

**Additional Table 1: qPCR primer sequences.**

S. No	Gene	Sense	Antisense
1	HMGCS1	GATGTGGGAATTGTTGCCCTT	ATTGTCTCTGTTCCAACCTCCAG
2	FDPS	TGTGACCGGCAAATTGGC	GCCCGTTGCAGACACTGAA
3	LSS	GCACTGGACGGGTGATTATGG	TCTCTTCTCTGTATCCGGCTG
4	EBP	CTCAGCACCTAAGACTGGACA	ACGACTAAGACCCCTGTGACA
5	MSMO1	TGCTTTGGTTGTGCAGTCATT	GGATGTGCATATTCAGCTTCCA
6	CYP51A1	GAAACGCAGACAGTCTCAAGA	ACGCCATCCTTGTATGTAGC
7	FDFT1	CCACCCCGAAGAGTTCTACAA	TGCGACTGGTCTGATTGAGATA
8	IDI1	TCCATTAAGCAATCCAGCCGA	CCCAGATACCATCAGACTGAGC
9	DHCR24	GCCGCTCTCGCTTATCTTCG	GTCTTGCTACCCTGCTCCTT
10	MVK	GGAGCAAGGTGATGTCACAAC	CGGCAGATGGACAGGTATAAGT
11	SQLE	GGCATTGCCACTTTCACCTAT	GGCCTGAGAGAATATCCGAGAAG
12	HSD17B7	TGGGATCATGCCTAATCCACA	CCAGTTCCCGAATCAGGATAAAA
13	SC5D	ACCATACGTGTATCCAGCCAC	GCTCAGTGTTGCACAGAAGAAA
14	DHCR7	GCTGCAAATCGCAACCCAA	GCTCGCCAGTGAAAACCAGT
15	NSDHL	ACGCCATCCTTGTATGTAGC	ACTGTGCATCTCTTGGCCTG
16	MVD	GGACCGGATTTGGCTGAATG	CCCATCCCGTGAGTTCCTC
17	HMGCR	TGATTGACCTTTCAGAGCAAG	CTAAAATTGCCATTCCACGAGC
18	TM7SF2	GTCGCCTGCGCTATCCTATTA	TGCGCCTTCATGTAGAGAAAGA
19	SREBP1	ACAGTGACTTCCCTGGCCTAT	GCATGGACGGGTACATCTTCAA
20	SREBP2	CCTGGGAGACATCGACGAGAT	TGAATGACCGTTGCACTGAAG
21	EGR1	GTCCCAGCTCATCAAACCCA	TTCAGCTCCTGGCAAACCT
22	IER2	ACTGGTCCCGAGCAAGAAAG	CGACTTCGGATGACGCTCC
23	LDLR	TCTGCAACATGGCTAGAGACT	TCCAAGCTAAGCTTGGTCCC
24	CDC20	GCACAGTTCGCGTTTCGAGA	CTGGATTTGCCAGGAGTTCGG
25	PPP2R2A	CATACCAGGTGCATGAATACCTC	GGGTTATGTCTCGCTTTGTGTTT
26	FOS	CCGGGGATAGCCTCTCTTACT	CCAGGTCCGTGCAGAAGTC
27	FOSB	GCTGCAAGATCCCCTACGAAG	ACGAAGAAGTGTACGAAGGGTT
28	BTG2	ACGGGAAGGGAACCGACAT	CAGTGGTGTTTGTAGTGCTCTG
29	BTGS2	CGCACTTATACTGGTCAAATCCC	CTGGCGCTCAGCCATACAG
30	JUN	TCCAAGTGCCGAAAAGGAAG	CGAGTTCTGAGCTTTC AAGGT
31	TNF	CCTCTCTCTAATCAGCCCTCTG	GAGGACCTGGGAGTAGATGAG

**Additional Table 2: ShRNA and siRNA sequences.**

## SREBP1 shRNA

SREBP1-sh1	5'-GACTTCCTCACCTCTTCTATTTCAAGAGAATAGAAGAGGGTGAGGAAGTCTTTTTT-3'
SREBP1-sh2	5'-CCTCAACCCAGCAGCAATTTGTTCAAGAGACAAATTGCTGCTGGGTTGAGGTTTTTT-3'
SREBP1-sh3	5'-GCTGGCCTTCTCTCGTCTGATTTCAAGAGAATCAGACGAGAGAAGGCCAGCTTTTTT-3'

**Additional Table 3:** Major clusters with biological functions regulated by A1542 compounds

C1 - cholesterol biosynthesis

C2 - Immune responses including response to cytokine

C3 - Positive regulation of macromolecule metabolic process

C4 - Cell Cycle

C5 - Regulation of cell growth and/or organization + cholesterol homeostasis

**Additional Table 4.** RNAseq data for expression of 67 genes regulated by A1542 in HEL cells treated for 24 h with A1542 (1µM).

Other Gene ID	HEL_DMSO FPKM	HEL_A1542 FPKM	Fold change (C/B)				
EGR1	6.82	149.33	21.896	LSS	55.04	143.58	2.609
CDKN1A	6.29	54.39	8.647	NFKBIA	10.89	28.32	2.601
CD69	9.24	70.29	7.607	PPP1R16B	7.86	20.11	2.559
CXCL2	3.2	23.75	7.422	IER2	61.57	156.31	2.539
TNF	21.93	150.36	6.856	IDI1	48.39	121.56	2.512
BHLHE40	6.17	38.61	6.258	CLCN6	8.86	21.99	2.482
HMGCS1	40.4	238.84	5.912	PMP22	9.19	22.35	2.432
CXCL3	3.53	20.82	5.898	VEGFA	19.3	46.12	2.390
RGS16	4.24	24.66	5.816	P4HA1	9.22	21.98	2.384
BCL3	4.49	21.02	4.682	HSD17B7	10.3	23.98	2.328
BTG2	23.56	104.97	4.455	FDFT1	90.55	210.36	2.323
GDF15	47.56	208.45	4.383	CXCR4	11.03	25.55	2.316
MAFF	5.84	23.09	3.954	ZFP36	9.82	22.69	2.311
INSIG1	25.21	97.24	3.857	FUT1	16.33	36.88	2.258
MSMO1	16.82	58.29	3.466	ACSS2	19.11	42.61	2.230
BNIP3	12.98	44.77	3.449	NSDHL	17.97	39.94	2.223
CD300A	8.18	27.94	3.416	ALAS1	27.23	59.93	2.201
ALDOC	38.57	124.11	3.218	ZFP36L1	12.08	26.55	2.198
TUBA1A	38.6	122.89	3.184	MVK	12.58	27.63	2.196
HMGCR	23.04	72.46	3.145	PTP4A3	16	34.47	2.154
JUNB	21.07	63.61	3.019	TMEM97	33.61	72.27	2.150
MVD	26	77.74	2.990	CD274	15.05	32.36	2.150
CYP51A1	9.03	26.92	2.981	TSC22D3	20.78	44.25	2.129
NFKB2	11.03	32.84	2.977	PLA2G6	10.09	21.36	2.117
DUSP6	29.61	85.48	2.887	CFAP161	22.74	47.84	2.104
SLC45A3	9.07	25.49	2.810	FDPS	126.58	266.17	2.103
IL1B	17.83	50.01	2.805	LDLR	22.21	45.83	2.063
HES1	18.48	51.19	2.770	TM7SF2	17.53	35.82	2.043
ACAT2	71.1	190.53	2.680	CCNB1	76.54	38.26	0.500
SLC2A3	56.98	151.48	2.658	HBQ1	20.48	9.41	0.459
DHCR7	57.14	150.73	2.638	CDC20	207.89	88.26	0.425
STARD4	12.41	32.73	2.637	PSRC1	21.39	8.92	0.417
WNT11	20.99	54.95	2.618	KIF20A	38.99	15.98	0.410
				PLK1	109.8	42.53	0.387