

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
0.GFP control	n/a	shGFP (#444)	n/a	n/a
0.GFP scrambled control	n/a	shSCR-GFP	n/a	n/a
0.IPTG scrambled control	n/a	shSCR-IPTG	n/a	n/a
0.Neo/G418 scrambled control	n/a	shSCR-neo	n/a	n/a
0.Puro scrambled control	n/a	shSCR (#665)	n/a	n/a
ABCB5	NM_178559	sh295.5	5	GCGAGGAAAGACAGTAGCATT
ABCB5	NM_178559	sh295.4	4	CCACCAATCTAAAGAGATAA
ABCB5	NM_178559	sh295.3	3	GCGGCATTATCGAGACCATAT
ABCB5	NM_178559	sh295.2	2	CCTCGAAGAAAGCACAGATTA
ABCB5	NM_178559	sh295.1	1	GCTGGAAAGATAGCAACTGAA
ABCB7	NM_004299	sh208.5	5	GCCATGAAGGATGTGGTCAAA
ABCB7	NM_004299	sh208.4	4	GCATTTATCTTGCTGGTCAAA
ABCB7	NM_004299	sh208.3	3	GCACAGAGATATGATGGATTT
ABCB7	NM_004299	sh208.2	2	CCTCATAGTATCTATTAGAA
ABCB7	NM_004299	sh208.1	1	GCAGATAATGATGCAGGTAAT
ABCG2	NM_004827	sh104.5	5	CCTGCCAATTTCAAATGTAAT
ABCG2	NM_004827	sh104.4	4	GCTGTGGCATTAAACAGAGAA
ABCG2	NM_004827	sh104.3	3	CCTTCTTCGTTATGATGTTTA
ABCG2	NM_004827	sh104.2	2	GCAACAACATATGACGAATCAT
ABCG2	NM_004827	sh104.1	1	GCCTCGATATTCATCTTCAA
ADAR	NM_001111	sh349.5	5	GCATGGGTTTCACAGAGGTAA
ADAR	NM_001111	sh349.4	4	GCAGGGTATGTTGACTTTGAA
ADAR	NM_001111	sh349.3	3	GCTGTTAGAATATGCCAGTT
ADAR	NM_001111	sh349.2	2	CGGATACTACACCCATCCATT
ADAR	NM_001111	sh349.1	1	GCCCACTGTTATCTTCACTTT
AIF1	NM_004208	sh265.5	5	CCTGGAAATAGACTCAGATTT
AIF1	NM_004208	sh265.4	4	GCCAAACTATTCAACATTCAT
AIF1	NM_004208	sh265.3	3	GCTCTCAAATAACCTATGAAA
AIF1	NM_004208	sh265.2	2	CCGAGAAAGGAAATATGGGAA
AIF1	NM_004208	sh265.1	1	CTGCGATTCAAACAGTGGAA
AIF2	NM_032797	sh266.5	5	CATTTCTACTCGGTGACTTT
AIF2	NM_032797	sh266.4	4	CGGGCAAGTTTAATGAGGTTT
AIF2	NM_032797	sh266.3	3	CAATGAGTACGAGATGACAT
AIF2	NM_032797	sh266.2	2	CAACATCGTCAACTCTGTGAA
AIF2	NM_032797	sh266.1	1	CCTGCCCTTCTCATCTTAT
AKT1	NM_005163	sh111.5	5	GGACTACCTGCACTCGGAGAA
AKT1	NM_005163	sh111.4	4	CTATGGCGCTGAGATTGTGTC
AKT1	NM_005163	sh111.3	3	CGAGTTTGAGTACCTGAAGCT
AKT1	NM_005163	sh111.2	2	GGACAAGGACGGGCACATTA
AKT1	NM_005163	sh111.1	1	GCCACGCTACTTCTCCTCAA
AKT2	NM_001626	sh040.5	5	CCTTAAACAACCTTCTCCGTAG
AKT2	NM_001626	sh040.4	4	ACGGGCTAAAGTGACCATGAA
AKT2	NM_001626	sh040.3	3	CTTCGACTATCTCAAACTCCT
AKT2	NM_001626	sh040.2	2	CCCTTAAACAACCTTCTCCGTA
AKT2	NM_001626	sh040.1	1	CGGGCTAAAGTGACCATGAAT
AKT3	NM_005465	sh094.5	5	AGAAACCTCAAGATGTGGATT
AKT3	NM_005465	sh094.4	4	GAAAGGGAAGATGGACAGAA
AKT3	NM_005465	sh094.3	3	ACTGGCAAGATGTATATGATA
AKT3	NM_005465	sh094.2	2	GCCTTACAACCCATCATAAA
AKT3	NM_005465	sh094.1	1	GCTGCTACTGTCTTACTATTA
ALDH16A1	NM_153329	sh428.5	5	GCTGCTCACTACCATGCAAT
ALDH16A1	NM_153329	sh428.4	4	GCCATGTGGTATTTCCGGATCA
ALDH16A1	NM_153329	sh428.3	3	CTCTCCAAGAACCTGAACTAT
ALDH16A1	NM_153329	sh428.2	2	CATGGGAGTAATTTGGCCTCAT
ALDH16A1	NM_153329	sh428.1	1	CCTTGAGATGATGTGGAGGAT
ALDH18A1	NM_002860	sh427.5	5	GCATCTATTGTTGAGCAGGTA
ALDH18A1	NM_002860	sh427.4	4	CCTCAGTCGTACACATGGAAA
ALDH18A1	NM_002860	sh427.3	3	CGGAACCTCAATGGAACTT
ALDH18A1	NM_002860	sh427.2	2	CCATTATTTGACCAGATCATT
ALDH18A1	NM_002860	sh427.1	1	GCCTTGTATGAGGCTATGTTT
ALDH1A1	NM_000689	sh421.5	5	CACCGATTTGAGATTCAATA
ALDH1A1	NM_000689	sh421.4	4	CCATGAATATACAGAGGTCAA
ALDH1A1	NM_000689	sh421.3	3	CGGGCTAAGAAGTATATCCTT

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ALDH1A1	NM_000689	sh421.2	2	GCTGATTTAATCGAAAGAGAT
ALDH1A1	NM_000689	sh421.1	1	GCCAAATCATTCTTGGGAATT
ALDH9A1	NM_000696	sh426.5	5	CCAGCATTAGCCTGTGGTAAT
ALDH9A1	NM_000696	sh426.4	4	GCTGCCAGGATAATAAGGGAA
ALDH9A1	NM_000696	sh426.3	3	GCTGCCAGGATAATAAGGGAA
ALDH9A1	NM_000696	sh426.2	2	CGTGCTTCATTAACAACATA
ALDH9A1	NM_000696	sh426.1	1	CCCAAATTAAGGATGGATAT
ALKBH2	NM_001001655	sh338.5	5	CATAAGGATTCCTGGGGAAA
ALKBH2	NM_001001655	sh338.4	4	CCCAGGAAGCAGGCAACGTAT
ALKBH2	NM_001001655	sh338.3	3	AGTTGGAGAAGAAGTAGAAT
ALKBH2	NM_001001655	sh338.2	2	CCACGGGAGCTTACTAATGAT
ALKBH2	NM_001001655	sh338.1	1	GTGCTCATCAACAGGTATAAA
ALKBH3	NM_139178	sh339.5	5	TGCCAAAGAATACCACTCTA
ALKBH3	NM_139178	sh339.4	4	CTCTGCAATCTTTATCGCAAT
ALKBH3	NM_139178	sh339.3	3	GTCTGTTTGTATCCTGGCTTT
ALKBH3	NM_139178	sh339.2	2	CCGGCATCAGAGAGGATATAA
ALKBH3	NM_139178	sh339.1	1	CGCACATAAAGAACCAGCATT
ANXA1	NM_000700	sh414.5	5	GCATTCTATCAGAAGGTGAT
ANXA1	NM_000700	sh414.4	4	CCAGCGCAATTTGATGCTGAT
ANXA1	NM_000700	sh414.3	3	GCAACCATCATTGACATTCTA
ANXA1	NM_000700	sh414.2	2	GCATTCTATCAGAAGGTGAT
ANXA1	NM_000700	sh414.1	1	GCCTTGATGAAGCAGGAGAA
ANXA2	NM_001002857	sh415.5	5	CGGGATGCTTTGAACATTGAA
ANXA2	NM_001002857	sh415.4	4	CTGTACTATTATCCAGCAA
ANXA2	NM_001002857	sh415.3	3	CCAGAAAGTATTTGATAGGTA
ANXA2	NM_001002857	sh415.2	2	GCAGGAAATTAACAGAGTCTA
ANXA2	NM_001002857	sh415.1	1	CCTGCTTTCAACTGAATTGTT
APEX1	NM_080649	sh006.4	4	GCCGGGTGATTGTGGCTGAAT
APEX1	NM_080649	sh006.3	3	CCTGGATTAAGAAGAAAGGAT
APEX1	NM_080649	sh006.2	2	GCCTGGACTCTCTCATCAATA
APEX1	NM_080649	sh006.1	1	CAGAGAAATCTGCATTCTATT
APEX2	NM_014481	sh007.5	5	AGAAGGAGTTACGGACCTCAT
APEX2	NM_014481	sh007.4	4	GCTAGTCTTTAAGATCGCCTT
APEX2	NM_014481	sh007.3	3	GCCACCTTCTGTAAGGACAAT
APEX2	NM_014481	sh007.2	2	CCTACCTTCTCTTCTCTTT
APEX2	NM_014481	sh007.1	1	GCTTCTATCGTTTGCTGCAAA
APTX	NM_017692	sh229.5	5	GCTGGTTATACATTCTCTGTTT
APTX	NM_017692	sh229.4	4	CGTTACCATTGGCTGGTCTTA
APTX	NM_017692	sh229.3	3	GTGGTGGTGATAAAGGATATAA
APTX	NM_017692	sh229.2	2	GCTGTGATCGAGATGGTACAA
APTX	NM_017692	sh229.1	1	CCGAGTATGAGCCATGTACAT
ASCIZ	NM_015251	sh186.5	5	GAAGTTATCCAACAAGACCAT
ASCIZ	NM_015251	sh186.4	4	CTTTACAACACCACCGAGAT
ASCIZ	NM_015251	sh186.3	3	CCAGTGGGATAGAAAGTCCAA
ASCIZ	NM_015251	sh186.2	2	GCAACGAAACTCAGACAGCAA
ASCIZ	NM_015251	sh186.1	1	CGGACTTCTTACTCGCAGATA
ATG5	NM_004849	sh110.5	5	CCTTTCATTAGAAGCTGTTT
ATG5	NM_004849	sh110.4	4	GATTCATGGAATTGAGCCAAT
ATG5	NM_004849	sh110.3	3	GCAGAACCATACTATTTGCTT
ATG5	NM_004849	sh110.2	2	CCTGAACAGAATCATCTTAA
ATG5	NM_004849	sh110.1	1	CCAGATATTCTGGAATGGAAA
ATG7	NM_006395	sh136.5	5	CCAAGGTCAAAGGACGAAGAT
ATG7	NM_006395	sh136.4	4	CCCAGCTATTGGAACACTGTA
ATG7	NM_006395	sh136.3	3	GCTTTGGGATTTGACACATT
ATG7	NM_006395	sh136.2	2	CCAGAGAGTTTACCTCTCATT
ATG7	NM_006395	sh136.1	1	GCCTGCTGAGGAGCTCTCCAT
ATM	NM_000051	sh236.10	10	GCTAGAATAATTCATGCTGTT
ATM	NM_000051	sh236.09	9	GCCTCAAATTTACAGTAA
ATM	NM_000051	sh236.08	8	CCTGAAACTTTGGATGAAATT
ATM	NM_000051	sh236.07	7	CCTTTCATTGAGCTTTAGAA
ATM	NM_000051	sh236.06	6	CGTGTCTTAATGAGACTCAA
ATM	NM_000051	sh236.05	5	GCACTGAAAGAGGATCGTAAA
ATM	NM_000051	sh236.04	4	GCCATAATTCAGGGTAGTTTA

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ATM	NM_000051	sh236.03	3	GCCGTCAACTAGAACATGATA
ATM	NM_000051	sh236.02	2	CCTGCCAACATACTTTAAGTA
ATM	NM_000051	sh236.01	1	TGATGGTCTTAAGGAACATCT
ATP13A2	NM_022089	sh196.5	5	GCCTCTGAATGAGATTGTAAT
ATP13A2	NM_022089	sh196.4	4	CGTTATCGAAATAAGAGACAA
ATP13A2	NM_022089	sh196.3	3	CCTGATCTCTACAGATCAA
ATP13A2	NM_022089	sh196.2	2	CCTGACGATAGGGACATCAAT
ATP13A2	NM_022089	sh196.1	1	GCCCATCAACTTCAAGTTCTA
ATR	NM_001184	sh239.8	8	GCTGATTATTTACAACCCAAA
ATR	NM_001184	sh239.7	7	GCCAAAGTATTTCTAGCCTAT
ATR	NM_001184	sh239.6	6	GCCGCTAATCTTCTAACATTA
ATR	NM_001184	sh239.5	5	CCGGATACTTACAGATGTAAA
ATR	NM_001184	sh239.4	4	CTGTGGTTGTATCTGTTCAAT
ATR	NM_001184	sh239.3	3	AATGCATTGGTATGAATCTG
ATR	NM_001184	sh239.2	2	AATGGAGTAAACCAGTGA
ATR	NM_001184	sh239.1	1	AAAGAGGCTCCTACCAACGA
ATRIP	NM_032166	sh402.5	5	TCTGAGAGGTGACTCCATAAA
ATRIP	NM_032166	sh402.4	4	GACCAGTGAACGACAATAA
ATRIP	NM_032166	sh402.3	3	GTGGGCAGAGAGGATAGTAAG
ATRIP	NM_032166	sh402.2	2	GAGCAGTCGTCTCCCTATTAC
ATRIP	NM_032166	sh402.1	1	GGACGTGTCCAGTGATCATAA
B4GALT7	NM_007255	sh330.5	5	CTCAACGAGGAGCTGGACTAT
B4GALT7	NM_007255	sh330.4	4	CACTGTCTCAACATCATGTT
B4GALT7	NM_007255	sh330.3	3	CTCGGAATCACAACTGGGTA
B4GALT7	NM_007255	sh330.2	2	CCACCTCTCTACCACTACAAC
B4GALT7	NM_007255	sh330.1	1	CTGAACACTGTGAAGTACCAT
BAT3	NM_004639	sh325.5	5	CCTATTATCCAGCAGGACATT
BAT3	NM_004639	sh325.4	4	CAGTGAAAGTATTGCTGCCT
BAT3	NM_004639	sh325.3	3	CCTTGGACTCTCAAACCTCGTA
BAT3	NM_004639	sh325.2	2	GCCATTCCCATACAGATCAAT
BAT3	NM_004639	sh325.1	1	GCTGTTATCAATGGCCGAATT
BAX	NM_004324	sh441.5	5	TCATCAGATGTGGTCTATAAT
BAX	NM_004324	sh441.4	4	GCCGGAECTGATCAGAACCAT
BAX	NM_004324	sh441.3	3	GCCCACCAGCTCTGAGCAGAT
BAX	NM_004324	sh441.2	2	GATGTGGTCTATAATGCGTTT
BAX	NM_004324	sh441.1	1	GCCTCAGGATGCGTCCACCAA
BBC3 (PUMA)	NM_014417	sh175.5	5	ACGGTCTCAGCCCTCGTCT
BBC3 (PUMA)	NM_014417	sh175.4	4	GAGGGTCTGTACAATTCAT
BBC3 (PUMA)	NM_014417	sh175.3	3	CGACCTCAACGCACAGTACGA
BBC3 (PUMA)	NM_014417	sh175.2	2	GTACAATCTCATGTTGGGACT
BBC3 (PUMA)	NM_014417	sh175.1	1	CGTGAAGAGCAAATGAGCCAA
BCL2L11	NM_138621	sh030.4	4	AGCCGAAGACCACCCACGAAT
BCL2L11	NM_138621	sh030.3	3	ACGAATGGTTATCTTACGACT
BCL2L11	NM_138621	sh030.2	2	GTCTCGATCCTCCAGTGGGTA
BCL2L11	NM_138621	sh030.1	1	ATGGTTATCTTACGACTGTTA
BECN1	NM_003766	sh087.5	5	GCTTGGGTGCTCTCACAATTT
BECN1	NM_003766	sh087.4	4	CTCAAGTTCATGCTGACGAAT
BECN1	NM_003766	sh087.3	3	GCCAGGATGATGTCCACAGAA
BECN1	NM_003766	sh087.2	2	CCGACTTGTTCTTACGGAAA
BECN1	NM_003766	sh087.1	1	CCCGTGGAAATGGAATGAGATT
BID	NM_001196	sh437.5	5	CAGGGATGAGTGCATCACAAA
BID	NM_001196	sh437.4	4	CCTCCAAAGCTGTTCTGACAA
BID	NM_001196	sh437.3	3	GTGAGGAGCTTAGCCAGAAAT
BID	NM_001196	sh437.2	2	TGGGAAGAATAGAGGCAGATT
BID	NM_001196	sh437.1	1	CTTTCACACAACAGTGAATTT
BID	NM_001196	sh054.5	5	CAGGGATGAGTGCATCACAAA
BID	NM_001196	sh054.4	4	GTGAGGAGCTTAGCCAGAAAT
BID	NM_001196	sh054.3	3	TGGGAAGAATAGAGGCAGATT
BID	NM_001196	sh054.2	2	CTTTCACACAACAGTGAATTT
BID	NM_001196	sh054.1	1	CCTCCAAAGCTGTTCTGACAA
BIM (BCL2L11)	NM_138621	sh442.5	5	AGCCGAAGACCACCCACGAAT
BIM (BCL2L11)	NM_138621	sh442.4	4	ACGAATGGTTATCTTACGACT
BIM (BCL2L11)	NM_138621	sh442.3	3	GTCTCGATCCTCCAGTGGGTA

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BIM (BCL2L11)	NM_138621	sh442.2	2	ATGGTTATCTTACGACTGTTA
BIM (BCL2L11)	NM_138621	sh442.1	1	TACGACTGTTACGTTACATTG
BLM	NM_000057	sh013.5	5	CGAAGGAAGTTGTATGCACTA
BLM	NM_000057	sh013.4	4	GCTACATATCTGACAGGTGAT
BLM	NM_000057	sh013.3	3	CGCTTATGTGATGCTCGGAAA
BLM	NM_000057	sh013.2	2	CCATCAATGATTGGGATGATA
BLM	NM_000057	sh013.1	1	GCCTTTATTCAATACCCATTT
BMI1	NM_005180	sh407.5	5	CCAGAACAGATTGGATCGGAA
BMI1	NM_005180	sh407.4	4	CGGAAAGTAAACAAGACAAA
BMI1	NM_005180	sh407.3	3	CCTAATACTTCCAGATTGAT
BMI1	NM_005180	sh407.2	2	CCAGACCACTACTGAATATAA
BMI1	NM_005180	sh407.1	1	CCTACATTTATACCTGGAGAA
BRCA1	NM_007294	sh139.5	5	GCCTACAAGAAAGTACGAGAT
BRCA1	NM_007294	sh139.4	4	CCCTTCTAAATGCCATCATT
BRCA1	NM_007294	sh139.3	3	CCCACCTAATTGACTGAATT
BRCA1	NM_007294	sh139.2	2	GCCCACCTAATTGACTGAAT
BRCA1	NM_007294	sh139.1	1	CCCTAAGTTTACTTCTCTAAA
BRCA2	NM_000059	sh022.5	5	GCCTTGAATAATCACAGGCAA
BRCA2	NM_000059	sh022.4	4	CCTCTGAAAGTGACTCGGAAA
BRCA2	NM_000059	sh022.3	3	GCGTTTCTAAACATTGCATAA
BRCA2	NM_000059	sh022.2	2	GCAGCCATTAATTTGCCATA
BRCA2	NM_000059	sh022.1	1	CGCTTAACCTTCCAGTTTAT
BTBD12	NM_032444	sh391.5	5	GCATTTGAGTCTGCAGGTGAA
BTBD12	NM_032444	sh391.4	4	GCTGGAGCTAGAACAACCAA
BTBD12	NM_032444	sh391.3	3	CAAAGGTGCTAATCGGAAGAA
BTBD12	NM_032444	sh391.2	2	CCAGGAACCTTGGAGTCAAT
BTBD12	NM_032444	sh391.1	1	GCTGTGCCATCAAAGCAGAAA
BUB1	NM_004336	sh244.4	4	CCTGGGTGAGGTATAGATAT
BUB1	NM_004336	sh244.3	3	CCAAGCAGAAATGGATGCAGAT
BUB1	NM_004336	sh244.2	2	CATGGAACCTACCAGATCGATT
BUB1	NM_004336	sh244.1	1	TACAACAGTGACCTCCATCAA
BUB1B	NM_001211	sh355.5	5	CCTCAGAAAGCATCACCTCAA
BUB1B	NM_001211	sh355.4	4	GAGACAACCTAACTGCAAAAT
BUB1B	NM_001211	sh355.3	3	CCAGTGTACCTTTCTCATT
BUB1B	NM_001211	sh355.2	2	GCGTTTTATGCAATGAGCCTTT
BUB1B	NM_001211	sh355.1	1	CTGAAACTGTATGTGCTGTAA
BUB1B	NM_001211	sh247.1	1	CTGAAACTGTATGTGCTGTAA
C2orf114	NM_033197	sh433.5	5	TCTGCAGCTTCCCTGACAATG
C2orf114	NM_033197	sh433.4	4	CGAACCAGAATGGCAAAATTA
C2orf114	NM_033197	sh433.3	3	GCTGAAGGTGATCACAGCTAA
C2orf114	NM_033197	sh433.2	2	GAAGGTGATCACAGCTAACAT
C2orf114	NM_033197	sh433.1	1	CTTGAATAACATCAGCTCTGA
C2orf13	NM_173545	sh035.4	4	GTTGGGCAACCCATGAGTAT
C2orf13	NM_173545	sh035.3	3	CCCCTGATTAATTTACCTCAT
C2orf13	NM_173545	sh035.2	2	CATCCTGGTGATAGTGATTAT
C2orf13	NM_173545	sh035.1	1	CAAAGATAAATCCAGCTAAA
C5orf39	NM_001014279	sh423.5	5	CCCTTATGTTTCTTTCTTGTT
C5orf39	NM_001014279	sh423.4	4	GCTGTGATTTGGGACTGCTTT
C5orf39	NM_001014279	sh423.3	3	CCAAACGTCTCCACCTAGAAA
C5orf39	NM_001014279	sh423.2	2	CCTATTGTGAGTTCAGAAGAT
C5orf39	NM_001014279	sh423.1	1	CGTCGCTTATTACTTTCAAGTT
CASP3	NM_004346	sh078.5	5	GTGGAATTGATGCGTGATGTT
CASP3	NM_004346	sh078.4	4	CTAAAGGTGGTGAGGCAATAA
CASP3	NM_004346	sh078.3	3	CCGAAAGGTGGCAACAGAATT
CASP3	NM_004346	sh078.2	2	CCTGAGATGGGTTTATGTATA
CASP3	NM_004346	sh078.1	1	GCGAATCAATGGACTCTGGAA
CASP7	NM_001227	sh041.5	5	GTAATCACTAATGCTCAACAA
CASP7	NM_001227	sh041.4	4	GCTGACTTCCCTCTCGCCTAT
CASP7	NM_001227	sh041.3	3	GCCTGCATCCTCTTAAAGCCAT
CASP7	NM_001227	sh041.2	2	CCTCGTTTGTACCGTCCCTCT
CASP7	NM_001227	sh041.1	1	AGGATTTGACAGCCACTTTA
CASP8	NM_001228	sh240.5	5	GCCTTGATGTTATTCCAGAGA
CASP8	NM_001228	sh240.4	4	TCACAGCATTAGGGACAGGAA

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CASP8	NM_001228	sh240.3	3	CCTGGCCGATGGTACTATTTA
CASP8	NM_001228	sh240.2	2	GACATGAACCTGCTGGATATT
CASP8	NM_001228	sh240.1	1	GAATCACAGACTTTGGACAAA
CASP9	NM_001229	sh42.5	5	CCACTGCCTCATTATCAACAA
CASP9	NM_001229	sh42.4	4	GATGCCTGGTGTCTTAATTT
CASP9	NM_001229	sh42.3	3	CCTTGTTCATCTCCTGCTTA
CASP9	NM_001229	sh42.2	2	CAGCTTCCAGATTGACGACAA
CASP9	NM_001229	sh42.1	1	CTTTGTGTCTACTCTACTTT
CAV1	NM_001753	sh044.5	5	GACCCACTTTTGAAGCTGTT
CAV1	NM_001753	sh044.4	4	GACGTGGTCAAGATTGACTTT
CAV1	NM_001753	sh044.3	3	GACCTAAACACCTCAACGAT
CAV1	NM_001753	sh044.2	2	CCACCTTCACTGTGACGAAAT
CAV1	NM_001753	sh044.1	1	GCTTTGTGATTCAATCTGTAA
CCNH	NM_001239	sh368.5	5	CGACCTGGTAGAATCTCTCTA
CCNH	NM_001239	sh368.4	4	CTTCCGAATGATCCAGTCTTT
CCNH	NM_001239	sh368.3	3	CGCTATCCCATATTGGAGAAT
CCNH	NM_001239	sh368.2	2	CCAGGATAAATAGTCTCACTT
CCNH	NM_001239	sh368.1	1	GCAACTTAATTTCCACTTAT
CD276	NM_001024736	sh435.5	5	GCTTGTGGTGTGACAGCA
CD276	NM_001024736	sh435.4	4	CTCTGAAACACTCTGACAGCA
CD276	NM_001024736	sh435.3	3	CTAGCCTTAATACTGGCCTTT
CD276	NM_001024736	sh435.2	2	CTGAAACACTCTGACAGCAAA
CD276	NM_001024736	sh435.1	1	CAAAGAAGATGATGGACAAGA
CD276	NM_001024736	sh296.5	5	CTGAAACACTCTGACAGCAAA
CD276	NM_001024736	sh296.4	4	CTAGCCTTAATACTGGCCTTT
CD276	NM_001024736	sh296.3	3	CAAAGAAGATGATGGACAAGA
CD276	NM_001024736	sh296.2	2	CTCTGAAACACTCTGACAGCA
CD276	NM_001024736	sh296.1	1	GCTTGTGGTGTGACAGCA
CD38	NM_001775	sh285.5	5	CCTCACATGGTGTGGTGAATT
CD38	NM_001775	sh285.4	4	CTGAGGATTCATCTTGACAT
CD38	NM_001775	sh285.3	3	CCAAGTGTATGGGATGCTTT
CD38	NM_001775	sh285.2	2	CCAGAGAAGGTTCCAGACTA
CD38	NM_001775	sh285.1	1	GCATACCTTTATTGTGATCTA
CDH1	NM_004360	sh324.5	5	ATACCAGAACCTCGAACTATA
CDH1	NM_004360	sh324.4	4	CCAACCCAAGAATCTATCAT
CDH1	NM_004360	sh324.3	3	CGATTCAAAGTGGGCACAGAT
CDH1	NM_004360	sh324.2	2	CCAAGCAGAATTGCTCACATT
CDH1	NM_004360	sh324.1	1	CCAGTGAACAACGATGGCATT
CDK7	NM_001799	sh367.5	5	CATTTAAGAGTTTCCCTGGAA
CDK7	NM_001799	sh367.4	4	GTGGGCTGTTGGCTGTATATT
CDK7	NM_001799	sh367.3	3	TCAGAAGCTAAAGATGGTATA
CDK7	NM_001799	sh367.2	2	GCAGGAGACGACTTACTAGAT
CDK7	NM_001799	sh367.1	1	GCTGTAGAAGTGAGTTTGTA
CDKN1A	NM_000389	sh020.5	5	GTCCTGTCTTGTACCCTTGT
CDKN1A	NM_000389	sh020.4	4	GACAGATTCTTACCCTCCAA
CDKN1A	NM_000389	sh020.3	3	GAGCGATGGAACCTCGACTTT
CDKN1A	NM_000389	sh020.2	2	GCTGATCTTCTCAAGAGGAA
CDKN1A	NM_000389	sh020.1	1	CGCTCTACATCTTCTGCCTTA
CDKN1B	NM_004064	sh088.5	5	CAGCGAAGTGGAAATTCGAT
CDKN1B	NM_004064	sh088.4	4	CCTCAGAAGACGTCAAACGTA
CDKN1B	NM_004064	sh088.3	3	GCGCAAGTGGAAATTCGATTT
CDKN1B	NM_004064	sh088.2	2	CCGACGATTCTTCTACTCAA
CDKN1B	NM_004064	sh088.1	1	GTAGGATAAGTGAATGGATA
CDKN1C	NM_000076	sh017.5	5	CCGCTGGGATTAGCACTTCCA
CDKN1C	NM_000076	sh017.4	4	GATCTCCGATTTCTTCGCCAA
CDKN1C	NM_000076	sh017.3	3	CGTGGGACCTTCCAGTACTA
CDKN1C	NM_000076	sh017.2	2	GCCTCTGATCTCCGATCTTT
CDKN1C	NM_000076	sh017.1	1	ATTCTGCACGGAAGGTACAC
CDKN2A	NM_058197	sh231.11	11	CCGATTGAAAGAACCAGAGA
CDKN2A	NM_058197	sh231.10	10	GCTCTGAGAAACCTCGGGAA
CDKN2A	NM_058197	sh231.09	9	ATCAGTCAACGAAGGTCTTA
CDKN2A	NM_058197	sh231.08	8	CCTCGGAAACTTAGATCAT
CDKN2A	NM_058197	sh231.07	7	CACTACCGTAAATGTCCATT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
CDKN2A	NM_058197	sh231.06	6	CCCTAAGCGCACATTCATGT
CDKN2A	NM_058197	sh231.05	5	GCGACTCTGGAGGACGAAGTT
CDKN2A	NM_058197	sh231.04	4	GAATCAGGTAGCGCTTCGATT
CDKN2A	NM_058197	sh231.03	3	TGGGAAACCAAGGAAGAGGAA
CDKN2A	NM_058197	sh231.02	2	GCGCTGCCAACCGCACCGAAT
CDKN2A	NM_058197	sh231.01	1	CGCACATTCATGTGGGCATTT
CDKN2B	NM_078487	sh267.4	4	GCGCGGATCCCAACGGAGTCA
CDKN2B	NM_078487	sh267.3	3	ACGGAGTCAACCGTTTCGGGA
CDKN2B	NM_078487	sh267.2	2	CCCAACGGAGTCAACCGTTTC
CDKN2B	NM_078487	sh267.1	1	ACTAGTGGAGAAGGTGCGACA
CDKN2C	NM_001262	sh233.5	5	TGGACACTTTACAGACTTTGC
CDKN2C	NM_001262	sh233.4	4	TGGATTTGGAAGGACTGCGCT
CDKN2C	NM_001262	sh233.3	3	CTATGGGAGGAATGAGGTTGT
CDKN2C	NM_001262	sh233.2	2	ACTGGTTTCGCTGTCAATCAT
CDKN2C	NM_001262	sh233.1	1	CCCACGTTGCCTCTACTTTAT
CDKN2D	NM_079421	sh268.4	4	CGCCCTCAACCGCTTCGGCAA
CDKN2D	NM_079421	sh268.3	3	GCGCTGCAGGTCATGATGTTT
CDKN2D	NM_079421	sh268.2	2	GCTGATGTCAACGTGCCTGAT
CDKN2D	NM_079421	sh268.1	1	CCAATCCATCTGGCAGTTCAA
CETN2	NM_004344	sh358.5	5	ACTGGCACCATAGATGTTAAA
CETN2	NM_004344	sh358.4	4	CCTAAGCCTGAGCTTACTGAA
CETN2	NM_004344	sh358.3	3	CTGGGCTTTGAACCCAAGAAA
CETN2	NM_004344	sh358.2	2	CCTGAGCTTACTGAAGAGCAA
CETN2	NM_004344	sh358.1	1	GAACCCAAGAAAGAAGAAATT
CFLAR (C-FLIP)	NM_003879	sh440.5	5	CACTCTGAGAAAGAAACTTAT
CFLAR (C-FLIP)	NM_003879	sh440.4	4	GCATCACATCAGGAGGATGTT
CFLAR (C-FLIP)	NM_003879	sh440.3	3	GCTCCATAATGGGAGAAGTAA
CFLAR (C-FLIP)	NM_003879	sh440.2	2	CCTCACCTGTTTCGGACTAT
CFLAR (C-FLIP)	NM_003879	sh440.1	1	CACCTGTAATCCAGCACTTT
CHAF1A	NM_005483	sh388.5	5	CGGCAATGTGAACGGGAGCAA
CHAF1A	NM_005483	sh388.4	4	GACATAGACTTTAGACCGAAA
CHAF1A	NM_005483	sh388.3	3	CCTCCGCAGAATAACTAAGAA
CHAF1A	NM_005483	sh388.2	2	CCACCCGGAATGCAGATATTT
CHAF1A	NM_005483	sh388.1	1	CCGACTCAATCCTGTGTAAA
CHEK1	NM_001274	sh048.5	5	CAAATCTTATCAATGCCTGAA
CHEK1	NM_001274	sh048.4	4	GCCCATGTCCTGATCATAT
CHEK1	NM_001274	sh048.3	3	GTTGTATGAATCAGGTTACTA
CHEK1	NM_001274	sh048.2	2	CTAAGCACATTCATCCAATT
CHEK1	NM_001274	sh048.1	1	GCAACAGTATTTCCGGTATAAT
CHEK2	NM_007194	sh142.5	5	GCTCTCAATGTTGAAACAGAA
CHEK2	NM_007194	sh142.4	4	GCCAATCTTGAATGTGTGAAT
CHEK2	NM_007194	sh142.3	3	CGCGTCTCTTTGAATAACAAT
CHEK2	NM_007194	sh142.2	2	CGTGACTTAAAGCCAGAGAAT
CHEK2	NM_007194	sh142.1	1	CTCCGTGGTTTGAACACGAAC
CHFR	NM_018223	sh171.5	5	GCAGCCTTCTGCCACCTGTA
CHFR	NM_018223	sh171.4	4	GCATACCTCTATGAATCTTTA
CHFR	NM_018223	sh171.3	3	GCAGTGAAGAAGATGTGCAAA
CHFR	NM_018223	sh171.2	2	CGCATGAAATTCATCATAT
CHFR	NM_018223	sh171.1	1	CCTGTTATCCTTGTTTGTTAAA
CHRM3	NM_000740	sh328.5	5	GCAAAGCATGAAACGCTCCAA
CHRM3	NM_000740	sh328.4	4	AGACCAGAAGTCAGATCACTA
CHRM3	NM_000740	sh328.3	3	CCGAGCCAACGAACAACAAA
CHRM3	NM_000740	sh328.2	2	CCTGTCACCATTATGACTATT
CHRM3	NM_000740	sh328.1	1	CCTGGTAATTGTGTCAATTTAA
CHUK	NM_001278	sh039.5	5	GCGTGCCATTGATCTATATAA
CHUK	NM_001278	sh039.4	4	GCAAATGAGGAACAGGGCAAT
CHUK	NM_001278	sh039.3	3	CCAGCCTCTCAATGTGTTCTA
CHUK	NM_001278	sh039.2	2	CCAGATTATGAAGAAGTTGAA
CHUK	NM_001278	sh039.1	1	GCATCATAAGGAGTTGGTGTA
CLIC1	NM_001288	sh315.5	5	CTTCAATGTTACCACCGTTGA
CLIC1	NM_001288	sh315.4	4	GTGGATGAAACCAGTGCTGAA
CLIC1	NM_001288	sh315.3	3	GACACCAACAAGATTGAGGAA
CLIC1	NM_001288	sh315.2	2	CCTGTTGCCAAAGTTACACAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
CLIC1	NM_001288	sh315.1	1	GCTGGACATATTTGCCAAATT
CLIC4	NM_013943	sh316.5	5	CCCAGTGATAAGGAGGTTGAA
CLIC4	NM_013943	sh316.4	4	GATGGCAATGAAATGACATTA
CLIC4	NM_013943	sh316.3	3	GCATATAGTGATGTAGCCAAA
CLIC4	NM_013943	sh316.2	2	CCCACCATTATAACTTTCAA
CLIC4	NM_013943	sh316.1	1	GCCGTAATGTTGAACAGAATT
CLOCK	NM_004898	sh292.5	5	CGTTCAACTTTCTTCTGGAAA
CLOCK	NM_004898	sh292.4	4	GCCAAGATTCTGGGTCAGATA
CLOCK	NM_004898	sh292.3	3	GCGAGGAACAATAGACCCAAA
CLOCK	NM_004898	sh292.2	2	CGCACACATAGGCCATCTTAT
CLOCK	NM_004898	sh292.1	1	CGACGAGAACTTGGCATTGAA
CSPG4	NM_001897	sh294.5	5	GACTTCATCTATGTGGACATA
CSPG4	NM_001897	sh294.4	4	CAACATGTTCCAGCGTCATCAT
CSPG4	NM_001897	sh294.3	3	CTTGCCACTGAGCCTTACAA
CSPG4	NM_001897	sh294.2	2	CATCACGGTGAGGGATGTAAA
CSPG4	NM_001897	sh294.1	1	CAATGCATCAGCCGTAGTGAA
CUL4A	NM_003589	sh375.5	5	CCAGAATATCTTAACCATGTA
CUL4A	NM_003589	sh375.4	4	GCAGAACTGATCGCAAGCAT
CUL4A	NM_003589	sh375.3	3	GCCAAAGGTTAATGCAGGAAA
CUL4A	NM_003589	sh375.2	2	GCAGGTGTATAAAGATTCATT
CUL4A	NM_003589	sh375.1	1	CCATGATATGGTCTAAGAA
DCLRE1A	NM_014881	sh392.5	5	GCATCATCAAGGATAACTGAA
DCLRE1A	NM_014881	sh392.4	4	CGGCTTTACAGTTGATGCCTT
DCLRE1A	NM_014881	sh392.3	3	GCAGGTTGTCAGACTTCTGTT
DCLRE1A	NM_014881	sh392.2	2	CGAGGATTCAGTAGTGTAA
DCLRE1A	NM_014881	sh392.1	1	CCCAAAGATACGGTCAGTTTA
DCLRE1B	NM_022836	sh393.5	5	CAGATCTCTATAGCAAAGAAT
DCLRE1B	NM_022836	sh393.4	4	CCCACAACATAACATAAAGAT
DCLRE1B	NM_022836	sh393.3	3	GCTGTTAGAAAGGAGGCTAAA
DCLRE1B	NM_022836	sh393.2	2	GCATCCATGCAGTAGACCATA
DCLRE1B	NM_022836	sh393.1	1	GCAGTGAAGAAGATTCATT
DCLRE1C	NM_022487	sh121.5	5	CGTTTCACAACTTTGTAGAT
DCLRE1C	NM_022487	sh121.4	4	CCAGTGGGAAGTATCTTTAA
DCLRE1C	NM_022487	sh121.3	3	CTGTGGAATTACTTCCAGAAA
DCLRE1C	NM_022487	sh121.2	2	GCAGAGATAAAGATGTGACAA
DCLRE1C	NM_022487	sh121.1	1	GCACAGAGATGACAGTCAATA
DDB1	NM_001923	sh056.5	5	CCTATCACAATGGTGACAAAT
DDB1	NM_001923	sh056.4	4	CGTGACTCTATGGTGGAAAT
DDB1	NM_001923	sh056.3	3	CGACCGTAAGAAGGTGACTTT
DDB1	NM_001923	sh056.2	2	CGACTCAATAAAGTCATCAA
DDB1	NM_001923	sh056.1	1	CCTTGATTGGTGTGCCAGTT
DDB2	NM_000107	sh028.5	5	GACACCATCAACATCTGGTT
DDB2	NM_000107	sh028.4	4	TCTGGATCTTACCGGATATT
DDB2	NM_000107	sh028.3	3	GCTGAAGTTTAAACCTCTCAA
DDB2	NM_000107	sh028.2	2	CCTCGCTACAACCTCATTGTT
DDB2	NM_000107	sh028.1	1	GCAGAGGTGGTGATTGTAA
DHX15	NM_001358	sh038.5	5	GCTTCAACAAATGCTATGCTT
DHX15	NM_001358	sh038.4	4	TGTAAGAGAATAAAGCGTGAA
DHX15	NM_001358	sh038.3	3	TGGAATACAAGGATAGGTTT
DHX15	NM_001358	sh038.2	2	ACTGTTCTAATGAGTCCTAT
DHX15	NM_001358	sh038.1	1	GTTGGTTCGATAATGGCCTTT
DHX9	NM_001357	sh411.5	5	TCGAGGAATCAGTCATGTAAT
DHX9	NM_001357	sh411.4	4	AGACTTAATATGGCTACACTAC
DHX9	NM_001357	sh411.3	3	GAAGGATTAATACTCAAGAAA
DHX9	NM_001357	sh411.2	2	CCAGAAGAATCAGTGCGGTTT
DHX9	NM_001357	sh411.1	1	GGCTTCGTTTAAATACAATAG
DICER1	NM_030621	sh010.5	5	GCTGGCTGTAAAGTACGACTA
DICER1	NM_030621	sh010.4	4	GCCAAGGAAATCAGCTAAATT
DICER1	NM_030621	sh010.3	3	CCACACATCTCAAGACTTAA
DICER1	NM_030621	sh010.2	2	CGGGAGAATTTCAACAGCCAA
DICER1	NM_030621	sh010.1	1	GCTCGAAATCTTACGCAATA
DMC1	NM_007068	sh149.5	5	CGGGAGCCAGGAATTTGATAA
DMC1	NM_007068	sh149.4	4	GCAGTGCCATGTGCTTGAAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
DMC1	NM_007068	sh149.3	3	CGCAATAACTGCTGGAGGAAT
DMC1	NM_007068	sh149.2	2	GCAAATTGCTTCTTAGTGCTT
DMC1	NM_007068	sh149.1	1	CTCATGCTTCAACAACAAGAA
DR4 (TNFRSF10A)	NM_003844	sh439.5	5	GATGCTGTTCTTTGACAAGTT
DR4 (TNFRSF10A)	NM_003844	sh439.4	4	CTCTGGAAAGTTCATCTACTT
DR4 (TNFRSF10A)	NM_003844	sh439.3	3	GCTTGTAATCAGATGAAGAA
DR4 (TNFRSF10A)	NM_003844	sh439.2	2	GCACACAGCAATGGGAACATA
DR4 (TNFRSF10A)	NM_003844	sh439.1	1	CTTAGGTGTTAGGAGTTAATA
DR5 (TNFRSF10B)	NM_003842	sh438.5	5	GCAGAAGATTGAGGACCCTT
DR5 (TNFRSF10B)	NM_003842	sh438.4	4	CTCACTGGAATGACCTCTTT
DR5 (TNFRSF10B)	NM_003842	sh438.3	3	GCTGAGGACAATGTCCTCAAT
DR5 (TNFRSF10B)	NM_003842	sh438.2	2	CCACAAAGAATCAGGTACAAA
DR5 (TNFRSF10B)	NM_003842	sh438.1	1	GCAGTCTCATTGACCCATA
DUT	NM_001948	sh385.5	5	GCTGGTGCATAGATGAAGAT
DUT	NM_001948	sh385.4	4	TGGTCCACTGAAAAGAATTA
DUT	NM_001948	sh385.3	3	GCGCTCCCTTCTGGGTGTTAT
DUT	NM_001948	sh385.2	2	CCAGAAATAGAAAGTTCAA
DUT	NM_001948	sh385.1	1	AGTGCCTATGATTACACAATA
DYNLL1	NM_003746	sh422.5	5	TCTTCTGTTCAAATCTGGTTA
DYNLL1	NM_003746	sh422.4	4	GCGCTGGAGAAAATACAACATA
DYNLL1	NM_003746	sh422.3	3	GTGGCCATTCTTCTGTTCAAA
DYNLL1	NM_003746	sh422.2	2	AGAAGGACATTGCGGCTCATA
DYNLL1	NM_003746	sh422.1	1	CGGTAGTTATGTGACACATGA
E2F1	NM_005225	sh103.5	5	CCTGAGGAGTTCATCAGCCTT
E2F1	NM_005225	sh103.4	4	ACCTGATGAATATCTGTAATA
E2F1	NM_005225	sh103.3	3	CGTGGACTCTTCGGAGAAGCTT
E2F1	NM_005225	sh103.2	2	CGTATGAGACCTCACTGAAT
E2F1	NM_005225	sh103.1	1	CAGGATGGATATGAGATGGGA
EAF1	NM_033083	sh453.5	5	GAACACCCTCAGAAATGACTT
EAF1	NM_033083	sh453.4	4	GCATCTATAGACACTTCTGT
EAF1	NM_033083	sh453.3	3	CTTCGGGAAGTGATGACGATA
EAF1	NM_033083	sh453.2	2	GCCCTGGTCTAAGTTACTCAA
EAF1	NM_033083	sh453.1	1	CCCTGGTCTAAGTTACTCAA
EAF2	NM_018456	sh448.5	5	GCTATGACTTCAAACCTGCTT
EAF2	NM_018456	sh448.4	4	GTGACCATAACTCTGCCAAAT
EAF2	NM_018456	sh448.3	3	GCAAATCCTCTACTTCTGATA
EAF2	NM_018456	sh448.2	2	CTGGAGAATGTCGGCTAGAAA
EAF2	NM_018456	sh448.1	1	CCTGATATAGATGCCAGTCAT
EAF2	NM_018456	sh190.5	5	GCTATGACTTCAAACCTGCTT
EAF2	NM_018456	sh190.4	4	GTGACCATAACTCTGCCAAAT
EAF2	NM_018456	sh190.3	3	GCAAATCCTCTACTTCTGATA
EAF2	NM_018456	sh190.2	2	CTGGAGAATGTCGGCTAGAAA
EAF2	NM_018456	sh190.1	1	CCTGATATAGATGCCAGTCAT
EDA2R	NM_021783	sh197.5	5	CTGCAGTTTGAGGCTGATAAA
EDA2R	NM_021783	sh197.4	4	TGTGCTGCATCAATCGTGTT
EDA2R	NM_021783	sh197.3	3	CAAGTGAGTGAGAACATCTTT
EDA2R	NM_021783	sh197.2	2	GCTATCCAAGGATTGTGGTTA
EDA2R	NM_021783	sh197.1	1	CCTCTACTGCAAGCAGTTCTT
EDAR	NM_022336	sh447.5	5	CGGGATTCAAAGCCGGAGGAA
EDAR	NM_022336	sh447.4	4	CGGTGAGAACGAGTACTACAA
EDAR	NM_022336	sh447.3	3	CGAGAAGGATGAATTTGAGAA
EDAR	NM_022336	sh447.2	2	GCCATTTGATTGCCTCGAGAA
EDAR	NM_022336	sh447.1	1	CCTCATCATCATGTTCTACAT
EDAR	NM_022336	sh198.5	5	CGGGATTCAAAGCCGGAGGAA
EDAR	NM_022336	sh198.4	4	CGGTGAGAACGAGTACTACAA
EDAR	NM_022336	sh198.3	3	CGAGAAGGATGAATTTGAGAA
EDAR	NM_022336	sh198.2	2	GCCATTTGATTGCCTCGAGAA
EDAR	NM_022336	sh198.1	1	CCTCATCATCATGTTCTACAT
EDARADD	NM_080738	sh125.5	5	CTGTACTTGTCTCTCTGCTT
EDARADD	NM_080738	sh125.4	4	CTGCCACGAAATTCAGATAT
EDARADD	NM_080738	sh125.3	3	CCCTAGCACTTTATCCTTTAA
EDARADD	NM_080738	sh125.2	2	CCCACGAAATTCAGATATGAA
EDARADD	NM_080738	sh125.1	1	CCGGTGTTCATGTATCAAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
EDNRB	NM_000115	sh446.5	5	CCATCGAGATCAAGGAGACTT
EDNRB	NM_000115	sh446.4	4	CTGTTGGTATTGGACTATATT
EDNRB	NM_000115	sh446.3	3	GCAGTCGTGCTTAAAGTTCAA
EDNRB	NM_000115	sh446.2	2	CAAAGGAAGTTATCTGCGAAT
EDNRB	NM_000115	sh446.1	1	CCTCACAAGAGAAATAGAAT
EFNA5	NM_001962	sh052.5	5	CAATCCCAGATAATGGAGAGAA
EFNA5	NM_001962	sh052.4	4	CCACACTTCCAAGGGTTCAA
EFNA5	NM_001962	sh052.3	3	CGCGGCACAAACCAAGGAT
EFNA5	NM_001962	sh052.2	2	GTCCTCTACATGGTGAACTTT
EFNA5	NM_001962	sh052.1	1	GAGACCAACAAATAGCTGTAT
EGFR	NM_005228	sh261.5	5	AGAGGAAATATGTACTACGAA
EGFR	NM_005228	sh261.4	4	CCTCCAGAGGATGTTCAATAA
EGFR	NM_005228	sh261.3	3	GCCAAGCCAAATGGCATCTTT
EGFR	NM_005228	sh261.2	2	GTCCGGGAACACAAGACAAT
EGFR	NM_005228	sh261.1	1	CCCTGTAACTGACTGGTTAA
EIF4E	NM_001968	sh290.5	5	CTGTTGTTAATGTTAGAGCTA
EIF4E	NM_001968	sh290.4	4	CGGCTGATCTCCAAGTTTGAT
EIF4E	NM_001968	sh290.3	3	CCAAAGATAGTGATTGGTTAT
EIF4E	NM_001968	sh290.2	2	CCGACTACAGAAGAGGAGAAA
EIF4E	NM_001968	sh290.1	1	CCACTCTGTAATAGTTCAGTA
ELL	NM_006532	sh235.5	5	GAGCTACAAGAACGACTTCAA
ELL	NM_006532	sh235.4	4	CCTGGGCAGCATACAGGACAA
ELL	NM_006532	sh235.3	3	CGCGCCAGACAGGATTCTGTT
ELL	NM_006532	sh235.2	2	GCCTGACTACTTGCTGAAGTA
ELL	NM_006532	sh235.1	1	GCAAGAAGGTTTCAGTTTCGGA
ELL2	NM_012081	sh150.5	5	CGACCTTCAATCCAGTCCAA
ELL2	NM_012081	sh150.4	4	CCCTGCAATACAATTCGAAA
ELL2	NM_012081	sh150.3	3	CCAGAATTATAAGGATGACTT
ELL2	NM_012081	sh150.2	2	GCCGTTCAGAATCTCCTGTAT
ELL2	NM_012081	sh150.1	1	CCTGGGATTTATACAAGATAA
EME1	NM_152463	sh033.5	5	CAGGCGTATCTACCTTCAGAT
EME1	NM_152463	sh033.4	4	CCCTGAGAAGACAGGAAAGAA
EME1	NM_152463	sh033.3	3	CCCTTTCCAAGATCCCTGAA
EME1	NM_152463	sh033.2	2	CGGATAAAGAACGCCAGAATT
EME1	NM_152463	sh033.1	1	GCACTATGAAAGGGAAGGAAA
ERBB2	NM_004448	sh313.5	5	AAGTACACGATGCGGAGACTC
ERBB2	NM_004448	sh313.4	4	ATCACAGGTTACCTATACATC
ERBB2	NM_004448	sh313.3	3	GAATATGTGAACCAGCCAGAT
ERBB2	NM_004448	sh313.2	2	CAGTGCCAATATCCAGGAGTT
ERBB2	NM_004448	sh313.1	1	TGTCAGTATCCAGGCTTTGTA
ERBB3	NM_001982	sh429.5	5	AGGTTAGGAGTAGATATTGAC
ERBB3	NM_001982	sh429.4	4	TATATGAATCGGCAACGAGAT
ERBB3	NM_001982	sh429.3	3	AATTCTCTACTCTACCATTGC
ERBB3	NM_001982	sh429.2	2	CTGCCTTTGATAACCTGATT
ERBB3	NM_001982	sh429.1	1	CCTGACAAGATGGAAGTAGAT
ERCC1	NM_001983	sh051.5	5	GCCGCCAGCAAGGAAGAAATT
ERCC1	NM_001983	sh051.4	4	GCTGGCTAAGATGTGTATCCT
ERCC1	NM_001983	sh051.3	3	CAAGAGAAGATCTGGCCTTAT
ERCC1	NM_001983	sh051.2	2	CCTGGGAATTTGGCGACGTAA
ERCC1	NM_001983	sh051.1	1	CCAAGCCCTTATCCGATCTA
ERCC2	NM_000400	sh014.5	5	CCCATACTTCCTGCTCGATA
ERCC2	NM_000400	sh014.4	4	CTGCCGATTCTATGAGGAATT
ERCC2	NM_000400	sh014.3	3	CCAGTTCAGATTCGTGAGAA
ERCC2	NM_000400	sh014.2	2	GCTTCGAAAGTTGCTCAACTT
ERCC2	NM_000400	sh014.1	1	GCGTTTCCAGTCTGTATCAT
ERCC3	NM_000122	sh015.5	5	CGGGAATATGTGGCAATCAAA
ERCC3	NM_000122	sh015.4	4	CCAGTTTACAAATATGCCAA
ERCC3	NM_000122	sh015.3	3	GCCCTAAAGGAATATGCCATT
ERCC3	NM_000122	sh015.2	2	CCGGAAGCAAATGTCTCATT
ERCC3	NM_000122	sh015.1	1	GCCATTCTAAGACTGCTGAA
ERCC4	NM_005236	sh105.5	5	CGGAAGTTGACCTTAACCTAA
ERCC4	NM_005236	sh105.4	4	CCAAGATACGTGGTTCTTTAT
ERCC4	NM_005236	sh105.3	3	GCTTGCTATACAGACTGCTAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
ERCC4	NM_005236	sh105.2	2	CCCACAGAATAATCGAGTCTT
ERCC4	NM_005236	sh105.1	1	GCGCAAGAGTATCAGTGATTT
ERCC5	NM_000123	sh023.5	5	CCAATGGAATTGACTCGGAA
ERCC5	NM_000123	sh023.4	4	CCTGTATTAAGCAACTCGAT
ERCC5	NM_000123	sh023.3	3	GCTTTCAGATTCTAAACGAAA
ERCC5	NM_000123	sh023.2	2	CCTCCTTTACAAGAGGAAGAA
ERCC5	NM_000123	sh023.1	1	CCAGCGAAATAGAAGCAGTTT
ERCC6	NM_000124	sh372.4	4	GCCACTGATTACGAGATACAA
ERCC6	NM_000124	sh372.3	3	GCGGTTAAGGAGATGGAATAA
ERCC6	NM_000124	sh372.2	2	CGACAAATCTTCAAGCAGTTT
ERCC6	NM_000124	sh372.1	1	CGTGGTTCAAATTACAGGTTT
ERCC8	NM_000082	sh371.5	5	GCGCTAATGCTTGAACCTTT
ERCC8	NM_000082	sh371.4	4	TGATGATGAGACTACAACAAA
ERCC8	NM_000082	sh371.3	3	GATGGTGTGATTGTACTTTAT
ERCC8	NM_000082	sh371.2	2	TGGAATTAACACCTTGACAT
ERCC8	NM_000082	sh371.1	1	GCAGCAGTGATGAAGAAGGAT
ESR2	NM_001437	sh228.4	4	GATGCTTTGGTTTGGGTGATT
ESR2	NM_001437	sh228.3	3	CCTTAATCTCCTTCCTCCTA
ESR2	NM_001437	sh228.2	2	CTTTCTCCTTAGTGGTCCAT
ESR2	NM_001437	sh228.1	1	GCGAGTAACAAGGGCATGGAA
EXO1	NM_130398	sh113.5	5	CCTGGTAAATGGACTACTAA
EXO1	NM_130398	sh113.4	4	CCAAGCTATGTTTATCTCATT
EXO1	NM_130398	sh113.3	3	GCCACAATACCTTCTCTAT
EXO1	NM_130398	sh113.2	2	GCCGTGTTCAAAGAGCAATAT
EXO1	NM_130398	sh113.1	1	TGCAGACTGCTCAAAGCTTT
FANCA	NM_000135	sh029.5	5	GCTGCTAATGTACAAACGGAT
FANCA	NM_000135	sh029.4	4	CAGAGTTCCTTTGTTGCTGAA
FANCA	NM_000135	sh029.3	3	GCACTGCACCTTGGCATTCAA
FANCA	NM_000135	sh029.2	2	GCACAGGAAATGAGGATATTA
FANCA	NM_000135	sh029.1	1	GCCGACCTCAAGTGTCTATA
FANCB	NM_152633	sh389.5	5	GCTGTATGGAAAGAGAGCTTT
FANCB	NM_152633	sh389.4	4	CGGCTGCTTTATCAGACAGAA
FANCB	NM_152633	sh389.3	3	CCAGTTAAGAATATCTCTCAT
FANCB	NM_152633	sh389.2	2	CCCTTTACAGAGAAATAACTT
FANCB	NM_152633	sh389.1	1	GTTGTTTATCTGAGGAAGAAT
FANCC	NM_000136	sh027.5	5	CCTGGATACAGGGTGTATTAT
FANCC	NM_000136	sh027.4	4	GTGAGAGAAATTGTCTGAGAA
FANCC	NM_000136	sh027.3	3	CACGAGATCATTGGCTTCTT
FANCC	NM_000136	sh027.2	2	CGAGTTTGTGCCACTTATT
FANCC	NM_000136	sh027.1	1	CCTGGAATCATAGCCACTAT
FANCD2	NM_033084	sh118.4	4	CCACTGAGGTATCTCTCAAAA
FANCD2	NM_033084	sh118.3	3	CCTCATACTGTTACTGTATT
FANCD2	NM_033084	sh118.2	2	GCGTCCACTTACTGCAGAATT
FANCD2	NM_033084	sh118.1	1	CGTCTATTAGATTGGAGGATT
FANCE	NM_021922	sh204.10	10	CCCGAACATAAGTCACTGGAA
FANCE	NM_021922	sh204.09	9	GAGCTTCTCCACTGTCTGAAA
FANCE	NM_021922	sh204.08	8	CAGCTTCTTACGAATGTAGT
FANCE	NM_021922	sh204.07	7	GTTCAGTGTCTTAATGGAGAA
FANCE	NM_021922	sh204.06	6	CAAATATACATACCTGTCT
FANCE	NM_021922	sh204.05	5	GATATGCCAGAGGAACCTGAT
FANCE	NM_021922	sh204.04	4	GATGACCAAGTATCAGGCTAA
FANCE	NM_021922	sh204.03	3	CCTCCTTCTGTGCCAAATATA
FANCE	NM_021922	sh204.02	2	CCCGAACATAAGTCACTGGAA
FANCE	NM_021922	sh204.01	1	CCTGAGAAGTTCAAGTGCTTA
FANCF	NM_022725	sh120.5	5	GCTCTTCGTAGTGGTGCATT
FANCF	NM_022725	sh120.4	4	CCTCCACCTCTGAAAGATAAA
FANCF	NM_022725	sh120.3	3	CCACCTGAAAAGATAAAGTT
FANCF	NM_022725	sh120.2	2	GCCTCAGAACAACCTTCTGAA
FANCF	NM_022725	sh120.1	1	GCCATCTTGTAGATTACATTT
FANCG	NM_004629	sh106.5	5	GCCAAAGTCTGTGACCTGTA
FANCG	NM_004629	sh106.4	4	CCTTGAATGTCCCATGCAGTT
FANCG	NM_004629	sh106.3	3	TGAGGAATTAGATGCTCCATT
FANCG	NM_004629	sh106.2	2	GCCTTAAGGATCTGCTGTTA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
FANCG	NM_004629	sh106.1	1	CCTGTGAAATTTGCCCTAGTT
FANCI	NM_018193	sh405.5	5	CAATTGCCACGAAACGGTAATG
FANCI	NM_018193	sh405.4	4	CTAGTTCCTCATAGATCTTAT
FANCI	NM_018193	sh405.3	3	CATGTGGAAGGCACCATTATT
FANCI	NM_018193	sh405.2	2	ATGTAAGCTCGGAGCTAATAT
FANCI	NM_018193	sh405.1	1	ACGGGCATCTGGGAGATATAG
FANCL	NM_018062	sh185.5	5	GCTGAGCAGGAACATACATTT
FANCL	NM_018062	sh185.4	4	GCAGAATTCATTAGGTAATA
FANCL	NM_018062	sh185.3	3	CCTTTCATCAAATATGCTTA
FANCL	NM_018062	sh185.2	2	GCCTTATTGAAGAGATAGGAA
FANCL	NM_018062	sh185.1	1	GCCTGAAGATTTACAAC TGAA
FANCM	NM_020937	sh406.5	5	AGTGTACTAAGGATAGTTTA
FANCM	NM_020937	sh406.4	4	CACACCAGGTAGTGATATAAA
FANCM	NM_020937	sh406.3	3	GACTTCATGAAACTCTATAAT
FANCM	NM_020937	sh406.2	2	ACGTGATGAGACCCGAGTTAT
FANCM	NM_020937	sh406.1	1	AGGACGAGAGGAACGTATTTA
FANCM	NM_020937	sh288.5	5	GACTTCATGAAACTCTATAAT
FANCM	NM_020937	sh288.4	4	ACGTGATGAGACCCGAGTTAT
FANCM	NM_020937	sh288.3	3	AGGACGAGAGGAACGTATTTA
FANCM	NM_020937	sh288.2	2	AGTGTACTAAGGATAGTTTA
FANCM	NM_020937	sh288.1	1	CACACCAGGTAGTGATATAAA
FBXL2	NM_012157	sh357.5	5	GTCTATTACAACAGCTCCTT
FBXL2	NM_012157	sh357.4	4	TGGCCTACTTTAATTCACAAT
FBXL2	NM_012157	sh357.3	3	CTCTCCATTCACTGTCTAAA
FBXL2	NM_012157	sh357.2	2	GATAACCGACAGCACACTCAT
FBXL2	NM_012157	sh357.1	1	GAACCTCAATGGATGCACAAA
FEN1	NM_004111	sh089.5	5	GATGCCTCTATGAGCATTAT
FEN1	NM_004111	sh089.4	4	GCAGTGACTACTGTGAGAGTA
FEN1	NM_004111	sh089.3	3	GCCAAATGAAGAAGAGCTGAT
FEN1	NM_004111	sh089.2	2	CAAGAGCTACTTTGGCCGTAA
FEN1	NM_004111	sh089.1	1	CGTGTATGTCTTTGATGGCAA
FGFR2	NM_000141	sh450.5	5	GCCAACTCTCGAACAGTATT
FGFR2	NM_000141	sh450.4	4	CCCAACAATAGGACAGTGCTT
FGFR2	NM_000141	sh450.3	3	CCGAATGAAGAACACGACCAA
FGFR2	NM_000141	sh450.2	2	GCCACCAACCAATATCCAAAT
FGFR2	NM_000141	sh450.1	1	GCACACACTTACAGAGCACAA
FKBP8	NM_012181	sh169.5	5	AGTGGACATGACGTTTCGAGGA
FKBP8	NM_012181	sh169.4	4	ACGTCGCTGGAGAATGGCACA
FKBP8	NM_012181	sh169.3	3	CAACAAGACGATCCACGCAGA
FKBP8	NM_012181	sh169.2	2	TGAAGGTGAAGTGTCTGAACA
FKBP8	NM_012181	sh169.1	1	GCTGTTGAGGAAGAAGACGCT
FLJ35220	NM_173627	sh037.5	5	CCTGAGCTCGAGTGGTGAT
FLJ35220	NM_173627	sh037.4	4	GAAACGCTGTCTGTGGAAA
FLJ35220	NM_173627	sh037.3	3	CCTGCCACCTTGGCGTCTTA
FLJ35220	NM_173627	sh037.2	2	GTTGACGTGTCTTCGTGAAA
FLJ35220	NM_173627	sh037.1	1	GAGAGTCCTCAGCACTTGT
FN1	NM_002026	sh456.5	5	GCCTGCTCCAAGAATTTGGTTT
FN1	NM_002026	sh456.4	4	TGCAGCACAACCTCGAATTAT
FN1	NM_002026	sh456.3	3	GCCTGCTCCAAGAATTTGGTTT
FN1	NM_002026	sh456.2	2	CGTTGTTATGACAATGGAAA
FN1	NM_002026	sh456.1	1	CGTGGTTGTATCAGGACTTATC
FOLH1	NM_004476	sh097.5	5	CCACTGTATCACAGTGTCTAT
FOLH1	NM_004476	sh097.4	4	CCCAAATAAGACTCATCCCAA
FOLH1	NM_004476	sh097.3	3	CCAATGAAGCTACTAACATTA
FOLH1	NM_004476	sh097.2	2	CCCAACTACATCTCAATAATT
FOLH1	NM_004476	sh097.1	1	GCACGAACTGAAGACTTCTTT
FOLR1	NM_016731	sh183.5	5	GTGAGCAATGGTGGGAAGATT
FOLR1	NM_016731	sh183.4	4	CCAACTTTCATTCTACTT
FOLR1	NM_016731	sh183.3	3	CCTATATAGATTCAACTGGAA
FOLR1	NM_016731	sh183.2	2	GCTTCTCAATGTCTGCATGAA
FOLR1	NM_016731	sh183.1	1	CCCACTGTTCTGTGCAATGAA
FOS	NM_005252	sh451.5	5	TCTGCTTGCAGACCGAGATT
FOS	NM_005252	sh451.4	4	GTGGAACAGTTATCTCCAGAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
FOS	NM_005252	sh451.3	3	CACTGCTTACAGTCTTCCTT
FOS	NM_005252	sh451.2	2	GCGGAGACAGACCAACTAGAA
FOS	NM_005252	sh451.1	1	GCTGGTAGTTAGTAGCATGTT
FOXO3A	NM_001455	sh049.5	5	GTCCTGCATAGTCGATTTCAT
FOXO3A	NM_001455	sh049.4	4	GCAGGCACCATGAATCTGAAT
FOXO3A	NM_001455	sh049.3	3	CTCCTTTAACAGCAGGGTGT
FOXO3A	NM_001455	sh049.2	2	CCACACAGAATGTTGTTGGTT
FOXO3A	NM_001455	sh049.1	1	CAGACCCTCAAAGTACACAA
FOXP3	NM_014009	sh173.5	5	GCCCGGATGTGAGAAGGTCTT
FOXP3	NM_014009	sh173.4	4	CTGAGTCTGCACAAGTGCTTT
FOXP3	NM_014009	sh173.3	3	GCTGGCAAATGGTGTCTGCAA
FOXP3	NM_014009	sh173.2	2	CACACGCATGTTTGCCTTCTT
FOXP3	NM_014009	sh173.1	1	CCTCCACAACATGGACTACTT
FRAP1	NM_004958	sh255.3	3	GCATGGAAGAATACACCTGTA
FRAP1	NM_004958	sh255.2	2	CCTCCTATTGTTAAGTTGTTT
FRAP1	NM_004958	sh255.1	1	CCTGGCAACAATAGGAGAATT
FXN	NM_000144	sh205.5	5	CCATACAGCTTTGAGGACTAT
FXN	NM_000144	sh205.4	4	CAACCAGATTTGGAATGTCAA
FXN	NM_000144	sh205.3	3	GCTGGACTCTTTAGCAGAGTT
FXN	NM_000144	sh205.2	2	GCAGACGCCAAACAAGCAAAT
FXN	NM_000144	sh205.1	1	CCCATCTGTAAATGAGAGAA
FYN	NM_002037	sh263.5	5	GTGCCAACATCCTAGTGCTT
FYN	NM_002037	sh263.4	4	CTTACCATCTGTCTGTCAAA
FYN	NM_002037	sh263.3	3	GCCTATTCACCTTCTATCCGT
FYN	NM_002037	sh263.2	2	GACTCTTAAACAGGCACAAT
FYN	NM_002037	sh263.1	1	GCGATCAGCAAACATTCTAGT
GAD1	NM_000817	sh055.4	4	CAACCAGATGTGTGCAGGATA
GAD1	NM_000817	sh055.3	3	GCTCTCCACTGGATTGGATAT
GAD1	NM_000817	sh055.2	2	GCACGACTGTTTATGGAGCTT
GAD1	NM_000817	sh055.1	1	CGCCATAAACTCAACGGCATA
GTF2H1	NM_005316	sh362.5	5	GTCCATTGAATATGAAGACTT
GTF2H1	NM_005316	sh362.4	4	CCTACAACAAGCTCCACACAT
GTF2H1	NM_005316	sh362.3	3	CCAACTCCAATCCAGTCACTA
GTF2H1	NM_005316	sh362.2	2	GCTGCCATCATCAAGAGATTT
GTF2H1	NM_005316	sh362.1	1	CCTGAATAATAAAGAGGGAAAT
GTF2H2	NM_001515	sh363.5	5	GCTCACTTATTCGTATGGGAT
GTF2H2	NM_001515	sh363.4	4	CCTATTAGTCAGATTGGAATA
GTF2H2	NM_001515	sh363.3	3	CCTGGCTGTATTCATAAGATT
GTF2H2	NM_001515	sh363.2	2	CGCCACCTTTATGTGGTAGTA
GTF2H2	NM_001515	sh363.1	1	GTCACAGAAATACCTGAAATT
GTF2H3	NM_001516	sh364.5	5	GCCTTCTCTCTGCAGTATTT
GTF2H3	NM_001516	sh364.4	4	GCTTGCTTCTGTCTATCGAAAT
GTF2H3	NM_001516	sh364.3	3	GCTGGGAAATTCGCATTTATT
GTF2H3	NM_001516	sh364.2	2	CCGATTCTTATATCTGGAAA
GTF2H3	NM_001516	sh364.1	1	GACTCATCATAGGCTTCTTAA
GTF2H4	NM_001517	sh365.5	5	GAGTGATTCTCTGTTGAACCT
GTF2H4	NM_001517	sh365.4	4	CAGCAGATAATCCATTTCTTA
GTF2H4	NM_001517	sh365.3	3	CTCTGAGATGCTCTATCGGTT
GTF2H4	NM_001517	sh365.2	2	CGGCTCAGCTCTGGTACTTTA
GTF2H4	NM_001517	sh365.1	1	GAACCGAGTACACCTACAATG
GTF2H5	NM_207118	sh366.5	5	GATGACACTCAGTCTTTTGTA
GTF2H5	NM_207118	sh366.4	4	GATCCTGCCATGAAGCAGTTT
GTF2H5	NM_207118	sh366.3	3	TGGGTGAATTAATGGACCAAA
GTF2H5	NM_207118	sh366.2	2	CTGTACTTGGATGAGTCCAAT
GTF2H5	NM_207118	sh366.1	1	CGTCTTTGTAATAGCAGAATT
GZMB	NM_004131	sh081.5	5	GCTTCCTGATACAAGACGACT
GZMB	NM_004131	sh081.4	4	CATTGTCTCTATGGACGAAA
GZMB	NM_004131	sh081.3	3	CATTATTACAGACGACTTACT
GZMB	NM_004131	sh081.2	2	GCTTATCTTATGATCTGGGAT
GZMB	NM_004131	sh081.1	1	CGAATCTGACTTACGCCATTA
H2AFX	NM_002105	sh387.5	5	CCTGCCAACATCCAGGCCGT
H2AFX	NM_002105	sh387.4	4	CAACAAGAAGACGCGAATCAT
H2AFX	NM_002105	sh387.3	3	CCAGGCTCCAGGAGTACTA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
H2AFX	NM_002105	sh387.2	2	CGACAACAAGAAGACGCGAAT
H2AFX	NM_002105	sh387.1	1	CGTTGGCTTCTGAACCTGGAAT
HCP1	NM_080669	sh128.4	4	CCAGGACATCTTAACCCITTA
HCP1	NM_080669	sh128.3	3	CCAGAGAAGTCCAGGAAACAT
HCP1	NM_080669	sh128.2	2	CAGGAAACATTTAGCCCTCTA
HCP1	NM_080669	sh128.1	1	CCTCTCATGTTACAGGATAT
HDAC7	NM_015401	sh420.5	5	GCCAGCAAGATCCTCATTGTA
HDAC7	NM_015401	sh420.4	4	TCCACACAGAAATGTGAACTT
HDAC7	NM_015401	sh420.3	3	GCTACCATGTTTCTGCCAAAT
HDAC7	NM_015401	sh420.2	2	GCTGATCTATGACTCGGCAT
HDAC7	NM_015401	sh420.1	1	GCCCTAGAAGAACAGTCCAT
HEL308	NM_133636	sh397.5	5	GCAACCTTACTGAATTACAAA
HEL308	NM_133636	sh397.4	4	CCCTGATTGGATGATATACTT
HEL308	NM_133636	sh397.3	3	CCTAGTAAGAAGAACTGTGAA
HEL308	NM_133636	sh397.2	2	GCAGAACTCTCAAATGATTT
HEL308	NM_133636	sh397.1	1	GCAAATTGTTTCATCAGCAAA
HGF	NM_000601	sh011.5	5	TGTCTGAAGCACCCACCAATA
HGF	NM_000601	sh011.4	4	GCAAGTAAGTGAATGAGAAT
HGF	NM_000601	sh011.3	3	GCAAAGACTACCTAATCAAAA
HGF	NM_000601	sh011.2	2	CAGACCAATGTGCTAATAGAT
HGF	NM_000601	sh011.1	1	CCCCTAATATCTTGTGCCAAA
HIF1A	NM_001530	sh209.5	5	TGCTCTTGTGGTTGGATCTA
HIF1A	NM_001530	sh209.4	4	CGGCGAAGTAAAGAATCTGAA
HIF1A	NM_001530	sh209.3	3	GTGATGAAAGAATTACCGAAT
HIF1A	NM_001530	sh209.2	2	CCAGTTATGATTGTGAAGTTA
HIF1A	NM_001530	sh209.1	1	CCGCTGGAGACACAATCATAT
HIF1A	NM_001530	sh043.5	5	TGCTCTTGTGGTTGGATCTA
HIF1A	NM_001530	sh043.4	4	CGGCGAAGTAAAGAATCTGAA
HIF1A	NM_001530	sh043.3	3	GTGATGAAAGAATTACCGAAT
HIF1A	NM_001530	sh043.2	2	CCAGTTATGATTGTGAAGTTA
HIF1A	NM_001530	sh043.1	1	CCGCTGGAGACACAATCATAT
HIST1H2BE	NM_003523	sh445.5	5	GAATTCCTTTGTCAACGACAT
HIST1H2BE	NM_003523	sh445.4	4	CGTGACCAAGCGCAGAAAGAA
HIST1H2BE	NM_003523	sh445.3	3	CTACTCCGTATACGTGTACAAA
HIST1H2BE	NM_003523	sh445.2	2	CGGCATCTCCTCTAAAGCCAT
HIST1H2BE	NM_003523	sh445.1	1	GATCATGAATTCCTTGTCAA
HMGB1	NM_002128	sh252.5	5	CCCAGATGCTTCAGTCAACTT
HMGB1	NM_002128	sh252.4	4	GCAGATGACAAGCAGCCTTAT
HMGB1	NM_002128	sh252.3	3	CCGTTATGAAAGAGAAATGAA
HMGB1	NM_002128	sh252.2	2	GAAGAAGATGAAGATGAAGAA
HMGB1	NM_002128	sh252.1	1	CGAGACTTTCATTACAAGTAT
HPGD	NM_000860	sh455.5	5	ACTCATAACAACACAGACATA
HPGD	NM_000860	sh455.4	4	GCTGGAGTGAATAATGAGAAA
HPGD	NM_000860	sh455.3	3	GCAACAACCTGAGAGACATTT
HPGD	NM_000860	sh455.2	2	GAAGGCGGCATCATTATCAAT
HPGD	NM_000860	sh455.1	1	CACAGCCATCCTTGAATCAAT
HSP90AA1	NM_005348	sh093.5	5	CCCTCTAAACATATCCCCTGA
HSP90AA1	NM_005348	sh093.4	4	GAAGGATGGTGACAAGAAGAA
HSP90AA1	NM_005348	sh093.3	3	TCATCAATACTTTCTACTCGA
HSP90AA1	NM_005348	sh093.2	2	CCAGAATGAAGGAGAACCAGA
HSP90AA1	NM_005348	sh093.1	1	GTTATCCTACACCTGAAAGAA
HSP90B1	NM_003299	sh293.5	5	GCGAGACTCTTCAGCAACATA
HSP90B1	NM_003299	sh293.4	4	GCTTTAGATAAGATAAGGCTA
HSP90B1	NM_003299	sh293.3	3	CGACGAATTAAGGAAGATGAA
HSP90B1	NM_003299	sh293.2	2	CGTGGTCTGTTTGACGAATAT
HSP90B1	NM_003299	sh293.1	1	CCTGTGGATGAATACTGTATT
HUS1	NM_004507	sh102.5	5	TCACCTTGTTATTGAAGCAAA
HUS1	NM_004507	sh102.4	4	CGTGTCCCTTCAGTATTTTCAAT
HUS1	NM_004507	sh102.3	3	CCACTTCACACGAATCAGTAA
HUS1	NM_004507	sh102.2	2	GAGAACTTCTTCAACGAATTT
HUS1	NM_004507	sh102.1	1	GCCTTATGCAATATTGTGAAT
ICMT	NM_012405	sh329.5	5	CCTGGAGTATAAGAAGAGGGT
ICMT	NM_012405	sh329.4	4	GATCGAACAGAAGAAGAAGAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
ICMT	NM_012405	sh329.3	3	GTTCCACTATTCTGAATACTT
ICMT	NM_012405	sh329.2	2	CTTCGGAGAATGCTGAGGAA
ICMT	NM_012405	sh329.1	1	GCTGCTCTTTCTTCTGGTTA
IFNG	NM_000619	sh053.5	5	TGTTTCAAGGTGCAAGAGCAT
IFNG	NM_000619	sh053.4	4	CTCATCCAAGTGATGGCTGAA
IFNG	NM_000619	sh053.3	3	GCAGAGCCAATTTGTCTCCTT
IFNG	NM_000619	sh053.2	2	CATTAGATGTAGCGGATAAT
IFNG	NM_000619	sh053.1	1	GACTTGAATGTCCAACGCAAA
IKBKB	NM_001556	sh046.5	5	CCATGATGAATCTCTCCGAA
IKBKB	NM_001556	sh046.4	4	CGGAAGTACCTGAACCACTTT
IKBKB	NM_001556	sh046.3	3	GCTGGTTCATATCTTGAACAT
IKBKB	NM_001556	sh046.2	2	CCAGCCAAGAAGAGTGAAGAA
IKBKB	NM_001556	sh046.1	1	GCACTGGGAAAGTATCTGAAA
IKBKG	NM_003639	sh086.5	5	GAGGGAGTACAGCAAACTGAA
IKBKG	NM_003639	sh086.4	4	GAGAATCAAGAGTCCGAGAT
IKBKG	NM_003639	sh086.3	3	GCAGCACAAGATTGTGATGGA
IKBKG	NM_003639	sh086.2	2	GCTCGATCTGAAGAGCCAGAA
IKBKG	NM_003639	sh086.1	1	CCAAGAATACGACAACCAT
IL1A	NM_000575	sh347.5	5	GCTTACCTTCAAGGAGAGCAT
IL1A	NM_000575	sh347.4	4	CCAATGACTCAGAGGAAGAAA
IL1A	NM_000575	sh347.3	3	CGTGATTCTAAGAATCTCAA
IL1A	NM_000575	sh347.2	2	CCACCTCTATCACTGACTTT
IL1A	NM_000575	sh347.1	1	GCCCTCAATCAAAGTATAATT
IL8	NM_000584	sh321.5	5	CAAGAGAATATCCGAACITTA
IL8	NM_000584	sh321.4	4	CCGAACITTAATTTTCAGGAAT
IL8	NM_000584	sh321.3	3	CAAGGAGTGCTAAAGAACTTA
IL8	NM_000584	sh321.2	2	GCTCTGTGTGAAGGTGCAGTT
IL8	NM_000584	sh321.1	1	ACTTAGATGTCAGTGCATAAA
IL8	NM_000584	sh024.5	5	CTGCGCCAACACAGAAATTAT
IL8	NM_000584	sh024.4	4	GCTCTGTGTGAAGGTGCAGTT
IL8	NM_000584	sh024.3	3	CAAGGAGTGCTAAAGAACTTA
IL8	NM_000584	sh024.2	2	GCCAACACAGAAATTATTGTA
IL8	NM_000584	sh024.1	1	CCGAACITTAATTTTCAGGAAT
IL8RB	NM_001557	sh045.5	5	CGTACTTGGTCAAATTCATA
IL8RB	NM_001557	sh045.4	4	GCACACTTCCACTACTCTCTA
IL8RB	NM_001557	sh045.3	3	CCGTCTACTCATCCAATGTTA
IL8RB	NM_001557	sh045.2	2	CCCTGGAAATCAACAAGTATT
IL8RB	NM_001557	sh045.1	1	GCCACTAAATTGACACTTAAA
IRF1	NM_002198	sh061.5	5	GCGTGTCTTCACAGATCTGAA
IRF1	NM_002198	sh061.4	4	AGATGCTAAGAGCAAGGCCAA
IRF1	NM_002198	sh061.3	3	GCAGATTAATTTCAACCAAT
IRF1	NM_002198	sh061.2	2	CCTCTGTCTATGGAGACTTTA
IRF1	NM_002198	sh061.1	1	CGTGTGGATCTTGCCACATTT
IRF2	NM_002199	sh062.5	5	GCAGATAAACTCCAACACGAT
IRF2	NM_002199	sh062.4	4	GCGGTCTGACTTCAACTATA
IRF2	NM_002199	sh062.3	3	CCAGGAGTAGATAAACCTGAT
IRF2	NM_002199	sh062.2	2	CCAGACATTTGCCAAGTTGTA
IRF2	NM_002199	sh062.1	1	CGGACGAGATAATGTGAACCTA
ITGA5	NM_002205	sh412.5	5	CTCCTATATGTGACCAGAGTT
ITGA5	NM_002205	sh412.4	4	CCTCAGGAACGAGTCAGAATT
ITGA5	NM_002205	sh412.3	3	CCACTGTGGATCATCATCCTA
ITGA5	NM_002205	sh412.2	2	CCATGATGAGTTTGGCCGATT
ITGA5	NM_002205	sh412.1	1	CCACAGATAACTTCAACCGAA
ITGB3	NM_000212	sh410.5	5	GATGCAGTGAATTTGACCTAT
ITGB3	NM_000212	sh410.4	4	CCTTAGCCTTTGTCCCAGAAT
ITGB3	NM_000212	sh410.3	3	CCACGTCTACCTTCAACCAATA
ITGB3	NM_000212	sh410.2	2	GTCGTGAGATCCAGACTAT
ITGB3	NM_000212	sh410.1	1	CTCATATAGCATTGGACGGAA
KDM1A (LSD1)	NM_001009999.2	sh417.5	5	CCACGAGTCAAACCTTTATTT
KDM1A (LSD1)	NM_001009999.2	sh417.4	4	GCCTAGACATTAACCTGAATA
KDM1A (LSD1)	NM_001009999.2	sh417.3	3	GCTACATCTTACCTTAGTCATC
KDM1A (LSD1)	NM_001009999.2	sh417.2	2	CCAACAATTAGAAGCACCTTA
KDM1A (LSD1)	NM_001009999.2	sh417.1	1	GCTCCAATACTGTTGGCACTA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
KDR	NM_002253	sh274.5	5	GTGGTCTCTCGTTGTGTAT
KDR	NM_002253	sh274.4	4	CTTFACTATCCCAGCTACAT
KDR	NM_002253	sh274.3	3	GTGCTGTTTCTGACTCCTAAT
KDR	NM_002253	sh274.2	2	AGGCTAATACAACCTTCAAA
KDR	NM_002253	sh274.1	1	GCGGCACGAAATATCCTCTTA
LAMP2	NM_002294	sh232.5	5	GAAGTGAACATCAGCATGTAT
LAMP2	NM_002294	sh232.4	4	CCAAGGCAGCATCTACTTATT
LAMP2	NM_002294	sh232.3	3	GCCATCAGAATTCATTGAAT
LAMP2	NM_002294	sh232.2	2	CTGGAGCATTTCAGATAAATA
LAMP2	NM_002294	sh232.1	1	GTACGCTATGAAACTACAAAT
LIG1	NM_000234	sh370.5	5	CTGAAACCAATGTTGGCCAT
LIG1	NM_000234	sh370.4	4	CCAAGAAAGAGGGTAAAGCAA
LIG1	NM_000234	sh370.3	3	GCTCAAGCTGAAGAAGGACTA
LIG1	NM_000234	sh370.2	2	CGGTTTATTCGAGTCCGTGAA
LIG1	NM_000234	sh370.1	1	CCTGCCAAGAACAACATCAT
LIG3	NM_002311	sh070.5	5	CAGGAGTCATTAAGACTGTTT
LIG3	NM_002311	sh070.4	4	GCCAGTACCAAGAAAGCAGAA
LIG3	NM_002311	sh070.3	3	GCTGAGTAACTCCAACAGCAA
LIG3	NM_002311	sh070.2	2	CCGGATCATGTTCTCAGAAAT
LIG3	NM_002311	sh070.1	1	GCCCACTTTAAGGACTACATT
LIG4	NM_002312	sh066.10	10	TTGCTATGGTGATAGTTATTT
LIG4	NM_002312	sh066.09	9	GGTGAGATGATGGCCTATAAT
LIG4	NM_002312	sh066.08	8	ATGCATTCAAAGCAGATATAC
LIG4	NM_002312	sh066.07	7	GCTGATTAGAATATCGGTAT
LIG4	NM_002312	sh066.06	6	GCCAGCAATAATTCTGCTAAA
LIG4	NM_002312	sh066.05	5	GCTGATTTAGAATATCGGTAT
LIG4	NM_002312	sh066.04	4	GCCAGCAATAATTCTGCTAAA
LIG4	NM_002312	sh066.03	3	GCTCGCATCTAAACACCTTTA
LIG4	NM_002312	sh066.02	2	GCCCGTGAATATGATTGCTAT
LIG4	NM_002312	sh066.01	1	GCTAGGTTTCTAGTAGGAGAA
LKB1	NM_000455	sh262.5	5	GAAGAAGAAGTTGCGAAGGAT
LKB1	NM_000455	sh262.4	4	CATCTACACTCAGGACTTCAC
LKB1	NM_000455	sh262.3	3	GAGTGTGCGGTCAATATTTAT
LKB1	NM_000455	sh262.2	2	GCCAACGTGAAGAAGGAAATT
LKB1	NM_000455	sh262.1	1	GATCCTCAAGAAGAAGAAGTT
MAD2L1	NM_002358	sh241.2	2	CGAGTTCTTCTCATTCCGCAT
MAD2L1	NM_002358	sh241.1	1	CCTATTGAATCAGTTTCCAAT
MAD2L2	NM_006341	sh379.5	5	CATCTTCCAGAAACGCAAGAA
MAD2L2	NM_006341	sh379.4	4	CACTCGCAACATGGAGAAGAT
MAD2L2	NM_006341	sh379.3	3	CCCAGTGGAGAAATTCGTCTT
MAD2L2	NM_006341	sh379.2	2	CCCGGAGCTGAATCAGTATAT
MAD2L2	NM_006341	sh379.1	1	CCCTGATTTCCAAGTCTCTTA
MAP1LC3B	NM_022818	sh129.5	5	CGCACCTTCAACAAAGAGTA
MAP1LC3B	NM_022818	sh129.4	4	CCCGGTGATAATAGAACGATA
MAP1LC3B	NM_022818	sh129.3	3	GAGTAGAAGATGTCCGACTTA
MAP1LC3B	NM_022818	sh129.2	2	CGAACAAAGAGTAGAAGATGT
MAP1LC3B	NM_022818	sh129.1	1	GTTTCGGGATGAAATTGTCACT
MAP3K7	NM_145332	sh031.5	5	TCCTGCCACAAATGATACTAT
MAP3K7	NM_145332	sh031.4	4	GACACACATGACCAATAACAA
MAP3K7	NM_145332	sh031.3	3	CAGTGTGCTTGTGATGGAAT
MAP3K7	NM_145332	sh031.2	2	CCCGTGTGAACCATCCTAATA
MAP3K7	NM_145332	sh031.1	1	GCAGTGATTCTTGATTGTTT
MAP3K7IP1	NM_006116	sh132.5	5	GCGATGATTGACTGAGTTT
MAP3K7IP1	NM_006116	sh132.4	4	GCCTCCTCAGTATCAGAAGAT
MAP3K7IP1	NM_006116	sh132.3	3	GTTGAGCCATATGTGGACTTT
MAP3K7IP1	NM_006116	sh132.2	2	CGTGCCAAGTCCAAACCAAT
MAP3K7IP1	NM_006116	sh132.1	1	CCTTTGAGACACAGTAACCTT
MAP3K7IP2	NM_015093	sh170.5	5	TGGCCCTGTATCTTCTCTAAA
MAP3K7IP2	NM_015093	sh170.4	4	CCTGCCTTTATTCATCCCAT
MAP3K7IP2	NM_015093	sh170.3	3	GCATCTAATCCTCTGTACAT
MAP3K7IP2	NM_015093	sh170.2	2	CCTGAAGTACCTGAAGTTGTT
MAP3K7IP2	NM_015093	sh170.1	1	AGATTGACATTGACTGCTTAA
MBD4	NM_003925	sh085.5	5	GTGTACTTTATCAGCCACAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
MBD4	NM_003925	sh085.4	4	GCAACGACTCTTACCGAATTT
MBD4	NM_003925	sh085.3	3	GCCAAGTAGTAGTTCAGAGTT
MBD4	NM_003925	sh085.2	2	CCCACGACGTAAGCCTTTAA
MBD4	NM_003925	sh085.1	1	GCCTAGTGTGTGTCTTTCTT
MCPH1	NM_024596	sh403.5	5	CGTAAATGTATGCAGCCAAA
MCPH1	NM_024596	sh403.4	4	GAGACGTTTGAAGAGAAGTAT
MCPH1	NM_024596	sh403.3	3	GCCAACAAGAACATTAGTCAT
MCPH1	NM_024596	sh403.2	2	GCAATGGAGAAGAGATTACAA
MCPH1	NM_024596	sh403.1	1	GCCATGTGTTGTGTTCTTAA
MEN1	NM_000244	sh269.5	5	GAGTTCCTTGAAGTAGCCAAT
MEN1	NM_000244	sh269.4	4	GCTGCGATTCTACGACGGCAT
MEN1	NM_000244	sh269.3	3	GTGCAGATGAAGAAGCAGAAA
MEN1	NM_000244	sh269.2	2	GCTGTACCTGAAAGGATCATA
MEN1	NM_000244	sh269.1	1	CCGAGTACAGTCTGTATCAAA
MET	NM_000245	sh018.5	5	GCCAGCCTGAATGATGACATT
MET	NM_000245	sh018.4	4	CGAGCTAAATATAGAGTGGAA
MET	NM_000245	sh018.3	3	CGTACTTATGTGAACGTAAA
MET	NM_000245	sh018.2	2	GCACGATGAATACATTGAAAT
MET	NM_000245	sh018.1	1	ATCAGAACCAGAGGCTTGTC
MGMT	NM_002412	sh340.5	5	GGAGGAGCAATGAGAGGCAAT
MGMT	NM_002412	sh340.4	4	TTACCAGCAATTAGCAGCCCT
MGMT	NM_002412	sh340.3	3	CTTACCAGCAATTAGCAGCC
MGMT	NM_002412	sh340.2	2	TCTTACCAGCAATTAGCAGCC
MGMT	NM_002412	sh340.1	1	GCTGTATTAAGGAAGTGGCA
MLH1	NM_000249	sh019.5	5	CCTCAGTAAAGAATGCGCTAT
MLH1	NM_000249	sh019.4	4	CCAAGTGAAGAATATGGGAAA
MLH1	NM_000249	sh019.3	3	GCAGACTATTTCTTTGGAA
MLH1	NM_000249	sh019.2	2	GCCTGATCTATACAAAGTCTT
MLH1	NM_000249	sh019.1	1	GTGTTCTTCTTCTCTGTATT
MLH3	NM_014381	sh336.5	5	CGCTTAGAGAACTCTGATGTTT
MLH3	NM_014381	sh336.4	4	CCACACAGGATAATTCCTTTA
MLH3	NM_014381	sh336.3	3	GCTACATAAACTCATTGACTT
MLH3	NM_014381	sh336.2	2	GCTGAGAGCTTAGCAGTTAACT
MLH3	NM_014381	sh336.1	1	GCTGACATAGACCATTGGAA
MLXIP	NM_014938	sh282.5	5	TGCTACTAAAGAACCAGGAGAT
MLXIP	NM_014938	sh282.4	4	GTGTCCTTGGTGTGAAGAAT
MLXIP	NM_014938	sh282.3	3	GCTCTCGAGTGCATGACTTT
MLXIP	NM_014938	sh282.2	2	CGCCAGTTTGATCACATGAAA
MLXIP	NM_014938	sh282.1	1	GAGATTGTGATCCGGGAGTAT
MLXIPL	NM_032951	sh280.5	5	CGCCTTCTGAGTCTTGATTT
MLXIPL	NM_032951	sh280.4	4	GCCTCTGTTTGAGCTTCAA
MLXIPL	NM_032951	sh280.3	3	GCAATGGTGCAACAGCTCTT
MLXIPL	NM_032951	sh280.2	2	CCCAAGTGAAGAATTTCAAA
MLXIPL	NM_032951	sh280.1	1	GCTGAGTACATCCTTATGCTA
MMP13	NM_002427	sh409.5	5	GCTCCGAGAAATGCAGTCTTT
MMP13	NM_002427	sh409.4	4	CCAACCGTATTGATGCTGCAT
MMP13	NM_002427	sh409.3	3	CGAACTCTTAAATGGTCCAAA
MMP13	NM_002427	sh409.2	2	CCGAGGAGAAACAATGATCTT
MMP13	NM_002427	sh409.1	1	CCGATGTAACCTCTGAATT
MMS19L	NM_022362	sh203.5	5	TGGAGCTATGAAGACAAAGAT
MMS19L	NM_022362	sh203.4	4	CCGACACAGCTTACAATAT
MMS19L	NM_022362	sh203.3	3	CCTGCCTCGAAATGTGGAAAT
MMS19L	NM_022362	sh203.2	2	CCAGCGGTTCTTACAGATAA
MMS19L	NM_022362	sh203.1	1	CCTGGGTCTCTTGACATTTATA
MNAT1	NM_002431	sh369.5	5	GCCACTGCAGATAGAGACATA
MNAT1	NM_002431	sh369.4	4	CTCTGTGAAAGTTGTGTAGAT
MNAT1	NM_002431	sh369.3	3	GTGGATTTGGACAACACCAAA
MNAT1	NM_002431	sh369.2	2	GCTATACTTCTTCTCTTGCTT
MNAT1	NM_002431	sh369.1	1	CCTAGTCTAAGAGAATACAAT
MPG	NM_002434	sh008.5	5	CCCATACCGCAGCATCTATTT
MPG	NM_002434	sh008.4	4	CCTGTACGTGTACATCATTTA
MPG	NM_002434	sh008.3	3	GTACATCATTTACGGCATGTA
MPG	NM_002434	sh008.2	2	CGACTTCTAATGGCAGAGAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
MPG	NM_002434	sh008.1	1	CATCTATTCTCAAGCCAAA
MRE11A	NM_005591	sh140.4	4	CGATTTCTTAAAGAAGCAT
MRE11A	NM_005591	sh140.3	3	CCACTCAAAGACAGATCAAA
MRE11A	NM_005591	sh140.2	2	GCTGCGTATTAAGGGAGGAA
MRE11A	NM_005591	sh140.1	1	GCCCACATCTTTATTGAAGCTT
MSH2	NM_000251	sh016.5	5	GCCAGTATATGAAATTGGATA
MSH2	NM_000251	sh016.4	4	GCATGTAATAGAGTGTGCTAA
MSH2	NM_000251	sh016.3	3	GCCTTGCTGAATAAGTGTAAG
MSH2	NM_000251	sh016.2	2	CCTGGCAATCTCTCAGTTT
MSH2	NM_000251	sh016.1	1	CCAGTAATGGAATGAAGGTAA
MSH3	NM_002439	sh317.5	5	GCAAGGAGTTATGGATTAAT
MSH3	NM_002439	sh317.4	4	CCACTCCTTAAATTAAGGGAA
MSH3	NM_002439	sh317.3	3	CGGAGTACATTTATGGAAGAA
MSH3	NM_002439	sh317.2	2	GCCATTTAGATCACAACCTTA
MSH3	NM_002439	sh317.1	1	GCACAGAAGGAATAAGGTCAT
MSH4	NM_002440	sh318.5	5	GAGGTGAAATAGGAATGGCAA
MSH4	NM_002440	sh318.4	4	CCAGATGACTACAGATTGTAT
MSH4	NM_002440	sh318.3	3	GCAGGAATGATATCACAACCT
MSH4	NM_002440	sh318.2	2	GCCAAGAATCTTTGAGAGAAA
MSH4	NM_002440	sh318.1	1	GCTAATGACAAATCGCTCATA
MSH5	NM_025259	sh319.5	5	GACGCCATCTTACACGAATT
MSH5	NM_025259	sh319.4	4	CCTCTCTCCATTATCCCTT
MSH5	NM_025259	sh319.3	3	CCAGACATTAGTGGAATAAGTT
MSH5	NM_025259	sh319.2	2	CCCAACATAGATCCTGAAATT
MSH5	NM_025259	sh319.1	1	CCACCCAGGATCAAAGGAA
MSH6	NM_000179	sh025.5	5	GCGGCGACTGTTCTATAACTT
MSH6	NM_000179	sh025.4	4	CGGGGACTGTTCTATAACTTT
MSH6	NM_000179	sh025.3	3	GCAGATTAAGTCTCAGAACTT
MSH6	NM_000179	sh025.2	2	CCAGAAGAATACGAGTTGAAA
MSH6	NM_000179	sh025.1	1	GCCAGAAGAATACGAGTTGAA
MUS81	NM_025128	sh116.5	5	CACGCGCTTCGTATTTAGAAA
MUS81	NM_025128	sh116.4	4	ACTCAGGTCATTGATGGCTTT
MUS81	NM_025128	sh116.3	3	CGCAGGAGCCATCAAGAATAA
MUS81	NM_025128	sh116.2	2	CCTAATGGTCAACCATCTTTA
MUS81	NM_025128	sh116.1	1	GAGTTGGTACTGGATCATT
MUTYH	NM_012222	sh182.4	4	AGCTGGTACGACCAAGAGAAA
MUTYH	NM_012222	sh182.3	3	CAAGTCCTGGATAATTTCTTT
MUTYH	NM_012222	sh182.2	2	CCACTGTGATCAACTACTATA
MUTYH	NM_012222	sh182.1	1	CAAGCTGACATATCAAGTATA
MYC	NM_002467	sh434.5	5	CAGGAACTATGACCTCGACTA
MYC	NM_002467	sh434.4	4	CAGTTGAAACACAAACTTGAA
MYC	NM_002467	sh434.3	3	CCATAATGTAAACTGCCTCAA
MYC	NM_002467	sh434.2	2	CCTGAGACAGATCAGCAACA
MYC	NM_002467	sh434.1	1	CCTGAGACAGATCAGCAACA
NADK	NM_023018	sh283.5	5	CCAGGAGAACATGATCGTGTA
NADK	NM_023018	sh283.4	4	GAGAACTTTCAGTCCCAAGTT
NADK	NM_023018	sh283.3	3	GCATCAGCATCACTACTCAT
NADK	NM_023018	sh283.2	2	TCGAGAAGATTATGATGACAT
NADK	NM_023018	sh283.1	1	CGATGAGACCTGGAGTTACAA
NAPRT1	NM_145201	sh309.5	5	GCAGTGAGGTGAATGTCATTG
NAPRT1	NM_145201	sh309.4	4	CTCATGGACATGCTGCAGTTA
NAPRT1	NM_145201	sh309.3	3	GTCAGTCTCATCGTAGTCAG
NAPRT1	NM_145201	sh309.2	2	CACCATGGCGTTGGGCTATTG
NAPRT1	NM_145201	sh309.1	1	TTCCCTGGGTGGCGTCTATAA
NBN	NM_002485	sh068.5	5	CCTCTTGATGAACATCTATT
NBN	NM_002485	sh068.4	4	GCAAGCAGATACATGGGATTT
NBN	NM_002485	sh068.3	3	GCTCGAAAAGAATACAGAACTA
NBN	NM_002485	sh068.2	2	GCCGAAATCATGCTGTGTTAA
NBN	NM_002485	sh068.1	1	GCTTATTTAGAGTCCAGTTT
NEIL1	NM_024608	sh115.5	5	CAGAGGTTCTTCAATGGCATT
NEIL1	NM_024608	sh115.4	4	GAGCCAGAAGATAAGGACCAA
NEIL1	NM_024608	sh115.3	3	CCGGAAGGTCAAGGCTGACAT
NEIL1	NM_024608	sh115.2	2	CGCCTATGTTTCGTGGACAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
NEIL1	NM_024608	sh115.1	1	GCTACGAAACCTAGCGGATAA
NEIL2	NM_145043	sh034.5	5	CCATGGAAAGAAATTATTCTCT
NEIL2	NM_145043	sh034.4	4	CATCATTAAAGAATGAAGCCTT
NEIL2	NM_145043	sh034.3	3	GAACGATTCTCCAGAGCCAA
NEIL2	NM_145043	sh034.2	2	GCTAGGGAACATCATTAAAGAA
NEIL2	NM_145043	sh034.1	1	CGTGTGAGCTTTGGTTTGTTT
NEIL3	NM_018248	sh172.5	5	GCTACCGACTAGAAATACTAT
NEIL3	NM_018248	sh172.4	4	GCCTGTTAATGGATATGTTT
NEIL3	NM_018248	sh172.3	3	CCTGGATATTCTAACAGTGAA
NEIL3	NM_018248	sh172.2	2	CGGATTCATTTGCGAATGAAA
NEIL3	NM_018248	sh172.1	1	CGGATATACAGCATATTTCCAT
NEK1	NM_012224	sh404.5	5	CCTTGCTGATTGGACTTTCAA
NEK1	NM_012224	sh404.4	4	CGCCAACAGATTAAGGCCAAA
NEK1	NM_012224	sh404.3	3	CCGCTAAATATGGAATACCTT
NEK1	NM_012224	sh404.2	2	CGAGAAATACTTCGTAGATTA
NEK1	NM_012224	sh404.1	1	CCTCAACTATATGAAAGCATT
NEK11	NM_024800	sh302.5	5	CCTTACCTTGATGAGCAGCTA
NEK11	NM_024800	sh302.4	4	CACCAAGGCTATGACACAAAAG
NEK11	NM_024800	sh302.3	3	GTTGGAGAATAATCCAAAT
NEK11	NM_024800	sh302.2	2	GAACCTAATGTGTAGATATTC
NEK11	NM_024800	sh302.1	1	GCCTATGCTTGGAGTCATAAG
NFKB1	NM_003998	sh083.5	5	CGAATGACAGAGGCGTGTATA
NFKB1	NM_003998	sh083.4	4	CCTTTCCTCTACTATCCTGAA
NFKB1	NM_003998	sh083.3	3	GCCTGAACAAATGTTTCATTT
NFKB1	NM_003998	sh083.2	2	CCAGAGTTTACATCTGATGAT
NFKB1	NM_003998	sh083.1	1	CGCCTGAATCATTCTCGATTT
NIBP	NM_031466	sh126.5	5	GCTTCTGTCATCTATCACTAT
NIBP	NM_031466	sh126.4	4	CCTCGAAAGTTCTCACCCTA
NIBP	NM_031466	sh126.3	3	CCGTTTGAACCTCGAGTTGAA
NIBP	NM_031466	sh126.2	2	CGTTTGAACCTCGAGTTGAAA
NIBP	NM_031466	sh126.1	1	CCTTTGGCCATAGAAAGAAAT
NIFUN	NM_014301	sh206.5	5	CCAGCTCATTAGCCTGAAT
NIFUN	NM_014301	sh206.4	4	AGATTGTGGATGCTAGGTTTA
NIFUN	NM_014301	sh206.3	3	GTCCCTTGACAAGACATCTAA
NIFUN	NM_014301	sh206.2	2	GCATGTGGTGACGTAATGAAA
NIFUN	NM_014301	sh206.1	1	CCTGGCTGATTACAAATTGAA
NMNAT1	NM_022787	sh225.5	5	GAAACACAAGATTCTAGTCAA
NMNAT1	NM_022787	sh225.4	4	GCAGATTTATTGGAGTCTTT
NMNAT1	NM_022787	sh225.3	3	CCCAATTTGTGGAAGAGTGAA
NMNAT1	NM_022787	sh225.2	2	CGCTACTTGGTACCAGATCTT
NMNAT1	NM_022787	sh225.1	1	GTGGAAGTTGATAACATGGGAA
NMNAT2	NM_015039	sh226.5	5	GCCCATTTACCAGAACAGCAA
NMNAT2	NM_015039	sh226.4	4	GAGGTGATTGTTGGTGACTTT
NMNAT2	NM_015039	sh226.3	3	CACTCCTCAATACTCCGCAA
NMNAT2	NM_015039	sh226.2	2	GCCAGGGATTATCTGCACAAA
NMNAT2	NM_015039	sh226.1	1	CGGTATGAAGAGATTGAGCTA
NMNAT3	NM_178177	sh227.5	5	CGATGCTGTCATCACGTACAT
NMNAT3	NM_178177	sh227.4	4	GAATGAGATCAGTGCCACATA
NMNAT3	NM_178177	sh227.3	3	TCTCCTGTCAACGACCTAT
NMNAT3	NM_178177	sh227.2	2	CAGGAAATAGTGGAGAAGTTT
NMNAT3	NM_178177	sh227.1	1	GCAGAGCGTAAAGTACCTGAT
NOTCH1	NM_017617	sh341.5	5	CAAAGACATGACCAGTGGCTA
NOTCH1	NM_017617	sh341.4	4	GCCGAACCAATACAACCTCT
NOTCH1	NM_017617	sh341.3	3	CGTGCCTGGACAAGATCAATC
NOTCH1	NM_017617	sh341.2	2	CTTTGTTTCAGTTTCAGTATT
NOTCH1	NM_017617	sh341.1	1	GATGCCAAATGCCTGCCAGAA
NOX4	NM_016931	sh413.5	5	GAGCCTCAGCATGTTCTTA
NOX4	NM_016931	sh413.4	4	CAGAGTTTACCAGCACAAAT
NOX4	NM_016931	sh413.3	3	CCTGTGGTGTACTATCTGTA
NOX4	NM_016931	sh413.2	2	CCCTCAACTTCTCAGTGAATT
NOX4	NM_016931	sh413.1	1	GCTGTATATTGATGGTCTTTC
NR4A1	NM_002135	sh444.5	5	GTACATCTGCCTGGCTAACAA
NR4A1	NM_002135	sh444.4	4	GCCAAACTGGACTACTCCAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
NR4A1	NM_002135	sh444.3	3	GTCACGTCTGTTGGGCAAACT
NR4A1	NM_002135	sh444.2	2	TCCTTCCACATGTACATAAAC
NR4A1	NM_002135	sh444.1	1	CAACGCTTCATGCCAGCATT
NRP1	NM_003873	sh275.5	5	CAGCCTTGAATGCACTTATAT
NRP1	NM_003873	sh275.4	4	CCGAGAGAACAAGGTGTTTCAT
NRP1	NM_003873	sh275.3	3	GCTGTGGATGACATTAGTATT
NRP1	NM_003873	sh275.2	2	CGGACCCATACCAGAGAATTA
NRP1	NM_003873	sh275.1	1	GCAACGATAAATGTGGCGATA
NT5E (CD73)	NM_002526.1	sh459.5	5	CAGGACTTATTTGCCATATA
NT5E (CD73)	NM_002526.1	sh459.4	4	GCACCTGGGAAATCATGAATTT
NT5E (CD73)	NM_002526.1	sh459.3	3	CCCATTGATGAACGCAACAAT
NT5E (CD73)	NM_002526.1	sh459.2	2	CCTCTCAATCATGCCGCTTTA
NT5E (CD73)	NM_002526.1	sh459.1	1	CCCAGTTATGACCTCTCAAA
NTHL1	NM_002528	sh060.5	5	GCACGAGATCAATGGACTCTT
NTHL1	NM_002528	sh060.4	4	GCATGTGCACAGATCGCCAA
NTHL1	NM_002528	sh060.3	3	GATGCTCTCCAGCAAACCAA
NTHL1	NM_002528	sh060.2	2	GAGCAAGGTGAAATACATCAA
NTHL1	NM_002528	sh060.1	1	CTGGAGGAGCAAGGTGAAATA
NUDT1	NM_002452	sh384.5	5	CGAGTTCTCTGGGCATGAAA
NUDT1	NM_002452	sh384.4	4	CGAGTTCTCTGGGCATGAAA
NUDT1	NM_002452	sh384.3	3	CCTGAGCTCATGGACGTGCAT
NUDT1	NM_002452	sh384.2	2	CCCACGACAGCTACTGGTTT
NUDT1	NM_002452	sh384.1	1	CCTGCTTCAGAAGAAGAAATT
NUDT12	NM_031438	sh307.5	5	GCCGAGCTATTGCACATCAAT
NUDT12	NM_031438	sh307.4	4	GCTGAACACACAGATATAAA
NUDT12	NM_031438	sh307.3	3	GCTCTAGGTATAGATCCTATT
NUDT12	NM_031438	sh307.2	2	CCAGTAGTAATCATGCAAGTT
NUDT12	NM_031438	sh307.1	1	GCTTAGCTCTAGCAGTGTCTA
NUDT14	NM_177533	sh308.5	5	GCGTCATCTTTGGTGTCTCAT
NUDT14	NM_177533	sh308.4	4	CTCCAGACAGACCATGTTCTA
NUDT14	NM_177533	sh308.3	3	CCAGAAGTCTGGGACTTCAT
NUDT14	NM_177533	sh308.2	2	CACGCTGCATTACGCCAGAA
NUDT14	NM_177533	sh308.1	1	CACGCTGCATTACGCCAGAA
NUDT2	NM_001161	sh299.5	5	GAAGGACTATGACGTGGAGAT
NUDT2	NM_001161	sh299.4	4	CACCAGTTTCTTGTCCATA
NUDT2	NM_001161	sh299.3	3	CAAAGTGGACAACAATGCAAT
NUDT2	NM_001161	sh299.2	2	CATCTCCGAAGATGCCTCAT
NUDT2	NM_001161	sh299.1	1	CAGGAGAGGATGACTTGGAAA
NUDT4	NM_019094	sh300.5	5	GTTGCCATCTAGTGTAAAGATA
NUDT4	NM_019094	sh300.4	4	CTGGGCATATTTGAGAACCAA
NUDT4	NM_019094	sh300.3	3	CCGATAAATAATGCCTTGT
NUDT4	NM_019094	sh300.2	2	GTTCTAACAGTCACTGAAATA
NUDT4	NM_019094	sh300.1	1	CTCCAGTGTCAATAAACCCTGTA
NUDT5	NM_014142	sh305.5	5	GAATGGCAAACAGTATATCAT
NUDT5	NM_014142	sh305.4	4	CGTACATGGATCCTACTGGTA
NUDT5	NM_014142	sh305.3	3	GCAGTCTCATAGATGATGGT
NUDT5	NM_014142	sh305.2	2	GCAAATGCAAAGCCATTTGAA
NUDT5	NM_014142	sh305.1	1	GCCATTTGAAGTGCCTTCTT
NUDT6	NM_007083	sh306.5	5	GCACAGGGTTACGTGCGGAAT
NUDT6	NM_007083	sh306.4	4	CCATCCTCCAAGCCGATTTA
NUDT6	NM_007083	sh306.3	3	GCTTCACATCAAGTAGGAGTT
NUDT6	NM_007083	sh306.2	2	GCAGATTACCAGGATATGCTT
NUDT6	NM_007083	sh306.1	1	GCCATATTCATTACCATAAAA
NUDT9	NM_024047	sh289.5	5	GCTGTGAACATACCATGACGAA
NUDT9	NM_024047	sh289.4	4	CCAACGTCATGTCTGGTTCTA
NUDT9	NM_024047	sh289.3	3	CCTAGTGATATATAAGGGATA
NUDT9	NM_024047	sh289.2	2	CCTCAGATCAGTGAAGTAAT
NUDT9	NM_024047	sh289.1	1	CCCATTATAACCAGATGGAAA
OGG1	NM_002542	sh059.5	5	CGGATCAAGTATGGACACTGA
OGG1	NM_002542	sh059.4	4	CGGCTCATCCAGCTTGATGAT
OGG1	NM_002542	sh059.3	3	GATGTCCATATGTGGCATT
OGG1	NM_002542	sh059.2	2	CGCAAGTACTCCAGCTAGAT
OGG1	NM_002542	sh059.1	1	CCTCCCTGTGACTACTCAAAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
OPA1	NM_130832	sh119.5	5	CCGCTTTATGACAGAACCGAA
OPA1	NM_130832	sh119.4	4	CCGGACCTTAGTGAATATAAA
OPA1	NM_130832	sh119.3	3	CCGGACCTTAGTGAATATAAAT
OPA1	NM_130832	sh119.2	2	CGGGAGTTTGATCTTACCAAA
OPA1	NM_130832	sh119.1	1	GCCCTCTTTGTATTCCCATTT
p53	NM_000546	sh238.4	4	CACCATCCACTACAACACAT
p53	NM_000546	sh238.3	3	GTCCAGATGAAGCTCCAGAA
p53	NM_000546	sh238.2	2	TCAGACCTATGGAAACTACTT
p53	NM_000546	sh238.1	1	CGGCGCACAGAGGAAGAGAAT
PADI1	NM_013358	sh327.5	5	GTCTGACTTTGGATATGTTA
PADI1	NM_013358	sh327.4	4	GCACAGCCAGTAAGGAATTAA
PADI1	NM_013358	sh327.3	3	CTTGCTTGAACGTGCCCTTT
PADI1	NM_013358	sh327.2	2	GACAACTTTCATGCACAGAAA
PADI1	NM_013358	sh327.1	1	GCACAGCCAGTAAGGAATTAA
PARG	NM_003631	sh243.5	5	GCAGTTTAGTAATGCTAACAT
PARG	NM_003631	sh243.4	4	GCTGAGCGAGATGTGTTTAT
PARG	NM_003631	sh243.3	3	GCCTAGGAAATCTCCTCCAT
PARG	NM_003631	sh243.2	2	CGATTGCATGTCACTACGAA
PARG	NM_003631	sh243.1	1	GCTAAGATGAAATCGGAGTAT
PARL	NM_018622	sh195.5	5	CCACAGGAAGATATGGACCAT
PARL	NM_018622	sh195.4	4	CGGACTGTGACAGGTATTATA
PARL	NM_018622	sh195.3	3	GCGGACAATGATCAGATATTT
PARL	NM_018622	sh195.2	2	GCTGCTATTTGGCAATATGAA
PARL	NM_018622	sh195.1	1	CGCAGGTTTAACTTCTTTATT
PARP1	NM_001618	sh002.5	5	CGACCTGATCTGGAACATCAA
PARP1	NM_001618	sh002.4	4	GCTTCACATATCAGCAGGTTA
PARP1	NM_001618	sh002.3	3	CCGAGAAATCTCTTACCTCAA
PARP1	NM_001618	sh002.2	2	GCAGCTTCATAACCGAAGATT
PARP1	NM_001618	sh002.1	1	CTTCGTTAGAATGTCTGCCTT
PARP2	NM_005484	sh003.5	5	GATGAGTAACTGGGTGGGAAT
PARP2	NM_005484	sh003.4	4	CCGAAGGATTGCTTCAAGGTA
PARP2	NM_005484	sh003.3	3	GCCTTGCTGTTAAAGGGCAAA
PARP2	NM_005484	sh003.2	2	CCATGAAAGTTACGAGTTCAA
PARP2	NM_005484	sh003.1	1	GCCACCAATCTCAGGATGAA
PARP3	NM_001003931	sh004.5	5	CCAGTCAAAGATCAACCACTT
PARP3	NM_001003931	sh004.4	4	GCACCATATCAACACGGACAA
PARP3	NM_001003931	sh004.3	3	CCAGACCAACATCGAGAACAA
PARP3	NM_001003931	sh004.2	2	GCACCTGAGTACAAGGTGATA
PARP3	NM_001003931	sh004.1	1	CCCTGAACCTTATGCCTCTAA
PARP4	NM_006437	sh460.5	5	CCGGCCTAAGCATATCACAAG
PARP4	NM_006437	sh460.4	4	CCGGCTCAGTACAAGATCA
PARP4	NM_006437	sh460.3	3	CCGGCCTAATAATCAAGAGAA
PARP4	NM_006437	sh460.2	2	CCGGCCTGGGACTATTGCTA
PARP4	NM_006437	sh460.1	1	CCGGGCATTCAATCTCTAGGT
PBEF1	NM_182790	sh224.5	5	GAAGCAAAGATGTCTACAAA
PBEF1	NM_182790	sh224.4	4	GTAACCTAGATGTCTGGAAT
PBEF1	NM_182790	sh224.3	3	CCTACAAGTTACTACTATA
PBEF1	NM_182790	sh224.2	2	CCACTAATAATCAGACCTGAT
PBEF1	NM_182790	sh224.1	1	CCACCTTATCTAGAGTTATT
PCNA	NM_002592	sh377.5	5	CACGTATATGCCGAGATCTCA
PCNA	NM_002592	sh377.4	4	ACGTCTCTTTGGTGCAGCTCA
PCNA	NM_002592	sh377.3	3	GAAGCACCAAACAGGAGAAA
PCNA	NM_002592	sh377.2	2	GATGCTGTTGTAATTTCTGT
PCNA	NM_002592	sh377.1	1	TGAAGCACCAAACAGGAGAAA
PDGFRA	NM_006206	sh431.5	5	CAATGGACTTACCTGGAGAA
PDGFRA	NM_006206	sh431.4	4	CCCAACTTCTTATCCAACCT
PDGFRA	NM_006206	sh431.3	3	CGGTGAAAGACAGTGGAGAT
PDGFRA	NM_006206	sh431.2	2	CCAGCTTTCATTACCTCTAT
PDGFRA	NM_006206	sh431.1	1	CCAGCCTCATATAAGAGAAA
PDGFRB	NM_002609	sh430.5	5	GACTCGAATTACATCTCCAAA
PDGFRB	NM_002609	sh430.4	4	GCTCACCATCATCTCCCTTAT
PDGFRB	NM_002609	sh430.3	3	GTGGATTCTGATGCCTACTAT
PDGFRB	NM_002609	sh430.2	2	CCCTCAGTCTTAATCCATCCAC

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
PDGFRB	NM_002609	sh430.1	1	CAAAGGAGGACCCATCTATA
PDHA1	NM_000284	sh210.5	5	CGAATGGAGTTGAAAGCAGAT
PDHA1	NM_000284	sh210.4	4	GCCAATCAGTGGATCAAGTTT
PDHA1	NM_000284	sh210.3	3	GTGAGAATAATCGCTATGGAA
PDHA1	NM_000284	sh210.2	2	GCTGGTAGCATCCCGTAATTT
PDHA1	NM_000284	sh210.1	1	CGAGAAATTCGCGAGAGCTT
PDK1	NM_002610	sh211.5	5	CGTGAATATGTTGAAGTAGAA
PDK1	NM_002610	sh211.4	4	CCAGGGTGTGATTGAATACAA
PDK1	NM_002610	sh211.3	3	CCAACTGCAATGTAATTGAA
PDK1	NM_002610	sh211.2	2	GCTCTGTCAACAGACTCAATA
PDK1	NM_002610	sh211.1	1	CGGATCAGAAACCGACACAAT
PDK2	NM_002611	sh212.5	5	ACCTTGTAGACCGAGAGCTT
PDK2	NM_002611	sh212.4	4	AGGAGATCAATGCAGCCAACT
PDK2	NM_002611	sh212.3	3	GTACATAGAGCACTTCAGCAA
PDK2	NM_002611	sh212.2	2	ACAGCCGATTCACATGGTCTA
PDK2	NM_002611	sh212.1	1	CACCTCTACCACATGCTCTTT
PLUNC	NM_016583	sh432.5	5	GAGAGATAAGCAGAGAGAGGAT
PLUNC	NM_016583	sh432.4	4	GAATAAAGTCTGCTGAGTT
PLUNC	NM_016583	sh432.3	3	GCAGAAATCTAGCTGTGAGA
PLUNC	NM_016583	sh432.2	2	GAAATCTTAGCTGTGAGAGAT
PLUNC	NM_016583	sh432.1	1	CGGCATAAAGCTCCAAGTGAA
PLXNB1	NM_002673	sh259.5	5	GTGGCCTACATCGAGTATGAT
PLXNB1	NM_002673	sh259.4	4	CCAACTGCATTCACCTCCAAT
PLXNB1	NM_002673	sh259.3	3	CCCATCAACAACTTCTGTGA
PLXNB1	NM_002673	sh259.2	2	GCTTGAGTATTCCTGACAT
PLXNB1	NM_002673	sh259.1	1	CGTGCAAACATCTGATAACAT
PMS1	NM_000534	sh335.5	5	CCTCGCAAAGTGATAAGTTAT
PMS1	NM_000534	sh335.4	4	ATTACAACAAGAACGGCTGCT
PMS1	NM_000534	sh335.3	3	GCACCTGTAATGGCAATGAAG
PMS1	NM_000534	sh335.2	2	CAAGCGTAGATGTTAAACTGG
PMS1	NM_000534	sh335.1	1	CTTCGGTGGTCACTGTTGTAA
PMS2	NM_000535	sh337.5	5	CCAGTCACTGAAAGGGCTAAA
PMS2	NM_000535	sh337.4	4	GACCTCTTTGATAGGAATGTT
PMS2	NM_000535	sh337.3	3	CGAGAAGTATAACTCGAGAT
PMS2	NM_000535	sh337.2	2	CGTGTGTGAAGAGTACGGTTT
PMS2	NM_000535	sh337.1	1	CCAGGAAGATACCGGATGTAA
PNKP	NM_007254	sh230.5	5	GTGTCAGACATGGTCATGTAT
PNKP	NM_007254	sh230.4	4	GACACACTGTATTTGGTCAAT
PNKP	NM_007254	sh230.3	3	CTTGGAGAAGTTGCTAGTGTT
PNKP	NM_007254	sh230.2	2	GTATGGCTACAGGAAGCAGTT
PNKP	NM_007254	sh230.1	1	GAAGCGTATGCGGAAGTCAAA
PoIb	NM_002690	sh001.5	5	GCAAGGAAGTTTGTAGATGAA
PoIb	NM_002690	sh001.4	4	CCTGTCAAAGGGTGAGACAAA
PoIb	NM_002690	sh001.3	3	CCAGCTTCACTTCAGAATCAA
PoIb	NM_002690	sh001.2	2	GCTAAGAAATTGCTGGAGTA
PoIb	NM_002690	sh001.1	1	CTCACAGAACTCGAAACTTT
POLD1	NM_002691	sh333.5	5	GCTTATCAGCAAGAAGCGCTA
POLD1	NM_002691	sh333.4	4	GTCCACCTTATCCGTATCAT
POLD1	NM_002691	sh333.3	3	CCTGCCATTGACACGCAGTA
POLD1	NM_002691	sh333.2	2	CCTGGCATTGATGGAGGAGAT
POLD1	NM_002691	sh333.1	1	CGGTTACAACATCCAGAACTT
POLD3	NM_006591	sh334.5	5	GCATCCAGAAAGCCATGCTAA
POLD3	NM_006591	sh334.4	4	ACTGGCTTCTCCAGAGGAAA
POLD3	NM_006591	sh334.3	3	GCCCAAAGGAATATGGGAAT
POLD3	NM_006591	sh334.2	2	CCTCTGTTCAATACTGACTAT
POLD3	NM_006591	sh334.1	1	CGAGTAGCATTATCTGATGAT
POLE	NM_006231	sh376.5	5	GCCAAATCACTGGTGGGTTT
POLE	NM_006231	sh376.4	4	CCTGTGTAAGACTCTTCCTT
POLE	NM_006231	sh376.3	3	GCTGACCAGTTGGACAACATT
POLE	NM_006231	sh376.2	2	CGTCCAACATGGTCTACAAT
POLE	NM_006231	sh376.1	1	GCAGTGGATTACTACTTTATT
POLG	NM_002693	sh071.5	5	GCAGAGGTGCACAGACTTTAT
POLG	NM_002693	sh071.4	4	GCTCACTGACAATAGTGCCAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
POLG	NM_002693	sh071.3	3	GCCATGAAGTGGCTGTTTGAA
POLG	NM_002693	sh071.2	2	CCTGCAAGAATTTAAGCAGAA
POLG	NM_002693	sh071.1	1	GCGCTTACTAATGCAGTTTAA
POLH	NM_006502	sh314.5	5	AGTTATGAAGCTCGTGCATTT
POLH	NM_006502	sh314.4	4	CATACAGGTAAACCTATTAT
POLH	NM_006502	sh314.3	3	GCTAAGAAGTTATGTCCAGAT
POLH	NM_006502	sh314.2	2	GCCGTATCTCATCAAGGCAAA
POLH	NM_006502	sh314.1	1	GTGCAGTTGTACAGTACAAT
POLI	NM_007195	sh381.5	5	GCCATAAGCAAACAGTAGCAA
POLI	NM_007195	sh381.4	4	CCTCAGTCCCTTAGTGAAGAA
POLI	NM_007195	sh381.3	3	CCAGATTCTGTTGATGAGAAA
POLI	NM_007195	sh381.2	2	CCCCTACAGAGAAAATGTCTT
POLI	NM_007195	sh381.1	1	GCAACCTTAAAGCACTAAATA
POLK	NM_016218	sh382.5	5	CAGTTAATCAACCCAAGAAA
POLK	NM_016218	sh382.4	4	CCCAAACATACCTTGATATA
POLK	NM_016218	sh382.3	3	GCCATTGCTAAGGAATTGCTA
POLK	NM_016218	sh382.2	2	CCTGTTTGTAACGTAGAACAA
POLK	NM_016218	sh382.1	1	GCATTGATCCTAGTGTCTTTA
POLL	NM_013274	sh180.5	5	AGCTGGATTCAGCATCTTCAT
POLL	NM_013274	sh180.4	4	CAAGAGGAGAATGGTCAGCAA
POLL	NM_013274	sh180.3	3	ACTCACATTGTGGTGGATGAA
POLL	NM_013274	sh180.2	2	CCTGAAGCATTACAGTGACTT
POLL	NM_013274	sh180.1	1	CGACCAATCACACCTCCATA
POLM	NM_013284	sh181.5	5	GCTCGTTGGACTGGCTCCAA
POLM	NM_013284	sh181.4	4	CGGGAAGACTGCGAACCTTA
POLM	NM_013284	sh181.3	3	GCCGTGAGAGTGGACTTGTA
POLM	NM_013284	sh181.2	2	TGCTGGACATAAGCTGGTTAA
POLM	NM_013284	sh181.1	1	GCGACACATGTTGTGATGGAA
POLN	NM_181808	sh383.5	5	CCTTCATCCATTACCCAAGAT
POLN	NM_181808	sh383.4	4	CCATGCCATTACAGGTGAACAA
POLN	NM_181808	sh383.3	3	GCATCCTAATATCCAAGGTAT
POLN	NM_181808	sh383.2	2	CCAGTGTGTCTCAGAAGATTAC
POLN	NM_181808	sh383.1	1	CCTGGTGATACTGTGATGTA
POLQ	NM_006596	sh144.5	5	CCCTGTTACATTCTAGTACAT
POLQ	NM_006596	sh144.4	4	GCTGACCAAGATTTGCTATAT
POLQ	NM_006596	sh144.3	3	CGTCGTCTCATTCAAGTGTTA
POLQ	NM_006596	sh144.2	2	CCTCAATCTTGCTTGCAGAAA
POLQ	NM_006596	sh144.1	1	CGGGCCTCTTAGATATAAAT
POU5F1	NM_002701	sh251.4	4	GAGATTGATAAAGTGGTGTGT
POU5F1	NM_002701	sh251.3	3	CCCTCACTTCACTGCACTGTA
POU5F1	NM_002701	sh251.2	2	CGTAGGTTCTTGAATCCCGAA
POU5F1	NM_002701	sh251.1	1	TCATTCACTAAGGAAGGAATT
PPARGC1A	NM_013261	sh250.5	5	GACAGCGAAGATGAAAGTGAT
PPARGC1A	NM_013261	sh250.4	4	CGACTTGGATACAGACAGCTT
PPARGC1A	NM_013261	sh250.3	3	CCTCCTCATAAAGCCAACCAA
PPARGC1A	NM_013261	sh250.2	2	CCGTATACCTGTGATGCTTT
PPARGC1A	NM_013261	sh250.1	1	GCAGAGTATGACGATGGTATT
PRF1	NM_005041	sh100.5	5	ACCTGAATCATGGCCACCTAA
PRF1	NM_005041	sh100.4	4	TGCCGCTTCTACAGTTCCAT
PRF1	NM_005041	sh100.3	3	CCTCAGGCTTATCTCAACTA
PRF1	NM_005041	sh100.2	2	GCCTATGTGAAGCTCTTCTTT
PRF1	NM_005041	sh100.1	1	CCAACACAATCTCTTCCAA
PRKAA1	NM_006251	sh131.5	5	GTTGCCTACCATCTCATAATA
PRKAA1	NM_006251	sh131.4	4	TGATTGATGATGAAGCCTTAA
PRKAA1	NM_006251	sh131.3	3	CCTGGAAGTCACACAATAGAA
PRKAA1	NM_006251	sh131.2	2	CCATCCTGAAAGAGTACCATT
PRKAA1	NM_006251	sh131.1	1	GCATAATAAGTCACGCCAAA
PRKAA2	NM_006252	sh133.5	5	GCTGTGTTTATCGCCAAATTT
PRKAA2	NM_006252	sh133.4	4	CCCACTGAAACGAGCAACTAT
PRKAA2	NM_006252	sh133.3	3	GTGGCTTATCATCTTATCATT
PRKAA2	NM_006252	sh133.2	2	CGCAGTTTAGATGTTGTTGGA
PRKAA2	NM_006252	sh133.1	1	GCTGTGAAAGAAGTGTGTGAA
PRKAB1	NM_006253	sh134.5	5	GCTGTCTATCAAGGATGGAGT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
PRKAB1	NM_006253	sh134.4	4	CAGCATGATCTGGAAGTGAAT
PRKAB1	NM_006253	sh134.3	3	CGTACCACCTTGTATACAA
PRKAB1	NM_006253	sh134.2	2	CCTCACCAGAAGCCACAATA
PRKAB1	NM_006253	sh134.1	1	GCCTGGCTATGGAACATAATA
PRKDC	NM_006904	sh350.5	5	GCAGCCTTATTACAAAGACA
PRKDC	NM_006904	sh350.4	4	CCACCTTTGTCTCTTGATT
PRKDC	NM_006904	sh350.3	3	CCAGTGAAAGTCTGAATCATT
PRKDC	NM_006904	sh350.2	2	CCGGTAAAGATCCTAATTCTA
PRKDC	NM_006904	sh350.1	1	GCAGATAGAAAGCATTACATT
PRKDC	NM_006904	sh135.5	5	GCAGCCTTATTACAAAGACAT
PRKDC	NM_006904	sh135.4	4	CCACCTTTGTCTCTTGATT
PRKDC	NM_006904	sh135.3	3	CCAGTGAAAGTCTGAATCATT
PRKDC	NM_006904	sh135.2	2	CCGGTAAAGATCCTAATTCTA
PRKDC	NM_006904	sh135.1	1	GCAGATAGAAAGCATTACATT
PRP8	NM_006445	sh264.5	5	GCCCTGTATGTGTACGTGAA
PRP8	NM_006445	sh264.4	4	CGCCTCATGAAACATGATGTT
PRP8	NM_006445	sh264.3	3	CGAGACATCAACCTACAGGAT
PRP8	NM_006445	sh264.2	2	CCCAACTTGTACCCGTACATA
PRP8	NM_006445	sh264.1	1	CCCAACATGAAATATGAGCTA
PTEN	NM_000314	sh304.5	5	CCACAAATGAAGGGATATAAA
PTEN	NM_000314	sh304.4	4	AGGCGCTATGTGTATTATTAT
PTEN	NM_000314	sh304.3	3	CGTGCAGATAATGACAAGGAA
PTEN	NM_000314	sh304.2	2	CCACAGCTAGAACCTTATCAAA
PTEN	NM_000314	sh304.1	1	CTAGAACTTATCAAACCCCTT
PTGS2	NM_000963	sh050.5	5	CCATTCTCCTTGAAGGACTT
PTGS2	NM_000963	sh050.4	4	CGTTGTGAATAACATCCCTT
PTGS2	NM_000963	sh050.3	3	CCAGGGCTCAAACATGATGTT
PTGS2	NM_000963	sh050.2	2	GCAGATGAAATACCAGTCTTT
PTGS2	NM_000963	sh050.1	1	GCTGAATTTAACCCCTCTAT
PXN	NM_002859	sh273.5	5	ACCCAACCTGGAACCACACAT
PXN	NM_002859	sh273.4	4	GCCTTACTGTGAGAACTGCTT
PXN	NM_002859	sh273.3	3	CCCAACTGGAAGACCACACATA
PXN	NM_002859	sh273.2	2	CCTGACGAAAGAGAACCTAA
PXN	NM_002859	sh273.1	1	CCCGACCTAATTGCTTTTGTT
RAD1	NM_133282	sh117.5	5	GAATTGGATATGACGAGTGAA
RAD1	NM_133282	sh117.4	4	GCAGCACCAATGTTATTAATA
RAD1	NM_133282	sh117.3	3	CCAAGTCAACAGATACAAGAT
RAD1	NM_133282	sh117.2	2	CCTGATGAAGAAGTTCCTGAA
RAD1	NM_133282	sh117.1	1	CCTATCTTGTAAAGGTATCTAT
RAD17	NM_133338	sh032.5	5	CGCTCTTACTCAGGGAATAT
RAD17	NM_133338	sh032.4	4	GCCCTCTCATTTATCAGAATA
RAD17	NM_133338	sh032.3	3	GCCACATCATTAGGTGTGAAT
RAD17	NM_133338	sh032.2	2	GCGACAAAGTATAACAAGTTA
RAD17	NM_133338	sh032.1	1	CCCAGCTTAATGGAGGACATT
RAD18	NM_020165	sh188.5	5	CAATGCCCAATGCGATGCTTT
RAD18	NM_020165	sh188.4	4	GCCCAAGGAAAGATGCTAAAT
RAD18	NM_020165	sh188.3	3	GAACCAAGAAACAAGCGTAAT
RAD18	NM_020165	sh188.2	2	TGCTTCGAGTATTTCAACATT
RAD18	NM_020165	sh188.1	1	CCCTCGACATCCACTTTGAAA
RAD21	NM_006265	sh352.5	5	GCTAATTGTTGACAGTGCTCAA
RAD21	NM_006265	sh352.4	4	GCCATTACTTTACCTGAAGAA
RAD21	NM_006265	sh352.3	3	CCAGATAGCATCAGAAATCAT
RAD21	NM_006265	sh352.2	2	GCTGAATCTATCAGTTTGCTT
RAD21	NM_006265	sh352.1	1	GCTAATTGTTGACAGTGCTCAA
RAD23A	NM_005053	sh095.5	5	GAAGAACTTTGTGGTCGTCAT
RAD23A	NM_005053	sh095.4	4	AGGCCTATTTGCGGTGTGAAA
RAD23A	NM_005053	sh095.3	3	GCAGACCTCAAGATCCGCAT
RAD23A	NM_005053	sh095.2	2	GATGTCCTTACAGGACTAT
RAD23A	NM_005053	sh095.1	1	CCCTACCTTATTCCATGAAA
RAD23B	NM_002874	sh057.5	5	CAGCAGATAGGTCGAGAGAAT
RAD23B	NM_002874	sh057.4	4	CTCCAGCATCAGCGACAGCAT
RAD23B	NM_002874	sh057.3	3	AGAAGCTGGAAGTGGTCATAT
RAD23B	NM_002874	sh057.2	2	GTGTACTAGATCCAGAAACTT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
RAD23B	NM_002874	sh057.1	1	CCAGCGTTACTACAGCAGATA
RAD50	NM_005732	sh143.5	5	GCTGTGCTAAATAATGTCATT
RAD50	NM_005732	sh143.4	4	GCCAAATTGAACAAGGAACATA
RAD50	NM_005732	sh143.3	3	CGACCATCATTGAATGCTTAA
RAD50	NM_005732	sh143.2	2	CGCCTAAAGAACGACATAGAA
RAD50	NM_005732	sh143.1	1	CGGGTCTTGATTACAGTACAT
RAD51	NM_002875	sh064.5	5	CCACAACCCATTTACCGGTTA
RAD51	NM_002875	sh064.4	4	CGGTCAGAGATCATAAGATT
RAD51	NM_002875	sh064.3	3	GCTGAAGCTATGTTGCCATT
RAD51	NM_002875	sh064.2	2	CGCCCTTTACAGAAGACTA
RAD51	NM_002875	sh064.1	1	GCTAAGACTAACTCAAGATAA
RAD51C	NM_002876	sh072.5	5	GCTTCATAATCACCTTCTGTT
RAD51C	NM_002876	sh072.4	4	GTTGGGATATCTAAAGCAGAA
RAD51C	NM_002876	sh072.3	3	GAAGCCTTAGAACTCTGCAA
RAD51C	NM_002876	sh072.2	2	GCAAAGAAGTTGGGATATCTA
RAD51C	NM_002876	sh072.1	1	CAGAAGAGAATGTCTCACAAA
RAD51L1	NM_002877	sh073.5	5	GCAAACGGCTTATGGGATAAA
RAD51L1	NM_002877	sh073.4	4	CCTGTGATGAAGTTCTACAAA
RAD51L1	NM_002877	sh073.3	3	CCCAGTTATCTTGACGAATCA
RAD51L1	NM_002877	sh073.2	2	CCCAAAGATGCAAACGGCTTA
RAD51L1	NM_002877	sh073.1	1	CCATTATGCAAGTGTCTCTAT
RAD51L3	NM_002878	sh074.5	5	GTCTCTATACTGGAGAAGTGA
RAD51L3	NM_002878	sh074.4	4	GCTGGTCTATACTGGAGAA
RAD51L3	NM_002878	sh074.3	3	CGTGTATGTTTCTGGTGGAAA
RAD51L3	NM_002878	sh074.2	2	CCACGTTTCCTTCCCTTATTT
RAD51L3	NM_002878	sh074.1	1	CCTGTGCTGTTGTTTGGGAAA
RAD52	NM_002879	sh063.5	5	GCAGGAGTGACTCAAGAATTA
RAD52	NM_002879	sh063.4	4	GCGAAGAGACAAGATCTTGAA
RAD52	NM_002879	sh063.3	3	GCACAACAGGAACTGGGAAT
RAD52	NM_002879	sh063.2	2	CCACCAGAACCACAAGCAAA
RAD52	NM_002879	sh063.1	1	CGGGTAATTAATCTGGCCAAT
RAD54B	NM_012415	sh179.5	5	GCAGATTGTTGATGGCTTTAA
RAD54B	NM_012415	sh179.4	4	GCTTTATCGAAAGCTGTTAAA
RAD54B	NM_012415	sh179.3	3	CCCTGGATCAAATTAAGAATA
RAD54B	NM_012415	sh179.2	2	GCAACATTAGATCCACCTCAT
RAD54B	NM_012415	sh179.1	1	CCAGAAATCTAACTCCCTGAA
RAD54L	NM_003579	sh075.5	5	GTCCATTAAGAAGCGAGCCAA
RAD54L	NM_003579	sh075.4	4	GTGAAGATTGAGCAGGTCGTT
RAD54L	NM_003579	sh075.3	3	CCTGGATTATATTCTGGCGGT
RAD54L	NM_003579	sh075.2	2	CTTTGTAAATCATCCAGCTCTA
RAD54L	NM_003579	sh075.1	1	CCAGAGTGAAGCCAGAAATT
RAD9A	NM_004584	sh101.5	5	GAAGACTACAACCTGTCTCT
RAD9A	NM_004584	sh101.4	4	GCGGAAGACAGTGAGGGTGAA
RAD9A	NM_004584	sh101.3	3	CCCCTCTTCTCCAGCAATA
RAD9A	NM_004584	sh101.2	2	GCAAACCTGAATCTTAGCATT
RAD9A	NM_004584	sh101.1	1	CGACATTGACTTTACATGAT
RAG2	NM_000536	sh303.5	5	GCCCTACTTGTGATGTGGATA
RAG2	NM_000536	sh303.4	4	CCCAGACATTAAGCACAGCAA
RAG2	NM_000536	sh303.3	3	CCAGTGCAATCCTGACTCAA
RAG2	NM_000536	sh303.2	2	CCAAACAATGAGGTTTCAGAT
RAG2	NM_000536	sh303.1	1	GCCATGATCTACTGCTCTCAT
RAGE	NM_014226	sh297.9	9	CAAGAAGACAGATCCGCAGAA
RAGE	NM_014226	sh297.8	8	CTGGTTCTCTTGCACTAATAT
RAGE	NM_014226	sh297.7	7	ACCTCTACTAACAACCAATTT
RAGE	NM_014226	sh297.6	6	CTGGGCTAATATACTTGTA
RAGE	NM_014226	sh297.5	5	CGGCTGTGTGTTCTACGAGAT
RAGE	NM_014226	sh297.4	4	CGAGGGAGAAGATACCCATTA
RAGE	NM_014226	sh297.3	3	GCAGCGCTTTGAAAGATTGA
RAGE	NM_014226	sh297.2	2	GCAGCGCTTTGAAAGATTGA
RAGE	NM_014226	sh297.1	1	GTGGTCAGACTGTCTCTTAC
RB1	NM_000321	sh021.5	5	CGAAATTGGATCACAGCGATA
RB1	NM_000321	sh021.4	4	CCTCCCATGTTGCTCAAAGAA
RB1	NM_000321	sh021.3	3	CGGCTAAATACACTTTGTGAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
RB1	NM_000321	sh021.2	2	CGCGTGTAATTCTACTGCAA
RB1	NM_000321	sh021.1	1	CCACATTATTTCTAGTCCAAA
RBBP7	NM_002893	sh443.5	5	GCGGATAAGACCGTAGCTTTA
RBBP7	NM_002893	sh443.4	4	GCACAGTTTGATGCTTCCCAT
RBBP7	NM_002893	sh443.3	3	CGTGTCAATGAAGAATAT
RBBP7	NM_002893	sh443.2	2	CCTCCAGAACTCCTGTTTATT
RBBP7	NM_002893	sh443.1	1	CGTTTCTATATGACCTGGTTA
RBL1	NM_002895	sh067.5	5	GCACAGGCTAATGTGGAGTAT
RBL1	NM_002895	sh067.4	4	CCAGAATACTACGTTACAGTA
RBL1	NM_002895	sh067.3	3	GCAGTGAATAAGGATATGAA
RBL1	NM_002895	sh067.2	2	CCAAGCTAATAGTCACGTATA
RBL1	NM_002895	sh067.1	1	CCCCTGTGGTAATCCACAT
RBL2	NM_005611	sh141.16	16	CAAGATACTGCTACGTGAAT
RBL2	NM_005611	sh141.15	15	CCACACCACTAACTGGTGTTA
RBL2	NM_005611	sh141.14	14	GAGCAGAGCTTAATCGAATTT
RBL2	NM_005611	sh141.13	13	GACTAGGAGACATGGATTAT
RBL2	NM_005611	sh141.12	12	AGACATCTGGAACCTATATTA
RBL2	NM_005611	sh141.11	11	ATTTCTGGAAACCCTATATTA
RBL2	NM_005611	sh141.10	10	CCTTACATGATGGCCTAGTTT
RBL2	NM_005611	sh141.09	9	GCTGAGAGAAATATGGAACCT
RBL2	NM_005611	sh141.08	8	TACTTCAGCAACAGTCCTTCA
RBL2	NM_005611	sh141.07	7	ATCTTATTGGTTAGCATGTC
RBL2	NM_005611	sh141.06	6	GCCAGGTGTATAGAAGTGTTT
RBL2	NM_005611	sh141.05	5	CCTTACATGATGGCCTAGTTT
RBL2	NM_005611	sh141.04	4	GCCAGGTGTATAGAAGTGTTT
RBL2	NM_005611	sh141.03	3	CCAGAACATTATGCGTTGTTA
RBL2	NM_005611	sh141.02	2	CCACACCACTAACTGGTGTTA
RBL2	NM_005611	sh141.01	1	GCTGAGAGAAATATGGAACCT
RDM1	NM_145654	sh398.5	5	GAAGTGGCGAATTACTACTTT
RDM1	NM_145654	sh398.4	4	GCATTCAGAAACTGTTGATT
RDM1	NM_145654	sh398.3	3	GCCAAGAAGTGGCGAATTA
RDM1	NM_145654	sh398.2	2	GAAGAAGAATACACGGTTTA
RDM1	NM_145654	sh398.1	1	GCGAGGTCATGTAACCTCCTT
RECQL	NM_002907	sh395.5	5	GCCGCTTGGAAATAAAGAGAT
RECQL	NM_002907	sh395.4	4	GCTTTATGAGATGGTATCATA
RECQL	NM_002907	sh395.3	3	GCACATGCTATTACTATGCAA
RECQL	NM_002907	sh395.2	2	GCCCTCAAACTGAAGATTT
RECQL	NM_002907	sh395.1	1	GCCAATGAAATCAGGTAGTA
RECQL4	NM_004260	sh090.5	5	CTCCCAATACAGCTTACCGTA
RECQL4	NM_004260	sh090.4	4	CGACCAAGAGTCCACAGCCTA
RECQL4	NM_004260	sh090.3	3	CAGATATGTGACTTCCCTCTAT
RECQL4	NM_004260	sh090.2	2	CCTCGATTCCATTATCATTTA
RECQL4	NM_004260	sh090.1	1	CGGCTCAACATGAAGCAGAAA
RECQL5	NM_001003715	sh396.5	5	GTACGCTGAAGAAGGTCTTTG
RECQL5	NM_001003715	sh396.4	4	GCCACTATCATGGCCTTTGAT
RECQL5	NM_001003715	sh396.3	3	CCCTAAAGGTACGAGTAAGTT
RECQL5	NM_001003715	sh396.2	2	CGTCTCTATTACTCCAGGAAT
RECQL5	NM_001003715	sh396.1	1	GCCTTGTTTACACTGGGAT
RELA	NM_021975	sh191.5	5	CCTGAGGCTATAACTCGCCTA
RELA	NM_021975	sh191.4	4	CACCATCAACTATGATGAGTT
RELA	NM_021975	sh191.3	3	GCAGGCTATCAGTCAGCGCAT
RELA	NM_021975	sh191.2	2	CGGATTGAGGAGAAACGTAAA
RELA	NM_021975	sh191.1	1	GCCTTAATAGTAGGGTAAGTT
RELB	NM_006509	sh137.5	5	CGAGAGCAAACGGCGGAAGAA
RELB	NM_006509	sh137.4	4	AGCCCGTCTATGACAAGAAAT
RELB	NM_006509	sh137.3	3	CACAGATGAATTGGAGATCAT
RELB	NM_006509	sh137.2	2	GCTGCGGATTTGCCGAATTA
RELB	NM_006509	sh137.1	1	CATGCTTCTGAAGTGGACATA
REV1L	NM_016316	sh380.5	5	GCTGCTTAACAGTCTGCAAAA
REV1L	NM_016316	sh380.4	4	CGGTGGAATCGGTTTGGAAATA
REV1L	NM_016316	sh380.3	3	GCTGTTGATGGAATCAAA
REV1L	NM_016316	sh380.2	2	CGAAGCAATGGAATTGATT
REV1L	NM_016316	sh380.1	1	CATAAGTGCTGTGAGGTATT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
REV3L	NM_002912	sh378.5	5	GCTGAGTTTGAGGGAGACTTT
REV3L	NM_002912	sh378.4	4	GCGTTCTCTAAAGCTGCTATT
REV3L	NM_002912	sh378.3	3	CGGAGCCATAATGAATAAATT
REV3L	NM_002912	sh378.2	2	CCGAAGATTGTGACTTGAATT
REV3L	NM_002912	sh378.1	1	CGAGCTATTAAGCTGGTGAAT
RFC5	NM_007370	sh301.5	5	GAAAGGCTTTAAGCTAGTGAT
RFC5	NM_007370	sh301.4	4	GAATGCCTTGAGAAGAGTAAT
RFC5	NM_007370	sh301.3	3	GTCACCAGAGACCTGATTGTT
RFC5	NM_007370	sh301.2	2	GCAGACATTGAGTACAGGCTT
RFC5	NM_007370	sh301.1	1	CAGAGGACAGTTCAGGATAA
RIPK1	NM_003804	sh076.5	5	CTTACAACAGAGAGGAGGAAA
RIPK1	NM_003804	sh076.4	4	CCTTGTTGATAATGACTTCCA
RIPK1	NM_003804	sh076.3	3	CAGGCCAATCCAAGTCATAT
RIPK1	NM_003804	sh076.2	2	CAGCACAAATACGAACCTCAA
RIPK1	NM_003804	sh076.1	1	AGGTCATGTTCTTTCAGCTTA
RNF146	NM_030963	sh461.5	5	GCTCATTTACAACCTCAGTGGG
RNF146	NM_030963	sh461.4	4	GCCAGTAGTGTACAGGATGAT
RNF146	NM_030963	sh461.3	3	CCTGTTCTAATACTGACCTT
RNF146	NM_030963	sh461.2	2	GCAGGAAGATTAAGCGAGATA
RNF146	NM_030963	sh461.1	1	CCTGTGAGATGTTTGATATTA
RPA1	NM_002945	sh359.5	5	CCTAGAACTGGTTGACGAAA
RPA1	NM_002945	sh359.4	4	GCGGCTACAAAGCGTTTCTTT
RPA1	NM_002945	sh359.3	3	CGTGCTGTCTCAAGCACTAT
RPA1	NM_002945	sh359.2	2	GTCATCAACATCCGTCCCATT
RPA1	NM_002945	sh359.1	1	CGACACCGAATTTCCCAATTT
RPA2	NM_002946	sh360.5	5	CAATCAAGCAAGCTGTGGATT
RPA2	NM_002946	sh360.4	4	CCGCACCTTCTCAAGCCGAAA
RPA2	NM_002946	sh360.3	3	GCACACATGGTACTAAGCAAA
RPA2	NM_002946	sh360.2	2	CCAGGTGTTGAATTTGATTAA
RPA2	NM_002946	sh360.1	1	GCTTGTTACAACATCAAGATA
RPA3	NM_002947	sh361.5	5	CCACCATCTTGTGTACATCTT
RPA3	NM_002947	sh361.4	4	GATCTTGGACTTTACAATGAA
RPA3	NM_002947	sh361.3	3	TCTGGAATTGTGGAAGTGTT
RPA3	NM_002947	sh361.2	2	GTACATCTTATGTCCAGTTTA
RPA3	NM_002947	sh361.1	1	GCTAGCTCAATTCATCGACAAC
RPA4	NM_013347	sh394.5	5	GTCGTGATACCACTGTAGAAA
RPA4	NM_013347	sh394.4	4	CGGAGTATATGTCAAAGTGTT
RPA4	NM_013347	sh394.3	3	CGGTGATGGATAAATTGACAA
RPA4	NM_013347	sh394.2	2	CCATCAAGGAAGCGATTGATT
RPA4	NM_013347	sh394.1	1	GCGATTGATTATCTGACCGTT
RPS6KB1	NM_003161	sh310.5	5	GCAATCTGAAGAGGATGTAAG
RPS6KB1	NM_003161	sh310.4	4	CCGGAGAATATCATGCTTAAT
RPS6KB1	NM_003161	sh310.3	3	GCGACATCTTCTCAACCTTA
RPS6KB1	NM_003161	sh310.2	2	CCCATGATCTCCAACGGCCA
RPS6KB1	NM_003161	sh310.1	1	AGCACAGCAAATCCTCAGACA
RRM2B	NM_015713	sh386.5	5	CCGGTTTGCATCTTCCAAT
RRM2B	NM_015713	sh386.4	4	GCAGCCAGTGATGGAATTGTA
RRM2B	NM_015713	sh386.3	3	GCTAAGAAGAGAGGTTCTTAT
RRM2B	NM_015713	sh386.2	2	GCGATGGATAGCAGATAGAAA
RRM2B	NM_015713	sh386.1	1	GCTGACAGATTACTTGTGGAA
S100A10	NM_002966	sh424.5	5	CTACTTAACAAGGAGGACCT
S100A10	NM_002966	sh424.4	4	ACCTGAGAGTACTCATGGAAA
S100A10	NM_002966	sh424.3	3	GACCAGTGTAGAGATGGCAAA
S100A10	NM_002966	sh424.2	2	CCATGATGTTTACATTTACA
S100A10	NM_002966	sh424.1	1	CCATTGCATGCAATGACTATT
SCO2	NM_005138	sh217.5	5	CGTGGACCACTCCATTGCCAT
SCO2	NM_005138	sh217.4	4	CTTCACTCACTGCCCTGACAT
SCO2	NM_005138	sh217.3	3	CAAACAGGTTGCCAGGCTA
SCO2	NM_005138	sh217.2	2	CAGTGGGTGCTGATGTACTTT
SCO2	NM_005138	sh217.1	1	CATTGCCATCTACCTGCTCAA
SDHA	NM_004168	sh213.5	5	GCATCTGCTAAAGTTTCAGAT
SDHA	NM_004168	sh213.4	4	GCAAGCTCTATGGAGACCTAA
SDHA	NM_004168	sh213.3	3	GCGATATGATACCAGCTATTT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
SDHA	NM_004168	sh213.2	2	GATTTGCTGATGGAAGCATAA
SDHA	NM_004168	sh213.1	1	TCGCTATTGCACACCTTATAT
SDHB	NM_003000	sh214.5	5	GCAGGACCCATTCTCTATA
SDHB	NM_003000	sh214.4	4	CCCATGGTATTGGATGCTTTA
SDHB	NM_003000	sh214.3	3	CCCGATTTGAGCAACTTCTAT
SDHB	NM_003000	sh214.2	2	GCAACCTATAAGGAGAAGAAA
SDHB	NM_003000	sh214.1	1	CCAACCTCAATAAGGTCTCAA
SDHC	NM_003001	sh215.5	5	GAGCGGTTCTGGAATAAGAAT
SDHC	NM_003001	sh215.4	4	CTCATGTATCATACTGGAAT
SDHC	NM_003001	sh215.3	3	CCCTCAGCTCTGTATCAGAAA
SDHC	NM_003001	sh215.2	2	CCTGGGAACCTTTGAGTCTTAT
SDHC	NM_003001	sh215.1	1	CCCACATTACTATCTACAGTT
SDHD	NM_003002	sh216.5	5	GCACTTTCAGCTTTAACCTTT
SDHD	NM_003002	sh216.4	4	GCCGAGCTCTGTTGCTTCGAA
SDHD	NM_003002	sh216.3	3	CATTTCTTCAGGACCGACCTA
SDHD	NM_003002	sh216.2	2	GCGAGAGGGTTGTCAAGTGT
SDHD	NM_003002	sh216.1	1	GCTACAATAAGGAAGAATA
SERPINB5	NM_002639	sh260.5	5	CCATCCCTTTATTACATCAT
SERPINB5	NM_002639	sh260.4	4	CCTTGTGGTTAATGCTGCCTA
SERPINB5	NM_002639	sh260.3	3	GCCGTTGATCTGTTCAAACAA
SERPINB5	NM_002639	sh260.2	2	CCACAAAGTGTGCTTAGAAAT
SERPINB5	NM_002639	sh260.1	1	CCCTATGCAAAGGAATTGGAA
SERPINB9	NM_004155	sh091.6	6	CAGAGCCAACAGCATTCTGTT
SERPINB9	NM_004155	sh091.5	5	CAGAGCCAACAGCATTCTGTT
SERPINB9	NM_004155	sh091.4	4	ACGTTTAAGGAATCCTGTCTT
SERPINB9	NM_004155	sh091.3	3	CTTCGGCATTGGGAATTGTT
SERPINB9	NM_004155	sh091.2	2	CTTCGCACAACGTTCTGTT
SERPINB9	NM_004155	sh091.1	1	CGTTTGACGAAACATACACAA
SHFM1	NM_006304	sh345.5	5	GCTGGCTTAGATGAAGATGAA
SHFM1	NM_006304	sh345.4	4	GTAGAGGATGACTTCTTAAT
SHFM1	NM_006304	sh345.3	3	GCTGAAGTAGAGAAACATGGT
SHFM1	NM_006304	sh345.2	2	GAAGTAGAGAAACATGGTTAT
SHFM1	NM_006304	sh345.1	1	CCAGAAGAAGTGTGAAGTAA
SHPRH	NM_173082	sh400.5	5	GCACACTAGTGAAGTGTAA
SHPRH	NM_173082	sh400.4	4	GCACTTCTATGGCGAGAGAT
SHPRH	NM_173082	sh400.3	3	CCAGGAGAAATCGCAGTAAAT
SHPRH	NM_173082	sh400.2	2	CCGCCTGTTCTTCATATCATT
SHPRH	NM_173082	sh400.1	1	CCAGCGTTGAGTGGGATTAA
SIRT1	NM_012238	sh009.5	5	GCGGCTTGATGGTAAATCAGTA
SIRT1	NM_012238	sh009.4	4	CGGTGATGAAATTAACACTAA
SIRT1	NM_012238	sh009.3	3	GCGGGAATCCAAAGGATAATT
SIRT1	NM_012238	sh009.2	2	CCTCGAACCAATCTTAAAGAT
SIRT1	NM_012238	sh009.1	1	GCAAAGCCTTTCTGAATCTAT
SIRT2	NM_012237	sh218.5	5	GCTAAGCTGGATGAAAGAGAA
SIRT2	NM_012237	sh218.4	4	GCCAACCATCTGTCACTACTT
SIRT2	NM_012237	sh218.3	3	CCTGCTCATCAACAAGGAGAA
SIRT2	NM_012237	sh218.2	2	GCCATCTTTGAGATCAGCTAT
SIRT2	NM_012237	sh218.1	1	CCTGTGGCTAAGTAAACCATA
SIRT3	NM_012239	sh219.4	4	GCGGCTCTACACGCAGAACAT
SIRT3	NM_012239	sh219.3	3	CCCAACGTCACCTCACTACTT
SIRT3	NM_012239	sh219.2	2	GTGGGTGCTTCAAGTGTGTT
SIRT3	NM_012239	sh219.1	1	TCTTGCTGCATGTGGTTGATT
SIRT4	NM_012240	sh220.10	10	GGATCATCCTTGCAGGTATAC
SIRT4	NM_012240	sh220.09	9	GAACCCTGACAAGGTTGATTT
SIRT4	NM_012240	sh220.08	8	ACAGGGACTTTCACTTGAATC
SIRT4	NM_012240	sh220.07	7	CTCCTGATGGTGACGTCTTTC
SIRT4	NM_012240	sh220.06	6	GCTGACCACGCCTGATATTC
SIRT4	NM_012240	sh220.05	5	CCAGCGGTACTGGCGGAGAAA
SIRT4	NM_012240	sh220.04	4	GCGCTTCATCACCTTTCCAA
SIRT4	NM_012240	sh220.03	3	GAACCCTGACAAGGTTGATTT
SIRT4	NM_012240	sh220.02	2	CCGTGCTCGAAAGCTCCATT
SIRT4	NM_012240	sh220.01	1	CCCGATTGCAATACTGAACAT
SIRT5	NM_012241	sh221.5	5	GAGCTGGTGTAGTGCAGAAA

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
SIRT5	NM_012241	sh221.4	4	CGTCCACACGAAACCAGATTT
SIRT5	NM_012241	sh221.3	3	GCTACGAACAGATTACAGGTTT
SIRT5	NM_012241	sh221.2	2	GAGTCCAATTTGTCCAGCTTT
SIRT5	NM_012241	sh221.1	1	CCAGCTATATTGTGGCCTGAA
SIRT6	NM_016539	sh222.10	10	ACCCGGATCAACGGCTCTATC
SIRT6	NM_016539	sh222.09	9	TGTCCATCACGCTGGGTACAT
SIRT6	NM_016539	sh222.08	8	GCTACGTTGACGAGGTACATGA
SIRT6	NM_016539	sh222.07	7	GAAGAATGTGCCAAGTGTAAAG
SIRT6	NM_016539	sh222.06	6	CTCCCTGGTCTCCAGCTTAAA
SIRT6	NM_016539	sh222.05	5	GCTGGGTACATCGCTGCAGAT
SIRT6	NM_016539	sh222.04	4	CACGGGAACATGTTTGTGGAA
SIRT6	NM_016539	sh222.03	3	CACCCGGATCAACGGCTCTAT
SIRT6	NM_016539	sh222.02	2	GCAGTCTCCAGTGTGGTGTT
SIRT6	NM_016539	sh222.01	1	TGGAAGAATGTGCCAAGTGTAA
SIRT7	NM_016538	sh223.4	4	CGGGACACCATTTGTGCATTT
SIRT7	NM_016538	sh223.3	3	CTTCAGAAAGGGAGAAGCGTT
SIRT7	NM_016538	sh223.2	2	GCCTGAAGTTCTAAAGAAGT
SIRT7	NM_016538	sh223.1	1	CGCCAAATCTTCTGTGCTCTA
SLC11A1	NM_000578	sh207.5	5	CTCCTTGAAGAGGACCAGAAA
SLC11A1	NM_000578	sh207.4	4	CCTTATAACCATTATGGCCTT
SLC11A1	NM_000578	sh207.3	3	CCCACCCTCATGCAGGAGTTT
SLC11A1	NM_000578	sh207.2	2	CTCCTTTATCATCAACCTCTT
SLC11A1	NM_000578	sh207.1	1	CCAGGAAACATCGAGTCAGAT
SLC19A1	NM_003056	sh069.5	5	CATCGCCTATTCCTCTACAT
SLC19A1	NM_003056	sh069.4	4	CCGCAAGCAGTCCAGTTATA
SLC19A1	NM_003056	sh069.3	3	GATTGCATCTTCTGTCTAA
SLC19A1	NM_003056	sh069.2	2	CGACGGTGTTCAGAATGTGAA
SLC19A1	NM_003056	sh069.1	1	CCAGTTATACTCCGTGACTT
SMAD4	NM_005359	sh344.5	5	GTACTTCATACCATGCCGATT
SMAD4	NM_005359	sh344.4	4	CGAGTTGTATCACCTGGAATT
SMAD4	NM_005359	sh344.3	3	GCTGCTGGAATGGTGTGGA
SMAD4	NM_005359	sh344.2	2	CCTGAGTATTGGTGTTCATT
SMAD4	NM_005359	sh344.1	1	GCAGACAGAACTGGATTAAA
SMARCA3	NM_003071	sh399.5	5	GCAGGTGGAGTTGGTTGAAT
SMARCA3	NM_003071	sh399.4	4	CGTATTAGAGAACCGGCCTTA
SMARCA3	NM_003071	sh399.3	3	GCAAGAAGTTATCATCACAAA
SMARCA3	NM_003071	sh399.2	2	GCTGTGTCTGAGGTATAAATA
SMARCA3	NM_003071	sh399.1	1	GTTGCCATACTTACCTTCTTA
SMC5	NM_015110	sh401.5	5	CAACAGATATTAAAGGAGGCAT
SMC5	NM_015110	sh401.4	4	GAGGTGAAAGAAGTGTTTCTA
SMC5	NM_015110	sh401.3	3	GAGAAAGAATTGAACGGGTAA
SMC5	NM_015110	sh401.2	2	GCATTATGTGAAGGCGAAATA
SMC5	NM_015110	sh401.1	1	GCGAAACTTGTTACCGAATTA
SMC6	NM_024624	sh351.5	5	CCTGGATGAATTTGATGTCTA
SMC6	NM_024624	sh351.4	4	GCCATCAGAGATAATATCAAA
SMC6	NM_024624	sh351.3	3	GCATCAATTCTGGACAAGAA
SMC6	NM_024624	sh351.2	2	CACCTACCAAGAGCTTATAA
SMC6	NM_024624	sh351.1	1	ACCGATCCTTAAACGAATATA
SMUG1	NM_014311	sh187.5	5	CATCTACAATCCCGTGGAGTA
SMUG1	NM_014311	sh187.4	4	CATCATCTACAATCCCGTGGGA
SMUG1	NM_014311	sh187.3	3	CCTCCTGATTCTGCTTTCTT
SMUG1	NM_014311	sh187.2	2	CCAAGACAAGCATGGGACAT
SMUG1	NM_014311	sh187.1	1	GCCAAGCAGATGACAACACAT
SND1	NM_014390	sh178.5	5	GCTGATGATGCAGACGAATTT
SND1	NM_014390	sh178.4	4	CGGGATCTCAAGTATACCATT
SND1	NM_014390	sh178.3	3	GCCAAAGGAACTTGCCCTTAT
SND1	NM_014390	sh178.2	2	GCGAGAGTATGGCATGACTA
SND1	NM_014390	sh178.1	1	CCCACAGCTAATTTGGACCAA
SPO11	NM_012444	sh177.5	5	GAGTGTACTTACCTAACAAAT
SPO11	NM_012444	sh177.4	4	CAAGAAATGAAGCACCTGCAT
SPO11	NM_012444	sh177.3	3	CCATCGAATATTCAAGGAATT
SPO11	NM_012444	sh177.2	2	GCATCTATAAGTATGGATCTA
SPO11	NM_012444	sh177.1	1	CGGCTCCTAGATGACAACTTT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
SSRP1	NM_003146	sh458.5	5	GCCATGGACTTAAACTGCTTA
SSRP1	NM_003146	sh458.4	4	CGCTTCGATGAGATCTCCTTT
SSRP1	NM_003146	sh458.3	3	GCATGGCAAGACCTTTGACTA
SSRP1	NM_003146	sh458.2	2	GCGATGACTCAGGAGAAGAAA
SSRP1	NM_003146	sh458.1	1	CGAGTCTTCTAAGAGGGACAA
STAT1	NM_007315	sh322.5	5	GAACAGAAATACACTACGAA
STAT1	NM_007315	sh322.4	4	CCCAAAGTATCAGGACGAGAAC
STAT1	NM_007315	sh322.3	3	CTGGAAGATTTACAAGATGAA
STAT1	NM_007315	sh322.2	2	CGACAGTATGATGAACACAGT
STAT1	NM_007315	sh322.1	1	CCCTGAAGTATCTGTATCCAA
STAT3	NM_003150	sh323.5	5	GCAAAGAATCACATGCCACTT
STAT3	NM_003150	sh323.4	4	GCACAATCTACGAAGAATCAA
STAT3	NM_003150	sh323.3	3	GCTGAAATCATCATGGGCTAT
STAT3	NM_003150	sh323.2	2	GCTGACCAACAATCCCAAGAA
STAT3	NM_003150	sh323.1	1	CGGATCATAAGGTCAGGAGAT
STUB1	NM_005861	sh452.5	5	CGCGAAGAAGAAGCGCTGGAA
STUB1	NM_005861	sh452.4	4	GCAGTCTGTGAAGCGCCTT
STUB1	NM_005861	sh452.3	3	GACGCATTCATCTGTAGAAT
STUB1	NM_005861	sh452.2	2	GAAGAGGAAGAAGCGAGACAT
STUB1	NM_005861	sh452.1	1	CCCAAGTCTGCTGTTGGACT
SUPT16H	NM_007192	sh457.5	5	CCCTGTGATGGAGAAATGATT
SUPT16H	NM_007192	sh457.4	4	CCTGCCATCACACTGTAATA
SUPT16H	NM_007192	sh457.3	3	CGGGCAGCATTACTTACAGAA
SUPT16H	NM_007192	sh457.2	2	CGCAAGTCTAATGTGTCTAT
SUPT16H	NM_007192	sh457.1	1	CCTAGAATACCCTGATGAGAA
TDG	NM_003211	sh272.4	4	GACATTGTCATTATTGGCATA
TDG	NM_003211	sh272.3	3	CCTTTAGTAATCACTGTGGAA
TDG	NM_003211	sh272.2	2	GAACGAAATATGGACGTTCAA
TDG	NM_003211	sh272.1	1	CAGTTGTGAATGAACAGCAAA
TDP1	NM_018319	sh176.5	5	CCTTATGTCAAAGCACCGGAT
TDP1	NM_018319	sh176.4	4	GCACGATCTCTGAAACAAA
TDP1	NM_018319	sh176.3	3	CCATATCTAGTAGTGATGAAA
TDP1	NM_018319	sh176.2	2	GCGGACCAGTTTAGAAGGATA
TDP1	NM_018319	sh176.1	1	CCGATGAATCAAAGTGGTTAT
TFF2	NM_005423	sh374.5	5	CTCCCAAAGCAAGAGTCGGAT
TFF2	NM_005423	sh374.4	4	ACTTCATCTTTGAAGTGCCCT
TFF2	NM_005423	sh374.3	3	CCCTGGAATCACCAAGTACCA
TFF2	NM_005423	sh374.2	2	AGTCTGTGGAAGACTGCCATT
TFF2	NM_005423	sh374.1	1	AGACCGAAGAAACTGTGGCTA
TMEM16A	NM_018043	sh258.5	5	GCTGATCCAGAACAACCTGTT
TMEM16A	NM_018043	sh258.4	4	CGACCTGGTCAGGAAGTATTT
TMEM16A	NM_018043	sh258.3	3	CATCGGAATCTGGTACAATAT
TMEM16A	NM_018043	sh258.2	2	CCTCACTAACTTGGTCTCCAT
TMEM16A	NM_018043	sh258.1	1	CGTCGAGTTCAACGACAGAAA
TOP3A	NM_004618	sh353.5	5	GCCAGAATGTTACCATGGTAA
TOP3A	NM_004618	sh353.4	4	CGGTGGCTAAAGCAAGAAAT
TOP3A	NM_004618	sh353.3	3	GCTTCTCGAAAGTTGAGAATA
TOP3A	NM_004618	sh353.2	2	CGAGTTTATTGTTGCGCCATT
TOP3A	NM_004618	sh353.1	1	CCAGAAATCTCCACAGAATT
TOP3B	NM_003935	sh354.5	5	CCAGGTTTCAGACTAAATATT
TOP3B	NM_003935	sh354.4	4	GCCAAGGTTAACACTGACAAA
TOP3B	NM_003935	sh354.3	3	CCGAGACATGAAGAAAGGCAT
TOP3B	NM_003935	sh354.2	2	CCCTGTGCATATCAACAACAT
TOP3B	NM_003935	sh354.1	1	CCCTGAGAACTTTGACCTGAA
TOPBP1	NM_007027	sh234.5	5	CCCTTTAATGATTCTACTCAT
TOPBP1	NM_007027	sh234.4	4	GCCTAGTTGCCCCACACAATA
TOPBP1	NM_007027	sh234.3	3	GCGTAAGTGAATCAATATGTA
TOPBP1	NM_007027	sh234.2	2	CCGTCGTTACACCTTTAGATA
TOPBP1	NM_007027	sh234.1	1	CCGTCGTTACACCTTTAGATA
TP53BP1	NM_005657	sh346.5	5	CCCTTGTTCCAGGACAGTCTTT
TP53BP1	NM_005657	sh346.4	4	CCCATAACAAAGATATTGCTT
TP53BP1	NM_005657	sh346.3	3	CCTCTCAACAAGACCTTGTTT
TP53BP1	NM_005657	sh346.2	2	CCAGTGTGATTAGTATTGATT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
TP53BP1	NM_005657	sh346.1	1	GATACTTGGTCTTACTGGTTT
TP73	NM_005427	sh096.5	5	CCAAGGGTTACAGAGCATTTA
TP73	NM_005427	sh096.4	4	CCCACCACCTTTGAGGTCACCTT
TP73	NM_005427	sh096.3	3	GTGTCCAAACTGCATCGAGTA
TP73	NM_005427	sh096.2	2	CCCCTCTTGAAGAACTCTA
TP73	NM_005427	sh096.1	1	CTCTCCTCTGTGTGTGCCAA
TP73L	NM_003722	sh082.5	5	CCGTTTCGTCAGAACACACAT
TP73L	NM_003722	sh082.4	4	CCCAGCTCATTCTCTTGGAA
TP73L	NM_003722	sh082.3	3	GAGTGGAAATGACTCAACTTT
TP73L	NM_003722	sh082.2	2	CCTAGTCATTTGATTCGAGTA
TP73L	NM_003722	sh082.1	1	GCCACATCAAACCTTTGAGTA
TRAF2	NM_021138	sh189.5	5	CGACCAGAATAACCGGGAGCA
TRAF2	NM_021138	sh189.4	4	CCCTGAAAGAATACGAGAGCT
TRAF2	NM_021138	sh189.3	3	CGAGACGGTAGAGGGTGAGAA
TRAF2	NM_021138	sh189.2	2	CTCGGGCATGACAGGCAGAAA
TRAF2	NM_021138	sh189.1	1	CCCTTGCAGATTCACGCCAT
TRAF3	NM_003300	sh065.5	5	GAGCAGTTAATGCTGGACAT
TRAF3	NM_003300	sh065.4	4	CCTTGGCCGTTTAAGCAGAAA
TRAF3	NM_003300	sh065.3	3	CCTTCATTTACAGCGAGTGAT
TRAF3	NM_003300	sh065.2	2	CGTGTCAAGAGAGCATCGTTA
TRAF3	NM_003300	sh065.1	1	CCAGCCTTTCTACACTGGTTA
TRAF5	NM_004619	sh098.5	5	CCTGTCAGTTTCGAAAGGAAA
TRAF5	NM_004619	sh098.4	4	GCTGGAGGGTACTTGCTATAA
TRAF5	NM_004619	sh098.3	3	CCCTGTAGATAAAGAGGTCAT
TRAF5	NM_004619	sh098.2	2	CCCAGTATAGAGTACCAGTTT
TRAF5	NM_004619	sh098.1	1	GCTGCATAAAGACTGGTGAAT
TRAF6	NM_004620	sh099.5	5	CCTGGATTCTACACTGGCAAA
TRAF6	NM_004620	sh099.4	4	CCCATCTGCTTGATGGCATT
TRAF6	NM_004620	sh099.3	3	CGAAGAGATAATGGATGCCAA
TRAF6	NM_004620	sh099.2	2	CGGAATTTCCAGGAACTATT
TRAF6	NM_004620	sh099.1	1	GCCACGGGAAATATGTAATAT
TREX1	NM_033629	sh246.5	5	CAAGACCATCTGCTGTACAAA
TREX1	NM_033629	sh246.4	4	CCAAGGAAGAGCTACGCCTA
TREX1	NM_033629	sh246.3	3	AGCATCTACACTCGCTGTAT
TREX1	NM_033629	sh246.2	2	CCTGCCCTTCTCCAGCCCAA
TREX1	NM_033629	sh246.1	1	CAAGGATCTTCTCCAGTGAA
TREX1	NM_033629	sh130.5	5	CCTGCCCTTCTCCAGCCCAA
TREX1	NM_033629	sh130.4	4	CCTGCCCTTCTCCAGCCCAA
TREX1	NM_033629	sh130.3	3	CAAGGATCTTCTCCAGTGAA
TREX1	NM_033629	sh130.2	2	CAAGGATCTTCTCCAGTGAA
TREX1	NM_033629	sh130.1	1	AGCATCTACACTCGCTGTAT
TREX2	NM_080701	sh112.5	5	CCACCGCTCCTCCCTGGAGAA
TREX2	NM_080701	sh112.4	4	CGGCAGCCTCTCCACCGCTA
TREX2	NM_080701	sh112.3	3	TGGATGATTGTGGCAGCAGAA
TREX2	NM_080701	sh112.2	2	CTCTAGTTTGAGGACTTGCTA
TREX2	NM_080701	sh112.1	1	TGGCCCAATGGCTTTGATT
TRPM2	NM_003307	sh291.4	4	GCCTGAGTTTGTGAAGCTCTT
TRPM2	NM_003307	sh291.3	3	CTGATCTATGACCCACCCTTT
TRPM2	NM_003307	sh291.2	2	GAAGAAAGAATCGGTGATTT
TRPM2	NM_003307	sh291.1	1	CCTGAACATCCTCTCCTACTT
TSC1	NM_000368	sh256.5	5	GCTACATATCATGGACTACAA
TSC1	NM_000368	sh256.4	4	GCAGCCATCTTGAAGCATAA
TSC1	NM_000368	sh256.3	3	GCCAAGAAAGACCACCTTCTT
TSC1	NM_000368	sh256.2	2	GCACTCTTTCATCGCCTTTAT
TSC1	NM_000368	sh256.1	1	CCACACATTTAATTGAGCTTT
TSC2	NM_000548	sh257.5	5	GAGGGTAAACAGACGGAGTTT
TSC2	NM_000548	sh257.4	4	CCAACGAAGACCTTACGAAA
TSC2	NM_000548	sh257.3	3	CGTATAAAGTGCTCATCTTT
TSC2	NM_000548	sh257.2	2	GCTCATCAACAGGCAGTTCTA
TSC2	NM_000548	sh257.1	1	CGACGAGTCAAACAAGCCAAT
UBE2A	NM_003336	sh058.5	5	ACCTCCCTACTCTGTCTATTA
UBE2A	NM_003336	sh058.4	4	CCAGGAGAACAACGGGAATA
UBE2A	NM_003336	sh058.3	3	CCATTCTAACATCCATACAGT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
UBE2A	NM_003336	sh058.2	2	TCTTCCATTCTAACATCCATA
UBE2A	NM_003336	sh058.1	1	CCAATCCCAATAGTCCAGCAA
UBE2B	NM_003337	sh079.5	5	CATGCGGGATTTCAAGCGGTT
UBE2B	NM_003337	sh079.4	4	CGGGATTTCAAGCGGTTACAA
UBE2B	NM_003337	sh079.3	3	GAATCCTAACAGTCCAGCCAA
UBE2B	NM_003337	sh079.2	2	GCAGTTATATTTGGACCAGAA
UBE2B	NM_003337	sh079.1	1	GCTTTAATTGTGTGGTGCTTT
UBE2N	NM_003348	sh084.5	5	CTAGGCTATATGCCATGAATA
UBE2N	NM_003348	sh084.4	4	CCTTCCAGAAGAATACCCAAT
UBE2N	NM_003348	sh084.3	3	CCATAGAAACAGCTAGAGCAT
UBE2N	NM_003348	sh084.2	2	GCCTTGTTAAGTGCTCCCAAT
UBE2N	NM_003348	sh084.1	1	GCTGAGGCATTTGTGAGTCTT
UBE2V2	NM_003350	sh080.5	5	GCCCGGAGCATACCAGTGTTA
UBE2V2	NM_003350	sh080.4	4	GCTCCTCGTCAAGTATAGATT
UBE2V2	NM_003350	sh080.3	3	GTCTTAAATCAACAACCTTCT
UBE2V2	NM_003350	sh080.2	2	CAGAAGGACAAAACATACAACA
UBE2V2	NM_003350	sh080.1	1	CAAGGTGGACAGGCATGATTA
UBE3B	NM_130466	sh331.5	5	GCTGGTCACTATCTCCTCTTT
UBE3B	NM_130466	sh331.4	4	CGTGCCATTTGCATCCTTCTT
UBE3B	NM_130466	sh331.3	3	CCCAGTGAAGAGTCTCCTAAA
UBE3B	NM_130466	sh331.2	2	CCGTGATGTATGTGAAAGTTT
UBE3B	NM_130466	sh331.1	1	GCTCGGTTCTTTGAAGATTT
ULK1	NM_003565	sh248.5	5	TACACGCCATCTCCTCAAGTT
ULK1	NM_003565	sh248.4	4	ACATCGAGAACGTCAACCAAGT
ULK1	NM_003565	sh248.3	3	CCTGGTTATGGAGTACTGCAA
ULK1	NM_003565	sh248.2	2	CAAGTGCAATTAACAAGAAGAA
ULK1	NM_003565	sh248.1	1	GCCCTTTGCGTTATATTGTAT
ULK2	NM_014683	sh249.5	5	TCCCAGAGAAACATCACCTTA
ULK2	NM_014683	sh249.4	4	GCAGACCGAAGATATTGTTTA
ULK2	NM_014683	sh249.3	3	GTCAGTGGTATTCGCATCAAAA
ULK2	NM_014683	sh249.2	2	CTCATCTATAATTGTGCTGTA
ULK2	NM_014683	sh249.1	1	GCAGTTTGATATTTGGAGTAA
UNG	NM_003362	sh092.5	5	GTCAGTGATAGAGGGTTCTT
UNG	NM_003362	sh092.4	4	CCGCCAGTTTGGAGAGTCAATT
UNG	NM_003362	sh092.3	3	GCAGTTGTCTCGGCTAAAT
UNG	NM_003362	sh092.2	2	GATCCATATCATGGACCTAAT
UNG	NM_003362	sh092.1	1	GCCCAGAAATTAGGGCTCAAT
UNG2	NM_021147	sh298.5	5	CATTAGCTTCTCCTGACATT
UNG2	NM_021147	sh298.4	4	CGTTTCTCTTTCTGAACTCTT
UNG2	NM_021147	sh298.3	3	GTTTCCAGTTTCCATTGCGGTT
UNG2	NM_021147	sh298.2	2	CAGTACTTCTTCTGACTACAT
UNG2	NM_021147	sh298.1	1	GATTCCTCTTGGCCCTTCTT
USP1	NM_003368	sh390.5	5	GCTAGTGGTTTGGAGTTTGAT
USP1	NM_003368	sh390.4	4	GCTCGTATTTGTATTCTCCAT
USP1	NM_003368	sh390.3	3	CCAGTGACCAAACAGGCATTA
USP1	NM_003368	sh390.2	2	CCAGAGACAAACTAGATCAAA
USP1	NM_003368	sh390.1	1	GACTGAATAATCTCGGCAATA
USP3	NM_006537	sh408.4	4	GCCCATGAATTCATGCGCTA
USP3	NM_006537	sh408.3	3	CAAACCATAAGAAATCAGAAA
USP3	NM_006537	sh408.2	2	GCCTCATATGTGGGACAGAAT
USP3	NM_006537	sh408.1	1	GCTGCCTTTCCACAGCTATAA
VEGF	NM_003376	sh077.5	5	ATGCGGATCAAACCTCACCAA
VEGF	NM_003376	sh077.4	4	GACGTGTAATGTTCTGCAA
VEGF	NM_003376	sh077.3	3	GCGCAAGAAATCCCGGTATAA
VEGF	NM_003376	sh077.2	2	CGAACGTAAGTGCAGATGTGA
VEGF	NM_003376	sh077.1	1	AGGGCAGAATCATCACGAAGT
WRN	NM_000553	sh012.5	5	GCTGGCAATTACGAGAACAAT
WRN	NM_000553	sh012.4	4	CCTGTTTATGTAGGCAAGATT
WRN	NM_000553	sh012.3	3	CCATTATAACAATAGAGGGAAA
WRN	NM_000553	sh012.2	2	CGTTGCTTAAATCTGAGAAAT
WRN	NM_000553	sh012.1	1	CCTGTAAGATTGCTTTAAGAA
XAB2	NM_020196	sh373.5	5	CGGAACCAATTCTCTGTCAAA
XAB2	NM_020196	sh373.4	4	GCAGTATGACATGTTCAACAT

GeneSymbol	pmID	LCFVector	shRNAClone	tarSeq
XAB2	NM_020196	sh373.3	3	GACCAAATTCATTGCCCGCTA
XAB2	NM_020196	sh373.2	2	GCTTCGCTACATCGAGTTCAA
XAB2	NM_020196	sh373.1	1	CCATCAAGGAAATGCTGCGTA
XPA	NM_000380	sh026.5	5	GACCTGTTATGGAATTTGATT
XPA	NM_000380	sh026.4	4	CATGAGTATGGACCAGAAGAA
XPA	NM_000380	sh026.3	3	GCTGATGATAAACACAAGCTT
XPA	NM_000380	sh026.2	2	GCATTAGAGAAGCAAAGGAA
XPA	NM_000380	sh026.1	1	GCACAATGTCATGTCTGTGAT
XPC	NM_004628	sh109.5	5	GCAACAGCAAAGGGAAGAAA
XPC	NM_004628	sh109.4	4	GCCTCTGACCTGTACAAGTA
XPC	NM_004628	sh109.3	3	GCAGGCAGTCATTGAAAGGAA
XPC	NM_004628	sh109.2	2	CCCCTGACCATTGGCTTATAT
XPC	NM_004628	sh109.1	1	CCAGTGGAGATAGAGATTGAA
XPO1	NM_003400	sh462.5	5	CCTCACCTACAAGATGCTCAA
XPO1	NM_003400	sh462.4	4	GCTCAAGAAGTACTGACACAT
XPO1	NM_003400	sh462.3	3	GCTCATTGTGAGCCTTCATT
XPO1	NM_003400	sh462.2	2	CCTTCATTAAGTGAAGTCAA
XPO1	NM_003400	sh462.1	1	CCATTGTAAGGACCTTCAAAA
XRCC1	NM_006297	sh005.5	5	CGATGGATCTACAGTTGCAAT
XRCC1	NM_006297	sh005.4	4	CGATACGTCACAGCCTTCAAT
XRCC1	NM_006297	sh005.3	3	GACCTAAATTGCCAGCTCCAA
XRCC1	NM_006297	sh005.2	2	CCAGTGTCCAGGAAGATATA
XRCC1	NM_006297	sh005.1	1	CCTTCTGGTCACTCATCTTT
XRCC2	NM_005431	sh108.5	5	ACCCACTTACTTCTTACACTT
XRCC2	NM_005431	sh108.4	4	CCAAACAAGATGATTTCTCAA
XRCC2	NM_005431	sh108.3	3	CCGACTTGAAGGTAGAAGTT
XRCC2	NM_005431	sh108.2	2	CCCCTTACTTCTTACACTTT
XRCC2	NM_005431	sh108.1	1	CCAGTCCAATGGCTATTATA
XRCC3	NM_005432	sh107.5	5	CTTGTTGGAGTGTGTAATAA
XRCC3	NM_005432	sh107.4	4	CTGCTTCAGAAGTCCGATTT
XRCC3	NM_005432	sh107.3	3	GCTGCAATTAAGAAAGCCAAA
XRCC3	NM_005432	sh107.2	2	CCCAGAATTATTGCTGCAATT
XRCC3	NM_005432	sh107.1	1	GCCTGCTTCTTCTCCATAT
XRCC4	NM_022406	sh114.7	7	TGTGTGAGTGCTAAGGAAGCT
XRCC4	NM_022406	sh114.6	6	TATTGCTTGGACACCATTGCA
XRCC4	NM_022406	sh114.5	5	CCTCAGGAGAATCAGCTTCAA
XRCC4	NM_022406	sh114.4	4	CCAGCTGATGTATACAGTTF
XRCC4	NM_022406	sh114.3	3	GCTGCTGTAAGTAAAGATGAT
XRCC4	NM_022406	sh114.2	2	CGGTTTATTCTGGTGTGAAT
XRCC4	NM_022406	sh114.1	1	GCACATTGAGTTCTAAACTAT
XRCC5	NM_021141	sh194.5	5	CGTGGGCTTTACCATGAGTAA
XRCC5	NM_021141	sh194.4	4	CCTCATATCAAGCATAACTAT
XRCC5	NM_021141	sh194.3	3	CCTGCAATTCTTCTGCCTTT
XRCC5	NM_021141	sh194.2	2	CGCTTTAAACACTTCTGAAA
XRCC5	NM_021141	sh194.1	1	GCAGCCCTTGTGATGTGATTA
XRCC6	NM_001469	sh047.5	5	GCTGGATAATCCAGGTGCAAA
XRCC6	NM_001469	sh047.4	4	CCCAAGGTTGAAGCAATGAAT
XRCC6	NM_001469	sh047.3	3	CGTCAGATTATACTGGAGAAA
XRCC6	NM_001469	sh047.2	2	GATGAGTCATAAGAGGATCAT
XRCC6	NM_001469	sh047.1	1	CGACATAAGTCGAGGGACTTT
YY1	NM_003403	sh253.5	5	GACGACGACTACATTGAACAA
YY1	NM_003403	sh253.4	4	CCTCCTGATTATTCAGAATAT
YY1	NM_003403	sh253.3	3	CGATGGTTGTAATAAGAAGTT
YY1	NM_003403	sh253.2	2	CCCAAACAAGTGCAGAAATTT
YY1	NM_003403	sh253.1	1	GCCTCTCCTTTGTATATTATT
ZSWIM7	NM_001042697	sh356.5	5	GTCCTTGGGAAGTTCAGTAAA
ZSWIM7	NM_001042697	sh356.4	4	AGCAGTTGACTGACATATTAT
ZSWIM7	NM_001042697	sh356.3	3	GTTTACCTGAGTCAGGTTATG
ZSWIM7	NM_001042697	sh356.2	2	TAGATGACAGAAGGAGTATTA
ZSWIM7	NM_001042697	sh356.1	1	TCGACAGTCCATCACCTAAT

<u>GFP</u>	<u>Neo</u>	<u>IPTG</u>
Y		
Y		Y
	Y	

GFP Neo IPTG

<u>GFP</u>	<u>Neo</u>	<u>IPTG</u>
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	Y	Y
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GFP Neo IPTG

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GFP Neo IPTG