Interferon α-induced SAMHD1 regulates human cultured megakaryocyte apoptosis and proplatelet formation

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Supplemental Data

Interferon Alpha-Induced SAMHD1 Regulates Human Cultured Megakaryocyte Apoptosis and Proplatelet Formation

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Supplemental Table 1. Changes in mRNA levels in differentiating human CD61+ cultured MKs on INFα stimulation.

EnsemblID	geneName	CONTROL-treated baseMean	IFNα-TREATED baseMean	log2 fold change IFNα / CONTROL	p-value	adjusted p-value
ENSG00000101347.9	SAMHD1	557.4	9633.0	4.11	6.74E-23	2.02E-18
ENSG00000136147.18	PHF11	243.9	1393.7	2.52	1.88E-22	2.82E-18
ENSG00000110057.8	UNC93B1	194.5	1310.9	2.75	1.19E-21	1.19E-17
ENSG00000172183.15	ISG20	177.7	3460.1	4.28	1.43E-15	1.07E-11
ENSG00000206190.11	ATP10A	24.6	520.3	4.41	1.85E-15	1.11E-11
ENSG00000142089.16	IFITM3	1237.0	7117.0	2.52	3.01E-15	1.51E-11
ENSG00000025708.14	TYMP	927.5	3560.7	1.94	1.21E-14	5.20E-11
ENSG00000185885.16	IFITM1	569.3	8065.2	3.82	3.22E-12	1.21E-08
ENSG00000110446.11	SLC15A3	13.0	215.4	4.05	7.15E-11	2.14E-07
ENSG00000138035.15	PNPT1	2179.2	7841.0	1.85	7.89E-11	2.15E-07
ENSG00000106785.15	TRIM14	148.3	1284.1	3.11	1.68E-10	4.20E-07
ENSG00000174808.12	BTC	33.6	221.8	2.72	2.95E-10	6.81E-07
ENSG00000130303.13	BST2	26.2	393.1	3.91	4.04E-10	8.65E-07
ENSG00000168394.11	TAP1	3302.4	12296.9	1.90	5.31E-10	9.95E-07
ENSG00000156587.16	UBE2L6	2131.2	11836.3	2.47	6.84E-10	1.21E-06
ENSG00000140511.11	HAPLN3	95.4	303.7	1.67	8.05E-10	1.31E-06
ENSG00000204642.14	HLA-F	803.2	2380.4	1.57	8.33E-10	1.31E-06
ENSG00000223960.6	PRKRA-AS1	172.1	608.8	1.82	1.46E-09	2.16E-06
ENSG00000240065.8	PSMB9	233.0	1127.3	2.27	1.52E-09	2.16E-06
ENSG00000178685.14	PARP10	1483.9	7248.1	2.29	4.87E-09	6.64E-06
ENSG00000135114.12	OASL	175.8	2279.7	3.70	1.42E-08	1.85E-05
ENSG00000125148.7	MT2A	96.3	758.6	2.98	1.55E-08	1.87E-05
ENSG00000116663.11	FBXO6	49.7	370.6	2.90	1.56E-08	1.87E-05
ENSG00000169248.12	CXCL11	528.5	2782.7	2.40	2.16E-08	2.43E-05
ENSG00000204267.14	TAP2	1314.2	5839.7	2.15	2.20E-08	2.43E-05
ENSG00000204264.10	PSMB8	2282.2	6010.9	1.40	2.27E-08	2.43E-05
ENSG00000108771.13	DHX58	730.8	5133.4	2.81	4.98E-08	4.98E-05
ENSG00000068079.7	IFI35	469.3	4305.6	3.20	5.64E-08	5.45E-05
ENSG00000173821.19	AC124319.1	9315.4	45655.9	2.29	7.29E-08	6.83E-05
ENSG00000221963.6	APOL6	1240.5	9540.8	2.94	1.03E-07	9.38E-05
ENSG00000002549.12	LAP3	5182.0	17514.4	1.76	2.13E-07	1.88E-04
ENSG00000137200.13	CMTR1	1800.0	5606.7	1.64	2.30E-07	1.97E-04
ENSG00000196141.14	SPATS2L	204.1	1161.9	2.51	2.61E-07	2.17E-04

ENSG00000198133.8	TMEM229B	112.2	348.5	1.63	**2.74E-07**	**2.22E-04**
ENSG00000140807.7	NKD1	168.1	596.2	1.83	**2.86E-07**	**2.26E-04**
ENSG00000185201.16	IFITM2	693.9	1877.8	1.44	**3.16E-07**	**2.43E-04**
ENSG00000130813.18	C19orf66	1155.3	4420.1	1.94	**4.75E-07**	**3.56E-04**
ENSG00000133943.20	DGLUCY	916.7	2003.2	1.13	**7.73E-07**	**5.65E-04**
ENSG00000184979.9	USP18	2711.5	13730.4	2.34	**1.11E-06**	**7.89E-04**
ENSG00000168961.17	LGALS9	92.9	453.3	2.29	**1.26E-06**	**8.57E-04**
ENSG00000163131.11	CTSS	129.1	422.1	1.71	**1.47E-06**	**9.55E-04**
ENSG00000181381.13	DDX60L	3513.3	24126.3	2.78	**1.50E-06**	**9.59E-04**
ENSG00000157601.14	MX1	5023.1	83193.7	4.05	**2.62E-06**	**1.54E-03**
ENSG00000188313.13	PLSCR1	3800.9	15297.0	2.01	**2.62E-06**	**1.54E-03**
ENSG00000173786.17	CNP	2354.2	6531.4	1.47	**3.79E-06**	**2.18E-03**
ENSG00000149131.15	SERPING1	87.5	316.1	1.85	**5.41E-06**	**3.00E-03**
ENSG00000177989.13	ODF3B	39.6	200.9	2.34	**7.23E-06**	**3.87E-03**
ENSG00000133106.14	EPSTI1	4814.2	24961.0	2.37	**8.60E-06**	**4.52E-03**
ENSG00000125826.20	RBCK1	1438.8	3844.5	1.42	**9.22E-06**	**4.76E-03**
ENSG00000060491.16	OGFR	564.4	1158.6	1.04	**9.52E-06**	**4.84E-03**
ENSG00000130589.16	HELZ2	1740.5	9537.4	2.45	**1.21E-05**	**6.02E-03**
ENSG00000111331.13	OAS3	2113.8	24324.4	3.52	**1.30E-05**	**6.39E-03**
ENSG00000138760.10	SCARB2	457.4	2349.6	2.36	**1.41E-05**	**6.83E-03**
ENSG00000132109.10	TRIM21	1617.5	5655.1	1.81	**1.45E-05**	**6.90E-03**
ENSG00000013364.19	MVP	870.1	1807.7	1.05	**1.60E-05**	**7.48E-03**
ENSG00000165806.19	CASP7	525.9	1444.6	1.46	**1.88E-05**	**8.66E-03**
ENSG00000010030.14	ETV7	204.6	527.5	1.37	**1.93E-05**	**8.77E-03**
ENSG00000035720.8	STAP1	37.7	180.1	2.26	**1.99E-05**	**8.91E-03**
ENSG00000177409.12	SAMD9L	1886.0	15436.3	3.03	**2.38E-05**	**1.05E-02**
ENSG00000239713.9	APOBEC3G	1232.6	3026.7	1.30	**3.13E-05**	**1.36E-02**
ENSG00000100342.20	APOL1	44.5	469.4	3.40	**4.49E-05**	**1.90E-02**
ENSG00000038210.13	PI4K2B	1754.2	3423.9	0.96	**6.54E-05**	**2.58E-02**
ENSG00000170581.14	STAT2	3168.3	10928.3	1.79	**6.84E-05**	**2.66E-02**
ENSG00000086065.14	CHMP5	3603.8	7951.9	1.14	**8.57E-05**	**3.25E-02**
ENSG00000160932.11	LY6E	2512.2	12768.5	2.35	**9.51E-05**	**3.56E-02**
ENSG00000134326.11	CMPK2	4480.2	32352.2	2.85	**1.29E-04**	**4.72E-02**
ENSG00000137628.17	DDX60	2923.1	14443.5	2.30	**1.46E-04**	5.25E-02
ENSG00000115415.18	STAT1	12649.1	50923.9	2.01	**1.48E-04**	5.27E-02
ENSG00000188157.15	AGRN	205.7	724.4	1.82	**1.57E-04**	5.40E-02
ENSG00000256043.3	CTSO	107.3	279.4	1.38	**1.78E-04**	6.08E-02
ENSG00000185507.20	IRF7	1450.1	7474.6	2.37	**1.92E-04**	6.48E-02
ENSG00000166750.10	SLFN5	140.7	811.0	2.53	**2.04E-04**	6.79E-02
ENSG00000059378.12	PARP12	2629.1	8620.5	1.71	**2.26E-04**	7.46E-02

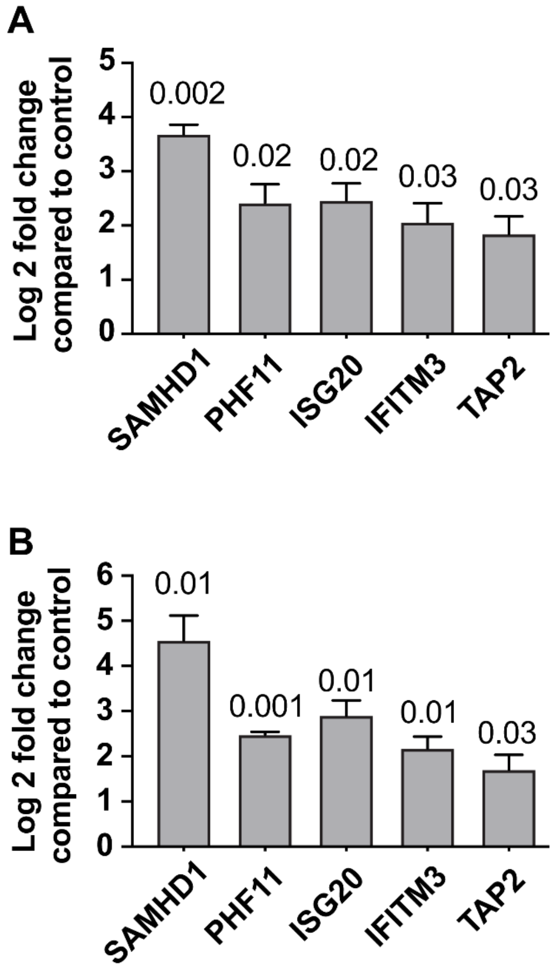
ENSG00000173193.15	PARP14	9488.7	54995.4	2.54	**2.32E-04**	7.56E-02
ENSG00000138646.9	HERC5	975.0	7430.7	2.93	**2.51E-04**	8.10E-02
ENSG00000111335.12	OAS2	839.3	16867.7	4.33	**2.63E-04**	8.40E-02
ENSG00000155363.18	MOV10	1808.9	6272.3	1.79	**3.22E-04**	1.02E-01
ENSG00000128335.14	APOL2	248.5	1142.5	2.20	**3.43E-04**	1.07E-01
ENSG00000196684.12	HSH2D	46.4	204.2	2.14	**3.85E-04**	1.18E-01
ENSG00000169245.6	CXCL10	77.1	1694.9	4.46	**4.50E-04**	1.35E-01
ENSG00000183486.13	MX2	880.3	15233.7	4.11	**4.71E-04**	1.40E-01
ENSG00000196116.8	TDRD7	978.1	2755.3	1.49	**4.99E-04**	1.45E-01
ENSG00000132274.16	TRIM22	785.6	13614.9	4.12	**5.06E-04**	1.46E-01
ENSG00000185404.16	SP140L	227.1	454.5	1.00	**5.53E-04**	1.58E-01
ENSG00000182240.16	BACE2	326.3	624.1	0.94	**5.99E-04**	1.69E-01
ENSG00000204525.16	HLA-C	6849.8	11846.0	0.79	**6.75E-04**	1.87E-01
ENSG00000108679.13	LGALS3BP	1011.0	3343.3	1.73	**7.43E-04**	2.02E-01
ENSG00000169228.14	RAB24	619.0	1071.7	0.79	**7.73E-04**	2.07E-01
ENSG00000105402.8	NAPA	3170.3	6024.1	0.93	**8.40E-04**	2.23E-01
ENSG00000164054.15	SHISA5	4357.2	11322.2	1.38	**9.29E-04**	2.44E-01
ENSG00000136514.3	RTP4	198.6	1332.3	2.75	**9.58E-04**	2.50E-01
ENSG00000138642.14	HERC6	2667.8	14155.6	2.41	**9.97E-04**	2.56E-01
ENSG00000169660.16	HEXD	433.7	839.0	0.95	**1.05E-03**	2.68E-01
ENSG00000183831.6	ANKRD45	441.0	1861.4	2.08	**1.09E-03**	2.73E-01
ENSG00000104419.14	NDRG1	533.8	944.9	0.82	**1.09E-03**	2.73E-01
ENSG00000166801.15	FAM111A	899.4	1768.6	0.98	**1.26E-03**	3.07E-01
ENSG00000172667.11	ZMAT3	4623.1	2197.7	-1.07	**1.34E-03**	3.21E-01
ENSG00000089127.13	OAS1	198.7	3332.0	4.07	**1.36E-03**	3.21E-01
ENSG00000128284.19	APOL3	202.3	664.1	1.72	**1.40E-03**	3.29E-01
ENSG00000132530.17	XAF1	1251.3	7526.3	2.59	**1.66E-03**	3.83E-01
ENSG00000275023.4	MLLT6	1237.6	1963.0	0.67	**1.68E-03**	3.84E-01
ENSG00000106560.11	GIMAP2	209.8	386.9	0.88	**1.70E-03**	3.86E-01
ENSG00000115271.11	GCA	905.5	1606.0	0.83	**1.87E-03**	4.10E-01
ENSG00000067066.17	SP100	2915.1	8358.1	1.52	**1.94E-03**	4.22E-01
ENSG00000134627.12	PIWIL4	157.3	306.8	0.96	**1.99E-03**	4.29E-01
ENSG00000013374.16	NUB1	1242.8	2370.0	0.93	**2.03E-03**	4.34E-01
ENSG00000137965.11	IFI44	1752.1	10207.0	2.54	**2.09E-03**	4.44E-01
ENSG00000168016.14	TRANK1	2174.0	4288.8	0.98	**2.12E-03**	4.47E-01
ENSG00000234883.5	MIR155HG	337.6	1267.9	1.91	**2.15E-03**	4.49E-01
ENSG00000182179.13	UBA7	12624.8	24525.3	0.96	**2.49E-03**	5.11E-01
ENSG00000121858.11	TNFSF10	31.0	733.3	4.56	**2.57E-03**	5.23E-01
ENSG00000185880.13	TRIM69	497.1	1365.4	1.46	**2.59E-03**	5.25E-01
ENSG00000160710.16	ADAR	16087.8	39436.4	1.29	**2.80E-03**	5.60E-01

ENSG00000107201.10	DDX58	3634.6	19534.0	2.43	**3.12E-03**	6.01E-01
ENSG00000133313.15	CNDP2	1520.8	2520.5	0.73	**3.16E-03**	6.02E-01
ENSG00000135899.17	SP110	532.7	2121.5	1.99	**3.17E-03**	6.02E-01
ENSG00000138496.16	PARP9	5077.8	18355.8	1.85	**3.24E-03**	6.11E-01
ENSG00000114450.10	GNB4	5897.1	10114.2	0.78	**3.27E-03**	6.13E-01
ENSG00000163121.10	NEURL3	82.3	255.2	1.63	**3.54E-03**	6.52E-01
ENSG00000111801.16	BTN3A3	65.1	141.9	1.12	**3.79E-03**	6.84E-01
ENSG00000175550.8	DRAP1	2880.9	6584.7	1.19	**3.90E-03**	6.99E-01
ENSG00000123609.10	NMI	1461.8	3073.6	1.07	**4.21E-03**	7.51E-01
ENSG00000205268.10	PDE7A	1835.2	3504.6	0.93	**4.23E-03**	7.51E-01
ENSG00000140464.19	PML	492.4	1368.9	1.48	**4.28E-03**	7.54E-01
ENSG00000168404.13	MLKL	448.8	923.3	1.04	**4.39E-03**	7.70E-01
ENSG00000258659.6	TRIM34	301.8	1200.3	1.99	**4.77E-03**	8.26E-01
ENSG00000132256.18	TRIM5	2165.4	4533.9	1.07	**5.03E-03**	8.62E-01
ENSG00000205413.8	SAMD9	9093.0	26651.4	1.55	**5.28E-03**	8.96E-01
ENSG00000172936.14	MYD88	346.7	730.7	1.08	**5.32E-03**	8.96E-01
ENSG00000205220.12	PSMB10	1328.1	2172.8	0.71	**5.37E-03**	8.99E-01
ENSG00000076321.11	KLHL20	2353.8	4469.1	0.93	**6.06E-03**	9.93E-01
ENSG00000100911.16	PSME2	1510.9	2628.9	0.80	**6.29E-03**	1.00E+00
ENSG00000204397.7	CARD16	135.4	276.5	1.03	**6.44E-03**	1.00E+00
ENSG00000092010.15	PSME1	2756.4	4333.7	0.65	**6.47E-03**	1.00E+00
ENSG00000163840.10	DTX3L	7989.0	24118.3	1.59	**6.67E-03**	1.00E+00
ENSG00000115267.7	IFIH1	1604.1	5665.2	1.82	**6.92E-03**	1.00E+00
ENSG00000127951.7	FGL2	162.2	365.2	1.17	**7.10E-03**	1.00E+00
ENSG00000112773.16	TENT5A	1159.0	2178.7	0.91	**7.49E-03**	1.00E+00
ENSG00000234127.9	TRIM26	132.7	311.1	1.23	**7.57E-03**	1.00E+00
ENSG00000105835.12	NAMPT	2757.5	6061.2	1.14	**7.64E-03**	1.00E+00
ENSG00000126709.15	IFI6	5259.8	24629.7	2.23	**8.03E-03**	1.00E+00
ENSG00000100226.16	GTPBP1	1432.1	2591.6	0.86	**8.05E-03**	1.00E+00
ENSG00000263740.2	RN7SL4P	5260.4	8890.4	0.76	**8.17E-03**	1.00E+00
ENSG00000164136.17	IL15	97.9	186.0	0.93	**8.32E-03**	1.00E+00
ENSG00000163644.15	PPM1K	3908.4	7376.0	0.92	**8.64E-03**	1.00E+00
ENSG00000197536.11	C5orf56	116.7	476.8	2.03	**8.69E-03**	1.00E+00
ENSG00000184992.11	BRI3BP	1098.7	600.4	-0.87	**9.29E-03**	1.00E+00
ENSG00000135052.16	GOLM1	392.6	898.0	1.19	**9.64E-03**	1.00E+00
ENSG00000106034.18	CPED1	901.5	2310.6	1.36	**1.07E-02**	1.00E+00
ENSG00000134321.12	RSAD2	7453.0	87283.2	3.55	**1.07E-02**	1.00E+00
ENSG00000165949.12	IFI27	94.8	1172.9	3.63	**1.10E-02**	1.00E+00
ENSG00000151338.18	MIPOL1	82.9	141.4	0.77	**1.10E-02**	1.00E+00
ENSG00000213689.14	TREX1	508.0	1006.3	0.99	**1.13E-02**	1.00E+00

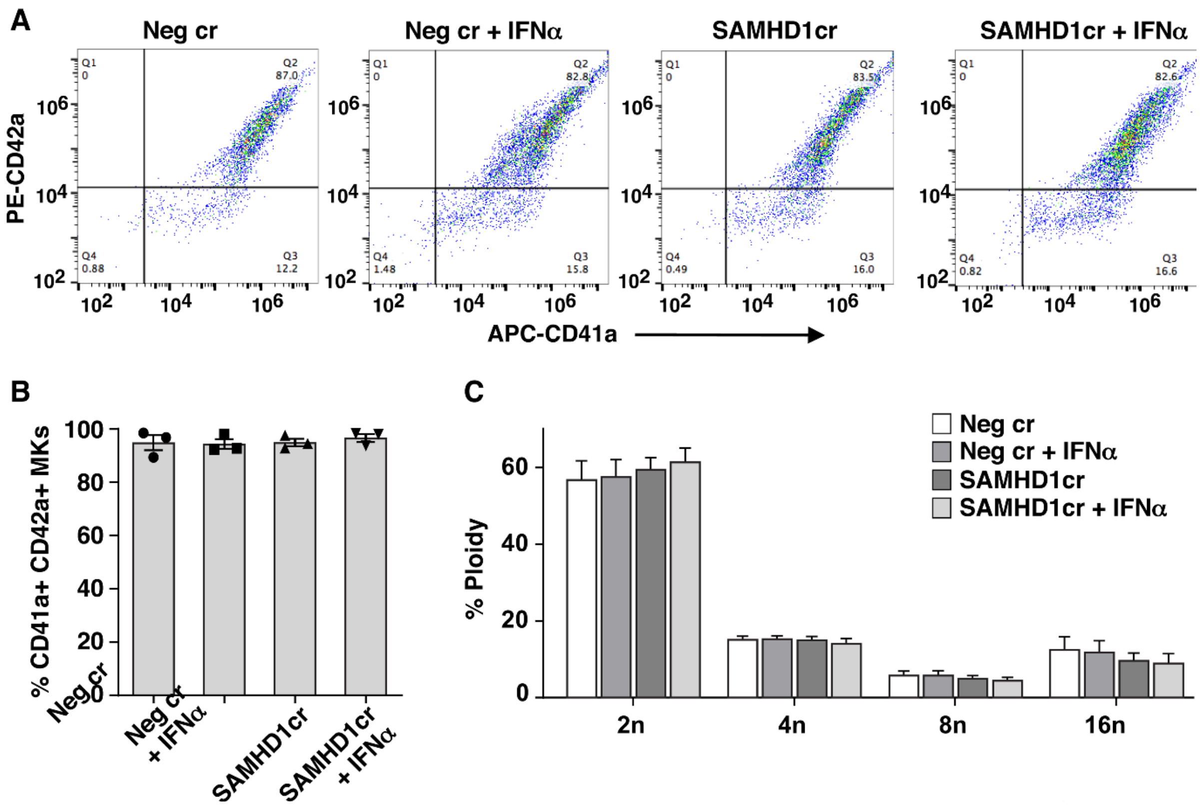
ENSG00000185722.18	ANKFY1	2550.3	4336.0	0.77	**1.14E-02**	1.00E+00
ENSG00000260249.2	AC007608.3	2157.8	6535.1	1.60	**1.24E-02**	1.00E+00
ENSG00000140105.18	WARS	3870.2	9213.5	1.25	**1.29E-02**	1.00E+00
ENSG00000129226.14	CD68	4152.3	6509.5	0.65	**1.46E-02**	1.00E+00
ENSG00000137767.14	SQOR	2011.6	3994.9	0.99	**1.51E-02**	1.00E+00
ENSG00000140853.15	NLRC5	5700.0	10202.1	0.84	**1.54E-02**	1.00E+00
ENSG00000187608.9	ISG15	4297.0	33110.7	2.95	**1.60E-02**	1.00E+00
ENSG00000137496.17	IL18BP	75.6	139.0	0.88	**1.64E-02**	1.00E+00
ENSG00000261609.6	GAN	1823.9	1141.0	-0.68	**1.80E-02**	1.00E+00
ENSG00000102524.11	TNFSF13B	1954.7	7555.9	1.95	**1.80E-02**	1.00E+00
ENSG00000276161.1	SNORA17B	276.2	180.5	-0.61	**1.83E-02**	1.00E+00
ENSG00000118507.17	AKAP7	169.2	282.1	0.74	**2.07E-02**	1.00E+00
ENSG00000130775.16	THEMIS2	1535.7	2602.9	0.76	**2.15E-02**	1.00E+00
ENSG00000163512.14	AZI2	2040.0	3124.4	0.62	**2.15E-02**	1.00E+00
ENSG00000234745.11	HLA-B	34259.0	53980.6	0.66	**2.15E-02**	1.00E+00
ENSG00000054219.11	LY75	119.4	255.7	1.10	**2.17E-02**	1.00E+00
ENSG00000152558.15	TMEM123	17122.2	27576.1	0.69	**2.17E-02**	1.00E+00
ENSG00000003400.14	CASP10	379.2	984.2	1.38	**2.19E-02**	1.00E+00
ENSG00000122694.16	GLIPR2	475.8	771.0	0.70	**2.19E-02**	1.00E+00
ENSG00000138166.6	DUSP5	3823.0	5876.2	0.62	**2.40E-02**	1.00E+00
ENSG00000168899.5	VAMP5	95.3	177.1	0.89	**2.40E-02**	1.00E+00
ENSG00000183688.4	RFLNB	1409.1	869.3	-0.70	**2.43E-02**	1.00E+00
ENSG00000000971.15	CFH	3106.7	5238.3	0.75	**2.47E-02**	1.00E+00
ENSG00000213928.8	IRF9	3373.7	7408.7	1.13	**2.67E-02**	1.00E+00
ENSG00000245556.2	SCAMP1-AS1	176.3	284.6	0.69	**2.88E-02**	1.00E+00
ENSG00000171714.11	ANO5	72.5	147.3	1.02	**3.01E-02**	1.00E+00
ENSG00000152778.9	IFIT5	2745.9	9069.5	1.72	**3.06E-02**	1.00E+00
ENSG00000104518.11	GSDMD	1216.8	2039.5	0.75	**3.17E-02**	1.00E+00
ENSG00000055332.18	EIF2AK2	5651.8	15920.6	1.49	**3.27E-02**	1.00E+00
ENSG00000285446.1	Z84488.2	78.6	173.7	1.14	**3.42E-02**	1.00E+00
ENSG00000119673.14	ACOT2	598.9	960.3	0.68	**3.42E-02**	1.00E+00
ENSG00000107262.22	BAG1	3181.4	4788.0	0.59	**3.55E-02**	1.00E+00
ENSG00000111224.14	PARP11	487.9	777.9	0.67	**3.57E-02**	1.00E+00
ENSG00000229474.6	PATL2	239.5	397.8	0.73	**3.62E-02**	1.00E+00
ENSG00000128604.20	IRF5	86.9	184.5	1.08	**3.76E-02**	1.00E+00
ENSG00000172123.12	SLFN12	697.7	1073.7	0.62	**3.92E-02**	1.00E+00
ENSG00000128512.21	DOCK4	208.2	329.0	0.66	**3.92E-02**	1.00E+00
ENSG00000017483.15	SLC38A5	1061.0	2055.2	0.95	**4.00E-02**	1.00E+00
ENSG00000146425.11	DYNLT1	864.1	1486.0	0.78	**4.00E-02**	1.00E+00
ENSG00000137842.7	TMEM62	546.3	834.8	0.61	**4.12E-02**	1.00E+00

ENSG00000167207.13	NOD2	135.8	485.6	1.84	**4.17E-02**	1.00E+00
ENSG00000085831.15	TTC39A	74.2	143.7	0.95	**4.23E-02**	1.00E+00
ENSG00000113319.13	RASGRF2	166.9	404.5	1.28	**4.39E-02**	1.00E+00
ENSG00000155629.15	PIK3AP1	3388.1	7823.8	1.21	**4.60E-02**	1.00E+00
ENSG00000259399.1	TGIF2-RAB5IF	102.4	230.5	1.17	**4.78E-02**	1.00E+00
ENSG00000137959.16	IFI44L	2318.0	20566.3	3.15	**4.80E-02**	1.00E+00
ENSG00000222489.1	SNORA79B	266.9	171.2	-0.64	**4.96E-02**	1.00E+00
ENSG00000078018.19	MAP2	2330.3	5761.3	1.31	**4.96E-02**	1.00E+00

List of cultured human MK RNA transcripts differentially expressed in response to INFα. FPKM>1000 was averaged from three independent, day 13 cord blood-derived CD61+ MKs. Log2 fold change of INFα treated MKs compared to control (PBS treated) were calculated, and presented by intensity of red color for up-regulated genes or by green color for down-regulated genes. The single noncoding RNA (MIR155) is highlighted. Table is ranked based on statistical significance p-value from highest to lowest.



Supplemental Figure 1. Validation of RNA-Seq of IFNα treatment in human cultured MKs. The validation of RNA-Seq analysis (Table 1) was performed by real time PCR using (A) technical and (B) biological replicates (CD61 purified day 13 MKs treated with 1000 U/ml IFNα or PBS, three independent cords). Most differentially expressed genes by FDR < 0.05 on IFNα stimulation from RNA-seq experiment is validated here. Log2 fold change was plotted for IFNα stimulated CD61+ MKs, normalized to PBS control. Actin was used as a housekeeping gene. Statistical significance was determined by one sample t-test. Error bars represent mean ± standard error of mean.



Supplemental Figure 2. IFNα-induced SAMHD1 is dispensable for human MK maturation and ploidy. CRISPR/Cas9 knock-down of *SAMHD1* (denoted as 'SAMHD1 cr') in CD34+ derived culture was performed at day 3. On day 9, cells are treated with 1000 U/ml IFNα or PBS. Results were compared with negative control CRISPR (denoted as 'neg cr'). (A) Day 13 cultured MKs were assayed for MK maturation by staining the cells with APC labeled anti-CD41a and PE labeled anti-CD42a antibodies at 37°C for 10 minutes. CD41a+CD42a+ MKs were analyzed by flow cytometry. Representative flow tracing is shown. (B) The percentage of CD41a+CD42a+ MKs by flow cytometry using neg cr vs. SAMHD1 cr treated with IFNα or PBS (n=3). (C) Neg cr vs. SAMHD1 cr MKs treated with IFNα or PBS were stained with APC labeled anti-CD41a antibody and propidium iodide, and ploidy was assessed by flow cytometry (n=3). No statistically significant difference was observed for B-C. Error bars represent mean ± standard error of mean.