

Additional file 7

Name	locus	strand	sequence	HU_KapB_eMyc	HU_KaposinB	HUVEC	IP_confidence	annotation
NM_hsa_3797	chr4:13629077-13629147	+	CGGGGCGGGCGGGCGGGCGGGT	0.0633175	0.0412051	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2842	chr17:36875913-36876031	+	AAGGGCCAGAGGAGCGTGGAAGT	0.0854786	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3150	chr1:26881016-26881096	+	CTCCTCGCCCTCTTGACTGTAG	0.0854786	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4884	chr3:18278766-18278778	+	AGTGCGTTAGATATGAATCTCGGA	0.113971	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1352	chr8:12151129-121511337	+	TTAGTCTACTCTTTGCCAGAA	0.170957	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1374	chr19:35500733-35500793	+	TTACCTCTCAAATCTCTCAGA	0.170957	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5201	chr17:8534364-8534480	-	CGGGCGGGCGGGCGGGCGGGC	0.170957	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_868	chr19:35652419-35652495	-	TCATGTCTGAACCAATGAGAGC	0.256436	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2856	chr17:42432096-42432164	-	GTCGGAAGGGCGGGCGGGCGG	0.303924	0.110371	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1090	chr21:4731396-4731479	+	CTCCCTTCTCGCTGGCTT	0.313421	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2182	chr10:29333102-29333178	+	GTGGATGTGACAAATGGTGTAT	0.313421	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4713	chr1:149900241-149900381	+	TAGAACCTCTGGCCCATCTCG	0.341914	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3678	chr3:38012172-38012248	+	CTACTTTTCCAGCCCTCTCG	0.7978	0.397335	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1953	chrY:19692289-19692341	-	GTCTGAGAGCAACTGGT	0.854786	0.79467	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3970	chr6:28732097-28732196	+	GCCAAAATTGCTATGGTGGAGA	4.87228	3.67535	0.329788	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3949	chr6:393743-3937467	-	AGCCGGCGGGCGGGCGGGCGG	232.559	137.345	15.2435	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4113	chr7:26371600-26371683	-	GCGCGGGCGGGCGGGCGGGCGG	0.186787	0.163717	0.0183216	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2631	chr14:49872786-49872879	-	GGGGGCGGGCGGGCGGGCGGGCGG	0.498625	0.463558	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4817	chr2:130653515-130653453	-	GCGCGGTGTGGGGGGCGGGCGG	1.13971	0.397335	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3773	chr3:138624104-138624175	-	TVAGGTAGGAGGTGACAGTGA	1.49113	0.960226	0.207644	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2506	chr12:127650709-127650800	-	TGGTGTGGCTTCGGATGGCTC	3.81804	3.70846	0.806149	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5210	chr17:65822043-65822163	-	GGGGGCGGGCGGGCGGGCGGGCGG	0.159877	0.13686	0.0299611	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3154	chr1:3381667-31381758	+	AGGAGGGCGGGCGGGCGGGCGG	0.455886	0.331113	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4450	chr21:9826690-9826778	+	CGGGGTCTGGCGGGCGGGCGG	0.341914	0.331113	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3332	chr1:167153912-167153981	-	TVAGGTAGTAGTGGTGGATG	10.2448	7.33598	1.62858	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_128	chr6:158914875-158914957	-	TVAGGTAGTAGTGGTGGTGGC	10.3954	7.70178	1.78214	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3536	chr2:73246462-73246545	+	GCGGAAGTAGTCAAGTGGGAG	48.9222	48.5742	11.396	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4644	chr9:79186665-79186763	+	CCCGCGGTGGCGGGCGGGGTCGG	79.3526	57.15	14.071	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4531	chr6:28757511-28757605	-	GCTTTCATGTATGAGTCCCGGTG	37.5536	29.2041	7.62177	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4273	chr9:134153375-134153457	+	TCGGCAGGGCGGGCGGGCGGGCGG	0.205757	0.137716	0.0374307	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2828	chr17:18965290-18965366	+	CCCCGAGGAAGAGAGGTAGCG	0.569857	0.52978	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1312	chr15:24972989-24971066	-	CGAGGGCGGGCGGGCGGGCGGGC	0.626493	0.26489	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3491	chr25:39711738-39711250	-	ACTGCGCGGGCGGGCGGGCGGGC	0.341914	0.65489	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_969	chr7:37043284-37043351	+	CAGGGTTTGACAGACCGGGTCT	0.289829	0.26489	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4689	chr1:180910059-180910189	+	CACCTCCCGCCCTCCCCCGCC	3.5901	2.25157	0.659576	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4528	chr7:7306127-73062227	+	GCGGGCGGGCGGGCGGGCGGGCGG	0.645838	0.52978	0.164894	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2185	chr10:35929773-35929871	+	GCGGGCGGGCGGGCGGGCGGGCGG	0.374742	0.268832	0.0875969	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3619	chr2:240322061-240322158	+	ACCCTCCCGCCCGGGCGGGCGG	10.2859	5.76136	1.90544	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2164	chr3:186505088-186505150	+	AAGCAGGATTCAAGTACAAT	1.76656	1.25823	0.439717	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3965	chr6:26328352-26328450	+	CAGGTTGCAGCTCGTGGCTGCTG	1.36615	9.90026	3.51774	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4791	chr16:33964220-33964318	+	CGCTGAGAAGACAGTCAACTGACTA	270.454	238.732	87.9435	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1054	chr16:57770361-57770453	+	TAGCTCTGCTTGGGAACTCGC	0.740814	0.397335	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_884	chr1:15027085-15027139	+	TVAGGGGAGAAGGCAACCGGA	0.455886	0.397335	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3296	chr1:35893406-35893490	-	TTTGGTATTGTAAGTCTG	14.4744	10.3307	3.81089	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_198	chr17:65822071-65822137	-	GGGGGCGGGCGGGCGGGCGGGCGG	0.168644	0.0927115	0.0355985	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3308	chr1:60809985-60810083	-	CACTAGTTTGGAGTCTCTTAA	33.4858	29.5816	11.9017	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1274	chr16:51272972-51273049	-	CACTAGATTGAGGCTGTGGAG	33.6282	29.6699	11.975	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4963	chr10:24497805-24497907	-	CCGTCCCGTCCCTCGCTGCTC	14.1799	8.15641	3.49331	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1727	chr10:94625410-94624568	+	TVAGGTCTAGACTGTGGTGG	0.3989	0.331113	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2470	chr12:112354552-112354633	+	AGATTGAGTATTTGGTTG	178.804	162.278	72.678	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4795	chr2:223184096-223184244	+	CCTCGGCAGGGCGGGCGGGCGGGCGT	0.319729	0.243672	0.110717	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2951	chr18:68879684-68879769	+	CGGGCGGGCGGGCGGGCGGGCGG	1.2005	0.708581	0.323681	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2719	chr16:90572599-9057333	+	CGCGGGCGGGCGGGCGGGCGGGC	1.36006	0.805707	0.382957	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3403	chr20:54606257-54606348	+	TTGCTGAGTAGTGTGGCTCT	325.458	293.394	147.771	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2154	chr1:70859275-70859325	+	TVAGGGAGTATTTGGCAA	313.671	284.254	145.109	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5244	chr16:33963146-33963264	+	GCTCTAGTTGGATCTGGAGCGGGC	23.82	12.5161	6.52248	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5254	chr19:3201433-3201551	+	TTCTCTCCCGCTCCCTGAT	0.04049	4.63558	2.41845	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4913	chr4:1006300-1006418	-	TGGGGCGGGCGGGCGGGCGGGCGG	1.11122	0.695336	0.366431	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2798	chr16:88519967-88520040	-	GCGGGCGGGCGGGCGGGCGGGCGG	0.968578	0.695336	0.366431	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3832	chr4:1006319-1006406	-	CGGGGCGGGCGGGCGGGCGGGGGA	0.940265	0.695336	0.366431	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5229	chr16:50903350-50903434	-	ATACGGGGTGTGAGGCTTAAAAA	420.624	273.136	147.951	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2566	chr14:65937572-65937650	+	CTGCACAGAGGGCGGGCGGGCTGT	0.626843	0.26489	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2910	chr17:38278611-38278692	-	GCTCCCGCCCGCTCTGCTGC	0.341914	0.26489	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2399	chr11:97593310-97593396	+	TVAGTAGATGTTTGTAGT	0.256436	0.110371	0.0610719	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2707	chr16:2222119-2222202	+	TTAGCACGCCCTCTCCCGAGA	0.284929	0.132445	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2772	chr16:89297532-89297619	+	AAGGTCATCAGATTACGGGGA	0.227943	0.132445	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2822	chr17:17598203-17598283	+	AGGGCGGGCGGGCGGGCGGGCGG	0.227943	0.132445	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2991	chr19:9653379-9653476	+	TTACAGTGGAGGCAAGTCTG	0.170957	0.132445	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5169	chr17:47269793-47269911	+	GAGACTCGGGCGGGCGGGCTAAGA	0.170957	0.132445	0.0732862	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5079	chrX:154003303-15400337	+	AAGTGGTGAGTTCTCTGCGACGG	0.626843	0.52978	0.293145	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1520	chr1:18073682-18073757	+	TVAGGTTTGGCTGGGACTGA	102.717	70.6594	40.3441	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4995	chr11:851195143-851195261	+	GAGGAGTCAACCCGGTGGGG	9.28867	7.28448	4.17732	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3989	chr6:43762884-43762978	+	CCAGGCTTCCCTCTGGCTCT	1.22519	1.05956	0.622933	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_2375	chr11:2102214-21022488	+	ACTGGCTGCTTACGGCTCTC	77.415	50.6657	31.8001	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3494	chr22:191490-42519567	+	AAGGAGGAGAAGACGGTGAAG	0.284929	0.231779	0.146572	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5175	chr17:46211097-4621207	+	TCCTGCCCTACTGTATCCCAAG	1.02574	0.463558	0.293145	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4425	chr20:2634868-2635014	+	CTGATGCTCCATGCTGTGAGCAAT	0.512871	0.463558	0.293145	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4447	chr21:9826183-9826277	+	CGGACAGGGCTGTGGCGACTGGT	0.0142464	0.0220742	0.0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_190	chr17:79919290-79919367	+	GCGGGCGGGCGGGCGGGCGGGCGG	0.0284929	0.0331113	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3374	chr20:30194978-30195067	+	CTCTCGTGAAGTCTGAGGA	0.0284929	0.0772596	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_35	chr19:7533656-7533712	+	TATCTGCTGTGTCCTCCAGG	0.0284929	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_5194	chr17:6347731-6347871	+	GTAGGTGGGGTGGGCAACAAGT	0.0284929	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1308	chr1:178712679-178712756	+	TTAGTCTGGGCAACTCGA	0.0569857	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_134	chr14:21460202-21460252	+	TTTAGCCCTGTTCTCCTAGG	0.0569857	0.132445	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_146	chr1:17156022-171560285	+	TAGGAGCTATCAGAATGAGTA	0.0569857	0.397335	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_1502	chr17:33760236-33760295	+	CACACTTCCCAGTGGCTCGG	0.0569857	0.463558	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_269	chr10:72082639-72082769	+	CCACTTGTATGGGAAATGGCTG	0.0569857	0.198668	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3094	chr19:59061035-59061102	+	TTGGGTTTGGGCTGTCTGGA	0.0569857	0.132445	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_3634	chr2:75340449-75340537	+	GTAGGCTTGAAGCTTGA	0.0569857	0.0662225	0	Yes	KaposinB+e-Myc+KaposinB
NM_hsa_4312	chrM:8153-8229	-	TAGGACGATGGGCATGAAACTGTG	0.0569857	0.198668	0	Yes	KaposinB