	22.85	12	1.16	4.33	94491
0.93	TCCTTGCTTC	10.36	22.85	12	1.16	4.33	457543
0.93	TAGGCCAAG	12.09	8.71	9.34	2.32	1.73	78880
0.93	TTGATGTACA	10.36	15.24	9.34	3.48	1.73	433581
0.93	CCCCAGTTGC	29.35	26.12	30.68	16.22	9.52	74451
0.93	ATCAAGGGTG	6.04	19.59	13.34	34.76	36.34	412370
0.93	ATCAAGGGTG	6.04	19.59	13.34	34.76	36.34	426460
0.93	GAAGATGTGT	3.45	2.18	2.67	19.7	9.52	112318
0.93	CAGTCTCTCA	0.86	3.26	1.33	11.59	8.65	172801
0.93	CAGTCTCTCA	0.86	3.26	1.33	11.59	8.65	406620
0.93	GGGGTAAGAA	0.86	2.18	0	5.79	9.52	80423
0.92	GAGAAATATC	1.73	11.97	2.67	0	0	169984
0.92	TAAGGAGCTG	40.57	35.91	49.35	97.32	63.17	299465
0.92	TAAGGAGCTG	40.57	35.91	49.35	97.32	63.17	355957
0.92	GGGGAAATCG	23.31	9.79	14.67	33.6	57.11	76293
0.92	CACTACTCAC	31.94	8.71	10.67	41.71	58.84	
0.92	CCAGTGGCCC	7.77	13.06	1.33	31.28	23.36	180920
0.92	CCAGTGGCCC	7.77	13.06	1.33	31.28	23.36	139876
0.92	CACACAGTTT	1.73	0	0	6.95	6.92	204354
0.92	CAGGCCCTGC	0.86	0	0	19.7	4.33	97087
0.91	TACAAAACCA	5.18	5.44	6.67	0	0.87	79110
0.91	AAGATTGGTG	7.77	6.53	12	2.32	0	1244
0.91	AAGATTGGTG	7.77	6.53	12	2.32	0	29205
0.91	ATCGCTTTCT	14.68	19.59	14.67	3.48	6.92	177486
0.91	GCTGGGAGGG	1.73	1.09	1.33	11.59	6.06	274701
0.91	GCTGGGAGGG	1.73	1.09	1.33	11.59	6.06	325650
0.91	GCTGGTGGCC	0.86	0	0	4.63	33.75	1734
0.9	TGCTCTGAAT	6.04	7.62	24.01	0	1.73	288390
0.9	TGCTCTGAAT	6.04	7.62	24.01	0	1.73	453714
0.9	CCTAGCTGGA	93.23	78.36	53.35	45.19	27.69	401787
0.9	GTGTTAACCA	5.18	7.62	4	12.74	19.04	74267

0.9	GTGTTAACCA	5.18	7.62	4	12.74	19.04	381219
0.9	CTGTTGGTGA	32.8	13.06	14.67	83.42	46.73	425392
0.9	CTGTTGGTGA	32.8	13.06	14.67	83.42	46.73	3463
0.9	GCTCAGCTGG	0	1.09	0	13.9	3.46	432848
0.89	CTAATAAATG	2.59	11.97	9.34	1.16	0	191045
0.89	AGTGTCTGTG	1.73	0	1.33	6.95	6.92	8867
0.89	GAAGTACAGT	0	0	0	1.16	17.31	347534
0.88	GCCCACATCC	15.54	1.09	2.67	0	0	84753
0.88	AATGCAGGCA	3.45	5.44	8	0	0.87	75206
0.88	AATGCAGGCA	3.45	5.44	8	0	0.87	172673
0.88	CCAAGCTAG	19.86	4.35	14.67	2.32	0	76067
0.88	GGCACAGTAA	3.45	7.62	5.33	1.16	0	11270
0.88	GGCACAGTAA	3.45	7.62	5.33	1.16	0	49169
0.88	TGCAATAAGC	6.91	2.18	6.67	1.16	0	411490
0.88	AGGCTACGGA	116.54	53.33	64.02	173.79	133.26	283429
0.88	AGGCTACGGA	116.54	53.33	64.02	173.79	133.26	416613
0.88	GCCCCAATA	13.81	6.53	22.67	64.88	32.02	382367
0.88	GGCTGCCCTG	5.18	2.18	0	12.74	11.25	352746
0.88	GGCTGCCCTG	5.18	2.18	0	12.74	11.25	74566
0.88	TAACAGCCAG	1.73	1.09	5.33	38.23	8.65	81328
0.88	TAACAGCCAG	1.73	1.09	5.33	38.23	8.65	235498
0.87	CACCATCAAA	6.91	4.35	2.67	1.16	0	268488
0.87	GAAGAACAGA	4.32	5.44	12	1.16	0.87	28144
0.87	GAAGAACAGA	4.32	5.44	12	1.16	0.87	400570
0.87	TTTTGTGTGA	7.77	4.35	6.67	1.16	0.87	182698
0.87	GCAGAAGAGG	8.63	4.35	5.33	1.16	0.87	118926
0.87	GCAGAAGAGG	8.63	4.35	5.33	1.16	0.87	396266
0.87	TCAGATCTTT	56.11	105.56	96.03	191.17	135.86	23492
0.87	TCAGATCTTT	56.11	105.56	96.03	191.17	135.86	85112
0.87	TCAGATCTTT	56.11	105.56	96.03	191.17	135.86	389933
0.87	GCCGAGGAAG	33.67	25.03	29.34	74.15	44.13	143067
0.87	GCCGAGGAAG	33.67	25.03	29.34	74.15	44.13	434029
0.87	TAGGTTGTCT	42.3	126.24	136.04	297.76	200.76	456734
0.87	ACCTGTATCC	6.91	6.53	8	22.01	13.85	433414
0.87	TGGAAAGTGA	0.86	1.09	22.67	38.23	108.17	25647
0.87	TGGAAAGTGA	0.86	1.09	22.67	38.23	108.17	276760
0.87	GGGTTTGT	0	0	1.33	2.32	10.38	75969
0.86	TGGTAATGGC	9.5	6.53	0	0	0	73149
0.86	TGGACACAAG	21.58	5.44	8	2.32	0.87	180832
0.86	GTTTTTGCTT	8.63	10.88	10.67	3.48	0	79110
0.86	CCTCCAGCTA	49.21	26.12	12	9.27	3.46	458103
0.86	CCTCCAGCTA	49.21	26.12	12	9.27	3.46	242463
0.86	TCACCCAGGG	4.32	4.35	1.33	19.7	8.65	

0.85	GAAACAAGAT	3.45	11.97	32.01	0	1.73	78771
0.85	CGTGGGGTGG	26.76	3.26	28.01	2.32	0	92679
0.85	AAAGTGCATC	3.45	28.3	24.01	2.32	0	193326
0.85	TGGTTTTTGG	5.18	3.26	5.33	0	0.87	283655
0.85	TGGTTTTTGG	5.18	3.26	5.33	0	0.87	7753
0.85	TATCACTCTG	6.91	4.35	1.33	0	0.87	278362
0.85	TCGGGGCCCC	2.59	7.62	4	1.16	0	248214
0.85	CCTGGATAAA	7.77	2.18	4	1.16	0	453557
0.85	CCTGGATAAA	7.77	2.18	4	1.16	0	325520
0.85	GTTTCTGCAA	6.04	3.26	4	1.16	0	179825
0.85	GTTTCTGCAA	6.04	3.26	4	1.16	0	278671
0.85	AGGATGTGGG	6.91	7.62	8	0	2.6	139648
0.85	GGCAACAAGA	5.18	16.32	22.67	3.48	1.73	301724
0.85	GGCAACAAGA	5.18	16.32	22.67	3.48	1.73	317017
0.85	GAAAAATGGT	18.13	417.91	120.04	42.87	57.11	433403
0.85	GAAAAATGGT	18.13	417.91	120.04	42.87	57.11	446421
0.85	ACAGTGGGGA	13.81	15.24	13.34	5.79	5.19	278270
0.85	ACAGTGGGGA	13.81	15.24	13.34	5.79	5.19	288443
0.85	ACAGTGGGGA	13.81	15.24	13.34	5.79	5.19	355693
0.85	ATGGCTGGTA	22.45	33.74	14.67	55.61	38.94	406341
0.85	ATGGCTGGTA	22.45	33.74	14.67	55.61	38.94	356363
0.85	TCGAAGCCCC	42.3	18.5	10.67	60.25	47.59	198281
0.85	TAGAAAGGCA	2.59	4.35	8	11.59	13.85	457718
0.85	AGCAGATCAG	0	0	10.67	13.9	8.65	400250
0.85	CCCATCCGAA	16.4	5.44	1.33	30.12	20.77	406682
0.85	CCCATCCGAA	16.4	5.44	1.33	30.12	20.77	458239
0.85	AAGAAGATAG	3.45	3.26	2.67	6.95	15.58	406616
0.85	AAGAAGATAG	3.45	3.26	2.67	6.95	15.58	458325
0.85	GGGGCGGGGT	2.59	0	0	5.79	7.79	25347
0.84	GGTTCAAGGC	20.72	16.32	0	0	0	353181
0.84	AGCAGAGACA	7.77	4.35	4	0	1.73	167382
0.84	CGGTTACTGT	6.04	5.44	5.33	1.16	0.87	49767
0.84	TACACGTGAG	7.77	4.35	4	1.16	0.87	11156
0.84	GCCTGCTCCC	6.04	7.62	6.67	2.32	0.87	355660
0.84	GCCTGCTCCC	6.04	7.62	6.67	2.32	0.87	375217
0.84	ACTTACCTGC	28.49	22.85	17.34	10.43	12.98	12504
0.84	ACTTACCTGC	28.49	22.85	17.34	10.43	12.98	431668
0.84	TGGGCAAAGC	48.34	51.15	45.35	100.8	64.03	256184
0.84	TGGGCAAAGC	48.34	51.15	45.35	100.8	64.03	381229
0.84	CCCCAGCCAG	23.31	19.59	20.01	118.18	32.02	232165
0.84	CCCCAGCCAG	23.31	19.59	20.01	118.18	32.02	354176
0.84	TCCAAATCGA	2.59	3.26	2.67	6.95	25.09	297753

0.83	TGCTGCCTCA	13.81	6.53	0	0	0	30792
0.83	GGCACCTCGG	10.36	4.35	0	0	0	37165
0.83	GAAATACAGT	11.22	29.38	68.02	5.79	7.79	343475
0.83	GAAATACAGT	11.22	29.38	68.02	5.79	7.79	67201
0.83	GAAACCGAGG	8.63	3.26	4	1.16	0.87	268053
0.83	GAAACCGAGG	8.63	3.26	4	1.16	0.87	279813
0.83	TGCCTGTAGT	13.81	16.32	21.34	6.95	7.79	274201
0.83	TGCCTGTAGT	13.81	16.32	21.34	6.95	7.79	283617
0.83	GTTGTGGTTA	8.63	9.79	160.05	76.47	71.82	99785
0.83	GTTGTGGTTA	8.63	9.79	160.05	76.47	71.82	48516
0.83	CTCCTCACCT	20.72	6.53	21.34	64.88	32.02	93213
0.83	CTCCTCACCT	20.72	6.53	21.34	64.88	32.02	317989
0.83	GGCCCTAGGC	0.86	2.18	1.33	9.27	4.33	78909
0.83	CACACCCCTG	1.73	0	1.33	3.48	12.98	90061
0.82	ATGTAGAGTG	8.63	0	5.33	0	0	29475
0.82	ATGTAGAGTG	8.63	0	5.33	0	0	181418
0.82	CCTGCTTGTC	3.45	11.97	2.67	1.16	0	2719
0.82	CCTGCTTGTC	3.45	11.97	2.67	1.16	0	82045
0.82	GCCTTGATCT	6.04	2.18	8	0	1.73	91146
0.82	TAATTCTTCT	3.45	8.71	4	0	1.73	345452
0.82	TAATTCTTCT	3.45	8.71	4	0	1.73	1708
0.82	TAATTCTTCT	3.45	8.71	4	0	1.73	239926
0.82	GGGAAGGCAC	6.91	3.26	5.33	0	1.73	79058
0.82	GGGAAGGCAC	6.91	3.26	5.33	0	1.73	13144
0.82	TTGGCCAGGA	20.72	14.15	9.34	31.28	26.83	131180
0.82	TTGGCCAGGA	20.72	14.15	9.34	31.28	26.83	233335
0.82	AAAACATTCT	8.63	8.71	25.34	25.49	34.61	323562
0.82	AAAACATTCT	8.63	8.71	25.34	25.49	34.61	194718
0.82	GTTCCCTGGC	18.99	5.44	9.34	27.81	25.09	12701
0.82	GTTCCCTGGC	18.99	5.44	9.34	27.81	25.09	177415
0.82	GCTGAACGCG	0	0	10.67	12.74	6.06	99029
0.81	TGCCGCTAAT	6.91	1.09	6.67	1.16	0	7331
0.81	TGGATCCTCG	6.04	8.71	4	1.16	1.73	5268
0.81	TCTCCAGGAA	9.5	6.53	5.33	2.32	1.73	237924
0.81	GGAATGTACG	27.63	13.06	20.01	8.11	9.52	429
0.81	TTGCCCAGGC	12.09	16.32	6.67	41.71	19.04	9711
0.81	TTGCCCAGGC	12.09	16.32	6.67	41.71	19.04	284256
0.81	AAGGTCGAGC	6.91	2.18	1.33	17.38	8.65	380948
0.81	AAGGTCGAGC	6.91	2.18	1.33	17.38	8.65	184582
0.81	ACCGGTCCGG	1.73	2.18	2.67	15.06	5.19	
0.81	AAGTGGGTGC	0	3.26	1.33	8.11	6.06	119475
0.81	TGTCCTGGTT	4.32	0	1.33	13.9	6.06	179665
0.81	TGTCCTGGTT	4.32	0	1.33	13.9	6.06	289063
0.8	CATTTCATAA	6.91	13.06	9.34	0	4.33	73851
0.8	TGAGGGAATA	32.8	32.65	58.68	2.32	22.5	83848

0.8	TGAGGGAATA	32.8	32.65	58.68	2.32	22.5	356372
0.8	GTGCTGGACC	9.5	5.44	9.34	3.48	1.73	20977
0.8	GTGCTGGACC	9.5	5.44	9.34	3.48	1.73	433810
0.8	GTTACATTA	2.59	5.44	189.39	31.28	20.77	84298
0.8	TACCCTAGAA	21.58	27.21	20.01	11.59	12.98	73734
0.8	TACCCTAGAA	21.58	27.21	20.01	11.59	12.98	118559
0.8	TACCTGCAGA	0	0	21.34	4.63	6.06	416073
0.8	AATAGGTCCA	34.53	31.56	33.34	42.87	95.19	409158
0.8	TTTAACGGCC	16.4	11.97	14.67	39.39	21.63	
0.8	GAACACATCC	24.17	2.18	2.67	28.97	24.23	426977
0.8	TTGGCCAGGT	2.59	1.09	2.67	8.11	6.92	182248
0.8	TTGGCCAGGT	2.59	1.09	2.67	8.11	6.92	273758
0.8	TCTGCAATGA	1.73	1.09	0	19.7	3.46	8170
0.79	CACGGACTCG	11.22	3.26	0	0	0	170195
0.79	CTGTTGCTGG	6.91	5.44	1.33	1.16	0.87	61976
0.79	CTGTTGCTGG	6.91	5.44	1.33	1.16	0.87	92260
0.79	CAAGGGCCAA	6.04	4.35	8	1.16	1.73	170160
0.79	TCTGGCAGTA	6.91	6.53	4	1.16	1.73	113503
0.79	GGGATGGCAG	12.95	9.79	4	2.32	3.46	159637
0.79	AGTTTCCCAA	10.36	4.35	12	2.32	3.46	279929
0.79	AGCTCTCCCT	42.3	14.15	25.34	75.31	46.73	82202
0.79	AGCTCTCCCT	42.3	14.15	25.34	75.31	46.73	406626
0.79	ACAAAGCATT	3.45	10.88	2.67	15.06	14.71	
0.79	CTCAACCCCC	1.73	2.18	0	8.11	4.33	446467
0.79	GGCGTTTAGA	0	3.26	0	4.63	6.92	
0.78	GTGGGGGGAG	8.63	8.71	2.67	2.32	1.73	446374
0.78	TGCACTTCAA	6.91	4.35	4	13.9	11.25	75445
0.78	CCCGTCCGGA	40.57	37	16	157.57	51.05	431392
0.78	CCAATAAAGT	10.36	33.74	8	35.92	100.38	101850
0.78	CCAATAAAGT	10.36	33.74	8	35.92	100.38	172051
0.77	TGTGTGCCAC	2.59	11.97	9.34	2.32	0.87	72925
0.77	GTGGCCACGG	0	0	8	4.63	6.92	
0.77	CCACGAGGTG	2.59	1.09	0	13.9	3.46	76293
0.76	ATGATGATGA	3.45	3.26	10.67	0	1.73	105445
0.76	ATGATGATGA	3.45	3.26	10.67	0	1.73	79172
0.76	TTTACCTGCC	3.45	6.53	4	0	1.73	340019
0.76	TTTACCTGCC	3.45	6.53	4	0	1.73	172572
0.76	TAATGGTAAC	5.18	2.18	6.67	1.16	0.87	323834
0.76	GAAGTCGGAA	3.45	10.88	9.34	1.16	2.6	
0.76	TGGTACACGT	23.31	11.97	5.33	5.79	1.73	279574
0.76	TGCATCTGGT	82.88	17.41	22.67	13.9	10.38	75410
0.76	CCACTGCCCT	6.91	9.79	5.33	2.32	2.6	167393
0.76	CCACTGCCCT	6.91	9.79	5.33	2.32	2.6	1010
0.76	CTGCACTTAC	11.22	4.35	9.34	3.48	2.6	77152
0.76	TTTGGTTTTTC	13.81	16.32	10.67	4.63	7.79	179573
0.76	TTTGGTTTTTC	13.81	16.32	10.67	4.63	7.79	21431

0.76	TGTACCTGTA	27.63	38.09	24.01	6.95	22.5	334842
0.76	TGTACCTGTA	27.63	38.09	24.01	6.95	22.5	458356
0.76	TGTACCTGTA	27.63	38.09	24.01	6.95	22.5	249922
0.76	AGTGCCGTGT	0	0	13.34	5.79	3.46	76391
0.76	AGTGCCGTGT	0	0	13.34	5.79	3.46	154654
0.76	CATTTGGTAT	0	0	8	5.79	5.19	
0.76	TTAGCCAGGA	4.32	7.62	8	20.86	10.38	196270
0.76	TTAGCCAGGA	4.32	7.62	8	20.86	10.38	350692
0.76	GCCATCCCCT	10.36	5.44	9.34	26.65	12.98	348389
0.76	GGAGTGGACA	4.32	4.35	2.67	8.11	11.25	409634
0.76	TGGCCTAATA	1.73	3.26	2.67	8.11	6.92	1501
0.76	AGGTGGCAAG	4.32	3.26	13.34	28.97	12.98	
0.76	TCACAGCTGT	1.73	1.09	4	6.95	6.92	77054
0.76	TCACAGCTGT	1.73	1.09	4	6.95	6.92	89463
0.75	ATGAAAAGAA	0	6.53	20.01	0	0	46783
0.75	ATGAAAAGAA	0	6.53	20.01	0	0	76550
0.75	TAGTTGTTTA	2.59	14.15	0	0	0	1098
0.75	TAGTTGTTTA	2.59	14.15	0	0	0	330741
0.75	TCCTCAACCC	11.22	2.18	0	0	0	118845
0.75	TTTTTAATGT	2.59	28.3	5.33	0	1.73	181307
0.75	TTTTTAATGT	2.59	28.3	5.33	0	1.73	367720
0.75	CAACTAATTC	5.18	14.15	109.37	5.79	4.33	69997
0.75	CAACTAATTC	5.18	14.15	109.37	5.79	4.33	75106
0.75	CTCCCCAAG	0	0	44.01	3.48	1.73	366
0.75	GATCTCGCAA	10.36	2.18	9.34	0	2.6	250773
0.75	TAGGAGTTAA	6.91	6.53	2.67	2.32	0.87	30743
0.75	TGTGTTGAGA	63.02	96.86	65.35	95.01	152.3	406283
0.75	TGTGTTGAGA	63.02	96.86	65.35	95.01	152.3	422118
0.75	TCAAAAGACC	0.86	1.09	22.67	15.06	19.9	
0.75	CCCTGGGTTT	18.13	4.35	21.34	39.39	25.09	395714
0.75	CCCTGGGTTT	18.13	4.35	21.34	39.39	25.09	406283
0.75	TCACCCACAC	32.8	9.79	8	47.5	30.29	406300
0.75	GGCTGTACCC	6.04	4.35	5.33	27.81	8.65	108080
0.75	ACCCCCCGC	8.63	0	1.33	20.86	8.65	
0.75	TCACCGGTCA	5.18	0	0	11.59	4.33	290070
0.75	CACCGGAAG	0.86	0	0	1.16	11.25	8008
0.75	CACCGGAAG	0.86	0	0	1.16	11.25	176901
0.74	TGTGCTAATA	3.45	10.88	2.67	0	1.73	60257
0.74	TGTGCTAATA	3.45	10.88	2.67	0	1.73	183037
0.74	TTAAGAGGGG	1.73	10.88	6.67	1.16	0.87	380400
0.74	GAGGAACTCA	10.36	5.44	2.67	0	2.6	5008
0.74	CAACATTCCT	8.63	2.18	6.67	1.16	1.73	180015
0.74	GAGGCTCAAT	6.04	7.62	5.33	2.32	1.73	406384
0.74	GCTTCCATCT	11.22	7.62	12	1.16	6.06	55296
0.74	GCTTCCATCT	11.22	7.62	12	1.16	6.06	78768
0.74	GGAGGTAGGG	9.5	11.97	4	3.48	3.46	6453
0.74	GGAGGTAGGG	9.5	11.97	4	3.48	3.46	90572

0.74	AGCCCTACAA	156.25	51.15	21.34	119.34	166.14	
0.74	GACTCACTTT	10.36	3.26	5.33	15.06	13.85	394389
0.74	GGAGGTGGAG	0	1.09	2.67	9.27	2.6	282835
0.74	GGAGGTGGAG	0	1.09	2.67	9.27	2.6	452330
0.73	ATTGTGAGGC	9.5	2.18	5.33	2.32	0	457301
0.73	ATTGTGAGGC	9.5	2.18	5.33	2.32	0	281434
0.73	ATGTGGCACA	6.91	2.18	12	1.16	1.73	1098
0.73	ATGTGGCACA	6.91	2.18	12	1.16	1.73	67776
0.73	GAGTTGGCAG	6.91	3.26	6.67	0	2.6	82292
0.73	GAGTTGGCAG	6.91	3.26	6.67	0	2.6	258730
0.73	AAGATCCCCG	18.13	4.35	9.34	2.32	3.46	107187
0.73	AGCCTTTGTT	18.13	6.53	13.34	0	7.79	9930
0.73	CAATAAAGGT	0	11.97	0	2.32	5.19	337445
0.73	CAATAAAGGT	0	11.97	0	2.32	5.19	171340
0.73	TGTGCTAAAT	21.58	38.09	10.67	53.3	36.34	11387
0.73	TGTGCTAAAT	21.58	38.09	10.67	53.3	36.34	250895
0.73	AGACCCACAA	11.22	2.18	13.34	20.86	18.17	
0.73	GCCTGTATGA	34.53	27.21	14.67	97.32	35.48	180450
0.73	ACAGTGCTTG	6.04	1.09	4	13.9	6.92	80350
0.72	GGAGAGGAAG	4.32	5.44	2.67	0	1.73	16313
0.72	TACCATCAAT	82.88	80.53	353.44	13.9	58.84	79877
0.72	TACCATCAAT	82.88	80.53	353.44	13.9	58.84	169476
0.72	TTGGGAGCAG	6.04	2.18	4	0	1.73	172801
0.72	CCCCCGCGGA	6.04	4.35	1.33	0	1.73	
0.72	GGATAAATGC	4.32	4.35	4	1.16	0.87	211608
0.72	TTATGGGGAG	5.18	3.26	4	1.16	0.87	355930
0.72	TGGAAGAGC	6.04	3.26	2.67	1.16	0.87	9043
0.72	TGGAATGCTG	17.27	8.71	20.01	8.11	6.92	290438
0.72	TGGAATGCTG	17.27	8.71	20.01	8.11	6.92	429621
0.72	GCCTGTACAA	0.86	23.94	0	9.27	9.52	433326
0.72	GTTTCGTGCCA	48.34	21.77	2.67	40.55	32.88	195464
0.72	GTTTCGTGCCA	48.34	21.77	2.67	40.55	32.88	288544
0.72	GAGCGGGATG	8.63	0	0	6.95	2.6	77060
0.72	GAAAAAAAAA	6.04	5.44	8	0	21.63	99843
0.72	GAAAAAAAAA	6.04	5.44	8	0	21.63	288102
0.72	AAGGGAGTTT	0	6.53	0	2.32	6.06	
0.72	GCGACAGCTC	18.99	4.35	4	25.49	16.44	184582
0.72	GCTTGGATCT	6.04	2.18	1.33	6.95	10.38	356623
0.72	GCTTGGATCT	6.04	2.18	1.33	6.95	10.38	457881
0.72	ATCTCGGCTC	4.32	6.53	1.33	17.38	6.92	156942
0.72	ATCTCGGCTC	4.32	6.53	1.33	17.38	6.92	271285
0.72	GATCCCAACT	4.32	1.09	1.33	8.11	6.06	77961
0.72	GATCCCAACT	4.32	1.09	1.33	8.11	6.06	118786
0.72	GGCAAGAAGA	13.81	6.53	2.67	35.92	13.85	83321
0.72	GGCAAGAAGA	13.81	6.53	2.67	35.92	13.85	405528
0.72	ATCCACATCG	3.45	2.18	0	4.63	7.79	119503

0.71	CCAAGAGGAA	3.45	1.09	16	0	0.87	288390
0.71	CCAAGAGGAA	3.45	1.09	16	0	0.87	331328
0.71	CCTGGGAAGT	17.27	5.44	28.01	6.95	0	89603
0.71	CCTGGGAAGT	17.27	5.44	28.01	6.95	0	249212
0.71	GCAGTGCCAC	6.91	1.09	6.67	1.16	0.87	22972
0.71	GCAGTGCCAC	6.91	1.09	6.67	1.16	0.87	198037
0.71	GTGTTGGGGG	5.18	4.35	4	2.32	0	55016
0.71	GTGTTGGGGG	5.18	4.35	4	2.32	0	41268
0.71	GCCTCCTCCC	47.48	15.24	16	12.74	4.33	250691
0.71	CCGTGCTCAT	9.5	7.62	4	4.63	0.87	9857
0.71	TGGCCTGCC	9.5	0	0	4.63	3.46	181002
0.71	CATATCATTA	6.04	2.18	10.67	11.59	14.71	119206
0.71	TTCTTGTGGC	19.86	4.35	2.67	19.7	19.9	182740
0.7	TTTAGTGACG	1.73	2.18	12	0	0.87	433788
0.7	AAAAATAAAG	3.45	18.5	45.35	0	4.33	405985
0.7	AAAAATAAAG	3.45	18.5	45.35	0	4.33	85100
0.7	TAAGTGAAT	2.59	3.26	20.01	0	1.73	24809
0.7	TAAGTGAAT	2.59	3.26	20.01	0	1.73	75103
0.7	GTGAGGGCTA	6.04	34.83	5.33	3.48	0	1244
0.7	GTGAGGGCTA	6.04	34.83	5.33	3.48	0	278311
0.7	GACTCGCTCC	8.63	1.09	2.67	1.16	0	69517
0.7	TACTGCTT	1.73	6.53	5.33	0	1.73	223669
0.7	TACTGCTT	1.73	6.53	5.33	0	1.73	337078
0.7	GCTGCTCCCT	12.95	5.44	5.33	4.63	0.87	343579
0.7	GCTGCTCCCT	12.95	5.44	5.33	4.63	0.87	109315
0.7	CTCCTGAAGG	11.22	13.06	2.67	4.63	1.73	4890
0.7	GGGAAGCAGA	4.32	18.5	96.03	23.17	14.71	175596
0.7	TGGAATGAC	27.63	39.18	26.67	8.11	25.96	172928
0.7	TGGAATGAC	27.63	39.18	26.67	8.11	25.96	193076
0.7	GCCTGCTGGG	31.94	16.32	18.67	16.22	8.65	2706
0.7	GCCTGCTGGG	31.94	16.32	18.67	16.22	8.65	214269
0.7	GGATTTGGCC	126.04	150.19	85.36	266.48	148.84	82506
0.7	GGATTTGGCC	126.04	150.19	85.36	266.48	148.84	302588
0.7	AGGGTGTTTT	13.81	6.53	12	18.54	19.04	75842
0.7	GTGAAGGCAG	27.63	84.89	20.01	121.65	70.96	356568
0.7	GTGAAGGCAG	27.63	84.89	20.01	121.65	70.96	77039
0.7	CCTATTTACT	5.18	2.18	2.67	5.79	10.38	430306
0.7	CGCAGTCTGC	1.73	1.09	1.33	6.95	3.46	6441
0.7	CGCAGTCTGC	1.73	1.09	1.33	6.95	3.46	24087
0.7	TACTGCTCGG	2.59	0	1.33	5.79	4.33	
0.7	TTCAGGAGGG	1.73	2.18	0	6.95	3.46	74647
0.7	TTCAGGAGGG	1.73	2.18	0	6.95	3.46	5890
0.7	ATAGTAGCTT	0	2.18	2.67	2.32	19.9	118400
0.69	GCAGGGCCTC	11.22	1.09	14.67	2.32	0	301350
0.69	TACCAGCACA	12.95	6.53	1.33	2.32	0	119908
0.69	TACCAGCACA	12.95	6.53	1.33	2.32	0	169476

0.69	ATAAAGTAAC	2.59	9.79	2.67	0	1.73	3727
0.69	TTAAAAGCCT	2.59	10.88	5.33	1.16	1.73	458348
0.69	TTAAAAGCCT	2.59	10.88	5.33	1.16	1.73	348669
0.69	TGTTTGTGTG	2.59	7.62	2.67	1.16	0.87	7188
0.69	TGTTTGTGTG	2.59	7.62	2.67	1.16	0.87	343214
0.69	TGGCTGGGAA	4.32	4.35	9.34	3.48	0	172684
0.69	GGAAGGGAGG	5.18	9.79	8	0	5.19	75510
0.69	GGAAGGGAGG	5.18	9.79	8	0	5.19	423103
0.69	TTCCGGTTCC	13.81	4.35	9.34	4.63	2.6	166172
0.69	TTCCGGTTCC	13.81	4.35	9.34	4.63	2.6	172609
0.69	CCACTACACT	13.81	5.44	17.34	5.79	4.33	172207
0.69	CCACTACACT	13.81	5.44	17.34	5.79	4.33	83429
0.69	GTGCTGAATG	38.85	35.91	22.67	25.49	19.9	77385
0.69	GTGCTGAATG	38.85	35.91	22.67	25.49	19.9	120260
0.69	TGGCCCCAGG	4.32	0	20.01	15.06	9.52	268571
0.69	TACAGAGGGA	10.36	4.35	18.67	19.7	21.63	406096
0.69	CAAGCATCCC	24.17	8.71	20.01	74.15	24.23	
0.68	GGAAAGCTGC	2.59	1.09	12	0	0.87	25237
0.68	GGAAAGCTGC	2.59	1.09	12	0	0.87	130643
0.68	TACTGTATGT	6.04	6.53	4	2.32	1.73	5867
0.68	TACTGTATGT	6.04	6.53	4	2.32	1.73	190466
0.68	TAATAAAGGT	25.9	200.25	185.39	48.66	75.28	126817
0.68	TAATAAAGGT	25.9	200.25	185.39	48.66	75.28	355986
0.68	TAATAAAGGT	25.9	200.25	185.39	48.66	75.28	399720
0.68	TTGGTCCTCT	258.99	205.69	62.69	285.02	221.52	381171
0.68	TTGGTCCTCT	258.99	205.69	62.69	285.02	221.52	356795
0.68	TTGGTCCTCT	258.99	205.69	62.69	285.02	221.52	356798
0.68	AGCCACCGTG	7.77	1.09	2.67	9.27	10.38	156051
0.68	AGCCACCGTG	7.77	1.09	2.67	9.27	10.38	240845
0.68	GTGGCACGCA	6.04	2.18	2.67	13.9	6.06	17680
0.68	GTGGCACGCA	6.04	2.18	2.67	13.9	6.06	77897
0.68	TGATTTCACT	2.59	25.03	6.67	19.7	60.57	
0.68	CCTGTGTTGG	2.59	5.44	6.67	50.98	3.46	
0.67	GTGCCCTGTT	12.09	2.18	2.67	1.16	0.87	278411
0.67	GTGCCCTGTT	12.09	2.18	2.67	1.16	0.87	337629
0.67	CTCCCCAAA	0	0	17.34	1.16	2.6	366
0.67	GGAGGTGGGA	8.63	4.35	2.67	3.48	0	89781
0.67	GGAGGTGGGA	8.63	4.35	2.67	3.48	0	178011
0.67	GACTCTGGTG	23.31	18.5	29.34	55.61	26.83	433406
0.67	GGTGAAGACA	3.45	5.44	10.67	8.11	22.5	26951
0.67	GGTGAAGACA	3.45	5.44	10.67	8.11	22.5	288181
0.66	TCTCCTGCAT	16.4	1.09	0	0	0	127973
0.66	TCTCCTGCAT	16.4	1.09	0	0	0	424414
0.66	GTGGAAGACG	18.13	1.09	0	0	0	80395
0.66	AAACCCCAAT	0	0	102.7	1.16	1.73	102950
0.66	GATTAACCA	1.73	7.62	4	0	1.73	90375

0.66	GATTAACCA	1.73	7.62	4	0	1.73	66881
0.66	GTTTTCATTC	1.73	9.79	17.34	1.16	2.6	173736
0.66	GTTTTCATTC	1.73	9.79	17.34	1.16	2.6	423525
0.66	TTATGCCTCC	5.18	2.18	5.33	2.32	0	43314
0.66	CACTTGCCCT	45.75	7.62	40.01	13.9	5.19	15977
0.66	CACTTGCCCT	45.75	7.62	40.01	13.9	5.19	14779
0.66	CCCATCATCC	7.77	3.26	2.67	2.32	0.87	458122
0.66	CCCATCATCC	7.77	3.26	2.67	2.32	0.87	306122
0.66	TTTTGAAGCA	5.18	6.53	8	1.16	3.46	433355
0.66	TTTTGAAGCA	5.18	6.53	8	1.16	3.46	194765
0.66	GGCAGCACAA	6.91	5.44	6.67	3.48	1.73	
0.66	GAAGCAGGAC	94.96	35.91	58.68	44.03	29.42	180370
0.66	CCTCCCCGT	7.77	0	0	2.32	4.33	433759
0.66	GACGACACGA	41.44	40.27	28.01	90.37	36.34	153177
0.66	GACGACACGA	41.44	40.27	28.01	90.37	36.34	457600
0.66	ACCAAAAACC	12.95	4.35	12	12.74	22.5	172928
0.66	GTGGCTCACG	17.27	2.18	1.33	13.9	13.85	127649
0.66	GTGGCTCACG	17.27	2.18	1.33	13.9	13.85	3454
0.66	CAGTTCTCTG	12.95	6.53	5.33	22.01	12.11	279921
0.66	TCTGTACACC	10.36	6.53	4	25.49	9.52	182740
0.66	GGGTCAGGAG	0	3.26	1.33	2.32	6.92	
0.66	GGGCCTGGGG	4.32	0	0	9.27	2.6	153042
0.66	GGGCCTGGGG	4.32	0	0	9.27	2.6	279953
0.65	GGCTGGTCTG	2.59	2.18	10.67	0	1.73	432419
0.65	AATAAAGGCT	2.59	2.18	10.67	1.16	0.87	1815
0.65	AATAAAGGCT	2.59	2.18	10.67	1.16	0.87	179735
0.65	TACTAAATG	9.5	1.09	9.34	1.16	1.73	155560
0.65	TACTAAATG	9.5	1.09	9.34	1.16	1.73	355732
0.65	TTTGTGACTG	6.91	5.44	24.01	1.16	5.19	343926
0.65	GGAGGTGGGG	18.13	3.26	8	3.48	2.6	180577
0.65	GGAGGTGGGG	18.13	3.26	8	3.48	2.6	178011
0.65	TGGCAACCTT	6.91	2.18	4	1.16	1.73	279952
0.65	TGGCAACCTT	6.91	2.18	4	1.16	1.73	75117
0.65	CTCAGCCTGA	5.18	6.53	1.33	1.16	1.73	3496
0.65	CTCAGCCTGA	5.18	6.53	1.33	1.16	1.73	89538
0.65	CCACTGCGCT	7.77	4.35	12	3.48	3.46	258193
0.65	CCACTGCGCT	7.77	4.35	12	3.48	3.46	260287
0.65	GTGCACTGAG	10.36	2.18	60.02	11.59	12.98	181244
0.65	GTGCACTGAG	10.36	2.18	60.02	11.59	12.98	277477
0.65	GAATTAACAT	6.04	7.62	6.67	0	6.92	79474
0.65	GAATTAACAT	6.04	7.62	6.67	0	6.92	90073
0.65	TCGTCTTTAT	3.45	11.97	0	6.95	12.98	301547
0.65	TCGTCTTTAT	3.45	11.97	0	6.95	12.98	374543
0.65	CTGACCTGTG	2.59	0	12	12.74	6.92	77961
0.65	CTGACCTGTG	2.59	0	12	12.74	6.92	145477

0.65	GCGGGAGGGC	4.32	2.18	0	9.27	4.33	399736
0.65	CTGAGGGCCG	0.86	1.09	2.67	8.11	2.6	12142
0.65	CTGAGGGCCG	0.86	1.09	2.67	8.11	2.6	321775
0.65	CAGGTTGTCT	0	4.35	0	2.32	18.17	75258
0.64	TGCAGATTGC	1.73	3.26	12	1.16	0.87	112360
0.64	TGCAGATTGC	1.73	3.26	12	1.16	0.87	352297
0.64	GGAGACAGAG	3.45	4.35	8	3.48	0	5996
0.64	GCACCTCCTA	7.77	3.26	4	1.16	2.6	155218
0.64	GGGGGTCACC	28.49	0	2.67	5.79	4.33	80986
0.64	TGTGATCAGA	20.72	35.91	38.68	19.7	19.9	107476
0.64	CCCATCGTCC	175.25	178.48	189.39	279.23	162.68	
0.64	CGCCGCCGGC	92.37	33.74	14.67	150.62	70.96	182825
0.64	ACGCAGGGAG	14.68	14.15	4	57.93	12.98	381246
0.63	GTGGACCCTG	9.5	3.26	2.67	0	2.6	7236
0.63	TAAACCGGAA	11.22	2.18	4	2.32	0.87	7870
0.63	AGAACCTTCC	6.04	5.44	52.02	8.11	5.19	181244
0.63	CCACTCCTCA	9.5	2.18	9.34	1.16	3.46	82890
0.63	GCTGTTGCGC	72.52	5.44	4	19.7	10.38	381038
0.63	CCACTGCACT	351.36	222.01	294.76	247.94	154.03	5338
0.63	CCACTGCACT	351.36	222.01	294.76	247.94	154.03	107003
0.63	GCAGGCGGCT	2.59	0	6.67	13.9	5.19	458179
0.62	CAAACCTAACC	0	1.09	516.16	0	0	153261
0.62	TGGTTTGCCT	12.95	1.09	6.67	2.32	0.87	6459
0.62	GCATTTAAAT	4.32	29.38	36.01	6.95	10.38	421608
0.62	GCATTTAAAT	4.32	29.38	36.01	6.95	10.38	458278
0.62	ATTGCACCAC	6.91	39.18	17.34	6.95	9.52	210778
0.62	ATTGCACCAC	6.91	39.18	17.34	6.95	9.52	326766
0.62	GCACTCCAGC	22.45	10.88	9.34	10.43	1.73	300485
0.62	GCACTCCAGC	22.45	10.88	9.34	10.43	1.73	153954
0.62	CACTTCAAGG	1.73	3.26	45.35	6.95	7.79	77667
0.62	ACCTCAGGAA	10.36	10.88	22.67	9.27	6.06	177516
0.62	ACCTCAGGAA	10.36	10.88	22.67	9.27	6.06	143504
0.62	GGCCGCGTTC	40.57	7.62	6.67	34.76	22.5	356625
0.62	GGCCGCGTTC	40.57	7.62	6.67	34.76	22.5	439420
0.62	CCTTTGTAAG	0.86	0	10.67	4.63	7.79	78465
0.62	GGTGAGACAC	6.04	16.32	12	23.17	15.58	407372
0.62	GGTGAGACAC	6.04	16.32	12	23.17	15.58	350927
0.62	TGTTCTGGAG	15.54	2.18	6.67	11.59	38.07	74471
0.62	ACAGGGTGAC	2.59	2.18	0	4.63	5.19	174050
0.62	ACTTTCCAAA	2.59	2.18	0	2.32	7.79	
0.61	ATGGCCATAG	4.32	6.53	1.33	1.16	1.73	155206
0.61	TACTTCCCC	4.32	5.44	2.67	2.32	0.87	184641
0.61	GTGAGACCTC	6.04	2.18	5.33	3.48	0	268541

0.61	GTGAGACCTC	6.04	2.18	5.33	3.48	0	341716
0.61	AGAATTGCTT	11.22	10.88	25.34	5.79	9.52	78060
0.61	AGAATTGCTT	11.22	10.88	25.34	5.79	9.52	190311
0.61	GTAAGTGTAC	5.18	3.26	45.35	15.06	12.11	
0.61	AAAAAAAAAA	4.32	22.85	13.34	0	28.56	78713
0.61	AAAAAAAAAA	4.32	22.85	13.34	0	28.56	11184
0.61	CCTTCGAGAT	6.91	6.53	8	12.74	12.11	237924
0.61	CCTTCGAGAT	6.91	6.53	8	12.74	12.11	356019
0.61	ATGGCAAGGG	6.91	5.44	6.67	11.59	11.25	295362
0.61	GCGACGAGGC	73.38	14.15	14.67	100.8	48.46	
0.61	GCCCCTCCGG	4.32	3.26	0	4.63	7.79	83753
0.61	GCCCCTCCGG	4.32	3.26	0	4.63	7.79	180859
0.61	GCAAATGTCA	1.73	4.35	0	4.63	6.06	8768
0.61	GCAAATGTCA	1.73	4.35	0	4.63	6.06	111301
0.61	ATGTCTTTTC	0	1.09	4	2.32	12.11	1516
0.6	CCCCCTGCAG	12.95	39.18	12	12.74	1.73	4084
0.6	CCCCCTGCAG	12.95	39.18	12	12.74	1.73	155981
0.6	TGGCCCCACC	14.68	5.44	2.67	3.48	1.73	146662
0.6	TGGCCCCACC	14.68	5.44	2.67	3.48	1.73	198281
0.6	CTAGCTTTTA	5.18	6.53	4	0	4.33	
0.6	GCATAGGCTG	11.22	3.26	6.67	3.48	2.6	12084
0.6	TACGTTGCAG	18.13	9.79	4	5.79	3.46	21756
0.6	CCGTTCTGGA	2.59	4.35	8	5.79	0	25413
0.6	CCGTTCTGGA	2.59	4.35	8	5.79	0	348412
0.6	ACCCTTGGCC	68.2	29.38	18.67	55.61	45	
0.6	GTCACACCAC	6.04	5.44	2.67	8.11	10.38	250655
0.6	GTCACACCAC	6.04	5.44	2.67	8.11	10.38	264317
0.6	GCGGCCAGTA	7.77	6.53	8	23.17	8.65	
0.6	TCTGCTTACA	3.45	5.44	1.33	9.27	6.06	74267
0.6	TCTGCTTACA	3.45	5.44	1.33	9.27	6.06	374641
0.6	CTGGAAATAA	0	0	0	0	15.58	69745
0.6	CTGGAAATAA	0	0	0	0	15.58	75576
0.6	GATAAATTGC	0	0	0	0	20.77	79946
0.59	ACTGAGGTGC	12.95	2.18	1.33	1.16	0.87	7768
0.59	CCCACTTGTA	7.77	2.18	8	1.16	3.46	343522
0.59	TTGTAAATGC	6.04	4.35	4	1.16	2.6	149436
0.59	TTGTAAATGC	6.04	4.35	4	1.16	2.6	171857
0.59	TACCCCTGAA	4.32	5.44	4	4.63	0	208912
0.59	TACCCCTGAA	4.32	5.44	4	4.63	0	244145
0.59	TACCCCTGAA	4.32	5.44	4	4.63	0	283550
0.59	CCACCCGAA	6.04	5.44	1.33	4.63	0	74637
0.59	CCACTGTACT	15.54	22.85	17.34	16.22	7.79	144852
0.59	CCACTGTACT	15.54	22.85	17.34	16.22	7.79	287515
0.59	CCACTGTACT	15.54	22.85	17.34	16.22	7.79	186679
0.59	CTAGCCTCAC	52.66	13.06	8	25.49	26.83	14376
0.59	GCGCAGAGGT	49.21	38.09	8	32.44	38.94	
0.59	TGGGTGAGCC	1.73	1.09	16	6.95	12.11	297939

0.59	TAAAAAAAAA	1.73	10.88	6.67	0	25.96	8257
0.59	TAAAAAAAAA	1.73	10.88	6.67	0	25.96	431584
0.59	CTGTGAGACC	6.04	1.09	0	6.95	5.19	111903
0.59	CCGTGGTCGT	12.95	3.26	1.33	25.49	8.65	99853
0.59	CCCCCTGGAT	0	3.26	4	12.74	3.46	275243
0.58	GACCACCTTT	7.77	19.59	1.33	1.16	3.46	389137
0.58	GCACGCGTAA	6.04	3.26	2.67	3.48	0	
0.58	CAGCTTCACC	6.91	3.26	6.67	3.48	1.73	311609
0.58	GGGACTGAA	6.91	5.44	6.67	3.48	2.6	3709
0.58	GGGACTGAA	6.91	5.44	6.67	3.48	2.6	438
0.58	CTGCTTAAGA	0	20.68	5.33	5.79	3.46	446421
0.58	GGCTCCCACT	42.3	6.53	2.67	8.11	11.25	74335
0.58	GGCTCCCACT	42.3	6.53	2.67	8.11	11.25	155566
0.58	GGCTGGGGGC	62.16	9.79	16	28.97	19.04	408943
0.58	GGCTGGGGGC	62.16	9.79	16	28.97	19.04	29189
0.58	GGCTGGGGGC	62.16	9.79	16	28.97	19.04	352407
0.58	TTCAATAAAA	20.72	25.03	42.68	4.63	66.63	424299
0.58	TTCAATAAAA	20.72	25.03	42.68	4.63	66.63	2012
0.58	CCCTCTCCCT	14.68	3.26	0	9.27	6.06	85087
0.58	GCATAATAGG	89.78	162.16	105.37	242.15	133.26	431927
0.58	GCATAATAGG	89.78	162.16	105.37	242.15	133.26	458236
0.58	CCTGGCTAAT	6.04	10.88	8	17.38	10.38	117062
0.58	CCTGGCTAAT	6.04	10.88	8	17.38	10.38	446774
0.58	ACCTTTACTG	6.04	0	0	9.27	1.73	77356
0.58	CCACCCTCAC	3.45	2.18	0	0	15.58	211573
0.58	CTGGGTCTCC	0.86	1.09	4	15.06	1.73	431392
0.57	GCAGGGTGGG	7.77	2.18	1.33	1.16	0.87	26232
0.57	GCAGGGTGGG	7.77	2.18	1.33	1.16	0.87	326445
0.57	AAGGAACTTG	2.59	5.44	6.67	0	3.46	179882
0.57	AAGGAACTTG	2.59	5.44	6.67	0	3.46	325825
0.57	TGATAATTCA	4.32	3.26	6.67	0	3.46	171625
0.57	TGGAAGGGCA	7.77	2.18	2.67	2.32	0.87	348388
0.57	ACAGCGGCAA	18.99	6.53	5.33	4.63	4.33	349499
0.57	TGGTGACAGT	14.68	5.44	6.67	6.95	0.87	301005
0.57	TGGAAGTGTG	4.32	13.06	12	6.95	2.6	279751
0.57	TGGAAGTGTG	4.32	13.06	12	6.95	2.6	454506
0.57	GCAAGACCCC	12.09	11.97	8	9.27	3.46	200595
0.57	GCAAGACCCC	12.09	11.97	8	9.27	3.46	453018
0.57	ACTAACACCC	60.43	40.27	16	53.3	44.13	
0.57	AAGGTGGAGG	42.3	66.39	36.01	67.2	59.71	414074
0.57	AAGGTGGAGG	42.3	66.39	36.01	67.2	59.71	337766
0.57	CGCCGGAACA	44.89	9.79	6.67	38.23	23.36	286
0.57	CGCCGGAACA	44.89	9.79	6.67	38.23	23.36	458141
0.57	CCAGCCTGGG	6.04	9.79	6.67	24.33	7.79	130082

0.57	CCAGCCTGGG	6.04	9.79	6.67	24.33	7.79	335432
0.57	GCTGGCAGGC	6.91	1.09	0	6.95	5.19	31146
0.57	GCTGGCAGGC	6.91	1.09	0	6.95	5.19	154886
0.57	GCGCGCCGCT	3.45	1.09	0	6.95	2.6	
0.56	AATCTTGTTT	7.77	9.79	0	1.16	0.87	32343
0.56	AATCTTGTTT	7.77	9.79	0	1.16	0.87	448718
0.56	CATTAAGGG	0.86	9.79	5.33	2.32	0	105509
0.56	TCCTGGGGCA	1.73	7.62	4	2.32	0.87	425276
0.56	CCTGGTCCCA	5.18	2.18	12	4.63	0	23881
0.56	CCTGGTCCCA	5.18	2.18	12	4.63	0	167679
0.56	TTACGATGAA	4.32	3.26	4	1.16	1.73	6335
0.56	TTACGATGAA	4.32	3.26	4	1.16	1.73	159384
0.56	TAACAGAAAG	1.73	4.35	6.67	2.32	0.87	97496
0.56	TTGGCTAGGC	4.32	3.26	4	2.32	0.87	324709
0.56	TTGGCTAGGC	4.32	3.26	4	2.32	0.87	374534
0.56	GCTGCACCGG	6.04	2.18	2.67	2.32	0.87	70582
0.56	CCTGAGCCCG	6.04	2.18	2.67	2.32	0.87	374575
0.56	GCAAGGTTGC	5.18	1.09	5.33	3.48	0	6764
0.56	GAAATGATGA	1.73	32.65	4	8.11	6.92	149158
0.56	GAAATGATGA	1.73	32.65	4	8.11	6.92	288856
0.56	AAGTTGCTAT	10.36	10.88	14.67	8.11	6.06	406455
0.56	CTCAACATCT	17.27	13.06	1.33	16.22	15.58	348311
0.56	CTCAACATCT	17.27	13.06	1.33	16.22	15.58	136470
0.56	GGGCTGGGGT	260.71	167.6	40.01	353.38	194.7	90436
0.56	GGGCTGGGGT	260.71	167.6	40.01	353.38	194.7	430207
0.56	GACAATGCCA	0.86	1.09	4	2.32	6.06	155433
0.56	GACAATGCCA	0.86	1.09	4	2.32	6.06	273415
0.56	TCACCTTAGG	1.73	1.09	4	4.63	5.19	171405
0.56	TCACCTTAGG	1.73	1.09	4	4.63	5.19	239625
0.56	TAAACTGAAA	0.86	2.18	2.67	2.32	6.06	
0.56	GCCTCCTCTT	0	5.44	1.33	6.95	3.46	97437
0.56	TGAAGTAACA	5.18	2.18	0	4.63	6.92	150580
0.56	GCCCCCACT	2.59	1.09	1.33	5.79	3.46	75074
0.56	CAATGCTGCC	14.68	7.62	2.67	39.39	9.52	458228
0.56	CTGGATGGGC	1.73	1.09	1.33	9.27	1.73	375214
0.55	CCCTCCTGGG	12.95	0	4	0	0.87	57301
0.55	CCCTCCTGGG	12.95	0	4	0	0.87	95867
0.55	GTGAAGCCCT	4.32	1.09	6.67	0	2.6	78871
0.55	GTGAAGCCCT	4.32	1.09	6.67	0	2.6	105407
0.55	GTGTGGTGGT	4.32	4.35	2.67	0	2.6	288932
0.55	CCTGTAGTCT	3.45	8.71	2.67	1.16	2.6	36679
0.55	CCTGTAGTCT	3.45	8.71	2.67	1.16	2.6	206882
0.55	CAGATTGCTG	2.59	8.71	6.67	3.48	1.73	21537
0.55	CTGCTGTGAT	8.63	2.18	4	3.48	0.87	1063
0.55	CTGCTGTGAT	8.63	2.18	4	3.48	0.87	169160
0.55	GCCTGCAGTC	16.4	11.97	4	8.11	3.46	31439
0.55	GATAGTTGTG	6.91	10.88	9.34	5.79	4.33	77558

0.55	GGGAGGGGTG	4.32	2.18	1.33	8.11	0	2399
0.55	AAGGCAATTT	6.04	5.44	2.67	6.95	10.38	278479
0.55	AAGGCAATTT	6.04	5.44	2.67	6.95	10.38	301626
0.55	AGCCACCGCG	6.04	6.53	2.67	5.79	12.98	145409
0.55	AGCCACCGCG	6.04	6.53	2.67	5.79	12.98	355874
0.55	TTGTGATGTA	3.45	3.26	2.67	4.63	7.79	356442
0.55	TTGTGATGTA	3.45	3.26	2.67	4.63	7.79	85844
0.55	CGCTGGTTCC	116.54	31.56	37.34	181.9	76.15	289019
0.55	CGCTGGTTCC	116.54	31.56	37.34	181.9	76.15	388664
0.55	CACCACCACA	6.04	1.09	0	10.43	3.46	105751
0.55	CACCACCACA	6.04	1.09	0	10.43	3.46	142856
0.55	CACCACCACA	6.04	1.09	0	10.43	3.46	257696
0.55	CGTGTTGAGA	0	4.35	0	1.16	12.11	
0.54	TGTTTTTATG	0	5.44	12	0	0.87	3192
0.54	GGCCCTCTGA	7.77	6.53	0	0	1.73	161362
0.54	ATTGCTGTAA	2.59	9.79	1.33	2.32	0	22370
0.54	GCCACTACCC	8.63	3.26	1.33	1.16	1.73	71475
0.54	GCCACTACCC	8.63	3.26	1.33	1.16	1.73	77448
0.54	GGTCACTGAG	4.32	3.26	9.34	2.32	2.6	
0.54	ACTGGTACGT	15.54	8.71	2.67	4.63	3.46	235557
0.54	GATTGGGGAT	4.32	5.44	6.67	3.48	1.73	103834
0.54	TACATCCGAA	6.91	4.35	4	2.32	2.6	21321
0.54	CTGTCAATTTG	6.91	6.53	4	3.48	2.6	388623
0.54	TGCTGGGTGG	7.77	6.53	2.67	4.63	1.73	198273
0.54	TGCTGGGTGG	7.77	6.53	2.67	4.63	1.73	754
0.54	TACTCTTGCC	17.27	14.15	10.67	6.95	11.25	2730
0.54	GTAGGGGTAA	14.68	15.24	9.34	4.63	32.88	
0.54	CTCATAGCAG	4.32	23.94	16	34.76	18.17	108636
0.54	CTCATAGCAG	4.32	23.94	16	34.76	18.17	401448
0.54	TCCGTGGTTG	5.18	0	4	5.79	6.92	79516
0.54	GCTTTGATGA	6.91	9.79	4	5.79	25.09	89649
0.54	GTGCGCTGAG	5.18	1.09	0	4.63	5.19	277477
0.53	AAAATAAAGA	0.86	17.41	12	1.16	4.33	73722
0.53	GAAATGTAAG	1.73	29.38	4	2.32	5.19	63525
0.53	GGTTTGATTA	6.91	1.09	8	2.32	1.73	
0.53	AGAACAAAAC	4.32	2.18	6.67	0	3.46	8402
0.53	AGAACAAAAC	4.32	2.18	6.67	0	3.46	180909
0.53	GTTGTCTTTG	0	2.18	102.7	24.33	3.46	258798
0.53	GTTGTCTTTG	0	2.18	102.7	24.33	3.46	284394
0.53	TTGGAACAAT	5.18	3.26	4	0	3.46	80305
0.53	TTCACAGTGG	6.04	2.18	5.33	2.32	1.73	406352
0.53	AATGTGAGTC	3.45	4.35	6.67	3.48	0.87	25001
0.53	TTTGCTCTCC	4.32	3.26	6.67	3.48	0.87	75350
0.53	TTTGCTCTCC	4.32	3.26	6.67	3.48	0.87	278027
0.53	GTGGCACACA	18.13	10.88	10.67	9.27	8.65	446459
0.53	GTGGCACACA	18.13	10.88	10.67	9.27	8.65	62654
0.53	GTGGCACACA	18.13	10.88	10.67	9.27	8.65	400556

0.53	CTCTGGGATA	5.18	1.09	2.67	6.95	0	334437
0.53	AACTAATACT	2.59	9.79	0	4.63	7.79	295362
0.53	TGGGAAGTGG	10.36	5.44	0	8.11	7.79	112844
0.53	GTGGCACGTG	20.72	8.71	13.34	24.33	19.04	29759
0.53	GTGGCACGTG	20.72	8.71	13.34	24.33	19.04	350936
0.53	GCTTTATTTG	1.73	5.44	6.67	4.63	11.25	426930
0.53	GACAAAAAAA	1.73	3.26	9.34	1.16	38.94	433406
0.52	ATCCTGAGTT	0.86	0	32.01	2.32	0.87	73931
0.52	TGGAACAGGA	8.63	1.09	4	0	2.6	90077
0.52	GCGGCAGCGG	7.77	1.09	4	2.32	0.87	348198
0.52	GCGGCAGCGG	7.77	1.09	4	2.32	0.87	75841
0.52	TGGTAGTTAC	12.95	3.26	4	4.63	0.87	66881
0.52	TGGTAGTTAC	12.95	3.26	4	4.63	0.87	355812
0.52	AGAAAGATGT	5.18	2.18	38.68	3.48	9.52	78225
0.52	AGAAAGATGT	5.18	2.18	38.68	3.48	9.52	86978
0.52	AGAAAGATGT	5.18	2.18	38.68	3.48	9.52	352541
0.52	ACAAGGTGCG	19.86	2.18	16	8.11	3.46	
0.52	ATTGTGCCAC	6.04	10.88	25.34	5.79	7.79	348525
0.52	ATTGTGCCAC	6.04	10.88	25.34	5.79	7.79	407560
0.52	CAATGTGTTA	6.91	7.62	32.01	8.11	6.92	74823
0.52	CTGTTAGTGT	14.68	5.44	13.34	9.27	4.33	75375
0.52	CTGGAAGGCC	3.45	2.18	4	5.79	0	
0.52	GCGCGGGCGA	10.36	1.09	0	3.48	5.19	
0.52	CTAAGACTTC	14.68	39.18	50.68	39.39	64.03	
0.52	GGGAAACCCC	4.32	8.71	0	6.95	7.79	237617
0.52	GGGAAACCCC	4.32	8.71	0	6.95	7.79	65135
0.52	AGCCACCACA	8.63	4.35	0	6.95	7.79	306212
0.52	AGCCACCACA	8.63	4.35	0	6.95	7.79	5999
0.52	CCTCCACCTA	6.91	7.62	0	8.11	8.65	432121
0.52	AGTGCAAGAC	1.73	4.35	2.67	9.27	3.46	
0.52	TCCATCGTCC	0	9.79	0	1.16	15.58	
0.51	GAAATAAAGC	0	0	901.61	0	4.33	413826
0.51	GAAATAAAGC	0	0	901.61	0	4.33	422345
0.51	CCACAGGGGA	9.5	0	2.67	0	0.87	119571
0.51	CTGCCAACTT	6.91	3.26	12	5.79	1.73	180370
0.51	TCAGCCTTCT	6.04	8.71	12	6.95	3.46	112165
0.51	TCAGCCTTCT	6.04	8.71	12	6.95	3.46	179986
0.51	GGGGGACGGC	16.4	26.12	12	17.38	5.19	349333
0.51	GGGGGACGGC	16.4	26.12	12	17.38	5.19	356298
0.51	CCGCCTCCGG	12.09	5.44	0	9.27	5.19	48375
0.51	TGGTGTTGAG	61.29	55.5	26.67	85.74	54.52	458163
0.51	TGGTGTTGAG	61.29	55.5	26.67	85.74	54.52	275865
0.51	GGCAAGCCCC	157.12	82.71	66.69	223.61	112.49	187577
0.51	GGCAAGCCCC	157.12	82.71	66.69	223.61	112.49	425293
0.51	GTGAAACTCT	7.77	5.44	4	11.59	8.65	334534
0.51	GTGAAACTCT	7.77	5.44	4	11.59	8.65	438816

0.5	TTGTGGGATC	0.86	8.71	5.33	1.16	1.73	278540
0.5	GTGTGTTTGT	1.73	3.26	16	3.48	0.87	118787
0.5	GCCCGCCTTG	12.09	5.44	8	8.11	2.6	220255
0.5	GCAAGCCAAC	43.16	15.24	8	40.55	24.23	
0.5	TGGCAGCTTT	6.04	0	6.67	5.79	7.79	22708
0.5	TGGCAGCTTT	6.04	0	6.67	5.79	7.79	6153

Description
- Homo sapiens transcribed sequence with weak similarity to protein ref:NP_062553.1 (H.sapiens) hypothetical protein FLJ11267 [Homo sapiens]
RASGRF1 Ras protein-specific guanine nucleotide-releasing factor 1
SEMA5B sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B
WINS1 WINS1 protein with Drosophila Lines (Lin) homologous domain
RHPN1 rhopilin, Rho GTPase binding protein 1
GAPD glyceraldehyde-3-phosphate dehydrogenase
HMGA1 high mobility group AT-hook 1
- Homo sapiens transcribed sequence with strong similarity to protein pir:A32794 (H.sapiens) A32794 nonhistone chromosomal protein HMG-I - human
FOLR1 folate receptor 1 (adult)
- Homo sapiens transcribed sequence with strong similarity to protein sp:P23131 (H.sapiens) RL23_HUMAN 60S ribosomal protein L23 (L17)
RPL23 ribosomal protein L23
RPL10 ribosomal protein L10
RPL5 ribosomal protein L5
TMSB4X thymosin, beta 4, X chromosome
- Homo sapiens transcribed sequence with strong similarity to protein sp:P10660 (H.sapiens) RS6_HUMAN 40S ribosomal protein S6 (Phosphoprotein NP33)
RPS6 ribosomal protein S6
KCNAB2 potassium voltage-gated channel, shaker-related subfamily, beta member 2
JUNB jun B proto-oncogene
na LOC349752
HBA2 hemoglobin, alpha 2
HBA1 hemoglobin, alpha 1
FOSB FBJ murine osteosarcoma viral oncogene homolog B
HBA2 hemoglobin, alpha 2
HBD hemoglobin, delta
HBB hemoglobin, beta
SPRR2A small proline-rich protein 2A
ZFP36 zinc finger protein 36, C3H type, homolog (mouse)
ITLN1 intelectin 1 (galactofuranose binding)
KLF2 Kruppel-like factor 2 (lung)
LPL lipoprotein lipase
FLJ22059 hypothetical protein FLJ22059
SERP1 stress-associated endoplasmic reticulum protein 1
C21orf51 chromosome 21 open reading frame 51
CD24 CD24 antigen (small cell lung carcinoma cluster 4 antigen)
PAX8 paired box gene 8
TACC3 transforming, acidic coiled-coil containing protein 3
PTPN13 protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
NR2F6 nuclear receptor subfamily 2, group F, member 6

RPL27A ribosomal protein L27a
- Homo sapiens transcribed sequence with strong similarity to protein pir:S55914 (H.sapiens) S55914 ribosomal protein L27a - human
ETR101 immediate early protein
NR4A1 nuclear receptor subfamily 4, group A, member 1
IGFBP6 insulin-like growth factor binding protein 6
ZNF262 zinc finger protein 262
FLJ31952 hypothetical protein FLJ31952
FLJ34922 hypothetical protein FLJ34922
CLDN3 claudin 3
HUMAGCGB chromosome 3p21.1 gene sequence
HSPC195 hypothetical protein HSPC195
D10S170 DNA segment on chromosome 10 (unique) 170
FKBP4 FK506 binding protein 4, 59kDa
RPL32 ribosomal protein L32
- Homo sapiens transcribed sequence with strong similarity to protein sp:P02433 (H.sapiens) RL32_HUMAN 60S ribosomal protein L32
MAPA monocyte and plasmacytoid activated molecule
VPS33A vacuolar protein sorting 33A (yeast)
SH3BP2 SH3-domain binding protein 2
TIMP2 tissue inhibitor of metalloproteinase 2
EGR1 early growth response 1
EGR1 early growth response 1
NR4A1 nuclear receptor subfamily 4, group A, member 1
GSTA1 glutathione S-transferase A1
RAB13 RAB13, member RAS oncogene family
MRPL3 mitochondrial ribosomal protein L3
DKFZP434C171 DKFZP434C171 protein
CD99 CD99 antigen
- Homo sapiens transcribed sequence with strong similarity to protein sp:P14209 (H.sapiens) MIC2_HUMAN T-cell surface glycoprotein E2 precursor (E2 antigen) (CD99) (MIC2 protein) (12E7)
COL18A1 collagen, type XVIII, alpha 1
LDHB lactate dehydrogenase B
MtFMT methionyl-tRNA formyltransferase, mitochondrial
SNARK likely ortholog of rat SNF1/AMP-activated protein kinase
RPL3 ribosomal protein L3
- Homo sapiens transcribed sequence with moderate similarity to protein pir:S34195 (H.sapiens) S34195 ribosomal protein L3, cytosolic - human
RPS13 ribosomal protein S13
- Homo sapiens transcribed sequence with strong similarity to protein sp:Q02546 (H.sapiens) RS13_HUMAN 40S ribosomal protein S13
- Homo sapiens transcribed sequence with moderate similarity to protein sp:P23411 (H.sapiens) RL38_HUMAN 60S ribosomal protein L38
RPL38 ribosomal protein L38
LOC285682 hypothetical protein LOC285682
HMOX1 heme oxygenase (decycling) 1
E46L like mouse brain protein E46
NR4A1 nuclear receptor subfamily 4, group A, member 1

- Sapiens cDNA FLJ10674 fis, clone NT2RP2006436.
ARMET arginine-rich, mutated in early stage tumors
- Homo sapiens transcribed sequences
JUP junction plakoglobin
MGC2615 hypothetical protein MGC2615
LOC128344 hypothetical protein LOC128344
CAD carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
- Homo sapiens transcribed sequences
CCND1 cyclin D1 (PRAD1: parathyroid adenomatosis 1)
na hypothetical gene supported by AL833510; AK097847
C10orf4 chromosome 10 open reading frame 4
HNRPD heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
RPS16 ribosomal protein S16
STAR steroidogenic acute regulatory protein
FLJ20297 hypothetical protein FLJ20297
na similar to hypothetical protein FLJ20756
ILVBL ilvB (bacterial acetolactate synthase)-like
SFRS11 splicing factor, arginine/serine-rich 11
CAPNS1 calpain, small subunit 1
RPL9 ribosomal protein L9
RPL9 ribosomal protein L9
TOM7 homolog of Tom7 (S. cerevisiae)
IARS isoleucine-tRNA synthetase
RPS10 ribosomal protein S10
PBP prostatic binding protein
NP220 NP220 nuclear protein
RPS26 ribosomal protein S26
RPS26 ribosomal protein S26
TMSB10 thymosin, beta 10
RPS9 ribosomal protein S9
- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_001004.2 (H.sapiens) ribosomal protein S9; 40S ribosomal protein S9 [Homo sapiens]
- HepG2 3' region cDNA, clone hmd1f06.
CD3Z CD3Z antigen, zeta polypeptide (TiT3 complex)
NCL nucleolin
CD9 CD9 antigen (p24)
HPS5 Hermansky-Pudlak syndrome 5
APP amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
na hypothetical gene supported by AK026041
EHD2 EH-domain containing 2
INHA inhibin, alpha
FLJ22795 hypothetical protein FLJ22795
FLJ12988 hypothetical protein FLJ12988
PPIA peptidylprolyl isomerase A (cyclophilin A)
RPL15 ribosomal protein L15

- Homo sapiens transcribed sequence with strong similarity to protein sp:P39030 (H.sapiens) RL15_HUMAN 60S ribosomal protein L15

- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_001016.1 (H.sapiens) ribosomal protein S23; 40S ribosomal protein S23; homolog of yeast ribosomal protein S28 [Homo sapiens] RPS23 ribosomal protein S23

EEF1D eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)

- Sapiens cDNA FLJ37884 fis, clone BRSTN2012451.

CYR61 cysteine-rich, angiogenic inducer, 61

KIAA1201 KIAA1201 protein

FLJ12442 hypothetical protein FLJ12442

PPP3CC protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)

AHCY S-adenosylhomocysteine hydrolase

HSPB1 heat shock 27kDa protein 1

MGC2491 hypothetical protein MGC2491

MAGI-3 membrane-associated guanylate kinase-related (MAGI-3)

LOC116228 hypothetical protein LOC116228

SMCX Smcx homolog, X chromosome (mouse)

FLJ34236 hypothetical protein FLJ34236

LGALS1 lectin, galactoside-binding, soluble, 1 (galectin 1)

KIAA1977 KIAA1977 protein

DPYSL3 dihydropyrimidinase-like 3

NFKBIA nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha

FLJ14075 hypothetical protein FLJ14075

KIAA1185 KIAA1185 protein

FSD1 fibronectin type 3 and SPRY domain-containing protein

- Sapiens, Similar to hypothetical protein FLJ22376, clone IMAGE:4128300, mRNA

MRPL20 mitochondrial ribosomal protein L20

SEN3 sentrin/SUMO-specific protease 3

LENG9 leukocyte receptor cluster (LRC) member 9

FLJ31295 hypothetical protein FLJ31295

IGF1 insulin-like growth factor 1 (somatomedin C)

RPS4X ribosomal protein S4, X-linked

KIAA1602 KIAA1602 protein

RPS12 ribosomal protein S12

- Sapiens, Similar to tumor protein, translationally-controlled 1, clone MGC:48852 IMAGE:5219529, mRNA, complete cds

IFITM3 interferon induced transmembrane protein 3 (1-8U)

FOS v-fos FBJ murine osteosarcoma viral oncogene homolog

- Sapiens cDNA FLJ40222 fis, clone TESTI2021785.

PROL2 proline rich 2

PAX8 paired box gene 8

RARS arginyl-tRNA synthetase

NCL nucleolin

- Homo sapiens transcribed sequence with moderate similarity to protein pir:I37982 (H.sapiens) I37982 Keratin 8 - human

KRT8 keratin 8

PGK1 phosphoglycerate kinase 1
KIFC2 likely ortholog of mouse kinesin family member C2
FGFRL1 fibroblast growth factor receptor-like 1
LYPLA2 lysophospholipase II
CALU calumenin
MEA male-enhanced antigen
CPLX1 complexin 1
LOC339091 hypothetical protein LOC339091
LAT1-3TM LAT1-3TM protein
RANBP2L1 RAN binding protein 2-like 1
GCC185 GRIP coiled-coil protein GCC185
KIF1C kinesin family member 1C
FLJ11301 hypothetical protein FLJ11301
- Homo sapiens transcribed sequence with moderate similarity to protein ref:NP_060265.1 (H.sapiens) hypothetical protein FLJ20378 [Homo sapiens]
- Homo sapiens transcribed sequence with strong similarity to protein sp:P08865 (H.sapiens) RSP4_HUMAN 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4)
LAMR1 laminin receptor 1 (ribosomal protein SA, 67kDa)
TEBP unactive progesterone receptor, 23 kD
- Homo sapiens transcribed sequences
- Homo sapiens transcribed sequence with strong similarity to protein pir:A56211 (H.sapiens) A56211 progesterone receptor-related protein p23 - human
RPS2 ribosomal protein S2
- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_002943.2 (H.sapiens) ribosomal protein S2; 40S ribosomal protein S2 [Homo sapiens]
PKM2 pyruvate kinase, muscle
na LOC151103
S100A10 S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
RPL26 ribosomal protein L26
- Homo sapiens transcribed sequence with strong similarity to protein sp:Q02877 (H.sapiens) RL26_HUMAN 60S ribosomal protein L26
RPL23A ribosomal protein L23a
RPL23A ribosomal protein L23a
RoXaN ubiquitous tetratricopeptide containing protein RoXaN
FLJ22635 hypothetical protein FLJ22635
NPR1 natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)
NDUFS6 NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
LOC51255 hypothetical protein LOC51255
PTR4 peptide-histidine transporter 4
ZIBRA zinc in-between-ring-finger ubiquitin-associated domain
RNF111 ring finger protein 111
COX6B cytochrome c oxidase subunit VIb
EEF1G eukaryotic translation elongation factor 1 gamma
- Homo sapiens transcribed sequence with strong similarity to protein pir:S22655 (H.sapiens) S22655 translation elongation factor eEF-1 gamma chain - human
PRV1 polycythemia rubra vera 1
RPS3 ribosomal protein S3
VIM vimentin

HOOK2 hook2 protein
COL9A2 collagen, type IX, alpha 2
CTSD cathepsin D (lysosomal aspartyl protease)
NT5C 5', 3'-nucleotidase, cytosolic
R3HDM R3H domain (binds single-stranded nucleic acids) containing
C13orf12 chromosome 13 open reading frame 12
C1orf33 chromosome 1 open reading frame 33
PRO1496 hypothetical protein PRO1496
- Sapiens cDNA: FLJ21245 fis, clone COL01184.
B2M beta-2-microglobulin
BAK1 BCL2-antagonist/killer 1
RPL13A ribosomal protein L13a
ZFP36L2 zinc finger protein 36, C3H type-like 2
PGRMC1 progesterone receptor membrane component 1
TYMS thymidylate synthetase
KIAA0152 KIAA0152 gene product
WFDC2 WAP four-disulfide core domain 2
MDK midkine (neurite growth-promoting factor 2)
PRKD2 protein kinase D2
- Homo sapiens transcribed sequence with weak similarity to protein ref:NP_060312.1 (H.sapiens) hypothetical protein FLJ20489 [Homo sapiens]
CCT3 chaperonin containing TCP1, subunit 3 (gamma)
SC4MOL sterol-C4-methyl oxidase-like
SUPT4H1 suppressor of Ty 4 homolog 1 (S. cerevisiae)
ORMDL2 ORM1-like 2 (S. cerevisiae)
C11orf17 chromosome 11 open reading frame 17
KIAA1465 KIAA1465 protein
DKFZp564K142 implantation-associated protein
ZNF265 zinc finger protein 265
TM4SF11 transmembrane 4 superfamily member 11 (plasmolipin)
FAU Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30
CEBPB CCAAT/enhancer binding protein (C/EBP), beta
ASRGL1 asparaginase like 1
ZDHHC4 zinc finger, DHHC domain containing 4
CGI-69 CGI-69 protein
ATP5G3 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
HSNOV1 novel protein
HIF3A hypoxia inducible factor 3, alpha subunit
- Homo sapiens transcribed sequence with strong similarity to protein pir:A35098 (H.sapiens) A35098 MHC class III histocompatibility antigen HLA-B-associated transcript 3 - human
RPL24 ribosomal protein L24
CIRBP cold inducible RNA binding protein
CDKN1A cyclin-dependent kinase inhibitor 1A (p21, Cip1)
FLJ22246 hypothetical protein FLJ22246
ATP5J ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
TPI1 triosephosphate isomerase 1

- Homo sapiens transcribed sequence with strong similarity to protein sp:P00938 (H.sapiens) TPIS_HUMAN Triosephosphate isomerase (TIM)
GDAP1L1 ganglioside-induced differentiation-associated protein 1-like 1
PSME2 proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
CD74 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
GP5 glycoprotein V (platelet)
GSG1 germ cell associated 1
S100A8 S100 calcium binding protein A8 (calgranulin A)
RPS25 ribosomal protein S25
RPL19 ribosomal protein L19
SQSTM1 sequestosome 1
C6orf59 chromosome 6 open reading frame 59
TINP1 TGF beta-inducible nuclear protein 1
BMP7 bone morphogenetic protein 7 (osteogenic protein 1)
DKFZp761B128 hypothetical protein DKFZp761B128
HMG2L1 high-mobility group protein 2-like 1
RAB2L RAB2, member RAS oncogene family-like
KPNB3 karyopherin (importin) beta 3
VARS2 valyl-tRNA synthetase 2
HSGP25L2G gp25L2 protein
RPL17 ribosomal protein L17
- Homo sapiens transcribed sequence with strong similarity to protein sp:P18621 (H.sapiens) RL17_HUMAN 60S ribosomal protein L17 (L23)
LRP1 low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)
HKE2 HLA class II region expressed gene KE2
SPARCL1 SPARC-like 1 (mast9, hevin)
RPL13 ribosomal protein L13
RBP1 retinol binding protein 1, cellular
- Homo sapiens transcribed sequences
C11orf13 chromosome 11 open reading frame 13
TMSB10 thymosin, beta 10
GFRA1 GDNF family receptor alpha 1
SLC25A5 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
C21orf81 chromosome 21 open reading frame 81
ANKRD10 ankyrin repeat domain 10
COX5A cytochrome c oxidase subunit Va
GRIM19 cell death-regulatory protein GRIM19
HSPA5 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
- Homo sapiens transcribed sequences
- Sapiens, clone IMAGE:4702418, mRNA
MCM7 MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
COL1A2 collagen, type I, alpha 2
SUFU suppressor of fused homolog (Drosophila)

K-ALPHA-1 tubulin, alpha, ubiquitous
- Homo sapiens transcribed sequence with moderate similarity to protein ref:NP_116093.1 (H.sapiens) tubulin alpha 6 [Homo sapiens]
- Homo sapiens transcribed sequence
MX1 myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
CYP1B1 cytochrome P450, family 1, subfamily B, polypeptide 1
MFTC mitochondrial folate transporter/carrier
- Sapiens cDNA FLJ32756 fis, clone TESTI2001758.
SFXN1 sideroflexin 1
RPL18 ribosomal protein L18
SDC2 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
BTG1 B-cell translocation gene 1, anti-proliferative
KCNMA1 potassium large conductance calcium-activated channel, subfamily M, alpha member 1
- Sapiens cDNA: FLJ22382 fis, clone HRC07514.
MAL2 mal, T-cell differentiation protein 2
ERdj5 ER-resident protein ERdj5
MGC12466 hypothetical protein MGC12466
TNNC1 troponin C, slow
H3F3A H3 histone, family 3A
H3F3A H3 histone, family 3A
ZNF238 zinc finger protein 238
CLU clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
MGC27165 hypothetical protein MGC27165
SSR1 signal sequence receptor, alpha (translocon-associated protein alpha)
PRAME preferentially expressed antigen in melanoma
- Sapiens mRNA expressed only in placental villi, clone SMAP83.
EEF1A1 eukaryotic translation elongation factor 1 alpha 1
FTL ferritin, light polypeptide
- Sapiens mRNA expressed only in placental villi, clone SMAP83.
RPL23 ribosomal protein L23
CSRP1 cysteine and glycine-rich protein 1
GSN gelsolin (amyloidosis, Finnish type)
DMAP1 DNA methyltransferase 1 associated protein 1
HSD17B1 hydroxysteroid (17-beta) dehydrogenase 1
- Sapiens cDNA FLJ13598 fis, clone PLACE1009921.
PRKAR1A protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
NASP nuclear autoantigenic sperm protein (histone-binding)
CGI-87 CGI-87 protein
DDT D-dopachrome tautomerase
CBX3 chromobox homolog 3 (HP1 gamma homolog, Drosophila)
BAT1 HLA-B associated transcript 1
LENG4 leukocyte receptor cluster (LRC) member 4
ITPK1 inositol 1,3,4-triphosphate 5/6 kinase
PTK7 PTK7 protein tyrosine kinase 7

PPIB peptidylprolyl isomerase B (cyclophilin B)
- Homo sapiens transcribed sequences
na similar to zinc finger protein 184 (Kruppel-like)
na LOC284303
- Sapiens, clone IMAGE:4800042, mRNA
ERdj5 ER-resident protein ERdj5
na hypothetical gene supported by BC033256; BC007264
KIAA0215 KIAA0215 gene product
HRI heme-regulated initiation factor 2-alpha kinase
C6orf82 chromosome 6 open reading frame 82
SERPINH1 serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
RPL37 ribosomal protein L37
- Homo sapiens transcribed sequence
KIAA1453 KIAA1453 protein
RPL34 ribosomal protein L34
RPS24 ribosomal protein S24
PPP2CB protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
GLIS2 Kruppel-like zinc finger protein GLIS2
MTMR6 myotubularin related protein 6
GAPD glyceraldehyde-3-phosphate dehydrogenase
IARS isoleucine-tRNA synthetase
NUP153 nucleoporin 153kDa
STIP1 stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
DKFZP564O092 DKFZP564O092 protein
- Homo sapiens transcribed sequence
WDR5 WD repeat domain 5
IGFBP2 insulin-like growth factor binding protein 2, 36kDa
FLNA filamin A, alpha (actin binding protein 280)
RPL35A ribosomal protein L35a
PSMB6 proteasome (prosome, macropain) subunit, beta type, 6
DKFZP586N0721 DKFZP586N0721 protein
PTGES2 prostaglandin E synthase 2
RPL24 ribosomal protein L24
- Homo sapiens transcribed sequence with moderate similarity to protein pir:I60307 (E. coli) I60307 beta-galactosidase, alpha peptide - Escherichia coli
- Homo sapiens transcribed sequence with weak similarity to protein ref:NP_008921.1 (H.sapiens) WAS protein family, member 2; WASP family Verprolin-homologous protein 2 [Homo sapiens]
LOC148137 hypothetical protein BC017947
KIAA1510 KIAA1510 protein
HLA-B major histocompatibility complex, class I, B
MT2A metallothionein 2A
NMB neuromedin B
RPL27 ribosomal protein L27
EIF3S6IP eukaryotic translation initiation factor 3, subunit 6 interacting protein

FLJ22795 hypothetical protein FLJ22795
FLJ13213 hypothetical protein FLJ13213
MUC1 mucin 1, transmembrane
RPC155 polymerase (RNA) III (DNA directed) (155kD)
FLJ13352 hypothetical protein FLJ13352
KIAA0599 KIAA0599 protein
EPS8L2 EPS8-like 2
- Homo sapiens transcribed sequences
eIF3k eukaryotic translation initiation factor 3 subunit k
DCXR dicarbonyl/L-xylulose reductase
MSF MLL septin-like fusion
IGFBP7 insulin-like growth factor binding protein 7
RPS11 ribosomal protein S11
- Sapiens mRNA; cDNA DKFZp761P06121 (from clone DKFZp761P06121)
ATP5A1 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
WDR1 WD repeat domain 1
FLJ10826 hypothetical protein FLJ10826
YWHAZ tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
CD9 CD9 antigen (p24)
PLXNB1 plexin B1
HSJ001348 cDNA for differentially expressed CO16 gene
- Homo sapiens transcribed sequence
UBE2Q ubiquitin-conjugating enzyme E2Q (putative)
MRPL14 mitochondrial ribosomal protein L14
PRex1 KIAA1415 protein
UBE2E3 ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
TA-WDRP T-cell activation WD repeat protein
COL1A1 collagen, type I, alpha 1
GRAP2 GRB2-related adaptor protein 2
GPX4 glutathione peroxidase 4 (phospholipid hydroperoxidase)
na similar to KIAA0664 protein
CPR8 cell cycle progression 8 protein
RPLP2 ribosomal protein, large P2
DYRK1A dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
- Homo sapiens transcribed sequence with strong similarity to protein sp:P49241 (H.sapiens)
RS3A_HUMAN 40S ribosomal protein S3A
RPS3A ribosomal protein S3A
COX4I1 cytochrome c oxidase subunit IV isoform 1
TIMP2 tissue inhibitor of metalloproteinase 2
AHRR arylhydrocarbon receptor repressor
TRA@ T cell receptor alpha locus
FLJ23306 hypothetical protein FLJ23306
FSCN1 fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)
FXVD3 FXVD domain containing ion transport regulator 3
NOP5/NOP58 nucleolar protein NOP5/NOP58
GAPD glyceraldehyde-3-phosphate dehydrogenase

UNRIP unr-interacting protein
- Homo sapiens transcribed sequence with strong similarity to protein pir:A36670 (H.sapiens) A36670 cell division control protein CKS1 - human
CKS1B CDC28 protein kinase regulatory subunit 1B
SEMA4C sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
CKLFSF7 chemokine-like factor super family 7
VAMP8 vesicle-associated membrane protein 8 (endobrevin)
ANXA11 annexin A11
HCFC1R1 host cell factor C1 regulator 1 (XPO1 dependant)
ARNT aryl hydrocarbon receptor nuclear translocator
NUCB1 nucleobindin 1
NONO non-POU domain containing, octamer-binding
TNFSF10 tumor necrosis factor (ligand) superfamily, member 10
MYL6 myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
IRTA1 immunoglobulin superfamily receptor translocation associated 1
APOC1 apolipoprotein C-I
ZNF216 zinc finger protein 216
LOC51337 mesenchymal stem cell protein DSCD75
- Homo sapiens transcribed sequences
SACM1L SAC1 suppressor of actin mutations 1-like (yeast)
- Sapiens, clone IMAGE:4815969, mRNA
TRALPUSH TRALPUSH
- Homo sapiens transcribed sequence with strong similarity to protein pir:S25022 (H.sapiens) S25022 ribosomal protein S8, cytosolic - human
RPS8 ribosomal protein S8
- Sapiens, clone IMAGE:5554909, mRNA
RPL41 ribosomal protein L41
RPL41 ribosomal protein L41
KIAA1443 KIAA1443 protein
DKFZP434D146 DKFZP434D146 protein
FUCA2 fucosidase, alpha-L- 2, plasma
SF3A3 splicing factor 3a, subunit 3, 60kDa
NCKAP1 NCK-associated protein 1
na similar to KIAA0752 protein
MGC27165 hypothetical protein MGC27165
UBTF upstream binding transcription factor, RNA polymerase I
FLJ20257 hypothetical protein FLJ20257
RPS15A ribosomal protein S15a
KIAA0375 KIAA0375 gene product
CTSH cathepsin H
- Homo sapiens transcribed sequences
MSX1 msh homeo box homolog 1 (Drosophila)
MAL mal, T-cell differentiation protein
IGLJ3 immunoglobulin lambda joining 3
FLJ10597 hypothetical protein FLJ10597

DNCI2 dynein, cytoplasmic, intermediate polypeptide 2
AUP1 ancient ubiquitous protein 1
na similar to hypothetical protein
LOC147912 hypothetical protein LOC147912
NDUFB9 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
ACAS2 acetyl-Coenzyme A synthetase 2 (ADP forming)
- Homo sapiens transcribed sequence with moderate similarity to protein pir:T50638 (H.sapiens) T50638 synaptic glycoprotein SC2 [imported] - human
GPSN2 glycoprotein, synaptic 2
HBXIP hepatitis B virus x interacting protein
LOC338645 hypothetical protein LOC338645
CFL1 cofilin 1 (non-muscle)
BANF1 barrier to autointegration factor 1
RPS28 ribosomal protein S28
- Homo sapiens transcribed sequence with strong similarity to protein sp:P25112 (H.sapiens) RS28_HUMAN
40S ribosomal protein S28
COL1A1 collagen, type I, alpha 1
ZNF297B zinc finger protein 297B
RAB11-FIP4 rab11-family interacting protein 4
MGC8721 hypothetical protein MGC8721
RPS11 ribosomal protein S11
LY9 lymphocyte antigen 9
EPN1 epsin 1
MGC4677 hypothetical protein MGC4677
MYL3 myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
ARHC ras homolog gene family, member C
CANX calnexin
HIG1 likely ortholog of mouse hypoxia induced gene 1
CTBP1 C-terminal binding protein 1
GRN granulin
FLJ20257 hypothetical protein FLJ20257
LOC51064 glutathione S-transferase subunit 13 homolog
ILF2 interleukin enhancer binding factor 2, 45kDa
LSM10 U7 snRNP-specific Sm-like protein LSM10
CETP cholesteryl ester transfer protein, plasma
- Sapiens cDNA FLJ14487 fis, clone MAMMA1002721.
KIAA1841 KIAA1841 protein
HLA-A major histocompatibility complex, class I, A
HLA-C major histocompatibility complex, class I, C
YWHAE tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
CSE1L CSE1 chromosome segregation 1-like (yeast)
RPS7 ribosomal protein S7
- Homo sapiens transcribed sequence with strong similarity to protein sp:P23821 (H.sapiens) RS7_HUMAN
40S ribosomal protein S7 (S8)
HLA-B major histocompatibility complex, class I, B
HCGIV-6 HCGIV-6 pseudogene

ARL2 ADP-ribosylation factor-like 2
WDR13 WD repeat domain 13
DKFZp434D1428 hypothetical protein DKFZp434D1428
H2AFY H2A histone family, member Y
PROM1 prominin 1
- Homo sapiens transcribed sequences
- Homo sapiens transcribed sequences
E1B-AP5 E1B-55kDa-associated protein 5
ATP5G1 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
ATP5L ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
RPL35 ribosomal protein L35
- Sapiens partial mRNA (non-coding TFEBA1 gene), tumor 3
NOSIP nitric oxide synthase interacting protein
LOC51240 hypothetical protein LOC51240
HLA-A major histocompatibility complex, class I, A
DAD1 defender against cell death 1
RPS20 ribosomal protein S20
CA12 carbonic anhydrase XII
HEI10 enhancer of invasion 10
- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_115610.1 (H.sapiens)
hypothetical protein FLJ23059 [Homo sapiens]
IGHM immunoglobulin heavy constant mu
FLJ11856 putative G-protein coupled receptor GPCR41
EEF1B2 eukaryotic translation elongation factor 1 beta 2
- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_066944.1 (H.sapiens)
eukaryotic translation elongation factor 1 beta 2; eukaryotic translation elongation factor 1 beta 1 [Homo sapiens]
QRSL1 glutamyl-tRNA synthase (glutamine-hydrolyzing)-like 1
LOC220070 hypothetical protein BC004224
- Sapiens cDNA FLJ40216 fis, clone TEST12021358.
TRAM2 translocation associated membrane protein 2
LY6E lymphocyte antigen 6 complex, locus E
HDLBP high density lipoprotein binding protein (vigilin)
FLJ12448 hypothetical protein FLJ12448
- Homo sapiens transcribed sequence with strong similarity to protein sp:P08708 (H.sapiens) RS17_HUMAN
40S ribosomal protein S17
RPS17 ribosomal protein S17
JUN v-jun sarcoma virus 17 oncogene homolog (avian)
SLC25A6 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
- Homo sapiens transcribed sequence with moderate similarity to protein sp:P12236 (H.sapiens)
ADT3_HUMAN ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3)
GJA1 gap junction protein, alpha 1, 43kDa (connexin 43)
EDF1 endothelial differentiation-related factor 1
STK25 serine/threonine kinase 25 (STE20 homolog, yeast)
FADS2 fatty acid desaturase 2
SH2D3A SH2 domain containing 3A

- Homo sapiens transcribed sequences
PHKB phosphorylase kinase, beta
NPHS1 nephrosis 1, congenital, Finnish type (nephrin)
SLC25A3 solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
UBE2R2 ubiquitin-conjugating enzyme E2R 2
CGI-69 CGI-69 protein
RPS5 ribosomal protein S5
MGC40157 hypothetical protein MGC40157
SNRPB small nuclear ribonucleoprotein polypeptides B and B1
LOC51142 16.7Kd protein
FLJ10849 hypothetical protein FLJ10849
MMP2 matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
IGFBP4 insulin-like growth factor binding protein 4
KIAA1025 KIAA1025 protein
MSLN mesothelin
FLJ36928 hypothetical protein FLJ36928
PKM2 pyruvate kinase, muscle
TUFM Tu translation elongation factor, mitochondrial
GC20 translation factor sui1 homolog
TOLLIP toll interacting protein
TCF7L2 transcription factor 7-like 2 (T-cell specific, HMG-box)
PTMA prothymosin, alpha (gene sequence 28)
- Homo sapiens transcribed sequence with strong similarity to protein sp:P06454 (H.sapiens)
THYA_HUMAN Prothymosin alpha
RPL15 ribosomal protein L15
- Homo sapiens transcribed sequence with strong similarity to protein sp:P39030 (H.sapiens) RL15_HUMAN
60S ribosomal protein L15
FDXR ferredoxin reductase
PLG plasminogen
CYP19A1 cytochrome P450, family 19, subfamily A, polypeptide 1
FIBP fibroblast growth factor (acidic) intracellular binding protein
ATP2B4 ATPase, Ca ⁺⁺ transporting, plasma membrane 4
KIF5B kinesin family member 5B
CYorf15A chromosome Y open reading frame 15A
C22orf18 chromosome 22 open reading frame 18
- Homo sapiens transcribed sequences
- Homo sapiens transcribed sequences
TEGT testis enhanced gene transcript (BAX inhibitor 1)
DKFZp434N074 hypothetical protein DKFZp434N074
FLJ12331 hypothetical protein FLJ12331
- Sapiens, Similar to zinc finger protein 254, clone IMAGE:4821872, mRNA, partial cds
ACTG1 actin, gamma 1
CTSB cathepsin B

CISH cytokine inducible SH2-containing protein
RPS14 ribosomal protein S14
FCGRT Fc fragment of IgG, receptor, transporter, alpha
FBL fibrillarlin
S100A6 S100 calcium binding protein A6 (calcyclin)
MFAP2 microfibrillar-associated protein 2
DDX39 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 39
QP-C low molecular mass ubiquinone-binding protein (9.5kD)
MEOX1 mesenchyme homeo box 1
LAMR1 laminin receptor 1 (ribosomal protein SA, 67kDa)
HSPCB heat shock 90kDa protein 1, beta
CRADD CASP2 and RIPK1 domain containing adaptor with death domain
PFN1 profilin 1
ATP11A ATPase, Class VI, type 11A
COAS3 chromosome 1 amplified sequence 3
RPLP1 ribosomal protein, large, P1
TCN1 transcobalamin I (vitamin B12 binding protein, R binder family)
LTBP4 latent transforming growth factor beta binding protein 4
RPL21 ribosomal protein L21
RPL21 ribosomal protein L21
AMID apoptosis-inducing factor (AIF)-homologous mitochondrion-associated inducer of death
FLJ31958 hypothetical protein FLJ31958
TFRC transferrin receptor (p90, CD71)
HSPG2 heparan sulfate proteoglycan 2 (perlecan)
RPL13 ribosomal protein L13
MAN2C1 mannosidase, alpha, class 2C, member 1
AKT2 v-akt murine thymoma viral oncogene homolog 2
FLJ12443 hypothetical protein FLJ12443
CKLFSF4 chemokine-like factor super family 4
MGC14697 upregulated during skeletal muscle growth 5
EAP30 EAP30 subunit of ELL complex
DSP desmoplakin
H2AV histone H2A.F/Z variant
SIGLEC8 sialic acid binding Ig-like lectin 8
FLJ20139 hypothetical protein FLJ20139
KIAA0562 KIAA0562 gene product
- Homo sapiens transcribed sequence with moderate similarity to protein pir:T42650 (H.sapiens) T42650 hypothetical protein DKFZp434D0215.1 - human (fragment)
- Homo sapiens transcribed sequence with strong similarity to protein ref:NP_000971.1 (H.sapiens) ribosomal protein L18a; 60S ribosomal protein L18a [Homo sapiens]
RPL18A ribosomal protein L18a
RPL4 ribosomal protein L4
- Homo sapiens transcribed sequence with moderate similarity to protein ref:NP_000959.2 (H.sapiens) ribosomal protein L4; 60S ribosomal protein L4; homologue of Xenopus ribosomal protein L1 [Homo sapiens]
na hypothetical gene supported by BC033667

- Homo sapiens transcribed sequence with weak similarity to protein ref:NP_060265.1 (H.sapiens)
hypothetical protein FLJ20378 [Homo sapiens]

MKL1 megakaryoblastic leukemia (translocation) 1

CHKL choline kinase-like

ZD52F10 hypothetical gene ZD52F10

- Sapiens cDNA FLJ34038 fis, clone FCBBF2005645.

CTL2 CTL2 gene

- Sapiens, clone MGC:35282 IMAGE:5175809, mRNA, complete cds

KRT7 keratin 7

SH3BP2 SH3-domain binding protein 2

PIP5K2B phosphatidylinositol-4-phosphate 5-kinase, type II, beta

SAFB2 scaffold attachment factor B2

YY1 YY1 transcription factor

MGC2474 hypothetical protein MGC2474

NXN nucleoredoxin

DDX54 DEAD (Asp-Glu-Ala-Asp) box polypeptide 54

VPS28 vacuolar protein sorting 28 (yeast)

HDAC6 histone deacetylase 6

- Homo sapiens transcribed sequences

PFDN5 prefoldin 5

PSAP prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)

RPLP0P2 ribosomal protein, large, P0 pseudogene 2

RPLP0 ribosomal protein, large, P0

SPAG7 sperm associated antigen 7

RPL29 ribosomal protein L29

ATP5C1 ATP synthase, H⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1

ALDOA aldolase A, fructose-bisphosphate

- Homo sapiens transcribed sequence

ITM2B integral membrane protein 2B

CEP1 centrosomal protein 1

SUI1 putative translation initiation factor

MAPKAPK2 mitogen-activated protein kinase-activated protein kinase 2

- Homo sapiens transcribed sequence with moderate similarity to protein sp:P23131 (H.sapiens)

RL23_HUMAN 60S ribosomal protein L23 (L17)

SIRT2 sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)

HMGA1 high mobility group AT-hook 1

C9orf16 chromosome 9 open reading frame 16

MESDC2 mesoderm development candidate 2

ED1 ectodermal dysplasia 1, anhidrotic

MAK3P likely ortholog of mouse Mak3p homolog (S. cerevisiae)

- Sapiens cDNA FLJ40954 fis, clone UTERU2010525.

KR18 KRAB zinc finger protein KR18

PPP1CB protein phosphatase 1, catalytic subunit, beta isoform

SNRPC small nuclear ribonucleoprotein polypeptide C

- Sapiens mRNA; cDNA DKFZp434N2116 (from clone DKFZp434N2116)

SPINT2 serine protease inhibitor, Kunitz type, 2

HMG3 high mobility group nucleosomal binding domain 3

MMP14 matrix metalloproteinase 14 (membrane-inserted)
TSPYL TSPY-like
- Sapiens cDNA FLJ11739 fis, clone HEMBA1005497.
RABL2A RAB, member of RAS oncogene family-like 2A
RABL2B RAB, member of RAS oncogene family-like 2B
PRO1073 PRO1073 protein
TPM3 tropomyosin 3
LTBP3 latent transforming growth factor beta binding protein 3
RPL11 ribosomal protein L11
SLK Ste20-related serine/threonine kinase
USP28 ubiquitin specific protease 28
- Sapiens cDNA FLJ12352 fis, clone MAMMA1002312.
PCBD 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)
PIN1 protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
- Sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)
ACP33 acid cluster protein 33
ALDH4A1 aldehyde dehydrogenase 4 family, member A1
ATP5J2 ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2
MGC5576 hypothetical protein MGC5576
MTPN myotrophin
SFRS3 splicing factor, arginine/serine-rich 3
NDUFB8 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
FPGS foylpolyglutamate synthase
HNRPL heterogeneous nuclear ribonucleoprotein L
C1orf9 chromosome 1 open reading frame 9
TPT1 tumor protein, translationally-controlled 1
BASP1 brain abundant, membrane attached signal protein 1
EPHX1 epoxide hydrolase 1, microsomal (xenobiotic)
HLA-C major histocompatibility complex, class I, C
APEX1 APEX nuclease (multifunctional DNA repair enzyme) 1
PCBP2 poly(rC) binding protein 2
ADCY3 adenylate cyclase 3
PRDX1 peroxiredoxin 1
FLJ20003 hypothetical protein FLJ20003
C3 complement component 3
MGC14258 hypothetical protein MGC14258
SDBCAG84 serologically defined breast cancer antigen 84
YWHAG tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
VCL vinculin
LIMK2 LIM domain kinase 2
SC65 nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein
KREMEN1 kringle containing transmembrane protein 1
BCAS1 breast carcinoma amplified sequence 1

MGC4248 hypothetical protein MGC4248
MGC40157 hypothetical protein MGC40157
MEG3 maternally expressed 3
PTRF polymerase I and transcript release factor
FLJ30194 hypothetical protein FLJ30194
ACTB actin, beta
RPS15A ribosomal protein S15a
HLA-DQB1 major histocompatibility complex, class II, DQ beta 1
TGIF TGFB-induced factor (TALE family homeobox)
PH-4 hypoxia-inducible factor prolyl 4-hydroxylase
C12orf8 chromosome 12 open reading frame 8
DNCI2 dynein, cytoplasmic, intermediate polypeptide 2
- Homo sapiens transcribed sequence with strong similarity to protein sp:Q13409 (H.sapiens) DYI2_HUMAN Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)
ANXA1 annexin A1
PREP prolyl endopeptidase
MGC29937 hypothetical protein MGC29937
na LOC145035
- Sapiens, Similar to SLIT-ROBO Rho GTPase-activating protein 3, clone MGC:39565 IMAGE:4830856, mRNA, complete cds
NDUFA1 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
MDH1 malate dehydrogenase 1, NAD (soluble)
DPP9 dipeptidylpeptidase 9
KIAA0913 KIAA0913 protein
- Sapiens, clone MGC:45813 IMAGE:4581020, mRNA, complete cds
FLJ10298 hypothetical protein FLJ10298
PRDX2 peroxiredoxin 2
IGHG3 immunoglobulin heavy constant gamma 3 (G3m marker)
IGHG4 immunoglobulin heavy constant gamma 4 (G4m marker)
COL3A1 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
CFL1 cofilin 1 (non-muscle)
- Sapiens cDNA FLJ12198 fis, clone MAMMA1000876.
FLOT1 flotillin 1
- Sapiens, Similar to RIKEN cDNA 1110049F14 gene, clone IMAGE:4156973, mRNA, partial cds
LOC58481 hypothetical protein LOC58481
SNRPN small nuclear ribonucleoprotein polypeptide N
na similar to ribosomal protein
RPS18 ribosomal protein S18
SOX21 SRY (sex determining region Y)-box 21
RPL10A ribosomal protein L10a
GNS glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
- Sapiens, clone IMAGE:5259991, mRNA, partial cds

PPP3R1 protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)

TGFB1 transforming growth factor, beta-induced, 68kDa

POLR2J polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa

MGC4268 hypothetical protein MGC4268

CGI-48 CGI-48 protein