

Supplementary Table 2

GeneSymbol	Log FC ([mix] Vs [alone])	p (Corr) ([mix] Vs [alone])	Upregulation genes	
			Sequence	
BCHC	6.430493	0.006100826	GACTGGAAAAATCAATTAACTAGATTACTAGCAAGAAAGAGCTGTGCGGGTCTCTAA	
PCSK1	6.3048544	0.001587217	TATAGCGACTATGTTGATGTTTCTATAACACGAAACCTTATAAGCACAGAGACGCGG	
SELL	5.6136956	3.82E-04	TGGTTACTGCTTTTGTGGGTGGCATTTATCATTTGGCTGGCGAAGAAGATTAAAGAAG	
DLA-DRA	5.2546477	0.006100826	GACCATTTTATCATCAAGGACATGCGCAAGGTCAAGCTGGTGAACGCCGAGGCGCTCT	
DLA-DRA	5.1716356	0.019792927	GTGAATGTTGCAACAGATATCTCTCTACACTTAAGTGTCTTGGTCTTCTCAAAATGTGGA	
MX2	4.9884806	0.001397632	TATTTTGCTGCTCAAGAAACGCGAGTTGCTGCGCAAGACCATGATGCAGATACACAG	
MX2	4.677125	0.001728301	CGGTTTAAATGTGTACCCTCTCCCTGGCTGGCAGGAGCTCCCATGCTATGTTAAGTCTT	
MUC13	4.667969	3.82E-04	ATTGAGAAGCACTTCAAGATCTGAGACTACAGACAGCAGGCTCAGCAATCTAGGA	
HLA-DRB1	4.6603117	0.009300616	CTTGCAATGGGCGTCTCATCTACTTACAGAAATCAGAAGGACACTTGGACTCAGGCCA	
BCHC	4.6050872	7.81E-04	AACAAGATCAAAAGTTTCCAGGTTTCTGCTGATCAGAGATGTGGAAACCCAAACATGAT	
LOC488622	4.583619	0.003459198	GACAAATGTGAAGAAGCTGAGATCTGTAAATTCACAGTTTCATGAAGTCACTAAGTCCAGG	
PKC1	4.4852066	0.002791285	AAGGCTAGGTGAGATCAACACGAAAGGAGCTTTCCACATCTCCCAAGGAGTCTTGGGAG	
SELP	4.4615984	8.16E-04	CACAGCCATCTAGGAACATATGGAGTTTITACGAATGCTGCATTGACCAACCCCTTAA	
HLA-DRB1	4.4391804	0.001728301	CATGGGAACCTCACCCTTGCTCATGTTCTTATAAGCTTTTCTCAATAAATGTGGATT	
PKC1	4.417198	8.16E-04	TATATCTCTGTTACTTGCTTTACGTAATTTACAGTGTITTCCTTGACACTCTGGAA	
GNPMB	4.31783	8.16E-04	GAAGGAGAGGCTGGATCTTCTAGCTTATCCGTGTAAACCAATGCATAAAACCAATATA	
IDO1	4.2823095	8.16E-04	ATGGATTCTCTGAAGAGTGAAGAATCAACACTGAGAAATTCCTGCTGATAGATCATTA	
KCNJ16	4.2793446	0.009534662	GAAGCCCTTACAGAAAGCTGCTTGACCTTAAATAGAAATCTCCGTGAATCCCAATG	
NA	4.231623	0.009534662	AAGGAATAGAGTGGTCTAGGGTAGTTTATTTTCTTTTATACCTTTGCTGGCAATC	
IFGB1	4.189995	0.001728301	GGAATCTGGAGTTTCTGACCACTGGAGGGGATAACACTTTGTGTAATGGTGTACTACATA	
CHDH	4.170151	0.04360071	CTCTTGACATCCCAAGAAAGGAGGAATATCATTTTGGAGAAATAAACACTTTGTTACC	
CIS	4.1073313	0.009534662	GGAATCTATACACAGTGAAGAATACATGACTGGATATAAGACAGACATGACGAAGAAC	
DHX58	4.084749	8.16E-04	GGATGAGTGTCCACACGCAACAGACACTGTCTACAACTCATCTGAGCGGTAACCT	
DLA-DRA	4.064752	0.012621684	GTGTGACAGAACATCTTTTGGCCAGAGAAGACCACTTTTCCGCAATTTCCACTATCTC	
HLA-DRB1	3.977394	0.014882946	CTTGGGCCAGGACACCCACCACTTCTTGGAGGTGGCAAGTCCGAGTGCTATTCA	
LOC100684769	3.9667258	7.81E-04	GTGACCATGTTGAGGGGGAAATAGCTCAAAAGTCTTTTGACACCTTGGCAATTTGGAA	
IFT1	3.9145572	8.16E-04	GTCTGGATAAAGCTCTCAGCTCTTAAATAGGCCAACAGGCAACACCTCTCTGCT	
ANTXR2	3.9128897	0.004607428	CTAGTCACCTTCGATACTGTACTCTAGATGCGAAATGGAATTCGACTCGAAACCTGACA	
GNPMB	3.9020047	0.013627986	TTGCTCTAGAGAACACGATTCACATCTCTCTTGAGGAGTGTGTTGGTGGAGTGGAA	
PPARGC1A	3.8937433	0.001397632	ACCTGACCAAGAGTGTGCGAGGCAACCGCTCTCAAATGGCAGCATTCCTGTGAAGACACA	
CDHR4	3.8740876	0.020093916	TGGAAATTTCTTCCATGATCATGGGCTGAGTCTCAAGCTGAATCAATAATAACAA	
DCDC2	3.8643227	0.004280022	GTAAAAATCACCAGCCACAGAACAAACAAACAAACAGGACTATGTGTCTATAGCATAG	
EDRF1	3.8399196	0.003897046	GGTTTITGAGGACTCCATCTCTGTCAGTATTACTGCTGTGTATAACAAAAATAAAAAAGG	
ANTXR2	3.8071766	0.000928849	TAGAGAAAGCCAAAAATGCTGTGTGAAGATTCTGGAAGATGTGAGGAACCTGTCCAGGC	
NA	3.6965823	0.001390219	TTGTTTITGACCAATCTCGAATGCTGAGAAGACAGTGTGCCGACCAATGCTCAATA	
OASL	3.6622124	0.003101108	TTATAAGCCATAAAGAAGATTCAAGAGAAGATGTGGCAAGCGCGTGTCTGCTCAGGCTT	
BASP1	3.5883174	0.002681907	AGTTCGGTTTCTCTTCCATCTGTGTCACAGACCAACCAACCACTCATTTGGAATAATG	
NLRCS	3.584126	0.004280022	GGCCCTTCCACACTTAAAGCAAAATAGACCAATAAATGTGGATGTGTTTACGCTCTA	
CCL20	3.568295	0.003778173	AAGAAGAAATGGGTGAACGGACTGTGCGTCTCTCCAGCCATAGAGTCAAGAAGATTGA	
IOCK	3.5622616	0.004664564	CTTCACCATCTCTTGGAACTAGAGCTCACTGTACATTGTATGACACTTAGTGTGAAGA	
BASP1	3.546532	0.002681907	TTAATGCAATGCTCGTGTGGTGTGCACTGTGATGCTTTTATTGTCATGGAGATGAA	
SELP	3.5264769	0.003258927	GAAATTTCACTATGATGCAACCTGTAGTCTCCATTGTCGCGAGGCGCACTTACTAATG	
CDL2	3.4728985	0.046358194	GAGACCTCTTGTATCTCCAGACTAGCTATAAGAGTCTGTGGCAGATAGTGAATCTA	
APOBEC1	3.408351	0.001475238	CCATTACCAAAACATTCACCTCTCTCTTTAGATATGGGGTGTATCAACACTCTGTG	
PER2	3.4006684	0.012595779	CGCAACAAACAACTCTCTTCCACCTAGTGAATATGTTGTTTACTGCTGTGTCTTTT	
NA	3.393124	0.01832375	ATTATCTTACGAGGTTCGACAGAAAAAGAAACCAATTAGAAAAAGAAAGCTTCCCG	
GNPMB	3.3812294	0.001475342	CTGGAAGACACCTCTGGTGAAGAGCTTTAAGTCTGACAGAAATGAAGATCTCTTACCG	
MX1	3.3770878	0.002681907	ATGAGTTCCACAAAAGGAGCGCTGTGTATGAAAAAGAGTCCAAAGAGGAGTCTGCTGCA	
MX1	3.3629365	0.004664564	TAGAGAAAGAAGCTGAGAAGTCCATCCGACTTCACTTCCAAATGGAGCAGATGCTCTACT	
KLHL13	3.3287573	0.014917472	AGAAATATGACCCAGATAAAGATGAGTGGCATAAAGTTTTCGATCTGCTGAGTCCCTTG	
GNPMB	3.3090959	0.012742206	AGCAAGACCAAGCAGTATGTTAGAGAAGCTCCGACTCTTATTTGCTGAACCTTGGTCTTG	
RNF213	3.2635403	0.005546489	CAAGCCAGGATACCTCTATGGGAATACCCACTCTGGTGTACAGAGCTGACGTGGGA	
NA	3.2619834	0.003101108	GGACTAGGTTAGAAACCTTTGGAAAAAGTGTATGGATCTTAGATGGAGAGACAGAGTTC	
RNF213	3.2286997	0.028879592	TTACATGGAAACCAAGACAGTGAATTTCTCTGAGCTAGAGTACCAGTTCACAGAGGA	
KIAA1551	3.2258122	0.001795421	TGTAAATCATGGAAGTTATTAATAGGGCTGGGGATCTTACCTGTGCTACACAGATATG	
RNF213	3.20642	0.018379502	AGGACTTGGAAAGGGAATCAACAGGAGAAAGCTTTCAGACAGATTGTATCTCTGTG	
HERC5	3.2045517	0.009534662	ATAGGGTAAACCAAGCTAAGTGTCAACTGCTGAAATATTTTCAAGTAAACGAGCTTA	
MX1	3.1717749	0.001907912	CGTGTGGGTGCTTTGAAGCTGTATTCTCACTGATTTGTAATAAATTTGTTATCCCGG	
KIAA1551	3.1703334	0.002218157	GGAAAAAGAGAAGCAGAAAGCTGTATAGCAGTCTTTAAACAAATTTGAGGCTAAATTTT	
IF44L	3.1643941	0.010580407	ATTATTTAGAAATTCGATTTCTCTGTGGGTGCAACTGGGTCTGGAAGTCTAGTTTAT	
KIAA1551	3.1544611	0.004658427	GTGTGGAAATCTGAGTATTGTATGATGAAGAAGAGGAGGCTTCTAGTCAAAATTTCTT	
GNPMB	3.1458988	0.001475238	CGATTTTATCTCCGTGCTGTCTTCTTGGAGGGAATAACGATTAACAGTAGCGCAACAA	
SYT13	3.1296473	0.011092977	TGCTGTGTCTCATCTGGGAGCGCAAAACCTTTACGTGGTAAATAAATAATTTGCAACT	
NA	3.1158066	0.007227312	CAGAGCGTGTGTATGAGAGATTGGCAATAGGGGATTAGGGGAAATTAAGTGTATTTC	
CYP4A37	3.1099863	0.01834368	GTGATCAATGAAGCAGTGTAGATGCTCTAAGGGATAATGGCTCTCTTGCATTTTCTGCC	
DDX60	3.1063557	0.002063574	ATTCCGTTGCCAAGATAGAAAACTATTAATCCCAAGCTTCTGCACTGAGAGGAGCAG	
CYP4A11	3.1016994	0.00794888	CTTGCTCTAGCTTCTCTCTGTGTGTTACCTGTGTACCAATTGTATCTACATACCTCT	
IF44L	3.0993123	0.013615503	TGCTAAGGCAGATGTTACGGATAGTAGATGACTCTTAGAGGATATGCTCTTGGAGAAA	
IF44L	3.0887225	0.013510066	CCTATCAAGTGCCCAATGAAGTGTAAAGTCTCTGGGCGAGCTGTGAAGTATACAGCT	
MYOT	3.0506325	0.001090103	GAAGGAGAAATTCAGCGCTGCGAGCTCAATCTGGACTATGAAAGTGAAGAATTTTAA	
GNPMB	3.0381374	0.012742206	CTGAATGTTCTTCTCAACCTGCGCAAGGCCATGTCTTACCTGGAAATCCAAAGAAAGAT	
PDE4B	3.025962	0.001475238	AAGCTGTGGAAATGTTATCGGCAATGGACAGACCGCATCTGGAAGAATTTTTCAGCAG	
IF44L	3.021646	0.016819654	TTCTAACTGATGTGCTCTCTGGGATCAGTATATCTCAAGTTCAAAGGCCAACCTTGAG	
OAS2	3.0162687	0.001397632	TTTCAAGAATGGAAGTGGATATCCGTGCAATCTGGAAGCTGCCAGTAAGATAATCTA	
HERC5	3.0086226	0.014849423	AATATTTACAGTGGAAAGAGTGGAAAGGCCCTTCAAGTCCATCAACAGCAGAG	
HAVCR1	2.9782524	0.024640199	GGGTGCCAAGCAGAAAGACATATCTACATATTCGAGGACAACTTTACGTCTAGATTAA	
OAS2	2.9774737	0.001475238	AGCAAAAGACGCTACCGAATGGTTGCTCTGCTGTTTCAAGAATGGAATGGATATCT	
DLA-DQB1	2.972374	0.041694704	AGAGACATCTATAACCGGGAGGAGTGTGCGCTCTGACAGCAGCTGGGGGAGTACCGG	
MMP21	2.8272858	0.001728301	TCAACCGCTTATTTCAAGCAGTCAATCTCAGAGCGGTGTTTGAATTTTGACGCTG	
STAG2	2.8222954	0.014917472	TAAITGACTGTTTCTGATTTGTTATTTATGTTTGAGACAGTAACTTTTGAATAAAAA	
BS2	2.8150039	0.014849423	ACTTCAGGAGAGATCGAGACTTGAAGCAGCAGCTGCAGCGCCCTTTGGAGGAGGTGAA	
ISG15	2.7756286	0.002557293	TTTTCAGGCGTATCTGCTGTCTGCTGCTGATGCCAGCATAGAGTCCCTCAAGGGCACCA	
KLHL13	2.7236705	0.001397632	AACTGCCACAGTAGAGTGTTCACATCCAAGAACAAACAGAGTGACCTACGTTGCGAAA	
CAMK1D	2.6419845	0.01245899	TCACTTCCGCTCTCTTGGTATGGGTAAACCTCTATGTGTGATTTTTCATTAATGACTA	
LOC119864113	2.6199727	0.015699476	TTGTTCTCAACCGCTCTCCGTGTGTTTTCGAAACAGTTTCCGAGATGGTAAACAACTACG	
NA	2.576849	0.013615503	TGGGGTTTGACAAAATATATAATGACATGTATCCATCTGTAACGAGATTTCACCTGCT	
MAP7D2	2.558522	0.038550276	ATGAATATCAGGGTAAATCCCTTTTATGCAACAGCACACAGAAAAATGATAGCATGGTCTG	
LOC106559934	2.5249524	0.009300616	TAAATTTTCCACATGCTGCTGTTTATAGAAACAGACATCCCATCCAATGACACAGCGTCA	
C16H8Ror4	2.5130775	0.04637118	ACGAAAGACAAAGCTTTTCCAAATTTCTGAAACTGCGGAAATATTCATCAAGTTTCACTGA	
LOC119871262	2.4975245	0.02387666	ATTAAGAAGCATACACTACTTAGCAAGCTGTGAAAGCCCTACTGTGACGACAGGAGCTG	
ISG15	2.4729118	0.002681907	AGTGCTGAGAGCCACCCCAAGCTCTGACCAAGTATGGGTAAATAAAGTTGACAAAA	
NA	2.45876	0.006927228	AGCTGAGATCAGGGCTCTGTAGCTGTGTTATTAAGATGGGTAATAAAGTGTGAATAAT	
LOC102151330	2.4418416	0.012757018	TATTTGCACTGCAACGTCAAAGGTATCTGCTCAATAAAGTAGGTGCTATACAAAGAA	
CLIC2	2.3951323	0.036439348	CTCAACAGATGGCCAAAGTTACAAAGACATATGCTCTATAAATGCTCTTATAAACA	
NEURL3	2.388929	0.007041358	GCTGTGCTTATTTCTTGCCAATTTTGAGGTGTCAAAATAAATGGATCTTTTGTAAG	
CMPE2	2.3867822	0.007227312	AGAAGAAACGTAAGTGGAGCCACAGCACTTCTCGTCAAGAGTGAATAATGCTCTATCA	
PNMB8	2.3862147	0.02896853	GTGAAAGTGGAAAGTACAGATGTCAATGAACACTGCAACCAATACCAAGAGGCCAATCAG	
DCDC2	2.385975	0.044969798	GGACATAGGAGAAATGAAGAAGAGACCTATGGAAGTATTATTAACAGAGGTGACATGTCT	
IF44	2.3741984	0.037521828	ATTCTGCTCTGGTCTCACTGGAGCTGGGAAGTCTAGCTTTTCACTGAGTTAAATCT	
GALNT16	2.3498178	0.006488228	CCTGAGGGCTTGTCTTTATGAACACACACTTGGATAAATAACCACTTCTCATGATATAA	
LOC119881591	2.3477383	0.047705047	AGGGGCTGACTGATGGATTCTCTAGGAGCTGTGCTGGGAAATAATGGTTAATGCAAAAA	
CITA	2.343522	0.013097328	TCCATCTGACGAGTCACTGTTTGGCACTAACTGTGCGAGGCCAAAGCTAGGCGTGGCT	
GNP6	2.3312025	0.006927228	GGAGAGATTGGTGTGAGATTGTTTCAATATTACTTCTCTGGTAGAATATTTGATG	
FAM13C	2.3192067	0.002571825	GCACATCCAGAGCTCAAGCGAAAAATTCGGAATTTGAAGAAAAATTTGAACAAAAAGAA	
CLIC2	2.317739	0.014849423	ATCAGCTGACACTGGCTGACTGACGCTTTGTTACCAAACTGGAACTATTAAAGTTGG	
IF44	2.3028407	0.02896853	CATGCACTATTACTTGGATGCTGACTTTCATGAGATTGTGATTGTTGATCTC	
IFT3	2.2967734	0.02024172	GATGCTCAGATTATGTGCAAAAGTGAAGACAGATGTGAAGAAATTTCAATCCATAT	
IF44	2.292231	0.04089313	TAAATTAACCTCAGATGGGAACTGGAACCCGTAAAGGACTCTTGATTTCTCTGCACT	
DLA-DMB	2.2811804	0.02852616	ACCAACAACTGTACAAAGTAGGCAAAATCACTCTTTTAACACGAAGGAGAGTGTGATGCT	
IFGC1	2.27413	0.025438935	ATATGACTTCTCATCAATATTCTCTCTCCGGGTATGCTCAATGATGCTTGCTGGG	
RSAD2	2.2362056	0.007327289	GAAAAACCATGTGGAAGAACTCCAGAAACTGAGAACGTGGTGTAGAGATTAACGATGGC	
RTN4	2.231507	0.011617051	TATCGCCATCTCTGTACAGATAATAGGAGTCTCTCTCTACATTTGGGTGACGTGTGCA	
DDX58	2.2230816	0.013436841	GCAAAAGTGGAGAGGACTTTCTTTTGAAGAGATACCTTTGGTGTCTCCAGAAATACCCGAA	
IFT3	2.2213154	0.014849423	TGGGACCCCTGGAAGGACCACTTTTGACTAACCTCAGATAATCTATCTTCAAAAA	
CMPE2	2.2107272	0.04089313	CATGGAATGGTGTGTTAAGTACTCACCAGGCTGATGTTATCAATTTCTCTCTT	

LMO2		2.1594825	0.004693125	ATATCTCTCATCAACTCCGACATAGTGTGCGAACAGGACATCTACGAGTGGACTAAGAT
DDX58		2.149151	0.006927228	TGGGTACAAAGTTGCAGGTAATTTCTGGAGCAACATCTGAGAAATCTACAGTGGGAAACAGA
CMPK2		2.1451101	0.011193037	TTCTTCTGCTCTTTTGTACTTGCAATGAAATAAGTTGCTGTGATTTGTATGTCGA
HGD		2.1355836	0.013627986	GGGGGGGTGTTAAATAGAGAACTATTTTTTCACAGTCAAGTAATTCAGACATTTGTGCA
NA		2.127853	0.01367179	TACTGTGTACGGCAGCTTGCCAAATCTTTAAATACCTCTATTGACTATTACAGAAAC
CCDC148		2.127264	0.0435245	CCAAAATCAACCCCTCAAAACCTCCAAGAAAGGACATGGAGTCTACTATTATTTAAATC
CYP4A11		2.1257048	0.04193724	AGGATTTCTAGTCTGTCTCTCTTTATGCCCTTCACCAACCCAAATGTGTGCCCAAA
CPM		2.0949588	0.007640783	ACACAAGCTACCTCTTTTGTATCAGAAACAAAGATCTTACCATTGGTACTCAACTTG
NA		2.0898328	0.02033887	TGTAATTCACAGATGCTCCACGATGGCATCTCATGGAAATTTATCTGCTTTTCAAGAA
EML6		2.0872984	0.041694704	ACCGACCTTTCTGTCATCAGACCTGTCATGTACAGAAACCCAGCTGGAGACTAAATTGA
CXCL10		2.084241	0.008582573	AAGATGTCTGAATCCAGAATCTAAGACCATCAAGAGTTTAGTGAAGCAATATGACAGAA
CCDC148		2.082622	0.049760997	AACCTCCAAGAAAGGACATGGAGTCTACTATATTTAAATCTAGAGTCTACTGTGCAATC
C1S		2.0665126	0.044996798	TTTGTGCTACTATTGTCTGTAGATATAAATGAGTGACAGACTTTGCGAGATGTCCTC
NA		2.0584185	0.025378237	CAAGTGAAGGCTTTGGATGGTATACAAATGACAGAAAGTGCAAGGTTCTGGGGGGGAGAAA
CTSS		2.0558534	0.035660136	GAACACAGTGGAAATCACTGTGGGATTGCTAGTTATCCCTCTACCCAGAAATCTAGACCT
SMIM6		2.0519853	0.024048297	TCCCATCCCAATGTGTCTGGCAGCAGTCAAGTTTCAGTCAATTTTGGTGGTGAATAAT
SYT13		2.0484342	0.030479088	AGGCCAGATGCGAGGAAAGTTTAATGGGGAAATAATGTCTACAAAGAAATGGGGGCTCTT
TMEM106A		2.0314426	0.014917472	TACAAAATCTGTTCTGGATGAAATCAAGTCCACCATGTGCTTTGTCACATCCAGGGC
NCALD		2.0290167	0.017858187	TTATGTCACCTCTTTCGGGGCTGTTCATGTCTATGGCTGGTGGTGGGACCTCTGGAAA
EHF		2.0253794	0.013615503	GTTTTTTGTGATGTCTGTGTTGATGGGTCCAGGACACACTAAATAAACCCTAGAGACC
DIA88		2.0252726	0.02896853	TCAGCACTTATGTGACCGCACTCAATTTGTACTGATTTTTCACAGGTGAGAGCAG
APOL5		2.0229833	0.015547871	AGTGTGCTCTTTGTGTATTGATAAGTGTGTACAGGCCTTCAAGAACCTCAAGGAAC
REP52		2.0092466	0.032174706	GGTTAAAAATCTCCAACCTTTGGAAAAATGATCATGATGTGAAACTGGGGTGTCTAAGTAA
CIR		2.006261	0.003479745	GAGGCATGTGAGAGCTGGCTCAGGAAAAATAAAGGAAGGAGTGTGTTTCTCAAAAGTTA
DUSP10		1.9875464	0.016092596	AAATTATTTCCCAACCTTAACTTCATGGGGCAATTACTGGAGTTGTAGGAAGACCTGAA
FAM78B		1.986277	0.014849423	GAATAAAGAAATCACTGATATGACAGACTGCTGTGATTACCATGCAAGTAGCCATAAAA
FBN2		1.9608256	0.012742206	GTGTGACCAAGATTCAATAACCAATATATCCATATCCAGTTGGGGGTTTGTGTTGTTT
IRF7		1.950927	0.008582573	CTCCAACAGCCCTACGAGGAGCTGGAACTCTCTCATGGAGGTAGAGCCACTGCTGTG
APOL5		1.9304924	0.012757018	AGTAAATCCAGGAAGGATCTCGAAACTGTGCGAAGGAGCCGGGAGTGAAACAAAGTTAT
SP100		1.9105384	0.013615503	CTGAAGACCTGATTGAGATAATAATACCTACAGACCCGCCAAGAAAGAAAGAAAGAGA
ALAS1		1.9050843	0.016092596	GTCGCGGTGCGAAATGCTGCTCAAAAACACTGAAGTCTGTGTGAACATAAGTAGAGACAT
ALAS1		1.8976617	0.006629123	TGATGAGTGAAGAGAGAAATCTTACTTCTTGCGATGAGCAAGTTGGTATCTGCCAAGG
DUSP10		1.8825595	0.013615503	GCCAGCTTGGAGATTGAAGGAATCTCAATAAAAAATCAATTACTTCTCCCACTTTT
LMO2		1.769426	0.016384536	AGATGTGCAATTGATTCTTCTTCTGGCTTTTATGACAAACCTGCTCAATCAGTGT
ELL2		1.8760643	0.024801938	TGTAGAAGCAAAAGCATTTCATTCAACAGTCTGTGACGTTTATTAATGTTGGGCAAA
ALAS1		1.8604196	0.0073944	CCAGGCCAGCTGTGATCCGGATAGTCTCCAGAGTGTCTTTATATGTGAATTAATATA
ALAS1		1.8507992	0.037521828	AAATATTCTGGAACTAGTAATATCCAATGTGGACCTGGAACAGGAGCTGGCTGATTTACA
RIMKLB		1.8360207	0.0398324	CAGTAGCTTAACCTGTGTTGATTTCAATGTGTTTCTCAATAAATAAACACAGAACTGGGA
TEX14		1.7708033	0.020093916	AGGGGGAAGAAAGATCAAACTCAGAGAGAGGGAAGTCAGACAGCTTTTAGGAAGCTTGA
SAMD9L		1.769326	0.014882946	GAGCAATACCTACTATAAAGACAAAAATCAAGTTCTCTCTCAGAGGTGAGATGTGTGCT
OAS1		1.7680743	0.027685806	AACTTTGAAACCCCGATTATCAAAACATACCTGATGAGGACGCTTGCAAAACCCAGGCGT
AASS		1.7581964	0.038401693	CCACATGTACCTCACTATAGAGACAGAAAAAGCAATCTTGCAAAATTTAAACCCCTGTCA
SAMD9L		1.7338874	0.014586864	GATATTTTATCAATTAAGAGAAAGAAATTTGGCAGCTGTCTGGAAAGGGCAACAGGGCCA
PARP14		1.7290585	0.012742206	TTTGTGGTATTTATGACTACCAGGCTTACCAGAGTACCTCACTTATCTTCACTTAA
CIR		1.7057194	0.02250385	GACCTGGAGCGTCTCCGAGGCTGTGTGATGACTATGTCAAGTCTCTGCTGACAAAAA
ETS2		1.6790198	0.014917472	ATTGGATTATAGCAATTCATAGGCTTTGGCTGGGACAAAGCAACGTATGGGGTGCAGA
ELL2		1.6704509	0.027768029	CAGTCCAGTCCCAATTATCATGAAGAAAAATATAGTGTGAGTATCTTCAATAACAGCTG
PSMD9		1.6697007	0.026458131	GCTGGTGTGGACTATCAAGTAATCTGGGTAAACGAACCTGCCAAATTCATGATGAGTGA
HIVEP1		1.654461	0.023998095	TCGCGCATCTCAGCAGCTGATGATGCGACGACGAGGACAGGCTGTGTATAGCCACCT
PSMD9		1.6366624	0.037204623	TATCAAGTAATCTGGGTAAACGAACCTGCCAAATTTATGATGAGTGAATCTGCTCTCCCT
SMIM3		1.6196502	0.013770033	TTTGGTCTGAATTTCAATGATGATGCGACAGTTTCCAATAAAGTGTGAGATGACCATG
PARP9		1.6175435	0.031440467	TCCAGCCCTGAACCTTTGTGATTTTATGATGATCACTAGCTAGCTCCCAAGTATTGTGG
USP18		1.6123757	0.021008676	CCTAATTAAGGACCAAAATCAGAGATGTGGACTTGGTATGAGAGGCTGAAGGCTCTGTATAC
PHYHIP1		1.5964211	0.012039664	AACTTGAAAGCCTAGAATTGTTCAGCACTTCCAACCTTGTGTTGTGACAGTGTTATTATGT
PIK3AP1		1.5915583	0.011819222	AGACAGAGAGAGAGCAAAAAATCAGGAAGAGCAGGAGATTGGAGATCAGCGTCCCAATT
OAS3		1.5877204	0.046567127	ATCTGCTTACTCTGAAGGAAACCTGCTTCCAGAAATTTGCCATCAAGGTGCTCAAAAGTG
RARRES3		1.5860928	0.043840606	ATTGCTCTCATGCTGTCTTGGATACCTCTCTTTTAAAGCGGCGATCCCAAAACCACTGA
LGAL59		1.5793939	0.02696063	TTTCTCAGCAGGGGGCGCTTCTTCTTCCAGTCTTCAAGAAAGAGCAAAATGCTTTGTGG
SLC35A1		1.5784938	0.019385379	GTGCTGTATTGTGCCATTCTATGCTCGGATTCATGTTCTTTTTCAGTTAGATGATCACTAC
EHF		1.5768689	0.022128865	AGTCACCTGAGATGAAAAAGGAGCAAGAGCACCCTGCAAAATCCCAACCAAAAAAGCATA
SLC35A1		1.5616436	0.026458131	AAGACACTCATCCATCCAACAGGAGAAATAGTCTTCAAAAGAGAGAGTTGGTGTGTAT
NA		1.5547235	0.04401138	CTATCAACCCCAACTATTTAAGCAAGTCCAACAGTAAAGGGGCACATTTTAATCTTAACT
EHF		1.5540632	0.0246018	TGAGATGAAAAAGGAGCAAGAGCACCCTGCAAAATCCCAACCAAAAAAGCATAATCCACG
NA		1.5456636	0.016819654	ACTAGGCAAGCATGAACATTGAAACCAACATGCCCTATAGGAAATCAAGTATGTTCTCT
OAS1		1.5193994	0.018163769	TCATAATTTCAGTCACTTGGGACACATTCAGAGAGTTCCTAGGATTGTGATACCCCTTCT
SP100		1.5079501	0.038550276	TTCAAAAACACATTTTGCAATTCAGGAAACAGGCGAGAACAGTTCTCAAGTTGGAGCCCAAT
HERC6		1.5077684	0.018163769	ATGGAGAAAGTGGAGGAAGCCCTTCAAGTAGCCATCAACAGCAACAAAGGATTGTGCTCA
LOC609817		1.4914365	0.019385379	CTGACTTTCTTATAGGGATTCTCTCAGATGGGCAACATAATAATCTTCTAGTAGTAG
ZNFR52		1.4671571	0.040400952	CATATCAAGTAGTCAATCTCTCTGTGAATGCTCATTAATACCAAGTTGAGGAGGATGACA
IFIH1		1.4426898	0.012595779	AAAGTGGGTAGAAATTAATCTGCTTTTCCGACTTTGACTACTCAGAACTAGCTTTGTT
CREM		1.4340565	0.020093916	TAACCTCTGACATTTCAAAATGCTCTCATGTGTTAACTCTAGCTATAACTTCGATT
NA		1.4073178	0.04626844	ATGCCCTTTTGGGAGACGTGGATGGTTAGTGTATCATTAAGTCTTGTGCTTGTGAA
NR3C2		1.3946095	0.04453826	CAAAATATACATAAAGAACTGAGGAAGATGGTAACATAAGTCTCCAGCACTCTGGGCGAGA
DTX3L		1.379942	0.018163769	CTGCTTTGTAGAGCCTTTTGAGCAAAAGGCTGATTTTACAGTGGGAGAGTCTGGAACACTA
RGS2		1.3617965	0.03892236	CCGTTTCTTGGAGTCTGAGATTTCTACAGGACTTGTGTAAAGGCCACAGATCGCCACAGA
DTX3L		1.3572886	0.047203712	CCTGATCCCGATTATCTGAAACGTGTCAAACAGGAGCTGAAAGATAAAGGAATTGAGTAA
NR4A2		1.343379	0.0398324	CTGTTCCAGAGTGCTTATAATATACATAACTCCCTGGAAATCTAGAGCACTTTGATTA
NUDT4		1.3501925	0.04089313	TGAAAAGGGGGCGAGGGGAATGACTGTTGTATATTCTAAATGGCTTTGCATGGTCTCTAT
SYTL2		1.3391902	0.024801938	AATCAAGCTAAAGTAGATAATCTGCTGGAAGAAATAGTACGTAGTGTGAGAGTGAATCTL
CABLES1		1.3388951	0.037595	CCACATTAAGTTAATCACTAGCAAGATAAAGAGTCTGAAGCGAGAGATGGGGAAGCTTGT
RABGAP1L		1.2710779	0.023311324	GAGGCGCATGTTCACTTCATCATAGTATTACACACTATTTATATGCTGTAGTATTGAG
RABGAP1L		1.2608447	0.026810586	GGCCATGTTTCAGTTCATATAGTATTACACACTATTTATATGCTGATGTTTAGTTGG
TLR3		1.2587512	0.028879592	CTTGAACTGGCCAGTTTCAGAAAGAGGGGTAAATGCTTTCTATCAATAATGCAAGTAGC
NUDT4		1.2562642	0.04844528	TGAGTAAATAGACUTTTTGTGCTACUTGTTACAGATTAGATTATATAGGCCACCTTA
PCYT1B		1.2059081	0.03758286	CCCTTTGGGACAGAGATGTTCTGTTCTTCTGGGCACTCATTCAGCACTAGTCTTGGCCAT
ABCBI1		1.1992997	0.037769947	TGCTACTAGATGAAGTACTCTTGCCCTAGACACAGAAAGTGAAAGACGGTGCAGGTT
MBP		1.1876957	0.037521828	TCCGAGGGGCTTGAATGTGATGGCTGCACAGAAAGACCTCCAGAGGCACGGATCCAA
GK		1.1825991	0.04564681	ATGGTAGCTTGCAATTGTCAGTTCGAATGTACTGTTTCTAAATATGAAATCTACTTGGG
KLKB1		1.1518855	0.04850343	TGTGATAAGGTTAAAGGAGACAGTGCACACAAAGCTGTGAGGAAAAATGTGTGACAG
MEIS1		1.1252414	0.041694704	GATGATCCAGATAAGGACAAAAAGGCTCACAAAAGCGTGGCACTTTTCCCAAGTATGCT
COL5A3		1.0828831	0.040294748	ATCCTAATGGTGTGCGCTATTTATACCTGGGTCTGGATTAAAGGGGAAATCCCAAAAA

Downregulation genes				
GeneSymbol	Log FC ([mix] Vs [alone])	p (Corr) ([mix] Vs [alone])	Sequence	
WNT7A	-2.1660843	0.004255209	TGCTGTTATGTCAAGTGCAACACCTGCAGCGAGCTACCGAGGTGTACACGTGCAAGTGA	
LOC118540810	-2.0817468	0.028495563	ATTTTGTGTCATATTGTGCTGCTCAATCAAGGGAAGGATAGAAGGACTTTGGAAAGGAGG	
NOG	-2.0132637	0.01437471	AAATAGCAGGTTAACAATATTAGCGACACACCAAGTAATAGGCTCTCTTGTCTGCTGCTT	
LOC477699	-1.86486	0.030554447	AAGATGTCCCACTGAAGAGATGCTGAAGCCAGCCATAGTGAAGTCTATGATTACTATGAGA	
NCKAP5	-1.7798468	0.03458291	AAACACCAAAATCTCTGTGGAAGAGTGAAGTCTTAGAGCACCAATGCTTCACTCCAA	
PLAU	-1.7239113	0.013627986	AGTTTCAATGTGGCCAGAAGGCTCTGAGGCGTCGCTTAAAGATTATGGTGGGAGAAATCA	
ABCB1	-1.6875682	0.013627986	CAGAAGCCATCGAAAACTCCGAAGTGTGTTTCTTTGACTAGGAGCAGAAAGTTTCAAC	
KRT14	-1.639804	0.018163769	CCTCACTCTTGTCCTCTGGCAATCAATAAAGCTTATATCTCAGTTGCATAAAAA	
COL2A1	-1.5615928	0.01245899	ACACAAATGGTGCTATTCTGTGTCAACACCTCTGATTTTTAAAAACATCAATTGATATT	
KRT14	-1.5266128	0.021088676	TGAGTCTGCTCCTACTCTTGTCCTCTGGCAATCAATAAAGCTTATATCTCAAGTGT	
ABCB1	-1.4816438	0.024801938	TTAATAGTGGTTTTCAGAAATGGCAAGTCAAGGAGCATGGGCACATCAACAGCTGCTG	
RUND3B	-1.4759988	0.037769947	ACAAATCTCTCAAGGTCTCAATCTAATGACTCACTTGCAAGTCCCAACACAGAGATGA	
LOC100688793	-1.3456538	0.018416796	TGTCATTGGTATGATGGCAATTTGCAAAATTTGGGGGTGAGTTTGGCCACATGAAATT	
ARL4C	-1.2813239	0.043840606	ATGGATGGGTTTACACAGAGGAAGTGTGCTCCCACTGTGAGACTTTGAAATTTTCT	
NA	-1.2612734	0.037405733	ATGCTTCTCGACCCACAGGAATTATAGCCACTCCGGGTAGAAAATTCAGAGGAGAAA	
EMP1	-1.2071683	0.039682474	TCTCTACTAGTCTTGAGAAAGAAATAAGGCTGAACAAATTCACAGGGAATCGGGGGGTG	