#	Accession	Targeted Region	Target Sequence	Tm_CP	Tm_RP	Gene	PN(CP;RP)
1	NM_001161857.1	1282-1382	AGGTCACGTCTGAGACGGACACCAGGTATTTTGATGAGGAGTTCACAGCCCAGATGATCACCATTACGCCACCTGACCAAGACGACGGCATGGAGGGGGA	86	86	AKT1	353407;253407
2	AY881028.1	110-210	CCATAACCAGTCAGAGGCAGTACACTCTAAGAATTGAGTTATTGGACTGGGAAGGAAACCGAGCCTATTCACAATACGACAGATTCCACATAGGAAATGA	82	83	ANGPT1	353424;253424
3	AY881029.1	149-249	AACACTCCCTTTCTACAAACAAATTGGAAAAACAGATTTTGGATCAGACCAGTGAAATAAGCAAACTGCAAGATAAGAACAGCTTCCTGGAAAAGAAAGT	78	84	ANGPT2	353410;253410
4	EE789237.1	391-491	GTGAAGAACATGTCACTTGAACTCGACTCAAAACTCGAAAGTCTCCTTGAAGAGAAAATTCTACTGCAACAGAAAGTGAGATACCTGGAGGACCAATTAA	80	84	ANGPTL3	353411;253411
5	EE823222.1	463-563	AGGGAAAGTGGATTGTTCCAGATCCAGCCCCAGGGATCCCCGCCTTTCCTGGTTAACTGCAAGATGACCTCAGATGGAGGCTGGACTGTAATTCAAAGGC	85	85	ANGPTL4	353404;253404
6	EE861424.1	290-390	TGATGGACCAATACAGCGAGATTAACGCCATCAGCACTGCCTGCTCCAATGGGTTGTCTAAGTGTGAGGAGCTGGCCAAAACACTTTTCAGCCAGTGGAT	86	85	ANPEP	353435;253435

7	EE828676.1	481-581	AGGACAGCAACTTCACCCTCATTGATAATCACGATAACACGGCCAACATCATAGTCAAGTACGGGTATTTTGACCGGGAGCGCGCCAAGGTCCACCACCT	84	85	CDH5	353412;253412
8	EE764535.1	267-367	AGGGACCGCCTGGCACGCCCGGAGTCAAGGGGGATCCTGGAGCTGTGGGGCCACCAGGGAGCAAGGGAGAAGTTGGAGCAGACGGAGCACCTGGCTTCCC	92	92	COL18A1	353383;253383
9	L47282.1	231-331	ATTACTGGCAAGGCCCTCGAGCCTTACATTAGCAGGTGCACCGTCTGTGAGGGTCCTGCGATTGCCATTGCCATCCACAGTCAAAGCACTGATGTTCCCC	85	86	COL4A3	353406;253406
10	NM_001164714.1	900-1000	CTTCCTGTGGAGTTCAAGTGTCCTGATGGGGAAGTCATGAAGAAGAGCATGATGTTCATCAAGACCTGTGCCTGCCATTACAACTGCCCCGGAGACAATG	84	86	CTGF	353461;253461
11	NM_001009358.1	116-216	GCGCCCGTGGTCAACGAACTGCGCTGCCAGTGCCTGCAGACCGTGCAGGGGATTCACCTCAAGAACATGCAGAGCGTGAAGGTGACGCCCCCGGGCCCCC	86	86	CXCL1	353375;253375
12	NM_001009191.1	135-235	CACGCTGCACCTGCATCGAGATCAGTAATGGATCTGTTAATCCAAGGTCCTTAGAAAAACTTGAACTGATTCCTGCAAGTCAATCCTGCCCACGTGTCGA	83	80	CXCL10	353445;253445

13	EE791361.1	295-395	TAAGAATGGTCAGGAAGCTTGTCTCAACCCTGAAGCTCCCATGGTTAAGAAAATCATCAATAAGATGCTAAACAAGGGCAGCACCAACTGACCTAGAGGG	85	85	CXCL2	353432;253432
14	DY496905.1	105-205	CCTGTCGCGGCCGTTGTGAGAGAGCTGCGTTGTGTGTGTTTAACCACCACCCCGGGAATTCATCCCAAAATGGTCAGTGATCTGCAGGTGACCGCCGCGG	83	85	CXCL5	353428;253428
15	GT875699.1	55-155	CCAGCCAAGGGATGATCCACCCAAAATCCATAAAGGACCTTAAACAATTTGCTCCAAGCCCTACTTGTGAGAAAATTGAAATCATCGCTACAGTGAAGAA	82	82	CXCL9	353440;253440
16	GT642504.1	319-419	TTCACAGGTTTTACCCTGAGCAAGGATTTCAAAGAGGGACACAACTACTACTACATCTCCAAGCCCATCCACAACCAGGAAGACCGTTGCTTGAGGCTGA	81	85	EFNA1	353416;253416
17	GO771352.1	374-474	TGGTTTGGATTGAATCCAAGTTTACAAGCAGACACCACTGCGGGGGGCCGCCGACAGTGGACAAGGGTGACGAGGGGTGGGCATTGGGGTGCCAGGCAGG	86	89	EFNA3	353387;253387
18	EE798517.1	65-165	TCAGCCCCAGTTAGTCAAACCCCAGCGACCTTTGCCCCTGGTTGCCAAGGGCTTTGCAGTGTGAAGCAGGGAAATAAGGATCTGTCTGTTTAGTGGATAC	86	81	EFNA5	353434;253434

19	CF116254.1	289-389	AGAGCCCGGCGAACATTTACTACAAGGTCTGAGCCTCGGCGGTGCCTTCGCTTCCCGGAGGAAACTTACTGTCCCCGCTGCCGCCCGCCGA	85	84	EFNB2	353374;253374
20	DY492950.1	329-429	TGTGCAGCCTCGGCCCCACAAGTCTTGCAGAAACAGTCTACTGTGACCTACAGCCTGTGGACTCCAAGGTGACATACACAATGAGCCAGGTTTCTGAGGG	85	85	ENG	353400;253400
21	EU340261.1	197-297	GACGACAGAATCACAGAACTGGTTGGTTACCACCCTGAAGAGCTGCTTGGCCGCTCAGCCTATGAGTTCTACCATGCGCTGGACTCAGAGAACATGACCA	85	86	EPAS1	353414;253414
22	DY521965.1	311-411	CCCCTTCTGGATCAGCGGCAGCCTCACTACTCAGCTTTTGGCTCCGTGGGGGAGTGGCTTCGAGCCATCAAAATGGGAAGATACGAAGAAAGCTTTGCAG	85	85	EPHB4	353402;253402
23	NM_001166195.1	1730-1830	CCCCTCTAACAACCGCTGGTATCAAATGGGCATCGTCTCATGGGGTGAAGGCTGTGACAGGGATGGAAAATATGGCTTCTACACACACGTCTTCCGCCTG	85	85	F2	353464;253464
24	DQ152951.1	35-135	AAGGCTGGAGGAAAACCATTATAACACCTACACATCCAAGAAGCATGCAGAGAAGAATTGGTTCATTGGTCTCAAGAAGAACGGAAGCTCCAAACTCGGT	84	82	FGF1	353426;253426

25	NM_001009769.1	355-455	AATACTCCAGTTGGTATGTGGCACTGAAACGAACTGGGCAGTATAAACTTGGACCCAAAACAGGACCTGGGCAGAAAGCTATACTTTTTCTTCCAATGTC	83	83	FGF2	353452;253452
26	AY737276.1	845-945	CCGCGGTGCACAAGGTCTCCCGCTTCCCGCTCAAGCGACAGGTGTCCTTGGAGTCCAGTTCATCCATGAGCTCCAACACGCCACTGGTACGCATCGCCCG	86	85	FGFR3	353423;253423
27	GW997725.1	565-665	ACCTGAATTAGTGCCTGTTAAAGTTGCCAACCATACAGGTTGTAAGTGCTTCCCAACGGCTCCCCGCCACCCATTCTCAATCATTAGAAGATCCATCCAG	80	84	FIGF	353444;253444
28	AF233077.1	130-230	TAAGAACCCTGACTATGTGAGAAAAGGAGATACGCGACTTCCTCTGAAGTGGATGGCTCCCGAGTCCATCTTTGACAAGATCTATAGCACCAAGAGCGAC	86	85	FLT1	353418;253418
29	EE796001.1	107-207	CTCTTCTTTCACATCTGTCTTCTTGATCTCTGCCTTGAAGGCCTCCGCCTCGCCGTTCTGGTCGTCCTTGGCCAGCAGGTCCATGAGGTAGGCGATGTAG	78	86	HAND2	353377;253377
30	AF213397.1	146-246	ACAGCTTTTTGCCTTCGAGCTATCGGGGTAAAGACCTACAGGAAAACTACTGTCGAAATCCTCGAGGGGAAGAAGGGGGACCTTGGTGTTTCACAAGCAA	83	85	HGF	353399;253399

31	AY485676.1	86-186	CTGTTATGAGGCTCACCATCAGCTATTTGCGTGTGAGGAAACTTCTGGATGCTGGTGATTTGGATATTGAAGATGAAATGAAGGCACAGATGAACTGCTT	81	82	HIF1A	353409;253409
32	GT873986.1	180-280	GGCAAGTGTTGTTTGGAGCCGGAAACTACCACCTAGTGGATGGAAATTTTGAACCTTTGCCTGATTATTGGCTCTCTCTTCTGTTCAAGAAACTGGTGGG	81	79	HPSE	353439;253439
33	EE798621.1	111-211	CAAAGCAATTAATTTCCTCAGAAATCTGAGAAGCACCAAACGTGACCATTTTTTAAATGTCCGCTTTTCAAAAAATAGAAACACACGAGGGGGGACTCCC	77	79	ID1	353403;253403
34	NM_001177678.1	135-235	ACGTGCGCGCGTTGCAGGCTGCTCCAGAGGGTCTCTGGCTTTCTCCTTCCTTCCAGCACTTCCCAACCTCATTGCTCAGTATGAAGGCGCTCAGCCCGGT	85	85	ID3	353465;253465
35	NM_001009803.1	470-570	TGATGAATGACCTGTCGCCAAAATCTAACCTCAGAAAGCGGAAGAGAAGTCAGAATCTCTTTCGAGGCCGGAGAGCATCAATGTAATGGTTCTCCTGCCT	85	82	IFNG	353454;253454
36	NM_001009774.2	244-344	GCGGGACCTGAGACCCTCTGCGGGGCTGAGTTGGTGGATGCTCTCCAGTTCGTGTGCGGAGACAGGGGCTTTTATTTCAACAAGCCCACGGGGTACGGCT	85	85	IGF1	353398;253398

37	X56972.1	685-785	TGTACCCTAACTGGTACATCAGCACTTCTCAAATCGAAGAAAAGCCCGTCTTCCTGGGACGTTTTAGAGGTGGCCAGGATATAACTGACTTCAGAATGGA	83	83	IL1B	353467;253467
38	NM_001009392.1	630-730	GAATTTCCTGCAGTTCAGCCTGAGAGCTATTCGGATGAAGTAGCTGCGGCTCCCATGATTGTGGTAGTTCCTGGGCATTCCCTCCTCTGGTCAGAAACCT	84	84	IL6	353448;253448
39	NM_001009401.1	50-150	AGAAGAAACCTGACAAAAAGCCTCTTGTTCAAGTATGACTTCCAAGCTGGCTGTTGCTCTCTTGGCCGCTTTCCTGCTCTCTGCAGCTCTGTGTGAAGCT	83	84	IL8	353450;253450
40	GT875990.1	606-706	GTTACTGCCAAGGGGGCTTCAGTGCCGAGTTCACCAAGACTGGGCGTGTGGTCCTGGGTGGACCAGGGAGCTATTTCTGGCAAGGCCAGATCCTGTCCGC	85	86	ITGA5	353396;253396
41	NM_001113771.1	2025-2125	TCCATCCCACTGCAGGCTGATTTCATCGGTGTTGTCCGTAACAGTGAAGCCTTAGCAAGACTTTCCTGCGCGTTTAAGACAGAAAACCAAACCCGCCAGG	82	83	ITGAV	353457;253457
42	AF349462.1	144-244	CAGGCTGAGGCTGAGCCTTACAGCCACCCGCTGCAACAATGGCAATGGGACCTTTGAGTGTGGGGTGTGCCGCTGTGGGCCTGGCTGGCTGGGGTCCCAG	89	89	ITGB3	353385;253385

43	DQ152971.1	40-140	ATATTCGCTTTACGTAGCTTGCGAGCCTTCCCCTTCTGCAAACAATGAAATGCATGTGGCCATTTCTGCTGAAGACATCCGGGATGATGGAAACCCTATC	77	86	JAG1	353427;253427
44	AF233076.1	305-405	GAGGAATTTTGTAGGCGACTGAAAGAAGGAACTAGAATGAGAGCCCCTGATTACACCACACCAGAAATGTACCAGACCATGCTTGATTGCTGGCATGGGG	85	85	KDR	353417;253417
45	DY493581.1	609-709	CAGGACCGCGGGGTACACAACGCCAGCCTGGCTCTGTCAGCCAGTATCAGCCGTGTGCGGGAAATCATTGCCCAGGCCCGTGGTGCAACCAGCAAAGTCA	85	85	LAMA5	353390;253390
46	U84247.1	5-105	CATCCGCAAGGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGGATCAATGACATCTCACACACGCAGTCCGTCTCCTCCAAACAGAGG	85	85	LEP	353466;253466
47	NM_001142894.1	1005-1105	ACGAATGGAAAAGTCTGACCTATGATGAAGTCATCAGCTTTGTGCCGCCACCCCTTGACCAAGAAGAGATGGAGTCTTGAGTGTCTGGTTTCTATTCTGT	83	79	MAPK14	353459;253459
48	GT881645.1	465-565	CACGCCCTCCCTCCACAGGCTCAAGATGTTACCCACCAGTGCCTTCTTCCTCCTCGTTAGCTTTATCAATCATGCCCTGCTTCTTCCCTCTCACTTGCCC	85	78	MDK	353443;253443

49	DY516990.1	290-390	GAGGACCCCTTCAACCAGAAGACCCTTAAATACCTGCTGCTGGGCCGCTGGAGAAAGAAGCATCTGACCTTCCGCATCTTGAACCTACCATCCACCCTAC	86	85	MMP19	353401;253401
50	NM_001166180.1	650-750	AGAAGGACAAGTGGTCCGTGTCAAGTACGGGAATGCTGACGGGGAATATTGCAAGTTCCCCTTCCGGTTCAACGGCAAGGAGTACACCAGCTGCACAGAC	85	86	MMP2	353462;253462
51	FJ185130.1	35-135	GGCATTCAGGGAGATGCCCACTTCGACGATGAAGAGTTATGGTCTCTGGGCAAAGGCGTTGTGATCCCGACCTACTTCGGAAACGCGAAGGGCGCCGCCT	85	86	MMP9	353437;253437
52	DY496911.1	546-646	GCTCCTGCATGCCCGGATGGACAGGTGAGCAGTGCCAGCTTCGAGACTTCTGCTCAGCCAACCCCTGCGTCAATGGAGGGGTGTGTCTGGGCACCTACCC	89	88	NOTCH4	353386;253386
53	EE867112.1	10-110	GCTGTCATAGACAATTTTGACGTATACAAGGTGGAGACCATCGGTGACGCCTACATGGTGGTGTCCGGGCTCCCGGTGCGGAACGGGAGGCTGCACGCCC	83	86	NPR1	353376;253376
54	AF395335.1	1455-1555	CTGCTGACGAAGAAGAAAGTATATTTTAGTGTGAGATGTCAGCCTCCAGGAAGGCAAGGGCTCCGAAGATTTGGCAACGTGGCTTAATCGTTCCGCTTTT	81	80	NRP1	353419;253419

55	EU366494.1	70-170	ATTTTCCTAGCTCTCTACTTTTCAGGACATGAAGTGAGAGGCCAAGCAGACCAACCCTGTGGAGGTCGTTTGAATTCCAAAGACGCTGGCTACATCACCT	81	85	NRP2	353436;253436
56	EE840398.1	202-302	AAGTGCCAGCCGTCGCGCGTCCACCACCGGAACGTCAAGGTGGCCAAGGTGGAGTACTTCAGGAAGAAGGCGAAGTTGAAAGAGGTGCAGGTGCGGCTGG	86	85	PDGFA	353395;253395
57	EE771049.1	339-439	GAGGAAAATTTGCCTGGACCAGCAGAATCCTCTGTATAAGAAAATAATCAAGAGGCTTTTGAAGAATTAGCTGCCTAAATCCCTACTGTTGCTATAGAAA	81	79	PF4	353393;253393
58	AY157708.1	172-272	GACAGCCAACGTCACCATGCAGCTCATGAAGTACCACTCTCTGGACCAGCCCTTCTTTGTGGAGATGAGCTTCTCTCAGCACGTCCGCTGCGAGTGCGAA	85	83	PGF	353389;253389
59	NM_001163593.1	1635-1735	GATCAGGATGGAAGGGTGGTCCTGAACCGGGATGGTATTGTCCATTTCTGGACTAAAGCTTCCTGGAGTTAAAAATGGCATCTCCTGTGCATAGGTGGAA	84	83	PLAU	353460;253460
60	EE768764.1	140-240	AGAGGATTGCGCAGCAAAGTGTGAGGAGGAGAAAGACTTCGTTTGCAAGGCATTCCAGTATCACGGTAAAGAGCAACAATGTGTCATAATGGGCGAAAGC	85	82	PLG	353431;253431

61	GO745129.1	220-320	TGCTCGCCCGACAGCTCCTTCATCCCCTTTGACGGATACTTCACCACCACCTCCTCCTCCCTCTTGATTGACAGCCTCACCACGGAATACGACACCAATG	85	86	PLXDC1	353438;253438
62	NM_001009476.1	1535-1635	TGCTTTGGAATTCTACCCGGGGCTACTTCTTGAGAAGTGCCATCCGAACTCCATCTTTGGGGAGAGTATGATAGAAATGGGGGCTCCTTTTTCCCTTAAG	84	79	PTGS1	353451;253451
63	EE794035.1	350-450	ACCACCCTATGACAAGAAAAAGCGAATGGTGGTTCCTGCTGCCCTCAAGGTTGTGCGTCTGAAGCCTACTCGCAAGTTTGCCTACCTAGGGCGCCTGGCT	86	86	RPL13A	353433;253433
64	CD288584.1	84-184	TCTCGGAGCTCGCTTGTATCTACTCTGCCCTCATTCTGCACGACGATGAGGTGACGGTCACGGAGGATAAGATCAATGCCCTCATTAAAGCAGCCGGTGT	84	86	RPLP1	353380;253380
65	GT879142.1	655-755	AGAGAACATCTTTGTTTTGCTGACCATCTGGAAAACCAAGAAGTTCCACCGACCCATGTACTATTTTATCGGCAACCTGGCCCTCTCAGACCTGTTGGCG	80	84	S1PR1	353442;253442
66	EE839061.1	216-316	ATTCTGGGCCTTCCGTATCGAAACCATGACCTCAGCATGTTCTTGCTGCTGCCCAATGACATCGACGGTCTGGAGAAGATTATAGATAAAATAACTCCTG	82	82	SERPINB5	353379;253379

67	NM_001139447.1	810-910	AACTGCAAGATCGCCCAGCTGCCCTTGACCGGGAGCACAAGTATCATCTTCTTCCTGCCTCAGAAAGTGACCCAGAACTTGACCTTGATAGAAGAGAGCC	86	85	SERPINF1	353458;253458
68	DY504212.1	375-475	GCCATCCAGAAGCCCCTGTGTAGCCTCCCGGCCGGCTCTGGCAATGCGATGGCCGCTTCTTTGAACTATTACGCCGGGTATGAGCAGGTGACTAAGGAAG	86	85	SPHK1	353391;253391
69	GO762530.1	291-391	CTGAGCTACGCCAATGCCACCCCGAGGGGTCTCGAGTTTCTGGACTTCCTGGACGACGAGCGCACCTACAAGACGCTCTTCGTCCCTGTCAATGAAGGTT	86	86	STAB1	353415;253415
70	AY881030.1	255-355	TCACCTCAGCCTTCACCAGGCTCATAGTCCGGAGATGTGAAGCTCAGAAGTGGGGACCTGAATGTAACCGCATCTGCACTGCTTGTATGAACAATGGGAT	86	85	TEK	353425;253425
71	L36232.1	176-276	CAGGTTTTTGTTGCAGGAGGAGAAGCCAGCGTGTGTCTGCCACTCTGGGTACGTCGGTGCACGCTGTGAACACGCAGACCTCCTGGCCGTGGTGGCTGCC	85	86	TGFA	353397;253397
72	NM_001009400.1	635-735	GGAAATAGAAGGCTTTCGCCTCAGTGCCCACTGTTCCTGTGACAGTAAGGATAACACGCTTCAAGTGGACATCAACGGGTTCAGTTCCGGCCGCCGGGGT	85	85	TGFB1	353449;253449

73	AY656797.1	880-980	AGCGTGCTCTGGACGCAGCCTATTGCTTTAGAAATGTGCAGGATAATTGTTGCCTACGCCCACTTTACATTGATTTCAAGAGGGATCTTGGGTGGAAATG	82	81	TGFB2	353420;253420
74	AY656798.1	570-670	ACGTCACAGACACTGTGCGTGAATGGCTCTCGCGGAGAGAATCCAACTTAGGTCTGGAAATCAGCATCCACTGTCCCTGTCACACCTTTCAGCCCAATGG	85	86	TGFB3	353421;253421
75	AY656799.1	70-170	ACGAGACAGGCCATTTGTATGTGCACCATCTTCAAAAACTGGGTCTACAACATATTGCTGCAACCAGGACCACTGCAATAAAATAGAACTTCCAACTGTC	82	83	TGFBR1	353422;253422
76	GO725318.1	96-196	ACTCAGGGCAGGAAGACTATGACAAGGATGGAATCGGCGATGCCTGTGATGATGACGATGACCATGATAAAATTCCAGATGACAGGGACAACTGTCCATT	86	83	THBS1	353405;253405
77	DY521350.1	385-485	ACAACCCCGACCAGACCGACGTGGACAATGACCTCGTGGGAGACCAGTGTGACGACAATGAGGACATCGATGAAGATGGCCACCAGAACAACCAGGACAA	86	85	THBS2	353392;253392
78	NM_001009319.2	345-445	ACTAAGATGTTCAAAGGGTTCAGTGCCTTGAGAGATGCCCCAGACATCCGATTCATCTACACCCCTGCCATGGAGAGCGTCTGCGGATACTTCCACAGGT	85	85	TIMP1	353447;253447

79	NM_001166186.1	174-274	AACGACATCTATGGCAACCCCATCAAGCGGATTCAGTATGAGATCAAGCAGATAAAGATGTTCAAGGGACCTGACCAGGACATAGAGTTTATCTACACAG	84	82	TIMP2	353408;253408
80	NM_001166187.1	250-350	CGGAAGCCTCTGAAAGTCTCTGTGGCCTTAAGCTTGAGGTCAACAAGTACCAGTACCTGCTGACAGGCCGTGTCTATGATGGCAAGATGTACACAGGACT	86	86	TIMP3	353463;253463
81	NM_001024860.1	1230-1330	CTTCAACTCTCCCTTCCTGCCAGTGTTTCCAGATTCCCCTGAGGTGGGAAGCCCAGCCCCAACCCCACTGGGCCAACTCCCTCTGTTTATGTTTGCACTT	83	86	TNF	353455;253455
82	GT643835.1	729-829	GCCCTGAAGGAGGGGTCAGGAGGGGTGTGTGGCTCGGGGACCCAGCTCTGGGATCACCGCCTGTTCACGAGATCCTGCCCCACCTGCCTGAGGACCGCCC	92	91	TNFAIP2	353384;253384
83	NM_001025110.1	115-215	TGATGAAGTTCATGGATGTCTACCAGCGCAGCTTCTGCCGTCCCATTGAGACCCTGGTGGACATCTTCCAGGAGTACCCAGATGAGATTGAGTTCATTTT	83	81	VEGFA	353456;253456
84	EE814744.1	41-141	GCTCCCGTCTCCCAGCCTGATGCCCCTGGTCACCAGAAGAAAGTGGTGTCATGGATAGACGTGTATGCTCGTGCCACCTGCCAGCCGCGGGAGGTGGTGG	85	85	VEGFB	353394;253394

85	DY521036.1	32-132	AAAAGTCAGTTTCCTGAACCACGTGGAGAATGTTACAGAAATGGACTGGAGCTCATCTGCAAAAGACCTCTTTAAAAGACTGGTTTTCTGCCAATGACCA	82	79	VEGFC	353381;253381
86	NM_001009784.1	1200-1300	GCAAATGCTTCTAGGCGGACTGTTAGCTGCGTTACACCCTTTTTCTTGACAAAACCTAACTTGCGCAGAAAACGAGATGAGATTGGCCTCGTGCGATTCG	79	83	ACTB	353453;253453
87	NM_001009284.1	285-385	CAACAGCAAGGATCAGTACAGCTGCCGAGTGAATCACGTTACTCTAACACAACCCAAGATAGTTAAGTGGGATCGAGACCTCTAAGCAGCACCATCAAGA	85	85	B2M	353446;253446
88	NM_001190390.1	1088-1188	TTCCTCAGCTGCTGGGGAGTCCTGCCCCACCTCCACCACACTGAGAATCTCCCGACCTCCATACATTTCCATCCTCAAGGCCCTGAGGAAAGGGAGGGGC	89	88	GAPDH	353382;253382
89	EE824765.1	698-798	AGATGAGAGTTCGAGTTGAGTTTGGAAATACCTGGCATCCCATTGAAATCACCAGTGACATGATCCCATGTTCTCATTCTGTGGCCAGCTGCTTAGTAGA	79	82	HPRT1	353378;253378
90	EE751721.1	175-275	TGATGGATCTCCAACATGGCAGCCTTTTCCTTAGAACACCAAAAATTGTCTCTGGCAAAGACTATAATGTAACAGCAAACTCCAGGCTGGTTATCATCAC	79	84	LDHA	353430;253430