Supplemental materials

Figure S1a Pathway network analysis of the top 100 genes regulated by Klotho in MO3.13 cells

Figure S1b Pathway network analysis of the top 100 genes genes regulated by Klotho in MO3.13 cells

Table S1: qPCR confirmation of the 91 regulated genes using RNA from cultured MO3.13 cells treated with Klotho for 1, 2.5 and 3.5 hrs.

Table S2: Signal Transduction Pathway Reporters.

Table S3. Up-regulated genes of Klotho treated MO3.3 cells vs. CGP database

Table S4. Down-regulated genes of Klotho treated MO3.3 cells vs. CGP database

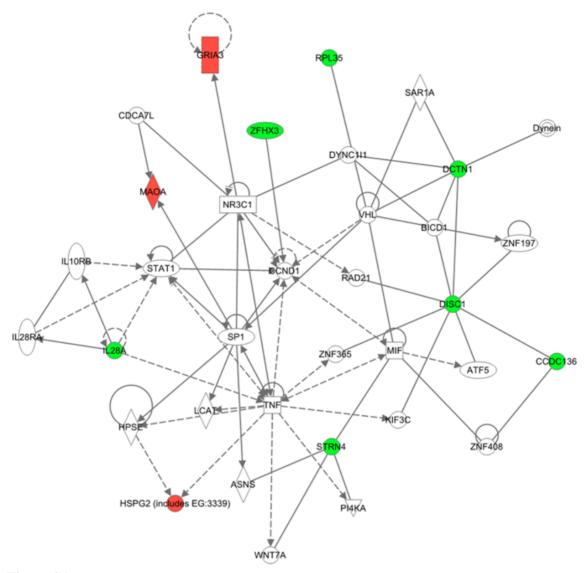


Figure S1a

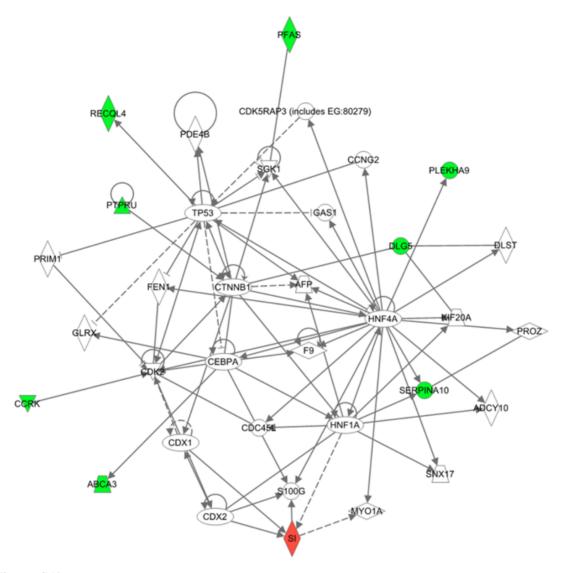


Figure S1b

Table S1: qPCR confirmation of the 91 regulated genes using RNA from cultured MO3.13 cells treated with Klotho for 1, 2.5 and 3 hrs.

Unregulated genes FNA1	Table S1: qPCR confi								
Cymogluided genes Cymo		Symbol	Accession	T-TEST	1 hr	T-TEST	2.5 hr	T-TEST	3.5 hr
minicroarray SLCSAB									Fold change
TGFEZ.X M., 13880 0, 0.48900591 7010_05685 0, 055555242 2, 20_251640 0, 0.40036239 2, 0.4003640 0, 0.40036239 0, 0									-6.744680017
ORAPE	in microarray	1	_						
CCENT M. M. 02271 0.01797/37 8.8.557927 2.5458055 0.36505039 0.4697032 4.917125 4.									
MAILSTAND MAIL 1927/2000 1986/2009									
MACA									
LGR0			_						
ORHAN NN, 097285 0.043937393 7665.400000 0.022064942 4.18786779 0.098000277 6.6564952 0.0476371942 0.04763									
TEPPELL NM 014553 0.0378333 2.0300016 0.45798601 1.70747907 0.60065203 0.91864691 NM 015916 NM 015916 0.467407307 1.5346711 0.21520300 2.258690014 0.050300503 3.7776511 NM 015916 0.467407307 1.5346711 0.21520300 2.258690014 0.050300503 3.7776511 NM 015916 0.46760707 0.25820300 0.25820300 0.258690014 0.05030050 0.7776511 0.2582030 0.25820300 0.2582030 0.258			_						
DKCF_1451A211			_						
SEMPINATION No. 1016186 0.45723387 1.33464711 0.21522080 2.256860034 0.055130864 0.77525518 0.2572518 0.25									
MCAM		1							
BLIZAA MM_172138 0.55132209 2.02216050 0.178506839 1.798060902 0.01850607 2.1096715 0.18616073 0.18616			_						
CHRPAMTA MM 198220 CASPBERTING 1210/09160 Desprisors Des			_						
KRT114 NM_000598 0.457271637 3.09843928 0.7159898 2.3659998 2.3659998 0.72159898 0.72159898 0.72159898 0.72159898 0.721598999 0.721598999 0.72159899 0.72159899 0.72159899 0.72159899 0.721598999 0.72159899 0.721598999 0.721598999 0.721598999 0.721598999 0.721598999 0.721598999 0.721598999 0.72159899999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.7215989999 0.72159899999999999999999999999999999999999		GPR112	_	0.661096047	69362.82321				42.80131846
NRXNN NM 001420 0.07758042 30-61.357 0.0596968002 178.691933 0.081291944 2-0-402573 3-87360140 0.07560141 0.07560		CHRFAM7A			12.31099105	0.982474495	1.018361653	0.071233849	-9.213504422
DOWN N.M. DOTS00 D. S98/25877 S97.199930 D. D. D. D. D. D. D. D		KRT14					1.162038725	0.611528688	23.96599058
Downregulated genes MSPG2 NM_005579 0.554416858 1.624739879 0.086737244 - 2.004794875 0.517144838 13.2193888 1.624739879 0.086737244 - 2.004794875 0.517144838 13.2193888 1.624739879 0.626737676 0.57676745 0.076767244 0.1015.05100 0.0967279 0.07676724		NRXN3	NM_004796	0.072158492	33461.357	0.095986602	178.6819383	0.831281944	-2.040255738
microarray		DCN	NM_001920	0.198235271	687.0993938	0.280765163	-1.587502785	0.267514773	-3.87380142
microarray									
FH-HDIL1	Downregulated genes	1							13.21938663
GIMAPE NN 024711 ACSM05 NN 126817	in microarray								138.5807763
ACSM/SB MM, 182617									18.37386633
WDDRS NM_145172 0.15442773 3.251542601 0.42562673 1.772312114 0.17397345 7.62330326 0.550687368 0.1231680									
IGF2									
MYO18B NM, 002608	Ī								-7.623305363
DCTN1									
RPL35									
CENTG1 NM 014770									
MMS1		1	_						
USP9Y			_						
NID2									
GLIJS MN_000168									
LOC151534			1						
Coord25			_						
CBWD5									
UNIC13B									
TCTIN2									
PPIG NM 004797			_						
DLGS									
LRP1									
AFAP1 PFAS NM_012393 POLR2A NM_000937 NN_004104 NM_001425 PPASN NM_004104 NM_000937 NN_004104 NM_000948 NN_004104 NM_000948 NN_004104 NM_000948 NN_004104 NM_000481 NM_000481 NM_00488 NM_00488 NM_00488 NM_001682 NSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		LRP1	NM_002332	0.803040683	1.331951607				-22.60782033
PFAS NNI_012393 POLR2A NNL_000937 POLR2A NNL_000937 POLR2A NNL_000937 POLR2A NNL_000937 POLR2A NNL_000937 POLR2A NNL_004104 NNL_0041		ZFHX3	NM_006885	0.099063823	-383.954532	0.04303407	-1.724667361	0.07303407	-4717.314264
PPCRAA NM_000337		AFAP1	NM_198595	0.084297753	3.010928259	0.119272069	-2.15317848	0.622013418	2.635207684
PPP2R1A		PFAS	NM_012393	0.092480741	-308.2858794	0.018420638	-2.891400474	0.135394378	-1102.897753
FASN NM_004104 0.160737298 192.0327192 0.305797886 - 1.647102934 0.03296448 -10.5104312 0.30904145 2.92183588 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41707858 0.41747848 0.4884181 0.48841		POLR2A	NM_000937	0.401410104	3.630600863	0.27314673	-1.330672444	0.015404594	-7.321216223
TNS1									9.688343388
HGFAC			_						
AMT									-6.974468766
FZDS									-3.58941815
PLEKHA9			_						
WIPF1 NM_00387 0.786642414			_						
DISC1			_						
CNAS NM_001077490 0.970104107 -1.100473954 0.314189142 -12.36979769 0.084669003 -160.944181									
PTPRU									
DENND3									
ABCA3									
ZBTB4									
RECQL4			_						
LPXN NM_004811									
C9orf58									-4.886325598
ZNF528									
CCDC40		ZNF528	1	0.13481532	129.2071114	0.203671997	-2.261946492	0.039867733	-8.085946548
MED25						0.004399933	-1.542719324		
SARM1									
NCLN									1.036162301
B4GALNT3			1						
ERBB3									
ITSN2									
SI									
DOCK5									
FLNB NM_001457		1							
MAP3K5 CCDC136 NM_005923 NM_022742 0.170903129 -114.4144136 0.054402028 -304.744914 0.024558563 -2.798796191 0.022811735 -3.098502335 0.676337097 -12.4127428 0.258920103 -324.127286 MBOAT1 KIF1A NM_001080480 NM_004321 0.078818954 6.861584024 0.3260589 147.9065022 0.177260069 2.966047427 0.221440729 10.26888996 THTPA 0.064730553 -1.911527472 0.056031879 1.763446763 0.056031879 1.763446763 0.056031879 1.763446763 0.040872913 -1.174214781 0.843468906 2.02967677 0.040872913 -1.797599419 0.040872913 -1.797599419 0.0387822894 -2.5381019 0.040872913 -1.797599419 0.0387822894 -2.5381019 0.040872913 -2.2244707165 0.387822894 -2.5381019 0.387822894 -2.5381019 0.05631879 -2.2244707165 0.084368896 0.04870255 0.083392285 -2.515250492 0.065496165 -2.822675542 0.09458827 -7.05550818 0.048839461 -1.932520951 0.065835079 5.46258314 0.056258314 KIF3C CCRK NM_002254 ARL4D NM_001661 0.845320304 -1.25248356 0.332798464 -1.885296805 0.048839461 -1.906205731 0.065835079 5.46258314			_						
CCDC136 NM_022742 0.054402028 -304.744914 0.022811735 -3.098502335 0.676337097 -12.4127425 MBOAT1 NM_001080480 0.078818954 6.861584024 0.114637753 -1.988414068 0.220659828 -3.6311251 KIF1A NM_004321 0.3260589 147.9065022 0.064730553 -1.911527472 0.23085106 -4.53284448 TCF7 NM_003202 0.177260069 2.966047427 0.056031879 1.763446763 0.120209567 -3.7505010 RTP1 NM_153708 0.221440729 10.26888996 0.638291 -1.174214781 0.843468906 2.02967677 THTPA NM_0024328 0.509161658 -2.623437342 0.040872913 -1.797599419 0.004072953 -8.85862838 NEFM NM_005382 0.00283283 4.590151167 0.146707289 -2.244707165 0.387822894 -2.5381019 COL6A3 NM_001039877 0.142666347 -24.08047035 0.049130673 -2.5294415 0.054270319 -366.774619 KIF3C NM_0178432 0.845320304									
MBOAT1									
KIF1A									
TCF7 RTP1 NM_003202 NM_153708 NM_024328 NEFM COL6A3 STRN4 NM_001039877 KIF3C CCRK NM_002254 NM_001661 NM_001661 NM_001661 NM_001661 NM_003202 0.177260069 2.966047427 0.056888996 0.221440729 10.26888996 0.0026838996 0.0026888996 0.0026888996 0.0026888996 0.0026888996 0.0026888996 0.0026888996 0.0026888996 0.0026888996 0.0040872913 0.056031879 0.056031879 1.763446763 0.843468906 0.84648906 0.84648906 0.84648906 0.84648906 0.84648906									
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THTPA NM_024328 NEFM NM_005382 0.00283283 4.590151167 0.146707289 -2.244707165 0.387822894 -2.53810197 0.065496165 -2.822675542 0.065496165 -2.822675542 0.054270319 -366.774619 0.0845320304 -1.25248356 ARL4D NM_001661 0.332798464 -1.885296805 0.048839461 -1.906205731 0.004072953 -8.85862838 0.387822894 -2.53810197 0.065496165 -2.822675542 0.236584631 50.8408648 0.049130673 -2.5294415 0.09458827 -7.05550818 0.083392285 -2.515250492 0.0065835079 5.46258314									
NEFM COL6A3 NM_005382 NM_004369 0.00283283 0.338999914 4.590151167 14.23175492 0.065496165 0.146707289 -2.244707165 0.065496165 0.387822894 0.236584631 -2.538101990 0.236584631 STRN4 KIF3C NM_001039877 NM_002254 0.142666347 0.213257683 -24.08047035 36.34138925 0.213257683 0.049130673 36.34138925 0.213257683 -2.5294415 0.189083464 0.054270319 -1.932520951 0.009458827 0.009458827 -7.05550818 0.0016137113 -4.32814850 -4.32814850 0.605835079 ARL4D NM_001661 0.332798464 -1.885296805 0.048839461 -1.906205731 0.605835079 5.46258314									
COL6A3 NM_004369 NM_001039877 NM_001039877 NM_002254 NM_002254 NM_178432 NM_001661 NM_001661 NM_001661 NM_001661 NM_001661 NM_002388999914 14.23175492 0.065496165 -2.822675542 0.054270319 -366.774619 0.0845320304 -1.25248356 0.083392285 -2.515250492 0.0065835079 5.46258314	l								
STRN4 NM_001039877 0.142666347 -24.08047035 0.049130673 -2.5294415 0.054270319 -366.774619 KIF3C NM_002254 0.213257683 36.34138925 0.083392285 -2.515250492 0.016137113 -4.32814850 CCRK NM_178432 0.0332798464 -1.885296805 0.048839461 -1.906205731 0.065835079 5.46258314		1							
KIF3C NM_002254 0.213257683 36.34138925 0.189083464 -1.932520951 0.009458827 -7.05550818 0.845320304 -1.25248356 0.083392285 -2.515250492 0.016137113 -4.32814850 0.332798464 -1.885296805 0.048839461 -1.906205731 0.605835079 5.46258314		1	_						
CCRK NM_178432 0.845320304 -1.25248356 0.083392285 -2.515250492 0.016137113 -4.32814850 ARL4D NM_001661 0.332798464 -1.885296805 0.048839461 -1.906205731 0.605835079 5.46258314		KIF3C						0.009458827	-7.055508189
PARD3B NM_057177 0.0097148									
Downregulated: green; upregulated: red; p < 0.05: red and bold					75553.36197	0.218329045	-2.263198286	0.604400297	17.02500519

Table S2: Signal Transduction Pathway Reporters.

Reporter	Pathway	Transciption Factor
C/EBP Reporter	C/EBP	C/EBP
E2F Reporter	Cell Cycle	E2F/DP1
p53 Reporter	p53/DNA Damage	p53
GATA Reporter	GATA	GATA
LXR Reporter	Liver X Receptor	LXRa
SRE Reporter	MAPK/ERK	Elk-1/SRF
AP1 Reporter	MAPK/JNK	AP-1
NF B Reporter	NF B	NF B
Pax3 Reporter	Pax3	Pax3
Pax6 Reporter	Pax6	Pax6
FOXO Reporter	PI3K/AKT	FOXO
PPAR Reporter	PPAR	PPAR
SP1 Reporter	SP1	SP1
VDR Reporter	Vitamin D Receptor	Vitamin D Receptor
TCF/LEF Reporter	Wnt	TCF/LEF
YY1 Reporter	YY1	YY1

Table S3. Up-regulated genes of Klotho treated MO3.3 cells vs. CGP database

Table S3. Up-regulated genes of Klotho treated MO3	3.3 cells vs. CGP database	
Database	Description	Category
UVB_NHEK3_C2		Cancer; Stress
HUMAN_TISSUE_TESTIS		hormone
BECKER_TAMOXIFEN_RESISTANT_UP		Cancer
LEE_E2F1_UP		Cancer
ZHAN_MULTIPLE_MYELOMA_VS_NORMAL_DN KANNAN_P53_DN		Cancer Cancer
GH_GHRHR_KO_24HRS_UP	Up-regulated at least 2-fold 24 hours following injection of human growth hormone (GH) into mice lacking functional GHRHR (lit/lit), and with no detectal	
BRENTANI_IMMUNE_FUNCTION		Cancer
BRCA1_OVEREXP_UP		Cancer
YAGI_AML_PROG_FAB	French-American-British (FAB) type-specific probe sets of acute myeloid leukemia (AML)	Cancer
BRCA1_OVEREXP_PROSTATE_UP		Cancer
GH_GHRHR_KO_24HRS_DN		hormone
ROSS_AML1_ETO		Cancer
VENTRICLES_UP		Cardiovascular
CHIARETTI_T_ALL CHIARETTI_T_ALL_DIFF	·	Cancer Cancer
SCHURINGA_STAT5A_UP		Cell proliferation differentiation and cell su
DIAB NEPH DN		Diabetes; insulin/IGF-1
MARTINELLI_IFNS_DIFF		immunoregulatory activities
GOLDRATH CYTOLYTIC		immunoregulatory activities
UVB_NHEK3_ALL		Cancer; Stress
MATSUDA_VALPHAINKT_DIFF	Differential gene expression between developmental stages of Va14i NKT cells	immunoregulatory activities
HSC_LATEPROGENITORS_FETAL	Up-regulated in mouse hematopoietic late progenitors from fetal liver (Late Progenitors Shared + Fetal)	cell fate decisions
TARTE_MATURE_PC	Genes overexpressed in polyclonal plasmablastic cells (PPCs) as compared to mature plasma cells isolated from tonsils (TPCs) and mature plasma cel	
WELCH_GATA1	We performed transcriptome analysis of G1E-ER4 cells a GATA-1-null erythroblast line that undergoes synchronous erythroid maturation when GATA-1	
YANG_OSTECLASTS_SIG		cell fate decisions; bone differentiation
HSC_LATEPROGENITORS_ADULT		cell fate decisions; bone differentiation
DAC_IFN_BLADDER_UP	Interferon-regulated genes upregulated by DAC (DNA methylation inhibitors 5-aza-2'-deoxycytidine (5-Aza-CdR)) treatment in T24 bladder carcinoma control of the control of	
HSC_LATEPROGENITORS_SHARED		cell fate decisions; bone differentiation
ASTON_OLIGODENDROGLIA_MYELINATION_SU		Depression; Myelin Cardiovascular
VEGF_HUVEC_30MIN_UP NAKAJIMA_MCSMBP_EOS		cell fate decisions; inflammation
VEGF_HUVEC_2HRS_UP	·	Cardiovascular
CPR_NULL-LOW_LIVER_UP	Up-regulated in mouse liver tissue from mice in which NADPH-cytochrome P450 reductase (CPR) was specifically deleted in the liver by cre-lox recomb	
RORIE_ES_PNET_DN	The 30 genes showing the greatest decrease in expression in NBa Ews/Fli-1 (Neuroblastoma (NB) and the Ewing sarcoma (ES)/peripheral primitive neuroblastoma (ES)/peripheral primitive neuroblastoma (NB) and the Ewing sarcoma (ES)/peripheral primitive neuroblastoma (NB) and the Ewing sarcoma (ES)/peripheral primitive neuroblastoma (NB) and the Ewing sarcoma (ES)/peripheral primitive neuroblastoma (ES)/peripheral primitive neuro	
HUMAN_TISSUE_PLACENTA	Genes expressed specifically in human placental tissue	hormone
LIAN_MYELOID_DIFF_GRANULE		cell fate decisions; bone differentiation
AGEING_LYMPH_DN		Stress; aging
DAC_BLADDER_UP		Cancer
CROONQUIST_IL6_RAS_UP	Genes upregulated in multiple myeloma cells exposed to the pro-proliferative cytokine IL-6 versus those with N-ras-activating mutations.	Cancer
HIPPOCAMPUS_DEVELOPMENT_PRENATAL		Brain development
GH_EXOGENOUS_EARLY_UP		hormone; Cancer
PENG_RAPAMYCIN_UP		Cancer
DAC_PANC_UP		Cancer
ZHAN_MULTIPLE_MYELOMA_VS_NORMAL_UP		Cancer
UVB_NHEK1_C2		Cancer; Stress
CPR_LOW_LIVER_UP		Stress
LVAD_HEARTFAILURE_DN TSA_CD4_DN	Downregulated in the left ventricle myocardium of patients with heart failure following implantation of a left ventricular assist device Down-regulated in mouse CD4+ T-cells following 4 hour treatment with 100 nM trichostatin A (a potent, reversible inhibitor of histone deacetylase (HDA0)	Cardiovascular
HOGERKORP_CD44_DN		immunoregulatory activities
AGUIRRE_PANCREAS_CHR6		Cancer
NAKAJIMA_MCS_UP		immunoregulatory activities
CREB_BRAIN_2WKS_UP	Up-regulated in the nucleus accumbens of mice after 2 weeks of induction of transgenic CREB (cAMP response element binding protein), transcription f	• •
BRCA1_SW480_UP		Cancer
CARIES_PULP_HIGH_UP		hormone
AGED_MOUSE_RETINA_ANY_UP	Up-regulated in the retina of 16-month aged mice from any of four strains (S8, S10, SR1, B6J), versus 3-month young controls	Aging
STAEGE_EFTS_UP	Summary of genes up-regulated in Ewing family tumors EFTs compared with normal body atlas	Cancer
BLEO_MOUSE_LYMPH_LOW_24HRS_DN		Stress
CPR_NULL_LIVER_UP	Up-regulated in mouse liver tissue from mice in which NADPH-cytochrome P450 reductase (CPR) was specifically deleted in the liver by cre-lox recomb	
	Genes downreglated in peripheral blood lymphocytes (PBLs) of immunosuppressed patients with a well functioning kidney transplant relative to PBLs of	
GRANDVAUX_IRF3_DN		immunoregulatory activities
TAKEDA_NUP8_HOXA9_3D_DN CPR_NULL_LIVER_DN		immunoregulatory activities; Cancer
YU_CMYC_DN	Down-regulated in mouse liver tissue from mice in which NADPH-cytochrome P450 reductase (CPR) was specifically deleted in the liver by cre-lox reco Myc-repressed genes in neoplastic transformation	Cancer
CROONQUIST_RAS_STROMA_UP		Cancer
TFF2_KO_UP		immunoregulatory activities
TNFALPHA_TGZ_ADIP_DN		Diabetes
HYPERME_COLONCA_SW48	Gene identified by chromatin IP and CpG island microarray as being hypermethylated in SW48 colon cancer cells, versus normal colon murcosa or WI3	
CMV_HCMV_TIMECOURSE_16HRS_DN		Stress; immunoregulatory activities
UV_UNIQUE_FIBRO_UP		Stress
XPB_TTD-CS_DN		DNA repair; skin cancer
UV_UNIQUE_FIBRO_DN		Cancer; Stress
TSADAC_RKOSILENT_UP		Cancer Proin development
CHESLER_BRAIN_NEURAL_HIGH_GENES		Brain development
HADDAD_CD45CD7_PLUS_VS_MINUS_UP TSADAC_PANC50_UP	50 most interesting genes upregulated by the combination of TSA and DAC in at least one of four pancreatic cancer cell lines, but not in normal (HPDE)	immunoregulatory activities Cancer
UVC_HIGH_ALL_UP		DNA repair; Stress
HOUSTIS_ROS		Stress
—		Cancer; Bone differentiation
WANG_HOXA9_VS_MEIS1_DN	Genomic signature of progenitors immortalized by Hoxa9 versus Hoxa9 plus Meis1 Increased expression in Hoxa9 plus Meis1-immortalized progenitors	·
MARSHALL_SPLEEN_BAL	Genes downregulated in influenza-specific CD8+ T cells isolated from spleen as compared to those from bronchoalveolar lavage (BAL) during influenza	
HANSON_NFKAPPB_IND		Cancer
TSA_CD4_UP	Up-regulated in mouse CD4+ T-cells following 4 hour treatment with 100 nM trichostatin A (a potent, reversible inhibitor of histone deacetylase (HDAC))	
	· · · · · · · · · · · · · · · · · · ·	immunoregulatory activities
IFNALPHA_NL_UP		immunoregulatory activities
HADDAD_HSC_CD7_UP	Genes upregulated in human hematopoietic stem cells of the line CD45RA(hi) CD7+, which are biased toward developing into T lymphocytes or natural	• •
GAMMA_UNIQUE_FIBRO_DN		Stress; DNA repair
LIZUKA_G2_GR_G3 RESISTANCE_XENOGRAFTS_UP		Cancer Cancer
YAGI_AML_PROGNOSIS		Cancer
PARP_KO_UP	Downregulated in MEF cells from PARP knockout mice; PARP deficiency also up-regulates genes that encode extracellular matrix or cytoskeletal protei	
LEE_ACOX1_UP		Cancer
IFNALPHA_NL_HCC_UP		Cancer
DAC_PANC50_UP		Cancer
BRG1_ALAB_DN		Cancer
LEE_MYC_TGFA_UP		Cancer
HOHENKIRK_MONOCYTE_DEND_DN		cell fate decisions; immunoregulatory acti
HUMAN_TISSUE_THYMUS	Genes expressed specifically in human thymus tissue	cell fate decisions
TPA_RESIST_MIDDLE_UP	Upregulated by TPA at two consecutive timepoints between 2-24hrs in resistant HL-525 cells. The tumor promoter 12-O-tetradecanoylphorbol-13-acetat	
MMS_MOUSE_LYMPH_HIGH_4HRS_UP	Up-regulated at 4 hours following treatment of mouse lymphocytes (TK 3.7.2C) with a high dose of methyl methanesulfonate (MMS) (DNA damage ager	nujna repair; Stress

Table S4. Down-regulated genes of Klotho treated MO3.3 cells vs. CGP database

Table S4. Down-regulated genes of Klotho treated MO3.3		
		Category
HEARTFAILURE_ATRIA_DN		Cardiovascular
IFN_BETA_GLIOMA_UP		Cancer
HEARTFAILURE_VENTRICLE_DN GUO_HEX_DN		Cardiovascular Cell fate decisions
JECHLINGER EMT UP		Cancer
NING_COPD_DN		Stress
ET743_SARCOMA_UP		Cancer
EMT_UP	Up-regulated during the TGFbeta-induced epithelial-to-mesenchymal transition (EMT) of Ras-transformed mouse mammary epithelial (EpH4) cells (EMT is representative of late-stage tι	
ET743_SARCOMA_72HRS_UP RADAEVA_IFNA_UP		Cancer Cancer
ZUCCHI_EPITHELIAL_UP		Cancer
ELONGINA_KO_DN		Cell fate decisions
IDX_TSA_DN_CLUSTER1	Down-regulated at 48-96 hours during differentiation of 3T3-L1 fibroblasts into adipocytes with IDX (insulin, dexamethasone and isobutylxanthine), vs. fibroblasts treated with IDX + TSA	Cancer
	, ,	Cancer
REOVIRUS_HEK293_UP IFNALPHA_HCC_UP		Stress; Viral infection Cancer
BENNETT_SLE_UP		Immunoregulatory activities
ET743_SARCOMA_6HRS_UP		Cancer
RIBAVIRIN_RSV_UP		Stress; Viral infection
DNMT1_KO_UP		Cell fate decisions
REOVIRUS_HEK293_DN		Stress; Viral infection
HDACI_COLON_TSA48HRS_UP AGUIRRE_PANCREAS_CHR9		Cancer Cancer
FALT_BCLL_UP		Cancer Immunoregulatory activities
CMV_ALL_DN		Stress; Viral infection
AGUIRRE_PANCREAS_CHR17	Genes on chromosome 17 with copy-number-driven expression in pancreatic adenocarcinoma.	Cancer
CMV_24HRS_DN	, , ,	Stress; Viral infection
NF90_DN		Stress; Viral infection
VHL_RCC_UP HDACI COLON CLUSTER10		Cancer Cancer
TGFBETA_LATE_UP		Cancer
NOUZOVA_CPG_H4_UP		Cancer
SRC_ONCOGENIC_SIGNATURE	Genes selected in supervised analyses to discriminate cells expressing activated H-Ras oncogene from control cells expressing GFP.	Cancer
HEARTFAILURE_ATRIA_UP		Cardiovascular
HDACI_COLON_TSABUT_UP ROTH_HTERT_DIFF	-1 -0	Cancer Stress: Call fate decisions
MANALO HYPOXIA DN	Expression of selected genes involved in DNA repair and cell-cycle control in hTERT-transduced T cells Genes downregulated in human pulmonary endothelial cells under hypoxic conditions or after exposure to AdCA5, an adenovirus carrying constitutively active hypoxia-inducible factor 1	Stress; Cell fate decisions Cardiovascular
FSH_OVARY_MCV152_DN		hormone
HDACI_COLON_TSA_UP		Cancer
BRCA2_BRCA1_UP		Cancer
LI_FETAL_VS_WT_KIDNEY_DN		Cell fate decisions
GH_GHRHR_KO_6HRS_DN HDACI_COLON_BUT30MIN_DN		hormone Cancer
TGFBETA_C5_UP		Cancer
UVC_TTD-XPCS_COMMON_DN		Stress
JNK_UP	Upregulated by expression of constitutively active JNK in 3T3 cells	Cancer
H2O2_CSBRESCUED_C1_UP		Stress
BRENTANI_REPAIR	· · · · · · · · · · · · · · · · · · ·	Cancer; DNA repair
UVB_NHEK1_DN BRENTANI PROTEIN MODIFICATION		Stress Cancer
P53_BRCA1_UP		Cancer
AGUIRRE_PANCREAS_CHR19		Cancer
TGFBETA_ALL_UP		Cancer
UVB_NHEK2_DN		Stress
		Cancer Cancer
ET743_RESIST_DN	······································	Cancer
CTNNB1_ONCOGENIC_SIGNATURE		Cancer
		Brain
		Cancer
BRCA1_OVEREXP_DN CROONQUIST_RAS_STROMA_DN		Cancer Cancer
NAB_LUNG_DN		Cancer
CMV_8HRS_DN		Stress; Viral infection
CHANG_SERUM_RESPONSE_UP		Immunoregulatory activities
		Stress; Viral infection
H2O2_CSBDIFF_C2 GH_EXOGENOUS_ALL_UP		Stress Cancer
WERNERONLY FIBRO DN		Cancer Aging
CROONQUIST_IL6_STROMA_UP		Cancer
HDACI_COLON_TSA2HRS_UP	Upregulated by TSA at 2 hrs in SW260 colon carcinoma cells	Cancer
		Cancer
OXSTRESS_RPE_HNETBH_DN HDACI COLON CLUSTER9		Stress Cancer
SMITH_HCV_INDUCED_HCC_UP		Cancer Cancer
YE_INTRAMETASTATIC_HCC_UP		Cancer
HDACI_COLON_TSA12HRS_UP	Upregulated by TSA at 12 hrs in SW260 colon carcinoma cells	Cancer
NADLER_OBESITY_UP		Cell fate decisions; Obesity
ET743_HELA_DN		Cancer
HBX_HCC_DN DORSAM HOXA9 DN		Cancer Cancer
LIAN_MYELOID_DIFF_RECEPTORS		Calicel Cell fate decisions
HUMAN_TISSUE_LIVER		Cell fate decisions
IDX_TSA_UP_CLUSTER2	Strongly up-regulated at 8 hours during differentiation of 3T3-L1 fibroblasts into adipocytes with IDX (insulin, dexamethasone and isobutylxanthine), vs. fibroblasts treated with IDX + TS/	
HASLINGER_B_CLL_13Q14		Cancer
MYOD_NIH3T3_UP MYOD BRG1 UP	Up-regulated at 24 hours in NIH 3T3 murine fibroblasts following transduction with MyoD and incubation in differentiation medium Genes up-regulated following transduction of MyoD in NIH 3T3 cells that fail to acheive full induction with expression of a dominant-negative BRG1 allele; induction thought to require fur	Cell fate decisions
HDACI_COLON_BUT24HRS_DN		Cancer
IGF_VS_PDGF_UP		Cancer
SERUM_FIBROBLAST_CORE_UP	Core group of genes consistently up-regulated following exposure to serum in a variety of human fibroblast cell lines	Cell fate decisions
		Stress
PENG_GLUTAMINE_UP		Stress
ADIP_VS_FIBRO_UP UVC_XPCS_4HR_DN		Cell fate decisions Stress
WALLACE_JAK2_DIFF		Cell fate decisions
UV-CMV_UNIQUE_HCMV_6HRS_DN		Stress; Viral infection
		Cancer
ET743PT650_COLONCA_DN		Cancer
	PPC genes overexpressed in TACI low patients. B-cell activating factor (BAFF) and a proliferation-inducing ligand (APRIL) have been shown to promote multiple myeloma (MM) cell grow List of YY1 target genes identified in MEFs expressing ~25% of YY1 Down	commencer Cell fate decisions
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