

Supplementary Table S2

List of 300 genes targeted by this custom siRNA library purchased from Qiagen.
Each well contains a pool of 4 siRNA duplexes targeting the indicated gene. The siRNA pools are arrayed into five 96-well plates.

PLATE ID	WELL	LOCUS ID	NCBI GENE SYMBOL	siRNA TARGET SEQUENCE 1	PRODUCT 1 ID	siRNA TARGET SEQUENCE 2	PRODUCT 2 ID	siRNA TARGET SEQUENCE 3	PRODUCT 3 ID	siRNA TARGET SEQUENCE 4	PRODUCT 4 ID
900097-1	B2	3832	KIF11	ACGGAGGAGATAGAACGTTTA	SI02653693	GCGGATAAGATAGAAGATATA	SI02653770	CTCGGGGAAGCTGGAATATATA	SI03019793	AACCTGGATCGTAAGAAGGCAG	1024738
900097-1	B3	4660	PPP1R12B	CGGGAGGTAGTAACTCCTACAA	SI00038472	CAGACACGGAAGGCTCTACTCAA	SI00363403	CCTGTAAGACTCTTGACCTCTAA	SI03074078	CCCACTGCTATGGACAACATA	SI03076374
900097-1	B4	3486	IGFBP3	CAAGGTTAATGTGGAGCTCAA	SI02780589	CCAAATATAGTAAGATCTATA	SI02623866	GAGAAGATATGTTCTTGTTAA	SI02623873	CACCCATGTGTTTGTGAACCTA	SI02623880
900097-1	B5	7027	TFDP1	CAGAACTTGTCCCGGGAAA	SI00094654	ATTGATTTATTGTGCCCTTAA	SI03052462	CACATTTGAAATCCACGATGA	SI03056858	CAGCAGAATGCACATCTTCAA	SI03065594
900097-1	B6	128178	EDARADD	CCGGACTTGAACAACCCACA	SI00148841	CCCTAGCACTTTATCCCTTAA	SI00153664	TACCCACAGCATTATATGTAA	SI02647778	TTGCTCAATGATCAGGACTTA	SI03024357
900097-1	B7	5151	PDE8A	ACGGAGATAAATACAACAAA	SI00040250	CAGGCTATTCAGATCATCAAA	SI00040257	CCCGGATACCTTCATGACAA	SI00040264	CCGGACCCCTAATCAACGGAAT	SI03081757
900097-1	B8	2906	GRIN2D	CCGCTACTGGTCGGTCGACAA	SI00016765	CCGGGATTACTCCTTCAATGA	SI00016772	GAGGATTGGTGCCCTCAACTA	SI00016779	CTCGGTGATTATGGTTTCTCTT	SI00016786
900097-1	B9	10460	TACC3	CAGGAAGTCTTGAGAACCCAA	SI00738423	AAGGAACCTTCCAAAGCGTAA	SI00738430	CTGCAGGTCTTAAACGACCTAA	SI00738444	CCCGTTCGGAGGTGACACCAA	SI03186568
900097-1	B10	3849	KRT2	CTGGTGGAAAGCCGAGATCAA	SI00464772	AAGCAGCACCTTTCATCAAA	SI00464779	AAGCAGTGTAAAGATGTGCAA	SI00464786	CAGGATCTTTGTGGAGGATTAT	SI00464793
900097-1	B11	8891	EIF2B3	CCGGAGTGAACGTGATCCATA	SI00377349	AAAGAGGAGGATCTAAAGAAA	SI00377363	CCAGTTGGGAACAACACCTTAA	SI00377370	AGGATTGAAGCCAAAGCTAAA	SI03145975
900097-1	C2	5764	PTN	TACCGTAGGCTTTGTATTCAA	SI00043750	CTGGAGCTGAGTGCAAGCAAA	SI00043764	CAGTGAGTCATCCGTCACGAA	SI03073049	CTGACCAAGCCCCAACCTCAA	SI03093083
900097-1	C3	1621	DBH	CACGTACTGGTGCTACATTAA	SI00015617	CCGGGAGTGGGAGATCGTGAA	SI00015624	GCGGGCTAATGAGCCAATAAA	SI00015638	CTCAGGCATCCGCTTGTACTA	SI03088785
900097-1	C4	5901	RAN	TAGTGTGAAGTTGATACGCCAA	SI00087493	TTGGGAATCTTGCTGTTAAA	SI00087507	TTGGCTAGGTAGGGTCACTTA	SI03025064	AATGTGTTTGTACATATCAA	SI03037447
900097-1	C5	1938	EEF2	CCGGCCATCATGGACAAGAA	SI00736369	TGCCGTTTCTTTCAATATTTA	SI00736376	CTGGCCGAGGACATCGATAAA	SI00376383	TTGGAATAATAAATTTGATAA	SI00376390
900097-1	C6	2308	FOXO1	AACAAGTAGCCCTGTTATCAA	SI02781415	CCCGAGTTTAGTAAACAGTGCA	SI02781450	AAGAGCTGCATCCATGGACAA	SI04435144	CTGGAACATGCCTCAATGTCTA	SI00031437
900097-1	C7	5791	PTPRE	CCGAGTGATCCTTTCCATGAA	SI02665635	ACCACGGGCAATTAACCTTTA	SI00089068	GACCATCGTCATGTTAAACAA	SI00089075	CAGTGAATTCACACCCCTGAA	SI00089082
900097-1	C8	6235	RPS29	GAAGGATATCGGTTCTATTAA	SI00707749	CCGCCAGTGTTTCCGTCAGTA	SI00707756	CTCGCTCTTGTCGTTGCTGTT	SI03204446	TCGTTGCACTGCTGAGACGAA	SI03235113
900097-1	C9	3543	IGLL1	ACCCCTCTTTGTCAACCAAGAA	SI00446628	CACAAGGACCTCTGACCCTGTA	SI00446635	CCCTAAATAAATACCCCTCTT	SI00446642	ACCCATAAATAATACCCCTCTT	SI00446649
900097-1	C10	6188	RPS3	GAGGTGTGGTGTCGCGGAAA	SI00707791	CGGCAAGTAGGCGATGCGCAAT	SI00707798	AAGAGGAAGTGTTCGCTGAT	SI03128741	CTGGAATGAAGTGGCGAGTTA	SI03210935
900097-1	C11	1316	KLIF6	CTGCGTAGAGCTGGGAACGTTA	SI00025074	GAGGTGGATCTCTTAGGCTAA	SI00025081	CACGGGCAAGTTTACCTCGGA	SI00025095	CAGGAAGATCTGTGGACCAAA	SI03068968
900097-1	D2	2633	GBP1	CAGGAAGAAGTTTATCTTCCA	SI0025495	AAGGCATGTACCTTAAGACTAA	SI00425495	AACACTCATCTTGAACTCTAA	SI03123176	ATGGGACACTTGTAGACATTAA	SI03154340
900097-1	D3	2958	GTF2A2	CAGAGAGGTGACAGAACTTAT	SI00431928	CAGAAATACTACTTTGGGAAA	SI00431935	CACCTTTATTATACAGCATGA	SI00431942	TCCAGTAGAAAGAAACTTGTGA	SI00431949
900097-1	D4	4437	MSH3	CTAGGTCGAAAGGATGGATAA	SI00037828	AGCCCGAGGCTCAATATTTAA	SI00037835	CAGCAAGGAGTATGTGGATTAA	SI02628591	CCGGCTAGAGTATAACATCAA	SI03084564
900097-1	D5	4256	MGP	CCAGATTGATAAGTAAATGAA	SI00645407	CAGCAGAGATGGAGAGCTCAA	SI00645414	ATGTGATTGTTCCATAATAAA	SI00645421	TAGCAGCATTAAGTAAATACA	SI00645428
900097-1	D6	9099	USP2	CCGATGTGGTTACTGCTTCTA	SI03246988	CAGCAATATGGCACACTTTCA	SI03247034	CCGAGTGGTACGAGCACTTAA	SI00758198	CCCGCTGTGTTTGGCTATAAT	SI00758212
900097-1	D7	86	ACTL6A	AAAGCTTTAACTGGCTCTATA	SI02779987	CACAGCTGGAACGAGGAGTTA	SI02779994	TACGAGTTTCTGGCACAATTA	SI00062405	TGGCAGGAGGAAACACACTAA	SI04433940
900097-1	D8	3549	IHH	CTGGGTGATTACGAGTCAAA	SI00446859	CCGCTGAAGTCCTGGCTATTA	SI00446866	CCGCTTGACTCGGCTGATTTA	SI00446873	CCCGGCTGCTTCTGAGTAGTA	SI04382714
900097-1	D9	1053	CEBPE	TAGAACCTGGATAAATGGCAA	SI00342909	CTCCGATCTCTTTCGCGTGAA	SI00342916	AGGACCCAGCATATAAGTATT	SI00342923	CGGCACTTACTCAGAGTGTGA	SI00342930
900097-1	D10	1557	CYP2C19	CAGAAACGTTTCGATTATAAA	SI00015162	AACCATAACAATTAACCTTAA	SI00015176	AAGGATGTTCAGAAATCCCTTA	SI00015183	TCCCACTATCACTTGATTATTT	SI03114076
900097-1	D11	53616	ADAM22	CCCAGTCATTAGCCCATATAA	SI00060823	TACGTGAGTTTATGAAATACA	SI00060837	TTAGACCTCGGCTAATTTCAA	SI03021298	CTCGATGCTGCTGCTAATATCA	SI03091228
900097-1	E2	11217	AKAP2	AAGAACAATACTGCTATTAGAA	SI00293818	AAGGATGATGACCATGGGATT	SI00293832	CAGGCTTGGAAATCAGCTACAA	SI03176096	CTGGTGCGAAGTGCACATTTAA	SI03213819
900097-1	E3	10594	PRPF8	ACGGCAGCTGATCGATACAAA	SI00088543	ATGGCTTGTCTATCCGTAATAA	SI00088550	CAACTGCTGCTCACTCAATATA	SI00088557	CTCATCTGCGTACCAACATATA	SI03089135
900097-1	E4	5618	PRLR	CCGGGACCTCTGAGAACATAA	SI00019047	AACCCATAAGTTTAACTGTAT	SI00019061	ACGCTCTCTGTATGAATTCGGA	SI00019068	CTCCGCTAAACCCCTTGGATTAA	SI03090052
900097-1	E5	54820	NDE1	ACGCAGCTGCAACAAGTATGAA	SI00655851	AGCCGACAGCCAAAAGCCATTAA	SI00655858	AGCCGCAAGAAATGAAGCGTAA	SI00655865	AAGACAATTTGCAGAAATACA	SI00655872
900097-1	E6	26271	FBXO5	CATGTTCATTCCGGAGCTTAAA	SI00097839	GAGAATTTCCGTGACAGTCTTA	SI00097853	AAGCAAGCGCTTGCATAACAAA	SI00097860	GTGGATTGTGATTATGTACGGA	SI03106999
900097-1	E7	53353	LRP1B	CCCTACTACTCTGCTTAGCAAA	SI02777782	TAGATGATTCATGATAGTTAA	SI00122290	AACGTTTATATCTGGACAGATA	SI00122297	CACCTGCGGCTGTGATAGCCAA	SI04439813
900097-1	E8	1325	CORT	TAAAGAGCAAAATCGCTTAA	SI00025102	CAGCTGGAGATTGGGCTTAAA	SI00025113	AAAGACCTGAAAGCTTTAAGTA	SI03026394	TCCAGGCGTTAGACATGTGATA	SI03113761
900097-1	E9	10732	TCLF5	CTCGGCTAGTCTGACTCGAAA	SI00090132	CTCATTCGACATCCCTCTGAAA	SI00090156	ATCCATGAATGTCTCTTAAATA	SI03047408	TACTGTACAGATGACGCTCTTA	SI03110310
900097-1	E10	6585	SLIT1	CCGGATCTGAACCCATGTGCAA	SI00726103	CACGGCAGAACTGCGATGTGAA	SI00726110	ACGGAGGATAGACCTGAGCAAA	SI00726117	CACCCAGCGCCTGGAACCTCAA	SI03058258
900097-1	E11	1298	COL9A2	ACGATAATTGGAGTATCTCTA	SI00029162	AAGCCCGGAGTATGATGGTTTA	SI00029169	AACGGCAAGGATGGAGATCGA	SI03029901	CTGGCGCAGATTAGAGGTGCTCA	SI03029908
900097-1	F2	4324	MMP15	CCACAAATCTGGAAATTCGAA	SI03648946	CTGGCTCTTTGCGAAGAAGCGAA	SI00037688	CCGGAGCGCTGAGCCAGACAAA	SI00037695	TACATTTATTTCTGTAATAATA	SI00037702
900097-1	F3	81029	WNT5B	CTTGTTGGTCATTAGTCTGAA	SI00763483	CAGGGTCTTGTCCAGAATGTGA	SI00763490	CAGGATGTAGGAGCTTGGAAA	SI00763497	CACAAAGTCTTATATTATATA	SI00763504
900097-1	F4	917	CD3G	CTCGAGGAGTGTATCAGTGTA	SI00001358	CTGGCTATCATTTCTTCTTCAA	SI00001365	CAGCCCTAAATCTAGACTCAA	SI02622893	ATGATCTCGGCTCTCAACTAGTA	SI03049592
900097-1	F5	14375	CSTB	CAAGAAGTTCCCTGCTTTTAA	SI00355936	TCCAATCTCTCCCTCATGAAA	SI00355950	CAGACATGATGAGCTGACCTAA	SI03157252	CAGCCGCTTGACCTTATCTCAA	SI04037375
900097-1	F6	9543	PUNC	CACCAAGGAGATCATCGGCTGA	SI00696031	CCACGTGAGGCTCAAGAAATGA	SI00696038	AGCCTACAGTTTCTACATACATA	SI00696045	TGGTCTCTTGATGATCCGCTCA	SI04347483
900097-1	F7	2132	EXT2	GAGGTCTCGGCTAACGTTTAA	SI00008827	CCGGTGGTTCTGGGAAGCGTGA	SI00008834	CCCATTTCTATCGAGTCTCTAA	SI00008841	CAGGTCAAGTGTGAGAGCTGCA	SI00008848
900097-1	F8	3720	JARID2	TCGGATTATTTCAAGGGCGAA	SI00449624	CCCGTGTGCGATTATATATATA	SI00449631	CAGCAAGTGACTGCACCTCAA	SI00449638	AGGGTGAAGTTTGGAGAAGCTAA	SI03147550
900097-1	F9	10893	MMP24	CCCTACAGCATCTCAACAATA	SI00091077	CAGGGTCTCTCCGAGACCCCA	SI00091084	AACGATCGAGTGGATGAAGAA	SI00091098	TAGGGCGAGAAACAAGCCGCTA	SI03111857
900097-1	F10	23481	PES1	CACCTTGAAGCTGGAGGATAA	SI00682339	CTCGACCACTATCATCAAGGAA	SI00682346	CCGGCTCACTGTGGAAGTTTAT	SI00682360	TAGGAGCTTTAAAGGACAATA	SI03226965
900097-1	F11	4194	MDM4	AGCCCTCTCTATGATAGCTGA	SI00037142	AAAGAGGTGATGCACTATTTAA	SI00037149	GACCTAAAGATCGCTATATATA	SI00037163	TACACAGAGACGGGAACATTTA	SI03010476
900097-1	G2	6125	RPL5	AAACCTATGAACACAGCACTAA	SI00706615	TTCTGTTGCAACAACAGAGATA	SI00706622	ACTGATATTATGTCTCGGAAA	SI03142433	TCGATATAGATAATAAAGCTT	SI03229856
900097-1	G3	5714	PSMD8	TCCAACCTGACATGTTCACTAA	SI00694967	AAGGGCGAGTGGAAAGCTAATA	SI00694974	CTCGAGGTTTTCGCCCAATATA	SI00694981	ATGCTACTACTTTGATTACATA	SI00694988
900097-1	G4	6135	RPL11	ATGGCGCAGAGTACAAGGTGAA	SI00705586	CGGGGAGTATGAGTTAAGAAA	SI00705593	CGGGAACCTCGCATCCGCAATA	SI03196683	CTGGTTCCAGCAGAGATGTAGA	SI03214127
900097-1	G5	330	BIRC3	AATGGGAACCGAAGGATAAT	SI00299439	AAGACCTTCAAGTATACACAG	SI02654458	TTCAAGATACCAAGTTTCTTAA	SI02654465	CAGAACATGCTGTATTATATA	SI02661918
900097-1	G6	7157	TP53	AAAGGGAATTTGCGTGTGGAGT	SI02655170	CGGCATGAACCGGAGGCCCAT	1024849	TTGTGTAACCTTAGTACCTTAA	SI04384079	CAGAGTGCATTGTGAGGGTTA	SI00011655
900097-1	G7	5224	PGAM2	CCAGGCGGATCATGGAGCTGAA	SI00682983	CTGCTACACGTCAGTGGCTGAA	SI00682990	CAGGCGCATCAAGGATGCCAA	SI00682997	TCGATGACAGAGCTGAGTGAAA	SI00683004
900097-1	G8	81930	KIF18A	ATTCGCTACAGATCAACCTTAA	SI00140224	CAGGTGGAACTAACTTGGTTTA	SI00140238	CAGGAGCACTTGGACTCTACA	SI00140245	CTGGAAGTGTAAATATCCGGA	SI03090941
900097-1	G9	3491	CYR61	AGGGCACACCTTAGACAACCAA	SI02626421	TCCTCTTACAGGCTGTTTCAA	SI02626428	AACCTCTTACAAGGCCAGAAA	SI03028655	CAGAAGCTGATCATGTATGCCA	SI03053477
900097-1	G10	1891	ECH1	ACCCAGTTTCCCAAGTTTATAA	SI00375921	CAGCCGGGTGTTTCCGACGAAA	SI00375928	CCGCTGACATCATCACTCGATA	SI00375935	CCCGTGTGCTGCGCTGCTCAT	SI03186330
900097-1	G11	27175	TUBG2	AAGCTTGGTGTGTCAGTATATA	SI00116067	CCGGGAGATCATCAACCTGCGA	SI00116074	TTACGCTCTCTAAAGAATATA	SI00116081	CAGGACGAGATGAGCGGACGTA	SI00116088
900097-2	B2	55558	PLXNA3	CTGCTATTATTGATAGCTGAA	SI02778055	CGCGGGAGACTCAGAGTTCTTA	SI00118510	ATGCTCTTCTGCTGAATATGTTA	SI02642661	ACGAGCTGTATTTCTTATGTTCA	SI02642668
900097-2	B3	6217	RPS16	CTGTTGGCCATTATACCGAATA	SI00707329	ATGATGAGCCGCGCCACGCTGA	SI03151960	CCCGCGCTCGCTACCGAAGAT	SI03184993	ACCGCGCAATGGGTTCTCATCAA	SI04367167
900097-2	B4	9782	MATR3	ACCAGCGTTAGTATTTGGCAAA	SI03137659	ATGGTTGACCATTTGTTGAAA	SI03155131	CAAGAGCTTGGACGTGTGATA	SI03156937	CACGCTTGCTGATTTTAAGTA	SI03163867
900097-2	B5	5973	RENBP	CTCGTCTATTGCATTGCGAATA	SI00701183	CACGTGATTGACAAGTTCTCTA	SI00701197	CGGGGTGTATGATGAACCTCAA	SI00701204	ATGATGATTGTTTTCGCGCTGA	SI03153801
900097-2	B6	5199	CFP	CGACGCTATCAACCCAGTATAA	SI00682787	CCGACGGAAACATGAGGTCCTAT	SI00682794	ACGAAACCTAAGGAGACACGAA	SI00682801	AAGGATCACTGGTCAAGATGGA	SI00682808
900097-2	B7	8467	SMARCA5	CTCAATTGTTATGTCATTTAA	SI00726775	AACCAAGTACTTCTTAAATTTA	SI00726782	CTGGATTCAATAGTCACTTCAA	SI00726789	CAGAGAGAGATGTAATACCTTAA	SI00726796
900097-2	B8	102	ADAM10	ATGGTAAGAAGAAGTCCCTTAA	SI00022029	ATGGTGTGTTGCGAGAGTGTTA	SI00022036	TTGGTGGGCGATTAATCTTAA	SI03025582	GAGAGATATATAAAGACCGGA	SI03102680
900097-2	B9	3375	IAPP	AATGCGGGTATTGCGAAACAAA	SI00009107	TTAGAGGACAATGTAACTCTTA	SI00009121	TTGGTGCCATTCTCTCATCTA	SI03025547	CACAGTGGGATCCAAATACATA	SI03053218
900097-2	B10	578	BAK1	AGGCGAAGTCTTTTGCTCTCTC	SI00299376	CAGGCTGCGAGGACACCTCAA	SI02654512	CTCAAGAGTACAGAAGCTTTTA	SI02654519	CTGAGCTTGAAGCGAAGCTCTT	SI02654526
900097-2	B11	1005	CDH7	CTCGAAGGTTCTTATCAATATA	SI00341852	ACGGATAGAAGCTGCAAAATAA	SI00341866	CACCAAGAGACTGGATCGTGA	SI03160444	CTCCTTATCGTCACTATGAGGA	SI03203732
900097-2	C2	3550	IK	AATGACATGTCTATTAGCAAG	SI00300531	AACCCGTAAACAAGAAGCTTAA	SI00084336	AACGGGAGCTGTGATCCGGAAA	SI03030013	CTGAGCTGATATAGACAACAAA	SI00084350
900097-2	C3	3817	KLK2	CTGAGGTTCCCTAGAGTTTCAA	SI00078743	CAGCATATAATTTCCCTCTGCA	SI00078750	TACCTTAATTAATTGACCTGAA	SI00078757	CAGGAGTATGAGGATCTTGAA	SI00078764
900097-2	C4	2539	G6PD	CTCGGTTTCCCTGACCTTCAA	SI00008855	ATCGGCTGACCTTGGCCAGAAA	SI00008862	CCCTATAATTTAGGACCGCGA	SI03079251	CCGGACGCTGTGATGACAACCA	SI03082450
900097-2	C5	6168	RPL37A	ATGGGTTAATTTATGTAACAA	SI00706489	AAAGTCGGGATGCTCGGTGAAA	SI03122413	CATGGCCCAAGCTACCAAGTAA	SI04277721	AGGAGTTGAAAGACCAAGTGA	SI04309788
900097-2	C6	10077	TSPAN32	TCAAATATACATCACATCAAA	SI00683739	CAGCAATGATGCTGATTAGGCAA	SI00683746	CACCATGTGACTCTTACCTA	SI00683753	CAGCTTGGACCGCAAGCTCTT	SI00683760
900097-2	C7	11093	ADAMTS13	TGGCGAGAGCTTCATCATGAA	SI00292047	CCAGAGCTAAACACTGCTCTAA	SI00292054	TGGGTGAGAGCCAGACCAATCAA			

900097-2	D7	6161	RPL32	CAGGTAATCCACCACGGTTAA	S100706251	AACCTAGTCAATAATTTAT	S100706265	AAGAACAGGATGATGTACAA	S100706272	CAGATTCTTACGGGATGCCTA	S103169299
900097-2	D8	5430	POLR2A	CTCGGGGAAGAACAAAGCTAAA	S100688975	CACCACAGTCTCCAACTTATA	S100688982	CCGCACTTAAGGAGCTCATCAA	S100688989	CAGGCACATTTCAGAACACTATT	S100688996
900097-2	D9	5071	PARK2	CACGTATAAATTAATAGCTAA	S100677845	CACGTTTAGAATGATTTCCTAA	S100677852	ATGGATTGGATTTCAGTCTTAA	S102661267	ATCCGATTAATCGAAATACCA	S103150301
900097-2	D10	3084	NRG1	CTCGGCTGCAGGTTCCAACTAA	S103116974	TGGCTGATTCTGGAGAGTATA	S103120530	CTAGTTGGCTCTTGAGATCTA	S103088071	TATCCACATCGCGGAAATCAAA	S103112487
900097-2	D11	7314	UBB	CAGGATCTCTGGTATCCGCTTAA	S100754243	CACCTGGTCTCTGCGTCTGAGA	S103059280	TAAAGGTTTCTGTTGCATGTGA	S103107328	TTCCGCCAGCCCGGAGGACTTTA	S103115105
900097-2	E2	3166	HMX1	ATGAATCTACTTATTTTCGGTA	S100439656	CTCTCGGGGTGCTGGTGGAGAA	S100439663	CTCTCTCTCTCTCATCGAGAA	S100439670	TGCCAGTGTCTCTACCACGAAA	S104342387
900097-2	E3	2954	GSTZ1	CGCGCTGAATTTTGGCGTGAA	S100153678	ACGTGGCCCATCAATCTCATATA	S100153685	CCCTACCATTACGCGTCCATCAA	S103079181	TGCGAATTGCTCTGGCCTTGAA	S103115987
900097-2	E4	4326	MMP17	AAGGACAATAACGTAGAGGAA	S102781086	CTGGGTGGTCAAGGACAATAA	S100113897	CACAGATCTGCTTCTCTTAA	S100113904	ATGACAGGACTTATTTCTTTA	S100113911
900097-2	E5	83416	FCRL5	AAGGTCCGCATGACACACAA	S103134425	CCCACCTATCAACGTATACCA	S103182795	CACACAGATATGCAACTTAA	S102658047	CAGTGAAGATGTGACACTGAA	S102658054
900097-2	E6	8633	UNC5C	CGGGCTCGTCTTGCATCCAA	S100055174	TTGAATTTAGCTATCAACCTA	S100055181	CCCATGTACATGCCCACTTTA	S100055188	CCGATGTGAGCGATGTGCTCTA	S103084382
900097-2	E7	1050	PDHX	CTGGTCAAGATGACATTAATA	S100681555	CTAGATGTAAATCAAAGTATA	S100681562	TCGGAATATATTTAAATAAT	S100681569	AGGCAATTAAGTCAATCTAAA	S100681576
900097-2	E8	6871	TADA2L	ACGGATCATCTTATGAAATA	S100738479	CCAGGTTAAAGGAGAGACAAA	S100738486	ACCTTAGAAAGTTTCAATTAA	S100738493	CAAGAGCATCATACTTATGAA	S100738500
900097-2	E9	83540	NUF2	CAGGAGCTACAACAATCTACTA	S100140630	CACAGTAATTTGAGGATTGCAA	S100140637	AGCGATCGGCTGAACGTTATA	S100140644	AAAGATCGGTTCCGCAAGCTTAA	S103032141
900097-2	E10	1786	DNMT1	ACAGGTGCTCATGCTTACAAC	S100300062	CCCATTGAGAGCTAGACATCAA	S102663409	CGGGAAGTGAATGGACGTTCTA	S102663416	CCCATCGGTTTCCGCGGAAA	S102663419
900097-2	E11	14	AAMP	GAGGAAGAGATACTAGTTAA	S100289051	CTGGATGTGGAAAGTCCCGAA	S100289065	CTGGACTTTGGCCCTCAGCAAA	S100289072	CCCATGTGAGTTCGGAATCGGA	S103188815
900097-2	F2	5202	PFND2	CTGGTGGAGCGCAACTGCTCAA	S100682850	CAGCGAGGCGCTCGCATCCAAA	S100682857	AAGGAGGTAGATGAAACCTCGT	S100682864	CACAAAGGAGGACGATACAGAA	S103155971
900097-2	F3	1117	CHI3L2	CAAGGTTTATCATCAAGGACAA	S100345849	AACCAAGAATCCCCAACTGAA	S100345856	ATGATTGATAACAGCTATCAAC	S100345863	AGGGCCAAAGCTCCTACTACAA	S104231626
900097-2	F4	8661	E1F3A	GAGGATCTAGATAATATTCAA	S103019107	CAGGAACATGAACAAATCAAA	S100377678	TTGGCTTGAAGTAGAATTTAA	S100377678	TACGAGGAACAGGAATATAAA	S102656752
900097-2	F5	5914	RARA	CTCCACCAAGTGCATCAITTA	S100019369	CCACATCTTTCATCACCAGCAA	S100019376	CTAGTGAGATCTACTGGATATA	S103062318	CAGGAAATGTTGGAGAACCTCA	S103068821
900097-2	F6	54971	BANP	CACITGTAATTTATGCAITTTCTA	S100310268	TGCGATGATGTTCGGGAACGCA	S100310275	TGCTATGGTGTTTATAACAAA	S100310282	CCCGAACAAACACGACGAGATA	S103184167
900097-2	F7	50640	PNPLA8	CTAGATGAAAGTCGAAATGAA	S100448056	AAGGGTGTAAATACATAGAA	S100448070	CACAAGATCTTATAACCAAAA	S100448077	AAGGTCGTGTTTGAAGATCAAC	S102657487
900097-2	F8	10581	IFITM2	CAGCATGAACCACATTTGCGCAA	S100446012	CAGCGATAGATCAGGAGGAT	S100446023	TCCCACTACTTACTTCTTCCA	S103231263	CTGGTCTGCTGTGACTTCAA	S102429705
900097-2	F9	3685	ITGAV	TAGCATGATGTTTACAGGAATA	S100034342	CACATACATGATACCATCCAA	S100034349	CAGGCAATAGAGATTATGCCA	S103070165	GAGTGCAATCTTGATGCATGAA	S103104374
900097-2	F10	8662	E1F3B	CGGGAAGATTGAACATCATCAA	S100377825	TTGCGTGATTTGTATGGACAA	S100377832	CAGGTTTGAACATGGAAATAAA	S100377839	CACGTTCTTCCATATTCTGAAA	S100377846
900097-2	F11	10578	GNLY	CAGGGTGACCTGTTGACCAAA	S102658239	CAGAAATTTTATCAGGAGGATA	S102658246	CCAGGGTGACCTGTTGACCAA	S102658253	ACTAAGAAGAAATGGTGGAATA	S102658260
900097-2	G2	8993	PGLYRP1	GAGGTCCAATGTTGCTGCTCAA	S100072261	CAGGATCTTGGGCAACTACAT	S102634352	CTGGTGGCAGCTGGGCTACAA	S102634359	TCAACTCTCTGATTTGGAGAA	S103107853
900097-2	G3	64231	MSA46A	AAGGGCTGATGACTTTTCAGAA	S103036054	CACATCTGCTATAGCTGTAA	S100365685	CACGCAAGAAATCAAGTTTAT	S100133364	ACCGTTGATGGGACTGAGAAA	S102645181
900097-2	G4	10081	ACTL7A	CTGCTCGGAGATGTTCTTCAA	S100291438	CAGCAAGAACTCTAGATCTCAA	S100291438	CAAGTGTGACATCGCGCACTAA	S100291445	CAGCTGGGCTCTCACACACCAA	S100291452
900097-2	G5	5494	PPM1A	AAGCGTGATTTCAAACCCATA	S102659258	TTCCATGAGTATGTCAGGTAA	S102659265	TCCGCTGGAGAAAGAACGAAT	S103115203	ACCTAGAGGATCAACAGATAA	S103040625
900097-2	G6	6261	RPL37	TCCGTGAAGGAACAAACCTCA	S104264176	AAGGTGAGTCTAGTAAAGTAAA	S104271127	AAGGAACAACCACTTAAACCCA	S103131856	CTGGGCTAGCTTCTATTCAGA	S103213140
900097-2	G7	3596	IL13	CAGCATGGTATGGAAGCATCAA	S100033831	TTCAATTGACTATCAAACTGAA	S100033838	ACAAGTGTGTTTCTATGACTA	S100033845	CAGCTCTCAGCACAACGAGTAA	S100033852
900097-2	G8	6587	SMARCA4	CCGCGCTACAACCAAGTGAAA	S100047579	TCACCTGGATGTCAAAAGCTAA	S100047586	CCCGTGGACTTCAAGAAGTAA	S102630208	CTGGGCTAGTCAGTTTGACAA	S100389984
900097-2	G9	10579	TACC2	CTGTATTTCCCTTCTAAATAA	S100738395	TGGATTTAATATGAACATGTA	S100738402	CACCTTTGTAAACGAGACCAA	S100738416	GAGCCTGGAGCAAGAAGATAA	S103216570
900097-2	G10	10370	C1TED2	TGGAAATCTGCTACGTGGCAA	S100084252	CAGATTTACAGAGTGAAGGAAA	S100084266	CTCCCTTATGATGTTGAATAA	S100084273	CACAGCTCTCAACAACGATAT	S103063102
900097-2	G11	6830	SUPT6H	TAGGAGCATCTTTGAAATGTA	S100736575	CAGCACAATTCAGAAGATCAA	S100736582	CAGGACAATTCCTCGAATCTA	S100736589	TCAGTGTATGCTAGGCAACAA	S103230171
900097-3	B2	80326	WNT10A	CTGAGCTGAAGTAATTTCCATA	S100763350	CATGGGCAATAAACAGCTAAA	S100763357	ATCCACGAATGCGCAACCAAA	S100763364	CAGGCTCATCCGCGCCACAA	S104312742
900097-3	B3	54700	RRN3	TAAAGACACATTTACATATA	S100708330	TCCGGGTTTTGGTGGAAAGTAA	S100708337	AAGGACATATGGAAGATGAA	S100708344	CAGGCACCTGATCCCACTCTTT	S103194296
900097-3	B4	6867	TACC1	AAGGCTCAGACTTATTAATAA	S100738367	CAGAGAAGCAAGAAATTTGAA	S100738381	CAGGAGATATGAGAACCTGAA	S100738388	CTCGGCAGCTCCTCGGAAACAA	S103204635
900097-3	B5	4001	LMBN1	AACGGCGCTGGTAGAGGTGGA	1022061	CAGCTTTCTTAATCTACAGAA	S102656248	TCAGTTTATAATATACTCTAA	S102656255	CAGGAGAGGAGGTGTGCTCAA	S102656262
900097-3	B6	3073	HEXA	CCCCAACAACCTTTCAAATCCAA	S100011039	AAGGCTCGGGAATGAACACTTAT	S103046029	CAAGGCGTGGTATATGGA	S103054562	CCCTGTGAGTATCAACCGTATA	S103079622
900097-3	B7	7316	UBC	GAGGTTGATCTTTGCGCGAAA	S100754271	GAGGTTGATCTTTGCTGGGAA	S100754278	AACGTCAAAAGCAAGATGCCAA	S100754285	ATGCTGTGATCGTCACTGGA	S103048423
900097-3	B8	5092	PCBD1	ATGGTTTAAACGTGTACAACAA	S100006139	CTGGCCAGCTCTCATCGAACAA	S100006146	ACCACCATCTCAATGGTTTAA	S100006153	AGGCGGTGATGCGATCTTCAA	S100006160
900097-3	B9	6651	SON	ATGATGTTGATTTATCTTTTAA	S100729246	AAAGATTTCAATCTTGCTTAA	S100729260	CAGCGCTGGAACTCTTATAAT	S103171861	TAGGCTTCTTGGTGTAGTAA	S103229009
900097-3	B10	9132	KCNQ4	CGCGCATCTCTGAGACTCAAA	S100067186	CCGCTCCATCAGGATTTCTCAA	S100067193	CAGCAATTACATTGACAACCAT	S100067200	CTGGTACTACTTATGACATAT	S100067207
900097-3	B11	64783	RBM15	AAGGTGATAGTTGGCGCATATA	S100699475	TTGCGTGATGTAAGTGTGAAA	S100699482	ACCCCGCAACATTAAGGAGTAA	S100699489	CCGGAAGCTCTTCTTGGGCAA	S100699496
900097-3	C2	5888	RAD51	AAGGGAATAGTGAAGCCAAA	S102663682	CAGGATAAAGCTTCCGGGAAA	S100045010	CACCTTCTAAATTAATGGTAAA	S102629837	CACGTTTAGAGCAGTGTGGCA	S103061338
900097-3	C3	7123	CLEC3B	CAAGAAGATGTAAATGCCAA	S100748559	CTGCCAGTTCCGGGATCGTGA	S100748566	CAACGGCAAGTGGTTCGACAA	S100748573	CTCGGAGAAGCAGCGCGCTGTA	S100748580
900097-3	C4	2524	FUT2	CTAGCGGCTAGCGAAGATTCAA	S100010892	CACGGGCGGAGACACCATCTA	S100010899	CACCATCTACCTGGCCAAITTA	S100010906	CAGTGTGAGCTCAACATCAA	S100010913
900097-3	C5	9024	SART1	CATCAACCTTCATATTAAATAA	S100710787	CCCGTGTACAGTAGCCACGAA	S100710794	AAGGAGAAGGACGCGCTACAA	S100710801	CAGCTCAGGAGAGACTAACAA	S100710808
900097-3	C6	5456	POU3F4	ACAGTTCGCCAAACCAATCAA	S100006748	TGGTCTTGAATCGAAGACAA	S103021214	CAGAAACTTCCCAAGTGAT	S103062675	CCGACAGCAATGTACAAGAT	S103077410
900097-3	C7	6883	TAF12	TTCCAATTTCTCATCCATAA	S100738598	CAGGGAATGGACAGCAATGTA	S100738615	CCAGAATAAAGAGTTTATTA	S100738612	CAGTATTGTACCAAGAAGAAA	S103177167
900097-3	C8	11096	ADAMTSS	CAGTGGTGACCTTGCAATATA	S100093940	CCCGTTAACTTCATAGCAAT	S100093947	AACCAATTAGATGTCGGTTATA	S100093954	AAGCACTTGATTGACCCGTTA	S100093961
900097-3	C9	57292	KIR2DL5A	CAGTCTATTTTGGGAACCTT	S100126910	AGGGAGAGCTCTGATGATCAA	S102694510	CAGCGTCAATGGAACATTGCA	S102717477	CACCATGTTCGCTGTAGCTCAT	S104346776
900097-3	C10	4622	MYH4	CTGGATCATCTTTGAAACTCTA	S100652743	CTGGGTTTCACTGCTGATGAA	S100652750	CGGCAATGAGTGTCTGAACCAA	S100652757	CAACTTATGAGAAACTCAA	S100652764
900097-3	C11	10213	PSMD14	CAGGCATTAATTGACGACTA	S100081396	TTGATACTGTCTGATTTTAA	S100081410	CACAGACTTATTCTCATTATA	S100081417	CTGGTCACTTAAACCAAGCCA	S103099152
900097-3	D2	84159	ARID5B	CTGGGAGGATATGAACAATA	S100303177	AAGGATAAACTCTTAGAGAA	S100303184	CCCGCGCTCAGTGGAAACATA	S100303198	CACCTAATTTATATACAGTTA	S13162362
900097-3	D3	4849	CNOT3	CTCGGACACTGTGGAATCTCTA	S100349601	AGGCTAGGAGACCAAAATCAA	S100349608	AAGAAGAGATTAAGGAGTAA	S100349615	GACACTTCTTCTCATCTTCTA	S100349622
900097-3	D4	5865	RAB3B	CAGCACTAGACTAAACATAACA	S100044814	CGGGTGCAGAACTCACTTACA	S100044821	CCGGACCATTCAACACAGCTTA	S100044828	CAGAGAGCTCAGACTCTCTAA	S100044835
900097-3	D5	7517	XRC3	CAGCAATTTTGTCTGCAATTA	S100077112	GAGACACTTAAGGGAAATTA	S100077119	AAGCCAACTGAAATCGGTA	S100077126	CCGCTGTAATTTTGACAGCCA	S100077133
900097-3	D6	51529	ANAPC11	CCGCCAGGAATGGAAGTTCAA	S102777691	ATGAATAAACATCTCCGTTAA	S100116270	AAGGAGCAGGATCAGACGCTA	S100116277	CAGGCCCATTTGAGATCTTTG	S102642304
900097-3	D7	84365	MKI67P	ATGGTTGAAGCTGGAAGTTTA	S100646023	CAAAACAATAACCAGAAATTA	S100646037	ACTAGGTACAATGGAATACAA	S103142356	TGGATGAAGATTGACACTTAA	S103237668
900097-3	D8	10771	ZMYND11	CCGGATGAAGTCGGACACCAA	S100090412	ACAGAGCGTGTGTTCCGAGAA	S103037706	ACCGAAGTATTAAGAGTTCTA	S103039694	CCACAGTAATGAGCAGCTAA	S103074470
900097-3	D9	5877	RAB1F	CTTCTCTCGCCGACAGCTTTT	S100301595	TAGAAGGAAGTTTATATATA	S102651075	CAGTCTCATCTCCAAAGATTA	S102651089	CAGTTTGATCTGAAAGAAATA	S102651096
900097-3	D10	54361	WNT4	CAGCAAGGCGCGATAATTTAA	S100139160	CAGACCTTAAGGTGGAGTAACA	S100139167	CTCATGTTTATTTTGTCCGAA	S100139174	CAGCGCAAGCTCGGAAGTCAT	S103054219
900097-3	D11	1203	CLN5	CACGTTTAAATATGTAATGTA	S100348425	TAGGATTGCTGTAAAGATGTA	S100348432	ATGGTTTCATATCAGTTATGTA	S100348439	CAGAAGTACATTAACCTGGCAA	S103048446
900097-3	E2	145282	MIPOL1	CAGGAGCTTTCATCATGTGAAA	S100645799	AAGAATCTAATGCTAACAA	S100645806	CACAGTATCTTGTGAACAGAA	S100645820	CAGGAATTAAGTCAAGGATATA	S103173716
900097-3	E3	648	BM11	ATGGGTCTATCAGCAACTCTTCT	S103051874	CAAGACGACAGCAACTCTGAA	S103053610	TTGGATCGGAAAGTAACAA	S100073311	CAGAGTTCGACCTACTTGTA	S100073325
900097-3	E4	6191	RPS4X	CAGATCTTTGTACGTAATTTAA	S100707875	CGGGAGAGAAATTTCCGCTGTA	S100707896	CTGGAGGTGCTAACCATAGGAA	S103210851	AAGGTTCCGCTTTGCTGTACAT	S104136062
900097-3	E5	412	STS	TAGATTAAATGACGTATACATA	S100007707	ACCCTACACGACCCACCTTTA	S100007721	CAGCATCAAGGCCCAACATCA	S100007728	CGGAAGTAAATGGGATCTATA	S103085628
900097-3	E6	55743	CHFR	AACCAAGAGTTTGACGATGGA	S102778125	AACAGTGTATTAACAAGCTGAA	S100121107	TCCGTTGGAGCGGATCTGTAA	S100121121	TCACCAAGCCCATGAAATTTAA	S100121128
900097-3	E7	8945	BTRC	CAGGATGAGCAACAACAGTAA	S102632322	CACGTTGATTCACCATTTGGA	S103061807	CTGGTTTTCAGGTGGAACCTTA	S100058072	CTGAGGCGAGATGACATCTAA	S100058079
900097-3	E8	10524	HTATIP	CACCACATTTGCTGCTCCTCTA	S102780897	CGGGCGGAACCCAGGACAAGAA	S100088053	CACCCGGATGAAGAACAATTGA	S100162981	CTGATCGAGTTACGATATGAA	S102637383
900097-3	E9	4594	MUT	CTGGGCTCACTTAAATAGAGAA	S100005565	AAGAGAGATACTATGACATTA	S100005572	AGGGAATACCTAAACTTCGAA	S100005579	CACGTTGACCATATCTTACCA	S103061639
900097-3	E10	1184	CLCN5	ATTCCTTGTTCTGTTTACAATA	S100001659	TAAGTTGGACTCTGGTTATCAA	S100001666	CACCGAGAGATTAACCAATAA	S100001673	CAGGTTCTGTTAGCTGTTTGA	S100724282
900097-3	E11	64147	KIF9	CGGAATTTGGTTTATAGAGACA	S100133280	AACAGACAGACTGGTCTGTTTA	S100133287	CACGCTCTGAAGGACTCGTTA	S102649850	CCCGGACCTTATCAGAGGAAA	S102649857
900097-3	F2	6227	RPS21	TAGGAATTTGTCTATAGATAA	S100707483	CGGCGAGTTCGTGGACCTGTA	S100707490	CAAGGTACACAGGCAGGTTTAA	S100707497	CGGGAAGTCTGCTCGGTGACAA	S100707504
900097-3	F3	2821	GPI	CCGGCTCTGGTATGCTCCAA	S102664011	GAGTTTGGAAATTGACCTTCAA	S102664018	ACGGAAAGGTTCTGCATCACAA	S100003738	GAGCTTGATGGCAGTGCTCAA	S103103268

900097-3	G9	7067	THRA	CCCGATGACATTGGCCAGTCA	SI00049798	CAGCGAGTTTACCAAGATCAT	SI00049805	TCCACCTATTCTGTCAAAATA	SI03114041	TCGCGGCACAATCCAGAAGAA	SI03116470
900097-3	G10	8239	USP9X	CCCGCAGATAGCACAACGATA	SI00066584	CAGCTAGTATTTGAGGCCAAAT	SI00066598	CCGCGTCGCAGTGGAAAGTGTA	SI00066605	GACGATGTATTCTCAATCGTA	SI03101973
900097-3	G11	8846	ALKBH1	CTGGGTACCAGAAATACGCAG	SI00294595	CACAGTGGTGACATCATGATA	SI00294602	CTGGGTGAACAGTGCCTTAA	SI00294609	CTGGGTTCTCTCTCAGAGCAA	SI00294616
900097-4	B2	10885	WDR3	CCGGGATGTTATCGGGCTCAA	SI00091868	AAGAGTGTGGCTCATCTTAA	SI00091875	CCAGCGGGTGACTAATATAGAA	SI00091889	TCCGCTGATAGGAATGTGAAA	SI02638055
900097-4	B3	9324	HMGN3	GAGGGCAAAGATGGATCCAAA	SI00061579	CTGCTGACTATTGTGGTTTA	SI00061586	AACCTGAACCCAAACCAAGAA	SI03029054	CAGAGGTGCTAAAGGGAAGAA	SI03064229
900097-4	B4	8643	PTCH2	CCGCACCTGGCTGCACATATTA	SI00055230	CTGGCGGATGATGACAGGTGAA	SI00055237	CAGGTACTCTCCCTGTACGA	SI03071796	CCCGGATATCCAGTGGACCAA	SI03078369
900097-4	B5	29920	PYCR2	AAGAGTGTTATTTAATGCTAA	SI00696501	CATGGATAGACTGGGTTTATA	SI00696598	CCGGCTTTCTCTGAAATGTGA	SI00696605	CAGCAACAAGGAGACGGTGAA	SI03069612
900097-4	B6	5742	PTGS1	TAGTCCCATGGAGTTCAACCA	SI00301511	AATACCGCAACCGCATTTGCCA	SI00301518	AATTGCCATGGAGTTTCAACGA	SI02655016	CTCGTCTTGGGAGTTTGTCAA	SI03100132
900097-4	B7	10531	PITRM1	CATTGTCTTCACGTACGGTAA	SI00108647	CCGGTGAATTACGTGGGTGAA	SI00108654	CAGGTTGAAAGTTTCCCGATA	SI00108661	TCGATATTAGAACCCACATA	SI01008668
900097-4	B8	9499	MYOT	CAGCAAAATATTAGCACTTAA	SI00752899	CAGGTTATAAATTAGTATCAA	SI00752906	AAGAGTTACTTTACTGATAAA	SI00752913	CAGGAACAATCATTTATAGTA	SI00752920
900097-4	B9	3442	IFNA5	CAGGAGGAGTTTGTATGATAAT	SI00033474	ATCCTTCTCTTTATCAGCAAA	SI00033481	ATGCAGGAGGTGTAGAGTGGAA	SI00033488	TGGGATGAGACACTTCTAGA	SI03025225
900097-4	B10	672	BRCA1	CAGCAGTTTATTACTCACTAA	SI02654575	CAGGAATAAGGCTGAACATAGAA	SI02664361	ACCATACAGCTTCATAAATAA	SI02664368	AACCTTATCGGAAGAAGGCAG	SI00299495
900097-4	B11	3978	LIG1	CCGGACGTTTGAGAGAGTCGA	SI02663542	CCCGCTCATTTTCTCAATAAA	SI02757482	CAGGCTCTGACCCCTGAAGATA	SI00050561	CCCTGTGTATCCGGGAAGCAAA	SI00050568
900097-4	C2	10979	FERMT2	AAGGATGGCTTGATTCTCTCAA	SI00686777	ACCGTAGAGTTTGCAGATGAA	SI00686784	TCGTCGGTGTGCTGATTGTTT	SI04331768	CTCCAGCGGCATAACAATATT	SI04376029
900097-4	C3	1840	DTX1	CACCAAGAAGAAGCACCTTAA	SI00374577	GTGGGAGTCAGCCAAAGATTTA	SI00374584	CCGGGAAGAGAGTTCACGCCAA	SI00374598	CTGCTACCTCATCTACTTCAA	SI03095743
900097-4	C4	183	AGT	CAGAGTCTACCCAACAGCTTA	SI00000350	ACCCAGCACGCTGTTTGTGAA	SI00000357	TCCTGGTGTAGTGTCTGTAATA	SI00000371	CAGGCTGTACACGGCTCGCTA	SI03070921
900097-4	C5	3265	HRAS	CCGGAAGCAGGTGGTCATTGA	SI02654806	CACAGATGGGATCACAGATAA	SI02662030	AGGAGCGATGACGGAATATAA	SI02662576	CTGAGGAGCGATGACGGAATA	SI04435368
900097-4	C6	26190	FBXW2	CAGCAGTCGACACAATCATTTA	SI00097706	CAGAGTGTATGCACCTTTACTA	SI00097713	ACGGAATGGGTGCTCAACAGTGA	SI00097720	CCAGTGGGACTTGTCCGAGTTA	SI00097727
900097-4	C7	7480	WNT10B	ACGAATGCGCAATCCACAACAA	SI00051800	CAGGATCGGGTGCAGGGCCAAA	SI00051807	AAACCTGAAGCGGAAATGCGAA	SI00051814	CAGGCAACTGTTTGGAGCCATA	SI00051821
900097-4	C8	3646	EIF3E	AAGCTGGCCTCTGAAATCTTAA	SI02619811	CCCAAGGTCGCGCATATAATT	SI02662499	CAGGATGTGTAGGATGTCTCTT	SI04228644	AAGGAATATTATCAAGATGAA	SI00377755
900097-4	C9	51514	DTL	CCGAGTCTACTGGGTATAACAA	SI02777684	CTGGGATACCCAGGTGCACAA	SI03098718	TGGCGTCTGAAATGAGGCTTAA	SI03120334	CACCTTACGCTTAACTGAATA	SI00116221
900097-4	C10	898	CCNE1	AAGGCAAACTGACGCGTTTTTT	SI00299691	CAGGATATCACTGTGCGCGACA	SI00204204	ACCGGTTTATCCCAAACCTCAA	SI02625569	AAGCGCCCTTAAGTGGCGTTTA	SI03035319
900097-4	C11	9412	MED21	CAGTTTATATTTGCCAAATAA	SI00736631	CACAATTAACAGAAACATTTAA	SI00736638	CTGGAGGATGTGTTTATATCGA	SI00736645	CTCGTGAAGGTGGGAATTGAA	SI00736652
900097-4	D2	6756	SSX1	TCGTTATAATTATGATGACAAA	SI00733887	AACGGTGAACACTTGAGCGCTCA	SI00733894	CTGTTTGTCTCTGAAGTGAG	SI00733901	AACAGATGGGAACAACCTGCA	SI00733908
900097-4	D3	59277	NTN4	CAGCATGACATTTAGCAGTAA	SI00662235	AAGGCATCTCTGTGAATGAAA	SI00662242	CCGAGGAAGGCGCAACTATTAA	SI00662249	CTCAGGTAATGCGAATGTAA	SI00662256
900097-4	D4	9266	PSD2	TCGGTTTATCTCCACAGACAA	SI00612292	CACGCTGTGTGTAATCTTATT	SI00612299	ATGAGGAGACGGCTGCACTGAA	SI03050894	CATCAAGCACTTCTGCAACGTAA	SI03072629
900097-4	D5	10565	ARFGEF1	CAGGATTTATTAGAATTGTT	SI00300825	TCCGGTATTACTGAATAGAAA	SI00300832	AGGGATGATTTTATTATATAA	SI00300839	CACAGTTGTGATGATCACTGAA	SI00300853
900097-4	D6	2057	EPOR	CCAGTGCAGACCTCAAGACTTA	SI02780351	CAGATATGATCAGGATGCAATA	SI02780400	CCGCGCGGCTCTGAAGCAGAA	SI04435060	CAGGAGGTGTGTGCTGAGCAA	SI00002408
900097-4	D7	2107	ETF1	CAGCATGATATCATTGATCAT	SI00381332	TCGGTGATATATTTGTCATTA	SI00381339	AGGGAGTATGCTCTTAATGTA	SI00381346	TTGGAACTGCATCTAACATTA	SI03244416
900097-4	D8	9509	ADAMTS2	CAGCTGCACCCCTGAACCATGA	SI03068310	CTGGCGCTACCTCCAGCAGAA	SI03098935	GAGGAGGAGTGTCTTGAGCTA	SI03103555	GGCGATCATCTCTTGAGCTA	SI03105368
900097-4	D9	3749	KCNK4	CAGCGCTGACCTTCGTCAGAAA	SI00070868	ACCCATGTAICTGCAAGTCTGA	SI00381948	AGAGGGTATGATGCGAGAGGAA	SI03042354	CCGGCGCGGAGGTGAGACAGAA	SI03082233
900097-4	D10	6134	RPL10	TGCGCTTATGTCACTGTGCTA	SI00083678	CAGAAACAGGTTGACAACTCA	SI00083685	CAGCAACCACTTGCAATCCCA	SI02636473	ACCAAGTCTGAAGTGTGATGA	SI04380957
900097-4	D11	7514	XPO1	CCCAATTGTAAGCGCACTTCAA	SI00051856	TACATGTTACTCCCTAATCAA	SI00051863	TTCTCAGAATATGAATACGAA	SI03023342	ATGGTTAGTCCGAATGCTAA	SI03052210
900097-4	E2	1719	DHFR	AACCTCCACAAGAGAGCTCAAT	SI00299992	TACGGAGAAACTGCAACTGAGA	SI00015729	TTAGGTACCGGAGAACCTGAA	SI00015736	ATGGTAAGTCAAGGAAGGAAA	SI00015750
900097-4	E3	4599	MX1	TCCGTTAGCCGCTGGTGATTTA	SI02781093	TAAAGTCAAGACACTCATCAA	SI00038185	TAGAGCTTACTTTCGAAGAAA	SI00038192	AGGAGACTCACCGAGATAATA	SI04435956
900097-4	E4	7321	UBE2D1	TCCACTGGCAAGCCACTATTA	SI00302085	CAGAAAGATTCAGTGATCTA	SI02651201	ATGGGTGTAGTCAATTAGCAA	SI02651208	TAGTATATTATTATATAAGCTA	SI02651222
900097-4	E5	26091	HERC4	GAGGGAATTATTGGATCTCTAA	SI00111531	TAGAAATACTACATAGGGTAA	SI00111545	CAGTGTGCTGTGTGTTACTAT	SI03072538	TAGACAGCTAGTGCATGAAA	SI03111528
900097-4	E6	2736	GLI2	TAGGGAGCATTTGGGTTTGAA	SI00074844	CCCGGACCCAGCATGCTCTCA	SI03078215	CTCGCTAGTGCGCTCATCAAA	SI03091445	TCCCGGGCTCATAGTCCGCAA	SI03108847
900097-4	E7	8288	EPX	CCCGGAATTTGGCAGCAGCTTA	SI00010668	AACGCTCAGGATGCCATGTGA	SI00010675	CTCGAATTATATGTGACAAATA	SI00010689	ACCGGCTGTTTTCGCAAGTGGA	SI03040247
900097-4	E8	4928	NUP98	CTGGGATAGCACTAACATATA	SI00115332	CAGTGTATTACTGCTATGAAA	SI02635115	AACCTTATTGCCAAACCTATT	SI03028578	CTCACTAAGGTTGGTTACTAT	SI03088491
900097-4	E9	9351	SLC9A3R2	CGCGCTCTAATAATTTGCAAT	SI00068376	TGGGCCATCGCGAGTCAACAAA	SI00068383	CCAGGCGGTGCGAAAGGATCAA	SI00375562	CGCGCCACAGATGAGCTGGAA	SI03084977
900097-4	E10	162466	PHOSPHO1	TACAACATAAAGGAGGTGAA	SI00161168	CGCCCAACATGTGCAACGACAAA	SI00161175	CCGTCCCTATTCTATTCAAGTTA	SI00161182	TCGGGTCCGGACAGCCAGTAA	SI00161189
900097-4	E11	5934	RBL2	ACCCTATATTAGGAACATTTA	SI02664473	TGCGGAGATGTTTACTATATA	SI02664480	GTGCAAGGATTTGCCAATGTGA	SI00079541	CTGATGAGTTTACAGCTTGTTA	SI00079548
900097-4	F2	112950	MED8	GCCGAACAAGCAGCACTTTTAA	SI00019775	AAGCAGCTTGAGGCATCTATTA	SI03032883	CAGATCCAGAGCTTGAAATATA	SI03064691	CAGGCAGGTCAACCAAGGAAA	SI00019768
900097-4	F3	10694	CCT8	AAACGTTGGATTAGATATTGA	SI03026212	AAGGTGATGTAACTATGCTGCA	SI03036460	TAGAGTGGATCAGATCATCAT	SI03110681	TCGTACCTCCATATTAGTAA	SI03117261
900097-4	F4	2734	GLG1	CCGGATTGAGATGTGGAGTTA	SI00097993	CCGCTGTGAGGCAGATCTATA	SI00098000	GTGGTGGAGTGTAGAGATATGA	SI00098007	CAGCCTACCGCAGTGAAGAA	SI03060218
900097-4	F5	84925	DIRC2	CAGAAATTACACATTAAFTTA	SI00364133	CACAGACTTGAAGAGTTTTAA	SI00364140	CTGATTACTTGAATTATGAA	SI00364147	CGGCTCTAAGATGCATACCTA	SI00364154
900097-4	F6	931	MS4A1	TTCAATCATGGACATCTTAA	SI00131572	TGGGCTTAAGTAAAGACTCTT	SI00205337	CAGGAACTCTCAACCAATGAA	SI03069059	CCCATCTACCCAATCATGTTA	SI03077123
900097-4	F7	65193	SLC2A1	CAGCGCTTGAATCGCATTAAT	SI00089257	CAGACACTAAGTTATAGTATA	SI00089271	CAGCTGGAATGAGACTTCGAAA	SI03068436	CTCCACGAGCTTCTCGAGTAA	SI03089401
900097-4	F8	7262	PHLD2	AGGTACGTGTACTTCAACCATC	SI00301182	CGCGCTCGGCAGCATGATGAAA	SI02225636	CTGGTTCTTGTGTAGTCACATA	SI02225643	CGCGCTTAAGTTATTGGAATA	SI00050561
900097-4	F9	25803	SPDEF	CCGGAATGGATAAATAAAGATA	SI00731311	CAAGGAGAAGGCGATCTCTCAA	SI00731318	CCGCTTCAAGGTGGTGGCTCAA	SI00731325	CAAGAAGGGCATCATCCGGAA	SI00731332
900097-4	F10	10291	SF3A1	CAGGATAAGCAGGAATTGAAA	SI00082194	CGCAAGGATTATGATCCCAA	SI00082201	CAGCATGTAGGTAGCGCTCTCA	SI00082208	CTCATTCAGGAGCGCTATGAA	SI03089233
900097-4	F11	55450	CAMK2N1	AGAGCGCGGTTGTTATTGAA	SI02224873	GGGTTGTATTGAAAGATGAT	SI02224880	AAGGCACCCTCTGGTGTCTAA	SI03035235	CAGCTATTGTGCCCAAGTTAA	SI04440047
900097-4	G2	8170	SLC14A2	AAGGGCATCAATCAATAACAA	SI00720111	CTCGGAGAAGTTAGACTACTA	SI00720118	CAGGAGTGATTTTACATCGA	SI00720125	AAGCCTATCTCTTAAAGAGAA	SI00720132
900097-4	G3	775	CACNA1C	CTGGTTTGGTTCGGTTTACTA	SI00373176	ACCGGAGGTAACCCAGCTGAA	SI03039862	TGGGTTAGCATTTGTGATATA	SI03107167	TCCAGGGATGTATGCTGTGAT	SI03113768
900097-4	G4	1659	DHX8	CCGAGAGAAGTGGGAGATCA	SI03019373	CCGGGAGAGGAATAAAGTGAA	SI00363909	CTGGAAGAAGATTAACACCCAA	SI00363916	CAGCAGGTTGCTTATATCCAT	SI04241797
900097-4	G5	8228	PNPLA4	AAGATTGAGAAATAGGCCAA	SI00688303	ACCAAGTAGCCTAGTAATAAT	SI00688310	AAACATGTAGTTTAACTCTTAA	SI00688324	CCAGTCTTAGGAGATTATCAA	SI00688332
900097-4	G6	9138	ARHGEF1	CAGCAGCTCTGAGAAACGGCAA	SI00302680	CAAGAAGAAATTTGGTCCACGA	SI00302694	CACCCATCACAAAGCGTCTTCA	SI03161900	TAGGGCTGACCTCATCTCCGA	SI03228771
900097-4	G7	200081	TXLNA	CCGAGCCTAGTGGCAAGGAAA	SI00159467	CGCGAGGAGATCATCGACAAA	SI00159474	AGCCGCAACTGGAAGACATA	SI03043376	CAGCAGGTTATTCCACCAATT	SI03066903
900097-4	G8	8664	EIF3D	TCGGAACATGTTGCAAGTCAA	SI00377797	CAGTTTGGTGGTGGAGTGCAA	SI00377811	CAGGAGCCACATCAACCAAGTA	SI00377818	GCCCTAGAATACTACGACAAA	SI03219741
900097-4	G9	8668	EIF3F	CATGATTAAGTATAAACCGGAA	SI00377713	AAGAATAAATTTGGTTGGTA	SI00377720	AAGGACCCATCTGCTCAATGTA	SI00377734	TCGGAGCCAGATTGACAACAA	SI04162368
900097-4	G10	51327	ERAF	CTGGATGAACCTTCTACATCAA	SI00380793	AAGGCAAGTGGCTCTTCTTAA	SI00380800	CAGGAGCTTCTGGAAGTCTCA	SI00380807	CCGACAGTGTGAAGGAGTTCA	SI03080814
900097-4	G11	1374	CPT1A	CAGCAAGCACATCGTGGTGTA	SI00029407	CTGGATGGGATGTGTCAGAT	SI00029414	AACGATGTACGCGAAGATCGA	SI00029421	AGGCTTCTTGTCGAGCTTGA	SI03044202
900097-5	B2	29929	ALG6	CGCCTATGTTTGGTGATTAT	SI00101598	CCGGTTGATCGTGGATTATTT	SI00101605	ACAGCTTATCATGATGTTCTCTA	SI00101612	AGGCTTATTTCTTATAGACTA	SI00101619
900097-5	B3	4839	NOL1	CAAGAAGGATCTGGGCACTTTA	SI00659974	CAGGAAATCTTGAACAGCGCA	SI00659981	CAGATCAATGTGGATGAGGAA	SI00659988	AGCGGTTGCTGCCCATTGAAA	SI03131121
900097-5	B4	825	CAPN3	ACCATCGGTACGCGACAGAAA	SI03038798	CCACCTCTGGAAACAGATTAA	SI03074554	CCGAGCGCGCTCGGTTCTGAA	SI03080147	TAGCATGATTTCGCGTCAATGA	SI03111003
900097-5	B5	32	ACACB	CCCGCTGTGCATAGAAATGTGA	SI00021798	TACCGTGGAATACCTCATTTAA	SI00021805	AAGGATCGATCCAGCTTCAAA	SI00021812	AAGGGTTGCGTGAAGAACGTTA	SI00021819
900097-5	B6	8532	CPZ	TACGGCAAAGCTCATCAAGAAA	SI00054229	CCGGATCTCAGTCAAAAGGCAT	SI00054236	CGCGCAGAACTGGATCTGAA	SI00054243	CCGCGAAGCAAAAGGACATCAT	SI00054250
900097-5	B7	29028	ATAD2	CTGTGACTTTAGGCACATTAATA	SI00103131	AAGGCTATTATAAAGATCGAA	SI00103138	AGAATAATGACAGCGCTTAA	SI00103145	CCGGATAAAGAAGAACCGGACA	SI02640232
900097-5	B8	22938	SNW1	AACGTCCTGGCTGCTGATGGA	SI00301812	CCCGATGGAAGAAGCTATTAA	SI02655478	TCGGATGGTAGAATGCGAAG	SI00098609	CACAGGCTCTCTCCAAGTGAA	SI00098616
900097-5	B9	3851	KRT4	AAGGTGCGAGTTCTTAGAGCAA	SI00464828	CAGGTTGAGAATGCCCTTAA	SI00464835	TCCATCTACATCAGAACCAAAA	SI00464842	CAGTCTTAATGACAGAGATCAA	SI00464849
900097-5	B10	10376	TUBA1B	TCCATCATATCTCAAAGTAA	SI00084308	AAGGAGAGGAATACTAATTAT	SI00084329	CCCGCTAGTGTGCGTTACTTAA	SI02636627	CAGCTTAACTGACAGAGCTTAA	SI02636634
900097-5	B11	30837	SOC57	CGGAAAGTTCTACTACTATGAA	SI00729218	CCACACTAGAATGAGGACATGA	SI00307440	GAGAGGCCAATTGACCATCCAA	SI03102687	TCGCCATTACAGAAATGTCAAA	SI03114356
900097-5	C2	6193	RPS5	CTCGAAGCTCTTATGCCATTTAA	SI00707980	CCGGGAGGACTCCACAGCAGTA	SI00707987	CGCGTGTGCTAGCCGAGTGTA	SI03195031	TCCGAGCTGCTGCGGCAATTA	SI03241469
900097-5	C3	8436	SDPR	CAGAGGATAAATTAAGATACTA	SI03246789	TACGTAGTAAAGTCCAGGACTA	SI04366915	TAAGCTAAACATATAAATATA	SI00713328	CCGGGACAACCTCAAGGTGAA	SI02656738
900097-5	C4	9994	CASP8AP2	CAGCTGATGTGCGGAAGTCAA	SI00097272	AACGAGAATTTGCGATTCTTA	SI00097279	CAGTGTGATCTCAATAAGGAA	SI02638937	CACATACGTAGATCTTAACGAA	SI03056501
900097-5	C5	10135	PBEF1	TACAAGGTTACTCACTAATTTA	SI00080836	ATGGGTTGCGATCAATTTCTTA	SI00080850	TTGTTGAGTCTGGTATATCCAA	SI03025897	CAGAGTGTACTGGCTTACAAA	SI03064432
900097-5	C6	81488	GRINL1A	CCGCGATCATCTGATACCT							

900097-5	D11	9960	USP3	AGCGCTCTAAGAATCAAGAAA	SI00089432	CTGGATCGGATAAACCTTTAAT	SI00089439	CAGAAGTAAGCGCTCTAAGAA	SI00089446	CAGGGCGGTTTCAACGGTGTT	SI03071432
900097-5	E2	10712	C1orf2	CCCAATTGCCTGCTCCATTAA	SI00323120	TTCAGGGGACCTTTATACCAAA	SI00323134	CACACGCTGTCTGTGACTAAA	SI04435228	AAGAAGGAATCGGATATAACA	SI00003276
900097-5	E3	6203	RPS9	ACGGCGTCTGTTCGAAGGCAA	SI00708071	CCCGCGGAGACCCCTTCGAGAA	SI00708078	CCCGGGCCGCGTGAAGAGGAA	SI00708092	CGGAGCTGGGTTTGTGCGCAA	SI04359782
900097-5	E4	3309	HSPA5	TAGGGTGTGTGTTCACTTCA	SI02780554	TGGGATAAGGAAACACTTCTA	SI02781016	CAAGCCCAATACAGCCATTAA	SI00075922	AACTGTTACAATCAAGGTCTA	SI00075929
900097-5	E5	10905	MAN1A2	TCACTTTAATTTTCATAATAA	SI00627375	CTGGCTGAATTTGGTACACTA	SI00627382	AAGACTTAATTAACATAATATA	SI00627389	AAGAATATTTATAGAATTCCA	SI00627396
900097-5	E6	2074	ERCC6	ATGGATGGTACCACACATAA	SI00002485	CAGAGCGTTTAGAAAGTGAAA	SI03064075	CAGGACTCGTGGTTCAAATTA	SI03069402	CAGGATGACATTAGCAGGTAT	SI03069934
900097-5	E7	7311	UBA52	AAACTGCCGCAAGAAGAAGTG	SI02780764	CTCCGCCAGCTTGCCAGAAA	SI00050939	CCCAATGGTGTAGAACGTTGA	SI03076255	CTCCTATGATAATCACTCTTA	SI03090465
900097-5	E8	2335	FN1	CCGGTGTATTATGACAATGGAA	SI02663997	CCCGGTTGTTATGACAATGGA	SI02664004	TACCCGAGTGGGTGACACTTAT	SI03108945	AACCGGGAACCGCAATATCAA	SI00031682
900097-5	E9	2877	GPX2	AACCCCTCGTGGTTGGTGATTCA	SI02627709	CCGCACCTTCCCAACCATCAA	SI02627716	CCGGGACTTCACCCAGCTCAA	SI02627723	CAGAATGATGGCACCTTCTCA	SI03063340
900097-5	E10	5519	PPP2R1B	CAGGAAATAACTACTAAGCAA	SI02653364	CAGAAGTAGGTCAAGATGAA	SI02653763	CTGAGCTTCGTTTGAATATCA	SI02659433	ATCGACGAGCTCCGCAATTGAA	SI03047996
900097-5	E11	80824	DUSP16	AACCCAGTTGTTACTCTCTTA	SI02759421	AAGGTTGTAGTTTACGATCAA	SI00374829	CCGGCCATTTTGGAATACAA	SI00374836	CAGGACAAAGTGTTAATTACA	SI00374843
900097-5	F2	6372	CXCL6	ACGCGTTACGCTGAGAGTAAA	SI00046669	TACGCTTCTCCTGAAGTTTA	SI00046676	CAAGTTTGCTGGACCCGGAA	SI00046683	TACCGTTATCTGTGCAGAATA	SI03109099
900097-5	F3	221150	C13orf3	CAGCTGGAAAGTATTATCTAA	SI00317940	AGGGAATATATTCAAAGTGTA	SI00317947	AAAGACAACATGAACATTAA	SI00317954	AAGAGAGTATTTCCAGAAGTA	SI04327995
900097-5	F4	10742	RAI2	CCGGAGCATAAAGTTAAAGAA	SI00697963	TAGGATGAATATTTTCACAATA	SI00697970	AAGCTGAGAATTAGGCTTAAA	SI00697977	CACCGAGGCTCGGAACATCAA	SI00697984
900097-5	F5	7980	TFPI2	ATGGTTGTATCTGAAGAATAA	SI00743519	CAGAAGAGGATCATAACTGAA	SI00743526	CAGCATGAGGAACCAATCAT	SI00743533	TTGCAATGCATAAGATATAAA	SI00743540
900097-5	F6	10426	TUBGCP3	CACGACTCGCATGGACTTTAA	SI00087465	CCACTACCTAAGAGTATTTAA	SI00087486	AAAGAGCTTATTCGACAACGA	SI03026464	CTCGATTATCATGTTGACGGA	SI03091235
900097-5	F7	11274	USP18	TAAGCGCTTCCTGGAAAGTGAA	SI00118034	AAGATGGAGTGCATATGGGAAA	SI00118041	TTCGCTTCCATTCACTGGGAA	SI03022915	CTGGATCTACGGAGTCTTCTA	SI03097570
900097-5	F8	3902	LAG3	CAGCAGCCCAGTCCAATAAAA	SI00467796	CAACGTCTCCATCATGTATAA	SI00467803	CCGGTCTTTCCCTCACTGCCAA	SI00467810	CCGCAGGCTCAGAGCAAGATA	SI00467817
900097-5	F9	8303	SNN	CAGGGCAGAGGTGAACCTGAA	SI00728203	AGGGATGTCACTCCTTCTTCAA	SI00728210	CTGCATAGACTCACTTGTTAA	SI00728217	CTGGAGGGTCATAGGCTTGTA	SI00728224
900097-5	F10	9112	MTA1	GCGCATCTTGTGGACATATT	SI02757699	CAGCATCATTGAGTACTACTA	SI00067130	TTGGACATATTGGAAGAAATA	SI00067151	CAGGGTCGGAGACTACGTCTA	SI02633736
900097-5	F11	79154	MGC4172	CCCAGTGGATTTCATGGTGAT	SI02778804	TGGGCACATCATTAAACATCAA	SI00136052	CGCCTTCAAACCTCCACGACAA	SI00136066	CAGATGTGACCTATCAAAATGA	SI00136073
900097-5	G2	55506	H2AFY2	CTCAAAGAAGATATAGGTAAA	SI00433076	CAGCTTGAAGAGACCATCAAA	SI00433083	AAGAAGGAACCTTCAAATTTCCA	SI00433090	CACAGATAGAACCCAAAGAAA	SI00433097
900097-5	G3	1312	COMT	CTGGAACGAGTTCATCCTGCA	SI00014868	CTGGCTAGCTATATTATCTTA	SI00014875	CCAGCTGAAGAAGAAGTATGA	SI03075191	CGGCCTGGAGAAGGCCATCTA	SI03086251
900097-5	G4	10346	TRIM22	ACCGCTAATGCCTTAATGAAA	SI00750708	AAGAGTGATTTCCGAGTACCA	SI03032057	CCGCATAAACGAGGTGGTCAA	SI03080644	CTCCAGATATAGACCTCAATA	SI03089485
900097-5	G5	55294	FBXW7	CCCTAAGAGTGGGCACTCTA	SI00146636	AAACATATGATGCAAGTGATA	SI03026023	CTCATTGATAGTTGTGAACCA	SI03089240	CTGGAGGCGAGGAGAACTCAA	SI03097241
900097-5	G6	2197	FAU	AAGCCACTTAGTTTCAGTCAA	SI00031122	CCGCCGTTCAAGTCGCAATAT	SI02627499	GGCCGCATGCTTGGAGGTAAA	SI02627513	AAGTGAGAGGTCAGACTCCTA	SI03036908
900097-5	G7	5713	PSMD7	AAGAATAGTTGGCTGGTACCA	SI00301483	CCGAATCGGCAAGGTTGGAAA	SI00043596	TTCCGTATTGGTCATCATTTGA	SI00043610	CACGTGACCAGTGAAATTGGA	SI03061541
900097-5	G8	29106	SCG3	AACACTGATTACTATCATGAA	SI02639749	CAGACATTGAGTTTACTTATA	SI02639756	TTCCCAAATTTCTATGCGCTA	SI03022138	CAGAGCCGTGTTTGACAAGAT	SI03064026
900097-5	G9	11331	PHB2	AACCCAGGAATTTCTCAATAA	SI02780918	CAGCCTCATCAAGGGTAAGAA	SI03066504	CTGGATGATGTGGCCATCACA	SI03097633	CAGAATCGTATCTATCTCACA	SI00096124
900097-5	G10	4809	NHP2L1	CAGCTACTCTCTATTGTTATA	SI00658539	CAGGGTGGTGGCACCGTTGAA	SI00658546	AACAGAGATGGTGGAGTCCAA	SI00658560	CAAGTGTGCTTTACTAATGTA	SI03158127
900097-5	G11	226	ALDOA	CAGGAGGAGTATGTCAAGCGA	SI03069675	CAGGCCATGCTTGCACTCAGA	SI03070340	CAGGGACAATGGCGAGACTA	SI03071005	TGCCAAATAAACAGCTATTTA	SI03118045