

Name	locus	strand	sequence	midsep2	miransep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1	chrM:15955-16024	-	GTTAAGAGCTTTTCTGAT	Yes	No	No	0.113971	0.26489	1.24587	Yes	H-KapB-KapB-cMye
NM_hsa_1000	chr1:35555045-9575500	-	GTCAGGGCTCCAGGGGTTGG	Yes	No	No	0.113971	0	0	No	
NM_hsa_1002	chr11:624936-625006	+	CCGACCGAGCCGCCCGCAT	Yes	No	No	0	0	0	No	
NM_hsa_1002	chr11:624925-625015	+	CCGACCGAGCCGCCCGCAT	Yes	Yes	No	0	0	0	No	
NM_hsa_1003	chr11:624936-625006	+	CGGGTGTGGCTTAGGACTGGCC	Yes	No	No	0	0	0	No	
NM_hsa_1004	chr16:261894-261899	+	TGGGCTGTGCTGGGCATT	Yes	Yes	No	0	0	0	No	
NM_hsa_1004	chr16:2681202-2681253	+	CTGCTGTGCTGTGGCATT	Yes	No	No	0	0	0	No	
NM_hsa_1004	chr16:2681193-2681263	+	TGGGCTGTGCTGGGCATT	Yes	Yes	No	0	0	0	No	
NM_hsa_1005	chr16:261894-261899	+	TGCCACAGCCAGCTCAGG	Yes	No	No	0	0	0	No	
NM_hsa_1005	chr16:2681202-2681253	+	TGCCACAGCCAGCTCAGG	Yes	No	No	0	0	0	No	
NM_hsa_1008	chrX:129299909-129299961	+	CCGTTTTCGCGAGTTTGTGG	Yes	Yes	Yes	0	0.0662225	0	No	
NM_hsa_1008	chrX:129299898-129299970	+	CCGTTTTCGCGAGTTTGTGG	Yes	Yes	Yes	0	0.0662225	0	No	
NM_hsa_1008	chrX:129299879-129299985	+	CCGTTTTCGCGAGTTTGTGG	Yes	Yes	Yes	0	0.0662225	0	No	
NM_hsa_1009	chrX:129299909-129299961	+	GCAAGCTGCCAAGAGCTGGCT	Yes	No	No	0	0	0	No	
NM_hsa_101	chr10:13505529-135055715	+	TGGGCGGGCTCCAGGT	Yes	No	No	0	0	0	No	
NM_hsa_1010	chr4:977692-9777035	+	CTCTGATGCTGCTAGGGCC	Yes	No	No	0	0	0	No	
NM_hsa_1011	chr4:977692-9777035	+	CCCTTCTTCTGCTTCTGGCT	Yes	No	No	0	0	0	Yes	
NM_hsa_1014	chr1:147829303-147829365	+	TCAGGCACAGCAATAGTGTGG	Yes	No	No	0	0	0	No	
NM_hsa_1015	chr20:60941181-60941248	+	CCTCACCAAGGCTGACCCAGGC	Yes	No	No	0	0	0	No	
NM_hsa_1016	chr2:74881271-74882325	+	AGTTCGGCTCGAGATGGT	Yes	No	No	0	0	0	No	
NM_hsa_1017	chr2:74881211-74881264	+	AGGCAGAGGGCGGAGTAG	Yes	No	No	0	0	0	No	
NM_hsa_1018	chr11:117049437-117049480	+	GTTCTGGCTCGAGGCGG	Yes	No	No	0	0	0	No	
NM_hsa_1019	chr11:117049437-117049480	+	CCAGCGCGCCAGCTCAC	Yes	No	No	0	0	0	No	
NM_hsa_1020	chr3:43757997-43758072	+	AAAAAGATTTGGGCGATGTAG	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1020	chr3:43757967-43758105	+	AAAAAGATTTGGGCGATGTAG	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1020	chr3:43758007-43758064	+	AAAAAGATTTGGGCGATGTAG	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1021	chr3:43758007-43758064	+	GTAGCCCTCACTTTTAAA	Yes	No	No	0	0	0	No	
NM_hsa_1022	chr14:106354391-106354459	+	TGGGTTTGTCTGTGGGAAA	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1022	chr14:106354381-106354459	+	TGGGTTTGTCTGTGGGAAA	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1022	chr14:106354356-106354484	+	TGGGTTTGTCTGTGGGAAA	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1023	chr14:106354391-106354459	+	CTCACAGTGAACAGACCCACACA	Yes	No	No	0	0	0	No	
NM_hsa_1024	chr12:122905573-122905640	+	TATTCGACTCAGGTGCTAG	Yes	No	No	0	0	0	No	
NM_hsa_1025	chr12:122905573-122905640	+	AAGCAGCTGAGTCAAGATACC	Yes	No	No	0	0	0	No	
NM_hsa_1026	chr9:3343645-3343653	+	CTGCTCTGCTGTCTAGCTGT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1026	chr9:33436473-3343638	+	CTGCTCTGCTGTCTAGCTGT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1026	chr9:33436463-3343658	+	CTGCTCTGCTGTCTAGCTGT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1027	chr9:33436473-3343638	+	AGCTGGAGCTTGGGGCAAGA	Yes	No	No	0	0	0	No	
NM_hsa_1029	chr19:5701933-57019264	+	CTGCCCACTCTGGA	Yes	No	No	0	0	0	No	
NM_hsa_1032	chr16:84004010-84004148	+	CTTCCATACTGTCTCAGT	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1032	chr16:84004035-84004118	+	CTTCCATACTGTCTCAGT	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1032	chr16:8400409-84004109	+	CTTCCATACTGTCTCAGT	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1033	chr16:8400409-84004109	+	TGAGTTCAGCCAGGAGGAGGG	Yes	No	No	0	0	0	Yes	
NM_hsa_1034	chr8:56821959-56822008	+	CTCTGGGATATGACTGA	Yes	No	No	2.2082	1.22512	1.81383	Yes	
NM_hsa_1035	chr8:56821959-56822008	+	AGTCAGATCCCACTCAGT	Yes	No	No	0	0	0	No	
NM_hsa_1036	chr8:22033947-22034012	+	TAGGGGGTGGGACTGCTGGA	Yes	Yes	No	0	0	0	Yes	
NM_hsa_1036	chr8:22033929-22034021	+	TAGGGGGTGGGACTGCTGGA	Yes	Yes	No	0	0	0	Yes	
NM_hsa_1037	chr1:2031947-2230412	+	CACGAGCTGCTCCAGAGA	Yes	No	No	0	0	0	No	
NM_hsa_1038	chr10:102798328-102798408	+	CATTGCTTTCTGTCTCCACA	Yes	Yes	Yes	0.170957	0	0.219859	Yes	
NM_hsa_1038	chr10:102798318-102798418	+	CATTGCTTTCTGTCTCCACA	Yes	Yes	Yes	0.170957	0	0.219859	Yes	
NM_hsa_1038	chr10:102798341-102798399	+	CATTGCTTTCTGTCTCCACA	Yes	Yes	Yes	0.170957	0	0.219859	Yes	
NM_hsa_1039	chr10:102798341-102798399	+	TGGGTTGACGTTGAGGAGGG	Yes	No	No	0	0	0	No	
NM_hsa_104	chr22:13024635-13025717	+	AACCACGGTTCGAGAGTGG	Yes	No	No	0	0	0	No	
NM_hsa_1040	chr11:120114220-120114275	+	GACTGGTGTACTGTGAGA	Yes	No	No	0	0	0	No	
NM_hsa_1041	chr11:120114220-120114275	+	GCCAGAATGGGCCAGGCTA	Yes	No	No	0	0	0	No	
NM_hsa_1042	chr11:155197297-155197340	+	GCGGACGGGTGGTGGGG	Yes	No	No	0	0	0	No	
NM_hsa_1043	chr11:155197297-155197340	+	CCCTCCCGACGGCTCTCT	Yes	No	No	0	0	0	No	
NM_hsa_1046	chr19:4816222-4816293	+	TCCCAAGGTGAGGCAAGGA	Yes	Yes	No	0	0	0	No	
NM_hsa_1046	chr19:4816212-4816300	+	TCCCAAGGTGAGGCAAGGA	Yes	Yes	No	0	0	0	No	
NM_hsa_1047	chr19:4816222-4816293	+	CTTGCTCTGGGGCTGGGACCC	Yes	No	No	0	0	0	No	
NM_hsa_1048	chr13:4988896-49889062	+	TTCAAATGATGGAGTAGAAC	Yes	Yes	No	0	0	0	No	
NM_hsa_1048	chr13:49888963-49889071	+	TTCAAATGATGGAGTAGAAC	Yes	Yes	No	0	0	0	No	
NM_hsa_1049	chr13:4988896-49889062	+	TCTACTCATGCATCAATG	Yes	No	No	0	0	0	No	
NM_hsa_1050	chrX:2846908-2846953	+	ACCAGAGCCGGTGCACGG	Yes	No	No	0	0	0	No	
NM_hsa_1051	chrX:2846908-2846953	+	TTCCTCCCTCCGGGCTC	Yes	No	No	0	0	0	No	
NM_hsa_1052	chr8:15403349-15403408	+	TTATGCTGTGACTGTGTAG	Yes	Yes	No	0	0	0	No	
NM_hsa_1052	chr8:15403339-15403415	+	TTATGCTGTGACTGTGTAG	Yes	Yes	No	0	0	0	No	
NM_hsa_1053	chr8:15403349-15403408	+	TCAGGCTTTATTGGCATGCA	Yes	No	No	0	0	0	No	
NM_hsa_1054	chr16:5770361-5770435	+	TGCTTGTGCTTGGGATCCG	Yes	Yes	No	0.740814	0.397335	0.146572	Yes	KapB-cMye-KapB-H
NM_hsa_1054	chr16:5770371-5770428	+	TAGCTTCTGCTTGGGATCCG	Yes	Yes	No	0.740814	0.397335	0.146572	Yes	KapB-cMye-KapB-H
NM_hsa_1055	chr17:27919433-27919569	+	GTTCTCTCTCGAGGACTGG	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1056	chr17:27919433-27919569	+	CTTCCCTCTGAGGGCCAG	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1056	chr17:27919472-27919530	+	CTTCCCTCTGAGGGCCAG	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1056	chr17:27919460-27919539	+	CTTCCCTCTGAGGGCCAG	Yes	Yes	Yes	0	0	0	Yes	
NM_hsa_1057	chr8:72756820-72756871	+	GTCATTCAGAGGAGGACAGT	Yes	No	No	0	0	0	No	
NM_hsa_1058	chr8:72756808-72756880	+	CTTGAAGCCAGCCGCGCTT	Yes	No	No	0	0	0	No	
NM_hsa_1058	chr8:72756820-72756871	+	CTTGAAGCCAGCCGCGCTT	Yes	Yes	No	0	0	0	No	
NM_hsa_1059	chr8:72756820-72756871	+	GCGGACCTCTTCGAGAGCC	Yes	No	No	0	0	0	No	
NM_hsa_106	chr17:16353818-16353875	+	TGTCACTCTGTGCTGGAG	Yes	Yes	No	0	0	0	No	
NM_hsa_106	chr17:16353804-16353884	+	TGTCACTCTGTGCTGGAG	Yes	Yes	No	0	0	0	Yes	
NM_hsa_1060	chr11:118661975-118662029	+	CGAAACCTCGCCCGCCGG	Yes	No	No	0	0	0	No	
NM_hsa_1061	chr11:118661975-118662029	+	GCGGCTCACTCGCTCTGGCC	Yes	No	No	0	0	0	No	
NM_hsa_1062	chr19:13278696-13278743	+	CTGGCTGTGCTTGGCGGTG	Yes	No	No	0	0	0	No	
NM_hsa_1063	chr19:13278696-13278743	+	TCTGACTCAGATGAGGTGG	Yes	No	No	0	0	0	No	
NM_hsa_1066	chr7:99691401-99691463	+	CTGACGAAGCAGCATTTGGA	Yes	Yes	No	0.113971	0	0	No	
NM_hsa_1066	chr7:99691388-99691472	+	CTGACGAAGCAGCATTTGGA	Yes	Yes	No	0.113971	0	0	No	
NM_hsa_1067	chr7:99691401-99691463	+	GGAAGTGTACTCAGAGATG	Yes	No	No	0	0	0	No	
NM_hsa_107	chr17:16353818-16353875	+	GTATCACCTCTGTGTTAACA	Yes	No	No	0	0	0	No	
NM_hsa_1070	chr19:4358028-4358079	+	CCATGGGCTCGGGCTGGTGA	Yes	Yes	No	0	0	0	No	
NM_hsa_1071	chr19:4358028-4358079	+	ACTGGTGTGTCTCCGCA	Yes	No	No	0	0	0	No	
NM_hsa_1072	chr22:1278908-1278962	+	TGGAAGGCTACAGATTGAG	Yes	Yes	No	0	0	0	No	
NM_hsa_1072	chr22:1278906-1278971	+	TGGAAGGCTACAGATTGAG	Yes	Yes	No	0	0	0	No	
NM_hsa_1073	chr22:1278906-1278962	+	CAATCTGAACTTGAAGCT	Yes	No	No	0.0569857	0	0	No	
NM_hsa_1074	chr3:123811949-123812008	+	TCCTCTCCCTCTGCTCTA	Yes	Yes	No	0	0.26489	0.146572	No	
NM_hsa_1074	chr3:123811937-123812017	+	TCCTCTCCCTCTGCTCTA	Yes	Yes	No	0	0.26489	0.146572	No	
NM_hsa_1075	chr3:123811949-123812008	+	GGGGGAGGGCTGGAGGTTGT	Yes	No	No	0	0	0	No	
NM_hsa_1076	chr17:452826-3745286	+	CTCCAGGGGAGCTCTGCT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1076	chr17:452826-3745286	+	CTCCAGGGGAGCTCTGCT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1077	chr17:452826-3745286	+	CTCCAGGGGAGCTCTGCT	Yes	Yes	Yes	0	0	0	No	
NM_hsa_1078	chr17:452826-3745286	+	ACATAGCCCTCGCTCTGCG	Yes	No	No					

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1125	chr14:106331738-106331791	-	CACAGTGTGGCAGCTTACAA	Yes	No	No	0	0	0	0	No
NM_hsa_1128	chr1:7593165-7593226	+	CACAGCCAGATCAGGGCTGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1128	chr1:7593165-7593226	+	CAAGCCCAAGATCAGGGCTGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1128	chr1:7593127-7593265	+	CAAGCCCAAGATCAGGGCTGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1129	chr1:7593165-7593226	+	CAGCAGTACAGGGCTGC	Yes	No	No	0	0	0	0	No
NM_hsa_113	chr10:104418545-104418608	+	CTTGGAGAGGGCTGC	Yes	No	No	0	0	0	0	No
NM_hsa_1130	chr19:4228474-42284823	-	GTGACTCCACATCTTTCTCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1130	chr1:193126397-193126457	+	CCTGTGCTAAATGTTAGTGA	Yes	Yes	Yes	0	0	0.0732862	0	Yes
NM_hsa_1130	chr1:193126387-193126457	+	CCTGTGCTAAATGTTAGTGA	Yes	Yes	Yes	0	0	0.0732862	0	Yes
NM_hsa_1131	chr1:193126397-193126457	+	CACTAACGTTTGAAGCACTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1132	chr1:1547688-15476884	+	TGCTTCTCTGTAAGTCAAGC	Yes	No	No	0.256436	0.430486	0.109929	0	No
NM_hsa_1132	chr1:1547618-1547677	+	TGCTTCTCTGTAAGTCAAGC	Yes	No	No	0.256436	0.430486	0.109929	0	No
NM_hsa_1133	chr1:1547618-1547677	+	CAGGTTGCTGGGAAGCACC	Yes	No	No	0	0	0.0732862	0	No
NM_hsa_1134	chr17:42284724-42284820	-	GTGACTCCACATCTTTCTCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1134	chr17:4228474-42284823	-	GTGACTCCACATCTTTCTCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1134	chr19:4228483-42284799	+	GTGACTCCACATCTTTCTCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1135	chr17:4228474-42284799	-	GGAGGGAGGGGAGCTGCGCA	Yes	No	No	0	0	0	0	No
NM_hsa_1136	chr19:39869073-39869161	+	CTGGAACATGGGAGAGGGCAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1136	chr19:39869083-39869142	+	CTGGAACATGGGAGAGGGCAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1137	chr19:39869083-39869142	+	CTGGAACATGGGAGAGGGCAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1138	chr2:99911236-99911322	+	GGAGGAACCTGGGTACCTGTA	Yes	Yes	Yes	0.284929	0	0	0	No
NM_hsa_1138	chr2:9991250-99911313	+	GGAGGAACCTGGGTACCTGTA	Yes	Yes	Yes	0.284929	0	0	0	No
NM_hsa_1138	chr3:99911214-99911352	+	GGAGGAACCTGGGTACCTGTA	Yes	Yes	Yes	0.284929	0	0	0	No
NM_hsa_1139	chr3:9991250-99911313	+	TAGTGTGGCAGCTCCCTCTTG	Yes	No	No	0	0	0	0	No
NM_hsa_114	chr3:18429817-184298188	+	CTGTGAGCTGCTGTGGCTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1140	chr3:4975272-49752795	+	TGCTGTGTGGCTGCTGGAACC	Yes	Yes	Yes	0.341914	0.79467	0	0	No
NM_hsa_1140	chr3:4975272-49752809	+	TGCTGTGTGGCTGCTGGAACC	Yes	Yes	Yes	0.341914	0.79467	0	0	No
NM_hsa_1141	chr3:4975272-49752795	+	TGCTGTGTGGCTGCTGGAACC	Yes	Yes	Yes	0.341914	0.79467	0	0	No
NM_hsa_1142	chr18:4855641-48556457	-	TGCTGTGTGGCTGCTGGAACC	Yes	No	No	0.0569857	0	0	0	No
NM_hsa_1142	chr18:48556362-48556433	-	CGGCTGTAATCGTACC	Yes	No	No	0	0	0	0	No
NM_hsa_1143	chr18:48556362-48556433	-	TTGAGGGAAGTGGT	Yes	No	No	0	0	0	0	No
NM_hsa_1144	chr10:104139225-104139277	+	CTTGACCTGATCTTCTCTCA	Yes	No	No	0	0.0662225	0	0	No
NM_hsa_1145	chr10:104139225-104139277	+	GGAGATCTGAGTCAAGAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1146	chr22:41732160-41732235	+	AGGTTGGAGTGGGAACATGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1146	chr22:41732170-41732225	+	AGGTTGGAGTGGGAACATGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1146	chr22:41732135-41732263	+	AGGTTGGAGTGGGAACATGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1147	chr22:41732170-41732225	+	CAGCTCTCCAGCCCACTTCC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1148	chr6:120216549-120216622	+	TTCGGAAGTACAGCAATAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1148	chr6:120216562-120216613	+	TTCGGAAGTACAGCAATAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1148	chr6:120216534-120216632	+	TTCGGAAGTACAGCAATAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1149	chr6:120216562-120216613	+	TATGCTCTTATCTCAGAGAT	Yes	No	No	0	0	0	0	No
NM_hsa_115	chr3:18429817-184298188	+	AGCTGTGAGTCTGCTGGAACC	Yes	No	No	0	0	0	0	No
NM_hsa_1152	chr2:2935294-2935232	-	AGACACAGAGTCTTAACTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1153	chr1:3588755-35887683	+	TCAATGACACCTTGGATTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1153	chr1:3588791-35887649	+	TCAATGACACCTTGGATTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1153	chr1:3588755-35887683	+	TCAATGACACCTTGGATTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1154	chr1:3588751-35887649	+	AGTTCACAGGACCATATGATA	Yes	No	No	0	0	0	0	No
NM_hsa_1155	chr20:2094889-2094973	+	AAAGAAGTACTTTGAGGCCAG	Yes	No	No	0.113971	0	0	0	No
NM_hsa_1156	chr20:2094889-2094973	+	GGCTCAAAAGTACTTTCTTG	Yes	No	No	0	0	0	0	No
NM_hsa_1157	chr4:80794850-80794921	+	TCTGTGTGAAATCTCTCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1157	chr4:80794840-80794929	+	TCTGTGTGAAATCTCTCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1158	chr4:80794850-80794921	+	TCAGAAAGTCTACACGGATA	Yes	No	No	0	0	0	0	No
NM_hsa_1159	chr19:49957932-49957988	+	TGATGACAGCCCTGGCACAGC	Yes	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_1159	chr19:49957925-49957997	+	TGATGACAGCCCTGGCACAGC	Yes	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_116	chr2:85109645-85109720	+	GGGCCACAGAAAGCCCCCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_116	chr2:85109655-85109713	+	GGGCCACAGAAAGCCCCCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1160	chr19:49957932-49957988	+	AGGAGGCCAGGCAATGATCCAA	Yes	No	No	0	0	0	0	No
NM_hsa_1161	chr1:11586568-11586642	-	TCAGGCTCCCTCCCTCT	Yes	No	No	0.379905	0.0662225	0.171001	0	Yes
NM_hsa_1161	chr1:11586622-11586649	-	TCAGGCTCCCTCCCTCT	Yes	No	No	0.379905	0.0662225	0.171001	0	Yes
NM_hsa_1161	chr1:11586568-11586642	-	GTGGCCAGAGAGCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_1163	chr17:79637501-79637564	+	TTCCCATCAGCCCTCTCAG	Yes	No	No	0	0	0	0	No
NM_hsa_1164	chr17:79637501-79637564	+	GGGAGGGGCTGCGCTGGGAGCC	Yes	No	No	0	0	0	0	No
NM_hsa_1165	chr14:70075944-70076005	+	TACTTTTCTGGCACTTTGG	Yes	Yes	No	0	0.132445	0	0	No
NM_hsa_1165	chr14:70075947-70076011	+	TACTTTTCTGGCACTTTGG	Yes	Yes	No	0	0.132445	0	0	No
NM_hsa_1165	chr14:70075957-70076008	+	TACTTTTCTGGCACTTTGG	Yes	Yes	No	0	0.132445	0	0	No
NM_hsa_1166	chr14:70075957-70076008	+	AAAGTCCACAGAAAGTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1167	chr20:49184677-49184805	+	TGCTTCTGCTGCTGCTGAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1167	chr20:49184712-49184778	+	TGCTTCTGCTGCTGCTGAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1167	chr20:49184712-49184778	+	TGCTTCTGCTGCTGCTGAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1168	chr20:49184712-49184778	+	CACCAGGACAGAGAGGTTGGT	Yes	No	No	0	0	0	0	No
NM_hsa_117	chr2:85109655-85109713	+	CTGGGCTTCTCTGGCCAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_1171	chr17:19882712-19882775	+	TTGTAGAGCAGGTTAAAGAT	Yes	Yes	Yes	0.113971	0	0	0	Yes
NM_hsa_1171	chr17:19882699-19882788	+	TTGTAGAGCAGGTTAAAGAT	Yes	Yes	Yes	0.113971	0	0	0	Yes
NM_hsa_1171	chr17:19882686-19882804	+	TTGTAGAGCAGGTTAAAGAT	Yes	Yes	Yes	0.113971	0	0	0	Yes
NM_hsa_1172	chr17:19882712-19882775	+	CCCTAACTCTCTTCTTCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1173	chr4:129471308-129471370	+	CTACGTGACAGAAAGTTCAG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1173	chr4:129471296-12947373	+	CTACGTGACAGAAAGTTCAG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1174	chr4:129471308-129471370	+	GAAATCTTGGCCCATAGGA	Yes	No	No	0	0	0	0	No
NM_hsa_1175	chrX:49021435-49021492	+	CTGGAAGCCCTTCACTGTAG	Yes	No	No	0	0	0	0	No
NM_hsa_1175	chrX:49021425-49021502	+	CTGGAAGCCCTTCACTGTAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1176	chr9:13209852-13209865	+	CGCTTGTGGGCTGCTCTCT	Yes	No	No	0	0	0	0	No
NM_hsa_1177	chr9:13209852-13209865	+	CACAGCTCTGGGAGTGGAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1177	chr9:13209862-13209865	+	CACAGCTCTGGGAGTGGAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1178	chr9:13209862-13209865	+	CGCCCCAGAGCCTGTGT	Yes	No	No	0	0	0	0	No
NM_hsa_1179	chr2:92820770-92820842	+	CGCCCGTCCAGAGGA	Yes	No	No	0	0	0	0	No
NM_hsa_118	chr3:42912126-42912110	+	TCAGGCTCTGAGCAAGTGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_118	chr3:42912126-42912216	+	TCAGGCTCTGAGCAAGTGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1180	chr2:92820770-92820842	+	TTCCCGCTCCAG	Yes	No	No	0	0	0	0	No
NM_hsa_1183	chr16:4384744-4384804	+	ATGGACGGGGGCTGGGCGAGC	Yes	No	No	0.113971	0.0662225	0	0	No
NM_hsa_1184	chr3:13784448-13784488	+	TACTCTCCCTCCGACCCAGGA	Yes	No	No	0.170957	0	0	0	No
NM_hsa_1185	chr3:13784448-13784454	+	TAGAAGTCTCTCTTCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1185	chr3:13784447-13784453	+	TAGAAGTCTCTCTTCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1186	chr3:13784448-13784454	+	GCTGAGAAAGAGATTCAGG	Yes	No	No	0	0	0	0	No
NM_hsa_1187	chr17:73752443-73752511	+	CGAGGAGGATCCAGCCAGGGTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1187	chr17:73752443-73752511	+	CGAGGAGGATCCAGCCAGGGTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1188	chr17:73752443-73752511	+	GCCCCAACTGATCCCCCGAG	Yes	No	No	0	0	0	0	No
NM_hsa_11											

Name	locus	strand	sequence	midrep2	mirseq	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1230	chr5:43467107-43467171	+	GTCAGTCAAGCTGGAAGGCA	Yes	No	No	0	0	0	0	No
NM_hsa_1231	chr7:3560232-3560242	-	TCATGCTTCATGTCAGAACTG	Yes	Yes	Yes	0.0569857	0.132445	0	0	No
NM_hsa_1231	chr7:35602346-3560247	-	TCATGCTTCATGTCAGAACTG	Yes	Yes	Yes	0.0569857	0.132445	0	0	No
NM_hsa_1231	chr7:35602339-35602417	-	TCATGCTTCATGTCAGAACTG	Yes	Yes	Yes	0.0569857	0.132445	0	0	No
NM_hsa_1232	chr7:35602346-35602407	-	GAGTGCACAACTGAGGATGGAA	Yes	No	No	0	0	0	0	No
NM_hsa_1233	chr5:13904436-13904449	+	AAGTGTGGGCTCTAGAGTTGGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1233	chr5:13904436-13904449	+	AAGTGTGGGCTCTAGAGTTGGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1233	chr5:13904436-139044418	+	AAGTGTGGGCTCTAGAGTTGGG	Yes	Yes	Yes	0.170957	0	0	0	Yes
NM_hsa_1234	chr5:13904436-139044418	+	CACCTCCACTGTCACACTTGC	Yes	No	No	0	0	0	0	Yes
NM_hsa_1235	chr8:18692018-18692089	+	CGCAGCGAGCCGCGAGCTTGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1236	chr8:18692018-18692089	+	CGCAGCTGTCTTCTCTGGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1237	chr4:14262045-14262026	+	CAGCAAGGGCATCGAGCTCTGC	Yes	No	No	0	0	0	0.0732862	Yes
NM_hsa_1238	chr4:14262045-14262026	+	AGGACTGGATCGGCGTGCA	Yes	No	No	0.170957	0	0	0	Yes
NM_hsa_1239	chr4:5209402-5209467	+	AGAAAGTGTCTGAGAGCTGAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_124	chr6:39042096-39042158	+	TTTTTGTGGAAACTTCTGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_124	chr6:39042078-39042169	+	TTTTTGTGGAAACTTCTGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1240	chr4:5209402-5209467	+	CGAGTCTCAGACACTTCTTA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1241	chr22:31459487-31459566	-	TAGGACTCATGCTTGTGCCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1243	chr4:7343950-73434019	+	CCGACTCTGGGCGACGAC	Yes	No	No	0	0	0	0	No
NM_hsa_1244	chr4:7343950-73434019	+	TGCCCCAAAACACTGGCTCAGTT	Yes	No	No	0	0	0	0	Yes
NM_hsa_1245	chr1:17617697-176176878	-	AATCCGGGAATGAGGTG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1246	chr1:17617697-176176878	-	CCACATCCGGAAGCG	Yes	No	No	0	0	0	0	No
NM_hsa_1247	chr3:48471674-48471746	+	AGGGAACCTGGGCTCAGAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1247	chr3:48471664-48471754	+	AGGGAACCTGGGCTCAGAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1248	chr3:48471674-48471746	+	TTCGAGCCAGCACTCCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1249	chr14:33409145-33409209	-	CCGAGCCAGGAGGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_125	chr6:39042096-39042158	+	GGAAATGTTCCAGCAAAAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1250	chr14:33409145-33409209	-	CCCTCCGCTGCCAAA	Yes	No	No	0	0	0	0	No
NM_hsa_1251	chr5:50373014-50373108	+	CCCGATGAGCTCTAGATAG	Yes	No	No	0.113971	0	0	0	No
NM_hsa_1252	chr19:50373014-50373108	+	GGAAAGCAGCCGGGGAT	Yes	No	No	0	0	0	0	No
NM_hsa_1254	chr9:131379970-131380054	+	GGCTATTCAGTAAGGAGGCCCG	Yes	No	No	0	0	0	0	No
NM_hsa_1255	chr16:47708273-47708330	+	CTGAAACCAAACTTCTTTTC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1255	chr16:47708238-47708364	+	CTGAAACCAAACTTCTTTTC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1255	chr16:47708241-47708369	+	CTGAAACCAAACTTCTTTTC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1256	chr16:47708273-47708330	+	AAAATGATCTGGTTTTTCC	Yes	No	No	1.58927	1.83573	1.85665	Yes	H-KapB+KapB+cMyc
NM_hsa_1257	chr1:32378944-32378997	-	ATTGCAATGACTGAACACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1257	chr1:32378944-32378997	-	ATTGCAATGACTGAACACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1257	chr1:32378944-32378997	-	ATTGCAATGACTGAACACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1258	chr1:32378944-32378997	-	AGTTTATGCTGATGCAATT	Yes	No	No	0	0	0	0	No
NM_hsa_1259	chr3:38367136-38367198	+	CTGCATCCAGGCTGCACCTCTG	Yes	No	No	0	0	0	0	No
NM_hsa_126	chr5:13916625-139166307	+	TGATTGTTCCAGGCTGGAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_126	chr5:13916625-139166307	+	TGATTGTTCCAGGCTGGAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1260	chr3:38367136-38367198	+	CAGGCAACTCTGGAGTGCAT	Yes	No	No	0	0	0	0	No
NM_hsa_1265	chr18:48556451-48556457	-	TACAGGGCAGCCAGCC	Yes	No	No	0	0	0	0	No
NM_hsa_1266	chr8:1128992-81129065	+	ATGCTGTAGTCTCTGCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1266	chr8:1129002-81129068	+	ATGCTGTAGTCTCTGCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1267	chr8:1129002-81129068	+	CAGCAAGAGACTGTGGTGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_127	chr5:13916625-139166307	+	TGCCAGGCTGGCCGATGAGACT	Yes	No	No	0	0	0	0	No
NM_hsa_1270	chr1:113424627-113424751	+	TTCAGTCTGGGCTGAAAACCTG	Yes	Yes	No	0.227943	0.26489	0.219899	0	No
NM_hsa_1270	chr1:113424627-113424751	+	TTCAGTCTGGGCTGAAAACCTG	Yes	Yes	No	0.227943	0.26489	0.219899	0	No
NM_hsa_1271	chr1:113424627-113424751	+	GAGGCACTGTTGAGAGCCAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1274	chr16:51272972-51273049	-	CACATGATTTGAGCTGCTTGG	Yes	No	No	33.6282	29.6699	11.975	Yes	KapB+cMyc-KapB-H
NM_hsa_1275	chr16:51272972-51273049	-	CGAGCACTGTCACATGGGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_1276	chr16:27181508-27181589	+	AGCTTAGGAGGCAAGGCTGTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1278	chr22:49144515-49144571	+	CTGGCCCTGAGGCAACTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1279	chr22:49144515-49144571	+	AGGAACCTAGCTGGCCAGG	Yes	No	No	0	0	0	0	No
NM_hsa_128	chr6:158914875-158914957	-	TGAGTGTAGTGGTGTGCTCAG	Yes	No	No	10.3954	7.70178	1.78214	Yes	KapB+cMyc-KapB-H
NM_hsa_1280	chr8:133962238-133962325	+	CTGTGTTCTAAAGGTGGTCCAG	Yes	No	No	0	0	0	0	No
NM_hsa_1281	chr2:225235712-225235792	+	GAAAGCTGTTGAGAATGACAG	Yes	Yes	Yes	0	0.132445	0	0	No
NM_hsa_1282	chr2:225235712-225235792	+	GAAAGCTGTTGAGAATGACAG	Yes	Yes	Yes	0	0.132445	0	0	No
NM_hsa_1282	chr2:225235712-225235792	+	GAAAGCTGTTGAGAATGACAG	Yes	Yes	Yes	0	0.132445	0	0	No
NM_hsa_1283	chr2:225235712-225235792	+	GAAAGCTGTTGAGAATGACAG	Yes	Yes	Yes	0	0.132445	0	0	No
NM_hsa_1284	chr6:33169450-33169518	+	TACTTGCAGTACTCTCCCTCA	Yes	Yes	No	2.50737	1.39067	1.02601	Yes	KapB+cMyc-KapB-H
NM_hsa_1285	chr6:33169450-33169518	+	TACTTGCAGTACTCTCCCTCA	Yes	Yes	No	2.50737	1.39067	1.02601	Yes	KapB+cMyc-KapB-H
NM_hsa_1285	chr6:33169450-33169518	+	TGGAGAGAGAGGCGGTGTTCT	Yes	No	No	0.284929	0.0662225	0.586295	Yes	KapB+cMyc-KapB-H
NM_hsa_1286	chr6:33055799-33055866	+	ACAGAGCTCTGGAGGACAGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1286	chr6:33055799-33055866	+	ACAGAGCTCTGGAGGACAGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1287	chr1:128556313-128556351	+	CATCTCTCTGGGATTTCTTGACA	Yes	No	No	0	0	0	0	No
NM_hsa_1288	chr1:128556313-128556351	+	CCCGGGCAGGCACTGAG	Yes	No	No	0	0	0	0	No
NM_hsa_1289	chr1:128556313-128556351	+	CACCGTCCCTGCC	Yes	No	No	0	0	0	0	No
NM_hsa_129	chr6:158914875-158914957	-	AAGTCAAGACTGGCTGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_1290	chr2:45622834-45622893	+	CTGGCCCTGAGGCAACTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1290	chr2:45622834-45622893	+	CTGGCCCTGAGGCAACTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1291	chr2:45622834-45622893	+	TCAGTAAATCTGTCAGCCGATGC	Yes	No	No	0	0	0	0	No
NM_hsa_1294	chr1:26515033-26515088	+	ACAAAGGCGCTGGAGCTCAGIA	Yes	No	No	0	0	0	0	Yes
NM_hsa_1295	chr1:26515033-26515088	+	TGTGTTCCACTCTGCTCTGCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1296	chr12:14743647-14743785	+	ACTTCTTTGAGCTAGGACTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1296	chr12:14743647-14743785	+	ACTTCTTTGAGCTAGGACTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1296	chr12:14743647-14743785	+	ACTTCTTTGAGCTAGGACTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1297	chr12:14743647-14743785	+	ACTTCTTTGAGCTAGGACTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1298	chr7:75508112-75508179	+	CTACTGGGCTGCTACTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1299	chr7:75508112-75508179	+	GGGGCAACTCCGGTAGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_13	chr1:149900286-149900341	+	TGGATGGATCGGAGCTTAGA	Yes	No	No	0.0569857	0	0	0	Yes
NM_hsa_13	chr1:149900286-149900341	+	TGGATGGATCGGAGCTTAGA	Yes	Yes	No	0.0569857	0	0	0	Yes
NM_hsa_1300	chr6:30710743-30710805	+	ATGGCAACTCTGAGCTCTGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1300	chr6:30710743-30710805	+	ATGGCAACTCTGAGCTCTGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1301	chr6:30710743-30710805	+	AAACCAGCACTGGGCAATGA	Yes	No	No	0	0	0	0	No
NM_hsa_1304	chr1:12601932-12602013	+	TTCCCCAAACTCTGATCCAC	Yes	Yes	Yes	0	0.0662225	0	0	No
NM_hsa_1304	chr1:12601943-12602004	+	TTCCCCAAACTCTGATCCAC	Yes	Yes	Yes	0	0.0662225	0	0	No
NM_hsa_1304	chr1:12601943-12602008	+	TTCCCCAAACTCTGATCCAC	Yes	Yes	Yes	0	0.0662225	0	0	No
NM_hsa_1305	chr1:12601943-12602004	+	TTCCCCAAACTCTGATCCAC	Yes	No	No	0	0	0	0	No
NM_hsa_1306	chr8:46951885-46951943	+	ACTATCTGTGGGATATAGC	Yes	Yes	Yes	2.48363	1.09267	1.16647	Yes	Yes
NM_hsa_1306	chr8:46951864-46951943	+	ACTATCTGTGGGATATAGC	Yes	Yes	Yes	2.48363	1.09267	1.16647	Yes	Yes
NM_hsa_1306	chr8:46951864-46951943	+	ACTATCTGTGGGATATAGC	Yes	Yes	Yes	2.48363	1.09267	1.16647	Yes	Yes
NM_hsa_1307	chr6:16951885-46951943	+	CAGATCCAGCCAGGATATAGG	Yes	Yes	Yes	0	0.0662225	0	0	Yes

Name	locus	strand	sequence	midsep2	mirap	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1354	chr8:7289977-7289713	+	ACCAATTCACAGATCAAGA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1354	chr8:72897021-72897084	+	ACCAATTCACAGATCAAGA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1355	chr8:72897021-72897084	+	TGGTCTGGGTTTGTGGTCC	Yes	No	No	0	0	0	0	
NM_hsa_1356	chr19:58024384-58024431	-	CACGTCCCTGTGGCCGGCCA	Yes	No	No	716.254	518.787	850.78	Yes	
NM_hsa_1357	chr19:58024384-58024431	-	GCTGTGGTTCGGAGTAA	Yes	No	No	0	0	0	0	
NM_hsa_1358	chr11:23242343-23242603	+	TCCAGAGACTGGAGCTGACTG	Yes	Yes	No	0	0	0	0	
NM_hsa_1358	chr11:23242343-23242603	+	TCCAGAGACTGGAGCTGACTG	Yes	Yes	No	0	0	0	0	
NM_hsa_1359	chr11:23242343-23242603	+	AGCCAAGTCAATCTGGACG	Yes	No	No	0	0	0	0	
NM_hsa_136	chr12:49061316-49061376	-	TGGCCCTGAACTCAAGC	Yes	No	No	0	0	0	0	
NM_hsa_1360	chr20:37078093-37078150	+	GCTGAAAGCGTTCCTCCGTTG	Yes	No	No	0	0	0	0	
NM_hsa_1361	chr10:37078093-37078150	+	CTGCGCTTTTCAACATG	Yes	Yes	No	0	0	0	0.0732862	H-KapB-KapB+cMyc
NM_hsa_1366	chr11:116708369-116708428	-	AGCCAGACCTGGCTGCAGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1366	chr11:116708369-116708428	-	AGCCAGACCTGGCTGCAGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1367	chr11:116708369-116708428	-	AGCAGCAACAGGGCCGGGCTGG	Yes	No	No	0	0	0	0	
NM_hsa_1368	chr11:126279097-126279155	+	TGGTGTGGATTTGAAGAACGG	Yes	Yes	No	0	0	0	0	
NM_hsa_1369	chr11:126279097-126279155	+	TGCTCTCTCTTGACCCCAT	Yes	No	No	0	0	0	0	
NM_hsa_137	chr12:49061316-49061376	-	TTCAGCAGAGCACTAA	Yes	No	No	0	0	0	0	
NM_hsa_1370	chr11:1075844-1075926	+	GATCCAGGTTGATCTGCTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1370	chr11:1075844-1075926	+	GATCCAGGTTGATCTGCTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1371	chr11:1075855-1075917	+	ATGCTCAGCTGGAACTC	Yes	No	No	0	0	0	0	
NM_hsa_1372	chr17:7754259-7754340	-	CTGCTGGCCCTCCTCCAGA	Yes	No	No	0	0	0	0.0732862	No
NM_hsa_1373	chr17:7754259-7754340	-	AGGAAGGAAAGAGCTGATGGG	Yes	No	No	0	0	0	0	
NM_hsa_1374	chr19:3550073-35500793	+	TCACCTCTCAAACTCTCTAGA	Yes	No	No	0.170957	0.0662225	0	Yes	KapB+cMyc-KapB-H
NM_hsa_1375	chr19:3550073-35500793	+	TGGGAGCAAGTTGGAGCTGA	Yes	No	No	0	0	0	0	
NM_hsa_1376	chr19:4058540-4058595	-	CTGGGGCCCGGAGTAC	Yes	No	No	0	0	0	0	
NM_hsa_1383	chr13:53029459-53029516	-	CGGTGGGACTGAGCTG	Yes	No	No	0	0	0	0	
NM_hsa_1384	chr13:53029459-53029516	-	GACTCAGTTGCGGGCCGGT	Yes	No	No	0	0	0	0	
NM_hsa_1385	chr16:6626064-66260782	+	YACTCTCTGACTGCTGAGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1385	chr16:6626064-66260782	+	YACTCTCTGACTGCTGAGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1385	chr16:6626064-66260782	+	TTCCCATCTGACACTGGTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1385	chr16:6626064-66260782	+	TTCCCATCTGACACTGGTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1386	chr12:6626093-66260743	+	TGCTGCTCAAGTAGGAAACA	Yes	No	No	0	0	0	0	
NM_hsa_1387	chr11:5422322-54223316	+	TAACCCAGAGCTGGAGTTGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_139	chr17:175636912-175637028	+	TAAAGTAACTGGTGGTGGT	Yes	Yes	No	0	0	0	0	
NM_hsa_139	chr17:175636912-175637028	+	TAAAGTAACTGGTGGTGGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1391	chr6:30854247-30854307	-	ACCCAGAGCTGAAGCAG	Yes	No	No	0	0	0	0	
NM_hsa_1392	chr6:30854247-30854307	-	CCCAATGACATAGGACAG	Yes	No	No	0	0	0	0	
NM_hsa_1397	chr12:2785651-27856679	+	TGTGGTAGACTTGGCATCG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1397	chr12:2785651-27856679	+	TGTGGTAGACTTGGCATCG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1397	chr12:2785651-27856679	+	TGTGGTAGACTTGGCATCG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1397	chr12:2785651-27856679	+	TGTGGTAGACTTGGCATCG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1398	chr12:2785651-27856679	+	ATGCCAGGCCCAACCCAGC	Yes	No	No	0	0	0	0	
NM_hsa_1399	chr9:12800393-12800392	+	CGCTTAGGGGCTCGGAGTCTG	Yes	No	No	0	0	0	0	
NM_hsa_14	chr14:4990206-4990341	+	TAGAAGCTCTGGCCATCG	Yes	Yes	No	0.0569857	0.0569857	0	Yes	
NM_hsa_14	chr14:4990206-4990341	+	TAGAAGCTCTGGCCATCG	Yes	Yes	No	0.0569857	0.0569857	0	Yes	
NM_hsa_1400	chr9:12800393-12800392	+	CTTCAAGCCGAGGATTTCCG	Yes	No	No	0	0	0	0	
NM_hsa_1401	chr22:25509168-25509240	+	CTCTGACTCCCACTCACGGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1401	chr22:25509168-25509240	+	CTCTGACTCCCACTCACGGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1402	chr22:25509168-25509231	+	CACAGTGGTAGTGGCAGAGCC	Yes	No	No	0.0569857	0.0569857	0	0	
NM_hsa_1403	chr22:114030814-114030897	+	CTGCCAGCCGGAGGAGGATG	Yes	No	No	0	0	0	0	
NM_hsa_1404	chr22:114030814-114030897	+	CTGCCAGCCGGAGGAGGATG	Yes	No	No	0	0	0	0	
NM_hsa_1405	chr11:60040796-60040879	+	GTCCAGAGACTCTGTGCAT	Yes	Yes	No	0	0	0	0	
NM_hsa_1405	chr11:60040796-60040879	+	GTCCAGAGACTCTGTGCAT	Yes	Yes	No	0	0	0	0	
NM_hsa_1406	chr11:60040796-60040879	+	GTAGCAGAGCTCTGGGAGAT	Yes	No	No	0	0	0	0	
NM_hsa_141	chr14:70449634-70449701	+	CCGCCTCCCAAGCCTGGAAT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_141	chr14:70449634-70449701	+	CCGCCTCCCAAGCCTGGAAT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1411	chr19:41316684-41316761	+	GCTCGCTGCTGAGCACTG	Yes	Yes	No	0	0	0	0	
NM_hsa_1411	chr19:41316684-41316761	+	GCTCGCTGCTGAGCACTG	Yes	Yes	No	0	0	0	0	
NM_hsa_1412	chr19:41316677-41316730	+	CCGTCACCAAGCAAGTCTGT	Yes	No	No	0	0	0	0	
NM_hsa_1413	chr17:61904846-61904939	+	GCTTGACGACACAGAGCAG	Yes	Yes	No	0	0	0	0	
NM_hsa_1413	chr17:61904846-61904939	+	GCTTGACGACACAGAGCAG	Yes	Yes	No	0	0	0	0	
NM_hsa_1414	chr17:61904846-61904932	+	CTGTGGTGGTGGAGGAGCT	Yes	Yes	No	0	0	0	0	
NM_hsa_1417	chr20:2520536-2520601	+	AGGAGTGGCTAAGAACTCCG	Yes	No	No	0	0	0	0	
NM_hsa_1418	chr20:2520536-2520601	+	AGGAGTGGCTAAGAACTCCG	Yes	No	No	0	0	0	0	
NM_hsa_1419	chr13:9921898-99219023	+	TAGTGGAAAGACTGAGCTCTG	Yes	Yes	No	0.227943	0.366431	0.366431	Yes	
NM_hsa_1419	chr13:9921898-99219023	+	TAGTGGAAAGACTGAGCTCTG	Yes	Yes	No	0.227943	0.366431	0.366431	Yes	
NM_hsa_142	chr14:70449634-70449701	+	TCCAAGCTGAAGAGGACGCT	Yes	No	No	0	0	0	0	Yes
NM_hsa_1420	chr13:99218947-99219010	+	GAGGTTTCTTCCCACTGCT	Yes	No	No	0	0	0	0	0
NM_hsa_1421	chr20:61899865-61899921	-	TCAAGTCCCGTGTGAACAG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1421	chr20:61899865-61899921	-	TCAAGTCCCGTGTGAACAG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1421	chr20:61899865-61899921	-	TCAAGTCCCGTGTGAACAG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1422	chr20:61899865-61899921	-	CATTCCCGGCTGCTTAAT	Yes	No	No	0	0	0	0	0
NM_hsa_1422	chr20:61899865-61899921	-	CATTCCCGGCTGCTTAAT	Yes	No	No	0	0	0	0	0
NM_hsa_1423	chr14:10282804-102828123	-	ATCTGTTACTTTGCAACAGC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1423	chr14:10282804-102828123	-	ATCTGTTACTTTGCAACAGC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1423	chr14:10282805-102828125	-	ATCTGTTACTTTGCAACAGC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1424	chr14:10282804-102828113	-	TGTTGCAAAAGTATGGCAATT	Yes	No	No	0	0	0	0	0
NM_hsa_1425	chr12:6980771-6980813	-	GGGCTGTAGAGTGGAGGCG	Yes	No	No	0	0	0	0	0
NM_hsa_1426	chr12:6980771-6980813	-	GGGCTGTAGAGTGGAGGCG	Yes	No	No	0	0	0	0	0
NM_hsa_1427	chr5:40798552-40798623	-	CTCTCCACTGAGCCCA	Yes	No	No	0	0	0	0	0
NM_hsa_1428	chr5:40798552-40798623	-	AAGTATGAGCCGAGCT	Yes	No	No	0	0	0	0.0732862	No
NM_hsa_1429	chr5:40798552-40798623	-	TGCCCGTGGATCTCC	Yes	No	No	0	0	0	0	0
NM_hsa_1429	chr5:40798552-40798623	-	TGCCCGTGGATCTCC	Yes	No	No	0	0	0	0	0
NM_hsa_1429	chr5:40798552-40798623	-	CACGCCAGGCTGGGAGCTG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1429	chr5:40798552-40798623	-	CACGCCAGGCTGGGAGCTG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1430	chr13:11214185-11214257	-	CCAGCCAGGCTGGGAGCTG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1431	chr5:175962811-175962880	+	CCGCTCCCGCTGGGAGCTG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1431	chr5:175962811-175962880	+	CCGCTCCCGCTGGGAGCTG	Yes	Yes	No	0	0	0	0	0
NM_hsa_1432	chr5:175962811-175962871	+	CCGCTCCCGCTGGGAGCTG	Yes	No	No	0	0	0	0	0
NM_hsa_1433	chr7:98617335-98617399	-	ACATCAGAGCCAGACTGTGT	Yes	No	No	0	0	0	0	0
NM_hsa_1434	chr7:98617335-98617399	-	ACATCAGAGCCAGACTGTGT	Yes	No	No	0	0	0	0	0
NM_hsa_1435	chr17:41409255-41409387	+	TACTGCTGAAGTCTGGAACATC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1435	chr17:41409255-41409387	+	TACTGCTGAAGTCTGGAACATC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1435	chr17:41409255-41409387	+	TACTGCTGAAGTCTGGAACATC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1436	chr17:41409255-41409387	+	TACTGCTGAAGTCTGGAACATC	Yes	Yes	Yes	0	0	0	0	0
NM_hsa_1437	chr11:109983414-109983497	+	CCAAAGGAGCTGCAAGTGTGA	Yes	Yes	No	0.113971	0.113971	0	Yes	
NM_hsa_1437	chr11:109983414-109983497	+	CCAAAGGAGCTGCAAGTGTGA	Yes	Yes	No	0.113971	0.113971	0	Yes	
NM_hsa_1438	chr11:109983427-109983488	+									

Name	locus	strand	sequence	midsep2	miranep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1496	chr3:133467577-133467661	+	TTTGTCTTCCACAGCAGATAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1497	chr1:23347592-1334762	+	AAATGTTCTGGAAAGAAAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_15	chr14:101506177-101506246	+	AGTCGGTGGCTCAGCAATCATGT	Yes	Yes	No	0.170957	0	0	0	No
NM_hsa_15	chr14:101506187-101506246	+	AGTCGGTGGCTCAGCAATCATGT	Yes	Yes	No	0.170957	0	0	0	No
NM_hsa_1500	chr7:1731872-1731930	+	ATTGCCAGAGGGTCTGTGATGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1500	chr7:1731898-1731984	+	ATTGCCAGAGGGTCTGTGATGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1501	chr7:1731872-1731930	+	CTCTCGAGGTTGTAGGCTCG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1502	chr17:33760236-33760295	+	CACACTCCCAAGCGGGCTGCTG	Yes	No	No	0.0569857	0	0	0.463558	0 Yes
NM_hsa_1503	chr17:33760236-33760295	+	AGCTGGGGCTCCGGAAGTGTCCG	Yes	No	No	0	0	0	0	No
NM_hsa_1504	chr16:78088162-78088233	+	ACTGACATCTCCAGGAAGTATG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1504	chr16:78088172-78088225	+	ACTGACATCTCCAGGAAGTATG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1505	chr16:78088172-78088225	+	GTCTTCCCAAGATGTCAGTTA	Yes	No	No	0	0	0	0	No
NM_hsa_1507	chr17:41363861-41363932	+	GAGTCAAGCTTGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_1508	chr20:37053929-37053969	-	GAAAGTGTCTGGGGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_1509	chr20:37053929-37053969	-	TCGCCGTGCTGATGATG	Yes	No	No	0	0	0	0	No
NM_hsa_1510	chr14:36278435-36278481	+	CTCTCGAGGTTGTAGGCTCG	Yes	Yes	No	0	0	0	0.0732862	No
NM_hsa_1510	chr14:36278435-36278481	+	CTCTCGAGGTTGTAGGCTCG	Yes	Yes	No	0	0	0	0.0732862	No
NM_hsa_1511	chr14:36278435-36278481	-	AGCTTCAACCTTAAAGGGGG	Yes	No	No	0	0	0	0	No
NM_hsa_1512	chr2:112109376-112109459	+	ATCCAGGTAACAGGTTGTATTAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1512	chr2:112109376-112109459	+	ATCCAGGTAACAGGTTGTATTAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1512	chr2:112109369-112109469	+	ATCCAGGTAACAGGTTGTATTAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1513	chr2:112109390-112109450	+	TGGCAGATCTGGATCCGGTAA	Yes	No	No	0	0	0	0	No
NM_hsa_1516	chr5:167517512-167517566	+	TGCTCATGATGATGACTCTCT	Yes	Yes	No	0	0	0	0	0 Yes
NM_hsa_1516	chr5:167517499-167517575	+	TGCTCATGATGATGACTCTCT	Yes	Yes	No	0	0	0	0	0 Yes
NM_hsa_1517	chr5:167517512-167517566	+	AAAGTAACAGGTTATGGGACAG	Yes	No	No	0	0	0	0	No
NM_hsa_1518	chr1:144984098-144984167	-	ATTCTTAGGACGATGACG	Yes	No	No	0	0	0	0	No
NM_hsa_1519	chr1:144984098-144984167	-	TACCAGGTAACCGGGATTA	Yes	No	No	0	0	0	0	No
NM_hsa_152	chr9:116310598-116310649	+	CAGCTGTGGGGTGTAAATGGA	Yes	No	No	0.0662225	0	0	0	No
NM_hsa_1520	chr10:8073862-18073783	+	TTAGGTTCTGGCTGGACTGTA	Yes	No	No	102.717	70.6594	0	40.3441	KapB+cMye+Kap-B-H
NM_hsa_1521	chr1:18073682-18073757	+	AAAAACAGGCAAAACAGATGAAT	Yes	No	No	0	0	0	0	No
NM_hsa_1526	chr3:184454966-184455062	+	TTCAGGTAACAGGCTGACAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1526	chr3:184455030-184455093	+	TTCAGGTAACAGGCTGACAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1527	chr3:184500180-18450093	+	CTCTCTAGCAAGGATCTGACAG	Yes	No	No	0	0	0	0	No
NM_hsa_1528	chr9:84706186-84706257	+	CAGTGAGCCAGCTGAGGATGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1528	chr9:84706186-84706264	+	CAGTGAGCCAGCTGAGGATGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1529	chr9:84706186-84706257	+	CAGCCCTCAATGAGCTCAGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_153	chr9:116310598-116310649	+	GAAAGCAGCTCAGTATGGCC	Yes	No	No	0	0	0	0	No
NM_hsa_1530	chr12:123193895-123193957	+	CCAGAAATCTGGTATGCCAGC	Yes	No	Yes	0	0	0	0	No
NM_hsa_1530	chr12:123193874-123193982	+	CCAGAAATCTGGTATGCCAGC	Yes	No	Yes	0	0	0	0	No
NM_hsa_1530	chr12:123180470-123180532	+	CCAGAAATCTGGTATGCCAGC	Yes	No	Yes	0	0	0	0	No
NM_hsa_1530	chr12:123180449-123180557	+	CCAGAAATCTGGTATGCCAGC	Yes	No	Yes	0	0	0	0	No
NM_hsa_1531	chr12:123193895-123193957	+	TGACAGCCAGCTCTGGCTGT	Yes	No	No	0	0	0	0	No
NM_hsa_1531	chr12:123180470-123180532	+	TGACAGCCAGCTCTGGCTGT	Yes	No	No	0	0	0	0	No
NM_hsa_1532	chr2:69402666-69402750	+	AGCCAGAAAGCTGGAATCGAG	Yes	Yes	No	0	0	0	0	0 Yes
NM_hsa_1534	chrX:36124372-36124449	+	AGATTGCTCTTGGACTAATAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1534	chrX:36124382-36124441	+	AGATTGCTCTTGGACTAATAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1535	chr16:156924088-156924168	+	AATTAACAGCAAGCAATCTTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1536	chr5:156924088-156924168	+	TCCTCTAATCTTGGCTCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1536	chr5:156924097-156924151	-	TCCTCTAATCTTGGCTCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1537	chr5:156924097-156924151	-	GGGTTGAGGCTGGGAGGAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1538	chr3:105289190-105289244	+	AAATTCAGATCTGGGAATGAG	Yes	No	No	0	0	0	0	0 Yes
NM_hsa_1539	chr3:105289190-105289244	+	AGTTCAGAAATCTGAAATTTG	Yes	No	No	0	0	0	0	No
NM_hsa_154	chr14:19318900-19319070	+	TTCTGGAATCTGTGGAGGG	Yes	No	No	0.0854786	0	0	0	0 Yes
NM_hsa_1540	chr13:110218012-110218076	-	TGAGACTCTTCCCTCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1541	chr13:110218012-110218076	-	TGAGAGGAGGGGACGACAG	Yes	No	No	0	0	0	0	No
NM_hsa_1542	chr6:46030731-46030801	+	TAAAGACTTTGAAAAGACAGCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1543	chr6:46030731-46030801	+	TGCTTTTGAAGTCTTTAT	Yes	No	No	0	0	0	0	No
NM_hsa_1544	chr5:114753411-114753498	+	TGGAGTGGAAACATATATAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1544	chr5:114753421-114753491	+	TGGAGTGGAAACATATATAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1545	chr5:114753421-114753491	+	ATCATATGCTCCAGTCCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_1548	chr7:50570219-50570283	+	CTCAGCTCTGAGTCAAGGATG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1549	chr7:50570219-50570283	+	TGAGGCTGATGAGTGTGACAGT	Yes	No	No	0	0	0	0	No
NM_hsa_155	chr15:19318900-19319070	+	CAAGAGCAGTGTGTGAAAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1552	chr15:91416192-91416261	-	ACTCTGTCCAGGCTGTGGC	Yes	No	No	0	0	0	0	No
NM_hsa_1553	chr15:91416192-91416261	-	TGTTCTTGGGCAAGGCC	Yes	No	No	0	0	0	0	No
NM_hsa_1554	chr12:226995009-226995070	+	CAGGGCTGAGGTCGGGAGGGA	Yes	No	No	0.0569857	0	0	0	No
NM_hsa_1555	chr12:226995009-226995070	+	GCTGCTGTGCAAGCTCAGCTTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1556	chr5:135314906-135314960	+	TACACAGCAAAAAGACATCA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1556	chr5:135314897-135314972	+	TACACAGCAAAAAGACATCA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1557	chr5:135314906-135314960	+	ATGCCCTTTATCTGGTAT	Yes	No	No	0	0	0	0	No
NM_hsa_1558	chr4:70075954-70076005	+	AAAGTGCACAGAAAAGTATT	Yes	No	No	0	0	0	0	No
NM_hsa_1559	chr4:160229023-160229118	+	AGCCCAAGGTTCTGAGAGGAG	Yes	Yes	No	0.198868	0	0	0.198868	0 Yes
NM_hsa_1559	chr4:160229043-160229108	+	AGCCCAAGGTTCTGAGAGGAG	Yes	Yes	No	0	0	0	0	0 Yes
NM_hsa_1560	chr4:160229023-160229108	+	GCACTCCAGCTTGGGGCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1561	chr12:101694587-101694655	+	ACTGTATGATCTTGGGACAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1561	chr12:101694574-101694644	+	ACTGTATGATCTTGGGACAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1562	chr12:101694587-101694655	+	CTCCAGCAATGCAAGTCTGTGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1563	chr14:69952747-69952808	+	TGGTATGGCTGGGAATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1563	chr14:69952736-69952817	+	TGGTATGGCTGGGAATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1563	chr14:69952712-69952842	+	TGGTATGGCTGGGAATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1564	chr14:69952712-69952842	+	TGCACTCTCCAGCTATTTCAAGT	Yes	No	No	0	0	0	0	No
NM_hsa_1565	chr9:112857459-112857512	+	TAGGAAACAAGGACTGCCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1566	chr9:112857459-112857512	+	CAGCAGTCTCTTGGCCCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_1567	chr5:14008155-14008197	+	GTCTACATCTGTGCTTACTG	Yes	No	No	0.113971	0.198868	0	0	0 No
NM_hsa_1568	chr5:14008155-14008197	+	GGGACAGATATGCTCCAAAG	Yes	No	No	0	0	0	0	No
NM_hsa_157	chr14:9458242-94582805	+	GCATCTCCATCTCTCCATCT	Yes	No	No	0	0	0	0	No
NM_hsa_1571	chr3:167452996-167453075	+	GGGCTGTCCGGCTGAGTATG	Yes	No	No	0	0	0	0	No
NM_hsa_1572	chr3:167452996-167453075	+	GGGGCGGGCTGACAGGACAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1573	chr17:38478846-38478929	+	GAGGAGGAGCTGAGGACTG	Yes	No	No	0	0	0	0	No
NM_hsa_1574	chr17:38478846-38478929	+	GCTTCTCTTCTCAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1575	chr16:15781178-15781233	+	CTCTGTTTTCTTCCGACG	Yes	No	No	0	0	0	0	No
NM_hsa_1576	chr16:15781178-15781233	+	TGGAGGGATGCTGGGGTTTG	Yes	No	No	0	0	0	0	No
NM_hsa_1579	chr16:18189384-18189522	+	GCCTTGAAGTGTGAGTCCACC	Yes	Yes	Yes	0	0	0	0	0 No
NM_hsa_1579	chr16:18189414-18189488	+	GCCTTGAAGTGTGAGTCCACC	Yes	Yes	Yes	0	0	0	0	0 No
NM_hsa_1579	chr16:18189423-18189488	+	GCCTTGAAGTGTGAGTCCACC	Yes	Yes	Yes	0	0	0	0	0 No
NM_hsa_1579	chr16:15277821-15277878	+	GCCTTGAAGTGTGAGTCCACC	Yes	Yes	Yes	0	0	0	0	0 No
NM_hsa_1579	chr16:15277782-15277920										

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1637	chr10:112064848-112064899	+	TCGCCAGCCGGGATTCACGG	Yes	No	No	0	0	0	0	
NM_hsa_1638	chr11:12064848-112064899	+	TGCGTTCGGCTGGGAATTT	Yes	No	No	0	0	0	0	
NM_hsa_1639	chr1:123140055-231400615	+	TCATGTTCCTGGCTGTGG	Yes	Yes	No	0	0	0	0	
NM_hsa_1639	chr1:231400543-231400624	+	TCATGTTCCTGGCTGTGG	Yes	Yes	No	0	0	0	0	
NM_hsa_1640	chr1:231400555-231400615	+	AGCAGCATGGCTAAAGACA	Yes	No	No	0	0	0	0	
NM_hsa_1647	chr9:92262506-92262591	+	AAGAAGATCTGTGTCTCGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1647	chr9:92262520-92262582	+	AAGAAGATCTGTGTCTCGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1648	chr9:92262520-92262582	+	GTGATCAAAAGGCTCTTTG	Yes	No	No	0	0	0	0	
NM_hsa_1649	chr3:160118979-160119035	-	TGGAATTTTGTGTGACCTG	Yes	Yes	No	0	0.049669	0.0732862	No	H-KapB-KapB-cMye
NM_hsa_1649	chr3:160118972-160119045	-	TGGAATTTTGTGTGACCTG	Yes	Yes	No	0	0.049669	0.0732862	No	H-KapB-KapB-cMye
NM_hsa_1650	chr1:160118979-160119035	-	GTGATCAAAAGGCTCTTTG	Yes	Yes	No	0	0	0	0	
NM_hsa_1651	chrX:2803667-2803793	+	TATCCTTTTCAGGGCTGAAC	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1651	chrX:28036692-28036769	+	TATCCTTTTCAGGGCTGAAC	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1651	chrX:28036702-28036761	+	TATCCTTTTCAGGGCTGAAC	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1652	chrX:28036702-28036761	+	TCAGACTAAAAGGATAACT	Yes	No	No	0	0	0	0	
NM_hsa_1659	chr16:23992370-23992485	+	CACCTCTCGCTTCTCCGGG	Yes	No	No	0	0	0	0	
NM_hsa_166	chr6:53141798-53141859	-	CGTGATAACTGCTGGGCTGT	Yes	Yes	No	0	0	0	0	
NM_hsa_166	chr6:53141789-53141871	-	CGTGATAACTGCTGGGCTGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1660	chr16:29923270-29923425	-	GGGGGAGTACAGTGGCTTTGGT	Yes	No	No	0	0	0	0	
NM_hsa_1661	chr14:23447386-23447450	+	GGGATCAACACTGCTCTGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1661	chr14:23447398-23447450	+	GGGATCAACACTGCTCTGT	Yes	Yes	No	0	0	0	0	
NM_hsa_1662	chr14:23447398-23447450	+	AGGAGCAGCTCGGACCTCA	Yes	No	No	0	0	0	0.0732862	No
NM_hsa_1663	chr19:35652401-35652451	+	TCTCATTTGGTTCAGCTGGAT	Yes	No	No	0	0	0	0	
NM_hsa_1664	chrX:3733961-37334013	+	TCTGAGCTCTGATCTAGTA	Yes	No	No	0.170957	0.176953	0.146572	Yes	
NM_hsa_1665	chr3:7333961-87334013	+	CTAGAGTTAGAGTGGAGC	Yes	No	No	0	0	0	0	
NM_hsa_1666	chr9:119179666-119179733	+	CTTGGACTCTGATTTTTCG	Yes	No	No	0	0	0	0	
NM_hsa_1667	chr9:119179666-119179733	+	AGAAAACACAGTCTGGCCG	Yes	No	No	0	0	0	0	
NM_hsa_1668	chrX:2449813-24498180	+	CCCGCTGACTGCTTACCACCT	Yes	Yes	No	0	0	0	0	
NM_hsa_1668	chrX:2449813-24498173	+	CCCGCTGACTGCTTACCACCT	Yes	Yes	No	0	0	0	0	
NM_hsa_1669	chrX:24498113-24498173	+	GTAGGTGAGGATTTGGCCCA	Yes	No	No	0	0	0	0	
NM_hsa_167	chr6:53141798-53141859	-	CAGCCCTGAGTATCACGGC	Yes	No	No	0	0	0	0	
NM_hsa_1670	chr16:31711876-31711952	+	CGCCTCCCTGCTGATCTG	Yes	No	No	0	0	0	0	
NM_hsa_1671	chr16:31711876-31711952	+	CGCGAAAAGGGGGCCGAC	Yes	No	No	0	0	0	0	
NM_hsa_1672	chr2:48925131-48925196	+	CGTGTGAGTCAACAGCACG	Yes	No	No	0	0	0	0	
NM_hsa_1673	chr20:48925131-48925196	+	CGAGGTGGTCAAGGAGAGGGA	Yes	No	No	0	0	0	0	
NM_hsa_1674	chrX:14485447-14485505	+	AATGCACTGATGAGTACT	Yes	Yes	No	0	0	0	0	
NM_hsa_1674	chrX:14485437-14485512	+	AATGCACTGATGAGTACT	Yes	Yes	No	0	0	0	0	
NM_hsa_1675	chrX:14485447-14485505	+	TACTATGAGTCTGCACTTC	Yes	No	No	0	0	0	0	
NM_hsa_1676	chr10:124169916-124169961	+	TGATTTTCAATGGCAAGTGG	Yes	No	No	0	0	0	0	
NM_hsa_1677	chr10:124169916-124169961	+	AACTGCCAGTGAATCACT	Yes	No	No	0	0	0	0	
NM_hsa_1678	chr3:50293915-50293974	+	TCTCGCTGATGCTGGTCAG	Yes	No	No	0	0	0	0	
NM_hsa_1679	chr3:50293915-50293974	+	CCACCCAGCTCTGCGAGCTCG	Yes	No	No	0	0	0	0	
NM_hsa_168	chr12:8202665-28202719	+	TTTGTAGCTGTACATAAGGGA	Yes	No	Yes	0	0	0	0	
NM_hsa_168	chr12:8202668-28202722	+	TTTGTAGCTGTACATAAGGGA	Yes	No	Yes	0	0	0	0	
NM_hsa_1680	chr10:6018981-6019043	+	CGCGTCCACAGCTTTGG	Yes	No	No	0	0	0	0	
NM_hsa_1681	chr15:75644307-75644383	+	TTTCTCCCTGGACCAGCA	Yes	Yes	No	0	0	0	0	
NM_hsa_1681	chr15:75644318-75644374	+	TTTCTCCCTGGACCAGCA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1681	chr15:75644300-75644388	+	TTTCTCCCTGGACCAGCA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1682	chr15:75644318-75644374	+	CGGGGGCAGGAGGAGGAACT	Yes	No	No	0	0.0732862	No	0	
NM_hsa_1685	chr11:61915507-61915569	+	TCATGAGCCAGTGTGTGGGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1685	chr11:61915407-61915573	+	TCATGAGCCAGTGTGTGGGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1686	chr11:61915507-61915569	+	CACAGCTCTGTTCTCATCT	Yes	No	No	0	0	0	0	
NM_hsa_1687	chr12:45449551-245449615	+	TTGGGAGCCAGTCACTTT	Yes	Yes	No	0	0	0	0	
NM_hsa_1688	chr12:45449551-245449615	+	TTGGGAGCCAGTCACTTT	Yes	Yes	No	0	0	0	0	
NM_hsa_1689	chr12:8202665-28202719	+	ACTGAGTGGTGTGGTGGCTCA	Yes	No	No	0	0	0	0	
NM_hsa_169	chr12:8202668-28202722	+	CCTTAGTGTACAGTCAAAAAT	Yes	No	No	0	0	0	0	
NM_hsa_1691	chr22:31560503-3156106	+	CGGAACCTAGAGCTCAAGC	Yes	Yes	No	0	0	0	0	
NM_hsa_1691	chr22:31560523-3156115	+	CGGAACCTAGAGCTCAAGC	Yes	Yes	No	0	0	0	0	
NM_hsa_1692	chr22:31560503-3156106	+	CGAAAGCTCAAGGCTCTG	Yes	No	No	0	0	0	0	
NM_hsa_1693	chr12:58388745-58388825	+	GATGCTGGGATTTGCCATCTG	Yes	No	No	2.67833	2.09705	2.36959	Yes	
NM_hsa_1694	chr12:58388745-58388825	+	AAGTGGCAGTCTTTTTTCT	Yes	No	No	0	0	0	0	
NM_hsa_1695	chr5:96271113-96271165	+	CTCTGCCAAAACACCTA	Yes	No	No	0	0	0	0	
NM_hsa_1696	chr11:119196271-9627165	+	CTCTGCCAAAACACCTA	Yes	No	No	0	0	0	0	
NM_hsa_1699	chr3:28282843-28282906	-	AAAGTCCAGCCCGCTC	Yes	No	No	0	0	0	0	
NM_hsa_170	chr8:127876737-127876873	-	TTTCTGAGTTCAGTCCAGG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_170	chr8:127876762-127876844	-	TTTCTGAGTTCAGTCCAGG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_170	chr8:127876762-127876833	-	TTTCTGAGTTCAGTCCAGG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_170	chr8:127876732-127876868	-	TTTCTGAGTTCAGTCCAGG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_170	chr8:127876732-127876836	-	TTTCTGAGTTCAGTCCAGG	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1700	chr2:76414851-76414910	+	TGAACTCTGATTTCACTGTT	Yes	Yes	No	0	0	0	0	
NM_hsa_1700	chr2:76414838-76414919	+	TGAACTCTGATTTCACTGTT	Yes	Yes	No	0	0	0	0	
NM_hsa_1701	chr2:76414851-76414910	+	AGGATGCAAAAGAGATTCATC	Yes	No	No	0	0	0	0	
NM_hsa_1702	chr19:18182978-91853032	+	GGCCCGCTTCAAGCTCTGT	Yes	No	No	0	0	0	0	
NM_hsa_1703	chr19:18182978-91853032	+	AGATCAAGGCACTTT	Yes	No	No	0	0	0	0	
NM_hsa_1704	chr5:138614607-138614669	+	TTTTCAGCTTCAGAGTGGAAATG	Yes	Yes	No	0.569857	0.26489	0.293145	Yes	
NM_hsa_1704	chr5:138614597-138614678	+	TTTTCAGCTTCAGAGTGGAAATG	Yes	Yes	No	0.569857	0.26489	0.293145	Yes	
NM_hsa_1705	chr5:138614607-138614669	+	TCTAGTCTGGTCAAAACAT	Yes	Yes	No	0	0	0	0	
NM_hsa_1705	chr5:138614597-138614678	+	TCTAGTCTGGTCAAAACAT	Yes	Yes	No	0	0	0	0	
NM_hsa_1706	chr1:94703309-94703351	+	GGGCTGGCTGGCTGCC	Yes	No	No	0	0	0	0	
NM_hsa_1707	chr22:30178248-30178315	+	CAGCCGAGACCCGGAGTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1707	chr22:30178236-30178322	+	CAGCCGAGACCCGGAGTGA	Yes	Yes	No	0	0	0	0	
NM_hsa_1708	chr22:30178248-30178315	+	CAGCCCGGCTCCCTGGGG	Yes	No	No	0	0	0	0	
NM_hsa_1709	chr6:27445250-27445302	-	AACTCAGATCCGAGGAGAGA	Yes	No	No	0	0	0	0	
NM_hsa_171	chr8:127876762-127876833	-	TGGGATCGAATCAGAAACT	Yes	No	No	0	0	0	0	
NM_hsa_171	chr8:127876732-127876836	-	TGGGATCGAATCAGAAACT	Yes	No	No	0	0	0	0	
NM_hsa_1710	chr6:27445250-27445302	-	TCTCGGAATCTGTAA	Yes	No	No	0	0	0	0	
NM_hsa_1711	chr8:8364894-8364964	-	AACTGGGCACTGTGAACTAAGC	Yes	Yes	No	0.151962	0.097715	0.097715	Yes	
NM_hsa_1711	chr8:8364894-8364974	-	AACTGGGCACTGTGAACTAAGC	Yes	Yes	No	0.151962	0.097715	0.097715	Yes	
NM_hsa_1711	chr4:7087114-7087177	+	AACTGGGCACTGTGAACTAAGC	Yes	Yes	No	0.151962	0.097715	0.097715	Yes	
NM_hsa_1712	chr3:13626901-8364964	-	TGATCTTCAATGGCCAGAGAT	Yes	No	No	0	0	0	0	
NM_hsa_1713	chr9:13166262-131662722	+	GATGCTGGCCCACTCAAGCA	Yes	No	No	0.3989	0.0662225	0	No	KapB-cMye-KapB-H
NM_hsa_1714	chr9:13166262-131662722	+	AGCATTTGGGGCTGGACGATGGC	Yes	No	No	0	0	0	0	
NM_hsa_1716	chr11:159895212-159895284	+	CAGTTCGGGGTACGGGGTGTG	Yes	No	No	0	0	0	0	
NM_hsa_1717	chr17:42344313-42344398	+	TTTGGGATTTCAAGGAGAA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1717	chr17:42344313-42344398	+	TTTGGGATTTCAAGGAGAA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1717	chr17:42344317-42344403	+	TTTGGGATTTCAAGGAGAA	Yes	Yes	Yes	0	0	0	0	
NM_hsa_1718	chr17:42344333-42344389	+	AACCTTAGATCCCAAAGC	Yes	No	No	0	0	0	0	
NM_hsa_172	chr9:13217588-132175666	+	CTCTGCGCTCCCGCCCA	Yes</							

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KaposinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_1767	chr22:42068981-42069027	+	GGGTATATGGCCCAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1768	chr16:11024671-11024712	+	CGTGGCTGTAGTCCAGGGAGA	Yes	No	No	0	0	0	0	No
NM_hsa_1769	chr16:11024671-11024712	+	TGCCCTCCAGCTCTGCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_177	chr8:949008931-94900922	-	AGAGTTGCAAGCAGTCCAAAG	Yes	No	No	0	0	0	0	No
NM_hsa_177	chr8:949008931-94900922	-	AGAGTTGCAAGCAGTCCAAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1770	chr19:35761295-35761351	+	TCTGCCCTCTACTCCCAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1771	chr19:35761295-35761351	+	AGCGGATGAGGAGCAAGAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1772	chr5:56162429-56162489	+	AGTGCCAGGTTGAAGGACTT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1772	chr5:56162429-56162489	+	AGTGCCAGGTTGAAGGACTT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1773	chr5:56162429-56162489	+	AGTGCCAGGTTGAAGGACTT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1774	chr11:17294640-17294699	+	TGAGCCCACTGGCCCTCCAGG	Yes	No	No	0	0.0662225	0	0	Yes
NM_hsa_1775	chr11:17294640-17294699	+	TGCGGGAGGTCGGGGTGCAC	Yes	No	No	0	0	0	0	No
NM_hsa_1776	chr7:74140308-74140373	+	CTTCCCTCCCTGGGCTCCAGC	Yes	No	No	0	0	0.293145	Yes	Yes
NM_hsa_1777	chr7:74140308-74140373	+	TGAGATCACTGGAGTGGAGTCC	Yes	No	No	0	0	0	0	Yes
NM_hsa_1778	chr7:129414758-129414832	+	TTATGGCCCTCGGTAATCACT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1778	chr7:129414758-129414832	+	TTATGGCCCTCGGTAATCACT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1779	chr7:129414758-129414832	+	TGAATCTACAGCTCCACTACAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_178	chr4:86594807-86594881	+	ATGCTTAGATCCCCCACTGGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_178	chr4:86594807-86594881	+	ATGCTTAGATCCCCCACTGGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1784	chr5:77863355-77863419	+	TTAGAAACATTTCCCTGTTACT	Yes	Yes	No	0	0	0.219859	No	Yes
NM_hsa_1784	chr5:77863355-77863419	+	TTAGAAACATTTCCCTGTTACT	Yes	Yes	No	0	0	0.219859	No	Yes
NM_hsa_1785	chr5:77863355-77863419	+	TAAGAGACTAATGTTTCTGAAA	Yes	No	No	0	0	0	0	No
NM_hsa_1786	chr26:28616037-28616087	-	GGCTCTGTGGCTTAATGGCC	Yes	No	No	0.569857	1.12578	0.513004	Yes	Yes
NM_hsa_1787	chr26:28616037-28616087	-	CATAAAGAGAGCAGCAAGTACG	Yes	No	No	0	0	0	0	No
NM_hsa_1789	chr1:204791131-204791188	+	AGGCCCACTGGAACAGTGTGC	Yes	No	No	0	0	0	0	No
NM_hsa_179	chr4:86594817-86594873	+	CAGTGGGGGACTTCAAGCATG	Yes	No	No	0	0	0	0	No
NM_hsa_1790	chr1:204791131-204791188	+	ATAACTCAGCTGGCCCACTG	Yes	No	No	0	0	0	0	No
NM_hsa_1792	chr12:624066-624124	+	TTTTCTGGGGTTTAAGTCT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1795	chr1:160232773-160232838	-	TGACTGTGAGGCTGTGTTA	Yes	No	No	0	0	0	0	No
NM_hsa_1796	chr3:160232773-160232838	-	CACACTGCCAATGATTAAACC	Yes	No	No	0	0	0	0	No
NM_hsa_1797	chr18:6094670-6094725	-	TACATGATAAATTTGGACCAAG	Yes	No	No	0	0	0	0	No
NM_hsa_1798	chr18:6094670-6094725	-	AGTCCCAAAATTTATCATAGC	Yes	No	No	0	0	0	0	No
NM_hsa_1799	chr3:126800613-126800644	+	TCAGGCCCTGCTCCCTCCAGC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1799	chr3:126800613-126800691	+	TCAGGCCCTGCTCCCTCCAGC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_180	chr1:203144249-203144326	+	CACCCACTGCCCTTCTTGCT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_180	chr1:203144249-203144346	+	CACCCACTGCCCTTCTTGCT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_180	chr1:203144249-203144373	+	CACCCACTGCCCTTCTTGCT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_1800	chr3:126800613-126800691	+	TGGTGTGGCAGGCTCTCTGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_1801	chr15:23916614-23916690	+	ACTGTGAAGTCAAACTGCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1801	chr15:23916627-23916681	+	ACTGTGAAGTCAAACTGCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1802	chr15:23916627-23916681	+	CACGATTTGCAGCTCAAGTAA	Yes	No	No	0	0	0	0	No
NM_hsa_1803	chr7:141466671-141466714	+	TTCTTGCTATGTTCTGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_1803	chr7:141466665-141466693	+	TTCTTGCTATGTTCTGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_1804	chr7:141466671-141466741	+	AGACAGTGTATTCACCCAGAGGA	Yes	No	No	0	0	0	0	No
NM_hsa_1805	chr23:3307804-3307866	+	ACTGTGTGATTTGCTGACTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1805	chr23:3307804-3307866	+	ACTGTGTGATTTGCTGACTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1806	chr23:3307804-3307866	+	CGTCCACCAAGTTCACACAGAAA	Yes	No	No	0	0	0	0	No
NM_hsa_1807	chr11:76155617-76155658	-	AGGTTAGGAGCAGTGGAG	Yes	No	No	0	0	0	0	No
NM_hsa_1808	chr11:76155617-76155658	-	CTTTGTTCTGAAGTGC	Yes	No	No	0	0	0	0	No
NM_hsa_181	chr1:203144257-203144316	+	CAGAAGAGGAGTGGTGGTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_1818	chr18:20814547-20814599	+	TTTTCTGCTGACTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_1819	chr13:112276339-112276401	+	TCCACAGGGTCCAGATCCGAGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_1819	chr13:112276369-112276457	+	TCCACAGGGTCCAGATCCGAGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_182	chr21:9824498-9824699	+	GGGGCCCGCCCTCCAGCCGGG	Yes	No	No	0	0	0	0	No
NM_hsa_1820	chr11:112726339-112726401	+	CGTGGCTGATCCCAAGTCCACT	Yes	No	No	0	0	0	0	No
NM_hsa_1825	chr12:110757493-110757547	+	TACTACCTTGTGGCTGTAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_1826	chr12:110757493-110757547	+	TATAGACCAATAGGTAAGACC	Yes	No	No	0	0	0	0	No
NM_hsa_1829	chr19:6393256-6393333	+	ACCTTCTAGGACTGTGGC	Yes	No	No	0	0	0	0	No
NM_hsa_183	chr1:9824498-9824699	+	CGGGCCCGCCAGCAGCCGGG	Yes	No	No	0	0.0662225	0	0	No
NM_hsa_1830	chr19:6393256-6393333	+	TATGCTGACTCAAAAGTCTC	Yes	No	No	0	0	0	0	No
NM_hsa_1831	chrX:118921315-118921385	-	AAAGCCGTTGTAATCAATTTGA	Yes	No	No	1.25369	1.72179	2.05201	Yes	H-KapB-KapB-cMye
NM_hsa_1832	chrX:118921315-118921385	-	AAAGCCGTTGTAATCAATTTGA	Yes	No	No	0	0	0	0	No
NM_hsa_1834	chr22:3435788-34358053	+	TGTGATGAGGAGGGGCTT	Yes	No	No	0	0	0	0	Yes
NM_hsa_1835	chr19:4635783-4635842	+	CTTGCTGCTGACTCTG	Yes	Yes	No	0.113971	0	0.0732862	No	Yes
NM_hsa_1835	chr19:4635783-4635842	+	CTTGCTGCTGACTCTG	Yes	Yes	No	0.113971	0	0.0732862	No	Yes
NM_hsa_1836	chr19:4635783-4635842	+	TCCCCTCTTGTCTGCTGCT	Yes	No	No	0	0	0	0	No
NM_hsa_1837	chr11:65192931-65193006	+	GATTTACACGAGGAGCATCG	Yes	No	No	0	0	0	0	No
NM_hsa_1838	chr11:65192931-65193006	+	CTTTGAAACTGCTGAGGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_184	chr20:23078428-23078489	+	TTTGCACAGCTTCCACAGGT	Yes	No	No	0	0	0	0	No
NM_hsa_184	chr20:23078428-23078489	+	TTTGCACAGCTTCCACAGGT	Yes	No	No	0	0	0	0	No
NM_hsa_1841	chr11:90010216-90010281	+	TGACCTTAGGCTCTTGTAGC	Yes	No	Yes	0.512871	0.331113	0.0732862	No	KapB-cMye-KapB-H
NM_hsa_1841	chr11:90010196-90010294	+	TGACCTTAGGCTCTTGTAGC	Yes	No	Yes	0.512871	0.331113	0.0732862	No	KapB-cMye-KapB-H
NM_hsa_1842	chr19:0010216-90010281	+	TACAGAGATCTTACAGAGTCC	Yes	Yes	No	0.512871	0	0.0732862	No	KapB-cMye-KapB-H
NM_hsa_1849	chr2:9146603-9146671	+	TGCTTCTTGGAGCACTTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_1849	chr2:9146590-9146680	+	TGCTTCTTGGAGCACTTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_185	chr20:23078428-23078489	+	CAGAGTATGGAAAGCTGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_185	chr20:23078428-23078489	+	CAGAGTATGGAAAGCTGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_1850	chr2:9146603-9146671	+	TAGAGTTTCCAGAGAACACAA	Yes	No	No	0	0	0	0	No
NM_hsa_1851	chr1:45277680-45277777	+	CACATTAATCTGCTCCAG	Yes	No	No	0.0569857	0	0	0	No
NM_hsa_1853	chr22:30234395-30234469	+	AGGCGGGCCCTGTGTGAT	Yes	No	No	0	0	0	0	No
NM_hsa_1854	chr22:30234395-30234469	+	CACCCGCCCTTCC	Yes	No	No	0	0	0	0	No
NM_hsa_1857	chr16:2683183-2683246	+	AACAATGGCTGAGGCTAGA	Yes	Yes	No	0.0569857	0	0	0	No
NM_hsa_1858	chr16:2683183-2683246	+	TGGCCGAGTGGACTTTCAGCA	Yes	No	No	0	0	0	0	No
NM_hsa_1859	chr19:51340286-51340341	+	CTTCTGGAACAGACAAAGCTGC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_1859	chr19:51340286-51340349	+	CTTCTGGAACAGACAAAGCTGC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_186	chr6:10963885-10963897	+	TGCAACAGCTGCACTGAGTCC	Yes	No	No	0	0	0	0	No
NM_hsa_1860	chr19:51340286-51340341	+	CGCTGGCTGCTGCTCCAGCAG	Yes	No	No	0	0	0	0	No
NM_hsa_1861	chr3:11245592-112456008	+	ACAGGCTCAAGAGCTGCAT	Yes	No	No	0	0	0	0	Yes
NM_hsa_1862	chr3:11245592-112456008	+	GTGGCTCAAGAGCTGCAT	Yes	No	No	0	0	0	0	Yes
NM_hsa_1864	chr5:149784624-149784677	+	TCAGAGGTTTCCCTGCTAGG	Yes	No	No	0	0	0	0	No
NM_hsa_1869	chr16:2683183-2683246	+	TACAGAGTCTCTTCCCAAGC	Yes	No	No	0	0	0	0	Yes
NM_hsa_187	chr6:10963885-10963897	+	TCAAGTCCAGAGCTGTCACGG	Yes	No	No	0	0	0	0	No
NM_hsa_1870	chr1:153750878-153750940	+	TGGCAGGAGGGGGCTCATGTACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1871	chr3:19545964-19546021	+	GCTGGCTTTTGTCTCCAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1871	chr3:19545964-19546000	+	GCTGGCTTTTGTCTCCAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1871	chr3:19545964-19546050	+	GCTGGCTTTTGTCTCCAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_1872	chr3:19545964-19546021	+	CTGGGAGCTTGGCTCCAGAT	Yes	Yes	No					

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation	
NM_hsa_193	chr4:8659814-8659870	-	CAGTGGGGAGTCTAAGCATTTG	Yes	No	No	0	0	0	0	No	
NM_hsa_1930	chr19:11202901-11202910	-	CTGAGAGGATCTGCTG	Yes	No	No	0.113971	0	0	0	No	
NM_hsa_1933	chr2:114035492-114035547	-	TGGACTGTGAGTCCACCCCG	Yes	No	No	0	0	0	0	No	
NM_hsa_1934	chr2:114035492-114035547	-	CGGGTGGCGGCGACTCTC	Yes	No	No	0	0	0	0	No	
NM_hsa_1935	chr13:42733748-42733817	+	ACCTCTGATGAAGCTGAG	Yes	Yes	No	0.113971	0.0662225	0	0	KapB+cMyc-KapB-H	
NM_hsa_1935	chr13:42733748-42733817	+	ACCTCTGATGAAGCTGAG	Yes	Yes	No	0.113971	0.0662225	0	0	KapB+cMyc-KapB-H	
NM_hsa_1936	chr13:42733748-42733817	+	CACTCTGGTGGTGGTGG	Yes	No	No	0	0	0	0	No	
NM_hsa_1937	chr20:45112781-45112832	-	CATCTGGATGTAATGAC	Yes	No	No	1.88528	0.695336	0.54354	Yes	KapB+cMyc-KapB-H	
NM_hsa_1938	chr20:45112781-45112832	-	CAGAATCCCAACCAAGA	Yes	No	No	0	0	0	0	No	
NM_hsa_194	chr6:51425076-51425132	-	TGCTAGATTTTGTCTGACT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_194	chr6:51425076-51425132	-	TGCTAGATTTTGTCTGACT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_194	chr6:51425076-51425132	+	TGCTAGATTTTGTCTGACT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1943	chr10:80831879-80831955	-	CTGTGAGAGAACAAAGAAC	Yes	No	No	0	0	0	0	No	
NM_hsa_1944	chr10:80831879-80831955	-	TTTTTCCCAACAAAGAAC	Yes	No	No	0	0	0	0	No	
NM_hsa_1945	chr5:167718384-167718447	-	AGGCTCTCGCAAGCTGG	Yes	No	No	0	0	0	0	No	
NM_hsa_1946	chr5:167718384-167718447	+	GCTCTGTATAAAGCTCTCTT	Yes	No	No	0	0	0	0	No	
NM_hsa_1949	chr1:28573685-28573735	-	CGAGAAGAGGCTGAAGT	Yes	No	No	0	0	0	0	No	
NM_hsa_195	chr6:51425076-51425132	-	TACAGGACAAATATAGCATG	Yes	No	No	0	0	0	0	No	
NM_hsa_195	chr6:51425076-51425132	+	TACAGGACAAATATAGCATG	Yes	No	No	0	0	0	0	No	
NM_hsa_1950	chr1:28573685-28573735	-	GTCCTGGCCCTGACTCTCT	Yes	No	No	0	0	0	0	No	
NM_hsa_1951	chr2:25898545-25898603	-	AAGTTTGTGTGACTGACT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1951	chr2:25898545-25898603	+	AAGTTTGTGTGACTGACT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1952	chr2:25898545-25898603	+	TGGAGTGTCTGAGCACTTG	Yes	No	No	0	0	0	0	No	
NM_hsa_1953	chrY:19692289-19692341	-	GTCGAGGAGCAAGTGGGTT	Yes	No	No	0.854786	0.79467	0	0	KapB+cMyc-KapB-H	
NM_hsa_1954	chrY:19692289-19692341	-	ATCCAGAGTTCAGACAT	Yes	No	No	0	0	0	0	No	
NM_hsa_1955	chr17:41368125-41368174	+	GTCAGAACTCCGGCCAGA	Yes	No	No	0	0	0	0	Yes	
NM_hsa_1956	chr17:41368125-41368174	+	TGTAAGGATTTGGGACTC	Yes	No	No	0	0	0	0	No	
NM_hsa_1957	chr2:20557545-20557545	-	TATCTCTGTGTGGGCTCGGA	Yes	No	No	0	0	0	0	No	
NM_hsa_1958	chr2:20557545-20557545	-	TAGGAAGTACTAGATTTCTGT	Yes	No	No	0	0	0	0	No	
NM_hsa_196	chr4:94280882-94280942	-	CTACTGTTTCTTCTTAAGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_196	chr4:94280882-94280942	-	CTACTGTTTCTTCTTAAGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_196	chr4:94280882-94280942	-	CTACTGTTTCTTCTTAAGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_196	chr4:94280882-94280942	-	CTACTGTTTCTTCTTAAGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_1961	chr12:76049395-76049444	-	GATAAAGACAAAGGCTAGG	Yes	No	No	0	0	0	0	No	
NM_hsa_1962	chr17:39739706-39739765	-	TTCCTTCCCTCCCTCACAGA	Yes	No	No	0	0	0	0	Yes	
NM_hsa_1962	chr17:39739706-39739765	-	TTCCTTCCCTCCCTCACAGA	Yes	No	No	0	0	0	0	Yes	
NM_hsa_1963	chr17:39739706-39739765	-	TGCGAGGAGGAGAACGGCCACA	Yes	No	No	0	0	0	0	No	
NM_hsa_1966	chr17:57233146-57233231	+	CTTGAGTAGTGGCCCTGTG	Yes	No	No	0	0	0	0	No	
NM_hsa_1968	chr4:129523249-129523330	+	TCCCAAGGACCTCACTGGAGC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1968	chr4:129523249-129523330	+	TCCCAAGGACCTCACTGGAGC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1969	chr4:129523249-129523330	+	TCCCTGTGCTCCATGATTAAGG	Yes	No	No	0	0	0	0	No	
NM_hsa_197	chr4:94280882-94280942	-	TTCAGTGTCTTCTTCTTAAGC	Yes	No	No	0	0	0	0	No	
NM_hsa_1972	chr19:35224647-35224731	-	GGGACACCTTCTTCTTAAGC	Yes	No	No	0	0	0	0	No	
NM_hsa_1973	chr19:35224647-35224731	-	GACTACTCGCTCCAC	Yes	No	No	0	0	0	0	No	
NM_hsa_1974	chr11:111412280-111412351	+	AGCTACCTCCGCTTGGGA	Yes	No	No	0	0	0	0	No	
NM_hsa_1975	chr11:111412280-111412351	+	TGCTCTTCTTCTTCTTCTG	Yes	No	No	0	0	0	0	No	
NM_hsa_1977	chr2:85555026-85555068	-	GGCGGTAAGACCTCCCA	Yes	No	No	0	0	0	0	No	
NM_hsa_1978	chr19:6729174-6729234	+	TGGGCTGAGTACTCTCCG	Yes	No	No	0	0	0	0	No	
NM_hsa_1979	chr19:6729174-6729234	+	TGGGCTGAGTACTCTCCG	Yes	No	No	0	0	0	0	No	
NM_hsa_198	chr17:6822073-6822137	-	GGGGGCGCGCGCGCGCGGG	Yes	No	No	0.168644	0.0927115	0.035985	Yes	KapB+cMyc-KapB-H	
NM_hsa_1980	chr22:3573241-35732471	+	TGTTTCTGCTCAGCTGGAC	Yes	No	No	0.113971	0	0	0	No	
NM_hsa_1980	chr22:3573241-35732480	+	TGTTTCTGCTCAGCTGGAC	Yes	Yes	No	0.113971	0	0	0	No	
NM_hsa_1981	chr22:3573241-35732471	+	CTTGGTGGAGGAAACACAGC	Yes	No	No	0	0	0	0	No	
NM_hsa_1982	chr19:51894688-51894766	+	TAGACACAGAACTGGACAC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1982	chr19:51894688-51894766	+	TAGACACAGAACTGGACAC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_1983	chr19:51894702-51894757	-	TGTCAGGCTTCTGATATAACT	Yes	No	No	0	0	0	0	No	
NM_hsa_1984	chr3:9933550-9933626	-	CTCTGCCAATCTCTCCCGC	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_1984	chr3:9933550-9933617	+	CTCTGCCAATCTCTCCCGC	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_1985	chr3:9933550-9933617	+	TGGAGAAGTATGGCGGCTGAG	Yes	No	No	0	0	0	0	No	
NM_hsa_199	chr17:46134631-46134716	+	AGCTCTGTTTGGCCCTAGT	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_1996	chr17:46134631-46134716	+	AGCTCTGTTTGGCCCTAGT	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_1997	chr17:46134631-46134707	+	TGGAGAAGAACCAAGTFTT	Yes	No	No	0	0	0	0	Yes	
NM_hsa_2	chr1:159551602	-	GACGAATAGTTAAATTAAT	Yes	No	No	0.512871	0.927115	1.46572	Yes	H-KapB-KapB+cMyc	
NM_hsa_200	chr10:50035510-50035600	+	CACCTAAGGCGAGCAACAAGA	Yes	No	No	0	0	0	0	No	
NM_hsa_200	chr10:50035510-50035600	+	TCTCTCCGCTCAGTGTGC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_200	chr10:50035523-50035591	+	TCTCTCCGCTCAGTGTGC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_2000	chr9:9493036-9493105	-	AGGGAGCGCAAGCTGTG	Yes	No	No	0.0662225	0	0	0	No	
NM_hsa_2001	chr9:9493036-9493105	-	AGGGAGCGCGCTGTGGG	Yes	No	No	0.113971	0	0	0	No	
NM_hsa_2002	chr12:96903118-9690256	+	TACATTTGACCTTTCAAGT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_2002	chr12:96903118-9690256	+	TACATTTGACCTTTCAAGT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_2002	chr12:96903118-9690256	+	TACATTTGACCTTTCAAGT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_2003	chr12:96903118-9690256	+	TACATTTGACCTTTCAAGT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_2006	chr12:46590639-46590712	-	ATTCTGTTTCTTCAAGCTG	Yes	No	No	0	0	0	0	No	
NM_hsa_2006	chr12:46590639-46590712	-	ATTCTGTTTCTTCAAGCTG	Yes	Yes	No	0	0	0	0	No	
NM_hsa_2007	chr12:46590639-46590712	-	AGACCTGATTAACAACATA	Yes	No	No	0	0	0	0	No	
NM_hsa_2008	chr9:7573376-7573438	+	AGCACTAAGTGTCTTCTTCCAG	Yes	Yes	No	0.170957	0	0	0	No	
NM_hsa_2008	chr9:7573376-7573438	+	AGCACTAAGTGTCTTCTTCCAG	Yes	Yes	No	0.170957	0	0	0	No	
NM_hsa_2009	chr9:7573376-7573438	+	GGAAGGAGAGTGTGTGGTGG	Yes	No	No	0	0	0	0	No	
NM_hsa_201	chr10:50035523-50035591	+	ACACTGACACAGAGAGAGA	Yes	No	No	0	0	0	0	No	
NM_hsa_2010	chr15:140700473-140700524	+	GACAGTGTCTGAGAAAG	Yes	No	No	0	0	0	0	No	
NM_hsa_2011	chr15:140700473-140700524	+	TTTCCGAGAGACTTGTTT	Yes	No	No	0	0	0	0	No	
NM_hsa_2012	chr3:8788889-8788950	+	TGGGAATAGGACGGAGGAC	Yes	No	No	0	0	0	0	No	
NM_hsa_2013	chr3:8788889-8788950	+	GCTTCCGCTCTAGTGCCTTT	Yes	No	No	0	0	0	0	No	
NM_hsa_2018	chr19:5218592-5218457	+	GCTTCCGCTCTAGTGCCTTT	Yes	No	No	0	0	0	0	No	
NM_hsa_2019	chr2:118588316-118588389	+	TTTCTTATATGTTGGCTCCAG	Yes	No	No	0	0	0	0	No	
NM_hsa_202	chr1:17121975-171218060	+	TAAGTACTGTGGGATGAT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_202	chr1:17121975-171218051	+	TAAGTACTGTGGGATGAT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_202	chr1:17121975-171218080	+	TAAGTACTGTGGGATGAT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_2021	chr4:102276058-102276095	-	GTCTTGTGGTGGCTGAGT	Yes	No	No	0	0	0	0	No	
NM_hsa_2022	chr4:102276058-102276095	-	CTTCAACAGCAAGA	Yes	No	No	0	0	0	0	No	
NM_hsa_2023	chr1:156711688-156711759	-	TATTTACAGACTTCCGCCACA	Yes	Yes	No	0	0	0	0	0.0732862	No
NM_hsa_2023	chr1:156711700-156711750	-	TATTTACAGACTTCCGCCACA	Yes	Yes	No	0	0	0	0	0.0732862	No
NM_hsa_2024	chr1:156711700-156711750	-	TGGGCAAGGATAGATGAA	Yes	No	No	0	0	0	0	No	
NM_hsa_2025	chr7:14466605-14466693	-	AAGCTCTGAGCAAGATTT	Yes	No	No	0	0	0	0	No	
NM_hsa_2026	chr1:22913925-229139341	+	CTTGTGCGCAAGCTGGAAG	Yes	No	No	0	0	0	0	No	
NM_hsa_2028	chr1:23607001-23607015	+	TCTGAGACTAGAGCAAGCCCT	Yes	Yes	Yes	0.0569857	0	0	0	Yes	
NM_hsa_2028	chr1:23607001-23607012	+	TCTGAGACTAGAGCAAGCCCT	Yes	Yes	Yes	0.0569857	0	0	0	Yes	
NM_hsa_2028												

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KaposinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_210	chr5:108949146-108949286	+	TGACCTCCAGAGTCTCTCCAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2100	chr1:173834848-173834912	+	TTCTGTGATGAATATCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2101	chr1:173834848-173834912	+	AGTGTTTATGTGTTTCT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2102	chr10:4989335-4989396	-	ATACAGGTTATGACTAG	Yes	No	No	0	0	0	0	No
NM_hsa_2103	chr10:4989335-4989396	-	ACAACCTGCTGTCTGCA	Yes	No	No	0	0	0	0	No
NM_hsa_2104	chr19:9202609-9202929	-	ACCTGCACCTGAAGCACTTGCAC	Yes	Yes	No	0	0	0	0	No
NM_hsa_2104	chr19:9202609-9202929	-	CGACCTGCTAGCACTTGCAC	Yes	Yes	No	0	0	0	0	No
NM_hsa_2105	chr19:9202609-9202929	-	TACAAGTCTCTCACTGAGTAG	Yes	No	No	0	0	0	0	No
NM_hsa_2106	chr3:98312729-98312789	+	TGGCAGAGTCCAGTCCCGCT	Yes	No	No	0	0	0	0	No
NM_hsa_211	chr5:108949146-108949247	+	AGCAAGGGTCCCGAAGCTCAT	Yes	No	No	0	0	0	0	No
NM_hsa_2110	chr2:1283073-20163143	+	GTAACTGTTTGTTAACCTGCTTT	Yes	No	No	0	0	0	0	No
NM_hsa_2111	chr11:110601597-110601657	+	CCTCAGAGCCAGCCCAAGA	Yes	No	No	0	0	0	0	No
NM_hsa_2112	chr11:110601597-110601657	+	TGCTGGGCTCCCTCCGGAT	Yes	No	No	0	0	0	0	No
NM_hsa_2113	chr6:3298687-32986955	+	GAGGTTGCTGGGTTCTG	Yes	No	No	0	0	0	0	No
NM_hsa_2114	chr6:3298687-32986955	+	GAAACAGCCAGCCCTC	Yes	No	No	0	0	0	0	No
NM_hsa_212	chr2:10304875-103048817	+	TGCAATTTTCCGTGATCAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_212	chr2:103048721-103048849	+	TGCAATTTTCCGTGATCAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_212	chr2:103048746-103048828	+	TGCAATTTTCCGTGATCAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2122	chr8:56826040-56826086	+	TGGTTTTCTTGTGGACT	Yes	No	No	0	0	0	0	No
NM_hsa_2123	chr12:71892246-71892292	+	GTTCTACTGTATGAGT	Yes	No	No	0	0	0	0	No
NM_hsa_2124	chr12:71892246-71892292	+	CCAACTTCAATGTATCCCT	Yes	No	No	0	0	0	0	No
NM_hsa_2127	chr20:8769037-8769096	+	GCAAAGTCAATTTCTTTTCCAG	Yes	No	No	0	0	0	0	No
NM_hsa_2128	chr20:8769037-8769096	+	GGGAAGGAAGCTGTTTGCAAA	Yes	No	No	0	0	0	0	No
NM_hsa_2129	chr12:4947007-4947046	+	CTGTAGCTTCTCTGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_213	chr2:10304875-103048817	+	TGTAATGAGCAAGGTCGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2130	chr12:4947007-4947046	+	AGCAGATGCAGTA	Yes	No	No	0	0	0	0	No
NM_hsa_2131	chr3:172241341-172241397	+	AGATGCTGTGGAAGGAG	Yes	No	No	0	0	0	0	No
NM_hsa_2132	chr3:172241341-172241397	+	CCCTTTTCTATGCCCA	Yes	No	No	0	0	0	0	No
NM_hsa_2135	chr16:50678624-50678679	+	CAGTGAATCTGTTGCTGCA	Yes	No	No	0	0	0	0	No
NM_hsa_2136	chr16:50678624-50678679	+	TCAAAGGCGAGCATGTTGGTAT	Yes	No	No	0	0	0	0	No
NM_hsa_2137	chr17:8125793-8125852	+	ACAGAGTCTCTCCAGCTGCAG	Yes	No	No	0	0	0	0	No
NM_hsa_2138	chr17:8125793-8125852	+	GACAGTCTTGGGCTCCCGAA	Yes	No	No	0	0	0	0	No
NM_hsa_214	chr2:144337526-144337628	+	TTTTTAAAGAAGAACACTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_214	chr2:144337526-144337628	+	TTTTTAAAGAAGAACACTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_214	chr2:144337529-144337594	+	TTTTTAAAGAAGAACACTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_214	chr2:144337497-144337615	+	TTTTTAAAGAAGAACACTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_214	chr2:144337526-144337591	+	TTTTTAAAGAAGAACACTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2142	chr12:104336300-104336342	+	TTTAGGTGATGGAAGA	Yes	No	No	0	0	0	0	No
NM_hsa_2143	chr11:170649590-170649650	+	TATGACATCATGGAACCCGCT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2143	chr11:170649581-170649659	+	TATGACATCATGGAACCCGCT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_2144	chr11:170649590-170649650	+	TGGATCTTGTGGATCATGAA	Yes	No	No	0	0	0	0	No
NM_hsa_2145	chr5:50698185-50698233	+	ATTGGCAGATGTTCTCAAAAT	Yes	No	No	0	0	0	0	No
NM_hsa_2146	chr5:50698185-50698233	+	GAATGAGAGTATGCTCAAGAT	Yes	No	No	0	0	0	0	No
NM_hsa_2147	chr5:168406096-168406140	+	GCTCAGTTTCCAGGAT	Yes	No	No	0	0	0	0	Yes
NM_hsa_2148	chr5:168406096-168406140	+	GCTCAGGATGAGTTGAAGGATAG	Yes	No	No	0	0	0	0	No
NM_hsa_2149	chr1:57532844-57532908	+	TTACTGTAGTCTGTATTTTA	Yes	No	No	0	0	0	0	No
NM_hsa_215	chr2:144337529-144337594	+	AGTGTCTTTTAAATAAACA	Yes	No	No	0	0	0	0	No
NM_hsa_215	chr2:144337526-144337591	+	AGTGTCTTTTAAATAAACA	Yes	No	No	0	0	0	0	No
NM_hsa_2150	chr11:57532844-57532908	+	AAACAACATGATTAATCAAA	Yes	No	No	0	0	0	0	No
NM_hsa_2152	chr13:118006387-118006454	+	TGGAGGAGGAAATGCCACCA	Yes	No	No	0	0	0	0	No
NM_hsa_2152	chr13:118006387-118006454	+	AAGTGGCAGTTGCCACTGT	Yes	No	No	2.70682	2.88068	1.42098	Yes	
NM_hsa_2153	chr13:118006387-118006454	+	AGTAAGCAGTCCGACAGGATA	Yes	No	No	0	0	0	0	No
NM_hsa_2154	chr17:70859275-70859325	+	TGAGGAGATGTTTGTGCAA	Yes	No	No	313.671	284.254	145.109	Yes	KapBcMye-KapB-H
NM_hsa_2155	chr17:70859275-70859325	+	GGGGGAAAGTATCCACAGT	Yes	No	No	0	0	0	0	No
NM_hsa_2157	chr20:47614704-47614761	+	TATTTTGTGGAATTAATCTCT	Yes	No	No	0	0	0	0	No
NM_hsa_2158	chr12:25409790-25409843	+	AGATGTGAGAGAACAGAG	Yes	No	No	0	0	0	0	No
NM_hsa_2159	chr12:25409790-25409843	+	CTTTAGCTCTATCTC	Yes	No	No	0	0	0	0	No
NM_hsa_216	chr3:138553852-138553972	+	TCTACCTGTCAGCCCGCTGCT	Yes	No	Yes	0.455886	0.52978	0.219899	Yes	
NM_hsa_216	chr3:138553876-138553943	+	TCTACCTGTCAGCCCGCTGCT	Yes	No	Yes	0.455886	0.52978	0.219899	Yes	
NM_hsa_2160	chr12:97856551-97856604	+	ATTCTGCAAGTCTGCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_2164	chr3:186505088-186505150	+	TACATATCTGCTGGAACAA	Yes	No	No	1.76656	1.25823	0.439717	Yes	KapBcMye-KapB-H
NM_hsa_2165	chr3:186505088-186505150	+	TAGTCTCCCTGCTAAA	Yes	No	No	0	0	0	0	No
NM_hsa_2166	chr6:50790656-50790749	+	TTTGTGTGATTTGACTCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_2166	chr6:50790656-50790749	+	TTTGTGTGATTTGACTCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_2167	chr6:50790631-50790689	+	AGGGGAGCAGCAGCAAAATA	Yes	No	No	0	0	0	0	No
NM_hsa_2169	chr20:3606545-36065501	+	AGAGTTTGTGACAGCTGCA	Yes	No	No	0.455886	0.463558	0.146572	Yes	
NM_hsa_217	chr3:138553876-138553943	+	AGTTGGGCTGGGAGGTTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_2170	chr20:3606545-36065501	+	GAGTGGGAGTGGGGTAGGA	Yes	No	No	0	0	0	0	No
NM_hsa_2171	chr11:2232652-12232721	+	ACAGGAACTCTGGCACTG	Yes	No	No	0	0	0	0	No
NM_hsa_2172	chr11:2232652-12232721	+	GGGAGAAAGAGTGTCTTCT	Yes	No	No	0	0	0	0	No
NM_hsa_218	chr11:62609168-62609210	+	AATGGATTTTGAAGTAAG	Yes	No	No	0.170957	0.52978	0.146572	Yes	
NM_hsa_22	chr10:5003136-5003219	+	TTAAGTGGCTCAATTTGAGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_22	chr10:5003136-5003219	+	TTAAGTGGCTCAATTTGAGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_220	chr14:81686538-81686614	+	CGGGGCTGCGCCCTGAGCA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_220	chr14:81686538-81686605	+	CGGGGCTGCGCCCTGAGCA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_221	chr14:81686538-81686605	+	CGGGGCTGCGCCCTGAGCC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_222	chr7:9964700-99647091	+	TGTCATAACCTGCTGAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_222	chr7:9964700-99647091	+	TGTCATAACCTGCTGAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_223	chr7:9964700-99647091	+	TGCTCCAGTGTATGAGCACT	Yes	No	No	0	0	0	0	No
NM_hsa_224	chr4:94280882-94280942	+	TAGCAATGAAACAGTAGCC	Yes	No	No	0	0	0	0	No
NM_hsa_225	chr16:31226793-31226860	+	CGCTTGGGCTGCTCTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_225	chr16:31226793-31226861	+	CGCTTGGGCTGCTCTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_226	chr16:31226781-31226851	+	GGGAGTCCAGCCCTCGGGCCC	Yes	No	No	0	0	0	0	No
NM_hsa_227	chr11:11256307-112563105	+	GAAGTGGGCTCAGACTGCTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_227	chr11:11256307-112563105	+	GAAGTGGGCTCAGACTGCTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_227	chr11:11256307-112563127	+	GAAGTGGGCTCAGACTGCTGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_228	chr11:11256307-112563097	+	AGCAAGTCTGAGGAGTCTG	Yes	No	No	0	0	0	0	No
NM_hsa_229	chr10:123790175-123790251	+	CTGGGTCATCTGCTGAGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_229	chr10:123790188-123790242	+	CTGGGTCATCTGCTGAGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_229	chr10:123790188-123790239	+	CTGGGTCATCTGCTGAGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_229	chr10:123790188-123790239	+	CTGGGTCATCTGCTGAGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_230	chr10:123790188-123790242	+	CTCAGCCAGCATGACCCTG	Yes	No	No	0	0	0	0	No
NM_hsa_231	chr6:120144241-120144322	+	CCACATACTCACTGTCTAGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_231	chr6:120144241-120144313	+	CCACATACTCACTGTCTAGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_232	chr6:120144241-120144313	+	TGAGCAAGTGAAGTATGTTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_235	chr17:59438884-59438972	+	TAATATCTGTGACACACTGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_235	chr17:59438897-59438963	+	TAATATCTGTGACACACTGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_236	chr17:59438897-59438										

Name	locus	strand	sequence	midexp2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_260	chr2:88932794-88932870	+	ATGCTAGGTTCTAGGAAACAGATA	Yes	No	No	0	0	0	0	No
NM_hsa_261	chr6:3504754-3504833	+	TGTCATGTTGGCGGTATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_261	chr6:3504762-3504823	-	TGTCATGTTGGCGGTATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_261	chr6:3504725-3504863	-	TGTCATGTTGGCGGTATGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_262	chr6:3504762-3504823	-	TCATCAGCCAAACATGACATA	Yes	No	No	0	0	0	0	No
NM_hsa_263	chrX:134459119-134459179	-	TGCATGCCACCACTGATCTAGA	Yes	Yes	Yes	0	0	0	0.0732862	Yes
NM_hsa_263	chrX:134459055-134459121	-	TGCATGCCACCACTGATCTAGA	Yes	Yes	Yes	0	0	0	0.0732862	Yes
NM_hsa_263	chrX:134459110-134459192	-	TGCATGCCACCACTGATCTAGA	Yes	Yes	Yes	0	0	0	0.0732862	Yes
NM_hsa_264	chrX:134459119-134459179	-	AGAACAGTGGCGGCACTGACCT	Yes	No	No	0	0	0	0	No
NM_hsa_265	chr6:12011806-12011991	+	CGGTTCTGGCGCCGGCGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_265	chr6:12011908-12011982	+	CGGTTCTGGCGCCGGCGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_266	chr6:10011908-12011982	+	GGGGCCGGCCGGCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_267	chr5:102123207-102123263	+	CAGATTCTGGGCTTAGTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_267	chr5:102123204-102123260	+	CAGATTCTGGGCTTAGTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_267	chr5:102123194-102123272	+	CAGATTCTGGGCTTAGTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_268	chr5:102123207-102123263	+	ACTAAGCCAGGAATTCTGTG	Yes	No	No	0	0	0	0	No
NM_hsa_269	chr10:72082639-72082769	+	CCCATCTGTAGGGGAAATGGCGTG	Yes	Yes	Yes	0.0569857	0.198668	0	0	Yes
NM_hsa_269	chr10:72082673-72082732	+	CCCATCTGTAGGGGAAATGGCGTG	Yes	Yes	Yes	0.0569857	0.198668	0	0	Yes
NM_hsa_269	chr10:72082644-72082744	+	CCCATCTGTAGGGGAAATGGCGTG	Yes	Yes	Yes	0.0569857	0.198668	0	0	Yes
NM_hsa_27	chr10:10780365-10780377	+	TAGGACACCATGGTCTATGACT	Yes	Yes	No	0	0	0	0	No
NM_hsa_27	chr10:107803665-107803746	+	TAGAGAAACATGGTCTATGACT	Yes	Yes	No	0	0	0	0	No
NM_hsa_270	chr10:72082673-72082732	+	GGCCATCCCATCAGATGAGTC	Yes	No	No	0	0	0	0	No
NM_hsa_273	chr18:15197815-15197866	+	GGACCAAGGCGCTTCCAGG	Yes	No	No	0	0	0	0	No
NM_hsa_274	chr18:15197815-15197866	+	TAGGAAAGAACCCCTGATGCCAG	Yes	No	No	0	0	0	0	No
NM_hsa_275	chr7:6318232-6318255	+	GGCCCGCCGGTGGGGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_277	chr14:91167034-91167114	-	CTTACAACCTGGAAAGCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_278	chr14:91167034-91167114	-	TGCTTTCCGGAGTGTAAAGTG	Yes	No	No	0	0	0	0.146572	No
NM_hsa_279	chr10:123790185-123790239	-	CTGTCAGACATGATGCTCTGTG	Yes	No	No	0	0	0	0	No
NM_hsa_28	chr10:10780365-10780377	+	TCTATGACCATGGTCTCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_28	chr10:107803665-107803746	+	TCTATGACCATGGTCTCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_28	chr10:107803645-107803763	+	TCTATGACCATGGTCTCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_280	chr19:40931563-40931619	+	CCCTCTCGGATCGCGGTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_280	chr19:40931520-40931658	+	CCCTCTCGGATCGCGGTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_280	chr19:40931563-40931621	+	CCCTCTCGGATCGCGGTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_281	chr19:40931563-40931619	+	ACCGACGGGACCAAGAACCGG	Yes	No	No	0	0	0	0	No
NM_hsa_282	chr5:71884923-71884987	+	ACTTTTATAGTAGTCTGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_282	chr5:71884910-71884996	+	ACTTTTATAGTAGTCTGGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_283	chr5:71884923-71884987	+	CCGACCTCTCTATAAAGTGA	Yes	No	No	0	0	0	0	No
NM_hsa_284	chr13:96705706-96705802	+	CGGACACTGGCCACCTCGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_284	chr13:96705730-96705793	+	CGGACACTGGCCACCTCGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_285	chr13:96705730-96705793	+	CGCCGGGTTTAAAGTGGT	Yes	No	No	0	0	0	0	No
NM_hsa_286	chr5:11866545-11866553	+	CATGTCAGACAAAGTTGGGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_286	chr5:118665478-11866553	+	CATGTCAGACAAAGTTGGGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_286	chr5:118665490-118665544	+	CATGTCAGACAAAGTTGGGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_287	chr5:118665490-118665544	+	CCAGCTTGTCTAGCATGGA	Yes	No	No	0	0	0	0	No
NM_hsa_288	chr17:3827861-38278692	-	CGTGGAGCCGAGGCTGAGAG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_290	chr13:80583310-80583399	+	TGTCATCTGTGGAAGAAGTGA	Yes	No	No	0	0	0	0	No
NM_hsa_291	chr13:80583310-80583399	+	ACTCTTCCACAGTGACTCAA	Yes	No	No	0	0	0	0	No
NM_hsa_292	chr3:189900523-189900590	+	GAATTAACCTCGGTCTGTG	Yes	Yes	Yes	0.0569857	0	0	0	Yes
NM_hsa_292	chr3:189900491-189900529	+	GAATTAACCTCGGTCTGTG	Yes	Yes	Yes	0.0569857	0	0	0	Yes
NM_hsa_292	chr3:189900510-189900599	+	GAATTAACCTCGGTCTGTG	Yes	Yes	Yes	0.0569857	0	0	0	Yes
NM_hsa_293	chr3:189900523-189900590	+	AGAGACTGAGTATATAGCA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_294	chr16:29937602-29937643	+	CCGTAGAGTCTGGCGTGT	Yes	No	No	0	0	0	0	No
NM_hsa_295	chr16:29937602-29937643	+	CGCAGTGGCTCGTGGGG	Yes	No	No	0	0	0	0	No
NM_hsa_296	chr5:34538010-34538072	+	AGGACCCCTGACTGCAACCG	Yes	No	No	0	0.0551854	0	0	No
NM_hsa_297	chr5:34538010-34538072	+	ATTCACCAAGGCGCTCCCTG	Yes	No	No	0	0	0	0	No
NM_hsa_298	chr9:127964182-127964229	+	ATAGAACAGGCGGCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_299	chr9:127964182-127964229	+	CGCCGACTTATTATT	Yes	No	No	0	0	0	0	No
NM_hsa_3	chr2:23221154-23221234	-	ATAGCAAGTTCTGGCCAG	Yes	No	No	0.113971	0.0662225	0.0732862	0	Yes
NM_hsa_300	chr5:102123204-102123260	+	ACTAAGCCAGGAATTCTGTG	Yes	No	No	0	0	0	0	No
NM_hsa_301	chr6:36020929-36021053	+	GAGAATATGGGATCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_301	chr6:36020960-36021021	+	GAGAATATGGGATCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_301	chr6:36020929-36021054	+	GAGAATATGGGATCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_301	chr6:36020957-36021018	+	GAGAATATGGGATCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_301	chr6:36020949-36021028	+	GAGAATATGGGATCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_302	chr6:36020960-36021021	+	ACAGACTCCCATATCTCAT	Yes	No	No	0	0	0	0	No
NM_hsa_302	chr6:36020957-36021018	+	ACAGACTCCCATATCTCAT	Yes	No	No	0	0	0	0	No
NM_hsa_303	chr21:41935303-41935365	+	CTCAGAGTCCACAGATCAAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_303	chr21:41935293-41935367	+	CTCAGAGTCCACAGATCAAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_303	chr21:41935263-41935401	+	CTCAGAGTCCACAGATCAAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_303	chr21:41935271-41935399	+	CTCAGAGTCCACAGATCAAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_304	chr21:41935293-41935373	+	ATTGATCTGGGAACTCGAG	Yes	No	No	0	0	0	0	No
NM_hsa_304	chr21:41935304-41935365	+	ATTGATCTGGGAACTCGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_305	chr9:2903556-29035619	+	TACTTGGTTTGACTCAAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_305	chr9:29035561-29035619	+	TACTTGGTTTGACTCAAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_305	chr9:29035554-29035630	+	TACTTGGTTTGACTCAAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_305	chr9:29035553-29035619	+	TACTTGGTTTGACTCAAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_306	chr9:2903556-29035622	+	TGGAAGTCAAACCAAGTACA	Yes	No	No	0	0	0	0	No
NM_hsa_306	chr9:29035561-29035619	+	TGGAAGTCAAACCAAGTACA	Yes	No	No	0	0	0	0	Yes
NM_hsa_307	chr4:185423377-185423433	+	TGGTGTAGCAATGGCACCGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_307	chr4:185423365-185423442	+	TGGTGTAGCAATGGCACCGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_307	chr4:18542334-18542342	+	TGGTGTAGCAATGGCACCGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_308	chr4:185423377-185423433	+	AGTGCACATGGTCTACACCGC	Yes	No	No	0	0	0	0	No
NM_hsa_312	chr13:51614829-51614915	+	TATTTGATTTCTGTAGGAC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_312	chr13:51614816-51614934	+	TATTTGATTTCTGTAGGAC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_312	chr13:51614839-51614907	+	TATTTGATTTCTGTAGGAC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_312	chr13:51614836-51614904	+	TATTTGATTTCTGTAGGAC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_313	chr13:51614839-51614907	+	CCTACAGAAAGAACTCAATAAG	Yes	No	No	0	0	0	0	No
NM_hsa_313	chr13:51614836-51614904	+	CCTACAGAAAGAACTCAATAAG	Yes	No	No	0	0	0	0	No
NM_hsa_314	chr18:8891641-8891690	+	TTCAGACTGACTGGAAGTGA	Yes	No	No	0	0	0	0	No
NM_hsa_315	chr18:8891641-8891690	+	TTCAGACTGACTGGAAGTGA	Yes	No	No	0	0	0	0	No
NM_hsa_316	chr3:193631983-19362050	+	ATGCTTAGTTGGACTATGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_316	chr3:193631943-193632081	+	ATGCTTAGTTGGACTATGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_316	chr3:193631973-193632058	+	ATGCTTAGTTGGACTATGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_317	chr3:193631983-19362050	+	ATGAGTCCAACTAAAGCACCC	Yes	No	No	0	0	0	0	No
NM_hsa_318	chr18:61089817-61089889	+	AGGCAGACTGAGCTGTG	Yes	No	No	0	0	0	0	No
NM_hsa_319	chr18:61089817-61089889	+	GGGAAAGTAGCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_320	chr15:80987263-80987301	+	GGAACACTTCTGCACCTG	Yes	No	No	0	0			

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_362	chr3:18654527-18654582	+	GAGGAGCCGGAGCTGGCTCGG	Yes	No	No	0	0	0	0	No
NM_hsa_363	chr2:174887523-174887628	+	CTTTAGTAGGAGAGCTGTGTA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_363	chr2:174887533-174887640	+	CTTTAGTAGGAGAGCTGTGTA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_363	chr2:174887565-174887631	+	CTTTAGTAGGAGAGCTGTGTA	Yes	Yes	No	0	0	0	0	No
NM_hsa_364	chr2:174887562-174887628	+	AACAGCCTCTACTAAAGCA	Yes	No	No	0	0	0	0	No
NM_hsa_364	chr2:174887565-174887631	+	AACAGCCTCTACTAAAGCA	Yes	No	No	0	0	0	0	No
NM_hsa_367	chr1:1283476-1283561	+	TGGACTAGGACTCAGTGAATCT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_367	chr1:1283445-1283499	+	TGGACTAGGACTCAGTGAATCT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_367	chr1:1283432-1283508	+	TGGACTAGGACTCAGTGAATCT	Yes	Yes	No	0	0	0	0	No
NM_hsa_368	chr1:1283476-1283561	+	GCTCCGCTCCCTGTCACAG	Yes	No	No	0	0	0	0	No
NM_hsa_369	chr8:4942725-4942727	+	ATGATAGCTGGGTTGAG	Yes	No	No	0	0	0	0	No
NM_hsa_369	chr8:4942712-4942722	+	ATGATAGCTGGGTTGAG	Yes	No	No	0	0	0	0	No
NM_hsa_37	chr1:52344884-5234492	+	CTACACCCCGGAGTGA	Yes	No	No	0.0569857	0	0.0732862	No	No
NM_hsa_370	chr8:49427212-4942722	+	GCGGCTCTGCTCCGGG	Yes	No	No	0	0	0	0	No
NM_hsa_371	chr3:143136911-143137029	+	TGCCAGATATACCTCACTAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_371	chr3:143136911-143136995	+	TGCCAGATATACCTCACTAG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_372	chr3:143136941-143136995	+	AGTAAGTGAATATCCGGCCTC	Yes	No	No	0	0	0	0	No
NM_hsa_373	chr22:38198608-38198708	+	CCGTCTTCCCTGCTTCCGCC	Yes	Yes	Yes	0	0	0	0.146572	No
NM_hsa_373	chr22:38198636-38198689	+	CCGTCTTCCCTGCTTCCGCC	Yes	Yes	Yes	0	0	0	0.146572	No
NM_hsa_373	chr22:38198619-38198698	+	CCGTCTTCCCTGCTTCCGCC	Yes	Yes	Yes	0	0	0	0.146572	No
NM_hsa_374	chr22:38198626-38198689	+	GAGGAGGAGGAGGAGGAGGCGCC	Yes	No	No	0	0	0	0	No
NM_hsa_375	chr8:99306385-99306465	+	GAGGAGGAGGAGGAGGAGGCGCC	Yes	Yes	No	0	0.331113	0	0	No
NM_hsa_375	chr8:99306399-99306456	+	GAGGAGGAGGAGGAGGAGGCGCC	Yes	Yes	No	0	0.331113	0	0	No
NM_hsa_376	chr8:99306399-99306456	+	GAGGAGGAGGAGGAGGAGGCGCC	Yes	Yes	No	0	0.331113	0	0	No
NM_hsa_377	chr21:36824270-36824331	+	TGAAACTCTGAGCAAGCACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_377	chr21:36824236-36824362	-	TGAAACTCTGAGCAAGCACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_377	chr21:36824261-36824344	+	TGAAACTCTGAGCAAGCACT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_378	chr21:36824270-36824331	+	GTCTTGCTCCAGAGTTCAGT	Yes	No	No	0	0	0	0	No
NM_hsa_379	chr21:17783606-17783678	-	TGCTGCTTCCCTGCCACAGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_379	chr3:17783597-17783693	-	TGCTGCTTCCCTGCCACAGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_38	chr1:52344884-5234492	+	AGAACCCGGAGATATT	Yes	No	No	0	0	0	0	No
NM_hsa_380	chr3:17783606-17783678	-	TGCGGGGAGGAGGAGGAGGCGCC	Yes	No	No	0	0	0	0	No
NM_hsa_383	chr1:50004055-50004123	+	TGCCCCCAAGCTCTGACAG	Yes	Yes	No	0.113971	0	0	0	No
NM_hsa_383	chr1:50004055-50004115	+	TGCCCCCAAGCTCTGACAG	Yes	Yes	No	0.113971	0	0	0	No
NM_hsa_384	chr1:50004055-50004115	+	GGTCAAGGTTGGGAGACAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_385	chr4:141073442-141073502	+	TCCGCCCTTCCCTCCAGGG	Yes	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_385	chr4:141073409-141073511	+	TCCGCCCTTCCCTCCAGGG	Yes	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_386	chr4:141073442-141073502	+	AAAGGGGTGGCTGGGAGGA	Yes	No	No	0.170957	0	0	0	No
NM_hsa_387	chr20:62321023-62321105	+	CTGGGTAAAGCGGCTGGTGA	Yes	No	No	0	0	0	0	Yes
NM_hsa_388	chr20:62321023-62321105	+	ACCGAGCCCTCCGCCACAGT	Yes	No	No	0	0	0	0	Yes
NM_hsa_389	chr4:43220997-43221078	+	TCCCAAGTCTCCAGCAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_389	chr4:43221007-43221070	+	TCCCAAGTCTCCAGCAGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_39	chr22:36309643-36309495	+	TTTGCTGGTCTCAGAGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_39	chr22:36309643-36309486	+	TTTGCTGGTCTCAGAGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_390	chr22:36309643-36309495	+	TTTGCTGGTCTCAGAGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_391	chr5:133840081-133840189	+	TGCTGAGCAATATGGGAAAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_391	chr5:133840081-133840189	+	TTGCTGGCTTAGGAGCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_391	chr5:133840081-133840219	-	TTGCTGGCTTAGGAGCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_392	chr5:133840111-133840179	-	TTGCTGGCTTAGGAGCTGTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_395	chr22:36309634-36309740	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_395	chr22:36309639-36309765	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_395	chr22:36309664-36309728	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_395	chr22:36309667-36309731	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_396	chr22:36309664-36309740	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_396	chr22:36309667-36309731	+	TAGATATCATAGAAATCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_398	chr1:64588680-4588751	-	GTGAGTCACTGATATCTATA	Yes	No	No	0	0	0	0	No
NM_hsa_399	chr2:70263108-70263246	+	AACCTTGAAGCTGAATCTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_399	chr2:70263107-70263206	+	AACCTTGAAGCTGAATCTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_399	chr2:70263140-70263209	+	AACCTTGAAGCTGAATCTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_399	chr2:70263115-70263223	+	AACCTTGAAGCTGAATCTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_399	chr2:70263129-70263216	+	AACCTTGAAGCTGAATCTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_40	chr1:7604937-7604915	+	CTCTGAAGCAAGCTGAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_40	chr1:7604943-7604949	+	CTCTGAAGCAAGCTGAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_40	chr1:76049423-76049486	+	CTCTGAAGCAAGCTGAGAGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_400	chr2:70263137-70263206	+	AGATATTCAGCTCAAGTCA	Yes	No	No	0	0	0	0	No
NM_hsa_400	chr2:70263104-70263209	+	AGATATTCAGCTCAAGTCA	Yes	No	No	0	0	0	0	No
NM_hsa_401	chr1:76553876-76553974	+	TAGATATCATAGAAATCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_401	chr1:76553888-76553965	+	TAGATATCATAGAAATCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_402	chr1:76553888-76553965	+	TGCTGCTGGAGATCTTCA	Yes	No	No	0	0	0	0	No
NM_hsa_403	chr1:55195301-55195363	+	AGAGGACCAAGCAATCTGTG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_403	chr1:55195298-55195360	+	AGAGGACCAAGCAATCTGTG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_403	chr1:55195291-55195331	+	AGAGGACCAAGCAATCTGTG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_403	chr1:55195262-55195400	+	AGAGGACCAAGCAATCTGTG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_404	chr1:55195298-55195360	+	CAGTATGTTGCTCCCTCTAG	Yes	No	No	0	0	0	0	No
NM_hsa_407	chr22:41048564-41048664	+	CTACCTCCCTCCAGCAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_407	chr22:41048574-41048649	+	CTACCTCCCTCCAGCAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_407	chr22:41048563-41048649	+	CTACCTCCCTCCAGCAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_408	chr22:41048574-41048640	+	GTGGGGTGGGAGGAGGCGCCGG	Yes	No	No	0	0	0	0	No
NM_hsa_409	chr8:103818795-103818931	+	CGCTGATGCTCAGCTGGAG	Yes	No	Yes	0	0	0	0	No
NM_hsa_409	chr8:103818834-103818892	+	CGCTGATGCTCAGCTGGAG	Yes	No	Yes	0	0	0	0	No
NM_hsa_41	chr1:1857597-1857655	+	AGGAGGAGGAGGAGGAGGCGCC	Yes	Yes	Yes	0.341914	0.0331113	0.0732862	No	No
NM_hsa_410	chr8:103818834-103818892	+	TGCGAAACTGTTGATCAGAGGGT	Yes	No	No	0	0	0	0	No
NM_hsa_411	chr1:133231459-133231531	+	TGCGAAACTGTTGATCAGAGGGT	Yes	No	No	0	0	0	0	No
NM_hsa_412	chr1:133231459-133231531	+	GCCCCGGAATGCTGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_415	chr1:1857597-1857655	+	CTGGCTACCCGCTGCTCAG	Yes	No	Yes	0	0	0	0	No
NM_hsa_415	chr1:1857556-1857694	+	CTGGCTACCCGCTGCTCAG	Yes	No	Yes	0	0	0	0	No
NM_hsa_416	chr1:1857597-1857655	+	GCGCAGCTGGTGGGCTGAGTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_417	chr1:229935783-229935923	+	CTCTGAACCAAGCAAGCCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_417	chr1:229935825-229935884	+	CTCTGAACCAAGCAAGCCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_417	chr1:229935809-229935931	+	CTCTGAACCAAGCAAGCCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_418	chr1:229935825-229935884	+	GCGGCTGGGAGGAGGAGGCGCC	Yes	No	No	0	0	0	0	No
NM_hsa_419	chr1:4640481-4640556	+	TTTGGCTGTCGACCCCGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_419	chr1:4640498-4640547	+	TTTGGCTGTCGACCCCGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_42	chr3:12875318-128753402	+	CCGTGAGCTCCAGCCTGCTG	Yes	No	No	0.113971	0.132445	0	0	No
NM_hsa_420	chr1:94464096-4640495	+	GTGGTGGGAGGAGGAGGCGCC	Yes	No	No	0	0	0	0	No
NM_hsa_421	chr1:57950479-57950542	+	TTATGGCTCCCTTGCTGCA	Yes	Yes	Yes	1.13971	0.79467	1.09929	Yes	Yes
NM_hsa_421	chr1:57950444-57950572	+	TTATGGCTCCCTTGCTGCA	Yes	Yes	Yes	1.13971	0.79467	1.09929	Yes	Yes
NM_hsa_421	chr1:57950409-57950549	+									

Name	locus	strand	sequence	midrep2	miraprep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_466	chr10:129535431-129535515	+	TCGCCAGTGGAGTTTCGGTCCGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_466	chr10:129535449-129535506	+	TCGCCAGTGGAGTTTCGGTCCGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_467	chr10:129535449-129535506	+	GCACCCGGGGCCCTCGCGCCGG	Yes	No	No	0	0	0	0	No
NM_hsa_468	chr18:30350208-30350271	+	AGCAGCTGTTCGGGGGGGGG	Yes	No	No	0	0	0	0	No
NM_hsa_469	chr18:30350208-30350271	+	TCTCGCGGGCCGCTGCTCG	Yes	No	No	0	0	0.146572	0	No
NM_hsa_47	chr2:188104481-188104551	+	ATGATCTGCATCTCTGGACC	Yes	Yes	No	0	0	0	0	No
NM_hsa_470	chr1:188104471-188104560	+	ATGATCTGCATCTCTGGACC	Yes	Yes	No	0	0	0	0	No
NM_hsa_470	chr1:237736806-237736886	-	GAACAACCCATCCCTTCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_470	chr1:237736815-237736874	-	GAACAACCCATCCCTTCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_470	chr1:237736803-237736891	-	GAACAACCCATCCCTTCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_470	chr1:237736818-237736877	-	GAACAACCCATCCCTTCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_470	chr1:237736791-237736899	-	GAACAACCCATCCCTTCCAG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_471	chr1:237736818-237736877	-	GGAAGAGGATAGGGTGTCTA	Yes	No	No	0	0	0	0	No
NM_hsa_472	chr13:27259465-27259541	+	TAGCCATAGCCACATGTCAGT	Yes	Yes	Yes	0	0.132445	0	0	Yes
NM_hsa_472	chr13:27259475-27259533	+	TAGCCATAGCCACATGTCAGT	Yes	Yes	Yes	0	0.132445	0	0	Yes
NM_hsa_472	chr15:27259402-27259570	+	TAGCCATAGCCACATGTCAGT	Yes	Yes	Yes	0	0.132445	0	0	Yes
NM_hsa_473	chr13:27259475-27259533	+	CTATATGTGCTAGTGGCTGCT	Yes	No	No	0	0	0.397335	0	Yes
NM_hsa_474	chr1:22170792-22170843	-	CTGACCTTCCCTCGCCCCAG	Yes	No	No	0.683829	0.0662225	0.219859	0	No
NM_hsa_475	chr1:22170792-22170843	-	GAGGACCTCAGGTCGCTCACTG	Yes	No	No	0	0	0	0	No
NM_hsa_476	chr8:13222065-13222068	+	CCGGAGCCCGCTGCTGAGT	Yes	No	No	0	0	0	0	No
NM_hsa_478	chr11:76156399-76156480	+	TATCCCGTGGCTATCTCTCT	Yes	Yes	Yes	0.626843	0.0662225	0.073262	0	Yes
NM_hsa_478	chr11:76156409-76156473	+	TATCCCGTGGCTATCTCTCT	Yes	Yes	Yes	0.626843	0.0662225	0.073435	0	Yes
NM_hsa_478	chr11:76156374-76156502	+	TATCCCGTGGCTATCTCTCT	Yes	Yes	Yes	0.626843	0.0662225	0.073435	0	Yes
NM_hsa_479	chr11:76156409-76156473	+	AGGGAGTGGAGCGGGGCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_48	chr2:188104481-188104551	+	AACAGAGTACACAGATCCACA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_48	chr2:188104446-188104574	+	AACAGAGTACACAGATCCACA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_48	chr2:188104471-188104560	+	AACAGAGTACACAGATCCACA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_480	chr1:55784366-55784417	+	AGCTCCAGTCCGCTCGTAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_480	chr1:55784352-55784426	+	AGCTCCAGTCCGCTCGTAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_481	chr1:55784366-55784417	+	CAGGCCAGGCTGGGAGGATGC	Yes	No	No	0	0	0	0	No
NM_hsa_482	chr11:133012742-133012794	+	CTGGGCAAAAGAACTCAAGTCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_482	chr11:133012730-133012803	+	CTGGGCAAAAGAACTCAAGTCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_483	chr11:133012742-133012794	+	AGTGGAGGCTTCTGCCATATC	Yes	No	No	0	0	0	0	No
NM_hsa_484	chr3:175325994-175326051	+	AGATTGGGATCTATGGCTAAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_484	chr3:175325997-175326065	+	AGATTGGGATCTATGGCTAAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_484	chr3:175325994-175326062	+	AGATTGGGATCTATGGCTAAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_485	chr3:175325997-175326065	+	TAGCCCAATGCCAATCTGTA	Yes	No	No	0	0	0	0	No
NM_hsa_485	chr3:175325994-175326062	+	TAGCCCAATGCCAATCTGTA	Yes	No	No	0	0	0	0	No
NM_hsa_488	chr17:59438889-59438965	-	CCTGTGACACATCATGATGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_488	chr17:59438880-59438977	-	CCTGTGACACATCATGATGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_489	chr17:59438889-59438965	-	CATCAGATGTGTCACAGATA	Yes	No	No	0	0	0	0	No
NM_hsa_490	chr7:29883565-29883636	+	CTGTGGCAGCAGGAAGTCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_490	chr7:29883546-29883635	+	CTGTGGCAGCAGGAAGTCCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_491	chr7:29883565-29883636	+	TGGCTCTGGCTCCAGGCC	Yes	No	No	0	0	0	0	No
NM_hsa_492	chr22:42816210-42816301	+	ACCTTAAGATCAGCTCGACA	Yes	Yes	No	0	0	0	0	No
NM_hsa_494	chr17:42993701-42993759	+	TCTGGCTTATAGGACTTTAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_494	chr17:42993701-42993759	+	TCTGGCTTATAGGACTTTAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_494	chr17:42993685-42993768	+	TCTGGCTTATAGGACTTTAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_495	chr17:42993701-42993759	+	GGAGGCTCTATGAGGCAAGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_498	chrX:126451083-126451191	+	TCTTTCAACCACTCCAGAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_498	chrX:126451108-126451166	+	TCTTTCAACCACTCCAGAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_498	chrX:126451099-126451176	+	TCTTTCAACCACTCCAGAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_498	chrX:126451086-126451194	+	TCTTTCAACCACTCCAGAGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_499	chrX:126451108-126451166	+	TCTGGAGGTTGTAAAGGAAA	Yes	No	No	0	0	0	0	No
NM_hsa_500	chr5:137673931-137674003	+	CTGGAGAAACCCGGGTAGT	Yes	No	No	0	0	0	0	No
NM_hsa_502	chr2:43454591-43454641	+	GCCTGGCGCTGTAAAG	Yes	No	No	0	0	0	0	No
NM_hsa_503	chr2:43454591-43454641	+	TCCGCTGCTGGCC	Yes	No	No	0	0	0	0	No
NM_hsa_504	chr9:7967909-7967992	+	TTAGGAATGGGCTGGATT	Yes	Yes	No	0	0	0	0	No
NM_hsa_504	chr9:7967921-7967983	+	TTAGGAATGGGCTGGATT	Yes	Yes	No	0	0	0	0	No
NM_hsa_505	chr9:7967921-7967983	+	TCCAGATCCCAATCTCAACG	Yes	No	No	0	0	0	0	No
NM_hsa_506	chr4:141677685-141677756	+	CCCGCCAGCCAGTGGCTCCG	Yes	No	No	0	0.132445	0.073262	0	No
NM_hsa_507	chr4:141677685-141677756	+	AGCTCCGAGTCCCGCCGCT	Yes	No	No	0	0.132445	0.073262	0	No
NM_hsa_508	chr8:18961076-18961133	+	CTCTGGAGATCTGAAATGTA	Yes	Yes	Yes	0	0.132445	0.073262	0	Yes
NM_hsa_508	chr8:18961039-18961167	+	CTCTGGAGATCTGAAATGTA	Yes	Yes	Yes	0	0.132445	0.073262	0	Yes
NM_hsa_508	chr8:18961061-18961142	+	CTCTGGAGATCTGAAATGTA	Yes	Yes	Yes	0	0.132445	0.073262	0	Yes
NM_hsa_509	chr8:18961076-18961133	+	TACTTGAATCCAGGACTA	Yes	No	No	0	0	0	0	No
NM_hsa_51	chr8:54111682-54111808	+	CATGTGAATCACTTTTACA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_51	chr8:54111717-54111776	+	CATGTGAATCACTTTTACA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_51	chr8:54111707-54111785	+	CATGTGAATCACTTTTACA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_510	chr20:3748726-3748807	+	CTTGAACCTGTTGAGGAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_510	chr20:3748726-3748799	+	CTTGAACCTGTTGAGGAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_511	chr20:3748726-3748799	+	TGGGGCGCTTCCGGCC	Yes	No	No	0	0	0	0	No
NM_hsa_512	chr8:126442070-126442070	+	GGGGCGGGGGGGGGGGGGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_512	chr8:126442038-126442095	+	GGGGCGGGGGGGGGGGGGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_513	chr8:126442038-126442095	+	GGCGCCCTATCCAGTAAGC	Yes	No	No	0	0	0	0	No
NM_hsa_514	chr22:5074254-50744313	-	AGGAGCTCTGGGCCACCCA	Yes	No	No	0	0	0	0	No
NM_hsa_515	chr22:5074254-50744313	-	AGTGGGCGAAGCCCTC	Yes	No	No	0	0	0	0	No
NM_hsa_518	chr10:10275735-102757604	+	TGCTCCAGCGGAGGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_519	chr10:10275735-102757604	+	CTCTCCGGGAACCCGAG	Yes	No	No	0	0	0	0	No
NM_hsa_52	chr8:54111689-54111805	+	TGAAAAGTGGTTCATAGGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_52	chr8:54111717-54111776	+	TGAAAAGTGGTTCATAGGGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_520	chr19:5978306-5978381	+	CATCTCCGCTCTTTCCGCCG	Yes	Yes	Yes	0.0569857	0.331113	0	0	No
NM_hsa_520	chr19:5978316-5978373	+	CATCTCCGCTCTTTCCGCCG	Yes	Yes	Yes	0.0569857	0.331113	0	0	Yes
NM_hsa_521	chr19:5978316-5978373	+	CGGGGAAGGCGGGGAGGGG	Yes	No	No	0	0	0.0662225	0	No
NM_hsa_522	chr5:17925113-179251183	+	CTCTGTAATCTCTCCCGCC	Yes	No	No	0.0569857	0.0662225	0	0	No
NM_hsa_523	chr5:17925113-179251183	+	TGGAGGAGCTCAGGGT	Yes	No	No	0	0	0	0	No
NM_hsa_524	chr8:145584178-145584244	+	TGGCGTGGAACTCAGGGCTG	Yes	No	No	0.0569857	0.0993338	0	0	No
NM_hsa_525	chr8:145584178-145584244	+	AGCCCTGACATCTCTGCTGCA	Yes	No	No	0	0	0	0	No
NM_hsa_526	chr22:41048069-41048125	+	AGTCACTCCCTCTGGCCAG	Yes	No	No	0	0	0	0	No
NM_hsa_527	chr22:41048069-41048125	+	GGCTGGAGGAGGAGGAGCCA	Yes	No	No	0	0	0	0	No
NM_hsa_528	chr10:82906028-82906089	+	CGAGATCTCTGTAACCTAGA	Yes	No	No	0.0569857	0	0	0	No
NM_hsa_529	chr10:82906028-82906089	+	TGAGTACACAGACATCTGTG	Yes	No	No	0	0	0	0	No
NM_hsa_53	chr22:50926246-50926313	+	CAGTCCCTCTCTCCCGCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_53	chr22:50926237-50926322	+	CAGTCCCTCTCTCCCGCC	Yes	Yes	No	0	0	0	0	No
NM_hsa_530	chr11:13044214-130442208	+	TTTGACTGCTGGGGAATGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_530	chr11:13044214-130442198	+	TTTGACTGCTGGGGAATGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_531	chr11:13044214-130442198	+	ATTCCAGTCCAGTGAAGAG								

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_57	chr11:131565798-131565873	+	ATCTGTCCCAAGATGACAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_57	chr11:131565798-131565906	+	ATCTGTCCCAAGATGACAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_570	chr7:38351095-38351153	+	GCCTTCCTCCGACAGC	No	No	No	0	0	0	0	No
NM_hsa_572	chr6:33175630-33175691	+	GACGTCCAGACTCACTCTC	Yes	No	No	0.0569857	0	0	0	Yes
NM_hsa_573	chr17:1633600-1633681	+	TGGGGTGGGAGGGTATGAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_573	chr17:1633610-1633673	+	TGGGGTGGGAGGGTATGAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_573	chr17:1633570-1633708	+	TGGGGTGGGAGGGTATGAGC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_574	chr17:1633610-1633673	+	TCAGGGCTCTCCACCCCCA	Yes	No	No	0	0	0	0.0732862	Yes
NM_hsa_575	chr2:23458968-23458973	-	CGCTCACTGTGTCTGCACAA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_575	chr2:23458971-23458973	-	CGCTCACTGTGTCTGCACAA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_575	chr2:23458975-23458973	-	CGCTCACTGTGTCTGCACAA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_576	chr2:23458971-23458973	-	CGAGAGACAGAGTGGCCACA	Yes	No	No	0	0	0	0	No
NM_hsa_579	chr8:70560149-70560265	+	CTTTGGATATAGCAGGAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_579	chr8:70560181-70560236	+	CTTTGGATATAGCAGGAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_579	chr8:70560168-70560245	+	CTTTGGATATAGCAGGAGC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_58	chr11:131565808-131565867	+	CCGCTCAAGGACAGGCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_580	chr8:70560181-70560236	+	TCTCTAGTATCAAAAGCC	Yes	No	No	0	0	0	0	No
NM_hsa_581	chr14:21493471-21493545	+	GGATCCCTCGGCTCCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_581	chr14:21493480-21493536	+	GGATCCCTCGGCTCCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_582	chr14:21493480-21493536	+	GGATCCCTCGGCTCCAGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_585	chr22:41621146-41621227	+	CTGCACCAGAGCTCCGACTT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_585	chr22:41621159-41621218	+	CTGCACCAGAGCTCCGACTT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_586	chr22:41621159-41621218	+	CTGCACCAGAGCTCCGACTT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_587	chr1:162531046-162531121	+	GTCGAGGGGGCTCTGCTCC	Yes	No	No	0	0	0	0	No
NM_hsa_587	chr1:162531103-162531146	+	GTCGAGGGGGCTCTGCTCC	Yes	No	No	0	0	0	0	No
NM_hsa_588	chr1:162531103-162531146	+	TGGCCTCACTGAGGCT	Yes	No	No	0	0	0	0	No
NM_hsa_589	chr20:44523532-44523672	+	GACCCACTGTCTGTCCCTCC	Yes	Yes	Yes	0.0569857	0	0	0	No
NM_hsa_589	chr20:44523548-44523623	+	GACCCACTGTCTGTCCCTCC	Yes	Yes	Yes	0.0569857	0	0	0	No
NM_hsa_589	chr20:44523567-44523623	+	GACCCACTGTCTGTCCCTCC	Yes	Yes	Yes	0.0569857	0	0	0	No
NM_hsa_59	chr6:41701281-41701358	+	CCCGGAGAGCTGGAGCCAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_59	chr6:41701251-41701387	+	CCCGGAGAGCTGGAGCCAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_59	chr6:41701290-41701348	+	CCCGGAGAGCTGGAGCCAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_590	chr20:44523567-44523623	+	CCCGGAGAGCTGGAGCCAGA	Yes	No	No	0	0	0	0	No
NM_hsa_591	chr13:13785734-13785795	+	TCTCTGAGAGTTCTGCTGTA	Yes	Yes	Yes	1.82354	2.0259	0.806149	0	No
NM_hsa_592	chr13:13785734-13785795	+	GGTCAAAAATCTGAGTGGAT	Yes	No	No	0	0	0	0.132445	No
NM_hsa_593	chr15:57608855-57608912	+	TCATCCCAAGAAAGGCTTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_593	chr15:57608845-57608920	+	TCATCCCAAGAAAGGCTTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_593	chr15:57608815-57608951	+	TCATCCCAAGAAAGGCTTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_594	chr15:57608855-57608912	+	CAAGTCACTTCTGGGGTCC	Yes	No	No	0	0	0	0	No
NM_hsa_597	chr6:25279591-25279649	+	AGGGCTGTAGTGGCGCGC	Yes	No	No	0	0	0	0	No
NM_hsa_598	chr6:25279591-25279649	+	AGGGCTGTAGTGGCGCGC	Yes	No	No	0	0	0	0	No
NM_hsa_599	chr5:156736971-156737087	+	CAAAAGGGCTCAGAGCAGAGC	Yes	Yes	Yes	0	0	0.0569857	0	Yes
NM_hsa_599	chr5:156736979-156737067	+	CAAAAGGGCTCAGAGCAGAGC	Yes	Yes	Yes	0	0	0.0569857	0	Yes
NM_hsa_599	chr5:156736995-156737058	+	CAAAAGGGCTCAGAGCAGAGC	Yes	Yes	Yes	0	0	0.0569857	0	Yes
NM_hsa_60	chr6:41701281-41701358	+	TGGTCCCTCTCTCCGCTGCG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_60	chr6:41701290-41701348	+	TGGTCCCTCTCTCCGCTGCG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_600	chr5:15673695-156737058	+	GGTCTCTGAGCTCTCTGCTG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_601	chr20:9491465-9491536	+	TCTTGGGACAGAACTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_601	chr20:9491457-9491546	+	TCTTGGGACAGAACTGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_602	chr20:9491465-9491536	+	AGTTTCTATCCCAAGGCT	Yes	No	No	0	0	0	0	No
NM_hsa_603	chr10:3827731-3827776	+	CTGTGAGGTCGGCCGCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_604	chr10:3827731-3827776	+	CGCCGGCCGGCCGAGGAGTC	Yes	No	No	0	0	0	0	No
NM_hsa_605	chr2:182013372-182013434	+	TCTTGGATCTGGTATCTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_605	chr2:182013347-182013455	+	TCTTGGATCTGGTATCTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_605	chr2:182013362-182013434	+	TCTTGGATCTGGTATCTGGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_606	chr2:182013372-182013434	+	ACAGATGAGAGTCCACAGATA	Yes	No	No	0	0	0	0	No
NM_hsa_608	chr14:4553280-4553345	+	TGACTTTTCCGCTCCAGGG	Yes	No	No	0	0	0	0	No
NM_hsa_609	chr1:44451113-44451190	+	TCTGCTCCCTCCCTCCTCAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_61	chr3:49824155-49824209	+	GCTACTACAGGCGGAGGCG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_61	chr3:49824149-49824250	+	GCTACTACAGGCGGAGGCG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_61	chr3:49824183-49824259	+	GCTACTACAGGCGGAGGCG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_610	chr1:44451113-44451190	+	GGAGGGGGGCTCAGAGT	Yes	No	No	0	0	0	0	No
NM_hsa_611	chr10:89307582-89307655	+	AGATTGATGATGCTCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_611	chr10:89307572-89307676	+	AGATTGATGATGCTCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_611	chr10:89307592-89307647	+	AGATTGATGATGCTCTGTGG	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_612	chr10:89307592-89307647	+	ATAGAGCCATCTGCAATATG	Yes	No	No	0	0	0	0.0732862	Yes
NM_hsa_613	chr1:45349964-45350026	+	CCCATCTTCCACCCCTCTC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_613	chr1:45349945-45350039	+	CCCATCTTCCACCCCTCTC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_614	chr5:9053936-9054009	+	GAGTGGTGGGAGATATGCA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_615	chr5:9053936-9054009	+	TAAAGGCTTGAACACGAGTTC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_615	chr5:9053938-9054000	+	TAAAGGCTTGAACACGAGTTC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_615	chr5:9053906-9054034	+	TAAAGGCTTGAACACGAGTTC	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_616	chr5:9053936-9054009	+	ACTGTGCTTGAAGCTTTCAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_617	chr3:5242790-5242803	+	CTTCTCGAGCTTGAAGTGGC	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_618	chr3:5242790-5242803	+	TGCTCAAGTCTTGAAGAGGCG	Yes	No	No	0	0	0	0	No
NM_hsa_619	chr3:3185631-31856375	+	GTGGGGCTGGGCTGGTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_619	chr3:31856311-31856385	+	GTGGGGCTGGGCTGGTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_62	chr3:49824193-49824250	+	TCTGTTCCGAGGCTGGCTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_62	chr3:49824183-49824259	+	TCTGTTCCGAGGCTGGCTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_62	chr3:49824155-49824287	+	TCTGTTCCGAGGCTGGCTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_620	chr3:1853131-1853175	+	CCCGCCCGCTCCAGCCAGC	Yes	No	No	0	0	0	0	No
NM_hsa_621	chr1:2266897-2266960	+	GGGTCTGGTCTCCACC	Yes	No	No	0	0	0	0	No
NM_hsa_622	chr3:126751433-126751525	+	GTAGGTGGAGGGTCCAGGGGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_622	chr3:126751443-126751518	+	GTAGGTGGAGGGTCCAGGGGT	Yes	Yes	No	0	0	0	0	No
NM_hsa_623	chr3:126751443-126751518	+	TGTTGCTCCAGCTCCAGGCA	Yes	No	No	0	0	0	0	No
NM_hsa_624	chr3:153106182-153106258	+	ATCAATGATTTGTTCACTGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_624	chr3:153106175-153106263	+	ATCAATGATTTGTTCACTGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_624	chr3:153106194-153106249	+	ATCAATGATTTGTTCACTGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_625	chr3:153106194-153106249	+	TCAGTGAATGATTTGACTA	Yes	No	No	0	0	0	0	No
NM_hsa_626	chr22:37942071-37942110	+	TGCTGCTCAGCAGGCTCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_627	chr22:37942071-37942110	+	GGGGCCGAGGCTTCA	Yes	No	No	0	0	0	0	No
NM_hsa_628	chr4:1737218-1737289	+	AGCCCAAGGAACTCTGACA	Yes	Yes	No	4.72982	17.0854	37.9623	No	H-KapB-KapB-cMye
NM_hsa_628	chr4:1737207-1737289	+	AGCCCAAGGAACTCTGACA	Yes	Yes	No	4.72982	17.0854	37.9623	No	H-KapB-KapB-cMye
NM_hsa_629	chr4:1737218-1737289	+	TCTAATGGTCTCTTGGCAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_63	chr15:101460156-101460250	+	TCTCTGAGGCTGGGCGGCGC	Yes	Yes	No	0	0	0.132445	0	No
NM_hsa_630	chr15:101460166-101460241	+	TCTCTGAGGCTGGGCGGCGC	Yes	Yes	No	0	0	0.132445	0	No
NM_hsa_630	chr11:65190840-65190882	+	TTTTCTCGGCTGGGAGC	Yes	No	No	0.0569857	0.0662225	0.0732862	0	H-KapB-KapB-cMye
NM_hsa_631	chr11:65190840-6519										

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation	
NM_hsa_676	chr19:1290067-1290078	-	CTCCGAGTCCAGGGCCGG	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_676	chr19:1290067-1290078	-	CTCCGAGTCCAGGGCCGG	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_676	chr19:1290067-1290078	-	CTCCGAGTCCAGGGCCGG	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_677	chr19:1290067-1290078	-	CTGCTGGGGCCCGAGCCAGAA	Yes	No	No	0	0	0	0	No	
NM_hsa_68	chr15:49622618-49622694	+	AGTGGTGGAAATCTGATACT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_68	chr15:49622598-49622714	+	AGTGGTGGAAATCTGATACT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_68	chr15:49622628-49622685	+	AGTGGTGGAAATCTGATACT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_680	chr17:2497441-2497524	+	CCCGGAGGAGGGGAGCTGT	Yes	No	No	0	0	0	0	No	
NM_hsa_681	chr17:2497441-2497524	+	CCTCCCTCTCTCTTCTTC	Yes	No	No	0	0	0	0	No	
NM_hsa_682	chr2:112662460-112662524	+	TCTGGCACTCGGGATCTGGCT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_682	chr2:112662425-112662524	+	TCTGGCACTCGGGATCTGGCT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_682	chr2:112662448-112662533	+	TCTGGCACTCGGGATCTGGCT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_683	chr2:112662460-112662524	+	CCAACCTCAGGTCGCGGAGG	Yes	No	No	0	0	0	0	No	
NM_hsa_686	chr8:138335349-138335424	+	TGTGTCAGTGGGCTGAAATGA	Yes	Yes	No	0	0	0	0	No	
NM_hsa_686	chr8:138335359-138335416	+	TGTGTCAGTGGGCTGAAATGA	Yes	Yes	No	0	0	0	0	No	
NM_hsa_687	chr8:138335359-138335416	+	TGTGTCAGTGGGCTGAAATGA	Yes	Yes	No	0	0	0	0	No	
NM_hsa_688	chr19:1003074-1003146	+	CACCCTCTCCAGAACCCATT	Yes	Yes	No	0.113971	0	0	0	Yes	
NM_hsa_688	chr19:1003074-1003137	+	CACCCTCTCCAGAACCCATT	Yes	Yes	No	0.113971	0	0	0	Yes	
NM_hsa_689	chr19:1003074-1003137	+	AGGGTTTGGGGGGTGA	Yes	No	No	0	0	0	0	No	
NM_hsa_69	chr9:129202091-12920292	+	CCTCTGTACAGCTCTGG	Yes	No	Yes	0	0	0	0	No	
NM_hsa_69	chr9:129202413-129202473	+	CCTCTGTACAGCTCTGG	Yes	No	Yes	0	0	0	0	No	
NM_hsa_690	chr1:110302413-110302499	+	GACTCTGTACTCCCTGCTGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_690	chr1:110302423-110302481	+	GACTCTGTACTCCCTGCTGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_690	chr1:110302393-110302513	+	GACTCTGTACTCCCTGCTGC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_691	chr1:110302423-110302481	+	CCTCAGGAGGAGGGGCTGT	Yes	No	No	0	0	0	0	No	
NM_hsa_693	chr10:113943427-113943506	+	CTCCAGGCGAGGCTGT	Yes	No	No	0	0	0	0	No	
NM_hsa_694	chr1:1560296-1560356	+	AGGGGCGGGCTCAGGGCTGG	Yes	No	No	0	0	0	0	No	
NM_hsa_695	chr1:1560296-1560356	+	CAGCTTAGCTCTGGGGG	Yes	No	No	0	0	0	0	No	
NM_hsa_696	chr7:73770615-73770754	+	GGCAGAGGATGAGGCTGTCT	Yes	No	Yes	0	0	0	0	No	
NM_hsa_697	chr7:73770655-73770761	+	CTTGGGCTCTCTCTTCCA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_697	chr7:73770674-73770737	+	CTTGGGCTCTCTCTTCCA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_697	chr7:73770661-73770746	+	CTTGGGCTCTCTCTTCCA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_698	chr7:73770674-73770737	+	GAGGAGGAGGAGGCTCCAGCT	Yes	No	No	0	0	0	0	Yes	
NM_hsa_7	chr14:94579986-94580044	+	TTTGTGTGTCAGGTCAGGTT	Yes	Yes	Yes	1.25369	1.58934	2.1253	1.58934	H-KapB-KapB-cMye	
NM_hsa_7	chr14:94579976-94580053	+	TTTGTGTGTCAGGTCAGGTT	Yes	Yes	Yes	1.25369	1.58934	2.1253	1.58934	H-KapB-KapB-cMye	
NM_hsa_70	chr9:129202393-129202491	+	CGAGGCCCTTCTGTATGGAG	Yes	No	Yes	0	0	0	0	No	
NM_hsa_70	chr9:129202413-129202473	+	CGAGGCCCTTCTGTATGGAG	Yes	No	Yes	0	0	0	0	No	
NM_hsa_701	chr15:68992906-68992955	+	CCGAGGAGGCGGGGGGGG	Yes	No	No	0	0	0	0	No	
NM_hsa_702	chr15:68992906-68992955	+	ACCAGGCCCTCCCCAGGGG	Yes	No	No	0	0	0	0	No	
NM_hsa_703	chr8:143557199-143557254	+	CTCTGAGAAAGCAGGACTAA	Yes	No	No	0	0	0	0	No	
NM_hsa_704	chr8:143557199-143557254	+	GGGCTCCAGAGGAGGCT	Yes	No	No	0	0	0	0	No	
NM_hsa_705	chr14:919251-1419256	+	CGAGGCGGGCTGAGTGGGA	Yes	No	No	0.484379	0.629114	0.622933	0.629114	H-KapB-KapB-cMye	
NM_hsa_705	chr19:1419251-1419256	+	CGAGGCGGGCTGAGTGGGA	Yes	No	No	0	0	0	0	No	
NM_hsa_707	chr9:139887231-139887339	+	TCTGCCCGCTTGTAGTGTAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_707	chr9:139887256-139887315	+	TCTGCCCGCTTGTAGTGTAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_707	chr9:139887256-139887315	+	TCTGCCCGCTTGTAGTGTAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_708	chr9:139887256-139887315	+	AGGGCTTGGGCTCGGCAAGTT	Yes	No	No	0	0	0	0	No	
NM_hsa_709	chr5:167592864-167592923	+	CCTCACTGGGATAAGCAATT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_709	chr5:167592881-167592932	+	CCTCACTGGGATAAGCAATT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_710	chr5:167592881-167592932	+	CCTCACTGGGATAAGCAATT	Yes	Yes	No	0	0	0	0	No	
NM_hsa_710	chr5:167592864-167592923	+	CTCTTGGGACTAAATGG	Yes	No	No	0	0	0	0	No	
NM_hsa_711	chr14:93581816-93581868	+	CTCTTGGGACTAAATGG	Yes	No	No	0	0	0	0	No	
NM_hsa_712	chr14:93581816-93581868	+	CTCTTGGGACTAAATGG	Yes	No	No	0	0	0	0	No	
NM_hsa_713	chr5:155143-155144	+	TGGTCTGGTTTGGGGCTCAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_713	chr5:155143-155144	+	TGGTCTGGTTTGGGGCTCAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_713	chr5:15525-315585	+	TGGTCTGGTTTGGGGCTCAG	Yes	Yes	Yes	0	0	0	0	Yes	
NM_hsa_714	chr5:15525-315585	+	CCAGCTCTTCTCCAGAGCTTC	Yes	No	No	0	0	0	0	Yes	
NM_hsa_715	chr8:49427253-49427297	+	CAGGCCCGGAGTCCACCC	Yes	No	No	0	0	0	0	No	
NM_hsa_718	chr1:67069157-67069203	+	CTGTGGGCTCTGGGCTCAG	Yes	No	No	0	0	0	0	Yes	
NM_hsa_719	chr1:67069157-67069203	+	CTGTGGGCTCTGGGCTCAG	Yes	No	No	0	0	0	0	Yes	
NM_hsa_722	chrX:48673316-48673370	+	GGCTCCCGGCTCAGCC	Yes	No	No	0	0	0	0	No	
NM_hsa_722	chrX:48673316-48673370	+	GGCTCCCGGCTCAGCC	Yes	No	No	0	0	0	0	No	
NM_hsa_726	chr12:98044116-98044189	+	ATAACGAAAGCTAGACTGA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_726	chr12:98044106-98044202	+	ATAACGAAAGCTAGACTGA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_726	chr12:98044126-98044181	+	ATAACGAAAGCTAGACTGA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_727	chr12:98044126-98044181	+	CAGTTTGGCTCTGATTTACT	Yes	No	No	0	0	0	0	No	
NM_hsa_73	chr15:66927983-66927986	+	AAGGCTGGAACCTAGATTTCT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_73	chr15:66927513-66927578	+	AAGGCTGGAACCTAGATTTCT	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_730	chr10:104229664-104229760	+	CTGTCTCCCTCTGGCTCAGA	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_730	chr10:104229675-104229751	+	CTGTCTCCCTCTGGCTCAGA	Yes	Yes	No	0	0	0	0	Yes	
NM_hsa_731	chr10:104229675-104229751	+	AGCAGGCTGAGGCGGAGGA	Yes	No	No	0	0	0	0	No	
NM_hsa_732	chr17:8149132-8149170	+	CTGTGGGACTGGCGGG	Yes	No	No	0	0	0	0	No	
NM_hsa_733	chr17:8149132-8149170	+	TTCGGCCCTCTCTTTC	Yes	No	No	0	0	0	0	No	
NM_hsa_734	chr22:37125466-3712602	+	AGGCCCGCTTGAAGGTT	Yes	No	No	0	0	0	0	No	
NM_hsa_735	chr22:37125466-3712602	+	CTCTAGGAGCTGTGG	Yes	No	No	0	0	0	0	No	
NM_hsa_736	chr19:7506733-7506799	+	CCACACTGCTCTCTCCAGAA	Yes	No	No	0	0	0	0	Yes	
NM_hsa_737	chr19:7506733-7506799	+	TACGGGAGGAAATGGGGTGGCAGTGGT	Yes	No	No	0	0	0	0	Yes	
NM_hsa_738	chr16:9375882-9375939	+	CTTCTGCCCTTCTCCAGCC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_739	chr16:9375882-9375939	+	CTTCTGCCCTTCTCCAGCC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_74	chr15:66927513-66927578	+	AATTCTAGGTCAGCCCTCGG	Yes	No	No	0	0	0	0	No	
NM_hsa_740	chr14:105293075-105293136	+	TCCTGCCCGGGGCTGATGAG	Yes	No	No	0	0	0	0	No	
NM_hsa_741	chr14:105293075-105293136	+	AATGCAACCTTGGACACGGT	Yes	No	No	0	0	0	0	No	
NM_hsa_742	chr2:161053361-161053428	-	TCTAGATTTGGGATGTGACA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_742	chr2:161053330-161053404	-	TCTAGATTTGGGATGTGACA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_742	chr2:161053361-161053428	-	TCTAGATTTGGGATGTGACA	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_742	chr2:161053361-161053428	-	TCAATCCAAATCTGGTGA	Yes	No	No	0	0	0	0	No	
NM_hsa_746	chr13:36104474-36104537	+	GGGCGCTCTCCCGAGT	Yes	No	No	0.370407	0.198668	0.256502	0.198668	Yes	
NM_hsa_747	chr13:36104474-36104537	+	GATGGGAGAGCCCGCC	Yes	Yes	Yes	0	0	0	0	No	
NM_hsa_75	chr22:23736575-23736648	-	TCAGACAGGCTCCCGCAGCC	Yes	Yes	Yes	0	0	0	0	0.0732862	No
NM_hsa_75	chr22:23736550-23736678	-	TCAGACAGGCTCCCGCAGCC	Yes	Yes	Yes	0	0	0	0	0.0732862	No
NM_hsa_75	chr22:23736575-23736648	-	TCAGACAGGCTCCCGCAGCC	Yes	Yes	Yes	0	0	0	0	0.0732862	No
NM_hsa_754	chr6:5773857-5773938	+	TTCAGGCTCTGCTCCCTGTC	Yes	No	No	0	0	0	0	No	
NM_hsa_755	chr6:5773857-5773938	+	TTCAGGCTCTGCTCCCTGTC	Yes	No	No	0	0	0	0	No	
NM_hsa_756	chr14:44045061-44045116	+	CTCAGGAAACGAGCCAGCC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_757	chr14:44045061-44045116	+	CTCAGGAAACGAGCCAGCC	Yes	Yes	No	0	0	0	0	No	
NM_hsa_758	chr9:37804215-37804292	+	TCTTCAAGTCTGGTAACT	Yes	Yes	No	0.0712322	0.0331113	0.146572	0.0331113	Yes	
NM_hsa_758	chr9:37804227-37804283	+	TCTTCAAGTCTGGTAACT	Yes	Yes	No	0.0712322	0.0331113	0.146572	0.0331113	Yes	
NM_hsa_759	chr9:37804227-378042											

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_801	chr7:27155186-27155241	+	TCTCCGTGAAGACCTGCCAGGGG	Yes	No	No	0	0	0	0	
NM_hsa_802	chr12:4215924-4215976	+	ACTCTGCTCCCTCCACAG	Yes	No	No	0	0	0	0	
NM_hsa_802	chr19:4215899-4215995	+	ACTCTGCTCCCTCCACAG	Yes	No	No	0	0	0	0	
NM_hsa_803	chr19:4215924-4215976	+	CACGGGGGCTGAGAGCAGAAC	Yes	No	No	0	0	0	0.072862	Yes
NM_hsa_804	chr6:78414402-78414452	+	ACTCTTTAAGGATAGGCTGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_804	chr6:78414389-78414461	+	ACTCTTTAAGGATAGGCTGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_805	chr6:78414402-78414452	+	ACTCTTTAAGGATAGGCTGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_806	chr8:71365480-71365551	+	CTTCCCTTACCTGGGTTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_806	chr8:71365480-71365573	+	CTTCCCTTACCTGGGTTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_807	chr1:1365480-71365543	+	AAATGTCAGACTGGGGAGGT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_808	chr22:31284149-31284211	+	AACTCTGTCTGTCTCTAGT	Yes	No	No	0	0	0.132445	0	Yes
NM_hsa_809	chr22:31284149-31284211	+	TAGGGAGGGGATTGAGCCTTT	Yes	No	No	0	0	0	0	Yes
NM_hsa_812	chr19:10946715-10946755	+	CGCGCGGATGGTAGAAA	Yes	No	No	0	0	0	0	Yes
NM_hsa_813	chr19:10946715-10946755	+	ACTGCTTCTCCCGCCGCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_814	chr3:47453513-47453585	+	TGCGCCCTCTCTTCCAGAGA	Yes	No	No	0	0	0	0	Yes
NM_hsa_815	chr3:47453513-47453585	+	TGCTGGAGGGATGAGGCTCAGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_816	chr4:1022123-1022167	+	ACCCTAAGGATCAGGACAGAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_817	chr4:1022123-1022167	+	ATCTCTGCTATGGGGCCC	Yes	No	No	0	0	0	0	Yes
NM_hsa_818	chr8:124171290-124171350	+	TTTCTCCGACTGTCGAGCAGA	Yes	No	No	0	0	0	0.132445	Yes
NM_hsa_819	chr8:124171290-124171350	+	GGACTGGGACTGGGAGTGCA	Yes	No	No	0	0	0	0	Yes
NM_hsa_820	chr1:756412670-56412723	+	AGAGGGATCGGGCTGGAAT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_820	chr1:756412660-56412751	+	AGAGGGATCGGGCTGGAAT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_821	chr1:756412670-56412723	+	TCCAGGCTATGGCCCTCACT	Yes	No	No	0	0	0	0	Yes
NM_hsa_822	chr12:124921989-124922046	-	CCCCCTTCCAGAGCTCG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_822	chr12:124921980-124922058	-	CCCCCTTCCAGAGCTCG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_823	chr12:124921989-124922046	-	AGGCTCAGGAACTGAGAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_824	chr9:97553116-97553194	+	AAITTTGTCAGTGTGGATGT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_824	chr9:97553128-97553185	+	AAITTTGTCAGTGTGGATGT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_825	chr9:97553128-97553185	+	ATCCAAATCCACCAAAATGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_826	chr5:41861017-41861078	+	CCCAGCTGGAGCTCTCTCC	Yes	No	No	0	0	0	0	Yes
NM_hsa_827	chr5:41861017-41861078	+	GTGGGGGCTTTCTGGCTCAGGA	Yes	No	No	0	0	0	0	Yes
NM_hsa_828	chr16:28858317-28858378	+	TGCTAGACTCACAGGGCAGA	Yes	Yes	Yes	0	0	0	0.132445	Yes
NM_hsa_828	chr16:28858284-28858378	+	TGCTAGACTCACAGGGCAGA	Yes	Yes	Yes	0	0	0	0.132445	Yes
NM_hsa_829	chr16:28858317-28858378	+	GGGCCCTGTGAGTCAGGACG	Yes	No	No	0	0	0	0	Yes
NM_hsa_83	chr22:31502901-31502999	+	AGGGCTGGAGCTCCAGAAATC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_83	chr22:31502893-31502929	+	AGGGCTGGAGCTCCAGAAATC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_83	chr22:31502914-31502989	+	AGGGCTGGAGCTCCAGAAATC	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_830	chr3:48357870-48357935	+	TCTAGCTCCATGAATCTGAT	Yes	Yes	No	0.370407	0.430446	0.659576	Yes	H-KapB-KapB-cMyc
NM_hsa_830	chr3:48357860-48357943	+	TCTAGCTCCATGAATCTGAT	Yes	Yes	No	0.370407	0.430446	0.659576	Yes	H-KapB-KapB-cMyc
NM_hsa_831	chr3:48357870-48357935	+	CAGGAGTCAATGGAAGCTGGA	Yes	No	No	0	0	0	0	Yes
NM_hsa_833	chr1:29989169-29989251	+	CCTGACGCTCCGCTCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_836	chr19:54651706-54651892	+	TCTGCTCTCTCCACCCGACG	Yes	Yes	No	0.0569857	0	0.0732862	Yes	
NM_hsa_836	chr19:54651814-54651883	+	TCTGCTCTCTCCACCCGACG	Yes	Yes	No	0.0569857	0	0.0732862	Yes	
NM_hsa_837	chr19:54651814-54651883	+	GAGTGTGGGGTGGTGGAG	Yes	No	No	0	0	0	0	Yes
NM_hsa_839	chr22:31502893-31502929	+	CCGAGTCCCGGTAACCCCGC	Yes	No	No	0	0	0	0	Yes
NM_hsa_84	chr22:31502914-31502989	+	CTTCTGGGTGCTCTCCCATTA	Yes	No	No	0	0	0	0	Yes
NM_hsa_840	chr7:8249160-8249230	+	TTGGGTCGAGGATGTTGAA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_840	chr7:8249170-8249222	+	TTGGGTCGAGGATGTTGAA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_841	chr7:8249170-8249222	+	TTACACATTTGAAACCCAAAT	Yes	No	No	0	0	0	0	Yes
NM_hsa_842	chr21:3044433-30444477	+	AAATCCAGGCTCAGGACT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_842	chr21:30444339-30444412	+	AAATCCAGGCTCAGGACT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_842	chr21:30444382-30444445	+	AAATCCAGGCTCAGGACT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_843	chr21:30444382-30444445	+	CCCTCGAGCTGGGCTGTTTC	Yes	No	No	0	0	0	0	Yes
NM_hsa_846	chr12:4184865-4184909	+	GAGAAGTCCAGACTCAGACT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_846	chr12:4184853-4184939	+	GAGAAGTCCAGACTCAGACT	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_847	chr12:4184865-4184909	+	TGTTAATGCTCAATTTCTCT	Yes	No	No	0	0	0	0	Yes
NM_hsa_849	chr11:43902347-43902407	+	GCCTGTGATGGGAGTGC	Yes	No	No	0	0	0	0	Yes
NM_hsa_85	chrX:44855632-44855718	+	AGTCAAGGCTGTGATTTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_85	chrX:44855625-44855733	+	AGTCAAGGCTGTGATTTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_85	chrX:44855640-44855708	+	AGTCAAGGCTGTGATTTGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_850	chr14:105147019-105147147	+	CTGGGCTGTGGGGACCCCTGG	Yes	No	Yes	0.341914	0.397335	0.366431	Yes	
NM_hsa_850	chr14:105147059-105147113	+	CTGGGCTGTGGGGACCCCTGG	Yes	No	Yes	0.341914	0.397335	0.366431	Yes	
NM_hsa_851	chr1:105147059-105147113	+	AGGAGTCCACAGCCCGCCAGCT	Yes	No	No	0	0	0	0	Yes
NM_hsa_852	chr1:9886185-9886243	+	AAATACCAGCTTTATGTGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_852	chr1:9886175-9886250	+	AAATACCAGCTTTATGTGG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_853	chr1:9886185-9886243	+	ACATAGACCTGGTGTCTCT	Yes	No	No	0	0	0	0	Yes
NM_hsa_854	chr9:98645113-98645170	+	TGATTTGTTGGGAATAAATGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_854	chr9:98645113-98645170	+	TGATTTGTTGGGAATAAATGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_854	chr9:98645083-98645201	+	TGATTTGTTGGGAATAAATGA	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_855	chr9:98645113-98645170	+	GTTATCCCAACAACTCAT	Yes	No	No	0	0	0	0	Yes
NM_hsa_856	chr5:98268282-98268336	+	ACTGTGTGCTCTGTATCACT	Yes	No	No	0	0.0662225	0	0	Yes
NM_hsa_857	chr5:98268282-98268336	+	AGTCAAGGCTCAACTATTCG	Yes	No	No	0.0569857	0	0	0	Yes
NM_hsa_858	chr10:4392339-4392404	+	CTGGGGAAGCCGCGCTCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_859	chr10:4392339-4392404	+	CTGGGGAAGCCGCGCTCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_86	chrX:44855640-44855708	+	AGAACTAAAGCTTGTCACTTA	Yes	No	No	0	0	0	0	Yes
NM_hsa_860	chr22:46773623-46773722	+	TGCTGCTGGCTCTCTCTGCG	Yes	Yes	No	0.0569857	0	0	0	Yes
NM_hsa_860	chr22:46773641-46773699	+	TGAAGCTGACCCGCTCTGCG	Yes	Yes	No	0.0569857	0	0	0	Yes
NM_hsa_861	chr22:46773641-46773699	+	CTGGAGGAGGCGACGGCCTC	Yes	No	No	0	0	0	0	Yes
NM_hsa_862	chr1:45273867-45273946	+	AAACCAGGTCGGGCGCTGACC	Yes	No	No	0	0	0	0	Yes
NM_hsa_863	chr1:45273867-45273946	+	TTTCCCGGCTGTCTCTAAC	Yes	No	No	0	0	0	0	Yes
NM_hsa_864	chr10:10366237-10366244	-	CTTCTACACAGCTCTTTGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_864	chr10:10366238-103662436	-	CTTCTACACAGCTCTTTGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_864	chr10:10366238-103662432	-	CTTCTACACAGCTCTTTGTT	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_865	chr10:10366237-10366244	-	CAAAAGACTGTGGTAGAAGTA	Yes	No	No	0	0	0	0	Yes
NM_hsa_866	chr19:39262615-39262690	+	CTGCTGCTGGGCGGCGACTCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_867	chr19:39262615-39262690	+	GGTCTGCTGGGCGGCGACTCG	Yes	No	No	0	0	0	0	Yes
NM_hsa_868	chr19:35652419-35652488	+	TCATGTGCAACCAATGAGACG	Yes	Yes	No	0.256436	0.0331113	0	0	Yes
NM_hsa_868	chr19:35652429-35652488	+	TCATGTGCAACCAATGAGACG	Yes	Yes	No	0.256436	0.0331113	0	0	Yes
NM_hsa_868	chr19:35652401-35652451	+	TCATGTGCAACCAATGAGACG	Yes	Yes	No	0.256436	0.0331113	0	0	Yes
NM_hsa_869	chr19:35652429-35652488	+	CTCTATGTCAGCTCTGAGT	Yes	No	No	0	0	0	0	Yes
NM_hsa_870	chr19:38882791-38882853	+	CTGCTCTCTCCACCCGACG	Yes	No	No	0	0.0662225	0.0732862	Yes	H-KapB-KapB-cMyc
NM_hsa_871	chr19:38882791-38882853	+	TGGGAGCGGGGAGGAACTGGG	Yes	No	No	0	0	0	0	Yes
NM_hsa_872	chr13:1627900-31627959	+	CTGGATCTCGGAAACGAG	Yes	No	No	0	0	0	0	Yes
NM_hsa_873	chr13:1627900-31627959	+	AGGGCGGGAGGGCGCC	Yes	No	No	0	0	0	0	Yes
NM_hsa_874	chr11:13259001-132590174	+	TGGAAGCTGCTCAGGGCCTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_874	chr11:132590090-132590198	+	TGGAAGCTGCTCAGGGCCTGG	Yes	Yes	Yes	0	0	0	0	Yes
NM_hsa_875	chr11:132590105-132590203	+	TGGAAGCTGCTCAGGG								

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_919	chr19:16198771-16198838	+	TGCAGTGGATGGGAGGACACCGG	Yes	No	No	0	0	0	0	No
NM_hsa_920	chr17:3967603-3967670	+	TGTTGGGATGAGCAATG	Yes	Yes	No	0	0	0	0	No
NM_hsa_920	chr17:3967603-3967670	+	TGTTGGGATGAGCAATG	Yes	Yes	No	0	0	0	0	No
NM_hsa_921	chr17:3967603-3967670	+	TGTTCTTAGCTCAACGGCA	Yes	No	No	0	0	0	0	No
NM_hsa_922	chr2:219292454-219292543	+	TAAGGTGCTCTCACTGTGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_923	chr2:219292454-219292543	+	TGACAGTGAAGTCCCTCTAAA	Yes	No	No	0	0	0	0	No
NM_hsa_924	chr3:31607430-31607485	+	CTCTCCATCCGGTGTCTGG	Yes	No	No	0	0	0	0	No
NM_hsa_925	chr3:31607430-31607485	+	AGGCGTCCCTGGAAGGAGGGA	Yes	No	No	0	0	0	0	Yes
NM_hsa_926	chr8:59223570-59223668	+	TTATCCCAAGTCACTGAGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_926	chr8:59223581-59223659	+	TACCTTCAAGTCACTGAGAT	Yes	Yes	No	0	0	0	0	No
NM_hsa_927	chr8:59223581-59223659	+	TCTCTCAAGTCACTGAGAT	Yes	No	No	0	0	0	0	No
NM_hsa_928	chr17:26322115-26322181	+	AGCTGTGATGAATTTGACACAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_928	chr17:26322102-26322190	+	AGCTGTGATGAATTTGACACAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_929	chr17:26322115-26322181	+	GGTGCAAAATGATTCGGTTTT	Yes	No	No	0	0	0	0	No
NM_hsa_93	chr17:18066909-18067053	+	AGTGGGCGCAGAAAGACAGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_930	chr16:54127346-54127437	+	CTGTGTTCTCTCACTCCCGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_930	chr16:54127373-54127428	+	CTGTGTTCTCTCACTCCCGC	Yes	Yes	No	0	0	0	0	No
NM_hsa_931	chr16:54127373-54127428	+	GGCAGGAGTCAACAGA	Yes	No	No	0	0	0	0	No
NM_hsa_932	chr12:12501072-12501102	-	CTCCACACTCAGGTCCTTA	Yes	No	No	0.0189952	0.0662225	0.0610719	0	Yes
NM_hsa_933	chr12:12501072-12501102	-	TGGGCGTCAAGCTTGGAT	Yes	No	No	0	0	0	0	No
NM_hsa_934	chr5:78566479-78566540	+	CTGCCCTCCGCACTGCGAGG	Yes	No	No	0	0	0	0	No
NM_hsa_935	chr5:78566479-78566540	+	AGCAGGAGCACTGGTAAGGA	Yes	No	No	0	0	0	0	No
NM_hsa_936	chr16:30670064-30670131	+	ACTGAACTCCGGCGAGCT	Yes	No	No	0	0	0	0	No
NM_hsa_938	chr10:104185989-104186048	+	TTGGGAGTCAAAAGCATGTAGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_938	chr10:104185989-104186048	+	TTGGGAGTCAAAAGCATGTAGA	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_939	chr10:104185989-104186048	+	CATATGCTCCAGTCCCAACC	Yes	No	No	0	0	0	0	No
NM_hsa_94	chr17:18066909-18067053	+	CATCTTCTCCGGCCCAACC	Yes	No	No	0	0	0	0	No
NM_hsa_940	chr3:52557374-52557442	+	CAACAGGCTCTGCTGCTCA	Yes	Yes	No	0.626843	0.927115	0.1985934	0	H-KapB+KapB+eMye
NM_hsa_940	chr3:52557374-52557442	+	CAACAGGCTCTGCTGCTCA	Yes	Yes	No	0.626843	0.927115	0.1985934	0	H-KapB+KapB+eMye
NM_hsa_941	chr3:52557374-52557442	+	TGGGAGAGCACTGGATTTGGC	Yes	No	No	0.0569857	0	0.293145	0	No
NM_hsa_942	chr16:72142304-72142384	+	TGTTGGGATGAAGGAGGCTGC	Yes	No	No	0	0	0	0	No
NM_hsa_943	chr16:72142304-72142384	+	TCTCTGCTCCATGGTCGGGAGGTG	Yes	No	No	0	0	0	0	No
NM_hsa_944	chr12:126468276-126468346	+	CTTAAACTCTGCAAGGCTC	Yes	No	No	0	0	0	0	No
NM_hsa_945	chr12:126468276-126468346	+	CCTCTCCACAGTAAAGAGGGG	Yes	No	No	0	0	0	0	No
NM_hsa_946	chr2:155586576-155586629	+	AGAGTTAAGAGCAAGAACAGC	Yes	No	No	0	0	0	0	No
NM_hsa_949	chr3:47043351-47043416	+	GTGAGATGTCGGGAGGCTC	Yes	No	No	0	0	0.0732862	0	No
NM_hsa_95	chr2:28563462-28563522	+	ACTGAGCCCGGACTGTGCTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_95	chr2:28563462-28563522	+	ACTGAGCCCGGACTGTGCTCTG	Yes	Yes	No	0	0	0	0	No
NM_hsa_950	chr3:47043351-47043416	+	TGCCGCCAAGCTGATC	Yes	No	No	0	0	0	0	No
NM_hsa_953	chr6:35453806-35453866	+	TATACGGGCTGTGGGATGCA	Yes	Yes	No	0	0	0	0	No
NM_hsa_953	chr6:35453818-35453866	+	TATACGGGCTGTGGGATGCA	Yes	Yes	No	0	0	0	0	No
NM_hsa_954	chr6:35453818-35453866	+	ACTCCACAGCCGCGACTGGA	Yes	Yes	No	0	0	0	0	No
NM_hsa_959	chr6:31621129-31621216	+	AACCTTCTGGGATCTGTAGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_959	chr6:31621129-31621245	+	AACCTTCTGGGATCTGTAGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_959	chr6:31621135-31621225	+	AACCTTCTGGGATCTGTAGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_96	chr2:28563462-28563522	+	AGAGCAAGCCAGGCTCACTCA	Yes	No	No	0	0	0	0	No
NM_hsa_960	chr6:31621155-31621216	+	TGGGAGTCTCCAGAAAGACACA	Yes	No	No	0	0	0	0	No
NM_hsa_961	chr4:18530682-185306150	+	ATAACTCGGCCAGGACAGCT	Yes	Yes	No	0	0	0	0	No
NM_hsa_961	chr4:18530672-185306150	+	ATAACTCGGCCAGGACAGCT	Yes	Yes	No	0	0	0	0	No
NM_hsa_962	chr4:18530682-185306150	+	CAGCTGGGAGCAGGAGGAGTCA	Yes	No	No	0	0	0	0	No
NM_hsa_965	chr13:33161460-33161550	+	AAGGCCACGACTGGCGTGA	Yes	No	Yes	0	0	0	0	No
NM_hsa_965	chr13:33161460-33161520	+	AAGGCCACGACTGGCGTGA	Yes	No	Yes	0	0	0	0	No
NM_hsa_966	chr13:33161460-33161520	+	CAGGCCACCAAGTGGTCTAGCTTCC	Yes	No	No	0	0	0	0	No
NM_hsa_967	chr4:6935683-69356892	+	ACGAGGCTGGACTCAAGCTG	Yes	No	No	0.0662225	0	0	0	No
NM_hsa_967	chr19:39028678-39028717	+	ACGAGGCTGGACTCAAGCTG	Yes	No	No	0.0662225	0	0	0	No
NM_hsa_969	chr17:37043284-37043351	+	CAGGTTTTCGAGCCGGCTCT	Yes	Yes	Yes	0.284929	0.26489	0.0732862	Yes	KapB+eMye-KapB-H
NM_hsa_969	chr17:37043257-37043385	+	CAGGTTTTCGAGCCGGCTCT	Yes	Yes	Yes	0.284929	0.26489	0.0732862	Yes	KapB+eMye-KapB-H
NM_hsa_969	chr17:37043272-37043360	+	CAGGTTTTCGAGCCGGCTCT	Yes	Yes	Yes	0.284929	0.26489	0.0732862	Yes	KapB+eMye-KapB-H
NM_hsa_97	chr8:8532082-85320911	+	ACAGCTGGTCTCTGAATGAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_97	chr8:8532089-85320911	+	ACAGCTGGTCTCTGAATGAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_97	chr8:8532083-85320941	+	ACAGCTGGTCTCTGAATGAT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_970	chr17:37043284-37043351	+	GCTGGCTGTTTAAACCTGTG	Yes	No	No	0.170957	0.26489	0	0	Yes
NM_hsa_971	chr4:2344245-23442521	+	TGCTCACTCTCTCTCCAGC	Yes	No	No	0	0	0	0	Yes
NM_hsa_972	chr10:104185989-104186048	+	CGAAGAGGCAAGGCTGAGTCA	Yes	No	No	0	0	0	0	Yes
NM_hsa_973	chr2:101618597-101618657	+	GAGCTATGATGTAACGGC	Yes	No	No	0	0	0	0	No
NM_hsa_974	chr4:25661109-25661198	+	TCATGAACAATAAACAGAGTT	Yes	Yes	No	0	0	0	0	No
NM_hsa_974	chr4:25661125-25661189	+	TCATGAACAATAAACAGAGTT	Yes	Yes	No	0	0	0	0	No
NM_hsa_975	chr4:25661125-25661189	+	CTCTTGTATTTGTTATGAGA	Yes	No	No	0	0	0	0	No
NM_hsa_976	chr14:23447395-23447447	+	GAGTTCGCGAGCTGCTGC	Yes	No	No	0	0	0	0	No
NM_hsa_977	chr14:23447395-23447447	+	AGAGCAAGCTGGTATGCCCCA	Yes	No	No	0	0	0	0	No
NM_hsa_98	chr8:85320839-85320902	+	TCATTCAAGAACAGGCTGGTGG	Yes	No	No	0	0	0	0	No
NM_hsa_980	chr2:23019549-23019591	+	TTTATTCAAGAGCAAGCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_980	chr2:23019549-23019572	+	TTTATTCAAGAGCAAGCTGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_981	chr2:23019549-23019591	+	TGCTGTCTTTGAAATAATA	Yes	No	No	0	0	0	0	No
NM_hsa_982	chr2:29352285-29352362	+	GCTATAAGACTCTGTGTCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_982	chr2:29352279-29352367	+	GCTATAAGACTCTGTGTCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_982	chr2:29352297-29352355	+	GCTATAAGACTCTGTGTCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_982	chr2:29352272-29352380	+	GCTATAAGACTCTGTGTCTGT	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_984	chr2:29352297-29352355	+	AGACACAGAGTCTTAAAGTCT	Yes	No	No	0	0	0	0	No
NM_hsa_985	chr20:61971594-6197208	+	AGGCTGTAGTCTCGAGAGC	Yes	No	No	0.26489	0.0732862	0	0	No
NM_hsa_985	chr20:61971594-6197208	+	CTCTCTGTCGAGAGCCCA	Yes	No	No	0	0	0	0	No
NM_hsa_986	chr17:76136837-76136896	+	GAGCAGCCGCTTCCCAACTCG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_986	chr17:76136812-76136905	+	GAGCAGCCGCTTCCCAACTCG	Yes	Yes	No	0	0	0	0	Yes
NM_hsa_987	chr17:76136837-76136896	+	AGTGTCTCCGCTGCTGCTC	Yes	No	No	0	0	0	0	No
NM_hsa_988	chr21:1484928-1484986	+	CTCTGAGGCCAATAGCCGGG	Yes	No	No	0	0	0	0	No
NM_hsa_989	chr21:1484928-1484986	+	CCTCTGAGGCCAATAGCCGGG	Yes	No	No	0	0	0	0	No
NM_hsa_99	chr22:20136497-20136550	+	GGCAGGATCCCTGGCTTGGGA	Yes	No	No	0	0	0	0	No
NM_hsa_990	chr15:40632542-40632608	+	CTCTGGCAGCGAAGCTG	Yes	No	No	0	0	0	0	No
NM_hsa_991	chr15:40632542-40632608	+	GGTCCGAGGGGAGCT	Yes	No	No	0	0	0	0	No
NM_hsa_992	chr12:679670-679762	+	CTCTGAGCGGAGGCGGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_992	chr12:679679-679743	+	CTCTGAGCGGAGGCGGGG	Yes	Yes	No	0	0	0	0	No
NM_hsa_993	chr12:679679-679743	+	CTCTGTCGCCCGCTGGG	Yes	No	No	0	0	0	0	No
NM_hsa_994	chr1:160092522-160092607	+	TAGCCAGGATTCAGAGTGGAG	Yes	Yes	No	0	0	0	0	No
NM_hsa_997	chr11:63606362-63606441	+	CGCTTGTGGATTTCCGTA	Yes	No	No	0.313421	0.0331113	0.0	0	KapB+eMye-KapB-H
NM_hsa_998	chrX:151128103-151128182	+	TTCTTTCAGATGAGCACTGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_998	chrX:151128078-151128206	+	TTCTTTCAGATGAGCACTGAGA	Yes	Yes	Yes	0	0	0	0	No
NM_hsa_998	chrX:151128113-151128174	+	TTCTTTCAGATGAGCACTGAGA	Yes	Yes	Yes	0	0	0	0	No</

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_2267	chr10:123790178-123790250	-	CTGGGTCATCTGCTGGCTAG	No	Yes	No	0	0	0	0	
NM_hsa_2268	chr10:125185703-125185760	-	CATCTCAAACTGGCAGAGGG	No	Yes	No	0	0	0	0	
NM_hsa_2270	chr10:130735313-130735398	-	TTGGACAGGCGCGCTACATA	No	Yes	No	0	0	0	0	
NM_hsa_2273	chr11:404451-404543	+	TTGGGCTCTCTCCACTGTAG	No	Yes	No	0	0	0	0	
NM_hsa_2274	chr11:448252-448349	+	CTCTGCACCCTGGAGGACGG	No	Yes	No	0	0	0	0	
NM_hsa_2276	chr11:104006-104093	+	CTGTAGGGCCAGAGCTCTAGC	No	Yes	No	0.113971	0	0	0	
NM_hsa_2277	chr11:777575-777655	+	CGCTCCGGGTCGGGCTGGCTG	No	Yes	Yes	0	0	0	0	
NM_hsa_2277	chr11:777535-777618	+	CGGTCCGGGTCGGGCTGGCTG	No	Yes	Yes	0	0	0	0	
NM_hsa_2278	chr11:833261-833363	+	GGGCCCTCCGGGCTGGGAC	No	Yes	Yes	0	0	0	0	
NM_hsa_2278	chr11:833276-833363	+	GGGCCCTCCGGGCTGGGAC	No	Yes	Yes	0	0	0	0	
NM_hsa_2281	chr11:386290-386387	+	TGCTCTGGAGCTGGACTGGA	No	Yes	Yes	0	0.0662225	0	0.146572	H-KapB->KapB+cMye
NM_hsa_2281	chr11:386299-386362	+	TGCTCTGGAGCTGGACTGGA	No	Yes	Yes	0	0.0662225	0	0.146572	H-KapB->KapB+cMye
NM_hsa_2285	chr11:11642548-11642640	+	ACTCTGAGCCGGACTTGTGTG	No	Yes	No	0	0	0	0	
NM_hsa_2287	chr11:16968511-16968609	+	TGGTCTATCTGGGCTGCTGGT	No	Yes	No	0	0	0	0	
NM_hsa_2288	chr11:18287900-18288023	+	AAGCAGGCTGGGGCTGGT	No	Yes	No	0.968757	0.463558	0	1.09929	Yes
NM_hsa_2290	chr12:2072492-2072569	+	TTCTGGAAAGCTCCCTTAGC	No	Yes	No	0	0	0	0	
NM_hsa_2291	chr11:22850970-22851058	+	GTCAGTGAAGTGAAGAAGA	No	Yes	No	0	0	0	0	
NM_hsa_2292	chr11:25410245-25410322	+	CACAGTATGAGCTCCTGCAG	No	Yes	No	0.0284929	0	0	0	
NM_hsa_2294	chr11:16175509-16175595	+	TTATCCAGACTGAAGGCCAGA	No	Yes	Yes	0.113971	0	0	0.0732862	No
NM_hsa_2294	chr11:16175905-16175982	+	TTCTCCAGACTGAAGGCCAGA	No	Yes	Yes	0.113971	0	0	0.0732862	No
NM_hsa_2296	chr11:43600200-43600288	+	GTGGGGCCGGAGTGTGGT	No	Yes	No	0	0	0	0	
NM_hsa_2298	chr11:4500652-45006648	+	CCAGCTTCCCTCCCCCC	No	Yes	No	0	0	0	0	
NM_hsa_2299	chr11:46182255-46182351	+	AGGGGAAAGCAAGCTGTAGCT	No	Yes	No	0	0	0	0	
NM_hsa_2300	chr11:4637990-46380074	+	CTCATCTCACTGCCCTCT	No	Yes	No	0	0.0569857	0	0	
NM_hsa_2302	chr11:4723599-4723607	+	CTCCCGGAGCCCTGAGAGG	No	Yes	No	0	0	0	0	
NM_hsa_2303	chr11:54750504-54750590	+	CTAGAAGGAACTTTGAGA	No	Yes	No	0	0	0	0	
NM_hsa_2306	chr11:58940659-58940731	+	CGCCGACCTGGCTGACCTGA	No	Yes	No	0	0	0	0	
NM_hsa_2307	chr11:5895678-58956893	+	TTGTCTCGTGGGACTAGG	No	Yes	No	0	0	0	0	
NM_hsa_2308	chr11:60508603-60508693	+	TGATGATGAGCTGAGCTCT	No	Yes	No	0.284929	0	1.2458	0	
NM_hsa_2309	chr11:61520105-6152109	+	GAGCCAGCCAGGACTCTGCC	No	Yes	No	0	0	0	0	
NM_hsa_2312	chr11:62761657-62761748	+	TGATGGAGTGGTGTGGGG	No	Yes	No	13.0402	9.00626	1.79551	0	
NM_hsa_2314	chr11:63536105-63536195	+	GCCTCCGGGCGCGGGGGCG	No	Yes	No	0	0	0	0	
NM_hsa_2315	chr11:64018944-64019014	+	CTCTGCTGGCCAGCACAGA	No	Yes	No	0	0	0	0	
NM_hsa_2316	chr11:6401423-6401562	+	CTCTCTCTCCCGCCCG	No	Yes	No	0	0	0	0	
NM_hsa_2317	chr11:64072814-64072905	+	GGCTCGGCGGGCTCGGGCG	No	Yes	No	0	0	0	0	
NM_hsa_2319	chr11:64128534-64128615	+	GCACCCCTTCCCTCCACAG	No	Yes	No	0	0	0	0	
NM_hsa_2323	chr11:65167989-65168061	+	GGCTCTGATGAAGACTGAGG	No	Yes	No	0	0	0	0	
NM_hsa_2324	chr11:65202608-65202685	+	AATGATATGGCTGTGAGCT	No	Yes	No	0	0	0	0	
NM_hsa_2325	chr11:65271877-65271949	+	AATGCATTGTGAAACACTGGAG	No	Yes	No	0	0.0569857	0	0	
NM_hsa_2326	chr11:65430748-65430823	+	AGGCCGGTGGTGAAGCTCCG	No	Yes	No	0.170957	0.132445	0	0	
NM_hsa_2328	chr11:65659226-65659300	+	CCCATCGGCGCCGGGACCG	No	Yes	No	0	0	0	0	
NM_hsa_2329	chr11:65744801-65744116	+	CTGGGCGGGCGCCGGGAC	No	Yes	No	0	0	0	0	
NM_hsa_2330	chr11:6611562-66115766	+	GGGGGGAAGATACACATTT	No	Yes	No	0	0	0	0	
NM_hsa_2331	chr11:66138873-66138953	+	TCGGCTGATGGAAATTTAGT	No	Yes	No	0	0	0	0	
NM_hsa_2332	chr11:66360675-66360763	+	TCTCCGCGGAGGAGTCTG	No	Yes	No	0	0	0	0	
NM_hsa_2334	chr11:67397703-67397771	+	GACGAGGAGGCGCGGGCGG	No	Yes	No	0.212747	0.101541	0.0671791	0	
NM_hsa_2335	chr11:68680879-68680957	+	CTACGACAGCACTGGAGCT	No	Yes	No	0	0.0662225	0	0.0732862	KapB+cMye->KapB-H
NM_hsa_2339	chr11:75986937-75987008	+	CGGGTGGGTAAGGAGGAGA	No	Yes	No	0	0	0	0	
NM_hsa_2340	chr11:76850623-76850705	+	CATTCACTCCCTCCCTCT	No	Yes	No	0	0	0.0244288	0	
NM_hsa_2341	chr11:77706131-77706222	+	GTAGGTTCTCGAGCACTCG	No	Yes	No	0	0	0	0	
NM_hsa_2342	chr11:79113064-79113157	+	CTCTAAGACTTACAGCTTAGT	No	Yes	No	4.39285	14.1363	8.83309	0	
NM_hsa_2344	chr11:9306373-93063876	+	TTCTCTCGGCGGGAGGCG	No	Yes	No	0	0	0	0	
NM_hsa_2346	chr11:100041472-100041544	+	TCTGAGACTGATCTGATGA	No	Yes	No	0	0	0	0	
NM_hsa_2347	chr11:102216848-102216929	+	CGGATCAACGGGCAAGAG	No	Yes	No	0	0	0	0	
NM_hsa_2348	chr11:104131597-104131694	+	TAGTATGATTCAGTGTGTT	No	Yes	No	0	0	0	0	
NM_hsa_2349	chr11:10833891-10833874	+	TTCTATTCAGCTGGCTGA	No	Yes	No	0	0	0	0	
NM_hsa_2350	chr11:110902182-110902276	+	GTATTGGACTTGGGAGCA	No	Yes	No	0	0	0	0	
NM_hsa_2355	chr11:12097373-12097465	+	CGGCTCTGGGGCTCTGGA	No	Yes	No	0	0	0	0	
NM_hsa_2356	chr11:113390477-113390459	+	TGCTGTAGGAGTCTTAAAG	No	Yes	No	1.39615	0.167159	0.329788	0	
NM_hsa_2362	chr11:12483714-124837988	+	TCGCTCTGAGGACTCACTGGCTG	No	Yes	No	0.940265	0.79467	0.696219	Yes	
NM_hsa_2363	chr11:12914983-12914967	+	CTCTTGTCTCGCGAGGCT	No	Yes	No	0	0	0	0	
NM_hsa_2364	chr11:134131135-134132127	+	AACGTGGCGGCTTCCCTCT	No	Yes	Yes	0.284929	0	0	0	
NM_hsa_2364	chr11:134131083-134131191	+	AACGTGGCGGCTTCCCTCT	No	Yes	Yes	0.284929	0	0	0	
NM_hsa_2366	chr11:1780805-1780899	+	CGACCCCTGCTCCCTGACG	No	Yes	No	0	0	0	0	
NM_hsa_2370	chr11:11005716-11005825	+	ACCAGATGTGAGCTTGGAGG	No	Yes	No	0.296326	0.200875	0.249172	0	
NM_hsa_2371	chr11:14521045-14521144	+	CGGGTGGGTTAGGAGGAGA	No	Yes	No	0	0	0	0	
NM_hsa_2372	chr11:17298021-17298107	+	CTGAGCAGGAGGAGGAGTGG	No	Yes	No	0	0	0	0	
NM_hsa_2373	chr11:18342206-18342292	+	AGGTTGACTGGAACAGAGGTTGG	No	Yes	No	0	0	0	0	
NM_hsa_2375	chr11:21022414-21022489	+	ACCGGGCTGTGTAAGGCTG	No	Yes	No	77.4151	50.6657	31.8001	0	
NM_hsa_2376	chr11:22852162-22851970	+	CCCAAGCAGCACTGTGAG	No	Yes	No	0	0	0	0	
NM_hsa_2377	chr11:22661102-22661170	+	AGGGACTTTGGGGGAAATA	No	Yes	No	0	0	0	0	
NM_hsa_2378	chr11:32379135-32379214	+	CTGAGCTTGGGTCAGAAAGC	No	Yes	No	0.0241758	0.00551854	0.00916078	Yes	
NM_hsa_2379	chr11:33902810-33902896	+	TTTCAGATGGAGGCGCAGC	No	Yes	No	0	0	0	0	
NM_hsa_2380	chr11:39009310-39009383	+	CCACTCCAGGACTGAGTGA	No	Yes	No	1.03524	0.982489	1.05044	0	
NM_hsa_2381	chr11:47170429-47170498	+	CTCTGGTCTATGGACACCG	No	Yes	No	0	0	0.132445	0	
NM_hsa_2382	chr11:47429705-47429775	+	GGGCTGGGAGGACTATGGT	No	Yes	No	0	0	0	0	
NM_hsa_2383	chr11:49594384-49594470	+	TGAGGATGAGAGTTATATTT	No	Yes	No	0	0	0	0	
NM_hsa_2386	chr11:64109305-64109392	+	TTGTGGTCTGGGCTTGGGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2386	chr11:64109301-64109407	+	TTGTGGTCTGGGCTTGGGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2387	chr11:64109305-64109392	+	CCCAAGACTCAGACCAACC	No	Yes	No	0	0	0	0	
NM_hsa_2388	chr11:64359146-64359223	+	CTGGCTGAGCCGCTGCTGT	No	Yes	No	0	0	0	0	
NM_hsa_2389	chr11:67140040-67140112	+	CCGCCCGCCCGCCGGGAC	No	Yes	No	0.0284929	0	0	0	
NM_hsa_2390	chr11:6807986-68080876	+	CTCTCCCGCCCGCCGGGAC	No	Yes	No	0.170957	0.26689	0.439717	0	
NM_hsa_2391	chr11:70592483-70592581	+	CACCCTGACCCCCACCTG	No	Yes	No	0	0	0	0	
NM_hsa_2393	chr11:76388047-76388140	+	GCAGGATGTATGTAACATGTG	No	Yes	No	0	0	0	0	
NM_hsa_2396	chr11:86488928-86488980	+	CAAAATGAGACTTGCAGAA	No	Yes	No	0	0	0	0	
NM_hsa_2397	chr11:8666782-86667125	+	TGGGGGCGGAGAGGCGGG	No	Yes	No	0	0	0	0	
NM_hsa_2398	chr11:91656157-91656241	+	TTTCACTGCTGCTCTGCTG	No	Yes	No	0	0	0	0	
NM_hsa_2399	chr11:9759310-97593396	+	TGATGATAGTATGTAATGT	No	Yes	No	0.256436	0.110371	0.0610719	Yes	
NM_hsa_2400	chr11:100120361-100120447	+	TCTCAGTGTGCTTAAATGT	No	Yes	No	0	0	0	0	
NM_hsa_2402	chr11:116643806-116643882	+	GAGCCGCTCCGGTGGCCGCA	No	Yes	No	0	0	0	0	
NM_hsa_2403	chr11:118120136-118120118	+	TGTTAGACTAGGAGCACTAG	No	Yes	No	0	0	0	0	
NM_hsa_2409	chr11:12579773-125797865	+	AGCTTCTAGCACTATGCTG	No	Yes	No	0	0	0	0	
NM_hsa_2410	chr11:125932755-125932822	+	CAGCCCGGGGGCGCCCGCC	No	Yes	No	0.0569857	0.132445	0	0	
NM_hsa_2411	chr11:133306823-133306907	+	GTCCGACATTAACCTCTGACA	No	Yes	No	0.0284929	0.0331113	0.0366431	Yes	
NM_hsa_2413	chr12:3068102-3068181	+	GGACCCCGGCTGGGGGGGG	No	Yes						

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation	
NM_hsa_2520	chr13:77524175-77524261	+	TCAGGTGTCCAGGTTGAGGAA	No	Yes	No	0	0	0	0	No	
NM_hsa_2521	chr13:80596381-80596467	+	GTCCATGAGGACAGGCTTAT	No	Yes	No	0	0	0	0	No	
NM_hsa_2522	chr13:80915894-80915966	+	GGGCTGGCCAGGAGGAGGAA	No	Yes	No	0	0	0	0	No	
NM_hsa_2526	chr13:92003261-92003335	+	ATGTGACAGCTTGTATGACAC	No	Yes	No	0.3989	0.860693	1.24587	Yes	H-KapB+KapB+eMye	
NM_hsa_2530	chr13:97079472-97079558	+	TTATGTACCTCGGATGAAT	No	Yes	No	0	0	0	0	0.146572	Yes
NM_hsa_2531	chr13:99739001-99739088	+	ACCGCGGACAGGAGGCTGG	No	Yes	No	0	0	0	0	0	No
NM_hsa_2532	chr13:113667070-113667148	+	GGAGAACTGGGAGGAGGCT	No	Yes	No	0	0	0	0	0	No
NM_hsa_2533	chr13:114542970-114543058	+	TGCTGGCTAGGCTGACAC	No	Yes	No	0	0	0	0	0	No
NM_hsa_2534	chr13:20357031-20357121	-	GGGGGTGAGTTGGGGAGGA	No	Yes	No	0	0	0	0	0	No
NM_hsa_2535	chr13:20981173-20981259	-	TTTGTAGAAAATAAATGTCCTT	No	Yes	No	0	0	0	0	0	No
NM_hsa_2536	chr13:24012704-24012790	-	CTCTGTGATGACCATACA	No	Yes	No	0	0	0	0	0	No
NM_hsa_2538	chr13:28546456-28546521	-	TGCTCGCTTAGATGTGACC	No	Yes	No	0	0	0	0	0	No
NM_hsa_2539	chr13:42030048-42030148	-	GTTCATGCCCGAGGGGAAACA	No	Yes	No	13.1067	19.9729	32.6124	Yes	H-KapB+KapB+eMye	
NM_hsa_2540	chr13:50570803-50570878	-	CGGGGAGGGCCGGCTGGG	No	Yes	No	0	0	0	0	0	No
NM_hsa_2543	chr13:52584493-52584589	-	CTGTGGCTCTCTGCTCCAGT	No	Yes	No	0	0	0	0	0	No
NM_hsa_2544	chr13:62980838-62980927	-	GAAGCAAGCTGGGAGCTTAT	No	Yes	No	0	0	0	0	0	No
NM_hsa_2547	chr13:103046759-103046827	-	GCGGCGTCCGGCTAGGGC	No	Yes	No	0	0	0	0	0	No
NM_hsa_2548	chr13:113830028-113830118	-	CCTGTGCTGTGGAGTTCATG	No	Yes	No	0	0	0	0	0	Yes
NM_hsa_2549	chr14:19285183-19285267	+	AACACAGTGGCTAGGTTCTG	No	Yes	No	0.303924	0.199868	0.268716	Yes		
NM_hsa_2550	chr14:21516021-2151672	+	TCCTGAGGACCGCTGATTT	No	Yes	No	0.0569857	0	0	0	Yes	
NM_hsa_2551	chr14:221152187-21152272	+	GCCTGTGGCTAGTTTT	No	Yes	No	0.0569857	0	0.0732862	Yes		
NM_hsa_2553	chr14:24657549-24657683	+	TTCAAGTCTCCGGTACAG	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2553	chr14:24657579-24657653	+	TTCAAGTCTCCGGTACAG	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2554	chr14:24657599-24657683	+	CGCGATCTAGGACGAGGAA	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2554	chr14:24657579-24657653	+	CGCGATCTAGGACGAGGAA	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2557	chr14:33843822-33843968	+	TTCTGTAGTACACCTTTTA	No	Yes	No	0	0	0	0	No	
NM_hsa_2558	chr14:34488656-34488728	+	GTGCAAAACAGCTGGCGTGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2559	chr14:52073519-52073599	+	TGCTAGTCTAGGACCAAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2561	chr14:55823863-55823169	+	CTGTGATCTAGCTTATG	No	Yes	No	0	0	0	0	No	
NM_hsa_2563	chr14:64108824-64108904	+	CTTCTCTGGCTAGCTGATG	No	Yes	No	0	0	0	0	No	
NM_hsa_2564	chr14:65092767-65092905	+	TGGGAGCCGGACCACTGATG	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2564	chr14:65092799-65092875	+	TGGGAGCCGGACCACTGATG	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2565	chr14:65213845-65213933	+	GTCTGTGGATGTCTGTGGA	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2565	chr14:65213811-65213891	+	GTCTGTGGATGTCTGTGGA	No	Yes	Yes	0	0	0	0	No	
NM_hsa_2566	chr14:65937572-65937650	+	CTGCAAGAGGGCCGGCGGTGT	No	Yes	No	0.626843	0.26489	0.146572	Yes	KapB+eMye+KapB-H	
NM_hsa_2567	chr14:65937572-65937650	+	TGTCGCCCTCTCTGTGGCT	No	Yes	Yes	0	0	0.146572	No		
NM_hsa_2567	chr14:65937572-65937650	+	TGTCGCCCTCTCTGTGGCT	No	Yes	Yes	0	0	0.146572	No		
NM_hsa_2570	chr14:7239081-72390971	+	CGTCGCCCGCCCGCGCGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2571	chr14:75593844-75593914	+	CCCGCTTCCGGGAGGCGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2574	chr14:77494049-77495027	+	ACGCTCCCGGAATGGGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2577	chr14:93152517-93152611	+	GCCTGTACTGCTGTGCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2615	chr14:104904651-104904718	+	CGCCGAGGATCTACCCAGC	No	Yes	No	0.0569857	0	0.0732862	No		
NM_hsa_2617	chr14:104314127-104314211	+	ACCGCGGAGCTGGGAGGCTGA	No	Yes	No	0	0	0	0	No	
NM_hsa_2619	chr14:105282492-105282580	+	CGCGAGGACCGGCGCTCCAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2620	chr14:105559750-105559841	+	CGCGGGGGCGGGTGGGGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2622	chr14:10588642-105886420	+	TACAGGCTCGAGTGAAGCCG	No	Yes	No	0	0.199868	0	0	Yes	
NM_hsa_2623	chr14:21675672-21675742	+	TATTAATGTGATGCTGACAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2624	chr14:22791151-22791232	-	TCTGTCTCTGCTCTCTCT	No	Yes	No	0	0	0	0	Yes	
NM_hsa_2626	chr14:34269620-34269698	-	GGCCGCCCGCCGGCCCGGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2627	chr14:35011618-35011690	-	CCCGGACCGCTCCACCAGA	No	Yes	No	0	0.0662225	0	0	No	
NM_hsa_2628	chr14:35481629-35481704	-	GCTTGCAGCTGGTCTCTG	No	Yes	No	0.0569857	0	0.364631	No		
NM_hsa_2629	chr14:48147155-48147253	+	CACAGATGCTGTCTCTGA	No	Yes	No	0	0	0	0	No	
NM_hsa_2631	chr14:74892786-74892879	-	GGGGCGGGCCGGCGGGCGGG	No	Yes	No	0.498625	0.463558	0.0732862	Yes	KapB+eMye+KapB-H	
NM_hsa_2633	chr14:77843371-77843459	-	GCAGATGCTGACCTGACAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2634	chr14:93581351-93581415	-	GGAGCCGGCCCGGCGCGCC	No	Yes	No	0	0	0	0	No	
NM_hsa_2635	chr14:96580591-96580677	-	TGCTAGGTTGACAGCGGCT	No	Yes	No	0	0	0	0	Yes	
NM_hsa_2638	chr14:105636831-105636928	-	CCGGCTGGGCTCTCTGAGG	No	Yes	No	0	0	0	0	No	
NM_hsa_2640	chr15:29284764-29284846	+	TTCTGTGGTGAATTTGCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2641	chr15:38856428-38856524	+	TGGCGGGCGGCGCCGGCT	No	Yes	No	0.142464	0	0	0	Yes	
NM_hsa_2642	chr15:40750666-40750667	+	TGGCCACCTTGTCTGCGAG	No	Yes	No	0.0569857	0	0	0	Yes	
NM_hsa_2644	chr15:42534065-42534100	+	TAAATTTAGTGGTGTAA	No	Yes	No	0	0	0	0	No	
NM_hsa_2646	chr15:52122214-52122293	+	CGCGAACCTGGGCTCCAGT	No	Yes	No	0	0	0	0	No	
NM_hsa_2647	chr15:59725246-59725308	+	GTGTGAATCCGGAGTGGAA	No	Yes	No	0	0	0	0	No	
NM_hsa_2651	chr15:6957847-69578508	+	GAACATGATCCGAGGACACC	No	Yes	No	0.3989	0.0662225	0.146572	Yes		
NM_hsa_2652	chr15:70262601-7026271	+	ATCTAGATTTGAGCTCTCT	No	Yes	No	0.142464	0	0.0732862	Yes		
NM_hsa_2653	chr15:72409959-7241025	+	GACGTGGCCAGGACGGGCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2654	chr15:72523986-72524081	+	ACGGAAGTGGGAGGAGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2657	chr15:75504622-75504715	+	CCAGCTGGCTGGCTTTGGTA	No	Yes	No	0	0	0	0	No	
NM_hsa_2658	chr15:78429800-78429819	+	CGCGCGTGGAGCTGAGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2662	chr15:83424751-83424828	+	AAGGTAGATGACAGGCTCT	No	Yes	No	13.819	13.7743	15.3168	Yes		
NM_hsa_2663	chr15:83629135-83629227	+	TGTTGAAAGAGGTTGGGCTGAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2664	chr15:85924258-85924348	+	GGGTGGGGGGCCCGCCGCG	No	Yes	No	0	0	0	0	No	
NM_hsa_2666	chr15:89529883-89529907	+	ACTCTTGGGCTGTGGTGAACA	No	Yes	No	0	0	0	0	No	
NM_hsa_2671	chr15:90836837-90836928	+	AGACCCGGCTATTGGCCAG	No	Yes	No	0	0	0	0	No	
NM_hsa_2675	chr15:91900044-91900139	+	TAACTGCTTACCCCGCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2677	chr15:97298885-97298953	+	TGTTGAAAAGGCAATCTCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2678	chr15:99191725-99191823	+	CGCGCGAAGCTGGGGCTTGT	No	Yes	No	0	0	0	0	No	
NM_hsa_2680	chr15:99791602-99791769	+	CGCTGGAGGTGAGTGAAGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2681	chr15:22466012-22466106	+	CTGAGATCTGAGACACGGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2682	chr15:28518177-28518257	-	TAAGCATGCTGTCTCTGAG	No	Yes	No	0	0	0	0	Yes	
NM_hsa_2690	chr15:66586037-66586119	+	TGCAAGGCGCGGCTCGCGCC	No	Yes	No	0	0	0	0	No	
NM_hsa_2691	chr15:69426666-69426741	+	GTAGTGTAGTCAAGAAATG	No	Yes	No	0	0	0	0	No	
NM_hsa_2693	chr15:75049173-75049250	+	CGCTGGAGCGGGGAGGAGCT	No	Yes	No	0.0331113	0	0.146572	No		
NM_hsa_2694	chr15:78017608-78017698	+	TGGCTTGGATGCTCTCTGAC	No	Yes	No	0	0	0	0	No	
NM_hsa_2695	chr15:89911257-89911330	-	TTCCGTTATCATCTTATGAC	No	Yes	No	0	0	0	0	Yes	
NM_hsa_2696	chr15:90684480-90684559	+	TATGGCATTTATGGCTATGTT	No	Yes	No	0	0	0	0	No	
NM_hsa_2697	chr15:96875213-96875305	+	TGTCGGGCGGGCGGGCGGG	No	Yes	No	0.0662225	0	0	0	Yes	
NM_hsa_2704	chr16:2128388-2128457	+	ATCCAACTCCCACTCCAGCT	No	Yes	No	0	0	0	0	No	
NM_hsa_2705	chr16:2185901-2185976	+	CGGCTCTCTCTCTCCCCCG	No	Yes	No	0.0569857	0.0331113	0.0636431	Yes		
NM_hsa_2707	chr16:2222119-2222202	+	TCAGCACCGCTCTCTCCAGA	No	Yes	No	0.284929	0.132445	0.0732862	Yes	KapB+eMye+KapB-H	
NM_hsa_2708	chr16:2228625-2228734	+	CCCCGACAGACAGCCACCCG	No	Yes	No	0	0	0	0	No	
NM_hsa_2710	chr16:2550728-2550814	+	CCACTGACTGAGACTCTGAG	No	Yes	No	0.113971	0	0.146572	No		
NM_hsa_2711	chr16:2618926-2619003	+	TGGCTGTGCTCTGGCCATG	No	Yes	No	0	0	0	0	No	
NM_hsa_2713	chr16:3174843-3174906	+	AGAAAGAAACCGCGGGCTG	No	Yes	No	0	0	0	0	No	
NM_hsa_2714	chr16:3208908-3208995	+	GTCTGGCTGTGTTGATGGG	No	Yes	No	0.455886	0.8				

Name	locus	strand	sequence	midsep2	mirsep	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_2798	chr16:88519967-88520040	-	GGCGGGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.968758	0.069536	0.366431	Yes	KapB+cMyc-KapB-H
NM_hsa_2799	chr10:102611331-10261134	-	GGCGGGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.284929	0.264809	0.366431	Yes	KapB+cMyc-KapB-H
NM_hsa_2802	chr17:22626123-22626393	+	CTGGCTCTCTCTTCCCAAGT	No	Yes	No	0	0	0	0	
NM_hsa_2803	chr17:2441320-2441417	+	TGCTGAGGCTGTGATGCGAGG	No	Yes	No	0	0	0	0	
NM_hsa_2804	chr17:2615300-2615387	+	ACTGTGACCTTGGGTGGAGA	No	Yes	No	0	0	0	0	
NM_hsa_2805	chr17:2885704-2885771	+	TTTACGTTTCCAGATTTGGG	No	Yes	No	0	0	0	0	
NM_hsa_2808	chr162:1452-462135	+	CTCCCTTACTGTGATCCAG	No	Yes	No	0.227943	0	0	0	
NM_hsa_2809	chr17:4794684-4794761	+	TCCTGTCTCTCCCTCCAGA	No	Yes	No	0	0	0	0	
NM_hsa_2810	chr17:6347800-6347869	+	TGATGTGGGGTGGGCAAGT	No	Yes	No	0.0284929	0	0	0	
NM_hsa_2811	chr17:6843859-6843928	+	AAGGATGATCGGGCTTGGT	No	Yes	Yes	0	0	0	0	
NM_hsa_2811	chr17:6843859-6843937	+	AAGGATGATCGGGCTTGGT	No	Yes	No	0	0	0	0	
NM_hsa_2812	chr17:6974383-6974476	+	CTCTGGGGTCTCTCTGTT	No	Yes	No	0	0	0	0	
NM_hsa_2816	chr17:8090489-8090581	+	CCGTGTTTCCCCACCTGTT	No	Yes	No	0.227943	0.198668	0.146572	Yes	KapB+cMyc-KapB-H
NM_hsa_2820	chr17:16342755-16342849	+	TGTCCTGATGATCTGTAAT	No	Yes	No	0	0.26489	0	0	
NM_hsa_2821	chr17:17598203-17598283	+	AGTCCACAGCTTCCGCCCGGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2821	chr17:17598188-17598286	+	AGTCCACAGCTTCCGCCCGGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2822	chr17:17598203-17598283	+	AGGCGGGGGCATCTGGGG	No	Yes	Yes	0.227943	0.132445	0.0732862	Yes	KapB+cMyc-KapB-H
NM_hsa_2822	chr17:17598192-17598298	+	AGGCGGGGGCATCTGGGG	No	Yes	Yes	0.227943	0.132445	0.0732862	Yes	KapB+cMyc-KapB-H
NM_hsa_2823	chr17:17717159-17717243	+	CAATGCAACAGCAATGACCCG	No	Yes	No	0	0.26489	0	0	
NM_hsa_2824	chr17:1993919-1993972	+	CTGGGGCTCCCTTACTCTG	No	Yes	No	0	0	0	0	
NM_hsa_2825	chr17:18156856-18156949	+	TGCACAGGCAAGCTCCCTG	No	Yes	No	0	0	0	0	
NM_hsa_2826	chr17:18266961-18267058	+	AGAAGTACCCTCTTGGCTG	No	Yes	No	0	0	0	0	
NM_hsa_2827	chr17:18684606-18684682	+	CAGGTGAGGGGAGGGGCTCG	No	Yes	No	0	0	0	0	
NM_hsa_2828	chr17:18962590-18963604	+	CCCCGAGGAGGAGGATAGCC	No	Yes	No	0.569857	0.52978	0.146572	Yes	KapB+cMyc-KapB-H
NM_hsa_2829	chr17:19266367-19266487	+	ACAGCTGTGGGGTAAGCTTGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2829	chr17:19266397-19266478	+	ACAGCTGTGGGGTAAGCTTGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2830	chr17:19651358-19651446	+	CGCGGATCCCTGGGACTCTGCC	No	Yes	Yes	0	0	0	0	
NM_hsa_2830	chr17:19651358-19651458	+	CGCGGATCCCTGGGACTCTGCC	No	Yes	Yes	0	0	0	0	
NM_hsa_2831	chr17:2707902-27079093	+	GGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2832	chr17:2707479-27074869	+	TGGGTTAGGGGGGGGAACTGA	No	Yes	No	0	0	0	0	
NM_hsa_2836	chr17:29892015-29892097	+	CCGCTGCTGATTTTCTCTG	No	Yes	No	0	0	0	0	
NM_hsa_2839	chr17:31149603-31149699	+	CGCGGGGACGGGGCGCTGG	No	Yes	No	0	0	0	0	
NM_hsa_2841	chr17:35996612-35996978	+	GCCTCGCCAGTGTGGGGGGT	No	Yes	No	0	0	0	0	
NM_hsa_2842	chr17:36875913-36876012	+	AAGCGCCAGGAGGAGCTGGAT	No	Yes	Yes	0.0854786	0.0331113	0.0732862	Yes	KapB+cMyc-KapB-H
NM_hsa_2842	chr17:36875933-36876012	+	AAGCGCCAGGAGGAGCTGGAT	No	Yes	Yes	0.0854786	0.0331113	0.0732862	Yes	KapB+cMyc-KapB-H
NM_hsa_2843	chr17:36875912-36876032	+	ACCCAGTTCCTCTGGCCGAG	No	Yes	Yes	0	0	0	0	
NM_hsa_2843	chr17:36875933-36876012	+	ACCCAGTTCCTCTGGCCGAG	No	Yes	Yes	0	0	0	0	
NM_hsa_2844	chr17:36955613-36955713	+	GGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.500817	0.534515	0.36844	Yes	KapB+cMyc-KapB-H
NM_hsa_2845	chr17:37202419-37202510	+	TTGGAATGAGAGGCTTCTG	No	Yes	No	0	0	0	0	
NM_hsa_2846	chr17:37896686-37896775	+	CCAGGCGGGGAGGCTCTCT	No	Yes	No	0	0	0	0	
NM_hsa_2849	chr17:39184971-39185044	+	AATGGCAATGTAGAACTCA	No	Yes	No	0	0	0	0	
NM_hsa_2850	chr17:39653271-39653336	+	ACCCAGGAGGATCAGAAAG	No	Yes	No	0	0	0	0	
NM_hsa_2851	chr17:39805762-39805844	+	CTCTGAGTGTCTCTGGGTTGG	No	Yes	No	0	0	0	0	
NM_hsa_2852	chr17:39845788-39845882	+	AAGCTGGCCCTCCGAGTAC	No	Yes	No	0	0	0	0	
NM_hsa_2853	chr17:39967644-39967712	+	CCCGGGTGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2855	chr17:41446157-41446246	+	CAGGTTCAAGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2856	chr17:423096-4230963	+	GGCGGAGGGGGGGGGGGGGGG	No	Yes	No	0.303924	0.110371	0	0	
NM_hsa_2857	chr17:46100953-46101041	+	CTCCGCCCACTGGGCTCTG	No	Yes	No	0	0	0	0	
NM_hsa_2858	chr17:47781712-47781794	+	CCCCCCCCCCCCCCCCCCCC	No	Yes	No	0	0	0	0	
NM_hsa_2859	chr17:48005564-48005663	+	GAGGGCTCTGCCCTGGGACCG	No	Yes	No	0	0	0	0	
NM_hsa_2861	chr17:53497607-53497694	+	CAGTCAATGATGAGTGGATG	No	Yes	No	0	0	0	0	
NM_hsa_2862	chr17:55062327-55062448	+	AATCCAGAGGATGAAAGCTGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2862	chr17:55062327-55062418	+	AATCCAGAGGATGAAAGCTGG	No	Yes	Yes	0	0	0	0	
NM_hsa_2864	chr17:56085681-56085752	+	TTGCAAGCTTGAATCTGGAT	No	Yes	No	0.113971	0	0	0	
NM_hsa_2865	chr17:56715137-56715230	+	GTTTCAACCTACTGCTTT	No	Yes	No	0	0	0	0	
NM_hsa_2870	chr17:59407920-59407996	+	AGCCATATGATGAACTGAGA	No	Yes	No	0	0	0	0	
NM_hsa_2871	chr17:61523780-61523850	+	GGCGCCAGCTGGGAGCCGG	No	Yes	No	0	0	0	0	
NM_hsa_2872	chr17:61777033-61777119	+	CTCCGCCCACTGGGAGCCGG	No	Yes	No	0	0	0	0	
NM_hsa_2873	chr17:62971766-62971863	+	CGCGCCAGAGGTTGAGTTCCG	No	Yes	No	0	0	0	0	
NM_hsa_2874	chr17:63557142-63557216	+	GGAGCGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2875	chr17:6599044-65990530	+	CGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2876	chr17:73084285-73084362	+	AGCCCAAGGGGGCTGGAGT	No	Yes	No	0	0	0	0	
NM_hsa_2878	chr17:74902025-74902109	+	TTGTGTCCCGCCACCAGC	No	Yes	No	0	0	0	0	
NM_hsa_2879	chr17:76349039-76349136	+	CTCTGAGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2880	chr17:7710281-77102835	+	AGCCAGGCTGGGTAAGCTTGG	No	Yes	No	0	0	0	0	
NM_hsa_2881	chr17:78234296-78234370	+	CGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.0427393	0.087193	0.128251	Yes	H-KapB-KapB+cMyc
NM_hsa_2887	chr17:78428687-78428769	+	GTGCTGGGGCTGGCCGCTAG	No	Yes	No	0	0	0	0	
NM_hsa_2889	chr17:79373923-79374016	+	CCTCGCCACCTCCCCCGCCC	No	Yes	No	0	0	0	0	
NM_hsa_2890	chr17:79982488-79982606	+	ACTACCGGCTTCTTCTCTCT	No	Yes	Yes	0	0	0	0	
NM_hsa_2890	chr17:79982491-79982576	+	ACTACCGGCTTCTTCTCTCT	No	Yes	Yes	0	0	0	0	
NM_hsa_2892	chr17:80376560-80376654	+	GGGGTGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2893	chr17:81053666-81053744	+	ACATTTGCTGATTTGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2895	chr17:817426-8174303	+	CGGTTGCCCCGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2897	chr17:819028-8190321	+	CGGCTGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0.0732862	Yes
NM_hsa_2898	chr17:8534381-8534460	+	GGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.0569857	0	0	0	
NM_hsa_2904	chr17:27507289-27507362	+	CGCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2907	chr17:32706138-32706226	+	AGGTTAGGTTGGTGGATTT	No	Yes	No	0.0455886	0.0662225	0.0439718	Yes	KapB+cMyc-KapB-H
NM_hsa_2908	chr17:3343293-3343322	+	GTCTAGTTTCTCTGGAAATTC	No	Yes	No	0	0	0	0	
NM_hsa_2909	chr17:36888003-36888086	+	GAATAGTCAAGTGTCTGAGGTT	No	Yes	No	65.9779	39.8119	39.6344	Yes	KapB+cMyc-KapB-H
NM_hsa_2910	chr17:38278611-38278692	+	GCCTCGCCCGCTTCTGGCTG	No	Yes	No	0.143914	0.26489	0.146572	Yes	KapB+cMyc-KapB-H
NM_hsa_2911	chr17:41907466-41907555	+	CGCTGTCTATCTTCTGACG	No	Yes	No	0.113971	0	0.0732862	Yes	KapB+cMyc-KapB-H
NM_hsa_2920	chr17:58154935-58154888	+	CAGTATGTTGGCTTTTGGAT	No	Yes	No	0.0142464	0	0	0	
NM_hsa_2921	chr17:6035231-60352386	+	ACTACCGGCTTCTGAGGCTGG	No	Yes	No	0	0	0	0	
NM_hsa_2922	chr17:65376258-65376340	+	AATCCAGGTTGGCGAGGTTGG	No	Yes	No	0	0	0	0	
NM_hsa_2923	chr17:7041705-70417181	+	TCCAGGAGGATGGGCTGTGG	No	Yes	No	0	0	0	0	
NM_hsa_2927	chr17:8034926-80349099	+	GGGAGCCGGTGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2931	chr18:5295513-5295593	+	CTCCGAGGCGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_2933	chr18:22731481-22731565	+	AAGCAGAACTTGAAGACTG	No	Yes	No	0	0	0	0	
NM_hsa_2936	chr18:24128979-24129074	+	GGGGGGTGGGGGGGGGGGGGGGG	No	Yes	No	1.37666	1.37576	2.74823	Yes	KapB+cMyc-KapB-H
NM_hsa_2937	chr18:24405104-24405180	+	AGTGATGAAGGAGGCTGAGG	No	Yes	No	0	0	0	0	
NM_hsa_2939	chr18:42260720-42260817	+	GAGTGGACTCGGAGGGGGGAGGG	No	Yes	No	0	0	0	0	
NM_hsa_2940	chr18:423096-4230963	+	TCTGAGCTTCTGAACTGAGAG	No	Yes	No	0	0	0	0	
NM_hsa_2941	chr18:45456878-45456945	+	GGCCCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.227943	0.397335	0.146572	Yes	KapB+cMyc-KapB-H
NM_hsa_2942	chr18:45711093-45711177	+	TGACTTCCCGCAGGACTCA	No	Yes	No	0	0	0	0	
NM_hsa_2943	chr18:46479149-46479215	+	TTTGACAACTCTTGAATG	No	Yes	No	0	0			

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_3035	chr19:44861166-44861231	+	TCTGACCTTGCGTCTCTTGG	No	Yes	No	0	0	0	0	
NM_hsa_3036	chr19:44861231-44861296	+	CTCAGCTACTGCTCTCTTGG	Yes	Yes	No	0.0284929	0	0	0	
NM_hsa_3041	chr19:46477190-46477288	+	CCCGGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3043	chr19:46891729-46891814	+	TGCTCTCCCTCTGCCACC	No	Yes	Yes	0	0	0	0	
NM_hsa_3043	chr19:46891718-46891834	+	TGCTCTCCCTCTGCCACC	No	Yes	Yes	0	0	0	0	
NM_hsa_3045	chr19:47880101-47880181	+	ATGAGAGGGTCTCGCTGCAG	No	Yes	No	0	0	0	0	
NM_hsa_3046	chr19:48199644-48197112	+	CAGCTCTCTCTCTCTCTCTCT	No	Yes	No	0.0569857	0	0	0	
NM_hsa_3047	chr19:48259161-48259229	+	GCTGCCCTCTGGTGGCCAGC	No	Yes	No	0	0	0	0	
NM_hsa_3048	chr19:48259161-48259229	+	CAATGCCAGGGGCTGAGGGCA	No	Yes	No	0.0569857	0.0662225	0	0	
NM_hsa_3050	chr19:50167878-50167975	+	CGCGCACTCCGGGTTTCAG	No	Yes	No	0	0	0	0	
NM_hsa_3052	chr19:5039137-50391390	+	TTCTCCCGCTCTCCACCAGC	No	Yes	No	0	0	0	0	
NM_hsa_3053	chr19:51925369-51925465	+	CGCCGACCCGGGACCTCCG	No	Yes	No	0	0	0	0	
NM_hsa_3061	chr19:53104501-53104584	+	AGATCAGCCGCACTGGAA	No	Yes	No	0	0	0	0	
NM_hsa_3062	chr19:53700319-53700395	+	CGGATCCGGGGGATGGAAGC	No	Yes	No	0	0	0	0	
NM_hsa_3088	chr19:54485225-54485310	+	CGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.968757	0.397335	0.293145	Yes	KapB+cMye+KapB-H
NM_hsa_3090	chr19:56112095-56112185	+	TTCTCTCTCTCTCTCTCTCT	No	Yes	No	0	0.0662225	0	0	
NM_hsa_3094	chr19:59061035-59061102	+	TCTGGTGTGGGGTGTGGGA	No	Yes	No	0.0569857	0.132445	0	0	
NM_hsa_3096	chr19:1469558-1469651	-	GCCTCCCGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3097	chr19:1652254-1652351	-	GCCTCCCGGGGGGGGGGGGG	No	Yes	No	0.0569857	0	0	0	
NM_hsa_3098	chr19:27252892-27252922	+	TCTGAGCTGGGGGAGTGGGA	No	Yes	No	0	0	0	0	
NM_hsa_3101	chr19:8152823-8152908	-	CACCTTCCGGGGTCCCGCA	No	Yes	No	0	0	0	0	
NM_hsa_3103	chr19:10926297-10926377	-	TGGCTTGCCATCCAGGAGC	No	Yes	No	0	0.0662225	0	0	
NM_hsa_3109	chr19:16199195-16199288	-	GTTAAGATCGGACAGCCCT	No	Yes	No	61.6586	96.7511	104.286	Yes	H-KapB+KapB+cMye
NM_hsa_3111	chr19:18631499-18631582	-	GGGGGGGGTCCCGGGGGGGGG	No	Yes	No	0	0.0662225	0.0732862	No	H-KapB+KapB+cMye
NM_hsa_3113	chr19:22224769-2222532	+	GTTATGTTGCTTCTCTCT	No	Yes	No	0	0	0	0	
NM_hsa_3114	chr19:32659206-32659303	-	TGAGGTAGAGGTTCTGTAT	No	Yes	No	0	0	0	0	
NM_hsa_3115	chr19:33967952-33968017	-	TGGAGGACAGCAGTGGCTG	No	Yes	No	0	0	0	0	
NM_hsa_3117	chr19:42112979-42113044	-	CTGGTACAGCCCTGGAGGTT	No	Yes	No	0	0	0	0	
NM_hsa_3118	chr19:45949632-45949706	-	CGCGGGGGGGGGGGGGGGGG	No	Yes	No	0	0.132445	0	0	
NM_hsa_3120	chr19:47734457-47734530	-	CGGGGGGGGGGGGGGGGGGG	No	Yes	No	0.0569857	0	0	0	
NM_hsa_3121	chr19:49149595-49149692	-	CGGCTGGGAGCCAGGAGCC	No	Yes	No	0	0	0	0	
NM_hsa_3122	chr19:49899167-49899254	-	AAAGTCCCTGGTTTACC	No	Yes	No	0	0	0	0	
NM_hsa_3125	chr19:875614-875697	-	GCCTCCCGGGGGGGGGGGGG	No	Yes	No	0.048786	0.165556	0.0732862	Yes	
NM_hsa_3126	chr19:1102442-1102513	-	CCCAAGCTGGGACGCTGGC	No	Yes	No	0	0	0	0	
NM_hsa_3130	chr19:1271612-1271709	-	GGCGGGGGGGGGGGGGGGGG	No	Yes	No	2.16544	2.0529	3.15131	Yes	
NM_hsa_3131	chr19:2158685-2158776	+	GGCGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3132	chr19:6268875-6268950	+	TGAGCCCGCTGGCCCGCCAG	No	Yes	No	0	0	0	0	
NM_hsa_3133	chr19:685748-685848	+	CAGGTGCGGAGGAGCGCTGGA	No	Yes	No	0	0	0	0	
NM_hsa_3136	chr19:9371339-9371424	+	TGATGGTCTCGCGTGGCTGA	No	Yes	No	0	0.0662225	0.0366431	No	
NM_hsa_3137	chr19:9750281-9750352	+	CTTCCCGGGGGGGGGGGGG	No	Yes	No	2.84929	2.84757	0.732862	No	KapB+cMye+KapB-H
NM_hsa_3141	chr19:10571690-10571772	+	TGTGGACCAGGAGCTCTGA	No	Yes	No	0.84929	0.860993	0.146572	Yes	
NM_hsa_3142	chr19:10683101-10683404	+	CGCCGTAGCTGTTCTCTCTCG	No	Yes	No	0	0.0662225	0	0	
NM_hsa_3143	chr19:10683264-10683337	+	ACTGAAGTGCAGTGTCTGTA	No	Yes	No	0	0	0	0	
NM_hsa_3144	chr19:12251751-12251851	+	TGCCCGCTCTCGCTCTGAGA	No	Yes	Yes	0	0	0	0	
NM_hsa_3145	chr19:12251760-12251841	+	TGCCCGCTCTCGCTCTGAGA	No	Yes	Yes	0	0	0	0	
NM_hsa_3145	chr19:19229446-19229530	+	TTGCGATGGGATCGACTGTA	No	Yes	No	0	0	0	0	
NM_hsa_3146	chr19:1924590-19245909	+	ACGAGTGAAGGAGCGACTGG	No	Yes	No	0	0	0	0	
NM_hsa_3147	chr19:21672033-21672107	+	GGCGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3148	chr19:23702353-23702432	+	GATAGGCCAATGCTGCTGACA	No	Yes	No	0	0.0662225	0	0	
NM_hsa_3149	chr19:25174649-25174743	+	GTATCTCTAGGCTGCTGCG	No	Yes	No	0	0	0	0	
NM_hsa_3150	chr19:26881016-26881096	+	CCTCTCCCTCTCTGCTGTAG	No	Yes	No	0.054786	0.031113	0	0	
NM_hsa_3152	chr19:2883367-28833937	+	TCCAAGTGTATGACAGTGG	No	Yes	No	0.0569857	0.513000	0.0732862	Yes	KapB+cMye+KapB-H
NM_hsa_3154	chr19:3131667-3131758	+	AGGAGGGGGGGGGGGGGGG	No	Yes	No	0.455886	0.331113	0.0732862	Yes	KapB+cMye+KapB-H
NM_hsa_3155	chr19:32686769-32686853	+	AGTGTAGTCCGCTACTGAG	No	Yes	No	0	0	0	0	
NM_hsa_3156	chr19:32817165-32817271	+	GCCTCCAGCACTGGCCAG	No	Yes	Yes	0	0	0	0	
NM_hsa_3156	chr19:32817174-32817256	+	GCCTCCAGCACTGGCCAG	No	Yes	Yes	0	0	0	0	
NM_hsa_3160	chr19:33545055-33545146	+	GTCGTCGGAGGAGGATGAG	No	Yes	No	0	0	0	0	
NM_hsa_3162	chr19:40505743-40505825	+	GACTCCGAGCCGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3163	chr19:41220011-41220095	+	CTTCTGGGCACTTTGTATC	No	Yes	No	0	0	0.219859	No	
NM_hsa_3166	chr19:41283765-41283852	+	CTGTGACTGGGCGCAGTGTG	No	Yes	No	0	0	0	0	
NM_hsa_3167	chr19:41931843-41931931	+	CTGTATCTCAGTGTCTGTG	No	Yes	No	0	0	0	0	
NM_hsa_3168	chr19:42801097-42801167	+	CAGTCCAGGAGGCTGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3172	chr19:43997256-43997335	+	TGGGTCGGGGTGGCCGGC	No	Yes	Yes	0	0	0	0	
NM_hsa_3172	chr19:43997256-43997335	+	TGGGTCGGGGTGGCCGGC	No	Yes	Yes	0	0	0	0	
NM_hsa_3174	chr19:44061219-4406210	+	CTCAGGACTGCTTCTCTCT	No	Yes	No	0.0569857	0	0.0732862	Yes	
NM_hsa_3174	chr19:44066099-44066237	+	CTCAGGACTGCTTCTCTCT	No	Yes	Yes	0.0569857	0	0.0732862	Yes	
NM_hsa_3176	chr19:46856415-46856501	+	TGAGGTCCTCTGGTGTGCCA	No	Yes	No	15.165	18.6343	23.4515	Yes	
NM_hsa_3177	chr19:47908900-47908987	+	TAGTTCGCTGTGCTTGG	No	Yes	No	0	0	0	0	
NM_hsa_3178	chr19:49378415-49378494	+	CTCTTAACCTATGCTCTCC	No	Yes	No	0	0	0	0	
NM_hsa_3180	chr19:4949286-49494370	+	CATTAGACCTGAGGCTCTGG	No	Yes	No	0	0	0	0	
NM_hsa_3181	chr19:61516056-61516146	+	CCGCTTCCGGCAGCTGTAG	No	Yes	No	0	0	0	0	
NM_hsa_3185	chr19:67529202-67529298	+	TCAGACTCTGGAAGAGAG	No	Yes	No	0.227943	0.26489	0	0	
NM_hsa_3189	chr19:90306769-90306854	+	AGACTCGGATGCTGATGG	No	Yes	No	0	0	0	0	
NM_hsa_3191	chr19:96079598-96079699	+	GCCTCCGCGGCTGTGTTGG	No	Yes	No	0.113971	0.055118	0.329788	Yes	
NM_hsa_3192	chr19:108742995-108743089	+	GAGTGGTCTCTGGGAGGTT	No	Yes	No	0	0	0	0	
NM_hsa_3193	chr19:109814148-109814223	+	AGGGAGCACTGGGCTGTGA	No	Yes	No	0	0	0	0	
NM_hsa_3196	chr19:11079923-11079997	+	TGTGATCCTCTGCTCTCTGA	No	Yes	No	0	0	0	0	
NM_hsa_3197	chr19:11077335-11077336	+	CACATAGCAGGAGGAGGCTG	No	Yes	No	0	0	0	0	
NM_hsa_3198	chr19:11742964-11743063	+	CAGTCCGCTGAGAGGAGCTGA	No	Yes	No	0.0569857	0	0	0	
NM_hsa_3199	chr19:112162347-112162425	+	TCTGGAGGAGGGCCAGCCG	No	Yes	No	7.23719	28.0686	Yes	H-KapB+KapB+cMye	
NM_hsa_3200	chr19:113162478-113162575	+	GTTCGGATGAGGAGGATGA	No	Yes	No	0	0	0	0	
NM_hsa_3201	chr19:117082010-117082138	+	TGGCCCACTGAGGAGTTGT	No	Yes	No	0	0	0	0	
NM_hsa_3203	chr19:12015844-12015951	+	CCGCGGAGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3204	chr19:120190942-120191034	+	GCCTCGGAGGTAGTGGGGCAG	No	Yes	No	0	0	0	0	
NM_hsa_3206	chr19:143910905-143910972	+	ACAATGAATCAGAACTTTGT	No	Yes	No	0	0	0	0	
NM_hsa_3208	chr19:14572648-14572693	+	TGGGATGGATGAATCAAGT	No	Yes	No	0	0	0	0	
NM_hsa_3210	chr19:149832910-149832929	+	CTGGTACTTGTAGTGCTTT	No	Yes	No	0	0	0	0	
NM_hsa_3211	chr19:150830001-150830070	+	CCCGGGGGTGGAGGCTGG	No	Yes	No	0	0	0	0	
NM_hsa_3212	chr19:15031668-150316648	+	TTGTCTCTTCACTGCAAT	No	Yes	No	0	0	0	0	
NM_hsa_3214	chr19:151512267-151512353	+	CTGATGAGCTGGAATCTGG	No	Yes	No	0	0	0	0	
NM_hsa_3215	chr19:1522861-152286207	+	CAGACTCGCTGTCAGATGA	No	Yes	No	0	0	0	0	
NM_hsa_3216	chr19:153880714-153880844	+	CTCAGGCTCTCTCTCCAGC	No	Yes	No	0.170957	0.397335	0.0732862	Yes	
NM_hsa_3216	chr19:153880714-153880844	+	TCACCCCTCTCTCTCCAGCA	No	Yes	Yes	0.170957	0.397335	0.0732862	Yes	
NM_hsa_3217	chr19:153750862-153750948	+	TACCCAGTCTCCCTTCCCAG	No	Yes	Yes	0	0	0	0	
NM_hsa_3217	chr19:153750862-153750948	+	TACCCAGTCTCCCTTCCCAG	No	Yes	Yes	0	0	0	0	
NM_hsa_3218	chr19:1539398										

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_3306	chr1:4779944-4779974	-	GGCCGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0	
NM_hsa_3308	chr1:6809983-6810873	-	CATGATCTGGAGCTCTTAA	No	Yes	No	33.4858	29.5816	11.8017	0	KapB+cMye-KapB-H
NM_hsa_3311	chr1:7427263-7427270	-	CTTCCAAATGATGGTGGG	No	Yes	No	0.79467	1.25369	0.886149	Yes	
NM_hsa_3312	chr1:77578428-77578500	-	TGTTCTCTAGCTGTATAT	No	Yes	No	0	0	0	0	
NM_hsa_3313	chr1:85345214-85345303	-	CGAGGTGGGTGATACAGAGCC	No	Yes	No	0	0.26489	0	0	
NM_hsa_3315	chr1:104314745-104314827	-	ATACCTCTATCTATCAAC	No	Yes	No	0	0	0	0	
NM_hsa_3316	chr1:117210401-117210485	-	CGCCGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0	0.0732862	Yes
NM_hsa_3317	chr1:120114212-120114292	-	AGACTGGTGTACTCTGGAG	No	Yes	No	0	0	0	0	
NM_hsa_3319	chr1:142667290-142667361	-	ATTTTCATAAGTCAGTACATA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3320	chr1:145195999-145196081	-	CTGTGGACTGAGAGTTATG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3321	chr1:145379281-145379353	-	ACAGTTCAACTCTCTAGGAG	No	Yes	No	0.0331113	0	0	0	Yes
NM_hsa_3322	chr1:146082600-146082775	-	CCGGAAGTCAGACTTGGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3323	chr1:147803755-147803834	-	ACACTCATCACTGTGCTGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3324	chr1:149937797-149937881	-	TTCCAGAAATAGGAAGGTGAA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3325	chr1:153278768-153278852	-	GAGAGGGAAAGAGAGAGTTGG	No	Yes	No	0	0	0	0.0732862	Yes
NM_hsa_3331	chr1:760013109-160013198	-	TGGGGTGTGAGCCAGCAATG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3332	chr1:167153912-167153981	-	TGAGATGTAGTTGGGAGT	No	Yes	No	10.2448	7.33598	1.62858	Yes	KapB+cMye-KapB-H
NM_hsa_3336	chr1:173532545-173532614	-	AAAAGCTGGTGGAGGAGCC	No	Yes	No	0.00518052	0.147161	0.0162858	Yes	
NM_hsa_3341	chr1:206136822-206136912	-	CTTCCCTCACCGCCGGGAAGTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3342	chr1:207893035-207893100	-	CGACTGTGGCTGGACTCTGCG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3345	chr1:210169848-210169929	-	TCTGTAGTTTGGTGGAGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3350	chr1:225615430-225615514	-	GGTCCGGGGCCGGCCGGGCGA	No	Yes	No	0	0.0220742	0.024288	Yes	H-KapB-KapB+cMye
NM_hsa_3353	chr1:233126373-233126428	-	CTCTGAGGTCTGGCGTGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3354	chr1:237271642-237272752	-	GGGTGGGGTGGGGGGTGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3355	chr1:240910395-240910463	-	TCTGTAGTGGTTTGTGAGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3356	chr2:6113399-6114096	+	CTAGCCAGTGAAGCTCTGGAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3359	chr2:3194751-3194835	+	CAAAATGAGTGAAGCTGATA	No	Yes	No	3.64709	10.132	12.1655	Yes	H-KapB-KapB+cMye
NM_hsa_3363	chr2:4527579-4527675	+	TAGCACAGTGAATATAATG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3365	chr1:1390976-13909788	+	TGGAAGTCAAGCTCTCTGAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3366	chr2:17486149-17486232	+	TGCCCGCGGTGTCCGGCCACA	No	Yes	No	0.91772	0.132445	0.58629	Yes	
NM_hsa_3367	chr2:17662487-17662571	+	CGGGCCGGCCGGCCGGCCGGC	No	Yes	No	0	0.0854786	0.0366431	Yes	
NM_hsa_3368	chr2:19739049-19739113	+	GGGTCCAGACGTGGGTGGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3371	chr2:21593222-21593223	+	CGGGCCGGTGGGGGGGGGG	No	Yes	No	2.87778	2.31779	0.769506	Yes	KapB+cMye-KapB-H
NM_hsa_3372	chr2:22328232-22328233	+	CGGGCCGGTGGGGGGGGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3373	chr2:25262596-25262678	+	TCCTCTTCTCTGTGTTCAG	No	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_3374	chr2:30194978-30195067	+	CTCTCGGTGATGCTGAGGA	No	Yes	No	0.0284929	0.0772956	0	0	Yes
NM_hsa_3377	chr2:35374639-35374735	+	CAGATTTTGGAGGGCGTGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3378	chr2:3660273-36602813	+	TGGAATAGGGTTTAAAAAA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3381	chr2:44563720-44563800	+	TGGCCGGCCGGCCGGCCGGC	No	Yes	No	0.0284929	0	0	0	Yes
NM_hsa_3384	chr2:47250126-47250208	+	AAGCCCAAGGTGTGCTGGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3385	chr2:57272577-57272666	+	TGGTCTAAAGGCTGGTCTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3390	chr2:60962291-60962386	+	GGCCCGCCGGTGAATCCCAAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3394	chr2:6191806-61918273	+	CTGAGTGGGGCCAGGGACAGGA	No	Yes	Yes	0.170957	0.0732862	0.0366431	Yes	
NM_hsa_3394	chr2:61918186-61918286	+	AGGTGGGGCCAGGGACAGGA	No	Yes	Yes	0.170957	0.0732862	Yes		
NM_hsa_3395	chr2:62711083-62711168	+	GTCCCGAAGCTCCCGCCAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3398	chr2:23078418-23078499	+	TTTTCAGACTCTTTCACAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3400	chr2:2619887-26198929	+	GTCTCCCTCTGGCGGTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3402	chr2:44151625-44151707	+	TGTCAGTGTGCACATACCAA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3403	chr2:54066257-54066348	+	TGAGTATGATTTGTGTCT	No	Yes	No	325.458	293.394	147.771	Yes	KapB+cMye-KapB-H
NM_hsa_3405	chr2:59177120-59177204	+	CTTTGGTTCAGTATGAGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3406	chr2:6120246-6120328	+	GACCGGTGGCTGTGGAA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3407	chr2:61809854-61809937	+	CAGAGTGTCTGTGCACAGCA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3408	chr2:61999828-61999925	+	CTCTGACTCGAGTCCCGTGG	No	Yes	No	0.018952	0	0.024288	Yes	
NM_hsa_3409	chr2:10906339-10906422	+	CGGAATGAAGAGTGTGTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3410	chr2:115399737-115399824	+	TCAGCCAGAGAGCGGGTGGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3419	chr2:13073186-13073233	+	CTGAGTGTCTGGAGCTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3421	chr2:134103288-134103363	+	TCAGGATCAAGATCTCAGAGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3423	chr2:134825454-134825530	+	CTCCCGGAGCCGGAGTCCAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3424	chr2:138071426-138071511	+	CTCCGGGCTGGTCTCCAGCC	No	Yes	No	0	0.198668	0	0	Yes
NM_hsa_3425	chr2:138639949-138640017	+	CTGTGTCTGGTGCACCTGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3426	chr2:141932594-14193373	+	CTCAAGATCTCCAGAGTAA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3430	chr2:145742814-145742907	+	CGAGTGTCTTGTACTGAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3431	chr2:146301281-146301367	+	GTCACTGCCAGGGATTTCC	No	Yes	No	0	0	0	0	Yes
NM_hsa_3435	chr2:14935294-14935367	+	TGTGGAAGTCTGGAATTTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3436	chr2:149324380-149324391	+	TCAGGAGAGTCTGAGAGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3437	chr2:19951638-19951732	+	GGCACTGACAGCCGCTGTCCAG	No	Yes	No	0.0569857	0	0	0	Yes
NM_hsa_3442	chr2:22090411-22090488	+	CGCGCTCGGACAGAGCTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3443	chr2:23267273-23267805	+	GGGCTCTGGGTGGGGTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3445	chr2:24257106-24257202	+	GGCCCGCCGGTCCCGGAGTGA	No	Yes	No	0.227943	0.0662225	0	0	Yes
NM_hsa_3446	chr2:24305832-24305913	+	ACTCCACAGCAGCTCTGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3447	chr2:24577371-24577461	+	TGTTCCGGCCCTCCGCTCCAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3448	chr2:24583848-24583937	+	CTGCACTCTGCCATCCCAAT	No	Yes	Yes	0.170957	0.331113	0.659576	Yes	H-KapB-KapB+cMye
NM_hsa_3448	chr2:24583872-24583967	+	CTGCACTCTGCCATCCCAAT	No	Yes	Yes	0.170957	0.170957	0.659576	Yes	H-KapB-KapB+cMye
NM_hsa_3450	chr2:2672320-26723282	+	AAATTTTCTCTGCACAC	No	Yes	No	0.113971	1.25533	0.659576	Yes	
NM_hsa_3454	chr2:3128134-31284219	+	AAGCTTGTCTGTCTCTAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3455	chr2:31742836-31742911	+	CAGTGGAGCGGGGTGGCTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3458	chr2:36784930-36784846	+	CTGGAAGAGTCTGGAATCT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3459	chr2:38012864-38012949	+	TAGTGTACAGCCGCTCCGTGG	No	Yes	No	0	0	0.219859	Yes	
NM_hsa_3462	chr2:39638464-39638557	+	GGCAGCCCGCTCTCCCTCC	No	Yes	No	0	0	0	0	Yes
NM_hsa_3464	chr2:39917748-39917818	+	ATCACTCAATGTTTCCAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3465	chr2:40706252-40706335	+	TTGCAAGTCTTTCCCTCAAT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3468	chr2:4154390-41543981	+	GTTAGTTGACTGCTGGAAT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3475	chr2:44691412-44692488	+	CCCTCTGTCTGGTCTGAGT	No	Yes	No	0.0993328	0	0	0	Yes
NM_hsa_3476	chr2:44983704-44983848	+	TCACCGGGGGCCGGGGGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3479	chr2:50913603-50913682	+	CCTCGGGCCGGGACCTGGAC	No	Yes	No	0	0	0	0	Yes
NM_hsa_3480	chr2:50969225-50969294	+	TTTGAACCCCTGGACTACGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3481	chr2:51066716-51066800	+	CTTGAAGCGGGTCTGGGAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3482	chr2:17082632-17082764	+	GGGAGCGGGCCGGGGGGGG	No	Yes	No	0.0284929	0	0	0	Yes
NM_hsa_3484	chr2:20786266-20786339	+	TGTCCTCTCTGGTCCAG	No	Yes	Yes	0	0	0	0	Yes
NM_hsa_3484	chr2:20786241-20786365	+	TGTCCTCTCTGGTCCAG	No	Yes	Yes	0	0	0	0	Yes
NM_hsa_3485	chr2:21871756-21871829	+	CGTGGGGGGGGTGGTGGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3486	chr2:23089510-23089609	+	TTGACCACTGGGCTGGCTGGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3487	chr2:24407605-24407699	+	GGCGCCGGCCGGGGTGGCG	No	Yes	No	0.0569857	0	0.146572	Yes	
NM_hsa_3491	chr2:3971178-39711250	+	ACTGCTCTCTTGAGAAACA	No	Yes	No	0.341914	0.26489	0.0732862	Yes	KapB+cMye-KapB-H
NM_hsa_3492	chr2:39715026-39715103	+	CGGACAGAACTGTGGTGA	No	Yes</						

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KaposinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_3583	chr2:18099601-18099675	+	TCCTTTGTATCTAGCAGAT	No	Yes	No	0	0	0	0	No
NM_hsa_3586	chr2:18754126-18754302	+	GAGCTCAAGATCAAGGTTCC	No	Yes	No	0	0	0	0	Yes
NM_hsa_3589	chr2:19187900-19187910	+	CGCCCGCCGGTGGAGCTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3590	chr2:19188284-19188382	+	ACGCTCGCCCTGGGGTGCAGA	No	Yes	No	0	0	0	0	No
NM_hsa_3591	chr2:19652276-19652282	+	CTTTTCCCGAAACCCCTT	No	Yes	No	0	0	0	0	No
NM_hsa_3592	chr2:198318719-19831877	+	AGAAGGCTCCCGCTCTGG	No	Yes	No	0	0.0569857	0.132445	0	Yes
NM_hsa_3593	chr2:20016386-20263929	+	AGTCCGATGGGGGAGCACTTTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3594	chr2:204126219-20412631	+	ACAGAGTCAGGTCAGTGA	No	Yes	No	0	0.26489	0.146572	Yes	Yes
NM_hsa_3595	chr2:204126219-20412631	+	CACGCGCAGCTCTCTGTAG	No	Yes	No	0.170957	0	0	0	Yes
NM_hsa_3599	chr2:218905708-21890575	+	CTTCAGATGCTCTCTAGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3600	chr2:218905708-21890575	+	CTCTAGAGACACCTCTGAAG	No	Yes	No	0	0	0	0	No
NM_hsa_3601	chr2:219206630-21920674	+	TCCCTGCTCCCTTTTCCCAAGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3602	chr2:219271110-21927119	+	AGAATCTTGGCTGGGTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3603	chr2:219925417-219925517	+	CGGGGGGGGGGGGGGGGGGG	No	Yes	No	0	0	0.0110371	0	Yes
NM_hsa_3605	chr2:220148015-220148106	+	AACCTGGACAGCCCTGCG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3606	chr2:22915765-22915851	+	AATGGGAATGGATCTCCGG	No	Yes	No	0	0	0	0	No
NM_hsa_3609	chr2:232379278-232379356	+	CGCGTGTCCAGGCTCTCCG	No	Yes	No	0	0	0	0	No
NM_hsa_3610	chr2:234184307-234184403	+	GGTCCATGTAGTTGTAATA	No	Yes	No	0.227943	0.331113	0.219859	0	No
NM_hsa_3611	chr2:234197478-234197559	+	TTTGTATTTGGAGTCTGGT	No	Yes	No	0	0	0	0	No
NM_hsa_3612	chr2:235230014-235230957	+	CTCCTCCCACTCTGTTCAGC	No	Yes	No	0	0	0	0	No
NM_hsa_3615	chr2:238886934-238887024	+	CACCTGTGATTTGGGCTGTAGT	No	Yes	Yes	0	0	0	0	No
NM_hsa_3615	chr2:238886939-238887016	+	CACCTGTGATTTGGGCTGTAGT	No	Yes	Yes	0	0	0	0	No
NM_hsa_3618	chr2:239404416-239404232	+	ACTCGGACTGACGCTTGAAG	No	Yes	No	0	0	0	0	No
NM_hsa_3619	chr2:240322061-240322158	+	ACCCTCCCGCCCGCCCGCCG	No	Yes	No	10.2859	5.76136	1.90544	Yes	KapB+cMye-KapB-H
NM_hsa_3622	chr2:2587876-2587952	+	TCGTATCTCAGGCTCTG	No	Yes	No	0	0	0	0	No
NM_hsa_3625	chr2:12122675-12122754	+	ACCCCAGAGATGGAGCTGCA	No	Yes	No	0	0	0	0	No
NM_hsa_3625	chr2:29862748-29862824	+	CTGGGAGGATTTGGGATGA	No	Yes	No	0	0	0	0	No
NM_hsa_3626	chr2:37193372-37193464	+	ACTTAAAGAAATTTGCGAT	No	Yes	No	0.113971	0	0	0	Yes
NM_hsa_3627	chr2:37883958-37884037	+	TAGAGATTTAGAGTGGAGGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_3628	chr2:48372001-48372079	+	CTAGATCACCAGACTTGAAG	No	Yes	No	0	0	0	0	No
NM_hsa_3633	chr2:69413998-69414092	+	CATCCATCTTCCCTGCTTCT	No	Yes	No	0	0	0	0	Yes
NM_hsa_3634	chr2:75340449-75340537	+	GTGAGCCTTGAAGCTTGAAG	No	Yes	No	0.0569857	0.0662225	0	0	Yes
NM_hsa_3636	chr2:85783045-85783123	+	AAAGGATTCAGTCTGGCTT	No	Yes	No	0	0	0	0	No
NM_hsa_3638	chr2:88519245-88519312	+	CTTGCATGCTCTGCTGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3639	chr2:90052219-90052305	+	CAGCATGTTGGATCTGAG	No	Yes	No	0.227943	0.0993338	0.182126	Yes	Yes
NM_hsa_3640	chr2:101440034-101440115	+	TCAGTGCATCCCAAACTTG	No	Yes	No	0	0	0	0	No
NM_hsa_3641	chr2:102313765-102313857	+	CGGGGAGGAGCGGGTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_3642	chr2:103089746-103089828	+	CTCTGATCACGAAAGTGCAG	No	Yes	No	0	0	0	0	No
NM_hsa_3644	chr2:113994289-113994373	+	TGACTTCTTCTTCCCCAG	No	Yes	No	0	0	0	0	No
NM_hsa_3645	chr2:117475329-117475394	+	TGGAATCTTCTGTCAGCC	No	Yes	No	1.05424	1.65556	2.78488	Yes	H-KapB-KapB+cMye
NM_hsa_3646	chr2:118874367-118874439	+	AGGACTTCAAGGACAGAGA	No	Yes	No	0.341914	0.298001	0.256502	Yes	KapB+cMye-KapB-H
NM_hsa_3649	chr2:146888421-146888508	+	CTTCAGAGAACCACTCAAG	No	Yes	No	0	0	0	0	No
NM_hsa_3651	chr2:169145666-169145683	+	TTTGGACCTCTGCTCACTG	No	Yes	No	0	0	0	0	No
NM_hsa_3653	chr2:197550903-197550996	+	TTTGGACCTCTGCTCACTG	No	Yes	No	0.0569857	0.132445	0.182126	Yes	H-KapB-KapB+cMye
NM_hsa_3654	chr2:204907212-204907293	+	TCAGATGAACACTGAAGTC	No	Yes	No	0	0	0	0	No
NM_hsa_3658	chr2:208634359-208634444	+	GGAGCGGCTGCTGGCGCTC	No	Yes	No	0	0	0	0	No
NM_hsa_3659	chr2:209190758-209190828	+	CCTCTTCCATTTCTTGA	No	Yes	No	0	0	0	0	No
NM_hsa_3664	chr2:241587123-241587210	+	GAGCCCTCTCTCTCCAGT	No	Yes	No	0	0	0	0	No
NM_hsa_3666	chr3:3841000-3841082	+	GGAAGAGGCTGGCGGGGA	No	Yes	No	0	0	0	0	No
NM_hsa_3667	chr3:5018997-5019093	+	GTCTTAGTCTGCAAGG	No	Yes	No	0	0	0	0	No
NM_hsa_3668	chr3:9439307-9439385	+	ACGAGCGGTGAGTGAAGTC	No	Yes	No	0	0	0	0	No
NM_hsa_3670	chr3:12969629-12969700	+	TTGCAAGTCTGCTGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3672	chr3:16259795-16259883	+	AGTGGAACTTGACATGGC	No	Yes	No	0	0	0	0	No
NM_hsa_3675	chr3:37902139-37902236	+	AGAGTGGCTGAGTTGGAAG	No	Yes	No	0.0569857	0	0.0732862	No	KapB+cMye-KapB-H
NM_hsa_3678	chr3:38012172-38012248	+	CTACTTTCAGCCCTCTGC	No	Yes	No	0.7978	0.397335	0	0	Yes
NM_hsa_3681	chr3:43663823-43663907	+	AGGAGAGGCTGTGGGCTGT	No	Yes	No	0	0	0	0	No
NM_hsa_3684	chr3:45883723-45883820	+	AGAGAGCGGGAGGTTGGCT	No	Yes	No	0	0.132445	0	0	No
NM_hsa_3687	chr3:49751453-49751532	+	CACGACCCCACTCCACAG	No	Yes	No	0	0	0	0	Yes
NM_hsa_3688	chr3:51229354-51229402	+	ACAGGTTGTCTTACTCAGG	No	Yes	Yes	0	0	0	0	Yes
NM_hsa_3688	chr3:51229354-51229402	+	ACAGGTTGTCTTACTCAGG	No	Yes	Yes	0	0	0	0	Yes
NM_hsa_3689	chr3:52525296-52525375	+	CTTGCAGCCCTCTCTCTGC	No	Yes	No	0	0	0	0	Yes
NM_hsa_3690	chr3:52535112-52535187	+	ACAGGTCAGACTGGCGGTG	No	Yes	No	0.0569857	0.26489	0	0	Yes
NM_hsa_3691	chr3:53222649-53222745	+	TTACCTGCCCTTCCCTTAA	No	Yes	No	0	0	0	0	No
NM_hsa_3693	chr3:64674698-64674778	+	TCGCTGTCTTCAAGCTGAGA	No	Yes	No	0	0	0	0	No
NM_hsa_3694	chr3:66025986-66025983	+	CTTCTAGGCTGGCTGCTG	No	Yes	No	0.0662225	0.219859	0	0	H-KapB-KapB+cMye
NM_hsa_3695	chr3:69063227-69063322	+	GTCTTCTGCTCTCACTGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3698	chr3:73779437-73779531	+	CCAAGGTCCGCACTGGAG	No	Yes	No	0.113971	0.331113	0.366431	0	H-KapB-KapB+cMye
NM_hsa_3700	chr3:77180423-77180505	+	CCTTCAGTACTGCTGTTT	No	Yes	No	0	0	0	0	No
NM_hsa_3702	chr3:80101686-80101779	+	CTCACTGCTTCTGGAGCGGTG	No	Yes	No	0.3989	0.397335	0.439717	Yes	Yes
NM_hsa_3703	chr3:88312719-88312798	+	FAGGAGCTGGGAGTGAAGC	No	Yes	No	0	0	0	0	No
NM_hsa_3704	chr3:100428819-10042895	+	GTCCCGCAGCTAATCCCTG	No	Yes	No	0	0	0	0	No
NM_hsa_3705	chr3:101567970-101568050	+	CGCCGCGCCCTTCCCGGG	No	Yes	No	0	0	0	0	No
NM_hsa_3706	chr3:107856084-107856167	+	TGGAAGGTGAGGCTGATGA	No	Yes	No	0	0	0	0	No
NM_hsa_3709	chr3:118838729-11883881	+	CTTGATGACTTTGACAGAC	No	Yes	No	0	0	0	0	No
NM_hsa_3711	chr3:122813448-122813514	+	CCAGTCCGCTGTGGTCTG	No	Yes	No	0	0	0	0	No
NM_hsa_3713	chr3:128567501-128567592	+	ACCCTGGCTAGTGTGATG	No	Yes	No	0	0	0	0	No
NM_hsa_3714	chr3:17880282-17880379	+	AGTTGGTCCAAGTTGTGGTT	No	Yes	No	0.788303	0.87193	0.818363	Yes	Yes
NM_hsa_3714	chr3:132291815-132291911	+	AGTTGGTCCAAGTTGTGGTT	No	Yes	No	0.788303	0.87193	0.818363	Yes	Yes
NM_hsa_3715	chr3:135915784-135915858	+	CTCCCTGGCTGGAGTGAAG	No	Yes	No	0.0569857	0.0662225	0	0	Yes
NM_hsa_3716	chr3:135929710-135929809	+	CCGTTGATGATGTTGAGCATA	No	Yes	No	0.170957	0	0	0	Yes
NM_hsa_3717	chr3:141205842-141205917	+	ACGAGGCGCAGGGCTCGCG	No	Yes	No	0.0569857	0	0.146572	No	Yes
NM_hsa_3719	chr3:155572840-155572610	+	CTGAAGTCTCTGGTGGTGA	No	Yes	No	0	0	0	0	No
NM_hsa_3720	chr3:156534821-156534905	+	CTTGCAGCTCCCGCTGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3721	chr3:156878029-156878118	+	CTCCGAGGGGAGTGTGGTG	No	Yes	No	0	0	0	0	No
NM_hsa_3724	chr3:159605671-159605741	+	TGAAATGCAAGGAAAGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_3727	chr3:169483089-169483136	+	CTCTCCAGCCAGACCGGTT	No	Yes	No	0	0	0	0	No
NM_hsa_3728	chr3:176232880-176232951	+	TTTCCAGCCAGCACCA	No	Yes	Yes	50.6663	48.7729	84.0224	Yes	Yes
NM_hsa_3729	chr3:178866236-178866356	+	CGCCCGCTTCCCTCCCGCC	No	Yes	Yes	0	0	0.0732862	Yes	Yes
NM_hsa_3729	chr3:178866243-178866331	+	CGCCCGCTTCCCTCCCGCC	No	Yes	Yes	0	0	0.0732862	Yes	Yes
NM_hsa_3731	chr3:181301731-181301813	+	AGTTGGCTAAGGAGGATGA	No	Yes	No	0.0569857	0	0	0	No
NM_hsa_3733	chr3:183907524-183907615	+	TTCCAGATGAGGCTAAGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_3736	chr3:186549502-186549584	+	CAGCACTAGATTTGAAGACTG	No	Yes	No	0	0	0.293145	Yes	Yes
NM_hsa_3737	chr3:187329742-187329812	+	CACAGGATGACAGTATGAG	No	Yes	No	0	0	0	0	No
NM_hsa_3738	chr3:187463609-187463698	+	GTGACATAAAGGGGAGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_3743	chr3:193921970-193922057	+	TTCCGCGGGGCTGTCTGCG	No							

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation	
NM_hsa_3848	chr4:15668106-156681165	-	CGCGCCCGCCGCGCCGAC	No	Yes	No	0	0	0	0		
NM_hsa_3849	chr4:170109194-170109150	-	CTGAAGGCTGATGAGAAATCC	No	Yes	No	0	0	0	0		
NM_hsa_3850	chr4:175204224-175204314	-	GACTCCAGTAAGCAACCAAG	No	Yes	No	0	0	0	0		
NM_hsa_3851	chr4:176881945-176882036	-	TCATTGCATCAGAAATTTTA	No	Yes	No	1.51012	0.860693	0.769056	Yes	KapB+cMye-KapB-H	
NM_hsa_3852	chr4:187010236-187010327	-	TGTGACTGGTGTGATGAGGG	No	Yes	No	0	0	0	0		
NM_hsa_3856	chr5:6713980-6714067	+	AGGCCCTCTGCTGCTCCCT	No	Yes	No	1.89952	1.53415	1.512325	Yes		
NM_hsa_3858	chr5:14441417-14441517	+	TCAGATGCTCCGCTGGCGCTGC	No	Yes	No	0	0	0	0		
NM_hsa_3859	chr5:14712519-14712612	+	CTCTGGCAAGTCTCTGCTGC	No	Yes	No	0	0	0	0		
NM_hsa_3860	chr5:14871905-14871990	+	ACGAGGGCCCGCCCGCCGGC	No	Yes	No	0	0	0	0.0732862	Yes	
NM_hsa_3861	chr5:2149575-21495842	+	TGATCGAAATCTCCAGGGGA	No	Yes	No	1.82354	1.72179	1.75887	Yes		
NM_hsa_3862	chr5:2150588-21509964	+	TCTCTCTCCCTCCCGCCCGC	No	Yes	No	0	0	0	0	Yes	
NM_hsa_3863	chr5:34537998-34538080	+	CAGGGCAAGCTGACTGCAACG	No	Yes	No	0	0	0	0.0220742	0	
NM_hsa_3864	chr5:38403574-38403661	+	ACAGTGAATCTGCAAACTGA	No	Yes	No	0.0569857	0.0662225	0	0	0	
NM_hsa_3865	chr5:39074595-39074658	+	CTGAGGGAGCACTGAGCCGAC	No	Yes	No	0	0	0	0	0	
NM_hsa_3866	chr5:56205885-56205967	+	GAGCTCCGACAGCCGATGTTG	No	Yes	No	0	0	0	0	0	
NM_hsa_3867	chr5:62451159-62452142	+	TCAGGGTTCCTCAAGTACAG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3867	chr5:62451129-62451267	+	TCAGGGTTCCTCAAGTACAG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3868	chr5:75480014-75480106	+	ACTAGGGTGGATCTCTGGAG	No	Yes	No	0	0	0	0	0	
NM_hsa_3869	chr5:78104703-78104777	+	GGGACACACAGGAAAGCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3870	chr5:78208075-78208062	+	AAGCCAGCTGCTGACAGCTAG	No	Yes	No	0	0	0	0	0	
NM_hsa_3871	chr5:91140647-91140736	+	TAGAAAGGTTGTGCCACCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3872	chr5:92916188-92916286	+	GTGCCACGACGACGCTCCAG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3872	chr5:92916198-92916279	+	GTGCCACGACGACGCTCCAG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3874	chr5:103289513-103289574	+	CAGCGGGACAGGCGCTCCCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3875	chr5:104899421-104899514	+	AAGTGGCTGGTAGAGGGGCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3876	chr5:107735053-107735130	+	TAAACGCTCTGCTGGCGAG	No	Yes	No	0	0	0	0	0	
NM_hsa_3878	chr5:116376612-116376689	+	GCATGTCTGAATGGGTGACT	No	Yes	No	0	0	0	0	0	
NM_hsa_3880	chr5:12240375-122403839	+	CGCGCCAGCGGCTGGTGTGG	No	Yes	No	0.0189952	0.0220742	0.0732862	Yes	H-KapB-KapB+cMye	
NM_hsa_3881	chr5:12666412-126664210	+	CGCGGGGCGGCTGCGGACTCT	No	Yes	No	0.113971	0	0	0	0	
NM_hsa_3882	chr5:127418874-127418967	+	CTCTGAAGCGTGGCTGGGG	No	Yes	No	0	0	0	0	0	
NM_hsa_3883	chr5:129606615-129606694	+	TGATGAAAGTGGAGTCTGAG	No	Yes	No	0	0	0	0	0	
NM_hsa_3884	chr5:132299919-132299988	+	ATAGATCTCGCTGTGTCGCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3885	chr5:132458988-132459055	+	CTCTGTGCTCCAGGCTGCTGT	No	Yes	No	0	0	0	0	0	
NM_hsa_3886	chr5:133340525-133340610	+	CGCTCAGGCGGCGGCGGAGT	No	Yes	No	0	0	0	0	0	
NM_hsa_3889	chr5:134261642-134261738	+	TGTTGGCACTCTCGCGGGTA	No	Yes	No	0.569857	0.463558	0.659576	Yes		
NM_hsa_3890	chr5:135359110-135359193	+	CAAGGGAATAGAGCACTGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3893	chr5:139903011-139903074	+	ATTCGCGGTTGGGCACTGGCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3894	chr5:141229306-141229381	+	TCTCTGTTTCCGACTCTCCGG	No	Yes	No	0.0569857	0.132485	0.0732862	Yes		
NM_hsa_3895	chr5:141229500-141229623	+	TATCCAGTTCGGCACTCAACT	No	Yes	No	0	0	0	0	0	
NM_hsa_3896	chr5:148686130-148686224	+	CGCTGGAATGGGAGTCAGAGGC	No	Yes	No	0	0	0	0	0	
NM_hsa_3900	chr5:149492511-149492607	+	ACACAGTGTAGGATCTGAGG	No	Yes	No	0	0	0	0	0	
NM_hsa_3903	chr5:157565600-157565769	+	GGCTTCTCAGCTGGGTGTTGA	No	Yes	No	0	0.0331113	0	0	0	
NM_hsa_3904	chr5:158432566-158433333	+	GTTAATGAAAGCTGTTTTTTT	No	Yes	No	0	0	0	0	0	
NM_hsa_3906	chr5:166485925-166486021	+	CGTGGGCGGCGGCTGTTGTG	No	Yes	No	0.132967	0.0551854	0.329788	Yes		
NM_hsa_3907	chr5:166592236-166592332	+	CGAGAGAGAGCAATGGCAAG	No	Yes	No	0.227943	0.463558	1.17258	Yes		
NM_hsa_3909	chr5:176833033-176833143	+	AAGAGGCTGGGCGGAGCGTCC	No	Yes	No	0	0	0	0	0	
NM_hsa_3912	chr5:180229833-180229924	+	GGTCCGCGGCGGCGGACTGCA	No	Yes	No	0	0	0	0	0.0732862	Yes
NM_hsa_3914	chr5:180689712-180689778	+	TACCCAGCTGTGAGGCCAAGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3915	chr5:473010-473106	+	CTCGGCCCTTCCACCGC	No	Yes	No	0	0	0	0	0	
NM_hsa_3916	chr5:38556867-38556952	+	CCCGCGGCGGGCGCGCGC	No	Yes	No	0	0	0	0	0	
NM_hsa_3917	chr5:40832754-40832843	+	TATCAGTGTGTGTAAAAAT	No	Yes	No	0	0	0	0	0	
NM_hsa_3918	chr5:40832754-40832843	+	TTCAGCAATTAAGTCAAGG	No	Yes	No	0	0	0	0	0	
NM_hsa_3919	chr5:41904043-41904130	+	GTGAGCTGTGGCGAGGCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3924	chr5:76376313-76376407	+	GTGGAGGACTGAGAGAGTGA	No	Yes	No	0	0	0	0	0.146572	No
NM_hsa_3925	chr5:77623407-77623501	+	TGAGTATGATAGATAAAGAT	No	Yes	No	0	0.0220742	0.0244288	Yes	H-KapB-KapB+cMye	
NM_hsa_3926	chr5:82360182-82360219	+	TKCATGTGGAATCTGCTGAG	No	Yes	No	0	0	0	0	0	
NM_hsa_3927	chr5:84844574-84845865	+	CTCCGGCACTCTCCACCA	No	Yes	No	28.6638	21.5223	24.4043	Yes		
NM_hsa_3930	chr5:113181176-113181272	+	TGAGGAAGCACTGAGTCACTA	No	Yes	No	0	0.0882967	0.097715	0	0	
NM_hsa_3932	chr5:138840660-138840735	+	CGCAGGCGAGGATGCGAGTGG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3932	chr5:138840660-138840735	+	CGCAGGCGAGGATGCGAGTGG	No	Yes	Yes	0	0	0	0	0	
NM_hsa_3933	chr5:142783411-142783497	+	CGCCGCTGCGGCGGCGGCGC	No	Yes	No	3.1912	3.04624	2.88516	Yes	KapB+cMye-KapB-H	
NM_hsa_3936	chr5:148808494-148808573	+	AGATGAGCACTGAGCCACTA	No	Yes	No	0	0	0	0	0	
NM_hsa_3937	chr5:155106164-155106248	+	TGTTAATGTCAGGAGGAGTGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3942	chr5:169356028-169356118	+	CAGGGCAATGAGCAACTCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3944	chr5:173214625-173214722	+	CGTGTATGAGGGTTGCAAGTT	No	Yes	No	0	0.0331113	0	0	0	
NM_hsa_3945	chr5:175158177-175158263	+	ATGGAACTGGATGCCACGCT	No	Yes	No	0.0569857	0	0	0	0	
NM_hsa_3946	chr5:176305523-176305603	+	CTCGCACACCCAGCTGCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3948	chr5:179316784-179316863	+	CTACAGCTCCATCCCGGACT	No	Yes	No	0.0569857	0	0.146572	Yes		
NM_hsa_3949	chr5:1993374-1993467	+	AGCCGGGCGGCGGCGGCGCG	No	Yes	No	232.459	137.346	15.2435	Yes	KapB+cMye-KapB-H	
NM_hsa_3950	chr5:1784455-1784495	+	TCTCTTGTGCTGCTGGCG	No	Yes	No	0.113971	0	0	0	0	
NM_hsa_3950	chr5:2784478-2784565	+	TCTCTTGTGCTGCTGGCG	No	Yes	Yes	0.113971	0	0	0	0	
NM_hsa_3951	chr5:3725451-3725536	+	TGCCCTCTCCCTGCGCAGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3952	chr5:67120217-67120313	+	GTGGATGATGCTGCTGCA	No	Yes	No	0.7978	1.05956	1.09929	Yes	H-KapB-KapB+cMye	
NM_hsa_3953	chr5:12012411-120124202	+	CGCCCGCCCGGCGGCGCGCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3958	chr5:18836381-18836465	+	ACTTGGCACTGATGACCTGA	No	Yes	No	38.1234	36.897	47.4525	Yes		
NM_hsa_3959	chr5:21686023-21686094	+	CACTTCTGCTGCTGGCTCGT	No	Yes	No	0	0	0	0	0.439717	0
NM_hsa_3960	chr5:21768025-21768090	+	TCTTGTGCTGAGTCACTGGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3961	chr5:4721902-24721908	+	GTTCAGAGGCTGCTGCTGGG	No	Yes	No	0	0.132485	0	0	0	
NM_hsa_3962	chr5:2612292-2612238	+	AGGCGCTAACTGGTGTCTCC	No	Yes	No	0	0	0	0	0	
NM_hsa_3963	chr5:2612292-2612238	+	GCCACAGCACTGGGGATG	No	Yes	No	0	0	0	0	0	
NM_hsa_3964	chr5:26328352-26328450	+	CGAAGGCGGCGGAGTGGCAATGA	No	Yes	No	17.8365	23.1117	60.3879	Yes	H-KapB-KapB+cMye	
NM_hsa_3965	chr5:26328352-26328450	+	TCATCTGCACTCGGCTGGCTG	No	Yes	No	13.9615	9.90026	3.51774	Yes	KapB+cMye-KapB-H	
NM_hsa_3966	chr5:271051-27107122	+	AGACACTTGTCTGCACTGA	No	Yes	No	0	0	0	0	0	
NM_hsa_3967	chr5:2719345-27219439	+	TCTGCACTCTGAGTCCCGCG	No	Yes	No	0	0	0	0	0	
NM_hsa_3969	chr5:28687504-28687569	+	GCATGCAAGGCGGCGGGGT	No	Yes	No	2.67833	2.78135	1.17258	Yes		
NM_hsa_3970	chr5:28722097-28723196	+	GCCAAATGCTGATGGTGGAGG	No	Yes	No	4.87228	3.67353	0.329788	Yes	KapB+cMye-KapB-H	
NM_hsa_3971	chr5:28918918-28918960	+	TCTGGCGGGATGCGGCTGTT	No	Yes	No	0.968757	1.72179	2.08866	Yes	H-KapB-KapB+cMye	
NM_hsa_3973	chr5:30683483-30685523	+	GTTCAGCTGCTGCTGGAGG	No	Yes	No	0	0	0	0	0	
NM_hsa_3975	chr5:31515849-31515949	+	CTGCTGCTTTTTCTCCACCA	No	Yes	No	0	0	0	0	0	
NM_hsa_3978	chr5:32147587-32147664	+	TTTCTCTCACTCTCCAGCA	No	Yes	No	0	0	0	0	0.0732862	Yes
NM_hsa_3985	chr5:3465534-3465612	+	TTCAGCTGCGCTCGGAGG	No	Yes	No	0	0	0	0	0	
NM_hsa_3986	chr5:32226041-32226271	+	CTGAGCTCCGAGTCAAGCAAG	No	Yes	No	2.82079	2.9887	2.45509	Yes		
NM_hsa_3987	chr5:43395613-43395687	+	AAGCCGCGTCTTACCTGCA	No	Yes	No	0	0	0	0	0.0732862	

Name	locus	strand	sequence	midseq2	mirseq	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_4088	chr7:13422049-14221508	+	CCCGTGTGATGTTACTGTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4089	chr7:13485523-13485624	+	CTGACTGGAGTCCGGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4091	chr7:13872042-138721027	+	CTGGACGTGGCTACCGCGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4093	chr7:13987620-139876499	+	CGGGCGCGCGCGCGCGCGG	No	Yes	No	0.0427393	0.087193	0	0.018216	Yes
NM_hsa_4094	chr7:143085697-143085782	+	GTGAAGTCGGCGTGTCTGGG	No	Yes	No	0.0569857	0	0	0.0732862	Yes
NM_hsa_4095	chr7:148638570-148638672	+	AGTTGATCCCAAGTGTGTGGTTAT	No	Yes	No	2.35541	1.76593	3.50979	1.80773	Yes
NM_hsa_4096	chr7:148638570-148638672	+	CTCTGTGACTGTCTGTCTGTT	No	Yes	No	0.51074	0	0	6.23993	No
NM_hsa_4097	chr7:148762972-148763044	+	CTCTGCTTTCTGTCTGGTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4098	chr7:148848165-148848256	+	GACCGCCAGCGGGTGTGGCG	No	Yes	No	0	0	0	0	No
NM_hsa_4099	chr7:149195257-149195333	+	TGCTGCCGAGTCTGTGGT	No	Yes	No	0	0.132445	0	0	No
NM_hsa_4100	chr7:15075338-15075363	+	CGGATCCACCGCCGCGGGAAG	No	Yes	No	0	0	0	0	No
NM_hsa_4106	chr7:157310013-157310102	+	GGTGAATGGTCCGGGGAGC	No	Yes	No	0	0	0	0	No
NM_hsa_4107	chr7:157520512-157520600	+	CCTGCAGTCTGCATCTTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4110	chr7:1488540-1488624	-	TGCAATATGGTGAAGTCAAG	No	Yes	No	0	0.0569857	0	0.219859	No
NM_hsa_4112	chr7:1596206-15962596	-	AGTTGCGGAATACAACTGA	No	Yes	No	0	0	0	0	Yes
NM_hsa_4113	chr7:2631600-2631683	+	GGCGCGCGCGCGCGCGCGG	No	Yes	No	0	0.163717	0	0.018216	Yes
NM_hsa_4114	chr7:29198723-29198792	+	CAGGATCTGCACATGCTT	No	Yes	No	0	0	0	0	No
NM_hsa_4115	chr7:37823130-37823210	+	CAGAACCACAGGAGCCGCTG	No	Yes	No	0	0	0	0	No
NM_hsa_4119	chr7:73228271-73228350	+	AAAGCCAGAGTGTGAAGTCCAG	No	Yes	No	0	0	0	0	No
NM_hsa_4120	chr7:14801768-17480774	+	CATCTCCCTCTCTACCCCTGC	No	Yes	No	0	0	0	0	Yes
NM_hsa_4121	chr7:91763389-91763469	+	GGCGCGCGCGCGCGCGCGG	No	Yes	No	0.341914	0.728448	0.439717	0	Yes
NM_hsa_4122	chr7:92165483-92165576	-	TGCTCATGTTACGCTTAA	No	Yes	No	0	0	0	0	No
NM_hsa_4123	chr7:97910948-97911033	-	GGCGGGCGCGCGCGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4124	chr7:9906365-99063748	-	CCCAAGTAAAGCTTTTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4126	chr7:99691220-99691311	+	TGCTCTCTCACAGGACAG	No	Yes	No	0	0	0	0	No
NM_hsa_4127	chr7:105924959-105925045	+	GGCGCGCGCGCGCGCGCGG	No	Yes	No	0.265933	0.362384	0.0427505	0	Yes
NM_hsa_4128	chr7:107301483-107301573	+	TCCCAAGAGCGCGCGCGCTG	No	Yes	No	0	0	0	0	No
NM_hsa_4130	chr7:12878477-128784872	-	CTCTCCCGGAGCGCGCGCGG	No	Yes	No	0.740814	0.866093	0.146572	0	No
NM_hsa_4135	chr4:42157422-42157470	+	TCGCTGTGTATCTCTGGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_4136	chr7:142625031-142625113	-	CTGGCGTGGAGACATCC	No	Yes	No	0	0	0	0	No
NM_hsa_4139	chr7:151216355-151216444	-	GGTCCGGCGCGCGCGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4140	chr7:152133530-152133619	+	CGGAGTTGAGAGGCTGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4141	chr7:156411756-156411832	+	GGCCAGTGTCCAGAGAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4142	chr7:158763287-158763377	+	GGTCAAGTATGACGTGAAGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4143	chr8:9760899-9760980	+	TCAAGTCCCTGTGAACACGG	No	Yes	No	0	0	0	0	No
NM_hsa_4145	chr8:12584738-12584821	+	CTGCTTTTGGCACTCCATT	No	Yes	No	0	0	0	0	No
NM_hsa_4147	chr8:2732578-27325862	+	TGTGGAGTGAAGTGTGTTA	No	Yes	No	0	0	0.0732862	0	Yes
NM_hsa_4150	chr8:4088486-40884937	+	GATCCAGGTCAGCACTGCT	No	Yes	No	0.142464	0.165556	0.219859	0	Yes
NM_hsa_4151	chr8:4133302-4133305	+	TAGCAAAATTTGACTCTGT	No	Yes	No	0	0	0	0	Yes
NM_hsa_4155	chr8:5493584-54935938	+	AATCTGCTGAGCTCTGGA	No	Yes	No	0	0	0	0	No
NM_hsa_4156	chr8:56884019-56884091	+	CACACTGTACAGGCTATG	No	Yes	No	0	0	0	0	No
NM_hsa_4157	chr8:6702521-67025598	+	TCGCTGCTGCTGAGTACG	No	Yes	No	0	0	0	0	No
NM_hsa_4158	chr7:1060464-10604643	+	CTGACTGTGACAGTAGAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4159	chr7:71951131-71951194	+	CTAAGGCTGAGAGGCTTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4160	chr8:8433363-84333434	+	TTAACTTGGCTAGCTTAAG	No	Yes	No	0	0	0	0	No
NM_hsa_4161	chr8:9987973-99879816	+	TCTACTACATACCTGCTCA	No	Yes	No	0	0	0	0	No
NM_hsa_4162	chr8:102218079-102218157	+	GGTCCAGCTCTGTCTCCAG	No	Yes	No	0	0	0	0	No
NM_hsa_4163	chr8:102218345-102218429	+	CGCGGGCGCGCGTGGCTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4164	chr8:102218345-102218429	+	CCAGGACACCGCGCGCGCGG	No	Yes	Yes	0	0	0.0732862	0	Yes
NM_hsa_4164	chr8:102218345-102218429	+	CCAGGACACCGCGCGCGCGG	No	Yes	Yes	0	0	0.0732862	0	Yes
NM_hsa_4166	chr8:10432523-104325322	+	TTTCCGCTGGATCCCTGGGGG	No	Yes	No	0.142464	0.199668	0.0732862	0	Yes
NM_hsa_4167	chr8:10381897-103818987	+	CAGGACGGCGCGCTGGGA	No	Yes	No	0	0	0	0	No
NM_hsa_4168	chr8:104008494-104008562	+	CTTCAGTGTCTCTGAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4169	chr8:106155317-106155413	+	TGAAATGACAGATGCTCCAC	No	Yes	No	0	0	0	0	No
NM_hsa_4170	chr8:12548698-125487033	+	GGGTTGCTGACTGACGG	No	Yes	No	0	0	0	0	No
NM_hsa_4171	chr8:12647302-12647324	+	GACCGATGATCCATGCTGCT	No	Yes	No	0	0	0	0	No
NM_hsa_4174	chr8:134058714-134058802	+	CAGCAAGACTGGAGTGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4175	chr8:134145639-134145723	+	TTTCTTCTCTATTGCCCAG	No	Yes	No	0	0	0	0	No
NM_hsa_4176	chr8:143823097-143823173	+	CCATCCCACTGCTGCTT	No	Yes	No	0	0	0	0	No
NM_hsa_4177	chr8:144905786-144905857	+	CTGGAATGCTTGGAGGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4178	chr8:14911634-14911728	+	GGCCAGCTGAGTGTGGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4179	chr8:145169753-145169844	+	GGTTGGCCCGGAGGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4185	chr8:146052940-146053013	+	CTCTCAGGAGGCTGATCCG	No	Yes	No	0	0	0	0	No
NM_hsa_4186	chr8:6333106-6333174	+	CTGGGATAGAGCATGCTCC	No	Yes	No	0.113971	0.132445	0	0	Yes
NM_hsa_4187	chr8:11334673-11334739	+	CTGGGAGGACACTCTCTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4188	chr8:11840580-11840671	+	CAAAGTGTAGATGCGAGC	No	Yes	No	0	0	0	0	Yes
NM_hsa_4192	chr8:25986983-25987052	+	CACGAAGAGTAAAGACAG	No	Yes	No	0	0	0	0	No
NM_hsa_4194	chr8:37264509-37264593	+	GCGCCAGCTGAGGACACTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4195	chr8:3829233-38292925	+	GGCCCGCGCGTGTGTAGTGC	No	Yes	No	0	0	0	0	No
NM_hsa_4199	chr8:5602876-56028846	+	TGAGATGAAGCTCTCTCAG	No	Yes	No	0	0	0	0	No
NM_hsa_4201	chr8:56418717-56418789	+	TGCCCTGTGACGAGAGAA	No	Yes	No	0	0	0	0	No
NM_hsa_4202	chr8:68522861-68522955	+	AAATGTTCCCTTCAAGTGT	No	Yes	No	0	0	0	0	No
NM_hsa_4204	chr8:81781151-81781229	+	TGATTAACACTAGTGTCTCT	No	Yes	No	0	0	0	0	No
NM_hsa_4205	chr7:173202-87178292	+	TGTGACTATGACAGTAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4207	chr8:94955044-94955121	+	GTAAGATGCGAGGACACAG	No	Yes	No	0.0662225	0	0	0	Yes
NM_hsa_4210	chr8:124926723-124926804	+	AAATCTGCTGTGTGATGG	No	Yes	No	0	0	0	0	Yes
NM_hsa_4212	chr8:133754177-133754260	+	TCCTTGTGTAGTGTGACG	No	Yes	No	0	0	0	0	Yes
NM_hsa_4215	chr8:14159339-14159416	+	ACAAGTGGCTTGGAGGAGG	No	Yes	No	0.142464	0.231779	0.219859	0	Yes
NM_hsa_4218	chr8:14258397-142583684	+	GAGTGAAGCATAGCGCTGTG	No	Yes	No	0	0	0	0	No
NM_hsa_4221	chr9:15306372-15306462	+	ACCAAAGAGCGCGCGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4223	chr9:34126774-34126847	+	CTCTGGTGTTCGCGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4224	chr9:35488981-35488955	+	CTTCCGCTGACTCGCGTGC	No	Yes	No	0	0	0	0	No
NM_hsa_4225	chr9:57253293-57282828	+	ATTTAGGCTGAGCTGAGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4227	chr9:5749111-35749194	+	CAGGTGCACCGCCGGGGAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4228	chr9:35755370-35755448	+	TCTGGCATAGACTCTGCAAC	No	Yes	No	0	0	0	0	No
NM_hsa_4229	chr9:35756452-35756530	+	CCGTTTACAGAGTGGCAAGA	No	Yes	No	0.0662225	0	0	0	No
NM_hsa_4231	chr9:35825019-35825277	+	GAGCGCGCGCGCGCGCGCGG	No	Yes	No	1.1967	1.52312	0.732862	0	Yes
NM_hsa_4234	chr9:3989454-39894618	+	CTCAAGAGCACTGCACTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4235	chr9:43128014-43128100	+	AAAAGGAGATTTTGAAGGA	No	Yes	No	2.50737	1.32445	3.95746	0	Yes
NM_hsa_4236	chr9:72287446-72287532	+	TCGTTGGCGCGCGCGCGCGG	No	Yes	No	0	0	0	0	No
NM_hsa_4237	chr9:73035234-73035409	+	CTGGTTCGAGAGCTGTGATAG	No	Yes	No	0	0	0	0	No
NM_hsa_4238	chr9:6535927-8635616	+	TGCTCTGTGAAGCGCGCGCTG	No	Yes	No	0.170957	0.132445	0.293147	0	No
NM_hsa_4241	chr9:91768732-91768812	+	GCTAGACTGCGATCTTCCAG	No	Yes	No	0.113971	0	0	0	No
NM_hsa_4242	chr9:94877793-94877882	+	GACGGGTCAGGTGGATGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4243	chr9:95862071-95862170	+	CCAGATATGGATGGCTGATGG	No	Yes	No	0	0.199668	0	0	No
NM_hsa_4244	chr9:96421763-96421829	+	TCGCTCGGTTGCTCCAGC	No	Yes	No	0	0	0	0	No
NM_h											

Name	locus	strand	sequence	midexp2	mirap	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_4361	chrX:153707368-153707433	+	TCCTCGAGAGAGCTGACTGG	No	Yes	No	0	0	0.0732862	No	
NM_hsa_4362	chrX:153908325-153908355	+	ATGCTCAAGAGGACTCACTGGG	Yes	Yes	Yes	0.113971	0	0	0	Yes
NM_hsa_4366	chrX:6301935-6302015	-	TGAGATGACACTGAGCTCCC	No	Yes	No	0	0	0	0	No
NM_hsa_4367	chrX:8541654-8541730	-	CTGGAAAGTATTTTGTAGT	No	Yes	No	0	0	0	0	No
NM_hsa_4368	chrX:10826203-10826301	-	CATGAGATTTGAGCCCTGCA	No	Yes	No	1.08273	1.25823	0.366431	Yes	
NM_hsa_4369	chrX:11846734-11846823	-	TTCTTCAGTTTCAGGACGAC	No	Yes	No	0	0	0	0	No
NM_hsa_4370	chrX:13279583-13279611	-	TCTTCACCTTTGGAGGGCA	No	Yes	No	0	0	0	0	No
NM_hsa_4373	chrX:29640709-29640797	-	TCTTGGTTTACTACTGTT	No	Yes	No	0	0	0	0	No
NM_hsa_4374	chrX:38420689-38420787	-	GGCCGGCCGGCCAGGCGGGCGGG	No	Yes	No	0.455886	0.364224	0.366431	Yes	
NM_hsa_4383	chrX:8733951-8733951	-	TCTGGACTCTGAACTATGAC	No	Yes	No	0.170957	0.176993	0.146572	Yes	
NM_hsa_4384	chrX:114948273-11494848	-	CAGATGGGACTCCGGGCGGAC	No	Yes	No	0.0569857	0.198688	0.146572	Yes	
NM_hsa_4385	chrX:125715185-125715267	-	GGGACGGGCTCCGGGAGCG	No	Yes	No	0	0	0	0	No
NM_hsa_4393	chrX:134562082-134562157	-	GGAAATCCAGAGTGTAAAGTCT	No	Yes	No	0.0596993	0.154519	0.024428	Yes	
NM_hsa_4394	chrX:139664947-139665039	-	TCCTTGAGACCTTCACTCTG	No	Yes	No	0	0	0	0	Yes
NM_hsa_4395	chrX:140008324-140008398	-	AAAAGCTGGGTGAGAGGAGCA	No	Yes	No	0.9608	1.14841	0.694794	Yes	
NM_hsa_4398	chrX:147582466-147582444	-	GGCCGGCGGGCGGGCGGGCG	No	Yes	No	0.0261185	0.00965745	0.00916078	Yes	KapB+cMye-KapB+H
NM_hsa_4399	chrX:149862037-149862125	-	GGCCGGGTGGGGCCCCCG	No	Yes	No	0	0	0	0	No
NM_hsa_4403	chrX:15303836-15303932	-	GGCCGGGTGGGGGGCGCC	No	Yes	No	0	0	0	0	No
NM_hsa_4404	chrX:153129925-153130000	-	CTGCCACCTCTCTCCCTGG	No	Yes	No	0.113971	0	0	0	No
NM_hsa_4406	chrX:153608932-153609279	-	CCCCCTCCCTCCCGCCGCG	No	Yes	No	0.113971	0.0662225	0.0732862	Yes	
NM_hsa_4408	chrY:20111101-201111190	+	AGAGTGGCAATGTGTGTA	No	Yes	No	0	0	0	0	No
NM_hsa_4409	chrY:8979486-8979564	-	GAGGTTCGGCTGTGTTAGTA	No	Yes	No	0	0	0	0	No
NM_hsa_4410	chrY:14320395-14320483	-	GTTCAAGTGGACAGGCCCTG	No	Yes	No	0	2.18334	1.97873	Yes	
NM_hsa_4411	chr20:23078388-23078530	-	CTTTCAGAGCTTGGCCGGCTG	No	Yes	No	0	0	0	0	No
NM_hsa_4411	chr20:23078387-23078529	-	CTTTCAGAGCTTGGCCGGCTG	No	Yes	No	0	0	0	0	No
NM_hsa_4413	chr20:37352999-37353127	-	CGGAGGGCGGGGGCGGGCGGG	No	Yes	No	3.61319	3.65229	2.55481	Yes	
NM_hsa_4415	chr20:37078607-37078169	+	AAATGCTGGCTTTCACACACT	No	Yes	No	0	0.0662225	0.146572	Yes	H-KapB+KapB+cMye
NM_hsa_4418	chr20:29611893-29611987	+	GAAGTGTTCGACAGAGTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4419	chr20:292086-292086	-	AGAGTGGGTCAAGAACCTGT	No	Yes	No	0	0	0	0	No
NM_hsa_4421	chr20:23078404-23078530	+	CAAGATCTGGCAAGCTGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4421	chr20:23078387-23078513	+	CAAGATCTGGCAAGCTGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4422	chr20:43272688-43272826	-	AATCTGACTAGTTGCTGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4423	chr20:6094141-60941277	+	CTAGGCTGGCTGGGGAGG	No	Yes	No	0	0	0	0	No
NM_hsa_4424	chr20:20194973-20194989	+	ACTCTGGCTGAGACTGGAGT	No	Yes	No	0.427393	1.26926	0.0732862	Yes	
NM_hsa_4425	chr20:2634868-2635014	+	CTGATGTCTCACTGTGAGCAAT	No	Yes	No	0.512871	0.463558	0.293145	Yes	KapB+cMye-KapB+H
NM_hsa_4426	chr20:2636705-2636851	+	TACAGGTGATGGCTGACAGGGTCC	No	Yes	No	0.170957	0.132445	0.513004	Yes	
NM_hsa_4428	chr20:4798074-4798178	+	GTGCTATAGGCTGAGACTGAGCT	No	Yes	No	0	0	0	0	No
NM_hsa_4429	chr20:24204893-24205025	+	CTGCTGGACTGACACTGTGGG	No	Yes	No	0.0569857	0	0	0	No
NM_hsa_4430	chr20:37078613-37078169	+	TTCAAATCTGGGCTTTCACA	No	Yes	No	0	0	0	0	Yes
NM_hsa_4431	chr20:37078623-37078162	+	TTGCTAAAGCCGTTCCCGTGTGGA	No	Yes	No	0.341914	0.52978	0	0	Yes
NM_hsa_4432	chr20:48330494-48330588	-	CTGTGGCCCGGAGGAGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4433	chr20:23078388-23078506	-	TCAGCTTGGCAAGCTTTCGA	No	Yes	No	0	0	0	0	No
NM_hsa_4433	chr20:23078406-23078524	-	TCAGCTTGGCAAGCTTTCGA	No	Yes	No	0	0	0	0	No
NM_hsa_4435	chr21:9826466-9826570	+	GGCCGACTCTCCCGGGCGGGCA	No	Yes	Yes	0.341914	0.728448	0.366431	Yes	
NM_hsa_4436	chr21:47705766-47705864	+	CCCTCGAGCCGGCTGGAAGGAC	No	Yes	No	0	0	0	0	No
NM_hsa_4437	chr21:9827223-9827213	+	GGGCGCCGGCTTTGGTACTTGA	No	Yes	No	5.35666	2.58268	3.9941	Yes	
NM_hsa_4439	chr21:41935264-41935384	+	TCTGTGGAAGCTTGAAGATTC	No	Yes	No	0	0	0	0	No
NM_hsa_4440	chr21:41935273-41935393	+	ATTGACTGTGGAACTTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4440	chr21:41935264-41935404	+	ATTGACTGTGGAACTTGA	No	Yes	No	0	0	0	0	No
NM_hsa_4441	chr21:9825733-9825811	+	GGGGTGGCTGGCCGGCGGGGG	No	Yes	No	0	0	0.219859	Yes	
NM_hsa_4442	chr21:9826739-9826870	+	CGGTGGCTGTGGCGGGGGGGT	No	Yes	No	0.113971	0	0	0	Yes
NM_hsa_4443	chr21:9825637-9825739	+	GGCTGGCGCCCGGGCTGGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4444	chr21:9826227-9826315	+	CGCTTCCGGCTGCTGGCCCT	No	Yes	No	0.113971	1.12578	0.879435	Yes	
NM_hsa_4445	chr21:9826410-9826542	+	CGCCCGCCGGCGGGCTGGAGCGGG	No	Yes	No	0.512871	0.52978	1.09929	Yes	H-KapB+KapB+cMye
NM_hsa_4446	chr21:46707943-46708053	+	CCGAGGGCTGGTGTGGTGGT	No	Yes	No	0	0	0	0	No
NM_hsa_4447	chr21:9826198-9826278	+	CGCACAGGCTTGGAGCACTGGT	No	Yes	No	0.0142464	0.0220742	0.0732862	Yes	
NM_hsa_4449	chr21:9826194-9826274	+	ACAGGGCTTGGTGGAGCTGGG	No	Yes	No	0.0142464	0	0.0732862	Yes	
NM_hsa_4450	chr21:9826690-9826778	+	CGCCGGTCTGGCGGGGGGG	No	Yes	No	0.341914	0.331113	0.0732862	Yes	KapB+cMye-KapB+H
NM_hsa_4451	chr21:36824232-36824374	+	CATGAACTTGGACAGAACTCC	No	Yes	No	0	0	0	0	No
NM_hsa_4452	chr21:9826739-9826819	+	GGGCGGGCGCCGGTGGTGG	No	Yes	No	0	0	0	0	No
NM_hsa_4453	chr21:9827210-9827320	+	GGGCGCCCGCCGGCTGGTACTCT	No	Yes	No	2.05149	1.4569	1.13594	Yes	KapB+cMye-KapB+H
NM_hsa_4454	chr21:9826739-9826871	+	GGGCGGGCTGGTGGGCTCGGG	No	Yes	No	0	0.0662225	0	0	Yes
NM_hsa_4455	chr21:9826749-9826881	+	GGGCGGGCTGGTGGGCTCGGG	No	Yes	No	0	0.132445	0	0	Yes
NM_hsa_4456	chr21:34103267-34103389	+	ATCAGATAGGATTCGACAGAT	No	Yes	No	0	0	0	0	Yes
NM_hsa_4457	chr21:36824231-36824384	+	TTGCAAGAACTTGGACAGAA	No	Yes	No	0	0	0	0	No
NM_hsa_4458	chr21:9827328-9827406	+	GGGCGGACGACCCCTGAAGCTGTG	No	Yes	No	1.02574	0.662225	1.39244	Yes	
NM_hsa_4459	chr21:9827260-9827348	+	GGCTGATGACCCCTCCCGGGCGG	No	Yes	No	1.82354	2.0529	3.44445	Yes	H-KapB+KapB+cMye
NM_hsa_4461	chr21:9826538-9826630	+	GGGCTGGCTTGGCTGGCCGGG	No	Yes	No	0.113971	0	0	0	No
NM_hsa_4463	chr21:45622813-45622913	+	TCTCGGCTGTGGCACTGAGCA	No	Yes	No	0	0.0662225	0	0	No
NM_hsa_4464	chr21:4670846-4670861	+	GGTCCGCTGGCCCGGGGGGGG	No	Yes	No	0	0.0662225	0.146572	Yes	H-KapB+KapB+cMye
NM_hsa_4465	chr21:46707948-46708054	+	GAGGCGGCTGGTGGTGGCGGGG	No	Yes	No	0.227943	0.132445	0.146572	Yes	
NM_hsa_4466	chr21:9826661-9826641	+	CTTCCAGCAAGCTGGCGGCTCCCG	No	Yes	No	1.1967	1.65556	2.34516	Yes	H-KapB+KapB+cMye
NM_hsa_4467	chr21:9826401-9826533	+	CGGCGCCGGCGGGCTCGAGCGGG	No	Yes	No	0.0569857	0	0	0	No
NM_hsa_4468	chr21:46853860-46853498	+	ACTTCTGAGCTTGGAGTGGTA	No	Yes	No	0	0	0	0	No
NM_hsa_4469	chr21:9825703-9825787	+	GGCCGGTGGCTTCCGAGAGGTT	No	Yes	No	0	0	0	0	No
NM_hsa_4472	chr22:4456487-4456495	+	CCTCAGTGGTGGGCTGAGCCTTC	No	Yes	No	0.170957	0.463558	0.366431	Yes	
NM_hsa_4473	chr22:43011313-43011415	+	GGGCTGGCTGGGATTCGATTCGCC	No	Yes	No	15.5911	10.706	7.86066	Yes	KapB+cMye-KapB+H
NM_hsa_4474	chr22:50928325-50928341	+	CACTGGCTTCTTCTCCCGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4477	chr22:24360156-24360228	+	TTTCCAGATGAGGCGCCAGCA	No	Yes	No	0.227943	0.0662225	0.0732862	Yes	
NM_hsa_4478	chr22:5075084-50757212	+	CTCACCCCTGGCACTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4479	chr22:21771619-21771717	+	GCCTGGGCGGGCGGCTGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4479	chr22:21871746-21871844	+	GGCTGGGCGGGCGGCTGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4479	chr22:2042772-20427876	+	GCCTGGGCGGGCGGCTGGAG	No	Yes	No	0	0	0	0	No
NM_hsa_4481	chr22:50926216-50926334	+	AGGGATGGAGAGGCTGTGTG	No	Yes	No	0	0	0	0	No
NM_hsa_4482	chr22:39097089-39097179	+	GACCGGGCGGCTGAGGGCGGCA	No	Yes	No	0	0	0	0	No
NM_hsa_4483	chr22:46973073-46973165	+	CGGCTCCCGGCGCCCTGGG	No	Yes	No	2.05149	2.18334	0.366431	Yes	
NM_hsa_4484	chr22:46984181-46984311	+	TCCGTCCTGGTGGCTGCTGGT	No	Yes	No	0.0993338	0	0	0	Yes
NM_hsa_4488	chr22:39097109-39097235	+	TTTCAAGGCTGGTGGTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4489	chr22:46773606-46773734	+	TGAAGCTGACCCGCTGCC	No	Yes	No	0.0569857	0	0	0	Yes
NM_hsa_4491	chr22:4148702-41487840	+	CTAGCTGTAAAGGAGATTGGG	No	Yes	No	0	0	0	0	No
NM_hsa_4492	chr21:138611848-138611954	+	CTCAGTGTAGGCAAGCTCTAGT	No	Yes	No	0.11772	0.397335	1.24857	No	
NM_hsa_4493	chr21:82626242-82626282	+	ACTGTGTGCTCTCTCCCTGCA	No	Yes	No	0	0.198688	0	0	No

Name	locus	strand	sequence	midexp2	midexp	minanalyser	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_4608	chr8:21906691-21906789	+	GGGGCGGAGAGCGGGTGTGGG	No	No	Yes	0	0	0	0	
NM_hsa_4610	chr8:65291688-65291688	+	GATGCGGCTGTGACACAGC28	No	No	Yes	0	0	0	0	
NM_hsa_4611	chr8:67026179-67026207	+	CGGAGGAGCTGTAGCGCGCCG	No	No	Yes	0	0	0	0	
NM_hsa_4614	chr1:12810711-1281177	+	GGGTGGCAGTGAAGAGGCTCT	No	No	Yes	0	0	0	0	
NM_hsa_4615	chr8:15403324-1540343	+	TTATCGCTGTACTCTGTAGA	No	No	Yes	0	0.198668	0.146572	0	
NM_hsa_4617	chr8:103452224-103452340	+	TTTCCCTGGATCTCCCTGGGCGAG	No	No	Yes	0	0.198668	0.439717	Yes	H-KapB-KapB-cMyc
NM_hsa_4620	chr8:4841646-4558467	+	GGGAGGAGGAGGAGGAGGAGG	No	No	Yes	0.1655697	0.146572	0	0	
NM_hsa_4622	chr8:109304621-109304715	+	CAGGACGGTCCGATGAAGTGAA	No	No	Yes	17.3806	11.7991	Yes	0	
NM_hsa_4624	chr8:42752844-42752882	+	CTGGCTGGGACCGCGGGCGG	No	No	Yes	0	0	0	0	
NM_hsa_4628	chr8:145582150-145582266	+	CTGTGCGCGCGCGCGCGGG	No	No	Yes	0	0	0	0	
NM_hsa_4629	chr10:1224117-1013225	+	CCCTGCGCGCGCGCGCGGG	No	No	Yes	0	0	0	0	
NM_hsa_4630	chr1:120868214-120868338	+	CCACGGCGCCAGCGGACTGGAGGA	No	No	Yes	0	0	0	0	
NM_hsa_4633	chr8:99405857-99405993	+	CTTATCTCCAGTACTAGCTAG	No	No	Yes	0	0	0	0	
NM_hsa_4634	chr8:146052957-146053065	+	GTCTCAGGAGGGGTAGCTCGG	No	No	Yes	0	0	0	0	
NM_hsa_4635	chr8:146027629-146027725	+	GTGCAACTGTCCACTCTGG	No	No	Yes	0	0.0662225	0	0	
NM_hsa_4636	chr8:10859511-10859503	+	GAGAGTGTCTGTGACTGTAAA	No	No	Yes	0.75981	1.10923	0.62904	Yes	
NM_hsa_4639	chr8:95961727-95961843	+	CCGGAGCTGAGCGTGAAGCG	No	No	Yes	0	0	0	0	
NM_hsa_4642	chr8:145164591-145164681	+	GCTGTGAGCCCGGAGGACTCG	No	No	Yes	0	0	0	0	
NM_hsa_4644	chr9:79186665-79186763	+	CCCGCGCTGCGAGCCGGGCTCG	No	No	Yes	79.3526	57.15	14.071	Yes	KapB-cMyc-KapB-H
NM_hsa_4645	chr2:92567879-92567959	+	TACTCGGCTCTGTAGAGCTGG	No	No	Yes	0.131971	0	0	0	
NM_hsa_4650	chr9:34049953-34050083	+	TTGTCCACCTATGCTCCGACG	No	No	Yes	4.61584	1.5869	0.439717	Yes	
NM_hsa_4652	chr9:132145419-132145525	+	TGGCCGTGGCTCTCAGGACTGCA	No	No	Yes	0	0	0	0	
NM_hsa_4654	chr9:96421752-96421848	+	CTGGGTCTGGTGTCTCGAG	No	No	Yes	0	0	0	0	
NM_hsa_4657	chr9:137343002-137343082	+	CATGTGCTGAAATCTGCTGATGT	No	No	Yes	0	0	0	0	
NM_hsa_4661	chr9:89293735-89294057	+	CAGCTGGGCTGTGCGAG	No	No	Yes	0.0569857	0	0	0.146572	Yes
NM_hsa_4663	chr9:88969518-88969646	+	CACCTGCTCAAGTGTCCGGCGCGG	No	No	Yes	0	0	0	0	
NM_hsa_4666	chr9:139760865-139760961	+	GACCTGGGCGGCTGGCTCGG	No	No	Yes	0	0	0.0732862	Yes	
NM_hsa_4669	chr9:79186824-79186942	+	ACCATCTGTAGACAGCTCTCTGTGG	No	No	Yes	79.78	64.445	57.3098	Yes	KapB-cMyc-KapB-H
NM_hsa_4670	chr9:79186824-79186942	+	TTTCTTAGGACTCTGCGCAACT	No	No	Yes	0.0423793	0.0331113	0.109929	0	
NM_hsa_4670	chr9:88969481-88969619	+	AGGTGTCCGGCGCGGCTCGG	No	No	Yes	0	0	0	0	
NM_hsa_4671	chr9:139565924-139566000	+	GCTGGACACTCAGCAGGACCCCG	No	No	Yes	54.0294	497.728	494.755	Yes	KapB-cMyc-KapB-H
NM_hsa_4672	chr9:37804197-37804303	+	TCTTCAGCAACTCTGGTCACTG	No	No	Yes	0.0712322	0.0331113	0.146572	Yes	
NM_hsa_4673	chr9:138623807-138623815	+	CCGCGCGCGCGCGCGCGGG	No	No	Yes	0	0.0110371	0	0	
NM_hsa_4675	chr1:38280002-38280106	+	CGCTGCGCGCGCGCGCGGG	No	No	Yes	1.79582	2.68129	1.711	0	
NM_hsa_4676	chr1:159111368-159111508	+	AGGTTCGGGCTGTGAGTCCCGG	No	No	Yes	0	0	0	0	
NM_hsa_4677	chr1:182643818-182643954	+	CCCAAGATATAGAGCTTGGTCTT	No	No	Yes	0	0	0	0	
NM_hsa_4678	chr1:9371329-9371439	+	CTGATGGCTCTGGCTGGCTGTA	No	No	Yes	0.113971	0.0662225	0.0366431	0	
NM_hsa_4679	chr1:1510345-1510431	+	GAAGAAGCGGCTCTGCGCGG	No	No	Yes	0.170957	0	0	0	
NM_hsa_4681	chr1:108962649-108962795	+	GGATTAGGCTGAAGACTTAAAGC	No	No	Yes	0	0	0	0	
NM_hsa_4681	chr1:108816829-108816975	+	GGAGTAGGCTGAAGACTTAAAGC	No	No	Yes	0	0	0	0	
NM_hsa_4682	chr1:36107183-36107307	+	TCTCCCGGAGCAGGCTGTGCAAG	No	No	Yes	0	0	0	0	
NM_hsa_4685	chr1:15423241-15423273	+	ATAAATCTGCAACTTCAACTTC	No	No	Yes	0	0	0	0	
NM_hsa_4687	chr1:13424623-13424747	+	TTCACGCTGTGGGCTGGCTGGG	No	No	Yes	0.227943	0.26489	0.219859	0	
NM_hsa_4689	chr1:180910059-18091109	+	CACCTCCGGGCTCCCGCCGCT	No	No	Yes	3.5901	2.25157	0.69576	Yes	KapB-cMyc-KapB-H
NM_hsa_4690	chr1:95582796-95582908	+	TGGCGCGCGCTCCGGGCGGG	No	No	Yes	7.00924	7.41692	1.46572	Yes	
NM_hsa_4692	chr1:32633007-32633135	+	TACAGTGTCAACTTGTGA	No	No	Yes	0	0	0	0	
NM_hsa_4693	chr1:5243445-4244170	+	GTGAGATATACTGCTGTGAGAGA	No	No	Yes	0.0854786	0	0	0	
NM_hsa_4694	chr1:26881010-26881102	+	TCTCTGCCCTCTGTGTGAGA	No	No	Yes	0.313421	0.364224	0.0366431	0	
NM_hsa_4695	chr1:20722686-20722686	+	GGAGCTGAGCCCGCGCGCGG	No	No	Yes	0	0	0	0	
NM_hsa_4696	chr1:569763-569853	+	GTCTATTAGAGGAGTGAAGGCG	No	No	Yes	1.42464	2.18334	0.879435	0	
NM_hsa_4702	chr1:32633019-32633147	+	TCTATTCCAGTTCAGTGAAGC	No	No	Yes	0	0	0	0	
NM_hsa_4704	chr1:2929171-2929199	+	CCTCGGAGGCGCGGCTGGG	No	No	Yes	0	0	0	0	
NM_hsa_4706	chr1:45244027-45244171	+	TCTCAGTGAAGAACTTGTCCAGTCTG	No	No	Yes	5.12872	2.78135	5.16133	Yes	
NM_hsa_4707	chr1:28202642-28202750	+	CCTGATTTGTAGCTGACTAC	No	No	Yes	0	0	0	0	
NM_hsa_4707	chr1:28202642-28202740	+	TTCGATTTGTAGCTGACTAC	No	No	Yes	0	0	0	0	
NM_hsa_4708	chr1:24748060-24748066	+	AGTCTGGGCAAGCTCTGCG	No	No	Yes	0	0	0	0	
NM_hsa_4713	chr1:149900241-149900381	+	CATGACTTCCCGCCCTCTGCG	No	No	Yes	0.341914	0.0662225	0.0366431	0	
NM_hsa_4714	chr1:22602629-22602639	+	CTGACTGCTCTGTCGCCCGAG	No	No	Yes	0	0	0	0	
NM_hsa_4716	chr1:109643120-109643274	+	CCCACTGATATGAGGCACTTGTATCGG	No	No	Yes	0.740814	0.0662225	0.146572	Yes	
NM_hsa_4717	chr1:7919127-17919299	+	TCCAGATTCGGGAGCACTAGTC	No	No	Yes	2.33641	1.05956	2.49173	No	
NM_hsa_4718	chr1:13162463-13162573	+	GTGTGGTGAAGGAGAGGAGTAA	No	No	Yes	0	0	0	0	
NM_hsa_4720	chr1:149822290-149822380	+	GCTGGTGTGGTCTGGTCTGG	No	No	Yes	0	0	0	0	
NM_hsa_4720	chr1:148214566-148214656	+	CTCGGCTGGTCTGGTCTGG	No	No	Yes	0	0	0	0	
NM_hsa_4721	chr1:45243499-45243599	+	TTCTGTGATGAAACTTGTCCAGTC	No	No	Yes	23.82	30.9259	34.6644	Yes	H-KapB-KapB-cMyc
NM_hsa_4723	chr1:38973835-38973925	+	CTGCTCCCTCACTCCACAG	No	No	Yes	0	0	0	0	
NM_hsa_4725	chr1:40254174-40254324	+	TGGCGCGCGCGCGCGCGGGGG	No	No	Yes	2.53017	1.92266	1.51458	Yes	KapB-cMyc-KapB-H
NM_hsa_4726	chr1:145726393-145726515	+	TGGGATGCGATGACTCAGGTTG	No	No	Yes	0	0	0	0	
NM_hsa_4729	chr1:203698757-203698843	+	ATTTCCAGGTTGTGGCTGG	No	No	Yes	0	0	0.146572	No	
NM_hsa_4731	chr1:203259533-203259673	+	AGCTGAGCAAGGCTGAGGCG	No	No	Yes	0	0	0	0	
NM_hsa_4732	chr1:164528359-164528493	+	AGCTGAGCGGGCTGTGGA	No	No	Yes	0	0	0	0	
NM_hsa_4733	chr1:158057677-158057825	+	ACTGGGAGCGCGGCTGTATGATG	No	No	Yes	0	0	0	0	
NM_hsa_4734	chr1:178995468-178995558	+	TGGGCTCCGGCTGCAAGGCGCG	No	No	Yes	0	0	0	0	
NM_hsa_4735	chr1:221400529-221400645	+	TGATGTGCTTGGTGTGG	No	No	Yes	0.68329	1.05956	0.0732862	Yes	KapB-cMyc-KapB-H
NM_hsa_4736	chr1:5865786-5865804	+	TCCAGTACCCCGCCACACA	No	No	Yes	124.001	94.560	80.0286	Yes	
NM_hsa_4738	chr1:23242323-23242323	+	CTGCGGAGGCGCGGCTGACTGT	No	No	Yes	0	0	0	0	
NM_hsa_4740	chr1:149900246-149900386	+	TGGATGGCTCCGAGCTCTAGAG	No	No	Yes	0.0569857	0	0	0	
NM_hsa_4741	chr1:78444938-78445075	+	TGATAGTGGCAACTGACTGGGA	No	No	Yes	0	0	0	0	
NM_hsa_4742	chr1:15618655-156186681	+	GGCGGCGCGCGCTGCTCG	No	No	Yes	0	0	0	0	
NM_hsa_4747	chr1:8524223-8524343	+	TCTGTGTTTGAAGCTTCACT	No	No	Yes	0	0	0	0	
NM_hsa_4749	chr1:144839419-144839519	+	TCAGATTCAGCTCACTGGGA	No	No	Yes	0	0.0331113	0.146572	Yes	H-KapB-KapB-cMyc
NM_hsa_4749	chr1:145379303-145379403	+	TCAGATTCAGCTCACTGGGA	No	No	Yes	0	0.0331113	0.146572	Yes	H-KapB-KapB-cMyc
NM_hsa_4750	chr1:244614485-244614625	+	AACCTGGCAGCGGCTGACTCT	No	No	Yes	0	0	0	0	
NM_hsa_4751	chr1:1342745-1342833	+	CTCTGAGGAGCTGGTGGTGTG	No	No	Yes	0	0	0	0	
NM_hsa_4754	chr1:15143194-151431274	+	GTGCGTGGAGCTGGGCTGG	No	No	Yes	0	0	0	0	
NM_hsa_4755	chr1:24668531-24668619	+	CAGCGGCCCTCTGTCTCCAG	No	No	Yes	0	0	0	0	
NM_hsa_4757	chr1:202858015-202858143	+	GCTCTCGGGGAGGACTGTGGG	No	No	Yes	0	0	0	0	
NM_hsa_4758	chr1:204964520-204965550	+	TTAGCTCTCTCTCCACTGCT	No	No	Yes	0	0	0	0	
NM_hsa_4759	chr1:154701480-154701570	+	TTACTGACTCTGGTGTGGG	No	No	Yes	0	0	0	0	
NM_hsa_4761	chr1:28202633-28202763	+	TTTGTAGCTGTCAACTAAGGAA	No	No	Yes	0	0	0	0	
NM_hsa_4762	chr1:1290479-1290617	+	GC CGCGCGCGCGCGCGGG	No	No	Yes	4.01749	2.28468	2.34516	Yes	
NM_hsa_4763	chr1:22693464-22693540	+	GAGTGGCTGGCAGTGGAGCTGGG	No	No	Yes	0	0	0.219859	No	
NM_hsa_4766	chr1:22633023-22633141	+	TCTCAGATTCAGTGAAGCTAT	No	No	Yes	0	0	0	0	
NM_hsa_4770	chr1:171070832-171070966	+	TTTCCAGCACTGAGGCTCAATC	No	No	Yes	0.0284929	0	0	0	
NM_hsa_4772	chr1:45244024-45244168	+	AGTGAAGA								

Name	locus	strand	sequence	midexp2	mirexp	miranalyzer	RPM_HU_KapB_cMye	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_4865	chr3:19462299-19462307	-	AAGGTGTAGACTGTAAGCATT	No	No	Yes	0	0	0	0	
NM_hsa_4868	chr3:12066833-12066840	-	AAGTGTAGACTGTAAGCATT	No	No	Yes	0	0	0	0	
NM_hsa_4870	chr3:156445497-156445627	+	ACTGACTGTCTCGAAGAAATCA	No	No	Yes	0	0	0	0	
NM_hsa_4874	chr3:156445498-156445618	+	ACTGACTGTCTCGAAGAAATCA	No	No	Yes	0	0	0	0	
NM_hsa_4874	chr3:156445498-156445618	+	CAGATGTGGCAATGGGGTAAT	No	No	Yes	0	0	0	0	
NM_hsa_4874	chr3:156445498-156445618	+	CAGATGTGGCAATGGGGTAAT	No	No	Yes	0	0	0	0	
NM_hsa_4878	chr3:129116035-12911639	+	GTGATTGGAAGCACTGGCCACAG	No	No	Yes	0.0854786	0.0331113	0.0732862	Yes	
NM_hsa_4879	chr3:18404307-18404345	+	TTCTCTGATGACTTCTGTGATGCC	No	No	Yes	3.70407	3.44537	4.17732	Yes	
NM_hsa_4880	chr3:18445495-18445503	+	TTCCAGGTCAAAGCTCGAGGAGT	No	No	Yes	0	0	0	0	
NM_hsa_4881	chr3:195270226-195270346	+	CTCTGAGAAGCTCGCGGAGACGG	No	No	Yes	0	0	0	0	
NM_hsa_4882	chr3:39452510-39452650	+	TGTGCACATTTGTGAAGCTTGAAGTTGA	No	No	Yes	4.84379	6.15869	3.00474	Yes	
NM_hsa_4884	chr3:182787676-182787778	+	AGTGGCTATGATATGAACCTACTGA	No	No	Yes	0.113971	0.0662225	0	Yes	KapB+cMye+KapB+H
NM_hsa_4887	chr3:48647162-48647298	+	TGGTGTACTGGCTGCACCGCGCTGC	No	No	Yes	0	0	0	0	
NM_hsa_4888	chr3:195459934-195460054	+	CTGGCCAGCTCATGGCCAGATG	No	No	Yes	0	0	0	0	
NM_hsa_4890	chr3:156071895-160119079	+	TGTGATATTTGTTTGTGACTGTGGA	No	No	Yes	0.113971	0.380779	0.1099229	Yes	
NM_hsa_4895	chr3:43220981-43221091	+	TTTCCCAAGTCTTGGCCAGCG	No	No	Yes	0	0	0	0	
NM_hsa_4896	chr3:164059128-164059220	+	GTTAATATTCCTCGTGGCCCTCCA	No	No	Yes	427.051	325.715	306.117	Yes	KapB+cMye+KapB+H
NM_hsa_4897	chr3:13784467-137844559	+	CTGAGACTCTTCTTCTGCAATG	No	No	Yes	0	0	0	0	
NM_hsa_4898	chr4:5353762-53537870	+	GTCGCCAGAGCTTCCGCCCG	No	No	Yes	0	0	0	0	
NM_hsa_4899	chr4:25235502-25235654	+	AGAAGAGTCTGGGGCGGGCGGGCCG	No	No	Yes	2.74637	1.80384	2.03518	Yes	
NM_hsa_4900	chr4:25661099-25661209	+	TGTCATGAACATAAACAAGAT	No	No	Yes	0	0	0	0	
NM_hsa_4902	chr4:125634189-125634297	+	AGGACTCCCGCGCTTGGT	No	No	Yes	0.0569857	0	0	0	
NM_hsa_4903	chr4:129576484-129576628	+	TCTCTTTATTCAGATCCAGGATA	No	No	Yes	0	0	0	0	
NM_hsa_4904	chr4:122618259-122618395	+	CCCGGGCGGGGAGCTCCCG	No	No	Yes	0.227943	0	0.0732862	Yes	
NM_hsa_4905	chr4:119200313-119200443	+	ATCTCATGATCTTGGGACTCTGAC	No	No	Yes	5.32642	4.96669	5.27661	Yes	
NM_hsa_4911	chr4:7087084-7087210	+	AAGTGGGCACTTGGCAATAAGTGA	No	No	Yes	0.322919	0	0.097715	Yes	
NM_hsa_4913	chr4:1006300-1006418	+	TGGCGGGCGGGCGGGCGGGCG	No	No	Yes	1.11122	0.695336	0.366431	Yes	KapB+cMye+KapB+H
NM_hsa_4916	chr4:1294955-4254904	+	CTGCGTTTGTGATGGAGACTGTGTT	No	No	Yes	0	0	0.219859	Yes	
NM_hsa_4918	chr4:25661121-25661193	+	TGTCATGAACATAAACAAGAT	No	No	Yes	0	0	0	0	
NM_hsa_4919	chr4:129471268-129471410	+	TCTACGTGACCAAGATTTACAGA	No	No	Yes	0	0	0	0	
NM_hsa_4920	chr4:3230266-3230358	+	CACCCACAGGAGCTGGCCACTGT	No	No	Yes	0.28429	0	0.0732862	Yes	
NM_hsa_4922	chr4:141073423-141073523	+	TTCCCGCTTCCCTCCAGGGGT	No	No	Yes	0	0.0662225	0	Yes	
NM_hsa_4923	chr4:8694782-8694989	+	AGACTTAGAGCTCCCACTGGTA	No	No	Yes	0	0	0	0	
NM_hsa_4924	chr4:5209394-5209480	+	AAGAAGTGTCTGAGACTGACGCTA	No	No	Yes	0	0	0	0	
NM_hsa_4925	chr4:53578771-53578869	+	CGCGCCAGAACGAGGGAGGAGCAG	No	No	Yes	0	0	0	0	
NM_hsa_4930	chr4:70947699-70947831	+	CACCGAGGCTGTGATGGT	No	No	Yes	0	0	0	0	
NM_hsa_4932	chr4:810468280	+	CCCTCAAAGAAGCAGGATCTGGGA	No	No	Yes	0	0	0	0	
NM_hsa_4933	chr4:20253489-20253597	+	CGCCCGGAGCCGGGAGCTGGT	No	No	Yes	0	0	0	0	
NM_hsa_4934	chr10:107803635-107803779	+	TAGAGAACCATTGCTAGACTAGT	No	No	Yes	0	0	0	0	
NM_hsa_4935	chr10:103870877-103870983	+	TCTCTCTTCACTTCCAG	No	No	Yes	0	0	0	0	
NM_hsa_4936	chr10:73580472-73580592	+	ACTTCTTCTTCCCAACAGCAG	No	No	Yes	0	0	0	0	
NM_hsa_4937	chr10:107803635-107803775	+	AGAAGCACTAGTCTTAGCACTAG	No	No	Yes	0	0	0	0	
NM_hsa_4938	chr10:38383735-38383845	+	CAGCGCGGACTCCCAACAGCAG	No	No	Yes	0.19945	0.26489	0.293145	Yes	H+KapB+KapB+cMye
NM_hsa_4939	chr10:123734372-123734508	+	CGGTACTGTGGCGGAGCTGGT	No	No	Yes	0	0	0	0	
NM_hsa_4941	chr10:107803635-107803763	+	AGAACAAGTGTATGACTAGT	No	No	Yes	0	0	0	0	
NM_hsa_4944	chr4:6047670-6047798	+	AATCCGCTGAGGAGTGTACAGT	No	No	Yes	0.284929	0.26489	1.02601	Yes	
NM_hsa_4945	chr10:100977961-100978071	+	TTACCTGACATCTGAGTTGGCT	No	No	Yes	0	0	0	0	
NM_hsa_4946	chr10:94624475-94624605	+	TCAGGCTCTCAGACTTGGCTCT	No	No	Yes	6.72432	6.82092	8.86764	Yes	H+KapB+KapB+cMye
NM_hsa_4947	chr10:123790151-123790271	+	TCTGGTACTGTCTGGTGGAGT	No	No	Yes	0	0	0	0	
NM_hsa_4948	chr10:100977961-100978071	+	TTACCTGACATCTGAGTTGGCT	No	No	Yes	0	0	0	0	
NM_hsa_4949	chr10:23003864-23003700	+	CTGCGCTCTGAGGCGGCTCT	No	No	Yes	0	0	0.0732862	Yes	
NM_hsa_4951	chr10:5003115-5003245	+	TTAAGTGGCTGAATTTGATAG	No	No	Yes	0	0	0	0	
NM_hsa_4954	chr10:3827699-3827797	+	CTGTGAGTGGCGGGCGGGCGG	No	No	Yes	0.0569857	0	0	0	
NM_hsa_4957	chr10:8290991-82906127	+	CGAGATCTCTGTAACCTGAG	No	No	Yes	0	0	0	0	
NM_hsa_4959	chr10:8396368-1963466	+	GCTGCTCCAGAACTGCTGCTCC	No	No	Yes	0	0	0	0	
NM_hsa_4960	chr10:79829488-79829586	+	CTGAAGGCTTAGGCCGGGAGA	No	No	Yes	0	0	0	0	
NM_hsa_4961	chr10:43966644-43966784	+	CGTGTCCAGATGGCCAGCAGGA	No	No	Yes	0	0	0	0	
NM_hsa_4962	chr10:43966644-43966772	+	TCAGAATGGCCAGCAGAGAT	No	No	Yes	0	0	0	0	
NM_hsa_4963	chr10:2447852-2447968	+	CCCTCGCTCGTCCGCTGGAGCT	No	No	Yes	14.1799	8.15641	3.49331	Yes	KapB+cMye+KapB+H
NM_hsa_4964	chr10:85992929-85992427	+	CTGAGGCTGAGGCGGCGGAGA	No	No	Yes	0.3989	0	0.293145	Yes	
NM_hsa_4965	chr10:1095176-1095268	+	TCAGAGCTCGAGTCCGCTGGCT	No	No	Yes	0	0	0.0732862	Yes	
NM_hsa_4967	chr10:129535410-129535542	+	TGCGCATGAGTTCGGTGGCGGA	No	No	Yes	0	0	0	0	
NM_hsa_4968	chr10:120514847-120514949	+	GTGGACTGGCAGGATGTGGAG	No	No	Yes	0.113971	0	0.219859	Yes	
NM_hsa_4970	chr10:32625374-32625492	+	TCTGCTGGCGGCGGAGCTCC	No	No	Yes	0	0	0	0	
NM_hsa_4974	chr11:118663740-118663891	+	AATCAAGTATGGTCCCGGCTGA	No	No	Yes	0	0	0	0	
NM_hsa_4975	chr11:130442110-130442238	+	CTTGACTGGAGCTGGGAATGAG	No	No	Yes	0	0	0	0	
NM_hsa_4976	chr11:123480409-123480509	+	TGGTGGGGAACACTTGGATGGG	No	No	Yes	0	0	0	0	
NM_hsa_4977	chr11:118798938-118799066	+	GGGCTGCTGGGCTGGAAGTGG	No	No	Yes	0	0	0	0	
NM_hsa_4980	chr11:130420975-130421394	+	TTTGCATGCTAGCTGGGAATGAT	No	No	Yes	0	0	0.0732862	Yes	
NM_hsa_4981	chr11:118798933-118799069	+	TGGCTCTGCTGGGAAAGT	No	No	Yes	0	0	0	0	
NM_hsa_4982	chr11:133012694-133012834	+	CTGGCAAAGACTCCAAGTCC	No	No	Yes	0	0	0	0	
NM_hsa_4983	chr11:101982901-101982105	+	TTCCACTCGCTGGGAGC	No	No	Yes	0	0	0	0	
NM_hsa_4986	chr11:2959463-2959583	+	GGAAGAAGGCTTCCCTGGCTCT	No	No	Yes	2.27943	2.45023	0.80616	Yes	
NM_hsa_4989	chr11:131565769-131565905	+	CGCCCTAAAGGAGCGGCTG	No	No	Yes	0	0	0	0	
NM_hsa_4991	chr11:67166298-67166412	+	CTGCTCCACTTCCGCCAG	No	No	Yes	0	0	0	0	
NM_hsa_4992	chr11:8705818-8705929	+	TGATGCAACAGGTAGAGACATCT	No	No	Yes	1.76656	3.50979	1.24887	Yes	
NM_hsa_4993	chr11:75019897-75019845	+	AGATGGCTGCTGTGTAGAGTATG	No	No	Yes	1.99485	2.53853	4.11624	Yes	H+KapB+KapB+cMye
NM_hsa_4995	chr11:85195143-85195261	+	GGAGATCTCAACCCGCTGGCG	No	No	Yes	9.28867	7.28448	4.17732	Yes	KapB+cMye+KapB+H
NM_hsa_4996	chr11:116708330-116708468	+	CAGCCAGACCTCGGCGAGA	No	No	Yes	0	0	0	0	
NM_hsa_5000	chr11:65326464-65326594	+	CGGGGCTGCTGGGCTCCAGA	No	No	Yes	0	0	0	0	
NM_hsa_5001	chr11:64789906-64788112	+	CTGTGACTCCCGCTCCAGAGA	No	No	Yes	0	0.198668	0	Yes	
NM_hsa_5004	chr11:8705818-8705929	+	TGAGACTCTTATGACTGCTGT	No	No	Yes	0	0	0	0	
NM_hsa_5005	chr11:66031423-66031551	+	CTGGCTCCTTCCATCCAGC	No	No	Yes	0	0	0	0	
NM_hsa_5006	chr11:2422423-2422561	+	CGGAGTCCCGCTGACCCAGC	No	No	Yes	0	0	0	0	
NM_hsa_5009	chr11:117827271-117827397	+	AAACAGGCTGAGGACTCAGG	No	No	Yes	0	0	0	0	
NM_hsa_5012	chr11:10845170-10841698	+	TTCCTGGGATTCAGCTCTGAG	No	No	Yes	0	0	0	0	
NM_hsa_5015	chr11:10830680-10830806	+	GCCTTTGATGCTGCTGTT	No	No	Yes	0	0	0	0	
NM_hsa_5016	chr11:118491757-118491865	+	ACAGGGGCTGGGAATGAACC	No	No	Yes	0.512871	0.132445	0	Yes	KapB+cMye+KapB+H
NM_hsa_5018	chr11:5957526-5957652	+	CATGCTCCGCTGACTAGT	No	No	Yes	0	0	0	0	
NM_hsa_5022	chr12:12290534-12290566	+	TATCTGACTAGTCTGCTTATG	No	No	Yes	0	0.132445	0	Yes	
NM_hsa_5025	chr12:9785694-9785686	+	ATTCCTGACAGCTCTGGGAGCA	No	No	Yes	0	0	0	0	
NM_hsa_5027	chr12:6965378-6965498	+	CTCTGAGTCTTCTCCAGC	No	No	Yes	0	0.132445	0.0732862	Yes	
NM_hsa_5030	chr12:5687326-56873958	+	TTCTGCTCTTTCGAGAGGTT	No	No	Yes	0	0.0662225	0	Yes	
NM_hsa_5031	chr12:7073183-7073305	+	TTCTGCTGCTGGGCTGGTCT	No	No	Yes	0	0	0	0	
NM_hsa_5032											

Name	locus	strand	sequence	mirdeep2	mirnap	miranalyzer	RPM_HU_KapB_cMyc	RPM_HU_KapoinB	RPM_HUVEC	IP_confidence	annotation
NM_hsa_5182	chr17:20841686-20841816	+	ATAATGATCTCCCAACTGTGATTG	No	No	Yes	0	0.0331113	0	0	Yes
NM_hsa_5184	chr17:209226128-20923222	+	ACCTCAGACACCGCGGTGAGGGTGTG	No	No	Yes	0.170957	0	0	0	No
NM_hsa_5185	chr17:63119528-63119636	+	GTCGAGGCGCGGAGCGCTGTGGT	No	No	Yes	0	0	0	0	No
NM_hsa_5186	chr17:19045346-19045454	-	CTGAGCAAACTCACAAGGCTGG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5186	chr17:18935718-18935826	+	CTGAGCAAACTCACAAGGCTGG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5189	chr17:46114780-46114920	+	CTCTCGGGTCCGGGCTGGGACGAA	No	No	Yes	0	0.0662225	0.0732862	Yes	H>KapB<KapB<cMyc
NM_hsa_5190	chr17:16343399-16343461	+	CTGCTCTGATGAACTACTAATAGGAAGT	No	No	Yes	7.09472	9.33737	9.52721	Yes	H>KapB<KapB<cMyc
NM_hsa_5192	chr17:31149412-31149526	+	TGCTTCTCTCTCCCGCCG	No	No	Yes	0	0	0	0	No
NM_hsa_5194	chr17:6347731-6347871	+	GTGAATGCGGGTGGGCAAACTG	No	No	Yes	0.0284929	0.0662225	0	0	Yes
NM_hsa_5196	chr17:37043120-37043204	+	TAAAACAGGCTCTCGCTGTGATCG	No	No	Yes	0.569857	0.662225	0.366431	Yes	KapB<cMyc>KapB<H
NM_hsa_5198	chr17:81037582-81037722	+	CCGGTCCGGCCCGCCGCGCCG	No	No	Yes	2.47888	1.22512	0.842792	No	KapB<cMyc>KapB<H
NM_hsa_5199	chr17:36888028-36888140	-	GAAATACACAGGTGTGTGAGGTTT	No	No	Yes	202.915	116.183	104.291	Yes	KapB<cMyc>KapB<H
NM_hsa_5201	chr17:8534364-8534480	-	CGCGCGCCCGCCGCGCGCCG	No	No	Yes	0.170957	0.662225	0	Yes	KapB<cMyc>KapB<H
NM_hsa_5202	chr17:17739712-17739838	+	TGTCGCCGCCCGGACGCCCA	No	No	Yes	0.740814	0.596003	0.659576	Yes	KapB<cMyc>KapB<H
NM_hsa_5203	chr17:7839280-7839384	+	AGGGACTGTGGCTCGCGGGTATGT	No	No	Yes	0	0	0	0	Yes
NM_hsa_5204	chr17:4458709-4458809	+	CGCTGTGCTGAGCGGAAGTCC	No	No	Yes	0	0	0	0	No
NM_hsa_5205	chr17:27507523-27507611	+	CTCCCTCGCTGGACTCCGA	No	No	Yes	0	0	0	0	No
NM_hsa_5206	chr17:29421336-29421474	+	CACCGGGTCACTATTGGATT	No	No	Yes	0	0	0	0	Yes
NM_hsa_5208	chr17:39676661-39676799	+	TGTCGTTGGCATAGAACATG	No	No	Yes	0	0	0	0	No
NM_hsa_5209	chr17:18886816-18886958	+	ATGCATCTTGACAGGTGTGAGC	No	No	Yes	0	0	0	0	No
NM_hsa_5210	chr17:65822043-65822163	-	GGGGGGCGCCGCGCGCGCCG	No	No	Yes	0.159877	0.13586	0.0299611	Yes	KapB<cMyc>KapB<H
NM_hsa_5212	chr17:62223671-62223791	+	GACCGGCTGTTTGAAGCCCGCCGAG	No	No	Yes	4.10297	3.11246	4.03074	Yes	KapB<cMyc>KapB<H
NM_hsa_5214	chr17:18066959-18067079	+	AGTGGGGCAGAGGACAGAGGT	No	No	Yes	0	0	0	0	No
NM_hsa_5216	chr17:748348-748480	+	GCTCCGGATCGGAAGCTGGCAGC	No	No	Yes	0.170957	0	0.0732862	No	KapB<cMyc>KapB<H
NM_hsa_5217	chr17:65628053-65628151	+	ATTCTGTGCGATCTGAGGCTG	No	No	Yes	0	0	0.0732862	Yes	KapB<cMyc>KapB<H
NM_hsa_5220	chr16:11891318-11891426	+	CTCGCTGGCCCGCCGCTGAG	No	No	Yes	0	0.198668	0.146572	No	KapB<cMyc>KapB<H
NM_hsa_5221	chr16:87887439-87887577	+	CTCGGGAGACACTGAGCACTCG	No	No	Yes	0.0569857	0	0.146572	No	KapB<cMyc>KapB<H
NM_hsa_5222	chr16:87799640-87799742	+	CGAGGTTCCGGTCTTGGAGTCCGT	No	No	Yes	0	0.198668	0.0732862	No	KapB<cMyc>KapB<H
NM_hsa_5223	chr16:33963171-33963263	+	TTGGAGCGCGCGGAGGCTGGCC	No	No	Yes	0.455886	0.397335	0.366431	Yes	KapB<cMyc>KapB<H
NM_hsa_5224	chr16:12594519-12594659	+	GAGCTGTGGATGTGACAGATT	No	No	Yes	0	0	0	0	Yes
NM_hsa_5227	chr16:78414378-78414468	+	ACTCTTAAAGTACGGCTGAAT	No	No	Yes	0	0	0	0	Yes
NM_hsa_5228	chr16:33966238-33966382	+	GTCGCCCATCGCCCGCCCTCCG	No	No	Yes	0	0	0	0	No
NM_hsa_5229	chr16:50903350-50903434	+	ATACCGGGTCTGTAGGCTTAAAAA	No	No	Yes	420.424	273.136	147.951	Yes	KapB<cMyc>KapB<H
NM_hsa_5231	chr16:33966232-33966378	+	GTGTGCTCCGCTACCGCCCGCCG	No	No	Yes	0.113971	0.397335	0.366431	Yes	KapB<cMyc>KapB<H
NM_hsa_5232	chr16:33963137-33963283	+	GCCACTCCGCTCCCGCCCTTGCCT	No	No	Yes	3.76106	2.91379	2.91345	Yes	KapB<cMyc>KapB<H
NM_hsa_5233	chr16:2128374-2128464	+	CATCCACTCTGACTCAGCCG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5235	chr16:67969865-67969955	+	GCGCAGATCCGAGTGACCTGG	No	No	Yes	0	0	0	0	No
NM_hsa_5236	chr16:89989864-89989958	+	TCTTGCTGGCTGTGGCTCTTGT	No	No	Yes	0.142464	0.0662225	0.0732862	Yes	KapB<cMyc>KapB<H
NM_hsa_5237	chr16:33963143-33963271	+	GGAGCCACTGACTCGCTCCGCG	No	No	Yes	0	0.662225	0.293145	Yes	KapB<cMyc>KapB<H
NM_hsa_5239	chr16:33966039-33966153	+	GTCGCCCGCCCGCGGCTGGCCCG	No	No	Yes	2.07998	2.48334	1.24587	Yes	KapB<cMyc>KapB<H
NM_hsa_5241	chr16:33964195-33964329	+	CTCTGTCAAGCCCGCCGCTG	No	No	Yes	0.284929	0.662225	0.293145	No	KapB<cMyc>KapB<H
NM_hsa_5243	chr16:33963388-33963496	+	TAGAGTGTGAAATCTTGGACCGGCCA	No	No	Yes	14.0755	7.74803	8.72106	Yes	KapB<cMyc>KapB<H
NM_hsa_5244	chr16:33963146-33963264	+	GCTCTGATTTGATTTGGGAGCGGGC	No	No	Yes	23.82	12.5161	6.52248	Yes	KapB<cMyc>KapB<H
NM_hsa_5245	chr16:30957964-30958080	+	ACCTCTATCGTGGTCCGAG	No	No	Yes	0	0	0	0	No
NM_hsa_5246	chr16:85507455-85507583	+	AGCTGTCATGCTGGGGAGA	No	No	Yes	0	0	0.0732862	Yes	KapB<cMyc>KapB<H
NM_hsa_5247	chr16:33966038-33966146	+	GAGCCCTCCGCGTCCCGCGGTTCCG	No	No	Yes	0.769307	1.15889	1.68558	Yes	H>KapB<KapB<cMyc
NM_hsa_5248	chr16:27561484-27561610	+	CCCTCCCGGAGGCGGGCTTATT	No	No	Yes	0.0569857	0	0	0	No
NM_hsa_5249	chr16:33965485-33965597	+	CAGATGATCTGACACTTCAAGCAAA	No	No	Yes	17.4946	15.2974	24.1112	Yes	H>KapB<KapB<cMyc
NM_hsa_5251	chr16:22206996-22207126	-	GGTTGAGCTGAGTGTGAGCTTCA	No	No	Yes	0.0569857	0.132445	0.146572	Yes	KapB<cMyc>KapB<H
NM_hsa_5252	chr16:50903359-50903455	-	AGGGAATACCGGGTGTGAGCTTCA	No	No	Yes	2644.2	2172.24	1560.78	Yes	KapB<cMyc>KapB<H
NM_hsa_5253	chr19:35652414-35652504	+	TCATGCTGAACTAAGTGAAGCC	No	No	Yes	0.712322	0.0993338	0.146572	Yes	KapB<cMyc>KapB<H
NM_hsa_5254	chr19:3201453-3201551	+	TGCTCTCCCGCTCTCTGATG	No	No	Yes	6.04049	4.63558	2.41845	Yes	KapB<cMyc>KapB<H
NM_hsa_5259	chr19:1253321-1253461	+	CTGGGAGCGGCTGGTCTGATG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5264	chr19:2418502-24185988	-	CCAGAGTCCGGTGTGGGAATGCA	No	No	Yes	1.42464	0.26489	0.659576	Yes	KapB<cMyc>KapB<H
NM_hsa_5265	chr19:17581269-17581365	+	GAGCGGGTCTGGGCGGGGGG	No	No	Yes	0.683829	0.198668	0.219859	Yes	KapB<cMyc>KapB<H
NM_hsa_5268	chr19:53700345-53700438	+	CGGATGCGGGGAGTGAAGCTCCG	No	No	Yes	0	0	0	0	No
NM_hsa_5271	chr19:14192493-14192583	+	CGAGCGCGGCTGACCTGCGAGA	No	No	Yes	2.64984	2.08601	3.9941	Yes	KapB<cMyc>KapB<H
NM_hsa_5281	chr19:50357813-50357949	+	CGCCCTCTCGCCCAACGA	No	No	Yes	0	0	0.0732862	Yes	KapB<cMyc>KapB<H
NM_hsa_5287	chr19:12606239-12606349	+	GCCTCGAACGTCCGATGGGCTG	No	No	Yes	0	0	0	0	No
NM_hsa_5288	chr19:39926776-39926896	+	TCTCTGTGATCGACTACCCGCG	No	No	Yes	0.455886	0.331113	0.513004	No	KapB<cMyc>KapB<H
NM_hsa_5290	chr19:48981443-48981561	+	TCTGTGACCTTGGTCTTCCAG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5295	chr19:39214988-39215088	+	TCCACACCGGCTCTCTTGCC	No	No	Yes	0.113971	0	0.0366431	Yes	KapB<cMyc>KapB<H
NM_hsa_5298	chr19:35500708-35500816	+	CTCACCTCTCAAACTTCTCAG	No	No	Yes	0	0	0	0	Yes
NM_hsa_5300	chr19:4285296-42853382	+	CTCTGCCAATGACCCCGAG	No	No	Yes	0	0	0	0	No
NM_hsa_5306	chr19:12897900-12898040	+	TAGCTGAACTAGCTGAGCA	No	No	Yes	0	0.0331113	0.0242828	Yes	KapB<cMyc>KapB<H
NM_hsa_5308	chr19:49993917-49994008	+	CACATGCACTACCACTGAGGCCA	No	No	Yes	5.5846	6.42358	5.20332	Yes	KapB<cMyc>KapB<H
NM_hsa_5310	chr19:38943362-38943498	+	ACAGTCGCGGCTCCGTGTAG	No	No	Yes	0	0	0	0	No
NM_hsa_5315	chr19:54940961-54941091	+	TGCTGTGGAGTGTGGATCCGG	No	No	Yes	0	0	0	0	No
NM_hsa_5318	chr18:34833624-34833752	+	CCCCCGTCCCGCCCGCCGCG	No	No	Yes	0	0	0	0	No
NM_hsa_5319	chr18:35147120-35147260	+	CGCCCGGAGCCGAGACTCCGCG	No	No	Yes	0	0	0	0	No
NM_hsa_5320	chr18:30350188-30350288	+	AGCAGTGTCTCGGGGGAGGA	No	No	Yes	0	0	0	0	No
NM_hsa_5322	chr18:33161789-33161871	-	CTAGGCGCGCGCGCGCGCGCG	No	No	Yes	3.26645	1.9943	1.41465	Yes	KapB<cMyc>KapB<H
NM_hsa_5323	chr18:53146428-53146544	-	TTGATGGAGTCTGATGGCCGTGCA	No	No	Yes	1.16821	1.09267	2.80931	No	KapB<cMyc>KapB<H
NM_hsa_5324	chr18:2750452-2750546	+	GGGATACAGGCTCTCTGGCTT	No	No	Yes	0.563073	0.739485	0.183216	Yes	KapB<cMyc>KapB<H
NM_hsa_5325	chr18:77748604-77748688	+	CGAACGTGTAGTGGCGGGTGTGAG	No	No	Yes	0	0	0	0	No
NM_hsa_5328	chr18:35424892-35424990	+	CTTGCTCTGGAGTTAGGA	No	No	Yes	0	0	0	0	No