Supplementary Information for:

Chaperone Probes and Bead-Based Enhancement Improve the Direct Detection of mRNA Using Silicon Photonic Sensor Arrays

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Nucleic Acid Sequences

C-myc

Table S-1. C-myc DNA capture probe, chaperone, and primary transcript sequences. Epitopes targeted by DNA capture probes are bolded and underlined

	Capture Probe Sequences	Length	Nucleotide position from 5’ End
Myc$_1$	5'-/5AmMC12/TTC GTG GAT GCG GCA AGG GT-3'	20	340-359
Myc$_2$	5'-/5AmMC12/GAG TTC CGT AGC TGT TCA AGT TTG TGT T-3'	28	1853-1880
Myc$_3$	5'-/5AmMC12/ACC ACC GAG GGG TCG ATG CA-3'	20	1132-1151
	Chaperone Sequences		
1	TGC GGA CCG CTG GCT GGG GGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
2	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA ACC GCT GCT ATG GGC AAA GT		
3	CTC TGA GGC GGC GGC GCT CAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
4	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA CGT TGA GAG GGT AGG GGA AG		
5	TCA ACT GTT CTC GTC GTT TCA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
6	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA TTA CTT TTC CTT ACG CAC AA		
7	AAA ACA ATT CTT AAA TAC AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
8	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA ATT GAA ATT CTG TGT AAC TG		
9	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA CTC CTC TGG CGC TCC AAG AC		
10	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA TCC AGA CTC TGA CCT TTT GC		
11	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA CCT GTT GGT GAA GCT AAC GT		
12	GGC GGC CGC GAG CAG CAC AGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		

1 GACCCCCGAG CTGTGCTGCT CGCGGCCGCC ACCGCCGGGC CCCGGCCGTC CCTGGCTCCC
61 CTCCTGCCTC GAGAAGGGCA GGGCTTCTCA GAGGCTTGGC GGGAAAAGA ACGGAGGGAG
121 GGATCGCGCT GAGTATAAA GCCGGTTTTC GGGGCTTTAT CTAACTCGCT GTAGTAATTC
181 CAGCGAGAGG CAGAGGGAGC GAGCGGGCGG CCGGCTAGGG TGGAAGAGCC GGGCGAGCAG
241 AGCTGCGCTG CGGGCGTCCT GGGAAGGGAG ATCCGGAGCG AATAGGGGGC TTCGCCTCTG
301 GCCCAGCCCT CCCGCTGATC CCCCAGCCAG CGGTCCGCA**A CCCTTGCCGC ATCCACGAA**A
361 CTTTGCCCAT AGCAGCGGGC GGGCACTTTG CACTGGAACT TACAACACCC GAGCAAGGAC
421 GCGACTCTCC CGACGCGGGG AGGCTATTCT GCCCATTTGG GGACACTTCC CCGCCGCTGC
481 CAGGACCCGC TTCTCTGAAA GGCTCTCCTT GCAGCTGCTT AGACGCTGGA TTTTTTTCGG
541 GTAGTGGAAA ACCAGCAGCC TCCCGCGACG ATGCCCCTCA ACGTTAGCTT CACCAACAGG
601 AACTATGACC TCGACTACGA CTCGGTGCAG CCGTATTTCT ACTGCGACGA GGAGGAGAAC
661 TTCTACCAGC AGCAGCAGCA GAGCGAGCTG CAGCCCCCGG CGCCCAGCGA GGATATCTGG
721 AAGAAATTCG AGCTGCTGCC CACCCCGCCC CTGTCCCCTA GCCGCCGCTC CGGGCTCTGC
781 TCGCCCTCCT ACGTTGCGGT CACACCCTTC TCCCTTCGGG GAGACAACGA CGGCGGTGGC
841 GGGAGCTTCT CCACGGCCGA CCAGCTGGAG ATGGTGACCG AGCTGCTGGG AGGAGGACATG
901 GTGAACCAGA GTTTCATCTG CGACCCGGAC GACGAGACCT TCATCAAAAA CATCATCATC
961 CAGGACTGTA TGTGGAGCGG CTTCTCGGCC GCCGCCAAGC TCGTCTCAGA GAAGCTGGCC
1021 TCCTACCAGG CTGCGCGCAA AGACAGCGGC AGCCCGAACC CCGCCCGCGG CCACAGCGTC
1081 TGCTCCACCT CCAGCTTGTA CCTGCAGGAT CTGAGCGCCG CCGCCTCAGA G**TGCATCGAC**
1141 **CCCTCGGTGG T**CTTCCCCTA CCCTCTCAAC GACAGCAGCT CGCCCAAGTC CTGCGCCTCG
1201 CAAGACTCCA GCGCCTTCTC TCCGTCCTCG GATTCTCTGC TCTCCTCGAC GGAGTCCTCC
1261 CCGCAGGGCA GCCCCGAGCC CCTGGTGCTC CATGAGGAGA CACCGCCCAC CACCAGCAGC
1321 GACTCTGAGG AGGAACAAGA AGATGAGGAA GAAATCGATG TTGTTTCTGT GGAAAAGAGG
1381 CAGGCTCCTG GCAAAAGGTC AGAGTCTGGA TCACCTTCTG CTGGAGGCCAA CAGCAAACCT
1441 CCTCACAGCC CACTGGTCCT CAAGAGGTGC CACGTCTCCA CACATCAGCA CAACTACGCA
1501 GCGCCTCCCT CCACTCGGAA GGACTATCCT GCTGCCAAGA GGTCAAGTT GGACAGTGTC
1561 AGAGTCCTGA GACAGATCAG CAACAACCGA AAATGCACCA GCCCCAGGTC CTCGGACACC
1621 GAGGAGAATG TCAAGAGGCG AACACACAAC GTCTTGGAGC GCCAGAGGAG GAACGAGCTA
1681 AAACGGAGCT TTTTTGCCCT GCGTGACCAG ATCCCGGAGT TGGAAAACAA TGAAAAGGCC
1741 CCCAAGGTAG TTATCCTTAA AAAAGCCACA GCATACATCC TGTCCGTCCA AGCAGAGGAG
1801 CAAAAGCTCA TTTCTGAAGA GGACTTGTTG CGGAAACGAC GAGAACAGTT GA**AACACAAA**
1861 **CTTGAACAGC TACGGAACTC** TTGTGCGTAA GGAAAAGTAA GGAAAACGAT TCCTTCTAAC
1921 AGAAATGTCC TGAGCAATCA CCTATGAACT TGTTTCAAAT GCATGATCAA ATGCAACCTC
1981 ACAACCTTGG CTGAGTCTTG AGACTGAAAG ATTTAGCCAT AATGTAAACT GCCTCAAATT
2041 GGACTTTGGG CATAAAAGAA CTTTTTTATG CTTACCATCT TTTTTTTTTC TTTAACAGAT
2101 TTGTATTTAAGAATTGTTTT TAAAAAATTTT TAAGATTTAC ACAATGTTTC TCTGTAAATA
2161 TTGCCATTAA ATGTAAATAA CTTTAATAAA ACGTTTATAG CAGTTACACA GAATTTCAAT
2221 CCTAGTATAT AGTACCTAGT ATTATAGGTA CTATAAACCC TAATTTTTTT TATTTAAGTA
2281 CATTTTGCTT TTTAAAGTTG ATTTTTTTCT ATTGTTTTTA GAAAAAATAA AATAACTGGC
2341 AAATATATCA TTGAGCCAAA TCTTAAAAAA AAAAAAAAAA

β-actin

Table S-2. β-actin DNA capture probe, chaperone, and primary transcript sequences. Epitopes targeted by DNA capture probes are bolded and underlined

	Capture Probe Sequence	Length	Nucleotide position from 5’ End
Act$_1$	5'-/5AmMC12/GCGGTTGGCCTTGGGGTTCA	20	413-432
Act$_2$	5'-/5AmMC12/TAGCCGCGCTCGGTGAGGAT	20	658-677
Act$_3$	5'-/5AmMC12/TGATCTCCTTCTGCATCCTGTCGGCAA	27	1010-1036
	Chaperones		
1	CGG CAA AGG CGA GGC TCT GTA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
2	GAG GAT GCC TCT CTT GCT CTA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
3	GGC CTC GGT CAG CAG CAC GGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
4	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA ATG ATC TGG GTC ATC TTC TC		
5	CTT CAT GAG GTA GTC AGT CAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
6	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA CGG CCG TGG TGG TGA AGC TG		
7	TGC CAG GGT ACA TGG TGG TGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
8	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA TGT GCT GGG TGC CAG GGC AG		
9	GTG TAA CGC AAC TAA GTC ATA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
10	CAT CTC ATA TTT GGA ATG ACA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
11	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAG TGG GGT GGC TTT TAG GA		
12	CCT TCA TAC ATC TCA AGT TGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		

1 ACCGCGUCCG CCCCGCGAGC ACAGAGCCUC GCCUUUGCCG AUCCGCCGCC CGUCCACACC
61 CGCCGCCAGC UCACCAUGGA UGAUGAUAUC GCCGCGCUCG UCGUCGACAA CGGCUCCGGC
121 AUGUGCAAGG CCGGCUUCGC GGGCGACGAU GCCCCCCGGG CCGUCUUCCC CUCCAUCGUG
181 GGGCGCCCCA GGCACCAGGG CGUGAUGGUG GGCAUGGGUC AGAAGGAUUC CUAUGUGGGC
241 GACGAGGCCC AGAGCAAGAG AGGCAUCCUC ACCCUGAAGU ACCCCAUCGA GCACGGCAUC
301 GUCACCAACU GGGACGACAU GGAGAAAAUC UGGCACCACA CCUUCUACAA UGAGCUGCGU
361 GUGGCUCCCG AGGAGCACCC CGUGCUGCUG ACCGAGGCCC CCC**UGAACCC CAAGGCCAAC**
421 **CGC**GAGAAGA UGACCCAGAU CAUGUUUGAG ACCUUCAACA CCCCAGCCAU GUACGUUGCU
481 AUCCAGGCUG UGCUAUCCCU GUACGCCUCU GGCCGUACCA CUGGCAUCGU GAUGGACUCC
541 GGUGACGGGG UCACCCACAC UGUGCCCAUC UACGAGGGGU AUGCCCUCCC CCAUGCCAUC
601 CUGCGUCUGG ACCUGGCUGG CCGGGACCUG ACUGACUACC UCAUGAAG**AU CCUCACCGAG**
661 **CGCGGCUA**CA GCUUCACCAC CACGGCCGAG CGGGAAAUCG UGCGUGACAU UAAGGAGAAG
721 CUGUGCUACG UCGCCCUGGA CUUCGAGCAA GAGAUGGCCA CGGCUGCUUC CAGCUCCUCC
781 CUGGAGAAGA GCUACGAGCU GCCUGACGGC CAGGUCAUCA CCAUUGGCAA UGAGCGGUUC
841 CGCUGCCCUG AGGCACUCUU CCAGCCUUCC UUCCUGGGCA UGGAGUCCUG UGGCAUCCAC
901 GAAACUACCU UCAACUCCAU CAUGAAGUGU GACGUGGACA UCCGCAAAGA CCUGUACGCC
961 AACACAGUGC UGUCUGGCGG CACCACCAUG UACCCUGGCA **UUGCCGACAG GAUGCAGAAG**
1021 **GAGAUCA**CUG CCCUGGCACC CAGCACAAUG AAGAUCAAGA UCAUUGCUCC UCCUGAGCGC
1081 AAGUACUCCG UGUGGAUCGG CGGCUCCAUC CUGGCCUCGC UGUCCACCUU CCAGCAGAUG
1141 UGGAUCAGCA AGCAGGAGUA UGACGAGUCC GGCCCCUCCA UCGUCCACCG CAAAUGCUUC
1201 UAGGCGGACU AUGACUUAGU UGCGUUACAC CCUUUCUUGA CAAAACCUAA CUUGCGCAGA
1261 AAACAAGAUG AGAUUGGCAU GGCUUUAUUU GUUUUUUUUG UUUUGUUUUG GUUUUUUUUU
1321 UUUUUUUUGG CUUGACUCAG GAUUUAAAAA CUGGAACGGU GAAGGUGACA GCAGUCGGUU
1381 GGAGCGAGCA UCCCCCAAAG UUCACAAUGU GGCCGAGGAC UUUGAUUGCA CAUUGUUGUU
1441 UUUUUAAUAG UCAUUCCAAA UAUGAGAUGC GUUGUUACAG GAAGUCCCUU GCCAUCCUAA
1501 AAGCCACCCC ACUUCUCUCU AAGGAGAAUG GCCCAGUCCU CUCCCAAGUC CACACAGGGG
1561 AGGUGAUAGC AUUGCUUUCG UGUAAAUUAU GUAAUGCAAA AUUUUUUUAA UCUUCGCCUU
1621 AAUACUUUUU UAUUUUGUUU UAUUUUGAAU GAUGAGCCUU CGUGCCCCCC CUUCCCCCUU
1681 UUUUGUCCCC CAACUUGAGA UGUAUGAAGG CUUUUGGUCU CCCUGGGAGU GGGUGGAGGC
1741 AGCCAGGGCU UACCUGUACA CUGACUUGAG ACCAGUUGAA UAAAAGUGCA CACCUUAAAA
1801 AAAAAAAAAA AAAAAAAAAA

IL-8

Table S-3. IL-8 DNA capture probe, chaperone, and primary transcript sequences. Epitopes targeted by DNA capture probes are bolded and underlined

	Capture Probe Sequence	Length	Nucleotide position from 5’ End
IL$_1$	TTCTGTGTTGGCGCAGTGTGGT	22	327-348
IL$_2$	TGGCCCTTGGCCTCAATTTTGCT	23	747-769
IL$_3$	ACTGTGAGGTAAGATGGTGGCTAAT	25	999-1023
	Chaperone Sequences		
1	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA TGG AAG TCA TGT TTA CAC AC		
2	CCA CTC TCA ATC ACT CTC AGA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
3	A AAA AAA AAA AAA AAA AAA AAA AAA AAA AA TCA GAA AGC TTT ACA ATA AT		
4	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA CCA GGA ATC TTG TAT TGC AT		
5	ATT TGT ATA TTC TCC CGT GCA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
6	A AAA AAA AAA AAA AAA AAA AAA AAA AAA AA TTA AAG TTC GGA TAT TCT CT		
7	AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AGG ATT TCC AGC TAA ATT TG		
8	ACT TTT TCC ACT TAG AAA TAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		
9	A AAA AAA AAA AAA AAA AAA AAA AAA AAA AA CCA CAT GTC CTC ACA ACA TC		
10	ATA ATG TAC TTA TAC TAA AAAAA AAA AAA AAA AAA AAA AAA AAA AAA AAA		
11	A AAA AAA AAA AAA AAA AAA AAA AAA AAA AATGG GAG TAT CAA ACT AGG AT		
12	GAA TCT ATT TGT ACA TAA TAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA		

1 GAAUUCGGCA CGAGGCAGCA GAGCACACAA GCUUCUAGGA CAAGAGCCAG GAAGAAACCA
61 CCGGAAGGAA CCAUCUCACU GUGUGUAAAC AUGACUUCCA AGCUGGCCGU GGCUCUCUUG
121 GCAGCCUUCC UGAUUUCUGC AGCUCUGUGU GAAGGUGCAG UUUUGCCAAG GAGUGCUAAA
181 GAACUUAGAU GUCAGUGCAU AAAGACAUAC UCCAAACCUU UCCACCCCAA AUUUAUCAAA
241 GAACUGAGAG UGAUUGAGAG UGG**ACCACAC UGCGCCAACA CAGAA**AUUAU UGUAAAGCUU
301 UCUGAUGGAA GAGAGCUCUG UCUGGACCCC AAGGAAAACU GGGUGCAGAG GGUUGUGGAG
361 AAGUUUUUGA AGAGGGCUGA GAAUUCAUAA AAAAAUUCAU UCUCUGUGGU AUCCAAGAAU
421 CAGUGAAGAU GCCAGUGAAA CUUCAAGCAA AUCUACUUCA ACACUUCAUG UAUUGUGUGG
481 GUCUGUUGUA GGGUUGCCAG AUGCAAUACA AGAUUCCUGG UUAAAUUUGA AUUUCAGUAA
541 ACAAUGAAUA GUUUUUCAUU GUACCAUGAA AUAUCCAGAA CAUACUUAUA UGUAAAGUAU
601 UAUUUAUUUG AAUCUACAAA AAACAACAAA UAAUUUUUAA AUAUAAGGAU UUUCCUAGAU
661 AUUGCACGGG AGAAUAUACA AAU**AGCAAAA UUGAGGCCAA GGGCCA**AGAG AAUAUCCGAA
721 CUUUAAUUUC AGGAAUUGAA UGGGUUUGCU AGAAUGUGAU AUUUGAAGCA UCACAUAAAA
781 AUGAUGGGAC AAUAAAUUUU GCCAUAAAGU CAAAUUUAGC UGGAAAUCCU GGAUUUUUUU
841 CUGUUAAAUC UGGCAACCCU AGUCUGCUAG CCAGGAUCCA CAAGUCCUUG UUCCACUGUG
901 CCUUGGUUUC UCCUUUAUUU CUAAGUGGAA AAAGU**AUUAG CCACCAUCUU ACCUCACAGU**
961 GAUGUUGUGA GGACAUGUGG AAGCACUUUA AGUUUUUUCA UCAUAACAUA AAUUAUUUUC
1021 AAGUGUAACU UAUUAACCUA UUUAUUAUUU AUGUAUUUAU UUAAGCAUCA AAUAUUUGUG
1081 CAAGAAUUUG GAAAAAUAGA AGAUGAAUCA UUGAUUGAAU AGUUAUAAAG AUGUUAUAGU
1141 AAAUUUAUUU UAUUUUAGAU AUUAAAUGAU GUUUUAUUAG AUAAAUUUCA AUCAGGGUUU
1201 UUAGAUUAAA CAAACAAACA AUUGGGUACC CAGUUAAAUU UUCAUUUCAG AUAUACAACA
1261 AAUAAUUUUU UAGUAUAAGU ACAUUAUUGU UUAUCUGAAA UUUUAAUUGA ACUAACAAUC
1321 CUAGUUUGAU ACUCCCAGUC UUGUCAUUGC CAGCUGUGUU GGUAGUGCUG UGUUGAAUUA
1381 CGGAAUAAUG AGUUAGAACU AUUAAAACAG CCAAAACUCC ACAGUCAAUA UUAGUAAUUU
1441 CUUGCUGGUU GAAACUUGUU UAUUAUGUAC AAAUAGAUUC UUAUAAUAUU AUUUAAAUGA
1501 CUGCAUUUUU AAAUACAAGG CUUUAUAUUU UUAACUUUAA GAUGUUUUUA UGUGCUCUCC
1561 AAAUUUUUUU UACUGUUUCU GAUUGUAUGG AAAUAUAAAA GUAAAUAUGA AACAUUUAAA
1621 AUAUAAUUUG UUGUCAAAGC AAAAAAAAAA AAAAAAAACU CGAC

Capture Probe Specificity

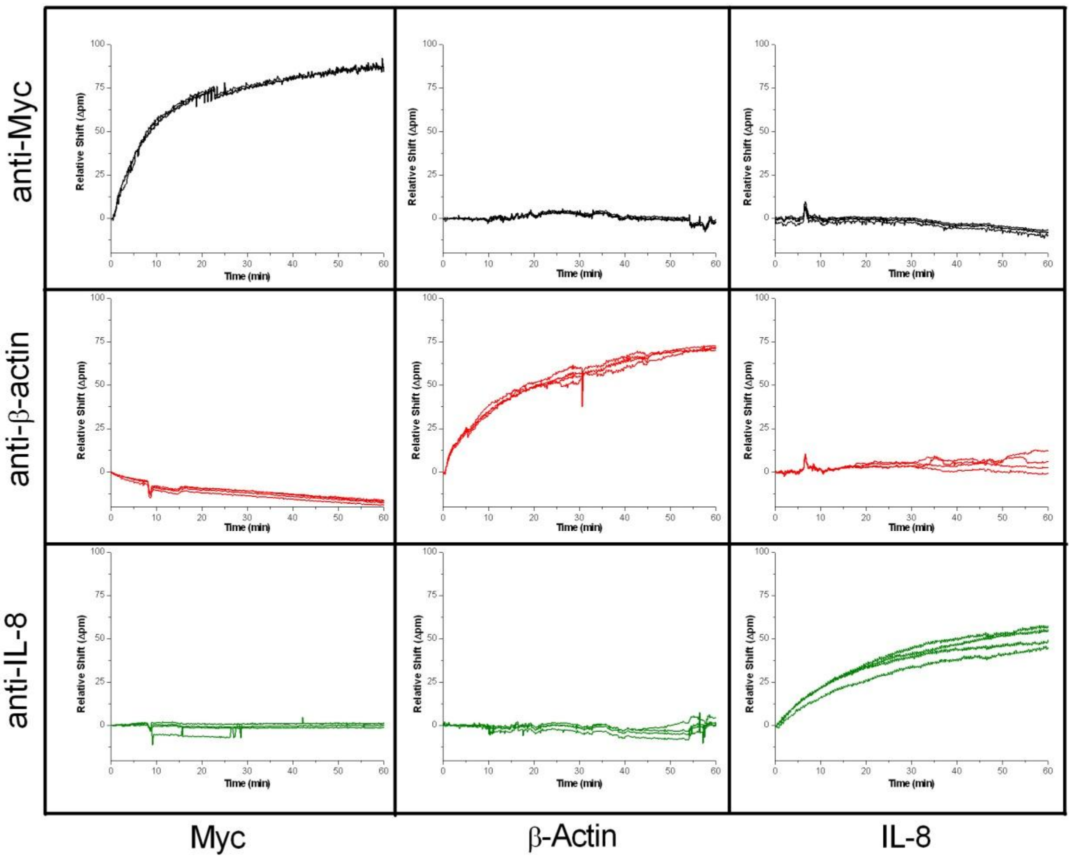

Figure S-1. (a) Array of sensor responses to 10 nM complementary and noncomplementary targets. Sensors functionalized towards a specific mRNA only illicit a response when incubated with the complementary mRNA target, as shown by the high responses diagonally across the array, confirming the specificity of the capture DNA probes.

HL-60 Flow Cytometry Analysis

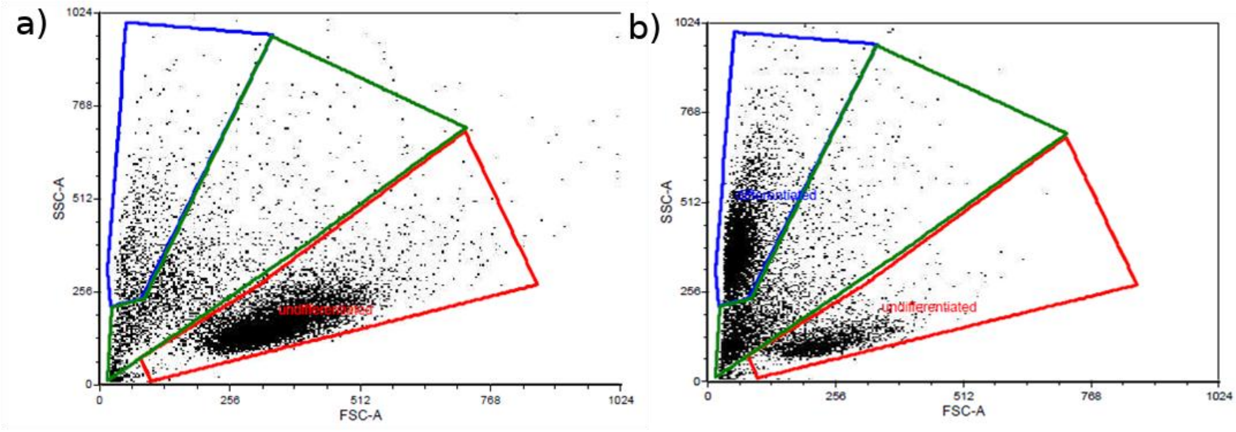

Figure S-3. (a) Flow Cytometry Analysis of native HL-60 cells and (b) seven days after differentiation. Cells are gated as undifferentiated (red), differentiated (blue), or nonviable (green).

Table S-4: Sharp changes in relative population abundances for HL-60 cells with and without 1.3% DMSO treatment indicate the efficacy of differentiation treatment.

	Untreated	DMSO Treated
Undifferentiated	75.94 %	18.98 %
Differentiated	7.00 %	53.64 %
Nonviable	17.05 %	27.37 %