

Supplementary table 2

Well	Gene Symbol	Gene Id	Accession Number	GI Number	Sequence
A02	<i>CASP1</i>	834	NM_033295	73622117	CCGCAAGGUUCGAUUUUCA
A02	<i>CASP1</i>	834	NM_033295	73622117	GAAUAUGCCUGUCCUGUG
A02	<i>CASP1</i>	834	NM_033295	73622117	GACUCAUUGAACAUUUGCA
A02	<i>CASP1</i>	834	NM_033295	73622117	AGACAUCCCACAAUGGGCU
A03	<i>CASP10</i>	843	NM_032974	98985797	GAAAUGACCUCCCUAAGUU
A03	<i>CASP10</i>	843	NM_032974	98985797	GAAGGCAGCUGGUUAUUAUC
A03	<i>CASP10</i>	843	NM_032974	98985797	CAAAGGGUUUCUCUGUUUA
A03	<i>CASP10</i>	843	NM_032974	98985797	ACAAUAAUGUGACGAAAGU
A04	<i>CASP14</i>	23581	NM_012114	6912285	GGACAUUUCUUGGAACUUC
A04	<i>CASP14</i>	23581	NM_012114	6912285	ACAGAUGCCUUGCACGUUU
A04	<i>CASP14</i>	23581	NM_012114	6912285	GAGCUAAGCCCAAGGUGUA
A04	<i>CASP14</i>	23581	NM_012114	6912285	GAGAUGAGAUUGUGAUGGU
A05	<i>CASP2</i>	835	NM_032983	39995060	GAACGCACUUAUCAAGGAU
A05	<i>CASP2</i>	835	NM_032983	39995060	GGAGAGUGAUGCCGGUAAA
A05	<i>CASP2</i>	835	NM_032983	39995060	GCACUGGUGUUGAGCAAUG
A05	<i>CASP2</i>	835	NM_032983	39995060	UGACGUCCAUGUUCUAUGU
A06	<i>CASP3</i>	836	NM_032991	73622122	CCGACAAGCUUGAAUUUUAU
A06	<i>CASP3</i>	836	NM_032991	73622122	GGUUUAUUUUCUUGGCGAA
A06	<i>CASP3</i>	836	NM_032991	73622122	UGAGAUGGGUUUAUGUAUA
A06	<i>CASP3</i>	836	NM_032991	73622122	GAUGCGUGAUGUUUCUAAA
A07	<i>CASP4</i>	837	NM_001225	73622123	GGACUUAUGUGUAGAUGUA
A07	<i>CASP4</i>	837	NM_001225	73622123	GAGGGAAUCUGCGGAACUG
A07	<i>CASP4</i>	837	NM_001225	73622123	GAGACUUAUGUAAAGAAAGA
A07	<i>CASP4</i>	837	NM_001225	73622123	UAGAGGAAGUAUUUCGGAA
A08	<i>CASP6</i>	839	NM_032992	73622127	CAUGGUACAUUCAAGAUUU
A08	<i>CASP6</i>	839	NM_032992	73622127	AAAUAUGGCUCCUCCUAG
A08	<i>CASP6</i>	839	NM_032992	73622127	CAACAUAAACUGAGGUGGAU
A08	<i>CASP6</i>	839	NM_032992	73622127	GUUCAAAGGAGACAAGUGU
A09	<i>CASP7</i>	840	NM_033340	73623014	GGGCAAUUGCAUCAUAAUA
A09	<i>CASP7</i>	840	NM_033340	73623014	GAACUCUACUUCAGUCAAU
A09	<i>CASP7</i>	840	NM_033340	73623014	UACCGUCCCUCUUCAGUAA
A09	<i>CASP7</i>	840	NM_033340	73623014	CCAGACCGGUCCUCGUUUG
A10	<i>CASP8</i>	841	NM_033358	122056472	GGACAAAGUUUACCAAUUG
A10	<i>CASP8</i>	841	NM_033358	122056472	GAAGAUAAUCAACGACUUA
A10	<i>CASP8</i>	841	NM_033358	122056472	CAACGACUAUGAAGAAUUC
A10	<i>CASP8</i>	841	NM_033358	122056472	GCAAGAACC CAUCAAGGAU
A11	<i>CASP9</i>	842	NM_032996	14790127	GCUUCCAGAUUGACGACAA
A11	<i>CASP9</i>	842	NM_032996	14790127	CCAGGCAGCUGAUCAUAGA
A11	<i>CASP9</i>	842	NM_032996	14790127	GGACAUUGCUGGCUUCGUUU
A11	<i>CASP9</i>	842	NM_032996	14790127	GGACUUUGCAGCCGGCACA
B02	<i>BCL10</i>	8915	NM_003921	119466529	GAAGAUUACAGAUGAAGUG
B02	<i>BCL10</i>	8915	NM_003921	119466529	GCCACCAGAUCUACAGUUA
B02	<i>BCL10</i>	8915	NM_003921	119466529	GAAAUUUUCUUGUCGAACAU
B02	<i>BCL10</i>	8915	NM_003921	119466529	GGGCAUCCACUGUCAUGUA
B03	<i>BCL2</i>	596	NM_000657	72198345	GGAGGAUUGUGGCCUUCUUCU
B03	<i>BCL2</i>	596	NM_000657	72198345	GGGAGAUAGUGAUGAAGUA
B03	<i>BCL2</i>	596	NM_000657	72198345	UCAUGUGUGUGGAGAGCGU
B03	<i>BCL2</i>	596	NM_000657	72198345	GAAGUACAUCUUAUAUUAAG
B04	<i>BCL2A1</i>	597	NM_004049	14574570	GGAAAGAUCUGUGAAAUGC
B04	<i>BCL2A1</i>	597	NM_004049	14574570	GAAGGUUAUCUCAUCAAGA
B04	<i>BCL2A1</i>	597	NM_004049	14574570	CCUAUAAGGAGAUUUCUAUA

B04	<i>BCL2A1</i>	597	NM_004049	14574570	UGACUGAUUUGGAAACGAU
B05	<i>BCL2L1</i>	598	NM_001191	20336333	CCUACAAGCUUUCCCAGAA
B05	<i>BCL2L1</i>	598	NM_001191	20336333	GGAGGCAGGCGACGAGUUU
B05	<i>BCL2L1</i>	598	NM_001191	20336333	GAUUCAGGCUGCUUGGGAU
B05	<i>BCL2L1</i>	598	NM_001191	20336333	GAAAGGGCCAGGAACGCUU
B06	<i>BCL2L10</i>	10017	NM_020396	20336328	UCUCUGGACACGAUUUUUA
B06	<i>BCL2L10</i>	10017	NM_020396	20336328	AGAGUGGUGACGCUCGUGA
B06	<i>BCL2L10</i>	10017	NM_020396	20336328	GGAGCAGGAGGGCGACGUC
B06	<i>BCL2L10</i>	10017	NM_020396	20336328	GGAACCGCUUCGAGCUGGU
B07	<i>BCL2L11</i>	10018	NM_207002	116734658	CCGAGAAGGUAGACAAUUG
B07	<i>BCL2L11</i>	10018	NM_207002	116734658	AUGUAAGUUCUGAGUGUGA
B07	<i>BCL2L11</i>	10018	NM_207002	116734658	GUUCUGAGUGUGACCGAGA
B07	<i>BCL2L11</i>	10018	NM_207002	116734658	UGAUGUAAGUUCUGAGUGU
B08	<i>BCL2L14</i>	79370	NM_030766	13540528	GAAAUUCCCAAUCCAGUGA
B08	<i>BCL2L14</i>	79370	NM_030766	13540528	GUCAAAGGACGUUGGAAUA
B08	<i>BCL2L14</i>	79370	NM_030766	13540528	UAACUGAGGGUCUCUCCUU
B08	<i>BCL2L14</i>	79370	NM_030766	13540528	GGAAUUGUUCAGCAAUGA
B09	<i>BCL2L2</i>	599	NM_004050	157266332	GGAAGAGUGAGCAGGACAC
B09	<i>BCL2L2</i>	599	NM_004050	157266332	CAUAAGUGCUGAUCUAGAA
B09	<i>BCL2L2</i>	599	NM_004050	157266332	GCAUAUGGGUUCUAGAGUA
B09	<i>BCL2L2</i>	599	NM_004050	157266332	GUUAUAAGCUGAGGCAGAA
B10	<i>BAD</i>	572	NM_004322	14670386	CAGAGUUUGAGCCGAGUGA
B10	<i>BAD</i>	572	NM_004322	14670386	GUUCCAGAUCCAGAGUUU
B10	<i>BAD</i>	572	NM_004322	14670386	GCAACGCAGAUCCGCGCAA
B10	<i>BAD</i>	572	NM_004322	14670386	GUGACGAGUUUGUGGACUC
B11	<i>BAG1</i>	573	NM_004323	124494250	GCGAAGAGAUCAAUCGGAG
B11	<i>BAG1</i>	573	NM_004323	124494250	GGGCAGCAGUGAACCCAGUU
B11	<i>BAG1</i>	573	NM_004323	124494250	ACACUGAUCCUGCCAGAAA
B11	<i>BAG1</i>	573	NM_004323	124494250	CAAUAGAGCAGUUUAUGAA
C02	<i>BAG4</i>	9530	NM_004874	14574569	GUUAUACUCAGACCAGUUA
C02	<i>BAG4</i>	9530	NM_004874	14574569	GAUAUCCGCCUUCACAGAA
C02	<i>BAG4</i>	9530	NM_004874	14574569	UAUCCUAGCUACAAUUCUA
C02	<i>BAG4</i>	9530	NM_004874	14574569	GAGAAGGUCCAGUAUCUUG
C03	<i>BAG5</i>	9529	NM_001015048	62548853	GAAGAAGGCAUCCAAGAUUA
C03	<i>BAG5</i>	9529	NM_001015048	62548853	GAAAUUCUGAUGAAUGGGAG
C03	<i>BAG5</i>	9529	NM_001015048	62548853	CAACAUCCUUCUUAUUAGUA
C03	<i>BAG5</i>	9529	NM_001015048	62548853	GAAAUUAUCGGAGGGAGGU
C04	<i>BAK1</i>	578	NM_001188	109698605	CAGAGAAUGCCUAUGAGUA
C04	<i>BAK1</i>	578	NM_001188	109698605	GCUUCGUGGUCGACUUCAU
C04	<i>BAK1</i>	578	NM_001188	109698605	CAACCGACGCUAUGACUCA
C04	<i>BAK1</i>	578	NM_001188	109698605	CGACAUCAACCGACGCUAU
C05	<i>BAX</i>	581	NM_138763	163659849	CUGAGCAGAUCAUGAAGAC
C05	<i>BAX</i>	581	NM_138763	163659849	GAACUGAUCAGAACCAUCA
C05	<i>BAX</i>	581	NM_138763	163659849	ACAUGUUUUCUGACGGCAA
C05	<i>BAX</i>	581	NM_138763	163659849	CAUUGGACUCCUCCGGGA
C06	<i>BBC3</i>	27113	NM_014417	24475588	CCGAGAUUGGAGCCAAUUA
C06	<i>BBC3</i>	27113	NM_014417	24475588	CGGACGACCUCAACGCACA
C06	<i>BBC3</i>	27113	NM_014417	24475588	CCUGGAGGGUCCUGUACAA
C06	<i>BBC3</i>	27113	NM_014417	24475588	GGCGGAGACAAGAGGAGCA
C07	<i>BMF</i>	90427	NM_001003943	51558703	GAACCAAAAUCGUGUGUGG
C07	<i>BMF</i>	90427	NM_001003943	51558703	AAUCGUGUGUGGUGGCAGA
C07	<i>BMF</i>	90427	NM_001003943	51558703	GAGUAACAGAUACGAUUA
C07	<i>BMF</i>	90427	NM_001003943	51558703	GAAUCUACCAGUUGUCGAA
C08	<i>BOK</i>	666	NM_032515	34335395	GGAGCGCGCCCGAGCGUGC

C08	<i>BOK</i>	666	NM_032515	34335395	GGCCCAGCGUCUACCGCAA
C08	<i>BOK</i>	666	NM_032515	34335395	AGAUCAUGGACGCCUUUGA
C08	<i>BOK</i>	666	NM_032515	34335395	GAUGGACUGAUGUCCUCA
C09	<i>MCL1</i>	4170	NM_182763	33519457	GGACCAACUACAAUUAAU
C09	<i>MCL1</i>	4170	NM_182763	33519457	GCUACGUAGUUCGGGCAA
C09	<i>MCL1</i>	4170	NM_182763	33519457	CGAAGGAAGUAUCGAAUUU
C09	<i>MCL1</i>	4170	NM_182763	33519457	AGAACGAAUUGAUGUGUAA
C10	<i>BID</i>	637	NM_197967	37574727	GCCAGAAGCUACUGCGAUG
C10	<i>BID</i>	637	NM_197967	37574727	UGCAAUACAUACCACGCUA
C10	<i>BID</i>	637	NM_197967	37574727	GCACCUACGUGAGGAGCUU
C10	<i>BID</i>	637	NM_197967	37574727	GAGUAAGGGCACUGACGGA
C11	<i>HRK</i>	8739	NM_003806	4504492	CUGCUCGGCAGGCGGAACU
C11	<i>HRK</i>	8739	NM_003806	4504492	UAGGCGACGAGCUGCACCA
C11	<i>HRK</i>	8739	NM_003806	4504492	GCUCAAGGCGCUAGGCGAC
C11	<i>HRK</i>	8739	NM_003806	4504492	UCAAGGCGCUAGGCGACGA
D02	<i>PMAIP1</i>	5366	NM_021127	148922873	AAACUGAACUCCGGCAGA
D02	<i>PMAIP1</i>	5366	NM_021127	148922873	AAUCUGAUUCCAAACUCU
D02	<i>PMAIP1</i>	5366	NM_021127	148922873	CUGGAAGUCGAGUGUCUA
D02	<i>PMAIP1</i>	5366	NM_021127	148922873	GCAAGAACGCUCAACCGAG
D03	<i>BIK</i>	638	NM_001197	21536418	CCAUGGAGGUUCUUGGCAU
D03	<i>BIK</i>	638	NM_001197	21536418	AAGAGGACCUGGACCCUAU
D03	<i>BIK</i>	638	NM_001197	21536418	GCACCUAGCUCUCAAGUGA
D03	<i>BIK</i>	638	NM_001197	21536418	GGAGGGCAGUGACGCAUUG
D04	<i>API5</i>	8539	NM_006595	5729729	CAAGGUUUGUGACAUUUU
D04	<i>API5</i>	8539	NM_006595	5729729	GAAAGGUGGUACUAAGGAA
D04	<i>API5</i>	8539	NM_006595	5729729	GAACAAGAUUAAAGUCGUU
D04	<i>API5</i>	8539	NM_006595	5729729	AAAGAUGCCUAUCAAGUGA
D05	<i>BIRC1</i>	4671	NM_022892	119393875	CAAGGGAUUUGUUGACUA
D05	<i>BIRC1</i>	4671	NM_022892	119393875	GUACAAGAUUCCCUGUCUA
D05	<i>BIRC1</i>	4671	NM_022892	119393875	GUAAGAGCUAUUUGGAUA
D05	<i>BIRC1</i>	4671	NM_022892	119393875	GAAAUUACCCAGUAUUAUUC
D06	<i>BIRC2</i>	329	NM_001166	41349435	UAUJAGGACCUGGAGAUAGG
D06	<i>BIRC2</i>	329	NM_001166	41349435	GAAACAAACAGUUCAAAGU
D06	<i>BIRC2</i>	329	NM_001166	41349435	CAAUUGACAUGUGUGCUUC
D06	<i>BIRC2</i>	329	NM_001166	41349435	GAACAGAAUGGCUCUCUUU
D07	<i>BIRC3</i>	330	NM_001165	33946283	CAUGUGAACUGUACCGAAU
D07	<i>BIRC3</i>	330	NM_001165	33946283	GAAGUGUCCAUGUGUUUA
D07	<i>BIRC3</i>	330	NM_001165	33946283	UCAUGAUCUUGUGUUAGA
D07	<i>BIRC3</i>	330	NM_001165	33946283	GAUGAAUACUCCUGUGAAU
D08	<i>BIRC5</i>	332	NM_001012270	59859879	CAAAGGAAACCAACAAUA
D08	<i>BIRC5</i>	332	NM_001012270	59859879	GCAAAGGAAACCAACAAUA
D08	<i>BIRC5</i>	332	NM_001012270	59859879	CACCGCAUCUCUCAUUA
D08	<i>BIRC5</i>	332	NM_001012270	59859879	CCACUGAGAACGAGCCAGA
D09	<i>BIRC6</i>	57448	NM_016252	153792693	CAAAGAUACGGUUACAUA
D09	<i>BIRC6</i>	57448	NM_016252	153792693	GGUCAAGAUCACUUAGUA
D09	<i>BIRC6</i>	57448	NM_016252	153792693	GCAACGAUGUGCAUGUUA
D09	<i>BIRC6</i>	57448	NM_016252	153792693	ACAAGCACCUCUCGCAUUA
D10	<i>DIABLO</i>	56616	NM_019887	42544195	GCAGAUACAGGCCUCUAUA
D10	<i>DIABLO</i>	56616	NM_019887	42544195	CCGACAAUAACAAGUUUA
D10	<i>DIABLO</i>	56616	NM_019887	42544195	GGAAACCACUUGGAUGACU
D10	<i>DIABLO</i>	56616	NM_019887	42544195	UAGAAGAGCUCCGUCAGAA
D11	<i>BIRC4</i>	331	NM_001167	32528298	GAGGAACCCUGCCAUGUAU
D11	<i>BIRC4</i>	331	NM_001167	32528298	GCACGGAUCUUUACUUUUG
D11	<i>BIRC4</i>	331	NM_001167	32528298	GAACUGGGCAGGUUGUAGA

D11	<i>BIRC4</i>	331	NM_001167	32528298	GAGGAGGGCUAACUGAUUG
E02	<i>PDCD8</i>	9131	NM_004208	22202627	GGUAGAAACUGACCACAUUA
E02	<i>PDCD8</i>	9131	NM_004208	22202627	CAAGGAAGAUCAUUAAGGA
E02	<i>PDCD8</i>	9131	NM_004208	22202627	GCAUGAAGAUCUCAUUGAA
E02	<i>PDCD8</i>	9131	NM_004208	22202627	GAACAUCUUUAACCGAAUG
E03	<i>APAF1</i>	317	NM_181869	32483362	GAACAAGCUCAUAGUUAUUA
E03	<i>APAF1</i>	317	NM_181869	32483362	GUAUGAUGGAGCUGCAAAU
E03	<i>APAF1</i>	317	NM_181869	32483362	AGAUAAUGAUUCCUACGUA
E03	<i>APAF1</i>	317	NM_181869	32483362	CAGUAAUGGGUCCUAAAUA
E04	<i>AVEN</i>	57099	NM_020371	56699476	UAACUGGGAUCGAUAUCAAA
E04	<i>AVEN</i>	57099	NM_020371	56699476	GAUUAGGGAUGCAGUUAAA
E04	<i>AVEN</i>	57099	NM_020371	56699476	GAACAGGGAAAUUAUUCUA
E04	<i>AVEN</i>	57099	NM_020371	56699476	GUUAUUGGUUCGAGCCCUU
E05	<i>BFAR</i>	51283	NM_016561	7706090	CAUCAUCAUUGCUAUGUUA
E05	<i>BFAR</i>	51283	NM_016561	7706090	ACGAGUAAAUGGAAGGUUG
E05	<i>BFAR</i>	51283	NM_016561	7706090	GCUACGACAUCUGGUUUA
E05	<i>BFAR</i>	51283	NM_016561	7706090	CAAGACGCCCUAUACCAUA
E06	<i>CFLAR</i>	8837	NM_003879	21361768	UAAAGAACAUCCACAGAAU
E06	<i>CFLAR</i>	8837	NM_003879	21361768	AAUAACUUCAGGCUCCAUA
E06	<i>CFLAR</i>	8837	NM_003879	21361768	GAUGUGUCCUCAUUAUUU
E06	<i>CFLAR</i>	8837	NM_003879	21361768	GCUAUGAAGUCCAGAAAU
E07	<i>CRADD</i>	8738	NM_003805	51988883	ACAAUGCUCUGCUGGAUA
E07	<i>CRADD</i>	8738	NM_003805	51988883	UAGAUUCCCUACAGGAGUU
E07	<i>CRADD</i>	8738	NM_003805	51988883	ACGGAUAUCUACCGCUGUA
E07	<i>CRADD</i>	8738	NM_003805	51988883	GGCCAGAGACAAACAAGUA
E08	<i>CYCS</i>	54205	NM_018947	34328939	GGAAGAAAGGGCAGACUUA
E08	<i>CYCS</i>	54205	NM_018947	34328939	GCAUUAGAAGAAGGAAGA
E08	<i>CYCS</i>	54205	NM_018947	34328939	ACACAGCCGCCAAUAAGAA
E08	<i>CYCS</i>	54205	NM_018947	34328939	GCACAAGACUGGGCCAAU
E09	<i>DAXX</i>	1616	NM_001350	53828721	GGAGUUGGAUCUCUCAGAA
E09	<i>DAXX</i>	1616	NM_001350	53828721	GGAAACAGCUAUGUGGAAA
E09	<i>DAXX</i>	1616	NM_001350	53828721	CUACAGAUCUCCAAUGAAA
E09	<i>DAXX</i>	1616	NM_001350	53828721	GCUACAAGCUGGAGAAUGA
E10	<i>DEDD</i>	9191	NM_001039712	89353286	GGACGUGACUUCUUAUUGG
E10	<i>DEDD</i>	9191	NM_001039712	89353286	GGCAAUGUCUUCUCUAAACA
E10	<i>DEDD</i>	9191	NM_001039712	89353286	UCACCUACCUCGAUGCAUU
E10	<i>DEDD</i>	9191	NM_001039712	89353286	CUACAUCAUUGGCUCUUUA
E11	<i>TOSO</i>	9214	NM_005449	34147517	GCAAGAAUCUGUCCUAGU
E11	<i>TOSO</i>	9214	NM_005449	34147517	GCAAUACCCACGCAAGAAU
E11	<i>TOSO</i>	9214	NM_005449	34147517	GGUUUCAUCUGCCCUAUUU
E11	<i>TOSO</i>	9214	NM_005449	34147517	GAAUACAAGGGCCGAGUUA
F02	<i>MOAP1</i>	64112	NM_022151	73747827	GAAGAGAAGGCGAUUGCUA
F02	<i>MOAP1</i>	64112	NM_022151	73747827	GAGGAGCAAUUGAGAGAGA
F02	<i>MOAP1</i>	64112	NM_022151	73747827	AGGAAAAGUUGUCGGCUUA
F02	<i>MOAP1</i>	64112	NM_022151	73747827	GGAAAGCGCUAUUGAUUGC

STable 2: siRNAs in apoptosis screen. All siRNAs present in the apoptosis screen are shown as well as gene id, asseccion number, GI number and sequence.