

Supplementary Information Titles

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Journal: Nature Medicine

Article Title:	Active Pin1 is a key target of all- <i>trans</i> retinoic acid in acute promyelocytic leukemia and breast cancer
Corresponding Author:	Kun Ping Lu

Supplementary Item & Number (add rows as necessary)	Title or Caption
Supplementary Figure 1	Summary of selected Pin1 substrates
Supplementary Figure 2	Characterization of the interaction between Pin1 and HTS probe pTide or ATRA
Supplementary Figure 3	ATRA-dose-dependently binds and fully inhibits Pin1, but not Cyclophilin or FKBP12
Supplementary Figure 4	The carboxylic group of ATRA as a pharmacophore for binding to Pin1 and co-crystal structure of ATRA and Pin1 PPIase domain
Supplementary Figure 5	Characterization of the ability of the pan-RAR activator AC-93253, the pan-RAR inhibitor Ro-415253, and ATRA to bind Pin1 and transactivate RAR downstream target genes
Supplementary Figure 6	Pin1 interacts with PML-RAR- α containing S581 and increase PML-RAR- α protein stability in NB4 cells
Supplementary Figure 7	Pin1 interacts with PML-RAR- α but much less with PLZF-RAR- α , and Pin1 knockdown reduces protein stability of PML-RAR- α but much less on PLZF-RAR- α in NB4
Supplementary Figure 8	Doxycycline-induced Pin1 KD or other structurally distinct Pin1 inhibitors effectively inhibits spleen size or cell proliferation of transplanted APL cells
Supplementary Figure 9	ATRA induces Pin1 and PML-RAR- α degradation in vitro
Supplementary Figure 10	Ser71 phosphorylation prevents ATRA from interacting with Pin1, and cytochrome P450 inhibitor, pan-RAR activator or inhibitor has no obvious effect on the ability of ATRA to inhibit cell growth or to induce Pin1 or cyclin D1 degradation of human breast cancer cells

Supplementary Figure 11	Summary schemes
Supplementary Table 1	Data collection and refinement statistics
Supplementary Table 2	Fold change of transcripts in ATRA-treated or Pin1 knockdown NB4 cells
Supplementary Table 3	Patient information on APL human samples
Supplementary Table 4	Patient information on triple negative breast cancer human samples
Supplementary Methods	

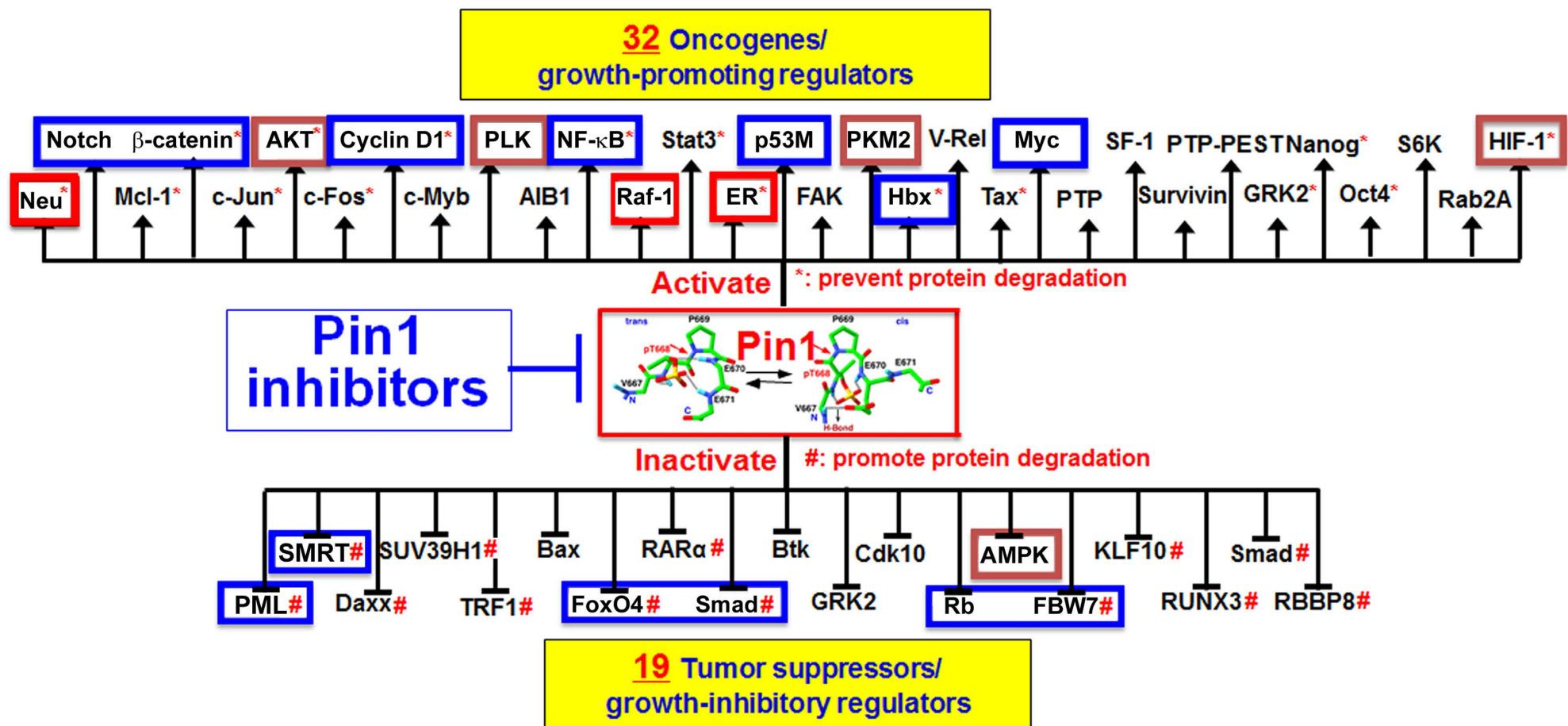


Figure S1: Summary of selected Pin1 substrates including 32 oncogenes and 19 tumor suppressors and their druggable potentials that have been color coded. Red box, drug targets; Brown box, hot targets; Blue box, dream targets but non-druggable. * denotes prevent protein degradation; # denotes promote protein degradation.

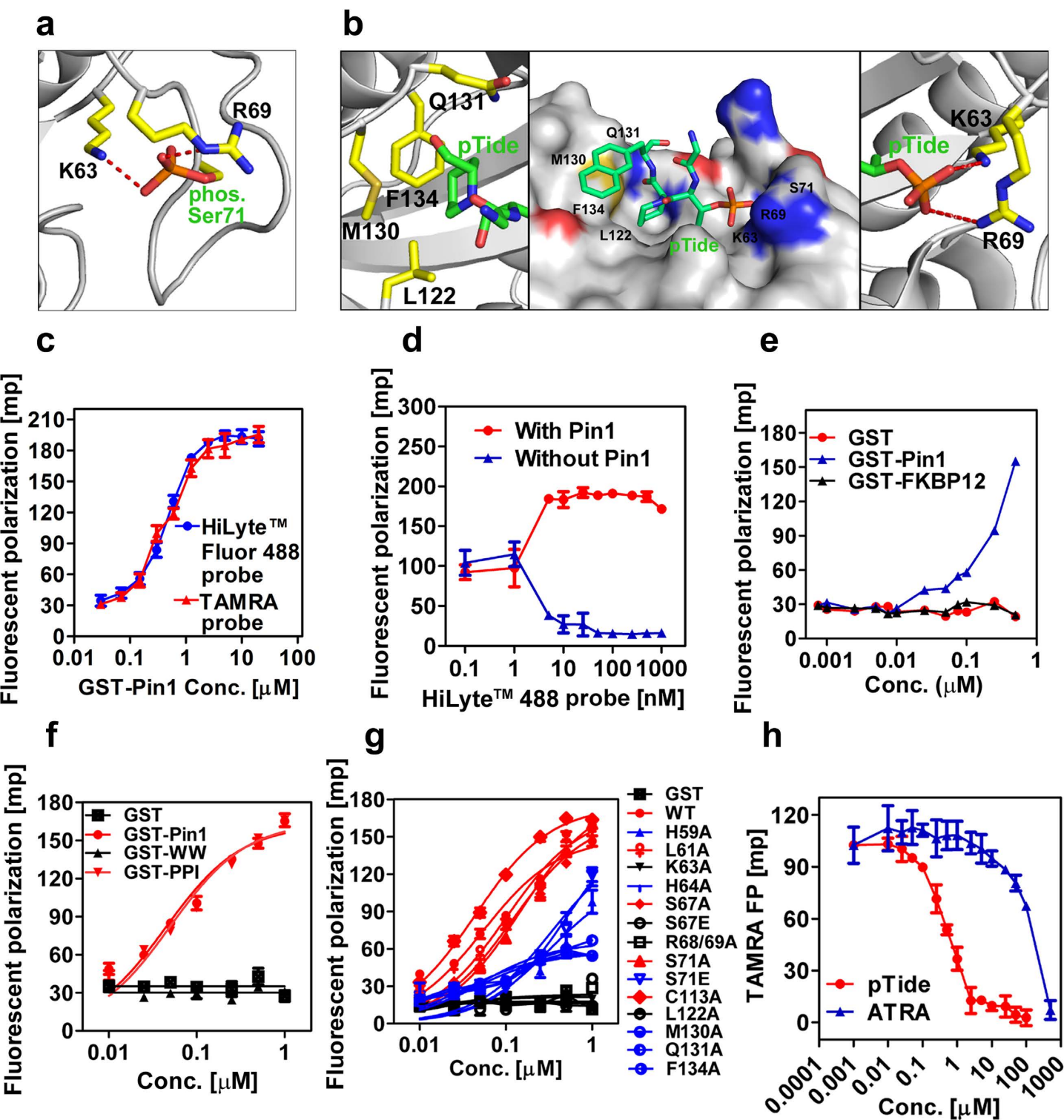


Figure S2: Characterization of the interaction between Pin1 and the HTS probe pTide or ATRA.

(a) Pin1 S71 phosphorylation inhibits its catalytic activity likely due to salt bridges between pS71 phosphate group and K63 and R69 residues, based on modeling⁷.

(b) The published Pin1-pTide structure²⁹ shows salt bridges between the phosphate group of pTide and K63 and R69 of Pin1 (right panel) and the hydrophobic interaction between homoproline (Pip) of pTide and L122, M130, Q131 and F134 of Pin1 (left panel).

(c) HiLyte™ Fluor 488- or TAMRA-conjugated probe pTide interacted with Pin1 in a dose-dependent manner.

(d) FP binding curve between HiLyte™ Fluor 488-conjugated pTide with or without Pin1.

(e) HiLyte™ Fluor 488 probe pTide specifically interacted with Pin1, but not FKBP12.

(f) HiLyte™ Fluor 488 probe pTide specifically interacted with Pin1 catalytic PPIase domain, but not WW domain.

(g) pTide-HiLyte™ Fluor 488 was incubated with different Pin1 point mutants for 0.5 h, before FP readout.

(h) ATRA was able to compete the interaction between TAMRA-conjugated pTide and Pin1.

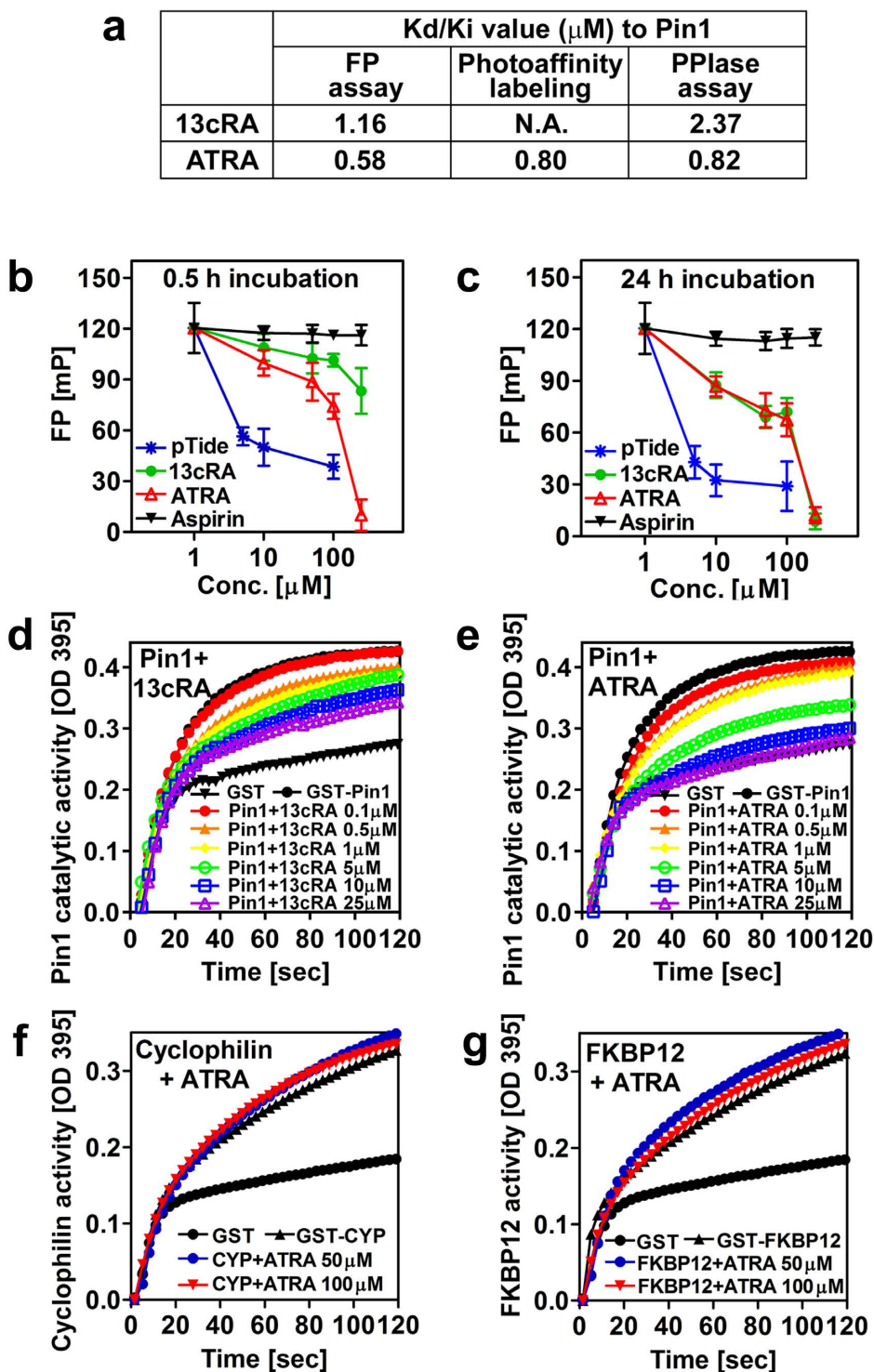


Figure S3: ATRA dose-dependently binds and fully inhibits Pin1, but not Cyclophilin or FKBP12.

(a) Summary table of the K_i or K_d values of ATRA and 13cRA for Pin1 obtained from FP, photoaffinity labeling and PPlase assays.

(b and c) HiLyte™ Fluor 488-pTide was added to Pin1, followed by incubation with different concentrations of cold pTide, ATRA, 13cRA or salicylic acid for 0.5 h (b) or 24 hr (c) before FP readout.

(d and e) 13cRA (d) and ATRA (e) dose-dependently inhibited Pin1 catalytic activity, as assayed using in vitro PPlase assay.

(f and g) In the in vitro PPlase assay, ATRA up to 100 μM remained unable to inhibit other isomerase families, Cyclophilin (f) and FKBP12 (g).

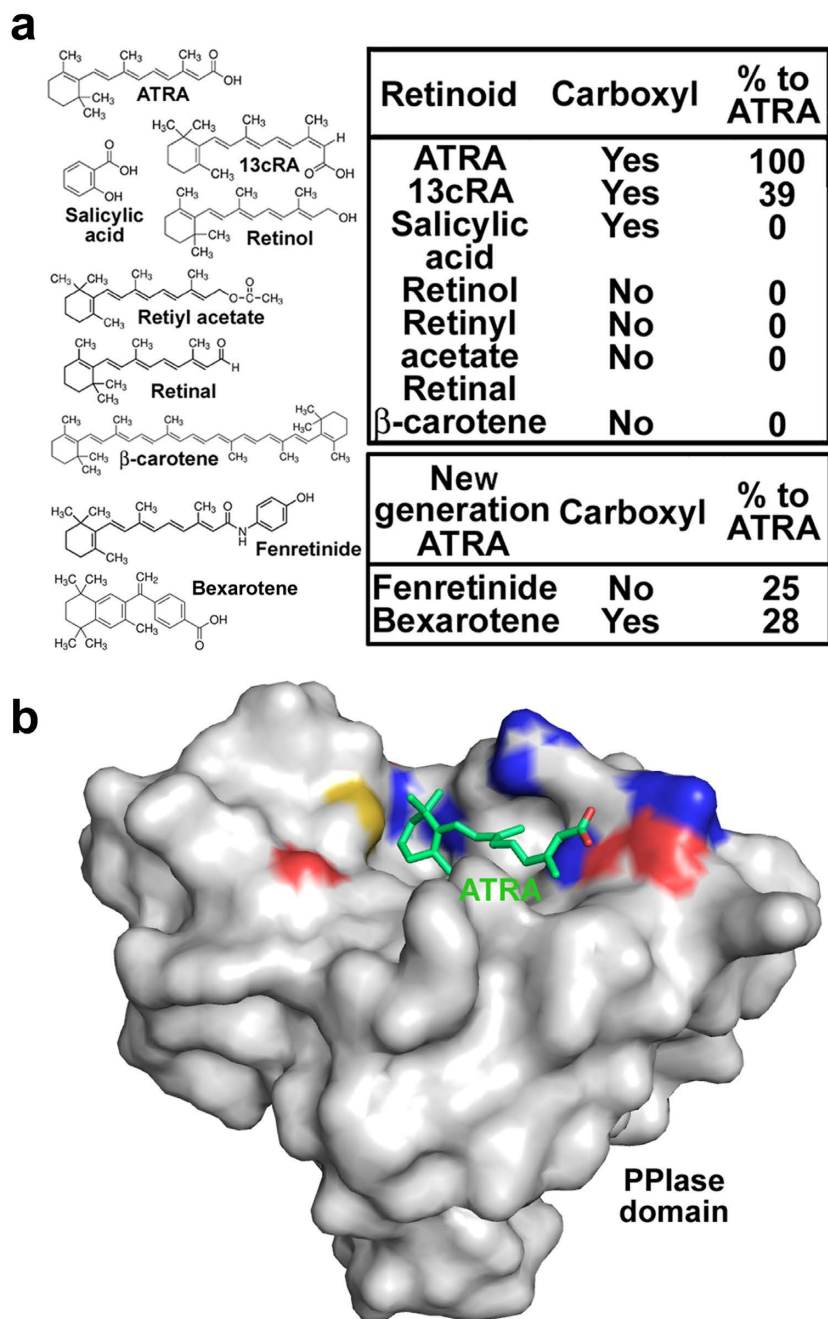


Figure S4: The carboxylic group of ATRA as a pharmacophore for binding to Pin1 and co-crystal structure of ATRA and Pin1 PPlase domain.

(a) Structures of ATRA and other retinoids including new generations of retinoid drugs and their binding to Pin1, as assayed by the FP assay. Carboxyl, carboxylic group (-COOH); % to ATRA, percentage of Pin1 inhibition compared to ATRA from the FP assay readout.
 (b) Full view of co-crystal structure of ATRA and Pin1 PPlase domain.

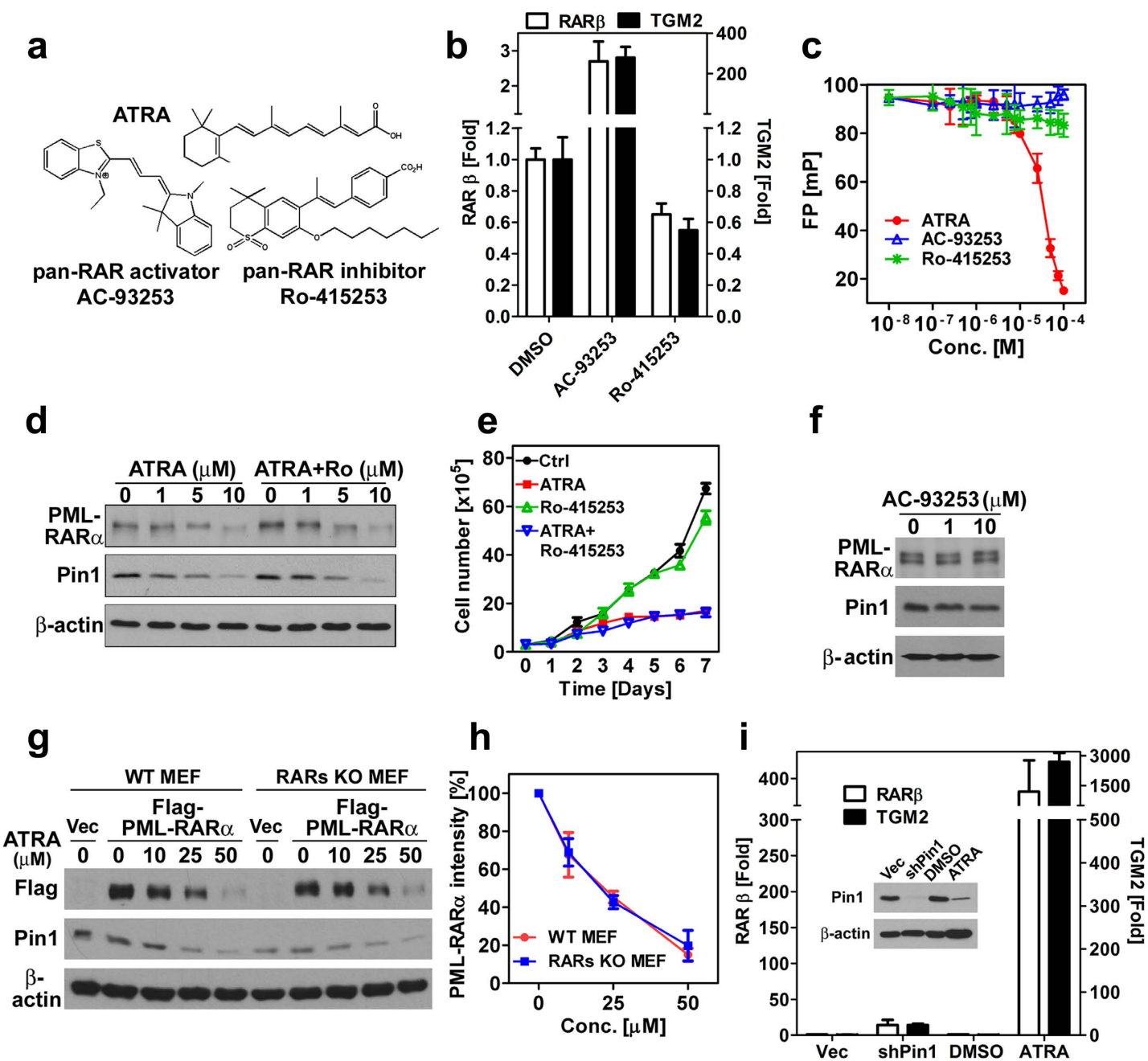


Figure S5: Characterization of the ability of the pan-RAR activator AC-93253, the pan-RAR inhibitor Ro-415253, and ATRA to bind Pin1 and transactivate RAR downstream target genes.

(a) Structures of the pan-RAR activator AC-93253 and the pan-RAR inhibitor Ro-415253.

(b) AC-93253 effectively transactivated RAR downstream targets, RARβ and TGM2, while Ro-415253 suppressed them.

(c) ATRA interacted with Pin1 but not AC-93253 or Ro-415253, as measured by FP assay.

(d) Ro-415253 was unable to restore ATRA-mediated Pin1 degradation.

(e) Ro-415253 was unable to rescue NB4 cell proliferation suppressed by ATRA.

(f) AC-93253 was unable to lead to Pin1 degradation in NB4 cells.

(g and h) ATRA caused degradation of Flag-PML-RARα and Pin1 in both WT and RARs triple KO MEFs.

(i) ATRA effectively and significantly transactivated RAR downstream targets, while Pin1 KD marginally induced it. Inset, Pin1 levels in response to different treatments.

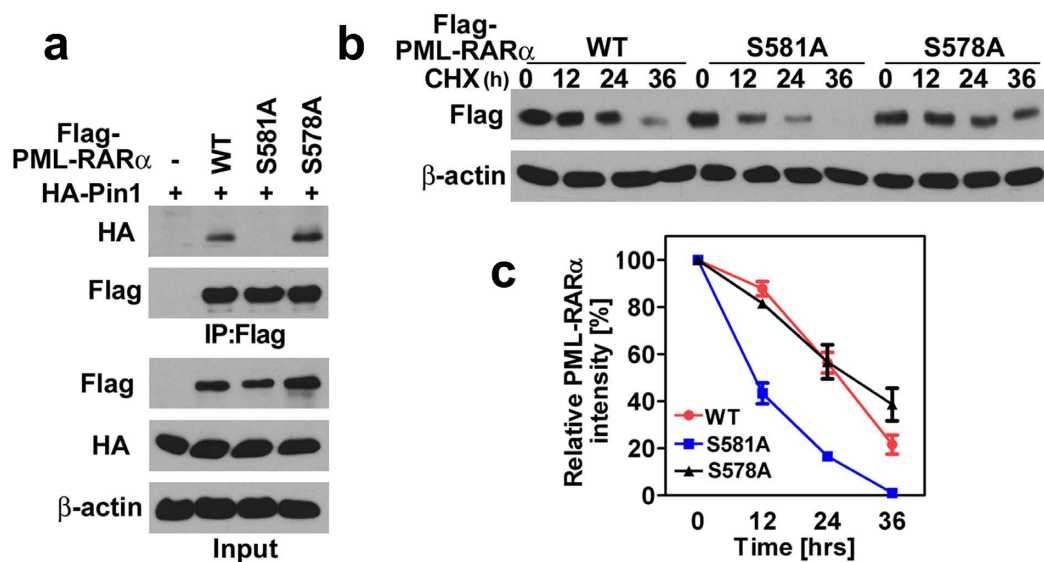


Figure S6: Pin1 interacts with PML-RAR α containing S581 and increases PML-RAR α protein stability in NB4 cells.

(a) HA-Pin1 Co-IPed with Flag-PML-RAR α , but not its S581A mutant.

(b and c) S581A Flag-PML-RAR α demonstrated shortened protein half-life than that of WT or S578A mutant Flag-PML-RAR α .

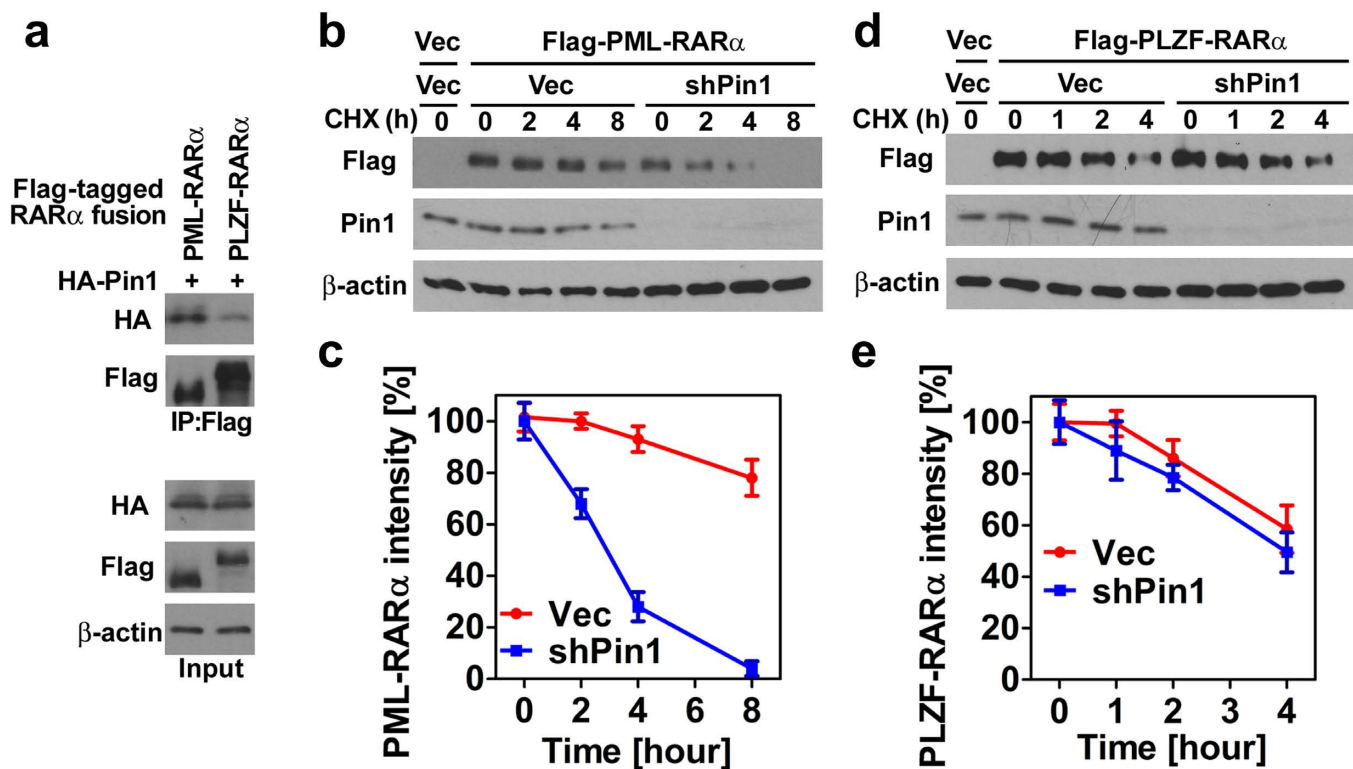


Figure S7: Pin1 interacts with PML-RAR α but much less with PLZF-RAR α , and Pin1 knockdown reduces protein stability of PML-RAR α but much less on PLZF-RAR α .

(a) HA-Pin1 Co-IPed with Flag-PML-RAR α more than Flag-PLZF-RAR α .

(b-e) Flag-PML-RAR α (b and c) but not Flag-PLZF-RAR α (d and e) demonstrated significantly shorter protein half-life in Pin1 knockdown cells.

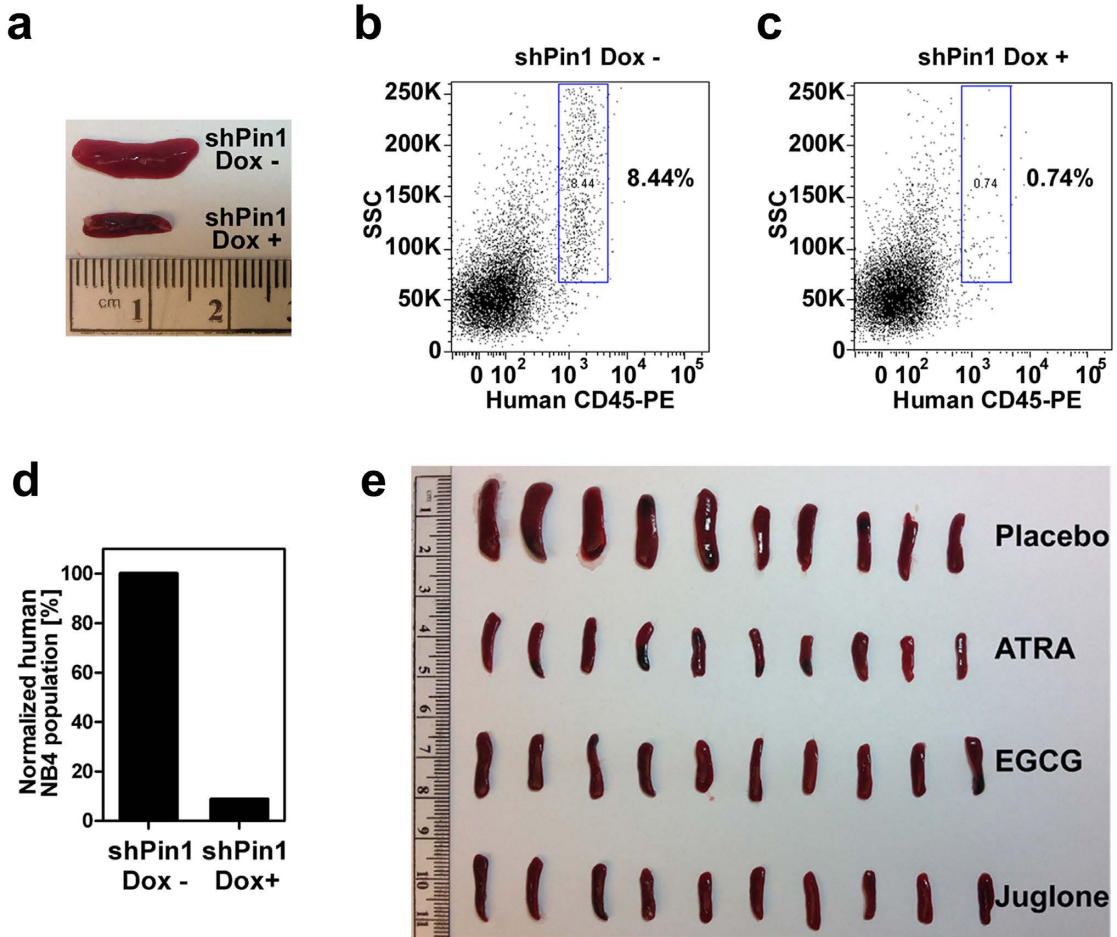


Figure S8: Doxycycline-induced Pin KD or other structurally distinct Pin1 inhibitors effectively inhibit spleen size or cell proliferation of transplanted APL cells.

(a) Splenomegaly of the mice fed doxycycline food was smaller than those fed regular food.
 (b-d) The number of NB4 cells in the transplanted mice fed doxycycline food (b) was significantly less than that in the mice fed regular food (c), with quantification results being presented (d).
 (e) Pin1 inhibitors, EGCG and Juglone, inhibited splenomegaly as nearly effective as ATRA did.

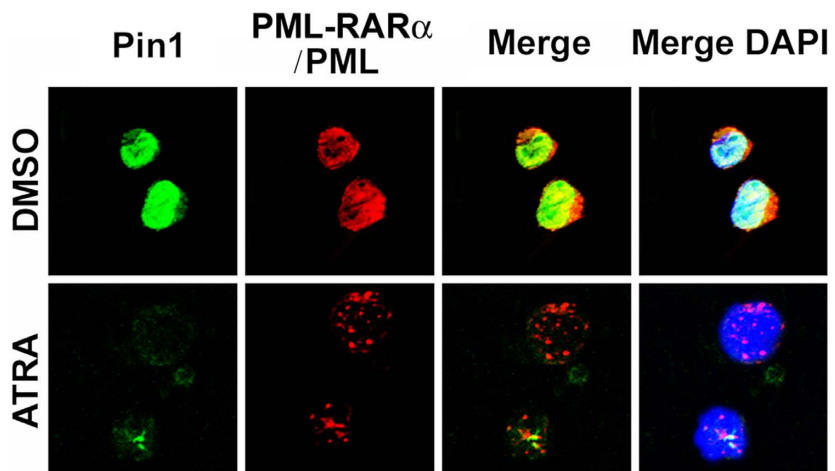


Figure S9: ATRA induces Pin1 and PML-RAR α degradation in vitro.
 Reduced expression of Pin1 and PML-RAR α was observed in APL NB4 cells received 10 μ M ATRA for 96 hours.

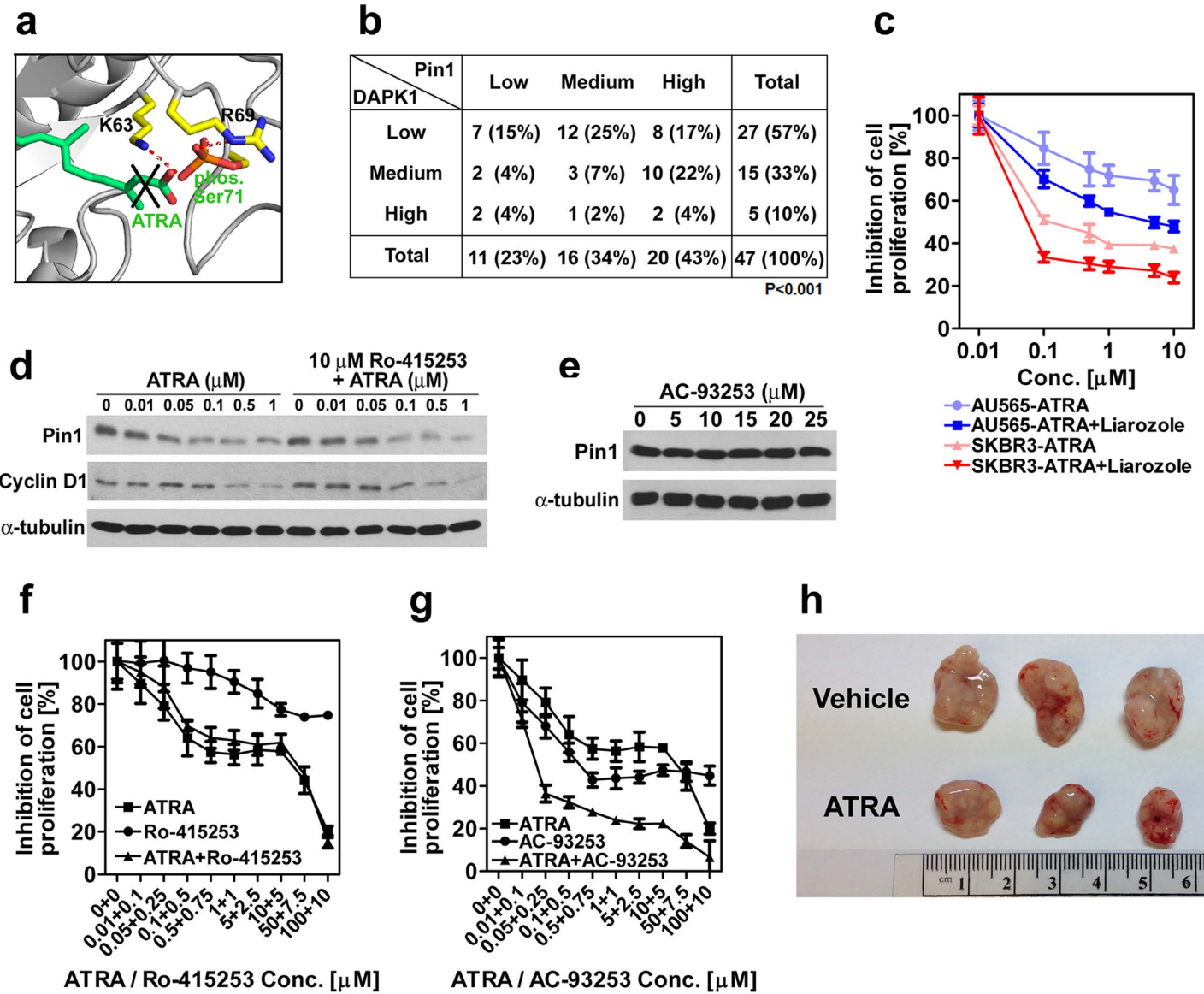


Figure S10: Ser71 phosphorylation prevents ATRA from interacting with Pin1, and cytochrome P450 inhibitor, pan-RAR activator or inhibitor has no obvious effect on the ability of ATRA to inhibit cell growth or to induce Pin1 or cyclin D1 degradation of human breast cancer cells.

(a) S71 phosphorylation formed hydrogen bonds with Arg69 and Lys63 in the Pin1 active site, preventing the carboxylic acid of ATRA from binding to the same active site residues.

(b) A quantification of the inverse correlation of Pin1 and DAPK1 shown in Fig. 5c (n=48).

(c) Cytochrome P450 inhibitor, Liarozole, generally enhanced the anti-proliferation effect of ATRA in ATRA-irresponsible AU565 or -responsive SKBR3 cells.

(d) Pan-RAR inhibitor Ro-415253 was unable to reverse ATRA-induced Pin1 or cyclin D1 degradation in T47D cells.

(e) Pan-RAR activator AC-93253 was unable to trigger Pin1 degradation in T47D cells.

(f and g) Pan-RAR inhibitor Ro-415253 was unable to rescue ATRA-mediated anti-proliferative effects (f), while co-treatment of ATRA and pan-RAR activator AC-93253 resulted in an additive effect on cell growth in T47D cells (g).

(h) Tumor sizes of MDA-MB-231-based xenograft tumors treated with placebo or ATRA intraperitoneally.

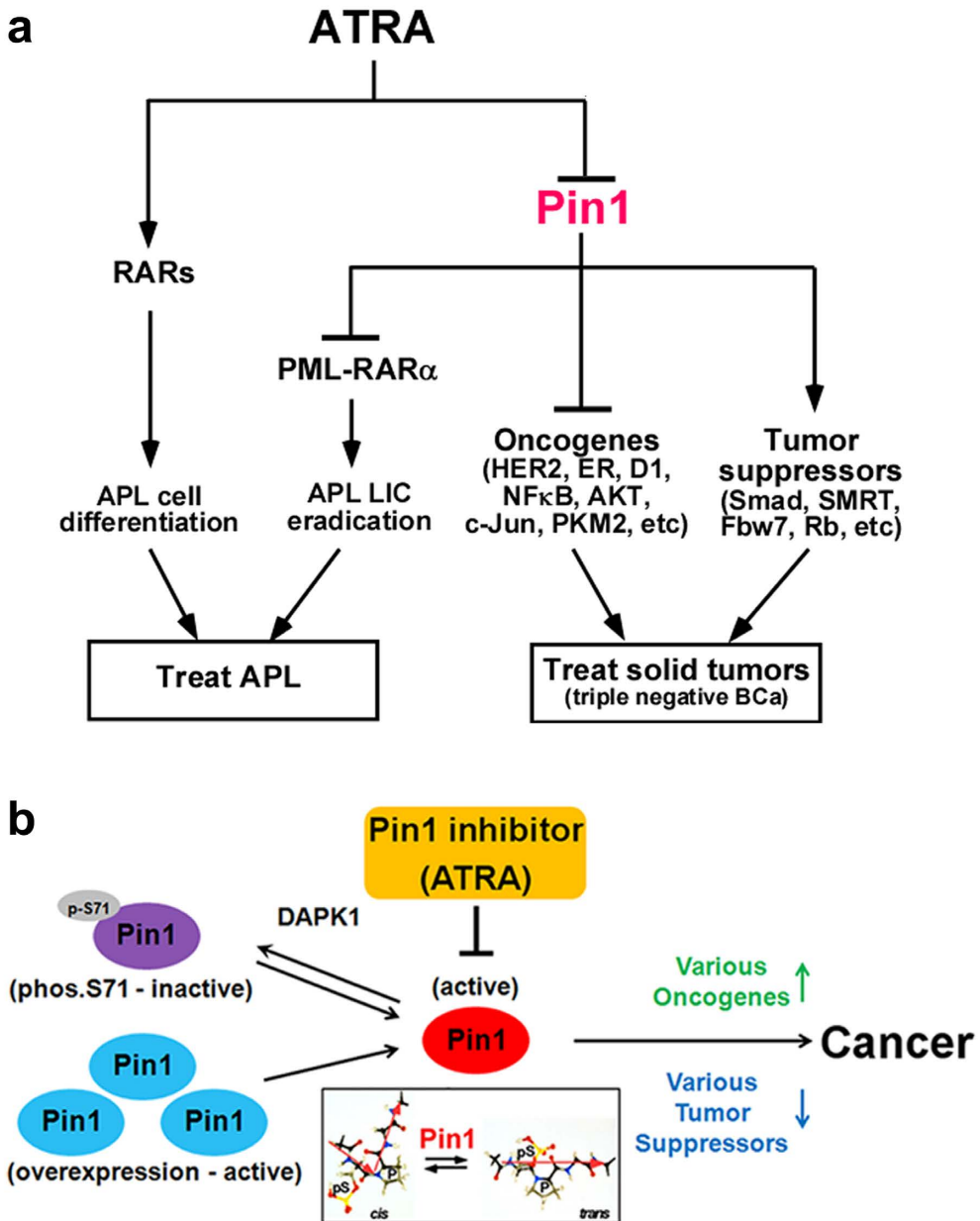


Figure S11: (a) A summary scheme depicting the molecular targets and their therapeutic effects of ATRA against APL and other solid cancers such as triple negative breast cancer. **(b)** In cancers, Pin1 becomes activated due to loss of the inhibitory kinase and tumor suppressor DAPK1 and/or overexpression, thereby activating many oncogenes and inactivating many tumor suppressors to promote tumorigenesis by catalyzing cis-trans isomerization of specific pSer/Thr-Pro motifs. ATRA directly binds, inhibits and ultimately degrades active Pin1 selectively in cancer cells to exert potent anticancer activity against both APL and TNBC by blocking multiple cancer-driving pathways simultaneously.

Table S1. Data Collection and Refinement Statistics

Data statistics	PPIase K7782Q ATRA	
Source	ALS 5.0.2	
Wavelength (Å)	1.00Å	
Resolution (Å)	50-1.33 (1.35-1.33)	
Space group	C2	
Unit Cell (Å) a, b, c	117.81, 36.29, 51.70	
Unit Cell Angel	90, 101, 90	
Data cutoff	$F > 0$	
Assymetric unit (asu)	2	
Number of unique reflections	49111	
Redundancy	3.6 (3.4)	
Completeness (%)	98.3 (96.7)	
$I/\sigma(I)$	64.9 (2.9)	
R_{sym} (%)	4.9	
Refinement statistics		
Refinement		
Resolution limit (Å)	57.84-1.33	
No. reflections (test)	46613 (3177)	
Data cutoff	None	
R_{work}/R_{free} (%) ^b	17.8/19.8	
No. atoms	2024	
protein	1880	
All trans RA	22	
Water	122	
B -factors (Å ²)	15.1	
protein	14.4	
All trans RA	36.4	
Water	22.2	
R.m.s deviations		
Bond lengths (Å)	0.02	
Bond angles (°)	1.96	
Ramachandran plot (%)		
Most favored regions	97	
Additional allowed regions	3	
Generously allowed regions	0	
Disallowed regions	0	
MolProbity score [^]	1.25	94 th percentile*
Bad Rotamer	0.97%	
Clashscore	4.83	88 th percentile*

* 100th percentile is the best among structures of comparable resolution; 0th percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006

[^] MolProbity score combines the clashscore, rotamer, and Ramachandran evaluations into a single score, normalized to be on the same scale as X-ray resolution.

Table S2. Fold change of transcripts in ATRA-treated or Pin1 knockdown NB4 cells

Transcript ID	Fold Change (DMSO vs ATRA)	Fold Change (Vector vs Pin1 KD)	Gene Symbol	Description	Group
TC03000107.hg.1	10.83	12.39	OTTHUMG0000155317	NULL	Coding
TC09000737.hg.1	8.52	6.23		ncrna:snoRNA chromosome:GRCh37:9:133325241:133325342:1 gene:ENSG00000238298 gene_biotype:snoRNA transcript_biotype:snoRNA	Coding
TC04002094.hg.1	5.94	5.67		accn=D21211 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=5112 cpcScore=16.5493000 cnci=-0.1473824	NonCoding
TC09000358.hg.1	6.45	5.59	PSAT1	phosphoserine aminotransferase 1; NULL	Coding
TC04000469.hg.1	5.79	5.49	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); NULL	Coding
TC05003094.hg.1	3.02	4.84		accn=AK123915 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=2971 cpcScore=-1.0632800 cnci=-0.2444438	NonCoding
TC09000736.hg.1	5.3	4.23	ASS1	argininosuccinate synthase 1; NULL	Coding
TC02001049.hg.1	7.35	3.77	HOXD13	homeobox D13; NULL	Coding
TC02001885.hg.1	2.88	3.6	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein); NULL	Coding
TC15002604.hg.1	2.92	3.38		accn=BC040579 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=333 cpcScore=-0.5628490 cnci=-0.2538815 linc-TLE3-1	NonCoding

				chr15::-70863297-70878945	
TC11001509.hg.1	2.57	3.32	LGR4	leucine-rich repeat containing G protein-coupled receptor 4; NULL	Coding
TC11002916.hg.1	6.45	3.31		accn=BC040643 class=mRNALike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=3607 cpcScore=-1.0975300 cnci=-0.3162465	NonCoding
TC07002265.hg.1	5.4	3.18		accn=NULL class=lncRNA name= ref=EnsemblNoncode transcriptId=ENST00000515771 cpcScore=0.0505312 cnci=-0.2863870	NonCoding
TC16001124.hg.1	3.9	3.11	IRX3	iroquois homeobox 3; NULL	Coding
TC17001727.hg.1	42.26	3.04	MPO	myeloperoxidase	Coding
TC01000314.hg.1	3.76	3.03	CLIC4	chloride intracellular channel 4; NULL	Coding
TC02004620.hg.1	5.95	3.02		accn=AF085983 class=mRNALike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=1403 cpcScore=-1.3254100 cnci=-0.3429003	NonCoding
TC11002566.hg.1	3.07	2.95		linc-CALCB-1 chr11:+:14934958-14969520	NonCoding
TC01001172.hg.1	2.57	2.93	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64); Fc fragment of IgG, high affinity Ib, receptor (CD64); NULL	Coding
TC02004536.hg.1	4.4	2.93		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc002tmi.1 cpcScore=-0.4862480 cnci=-0.1784094	NonCoding
TC01001161.hg.1	2.35	2.76	FCGR1C	Fc fragment of IgG, high affinity Ic, receptor (CD64), pseudogene	Coding
TC09002619.hg.1	2.09	2.73		accn=NR_037638 class=lncRNA name=	NonCoding

				ref=RefGeneNoncode transcriptId=NR_037638 cpcScore=7.7978900 cnci=- 0.2782276	
TC17002261.hg.1	6.71	2.69		accn=AK095573 class=mRNALike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=3199 cpcScore=-0.8604430 cnci=- 0.2462343	NonCoding
TC10000808.hg.1	6.77	2.67	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor); microRNA 4680; NULL	Coding
TC17001406.hg.1	2.45	2.54	ACACA	acetyl-CoA carboxylase alpha; NULL	Coding
TC13000738.hg.1	2.41	2.51	TBC1D4	TBC1 domain family, member 4; NULL	Coding
TC01005212.hg.1	4.01	2.5		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc001aia.1 cpcScore=1.1647500 cnci=- 0.2131817	NonCoding
TC11003010.hg.1	4.16	2.47		accn=NR_036542 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_036542 cpcScore=11.5355000 cnci=- 0.1951032	NonCoding
TC07000159.hg.1	2.54	2.45	NFE2L3	nuclear factor (erythroid- derived 2)-like 3; NULL	Coding
TC01000494.hg.1	3.32	2.43	KIAA0754	KIAA0754	Coding
TC19002198.hg.1	6.66	2.41		accn=BC000847 class=mRNALike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000085900 cpcScore=-1.3886400 cnci=- 0.2095920	NonCoding
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TC02001145.hg.1	-3.42	2.37		[retired] ncrna:snoRNA chromosome:GRCh37:2:198 266282:198266315:1 gene:ENSG00000238956	Coding

				gene_biotype:snoRNA transcript_biotype:snoRNA	
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TC02000511.hg.1	7.16	2.32	MAT2A	methionine adenosyltransferase II, alpha; NULL	Coding
TC10002884.hg.1	5.5	2.31		accn=AF427341 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000079492 cpcScore=1.0804600 cnci=- 0.3571220	NonCoding
TC01004727.hg.1	3.05	2.3		linc-PPIAL4A-11 chr1:+:149369293- 149378365 linc-PPIAL4A-11 chr1:+:149369293- 149378295 linc-PPIAL4A-11 chr1:+:149369293- 149370314 linc-PPIAL4A-11 chr1:+:149369308- 149379201 linc-PPIAL4A-11 chr1:+:149369359- 149375183 linc-PPIAL4A-11 chr1:+:149370546-1493752	NonCoding
TC02002256.hg.1	5.11	2.27	TMEM185B	transmembrane protein 185B	Coding
TC10001924.hg.1	2.3	2.23		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc001iqe.2 cpcScore=-1.2488100 cnci=- 0.4433531	NonCoding
TC20001302.hg.1	3.16	2.22		accn=L17329 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000192308 cpcScore=-1.3871500 cnci=- 0.3295578	NonCoding
TC17002479.hg.1	3.37	2.21		accn=BC008968 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000087180 cpcScore=4.1403600 cnci=-	NonCoding

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TC11000571.hg.1	2.04	2.19	LGALS12	lectin, galactoside-binding, soluble, 12	Coding
TC11001289.hg.1	2.85	2.18	CARS	cysteinyl-tRNA synthetase; NULL	Coding
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TC06002723.hg.1	2.14	2.16		accn=NR_037861 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_037861 cpcScore=4.9579600 cnci=-0.1227873 accn=NR_037860 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_037860 cpcScore=3.1905200 cnci=-0.1085205	NonCoding
TC20000603.hg.1	2.14	2.16	FERMT1	fermitin family member 1; NULL	Coding
TC11002205.hg.1	3.69	2.15	SESN3	sestrin 3	Coding
TC02003715.hg.1	4.57	2.13		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc002umb.1 cpcScore=-1.2398600 cnci=-0.1985030 accn=NULL class=lncRNA name= ref=EnsemblNoncode transcriptId=ENST00000420672 cpcScore=-1.0201700 cnci=-0.2972254 accn=NULL class=lncRNA name= ref=	NonCoding
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TC07003326.hg.1	3.35	2.06	GBAS	glioblastoma amplified sequence; NULL	Coding
TC11001107.hg.1	2.5	2.05	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	Coding
TC22000381.hg.1	4.25	2.05		DQ586951,uc021wrj.1	Coding
TC06002106.hg.1	2.48	2.04	EPB41L2	erythrocyte membrane protein band 4.1-like 2; NULL	Coding
TC09001547.hg.1	3.76	2.03	STOM	stomatin; NULL	Coding
TC08000749.hg.1	4.28	2.01	MYC	v-myc myelocytomatosis viral oncogene homolog (avian); NULL	Coding
TC16001234.hg.1	2.73	2.01	AARS	alanyl-tRNA synthetase	Coding
TC06002149.hg.1	-3.47	-2.01	NHEG1	neuroblastoma highly expressed 1; NULL	Coding
TC09001935.hg.1	-6.46	-2.01		linc-CNTNAP3B-3 chr9:+:42858151-42893135	NonCoding
TC11001673.hg.1	-2.96	-2.01		DQ595836,uc001nap.1	Coding
TC11001680.hg.1	-4.38	-2.01		DQ589460,uc010rgf.2	Coding
TC12000236.hg.1	-5.56	-2.01		cdna:known chromosome:GRCh37:12:21 980144:22040891:1 gene:ENSG00000257022 gene_biotype:antisense transcript_biotype:antisens e	Coding
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TC07002244.hg.1	-3.69	-2.02		linc-BMPER chr7:+:33900207-33917087	NonCoding
TC09000278.hg.1	-5.44	-2.02		ENSG00000256208,ENST0000542122.1	Coding
TC09000305.hg.1	-6.04	-2.02		ENSG00000255706,ENST0000537313.1	Coding
TC01006262.hg.1	-2.91	-2.03		accn=AF399612 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000384019 cpcScore=5.0364600 cnci=- 0.0404239	NonCoding
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TC07003153.hg.1	-3.16	-2.03		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=Gencode transcriptId=OTTHUMT0000 0141831 cpcScore=- 0.5360430 cnci=-0.3446831	NonCoding
TC08000450.hg.1	-2.84	-2.03		ncrna:miRNA chromosome:GRCh37:8:686 23867:68623958:1 gene:ENSG00000221660 gene_biotype:miRNA transcript_biotype:miRNA	Coding
TC11002671.hg.1	-5.7	-2.03		accn=X64990 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=5265 cpcScore=1.2101900 cnci=- 0.3632053	NonCoding
TC13000252.hg.1	-4.72	-2.03	OTTHUMG0000017023	NULL	Coding
TC19000160.hg.1	-3.47	-2.03		[retired] ncrna:lincRNA chromosome:GRCh37:19:96 49409:9650402:1 gene:ENSG00000247585	Coding

TC21000877.hg.1	-5.14	-2.03		linc-TMPRSS15-15 chr21:- :26258989-26275070	NonCoding
TC05001948.hg.1	-4.5	-2.04	OTTHUMG00 000164977	NULL	Coding
TC10000590.hg.1	-4.18	-2.04		ncrna:snRNA chromosome:GRCh37:10:85 763088:85763235:1 gene:ENSG00000200789 gene_biotype:snRNA transcript_biotype:snRNA	Coding
TC14001601.hg.1	-8.32	-2.04		linc-DHRS2-1 chr14:+:24096369- 24096959	NonCoding
TC01000921.hg.1	-7.29	-2.05	AMY1B	amylase, alpha 1B (salivary); amylase, alpha 1C (salivary); amylase, alpha 1A (salivary); NULL	Coding
TC02004912.hg.1	-4.52	-2.05		linc-PDCD1-3 chr2:- :242961959- 242968317 linc-PDCD1-3 chr2:-:242967333- 242968327	NonCoding
TC05001189.hg.1	-2.52	-2.05	FTH1P3	ferritin, heavy polypeptide 1 pseudogene 3	Coding
TC07003110.hg.1	-4.08	-2.05		linc-C7orf66-3 chr7:- :109162037-109237223	NonCoding
TC12002787.hg.1	-2.41	-2.05		linc-PLCZ1-4 chr12:- :20387840-20417097	NonCoding
TC02003420.hg.1	-4.66	-2.06		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_1936 cpcScore=-1.4988900 cnci=- 0.1588102 linc-LOC285033- 4 chr2:+:96477741- 96479705	NonCoding
TC03000780.hg.1	-4.6	-2.06	SLC9A9-AS2	SLC9A9 antisense RNA 2; NULL	Coding
TC08002109.hg.1	-6.72	-2.06		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_1451 cpcScore=-1.3778800 cnci=-	NonCoding

				0.2708561	
TC09001709.hg.1	-5.13	-2.06	MIR3689F	microRNA 3689f	Coding
TC12001808.hg.1	-3.91	-2.06		ncrna:misc_RNA chromosome:GRCh37:12:92564129:92564229:-1 gene:ENSG00000199895 gene_biotype:misc_RNA transcript_biotype:misc_RNA	Coding
TC02003400.hg.1	-4.05	-2.07		accn=Z69008 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000327645_03 cpcScore=2.1100800 cnci=-0.2912141 accn=Z68955 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000327592_03 cpcScore=2.2525300 cnci=-0	NonCoding
TC02003448.hg.1	-4.14	-2.07		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=Gencode transcriptId=OTTHUMT00000329516 cpcScore=-1.1853900 cnci=-0.2758929	NonCoding
TC02004595.hg.1	-4.43	-2.07		linc-C2orf27B-5 chr2:- :132889689-132893383	NonCoding
TC06002303.hg.1	-3.68	-2.07		ncrna:miRNA chromosome:GRCh37:6:166355759:166355829:-1 gene:ENSG00000252196 gene_biotype:miRNA transcript_biotype:miRNA	Coding
TC0X002055.hg.1	-5.27	-2.07		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=Gencode transcriptId=OTTHUMT00000056483 cpcScore=-1.1776400 cnci=-0.1236370	NonCoding
TC15000079.hg.1	-10.32	-2.07	SNORD115-5	small nucleolar RNA, C/D box 115-5; small nucleolar RNA, C/D box 115-9	Coding
TC15000082.hg.1	-10.32	-2.07	SNORD115-	small nucleolar RNA, C/D	Coding

			12	box 115-12; small nucleolar RNA, C/D box 115-9	
TC15000084.hg.1	-10.31	-2.07	SNORD115-11	small nucleolar RNA, C/D box 115-11; small nucleolar RNA, C/D box 115-43; small nucleolar RNA, C/D box 115-36; small nucleolar RNA, C/D box 115-29	Coding
TC15000085.hg.1	-10.32	-2.07	SNORD115-12	small nucleolar RNA, C/D box 115-12; small nucleolar RNA, C/D box 115-9	Coding
TC15000099.hg.1	-10.31	-2.07	SNORD115-43	small nucleolar RNA, C/D box 115-43; small nucleolar RNA, C/D box 115-36; small nucleolar RNA, C/D box 115-29; small nucleolar RNA, C/D box 115-11	Coding
TC15000105.hg.1	-10.31	-2.07	SNORD115-43	small nucleolar RNA, C/D box 115-43; small nucleolar RNA, C/D box 115-36; small nucleolar RNA, C/D box 115-29; small nucleolar RNA, C/D box 115-11	Coding
TC15000112.hg.1	-10.31	-2.07	SNORD115-43	small nucleolar RNA, C/D box 115-43; small nucleolar RNA, C/D box 115-36; small nucleolar RNA, C/D box 115-29; small nucleolar RNA, C/D box 115-11	Coding
TC01000307.hg.1	-2.38	-2.08	OTTHUMG0000003037	NULL	Coding
TC01005778.hg.1	-5.42	-2.08		accn=NULL class=IncRNA name= ref=UCSCGeneNoncode transcriptId=uc001eng.1 cpcScore=0.1574640 cnci=-0.2691133	NonCoding
TC02002932.hg.1	-3.12	-2.08	OR6B3	olfactory receptor, family 6, subfamily B, member 3; NULL	Coding
TC02003970.hg.1	-3.65	-2.08		accn=NULL class=mRNALike lncRNA name=vega lncRNA ref=GENCODE transcriptId=OTTHUMT00000322440 cpcScore=-1.1150400 cnci=-0.2497148	NonCoding
TC05001719.hg.1	-4.44	-2.08	MGC32805	uncharacterized	Coding

				LOC153163; NULL	
TC07002969.hg.1	-2.34	-2.08		linc-ZNF479-11 chr7:- :57469683-57472194	NonCoding
TC11001646.hg.1	-4.01	-2.08		DQ594870,uc001mzz.2	Coding
TC12001449.hg.1	-3.38	-2.08		[retired] ncrna:miRNA chromosome:GRCh37:12:48 876841:48876921:-1 gene:ENSG00000221171 gene_biotype:miRNA transcript_biotype:miRNA	Coding
TC17000414.hg.1	-5.49	-2.09		DQ575686,uc021tvc.1	Coding
TC17000421.hg.1	-5.49	-2.09		DQ575686,uc021tvf.1	Coding
TC17000428.hg.1	-5.49	-2.09		DQ575686,uc002hmi.3	Coding
TC17000434.hg.1	-5.49	-2.09		DQ575686,uc002hmq.3	Coding
TC17000457.hg.1	-5.49	-2.09		DQ575686,uc002hpu.3	Coding
TC17000734.hg.1	-5.49	-2.09		DQ575686,uc021uay.1	Coding
TC17001414.hg.1	-5.49	-2.09		DQ587906,uc002hor.3	Coding
TC17002510.hg.1	-5.21	-2.09		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=Gencode transcriptId=OTTHUMT0000 0131039 cpcScore=- 0.2197860 cnci=-0.2135483	NonCoding
TC18000363.hg.1	-3.84	-2.09		DQ600844,uc002kpv.1	Coding
TC03002148.hg.1	-5.27	-2.1		BC053580,uc011bta.1	Coding
TC09001920.hg.1	-5.51	-2.1		linc-FAM75A3-2 chr9:+:40308215- 40322860 linc-FAM75A3-2 chr9:+:40308742-40324812	NonCoding
TC15000094.hg.1	-10.05	-2.1	SNORD115- 22	small nucleolar RNA, C/D box 115-22	Coding
TC17002014.hg.1	-4.49	-2.1		accn=NR_033795 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_033795 cpcScore=4.7796000 cnci=- 0.0475037	NonCoding
TC06002340.hg.1	-4.82	-2.11	OTTHUMG00 000016072	NULL	Coding
TC17000313.hg.1	-4.18	-2.11		DQ586005,uc021tth.1	Coding
TC02000730.hg.1	-7.31	-2.12	FAM138B	family with sequence similarity 138, member B; family with sequence similarity 138, member D; NULL	Coding
TC16000375.hg.1	-2.89	-2.12	ITGAX	integrin, alpha X (complement component 3	Coding

				receptor 4 subunit); NULL	
TC02003395.hg.1	-5.75	-2.13		accn=X72451 class=mRNALike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000323293 cpcScore=2.3912500 cnci=- 0.1347265	NonCoding
TC04002904.hg.1	-5.27	-2.13		linc-TRIML2-6 chr4:- :190598434-190600102	NonCoding
TC07002689.hg.1	-6.12	-2.13		linc-DPP6-2 chr7:+:153119375- 153120601	NonCoding
TC09000771.hg.1	-4.55	-2.13		ncrna:misc_RNA chromosome:GRCh37:9:136 177953:136178046:1 gene:ENSG00000201843 gene_biotype:misc_RNA transcript_biotype:misc_RN A	Coding
TC10001166.hg.1	-2.03	-2.13	NRP1	neuropilin 1; NULL	Coding
TC15002068.hg.1	-6.09	-2.13		linc-GOLGA6L1-1 chr15:+:22512032- 22512452	NonCoding
TC22000007.hg.1	-9.04	-2.13	LOC1005080 46	uncharacterized LOC100508046; NULL	Coding
TC01002058.hg.1	-5	-2.14	OTTHUMG00 000002855	NULL	Coding
TC03002939.hg.1	-3.78	-2.14		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc011bfh.1 cpcScore=1.6423300 cnci=- 0.2776299	NonCoding
TC0X000833.hg.1	-9.45	-2.14		DQ595787,uc004csk.3	Coding
TC0X000836.hg.1	-9.45	-2.14		DQ595787,uc011mhx.2	Coding
TC0X000838.hg.1	-9.45	-2.14		DQ595787,uc022bsm.1	Coding
TC0X000843.hg.1	-9.45	-2.14		DQ595787,uc011mia.2	Coding
TC0X000844.hg.1	-9.45	-2.14		DQ595787,uc011mib.2	Coding
TC0X000846.hg.1	-9.45	-2.14		DQ595787,uc022bsp.1	Coding
TC0X000848.hg.1	-9.45	-2.14		DQ595787,uc022bsr.1	Coding
TC22001200.hg.1	-7.5	-2.14		linc-MICAL3-2 chr22:- :18660804-18688682 linc- MICAL3-2 chr22:- :18660804-18685242	NonCoding
TC02000623.hg.1	-3.36	-2.15	IL18RAP	interleukin 18 receptor accessory protein; NULL	Coding

TC0400999.hg.1	-6.54	-2.15	MIR378D1	microRNA 378d-1	Coding
TC08000001.hg.1	-4.63	-2.15	OTTHUMG00000163939	NULL	Coding
TC02000559.hg.1	-5.55	-2.16	IGKV3D-7	immunoglobulin kappa variable 3D-7; NULL	Coding
TC03002147.hg.1	-6.47	-2.16		BC044310,uc011bsy.2	Coding
TC06001823.hg.1	-4.4	-2.16	OTTHUMG0000014898	NULL	Coding
TC08000130.hg.1	-3.46	-2.16	RNA5SP256	RNA, 5S ribosomal pseudogene 256	Coding
TC09000861.hg.1	-5.7	-2.16	OTTHUMG0000021018	NULL	Coding
TC10002919.hg.1	-9.8	-2.16		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_1386 cpcScore=-1.4896900 cnci=-0.2016896 linc-C10orf93-1 chr10:-:134824439-134825072 linc-C10orf93-1 chr10:-:134824448-134825220 linc-C10orf93-1	NonCoding
TC14000705.hg.1	-4.35	-2.16	SNORD114-25	small nucleolar RNA, C/D box 114-25	Coding
TC18000333.hg.1	-3.11	-2.16		DQ582047,uc021uha.1	Coding
TC08002172.hg.1	-6.4	-2.17		linc-ERICH1-7 chr8:-:1236402-1237027 linc-ERICH1-7 chr8:-:1236493-1237155 linc-ERICH1-7 chr8:-:1236612-1237971 linc-ERICH1-7 chr8:-:1236703-1237178 linc-ERICH1-7 chr8:-:1236887-1237155	NonCoding
TC14001575.hg.1	-4.99	-2.17		accn=NULL class=lncRNA name= ref=EnsemblNoncode transcriptId=ENST00000547584 cpcScore=-1.1980100 cnci=-0.3683500	NonCoding
TC04002491.hg.1	-3.53	-2.18		accn=BC015108 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=2339	NonCoding

				cpcScore=-1.1526500 cnci=-0.2173938 linc-GPR125-2 chr4:-:23724884-23735202 linc-GPR125-2 chr4:-:23730408-23735559	
TCOX000603.hg.1	-4.15	-2.18	OTTHUMG0000022331	NULL	Coding
TC02004202.hg.1	-3.31	-2.19		linc-LRPPRC-1 chr2:-:44286098-44294916	NonCoding
TCOX001857.hg.1	-3.05	-2.19		linc-THOC2-AS chrX:+:122867023-122868144	NonCoding
TC12000478.hg.1	-4.24	-2.19	OR6C3	olfactory receptor, family 6, subfamily C, member 3	Coding
TC02003520.hg.1	-8.88	-2.2		linc-RABL2A-1 chr2:+:114334958-114336486 linc-RABL2A-1 chr2:+:114334958-114336428	NonCoding
TC03001759.hg.1	-2.48	-2.2	FTH1P4	ferritin, heavy polypeptide 1 pseudogene 4	Coding
TC12002388.hg.1	-3.35	-2.2		accn=U88357 class=mRNAlike lincRNA name=NULL ref=H-invitational v7.5 transcriptId=HIT000222077 cpcScore=0.4891320 cnci=-0.2568067	NonCoding
TC02001926.hg.1	-4.61	-2.21		ncrna:misc_RNA chromosome:GRCh37:2:65782566:65782668:-1 gene:ENSG00000251900 gene_biotype:misc_RNA transcript_biotype:misc_RNA	Coding
TC10000605.hg.1	-4.93	-2.21	RNA5SP322	RNA, 5S ribosomal pseudogene 322	Coding
TC10001942.hg.1	-2.8	-2.21		accn=NULL class=mRNAlike lincRNA name=vega lincRNA ref=Gencode transcriptId=OTTHUMT00000047252 cpcScore=-1.1365300 cnci=-0.1967077	NonCoding
TC13001093.hg.1	-4.1	-2.21		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By	NonCoding

				Luo transcriptId=linc_luo_257 cpcScore=-1.4103200 cnci=- 0.2829408	
TC03001171.hg.1	-4.49	-2.22	RNA5SP123	RNA, 5S ribosomal pseudogene 123	Coding
TC0X001962.hg.1	-4.52	-2.22		linc-PRKX-3 chrX:-:4545240- 4551613	NonCoding
TC13000405.hg.1	-6.14	-2.22		ncrna:snoRNA chromosome:GRCh37:13:11 2706392:112706452:1 gene:ENSG00000200072 gene_biotype:snoRNA transcript_biotype:snoRNA	Coding
TC19002237.hg.1	-4.41	-2.22		accn=X90753 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000324414 cpcScore=0.9822840 cnci=- 0.1848652	NonCoding
TC05003051.hg.1	-10.29	-2.23		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc003jxs.3 cpcScore=1.5112400 cnci=- 0.2519878	NonCoding
TC06002110.hg.1	-7.84	-2.23	OR2A4	olfactory receptor, family 2, subfamily A, member 4; NULL	Coding
TC08000679.hg.1	-4.97	-2.23	OTTHUMG00 000164897	NULL	Coding
TC04002398.hg.1	-5.44	-2.24		linc-FRG1-1 chr4:+:190802232- 190806061 linc-FRG1-1 chr4:+:190802669- 190806023	NonCoding
TC05001446.hg.1	-10.2	-2.24		DQ575504,uc003jxs.4	Coding
TC05002798.hg.1	-5.89	-2.24		linc-SLC9A3-1 chr5:- :553526-554002	NonCoding
TC08000916.hg.1	-7.04	-2.25	LINC00965	long intergenic non-protein coding RNA 965	Coding
TC01001150.hg.1	-9.25	-2.26	OTTHUMG00 000040701	NULL	Coding
TC19002432.hg.1	-5.54	-2.26		linc-UQCRFS1-2 chr19:- :30186599-30187171	NonCoding
TC08000534.hg.1	-7.66	-2.27		[retired] ncrna:lincRNA	Coding

				chromosome:GRCh37:8:86776895:86804123:1 gene:ENSG00000250531	
TC02001429.hg.1	-3.62	-2.28		ncrna:miRNA chromosome:GRCh37:2:236235002:236235095:1 gene:ENSG00000216002 gene_biotype:miRNA transcript_biotype:miRNA	Coding
TC09001559.hg.1	-4.54	-2.28	OR1N1	olfactory receptor, family 1, subfamily N, member 1; NULL	Coding
TC11000115.hg.1	-3.81	-2.28	OR52B6	olfactory receptor, family 52, subfamily B, member 6; NULL	Coding
TC15001873.hg.1	-3.8	-2.28		DQ601487,uc021suq.1	Coding
TC22000518.hg.1	-6.51	-2.28	LOC729461	uncharacterized LOC729461; uncharacterized LOC642633; NULL	Coding
TC19001246.hg.1	-6.75	-2.3		cdna:pseudogene chromosome:GRCh37:19:14974598:14975527:-1 gene:ENSG00000172148 gene_biotype:pseudogene transcript_biotype:unprocessed_pseudogene	Coding
TC07002496.hg.1	-12.81	-2.31		accn=AF016693 class=mRNAlike lncRNA name=NULL ref=H-invitational v7.5 transcriptId=HIT000062404 cpcScore=2.2948300 cnci=-0.1207372	NonCoding
TC19000120.hg.1	-5.12	-2.31	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	Coding
TC07000757.hg.1	-5.44	-2.32	OTTHUMG0000157151	NULL	Coding
TC22000534.hg.1	-11.66	-2.32	OTTHUMG0000150794	NULL	Coding
TC02004483.hg.1	-7.97	-2.33		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=GENCODE transcriptId=OTTHUMT00000329963 cpcScore=-1.0952600 cnci=-0.1940687	NonCoding

TC10000958.hg.1	-11.29	-2.33		[retired] havana:lincRNA chromosome:GRCh37:10:60001:60544:-1 gene:ENSG00000224285 gene_biotype:lincRNA transcript_biotype:lincRNA [retired] cdna:all chromosome:VEGA50:10:60001:60544:-1 Gene:OTTHUMG00000017523	Coding
TC19001244.hg.1	-5.74	-2.33	OR7A5	olfactory receptor, family 7, subfamily A, member 5	Coding
TC01003067.hg.1	-15.63	-2.34	OTTHUMG0000085417	NULL	Coding
TC08000034.hg.1	-8.22	-2.34	USP17L1P	NULL	Coding
TC0X001908.hg.1	-2.28	-2.34		linc-AFF2 chrX:+:147133552-147134419 linc-AFF2 chrX:+:147133558-147134430	NonCoding
TC11003421.hg.1	-3.34	-2.34		linc-SNX19 chr11:-:130949312-130953304	NonCoding
TC06003051.hg.1	-4.86	-2.39		linc-TAAR9-3 chr6:+:132223102-132241705 linc-TAAR9-3 chr6:+:132223103-132228670 linc-TAAR9-3 chr6:+:132224787-132228670	NonCoding
TC15000015.hg.1	-6.9	-2.39		DQ582260,uc001yts.3	Coding
TC19000264.hg.1	-6.58	-2.39	OR7C2	olfactory receptor, family 7, subfamily C, member 2	Coding
TC02002994.hg.1	-12.34	-2.4		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_1893 cpcScore=-1.3204600 cnci=-0.0921625	NonCoding
TC07003092.hg.1	-5.85	-2.4		accn=AJ011910 class=mRNAlike lincRNA name=Human lincRNA ref=JournalRNA transcriptId=5322 cpcScore=-1.0171800 cnci=-	NonCoding

				0.4715375	
TC18000358.hg.1	-6.98	-2.4		DQ591184,uc002kpr.3	Coding
TC04001083.hg.1	-5.01	-2.41	OTTHUMG0000160276	NULL	Coding
TC10000515.hg.1	-11.05	-2.41		DQ579258,uc021puh.1	Coding
TC15000998.hg.1	-9.11	-2.41		DQ596816,uc002cdb.3	Coding
TC15001866.hg.1	-4.43	-2.41		DQ597717,uc021sun.1	Coding
TC04002870.hg.1	-4.31	-2.42		linc-RWDD4 chr4:-:184653377-184658726	NonCoding
TC05002245.hg.1	-6.5	-2.42		accn=U10508 class=mRNAlike lncRNA name=Human lncRNA ref=JounralRNA transcriptId=2801 cpcScore=-0.8310320 cnci=-0.1494575	NonCoding
TC11002476.hg.1	-3.72	-2.43		[retired] ncrna:miRNA chromosome:GRCh37:11:134320648:134320733:-1 gene:ENSG00000216049 gene_biotype:miRNA transcript_biotype:miRNA	Coding
TC13000108.hg.1	-5.09	-2.43	OTTHUMG0000153574	NULL	Coding
TC22000538.hg.1	-7.63	-2.43	FAM230C	family with sequence similarity 230, member C; uncharacterized LOC642633; long intergenic non-protein coding RNA 281; NULL	Coding
TC02000811.hg.1	-7.12	-2.44		DQ582260,uc002trj.1	Coding
TC02002310.hg.1	-7.12	-2.44		DQ587539,uc010yzt.2	Coding
TC02002334.hg.1	-7.12	-2.44		DQ587539,uc002tri.2	Coding
TC09000251.hg.1	-7.12	-2.44		DQ582260,uc011lqx.1	Coding
TC09000299.hg.1	-7.12	-2.44		DQ582260,uc011lri.1	Coding
TC09001108.hg.1	-7.12	-2.44		DQ587539,uc004acf.1	Coding
TC09001121.hg.1	-7.12	-2.44		DQ587539,uc022bhh.1	Coding
TC09001148.hg.1	-7.12	-2.44		DQ587539,uc022bhq.1	Coding
TC09001172.hg.1	-7.12	-2.44		DQ587539,uc022bhw.1	Coding
TC13000442.hg.1	-7.04	-2.44		DQ587539,uc001uly.1	Coding
TC13001134.hg.1	-6.51	-2.44		accn=NULL class=lncRNA name= ref=UCSCGeneNoncode transcriptId=uc010thk.1 cpcScore=0.8870790 cnci=-0.0516855	NonCoding
TC18000083.hg.1	-6.81	-2.44		DQ582260,uc021uhw.1	Coding

TC21000279.hg.1	-7.04	-2.44		DQ587539,uc021whd.1	Coding
TC22000446.hg.1	-7.12	-2.44		DQ587539,uc021wkf.1	Coding
TC01004717.hg.1	-9.07	-2.46		linc-PPIAL4A-6 chr1:+:148852392- 148853717	NonCoding
TC03003284.hg.1	-7.27	-2.48		linc-LSG1-2 chr3:- :194565037-194567506	NonCoding
TC17001282.hg.1	-11.54	-2.48		DQ585914,uc002haf.2	Coding
TC14000016.hg.1	-7.1	-2.49		DQ582260,uc021rnb.1	Coding
TC02004978.hg.1	-6.18	-2.5	IGKV2D-28	immunoglobulin kappa variable 2D-28; NULL	Coding
TC02004946.hg.1	-5.2	-2.51	IGKV2-28	immunoglobulin kappa variable 2-28; NULL	Coding
TC01004677.hg.1	-12.85	-2.53		linc-NBPF9-8 chr1:+:142553292- 142559170	NonCoding
TC04000120.hg.1	-4.54	-2.53		DQ584082,uc021xmd.1	Coding
TC11001644.hg.1	-9.45	-2.53		DQ585153,uc001mzx.1	Coding
TC13001526.hg.1	-6.88	-2.53		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_142 cpcScore=-1.3063300 cnci=- 0.2426910	NonCoding
TC06000474.hg.1	-7.36	-2.54		DQ573430,uc003ohv.3	Coding
TCOX000847.hg.1	-8.47	-2.55		DQ580770,uc022bsq.1	Coding
TC22000059.hg.1	-7.92	-2.55	LOC729444	uncharacterized LOC729444; NULL	Coding
TC19002656.hg.1	-2.17	-2.58	KIR2DL4	killer cell immunoglobulin- like receptor, two domains, long cytoplasmic tail, 4; NULL	Coding
TC08002004.hg.1	-8.43	-2.6		accn=NULL class=lncRNA name= ref=EnsemblNoncode transcriptId=ENST00000508 419 cpcScore=2.1115700 cnci=-0.1978256	NonCoding
TC17001289.hg.1	-12.76	-2.6		DQ581055,DQ585914,uc02 1ttn.1,uc002hao.3	Coding
TCUn_gl0002280 00014.hg.1	-10.62	-2.6		DUX4,HQ266764,NM_0331 78,NR_038191,uc022bro.1	Coding
TC10000296.hg.1	-7.19	-2.61	RNA5SP310	RNA, 5S ribosomal pseudogene 310	Coding
TC10000333.hg.1	-7.19	-2.61	RNA5SP316	RNA, 5S ribosomal	Coding

				pseudogene 316	
TC05003371.hg.1	-6.9	-2.63		linc-FAM153A-2 chr5:- :177387461- 177391278 linc-FAM153A-2 chr5:-:177387471- 177392855 linc-FAM153A-2 chr5:-:177388523- 177388871	NonCoding
TC15001949.hg.1	-8.43	-2.63		DQ595853,uc002bua.1	Coding
TC22001237.hg.1	-8.97	-2.63		linc-SLC7A4-6 chr22:- :21655278-21679331 linc- SLC7A4-6 chr22:-:21655279- 21664170 linc-SLC7A4-6 chr22:-:21655285- 21679331 linc-SLC7A4-6 chr22:-:21664109- 21677143 linc-SLC7A4-6 chr22:-:21666028- 21679331 linc-SLC7A4-6 chr22:-:21673555- 21679433 linc-SLC7A4-6 c	NonCoding
TC10000305.hg.1	-7.27	-2.65	RNA5SP312	RNA, 5S ribosomal pseudogene 312	Coding
TC10000321.hg.1	-7.27	-2.65	RNA5SP315	RNA, 5S ribosomal pseudogene 315	Coding
TC10001247.hg.1	-7.27	-2.65	RNA5SP313	RNA, 5S ribosomal pseudogene 313	Coding
TC12002520.hg.1	-7.9	-2.65		accn=NR_037687 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_037687 cpcScore=6.7736100 cnci=- 0.2530751	NonCoding
TC19002358.hg.1	-11.22	-2.65		accn=AF399542 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000383959 cpcScore=5.5736800 cnci=- 0.1055078	NonCoding
TC01002356.hg.1	-4.03	-2.66		DQ588542,uc021oit.1	Coding
TC05002149.hg.1	-7.4	-2.67		DQ589679,uc021yjm.1	Coding
TC17000278.hg.1	-9.11	-2.67		DQ578310,uc010vzu.2	Coding
TC06000488.hg.1	-6.57	-2.71		DQ589595,uc011dsg.1	Coding
TC10000466.hg.1	-9.34	-2.72	RNA5SP320	RNA, 5S ribosomal pseudogene 320	Coding
TC22000973.hg.1	-9.48	-2.72		linc-ZNF74-4	NonCoding

				chr22:+:20325556-20332103 linc-ZNF74-4 chr22:+:20325589-20329425 linc-ZNF74-4 chr22:+:20325665-20350461 linc-ZNF74-4 chr22:+:20325665-20350461 linc-ZNF74-4 chr22:+:20326398-20350450 linc-ZNF74-4 chr22:+:20326398-20350461 linc-ZNF74-4 chr22:+:	
TC14000036.hg.1	-6.95	-2.74	OR4N2	olfactory receptor, family 4, subfamily N, member 2	Coding
TC01004099.hg.1	-11.5	-2.75		accn=NULL class=mRNALike lincRNA name=vega lincRNA ref=GENCODE transcriptId=OTTHUMT00000007169 cpcScore=-0.9192430 cnci=-0.2066822	NonCoding
TC04000460.hg.1	-2.15	-2.75	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9; NULL	Coding
TC0Y000217.hg.1	-6.38	-2.75		DQ596138,uc011nbx.1	Coding
TC09001705.hg.1	-8.07	-2.77	MIR3689C	microRNA 3689c	Coding
TC01000920.hg.1	-11.81	-2.78		CU675524,uc010our.1	Coding
TC20000381.hg.1	-8.96	-2.78		[retired] havana:lincRNA chromosome:GRCh37:20:47100223:47130447:1 gene:ENSG00000229963 gene_biotype:lincRNA transcript_biotype:lincRNA	Coding
TC04002624.hg.1	-7.01	-2.8		accn=AF094508 class=mRNALike lincRNA name=NULL ref=H-invitational v7.5 transcriptId=HIT000068406 cpcScore=6.8551300 cnci=-0.0396781	NonCoding
TC17000280.hg.1	-6.25	-2.8		DQ580080,uc010vzw.1	Coding
TC17000272.hg.1	-5.29	-2.81		DQ598304,uc010vzo.2	Coding
TC20001334.hg.1	-10.81	-2.83		linc-LSM14B-2 chr20:+:60520107-60523627	NonCoding
TC22001089.hg.1	-6.08	-2.83		accn=M23041 class=mRNALike lincRNA name=NULL ref=H-	NonCoding

				invitational v7.5 transcriptId=HIT000194871 cpcScore=2.1104100 cnci=- 0.0596197	
TC01003165.hg.1	-9.45	-2.84		ncrna:snRNA chromosome:GRCh37:1:149 286177:149286322:-1 gene:ENSG00000252105 gene_biotype:snRNA transcript_biotype:snRNA	Coding
TC01003181.hg.1	-9.45	-2.84		ncrna:snRNA chromosome:GRCh37:1:149 671723:149671868:-1 gene:ENSG00000252925 gene_biotype:snRNA transcript_biotype:snRNA	Coding
TC08000036.hg.1	-4.8	-2.86	DEFB108P2	NULL	Coding
TC11001603.hg.1	-8.66	-2.88		DQ583612,uc001mza.3	Coding
TC18000910.hg.1	-9.17	-2.9		accn=AF133658 class=mRNAlike lincRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000070983 cpcScore=-0.1775420 cnci=- 0.2149474	NonCoding
TC10002567.hg.1	-9.68	-2.91		linc-ZNF25-1 chr10:- :42383278-42391866	NonCoding
TC01003061.hg.1	-9.76	-2.92	OTTHUMG00 000013378	NULL	Coding
TC01005754.hg.1	-8.19	-2.92		linc-FCGR1B-7 chr1:- :121484056- 121485434 linc-FCGR1B-7 chr1:-:121484423- 121485429	NonCoding
TC12001220.hg.1	-7.43	-2.92		havana:lincRNA chromosome:GRCh37:12:10 485460:10490891:-1 gene:ENSG00000256288 gene_biotype:lincRNA transcript_biotype:lincRNA	Coding
TC12000730.hg.1	-8.31	-2.95	PLXNC1	plexin C1	Coding
TC14000012.hg.1	-15.08	-2.96		DQ595091,uc021rmy.1	Coding
TC14000018.hg.1	-15.08	-2.96		DQ595091,uc021rne.1	Coding
TC14000864.hg.1	-15.08	-2.96		DQ582484,uc021rnl.1	Coding
TC14000867.hg.1	-15.08	-2.96		DQ582484,uc021rnn.1	Coding
TC22000447.hg.1	-15.08	-2.96		DQ582484,uc002zlb.3	Coding
TC22000452.hg.1	-15.08	-2.96		DQ582484,uc002zld.3	Coding

TC02000533.hg.1	-13.4	-3		DQ576039,uc002ssi.2	Coding
TC02000561.hg.1	-13.4	-3		DQ576039,uc010ytw.2	Coding
TC02002078.hg.1	-13.4	-3		DQ576041,uc010yty.2	Coding
TC02002081.hg.1	-13.4	-3		DQ576041,uc002stq.2	Coding
TC02004870.hg.1	-8.09	-3.02		linc-IQCA1-2 chr2:- :238037369-238039886	NonCoding
TC11002928.hg.1	-8.05	-3.04		accn=X89669 class=mRNALike lincRNA name=Human lincRNA ref=JounralRNA transcriptId=5293 cpcScore=3.8293500 cnci=- 0.1633526	NonCoding
TC12000663.hg.1	-6.43	-3.04		havana:lincRNA chromosome:GRCh37:12:79 933983:79940334:1 gene:ENSG00000257474 gene_biotype:lincRNA transcript_biotype:lincRNA	Coding
TC02000729.hg.1	-15.25	-3.05		DQ598479,uc002tjy.1	Coding
TC04000716.hg.1	-4.71	-3.05	OTTHUMG00 000162028	NULL	Coding
TC20001263.hg.1	-8.8	-3.07		linc-ARFGEF2-2 chr20:+:47126390- 47133386 linc-ARFGEF2-2 chr20:+:47126390- 47133386 linc-ARFGEF2-2 chr20:+:47129834- 47133716	NonCoding
TC04002789.hg.1	-6.06	-3.09		linc-TMEM154 chr4:- :153662549-153667773	NonCoding
TC04001512.hg.1	-8.48	-3.15		ncrna:snRNA chromosome:GRCh37:4:122 113952:122114058:-1 gene:ENSG00000252183 gene_biotype:snRNA transcript_biotype:snRNA	Coding
TC11002453.hg.1	-6.65	-3.15		ENSG00000255658,ENST00 000538996.1	Coding
TC01005755.hg.1	-13.44	-3.16		linc-FCGR1B-8 chr1:- :142569265-142588234	NonCoding
TC18000331.hg.1	-5.14	-3.17		DQ578665,uc002kpb.1	Coding
TC11003415.hg.1	-7.42	-3.2		accn=NULL class=lincRNA name= ref=EnsemblNoncode transcriptId=ENST00000538 996 cpcScore=-1.1912700	NonCoding

				cnci=-0.2738760	
TC04001117.hg.1	-5.37	-3.23		ncrna:misc_RNA chromosome:GRCh37:4:37701517:37701624:-1 gene:ENSG00000207075 gene_biotype:misc_RNA transcript_biotype:misc_RNA	Coding
TC16001920.hg.1	-9.05	-3.24		accn=NULL class=lincRNA name=Human lincRNA ref=Scripture Reconstruction LincRNAs By Luo transcriptId=linc_luo_168 cpcScore=-1.3471600 cnci=-0.3408175	NonCoding
TC02000836.hg.1	-12.86	-3.25		DQ600792,uc021vpc.1	Coding
TC02000839.hg.1	-12.86	-3.25		DQ600792,uc021vpe.1	Coding
TC02002312.hg.1	-12.86	-3.25		DQ589348,uc021vnv.1	Coding
TC06001608.hg.1	-8.35	-3.26		DQ577977,uc003ofl.1	Coding
TC19001245.hg.1	-11.4	-3.3	OR7A10	olfactory receptor, family 7, subfamily A, member 10	Coding
TC02000819.hg.1	-10.2	-3.36		DQ600792,uc021vot.1	Coding
TC02000822.hg.1	-10.2	-3.36		DQ600792,uc021vow.1	Coding
TC02000823.hg.1	-10.2	-3.36		DQ600792,uc021vox.1	Coding
TC02002333.hg.1	-10.2	-3.36		DQ589348,uc021vom.1	Coding
TC02002335.hg.1	-10.2	-3.36		DQ589348,uc021von.1	Coding
TC02002336.hg.1	-10.2	-3.36		DQ589348,uc021voo.1	Coding
TC04000095.hg.1	-18.57	-3.36	USP17L10	ubiquitin specific peptidase 17-like family member 10; ubiquitin specific peptidase 17-like family member 13; NULL	Coding
TC09001343.hg.1	-21.92	-3.36		DQ573684,uc022bkb.1	Coding
TC02002219.hg.1	-18.53	-3.39	IL1B	interleukin 1, beta; NULL	Coding
TC02000859.hg.1	-23.42	-3.41		DQ583165,uc010zbc.2	Coding
TC22000444.hg.1	-23.42	-3.41		DQ573684,uc021wke.1	Coding
TC08001383.hg.1	-10.38	-3.46	REXO1L2P	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 2 (pseudogene)	Coding
TCUn_gl00022100001.hg.1	-8.38	-3.46		DQ592442,uc011mfv.1	Coding
TC01000388.hg.1	-7.88	-3.51	RNU11	RNA, U11 small nuclear	Coding
TC08002406.hg.1	-15.96	-3.51		accn=NR_003594 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_003594	NonCoding

				cpcScore=5.4541000 cnci=-0.0385011	
TC18000797.hg.1	-8.72	-3.53		linc-PARD6G-2 chr18:-:106601-108335	NonCoding
TC15000172.hg.1	-13	-3.6		DQ583847,uc021shg.1	Coding
TC15000215.hg.1	-13	-3.6		DQ583847,uc001zgl.3	Coding
TC15001121.hg.1	-13	-3.6		DQ577333,uc001zda.3	Coding
TC15001148.hg.1	-13	-3.6		DQ577333,uc001zem.3	Coding
TC07002493.hg.1	-7.17	-3.62		accn=AF007193 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000061898 cpcScore=1.0854600 cnci=-0.1825470 accn=M55405 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000195782 cpcScore=-0.9085650 cnci=-1.00	NonCoding
TC05001890.hg.1	-9.72	-3.72		ncrna:snRNA chromosome:GRCh37:5:142922079:142922152:-1 gene:ENSG00000253023 gene_biotype:snRNA transcript_biotype:snRNA	Coding
TC04002853.hg.1	-8.65	-3.78		linc-AGA-10 chr4:-:180087669-180091375 linc-AGA-10 chr4:-:180087669-180091246	NonCoding
TC0Y000099.hg.1	-14.99	-3.82		DQ600137,uc011nby.2	Coding
TC0Y000204.hg.1	-14.99	-3.82		DQ577902,uc011nbq.1	Coding
TC06002606.hg.1	-14.93	-3.9		linc-FAM8A1 chr6:+:17587063-17587418	NonCoding
TC19001925.hg.1	-11.16	-4.18		linc-MADCAM1 chr19:+:302197-304321 linc-MADCAM1 chr19:+:302227-303170 linc-MADCAM1 chr19:+:302322-302944 linc-MADCAM1 chr19:+:303035-304321 linc-MADCAM1 chr19:+:303339-304460	NonCoding
TC12002492.hg.1	-11.08	-4.22		linc-CLLU1-11	NonCoding

				chr12:+:88811914-88813084	
TC01001069.hg.1	-14.61	-4.23	OTTHUMG0000013631	NULL	Coding
TC01004685.hg.1	-15.31	-4.23		linc-NBPF9-2 chr1:+:143498343-143517299	NonCoding
TC09001627.hg.1	-9.62	-4.24		DQ575742,uc004buf.1	Coding
TC15002336.hg.1	-8.86	-4.32		linc-ZSCAN2-2 chr15:+:85054685-85055992	NonCoding
TC04000100.hg.1	-18.34	-4.37	USP17L19	ubiquitin specific peptidase 17-like family member 19; NULL	Coding
TC08001384.hg.1	-17.27	-4.5	REXO1L1	REX1, RNA exonuclease 1 homolog (<i>S. cerevisiae</i>)-like 1; exonuclease GOR-like; NULL	Coding
TC15002028.hg.1	-10.09	-4.56		DQ582666,uc002byc.3	Coding
TC15002031.hg.1	-10.09	-4.56		DQ593627,uc002byj.3	Coding
TC15002034.hg.1	-10.09	-4.56		DQ593627,uc010usn.2	Coding
TC15002043.hg.1	-10.09	-4.56		DQ593627,uc002bzk.3	Coding
TC15002046.hg.1	-10.09	-4.56		DQ593627,uc002bzs.3	Coding
TC15002049.hg.1	-10.09	-4.56		DQ593627,uc021syq.1	Coding
TC01005189.hg.1	-11.29	-4.66		accn=NULL class=mRNAlike lincRNA name=vega lincRNA ref=GENCODE transcriptId=OTTHUMT0000007988 cpcScore=-0.8871240 cnci=-0.0601337 accn=NULL class=mRNAlike lincRNA name=vega lincRNA ref=GENCODE transcriptId=OTTHUMT0000007987 cpcScore=-0.9979760 cnci=-0.04890	NonCoding
TC15000159.hg.1	-12.25	-4.66		DQ575741,uc021sgz.1	Coding
TC15000185.hg.1	-12.25	-4.66		DQ575741,uc021shr.1	Coding
TC15000960.hg.1	-12.25	-4.66		DQ575741,uc002bvt.1	Coding
TC15001139.hg.1	-12.25	-4.66		DQ575741,uc010uay.1	Coding
TC15001173.hg.1	-12.25	-4.66		DQ575741,uc021sif.1	Coding
TC04000097.hg.1	-18.99	-4.78	USP17L12	ubiquitin specific peptidase 17-like family member 12; NULL	Coding
TC03003289.hg.1	-7.85	-4.82		accn=AF058804 class=mRNAlike lincRNA	NonCoding

				name=NULL ref=H- invitational v7.5 transcriptId=HIT000064809 cpcScore=-0.8819030 cnci=- 0.0161171	
TC04000098.hg.1	-16.23	-4.89	USP17L15	ubiquitin specific peptidase 17-like family member 15; NULL	Coding
TC04000101.hg.1	-17.46	-4.89	USP17L21	ubiquitin specific peptidase 17-like family member 21; NULL	Coding
TC08001385.hg.1	-18.35	-4.91	REXO1L1	REX1, RNA exonuclease 1 homolog (<i>S. cerevisiae</i>)-like 1; exonuclease GOR-like	Coding
TC01005132.hg.1	-9.61	-4.98		linc-GPR137B-1 chr1+:236260401- 236261074 linc-GPR137B-1 chr1+:236260401- 236261074 linc-GPR137B-1 chr1+:236260401- 236261074 linc-GPR137B-1 chr1+:236260401- 236261074	NonCoding
TC07001516.hg.1	-28.26	-4.98	NCF1C	neutrophil cytosolic factor 1C pseudogene	Coding
TC10002908.hg.1	-23.72	-5		linc-TCERG1L-3 chr10:- :133730127-133733387	NonCoding
TC04000099.hg.1	-17.63	-5.03	USP17L18	ubiquitin specific peptidase 17-like family member 18; NULL	Coding
TC07002494.hg.1	-21.34	-5.15		accn=AK025404 class=mRNAlike lincRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000008678 cpcScore=2.1611700 cnci=- 0.0825375	NonCoding
TC15002025.hg.1	-8.62	-5.17		DQ582666,uc002bxy.2	Coding
TC15000769.hg.1	-17.61	-5.34		DQ601279,uc002bhd.1	Coding
TC15000782.hg.1	-17.61	-5.34		DQ601279,uc021stc.1	Coding
TC15000804.hg.1	-17.61	-5.34		DQ601279,uc021sti.1	Coding
TC15001780.hg.1	-17.61	-5.34		DQ601279,uc002bkj.1	Coding
TC15002052.hg.1	-18.77	-5.37		DQ582462,uc002car.3	Coding
TC15002053.hg.1	-18.77	-5.37		DQ582462,uc021syy.1	Coding
TC15002029.hg.1	-9.79	-5.45		DQ593630,uc021syf.1	Coding
TC04000111.hg.1	-17.58	-5.69	USP17L6P	ubiquitin specific peptidase 17-like family member 6,	Coding

				pseudogene; NULL	
TC0Y000098.hg.1	-32.7	-5.8		DQ581594,uc004fxd.3	Coding
TC0Y000205.hg.1	-32.7	-5.8		DQ574758,uc022cop.1	Coding
TC15000772.hg.1	-32.7	-5.8		DQ581594,uc002bhk.3	Coding
TC15000779.hg.1	-32.7	-5.8		DQ581594,uc002bhz.3	Coding
TC15000785.hg.1	-32.7	-5.8		DQ581594,uc002bik.3	Coding
TC15000807.hg.1	-32.7	-5.8		DQ574760,uc002bkd.3	Coding
TC15000811.hg.1	-32.7	-5.8		DQ581594,uc002bki.3	Coding
TC15000826.hg.1	-32.7	-5.8		DQ574760,uc002blq.3	Coding
TC15001740.hg.1	-32.7	-5.8		DQ574758,uc002bhc.3	Coding
TC15001742.hg.1	-32.7	-5.8		DQ574758,uc002bhp.2	Coding
TC15001747.hg.1	-32.7	-5.8		DQ574758,uc002bhx.3	Coding
TC15001751.hg.1	-32.7	-5.8		DQ574758,uc002cfa.3	Coding
TC15001753.hg.1	-32.7	-5.8		DQ574758,uc002bim.3	Coding
TC15001770.hg.1	-32.7	-5.8		DQ574758,uc010uou.2	Coding
TC04001892.hg.1	-19.99	-5.85		accn=NR_027279 class=lncRNA name= ref=RefGeneNoncode transcriptId=NR_027279 cpcScore=4.2575600 cnci=- 0.0492218	NonCoding
TC07000438.hg.1	-30.2	-5.92	NCF1B	neutrophil cytosolic factor 1B pseudogene	Coding
TC03003290.hg.1	-17.03	-5.96		accn=AF177925 class=mRNAlike lncRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000072731 _03 cpcScore=1.9245000 cnci=-0.0315219	NonCoding
TC0Y000085.hg.1	-36.28	-6.05		DQ581594,uc022cot.1	Coding
TC0Y000220.hg.1	-36.28	-6.05		DQ574758,uc004fwz.3	Coding
TC06003171.hg.1	-24.58	-6.55		accn=NULL class=mRNAlike lncRNA name=vega lncRNA ref=Gencode transcriptId=OTTHUMT0000 0042954 cpcScore=- 1.0629000 cnci=-0.0971014	NonCoding
TC04000102.hg.1	-19.63	-6.64	USP17L23	ubiquitin specific peptidase 17-like family member 23; NULL	Coding
TC15001627.hg.1	-31.04	-6.67		DQ582073,uc002aux.1	Coding
TC04000408.hg.1	-13.18	-7.85	IL8	interleukin 8; NULL	Coding
TC17000383.hg.1	-76.1	-8.4	CCL2	chemokine (C-C motif) ligand 2; NULL	Coding
TC04000478.hg.1	-22.44	-8.44	SPP1	secreted phosphoprotein 1; NULL	Coding

TC16001514.hg.1	-15.03	-8.69		linc-ORC6-7 chr16:+:33340192- 33343609	NonCoding
TC01004129.hg.1	-29.17	-9.25		linc-TMEM88B-1 chr1:+:1317608- 1318166 linc-TMEM88B-1 chr1:+:1317652-1318166	NonCoding
TC05001641.hg.1	-18.69	-11.47	SLCO4C1	solute carrier organic anion transporter family, member 4C1; NULL	Coding
TC04002100.hg.1	-29.9	-12.25		accn=AY956318 class=mRNAlike lincRNA name=NULL ref=H- invitational v7.5 transcriptId=HIT000333296 cpcScore=0.3543570 cnci=- 0.3343817	NonCoding

Table S3. Patient information on APL human samples

No.	Sex	Age	Tissue	Diagnosis
1	F	66	Bone marrow	Normal
2	M	62	Bone marrow	Normal
3	M	66	Bone marrow	Normal
4	M	53	Bone marrow	Normal
5	M	62	Bone marrow	Normal
6	M	36	Bone marrow	Normal
7	M	30	Bone marrow	Normal
8	F	61	Bone marrow	Normal
9	M	72	Bone marrow	Normal
10	F	62	Bone marrow	Normal
11	M	71	Bone marrow	Normal
12	M	45	Bone marrow	Normal
13	M	63	Bone marrow	Normal
14	F	43	Bone marrow	Normal
15	M	58	Bone marrow	Normal
16	M	75	Bone marrow	Normal
17	F	21	Bone marrow	Normal
18	M	66	Bone marrow	Normal
19	M	53	Bone marrow	Normal
20	M	41	Bone marrow	Normal
21	M	60	Bone marrow	Normal
22	M	75	Bone marrow	Normal
23	M	63	Bone marrow	Normal
24	F	50	Bone marrow	Normal
25	F	23	Bone marrow	APL
26	M	38	Bone marrow	APL
27	F	32	Bone marrow	APL
28	F	59	Bone marrow	APL
29	F	28	Bone marrow	APL
30	F	61	Bone marrow	APL
31	M	22	Bone marrow	APL
32	M	51	Bone marrow	APL
33	M	33	Bone marrow	APL
34	F	27	Bone marrow	APL
35	M	33	Bone marrow	APL
36	M	22	Bone marrow	APL
37	F	58	Blood	APL
38	M	16	Bone marrow	APL
39	M	5	Blood	APL
40	M	5	Bone marrow	APL
41	F	57	Blood + Bone marrow	APL
42	F	42	Bone marrow	APL
43	F	24	Bone marrow	APL
44	M	21	Bone marrow	APL
45	M	69	Bone marrow	APL
46	F	4	Bone marrow	APL
47	M	82	Bone marrow	APL
48	F	78	Bone marrow	APL
49	M	22	Bone marrow	APL
50	M	31	Bone marrow	Remission

51	M	3	Bone marrow	Remission
52	F	7	Bone marrow	Remission
53	M	11	Bone marrow	Remission
54	M	13	Bone marrow	Remission
55	F	57	Bone marrow	Remission
56	F	38	Bone marrow	Remission
57	F	54	Bone marrow	Remission
58	M	31	Bone marrow	Remission
59	M	12	Bone marrow	Remission
60	M	20	Bone marrow	Remission
61	M	20	Bone marrow	Remission
62	M	50	Bone marrow	Remission
63	M	58	Bone marrow	Remission
64	M	54	Bone marrow	Remission
65	F	27	Bone marrow	Remission
66	F	51	Bone marrow	Remission

Table S4. Patient information on triple negative breast cancer human samples

No.	Sex	Age	Organ	Pathology diagnosis	Grade	Stage	TNM	ER	PR	HER2
1	F	40	Breast	Invasive ductal carcinoma	1	IIB	T2N1M0	-	-	-
2	F	45	Breast	Invasive ductal carcinoma	1	IIB	T3N0M0	-	-	-
3	F	39	Breast	Invasive ductal carcinoma	1	IIA	T2N0M0	-	-	-
4	F	32	Breast	Invasive ductal carcinoma	1	IIB	T2N1M0	-	-	-
5	F	68	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
6	F	45	Breast	Invasive ductal carcinoma	1	IIA	T1N1M0	-	-	-
7	F	50	Breast	Invasive ductal carcinoma	1	IIB	T2N1M0	-	-	-
8	F	54	Breast	Invasive ductal carcinoma	2	IIIA	T2N2M0	-	-	-
9	F	87	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
10	F	39	Breast	Invasive ductal carcinoma	2	IIIB	T4N2M0	-	-	-
11	F	52	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
12	F	58	Breast	Invasive ductal carcinoma	2	IV	T3N2M1	-	-	-
13	F	56	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
14	F	45	Breast	Invasive ductal carcinoma	2	I	T1N0M0	-	-	-
15	F	60	Breast	Invasive ductal carcinoma	2	IIA	T2N0M0	-	-	2+
16	F	66	Breast	Invasive ductal carcinoma	2	IIA	T2N0M0	-	-	-
17	F	32	Breast	Invasive ductal carcinoma	2	IIIA	T3N1M0	-	+	-
18	F	41	Breast	Invasive ductal carcinoma	2	IIIB	T4N1M0	-	-	-
19	F	51	Breast	Invasive ductal carcinoma	2	IIIA	T2N2M0	-	-	-
20	F	42	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
21	F	79	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
22	F	72	Breast	Invasive ductal carcinoma (chronic mastitis)	-	IIB	T2N1M0	-	-	2+
23	F	50	Breast	Invasive ductal carcinoma	2	IIB	T2N1M0	-	-	-
24	F	68	Breast	Invasive ductal carcinoma	2	IIA	T2N0M0	-	-	-
25	F	37	Breast	Invasive ductal carcinoma	2	IIB	T3N0M0	-	-	-
26	F	40	Breast	Invasive ductal carcinoma	2	IIIA	T3N2M0	-	-	-
27	F	49	Breast	Invasive ductal carcinoma	2	IIIA	T2N2M0	-	-	-
28	F	47	Breast	Invasive ductal carcinoma	3	IIIB	T4N1M0	-	-	-
29	F	49	Breast	Invasive ductal carcinoma	3	IIA	T2N0M0	-	-	-
30	F	44	Breast	Invasive ductal carcinoma	3	IIA	T2N0M0	-	-	-
31	F	47	Breast	Invasive ductal carcinoma	3	IIIB	T4N0M0	-	-	-
32	F	57	Breast	Invasive ductal carcinoma	2	IIB	T3N0M0	-	-	-
33	F	34	Breast	Invasive ductal carcinoma	3	IIA	T2N0M0	-	-	-
34	F	51	Breast	Invasive ductal carcinoma (sparse)	3	IIA	T2N0M0	-	-	-
35	F	75	Breast	Invasive ductal carcinoma	3	IIB	T2N1M0	-	-	-
36	F	48	Breast	Invasive ductal carcinoma	3	IIB	T2N1M0	-	-	-
37	F	49	Breast	Invasive ductal carcinoma	3	IIIA	T3N1M0	-	-	-
38	F	40	Breast	Invasive ductal carcinoma	3	IIA	T2N0M0	-	-	-
39	F	46	Breast	Invasive ductal carcinoma	3	IIA	T2N0M0	-	-	-
40	F	45	Breast	Lobular ductal mixed carcinoma	-	IIB	T2N1M0	-	-	-
41	F	55	Breast	Lobular ductal mixed carcinoma	-	IIA	T2N0M0	-	-	-
42	F	54	Breast	Lobular ductal mixed carcinoma	-	IIB	T2N1M0	+	-	-
43	F	74	Breast	Invasive lobular carcinoma	-	IIB	T2N1M0	-	-	-
44	F	50	Breast	Invasive lobular carcinoma	-	IIB	T2N1M0	-	-	-
45	F	45	Breast	Invasive lobular carcinoma	-	IIB	T2N1M0	-	-	-
46	F	51	Breast	Medullary carcinoma	-	IIA	T2N0M0	-	-	-
47	F	45	Breast	Medullary carcinoma	-	IIA	T2N0M0	-	-	-
48	F	50	Breast	Medullary carcinoma	-	IIIA	T3N1M0	-	-	-