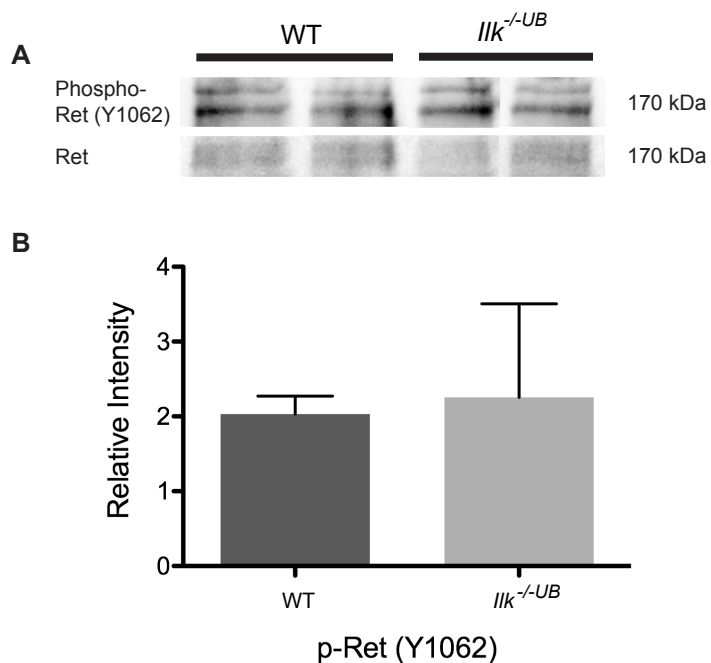


Supplemental Figure 1



Supplemental Figure 1: Embryonic *Ilk<sup>-UB</sup>* kidneys show no difference in Ret tyrosine 1062 phosphorylation. A) Western blot analysis of E13.5 kidney lysates for expression of phospho-Ret (Y1062). B) Quantification of phosphorylated protein relative to total protein demonstrated no significant difference in phospho-Ret (Y1062) in *Ilk<sup>-UB</sup>* kidneys (n=6).

Supplemental Table 1: Primer sequences for qRT-PCR

<b>Gene Primer</b>	<b>Primer Sequence</b>
B2M fwd	GAATGGGAAGCCGAACATAC
B2M rev	CCGTTCTTCAGCATTTGGAT
CXCR4 fwd	GAGGCGTTTGGTGCTCCGGT
CXCR4 rev	TCCCGGAAGCAGGGTTCCTTGT
Dusp8 fwd	CACTCTACCGTCCATGAGCC
Dusp8 rev	TTTAGGGCAGGAGTTGCTGG
Etv4 fwd	ACCTCAGGTCTCTGCCTCCGC
Etv4 rev	GACCATCAGCGCTTCGCCCA
Etv5 fwd	CCAGCTGCAGGAGGCTTGGTT
Etv5 rev	GGGCTGTGCAGCTCCCGTTT
Homer2 fwd	AGGGACCTTGGGTCACGGGT
Homer2 rev	GCTTGCCGGCACCCAGTTCT
Kitl fwd	CCGAGAGTGCCGCGGAAA
Kitl rev	CCAGCATATTGCACCAGCAGCG
Krt23 fwd	CTCAACGATCGCCTGGCCACA
Krt23 rev	TCCTGCAGGCGGCTGATGTTT
Lama1 fwd	CGAGCACGGGCGAGACCTTC
Lama1 rev	CTCTCTGCTGGCTCCGCACG
Myb fwd	CCAAAGCCAGCCAGACGCCA
Myb rev	ACGGAGGACTGGCCACTTGA
Pou3f4 fwd	GGCATGCAGCAGGGAAGTCCT
Pou3f4 rev	GCGTCCCGGCTTCACGTCTT
Slco4c1 fwd	CCCGGCTTTCGTCCCTTCCAG
Slco4c1 rev	ACCCCGGCGGCTCATCAGA
Sox8 fwd	AGACTGAGCTACTGCGGCGGA
Sox8 rev	AGGGGCACTCAGTGGGGATGG
Spry1 fwd	AGCAGCTACGAGCACCGACCT
Spry1 rev	GGTGGGCGGAGACCGTCCTA
Taf4b fwd	CGGCTCGCCTCGCTTCAGTT
Taf4b rev	CCCGACGCGCTCGAGACTAC
Wnt11 fwd	GGCGCGGCTACAACCCCTAC
Wnt11 rev	CCTCCTCAGGGGTGGGGCAT

Supplemental Table 2: mRNA transcripts downregulated in *Ilk<sup>-/-UB</sup>* kidneys (p<0.003)

Probe ID	Gene Name	Gene Symbol	Fold Change
1416468_at	aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1	-2.148623186
1435438_at	SRY-box containing gene 8	Sox8	-2.037065358
1437870_at	solute carrier organic anion transporter family, member 4C1	Sloca4c1	-1.963658776
1448304_a_at	similar to Rab6 protein; predicted gene 13082; RAB6, member RAS oncogene family similar to tripartite motif protein TRIM34 alpha; tripartite motif-containing 34; similar to Tripartite motif protein 34	Rab6	-1.903923252
1424857_a_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Trim34a	-1.88213653
1433977_at	keratin 23	Hs3st3b1	-1.867756375
1418213_at	integrin linked kinase; predicted gene 6263	Krt23	-1.835321044
1449942_a_at	tripartite motif-containing 12	Ilk	-1.783115674
1437432_a_at	aldehyde dehydrogenase family 1, subfamily A7	Trim12a	-1.72206885
1418601_at	RIKEN cDNA 5730510P18 gene	Aldh1a7	-1.652019446
1432463_at	RIKEN cDNA 6332401O19 gene	5730510P18Rik	-1.64085918
1455963_at	solute carrier organic anion transporter family, member 4C1	Tmem229a	-1.636875596
1460616_at	chemokine (C-X-C motif) receptor 4	Sloca4c1	-1.623859999
1448710_at	myosin VIIA	Cxcr4	-1.613128354
1421385_a_at	wingless-related MMTV integration site 11	Myo7a	-1.593751951
1450772_at	essential meiotic endonuclease 1 homolog 2 (S. pombe)	Wnt11	-1.572346139
1460628_at	LINE-1 type transposase domain containing 1	Eme2	-1.525193787
1457314_at	ribonucleotide reductase M1	L1td1	-1.518304129
1440073_at	cholinergic receptor, nicotinic, alpha polypeptide 7	Rrm1	-1.514190901
1440681_at	fibroblast growth factor 9	Chma7	-1.497942619
1438718_at	fibroblast growth factor 1	Fgf9	-1.497274747
1423136_at	ets variant gene 5	Fgf1	-1.495758655
1450082_s_at	chemokine (C-X-C motif) ligand 14	Etv6	-1.494461582
1418457_at	sclerostin domain containing 1	Cxcl14	-1.494057497
1449340_at	Fras1 related extracellular matrix protein 2	Sostdc1	-1.48307694
1457038_at	ets variant gene 5	Frem2	-1.473208747
1420998_at	mal, T-cell differentiation protein 2	Etv5	-1.459696529
1427042_at	major facilitator superfamily domain containing 2	Mal2	-1.45674724
1428223_at	RIKEN cDNA 1700011H14 gene	Mfsd2a	-1.455394415
1419294_at	chemokine (C-X-C motif) ligand 14	1700011H14Rik	-1.451580738
1418456_a_at	arginase type II	Cxcl14	-1.445357692
1418847_at	ets variant gene 5	Arg2	-1.44296205
1428142_at	homeo box D1	Etv5	-1.43919854
1420573_at	RIKEN cDNA D630045M09 gene	Hoxd1	-1.436256375
1436619_at	aquaporin 4	D630045M09Rik	-1.433271454
1434449_at	RIKEN cDNA 6332401O19 gene	Aqp4	-1.43185887
1434279_at	Fas (TNF receptor superfamily member 6)	Tmem229a	-1.429280299
1434301_at	RIKEN cDNA D330050I23 gene	NA	-1.417486893
1444128_at	RIKEN cDNA 9630014M24 gene; Rho GTPase activating protein 26; predicted gene 5820	Fam84b	-1.417477142
1435303_at	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	Arhgap26	-1.415957998
1421279_at	laminin, gamma 2	Taf4b	-1.413147086
1456478_at	phosphoglucosyltransferase 2-like 1	Lamc2	-1.400053855
1441316_at	similar to wingless related MMTV integration site 8b; wingless related MMTV integration site 8b	Pgm2l1	-1.390517028
1421161_at	betacellulin, epidermal growth factor family member	Wnt8b	-1.390118093
1425970_a_at	Ros1 proto-oncogene	Btc	-1.389427753
1435670_at	transcription factor AP-2 beta	Ros1	-1.387583768
1415965_at	stearyl-Coenzyme A desaturase 1	Tcfap2b	-1.3862589
1431897_at	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9	Scd1	-1.385529867
1422165_at	POU domain, class 3, transcription factor 4	Chst9	-1.382431504
1423232_at	ets variant gene 4 (E1A enhancer binding protein, E1AF)	Pou3f4	-1.379100185
1430688_s_at	RIKEN cDNA D730039F16 gene	Etv4	-1.368048482
1438841_s_at	arginase type II	D730039F16Rik	-1.366240969
1444214_at	tubulin, beta 1	NA	-1.365761591
1422967_a_at	transferrin receptor	Tubb1	-1.365211736
1443770_x_at	---	Tfrc	-1.359242927
1421317_x_at	myeloblastosis oncogene	NA	-1.358863301
1443969_at	insulin receptor substrate 2	Myb	-1.358088739
1415857_at	embigin	Irs2	-1.357979221
1440409_at	glucosaminyl (N-acetyl) transferase 3, mucin type	Emb	-1.354260499
1420964_at	ectodermal-neural cortex 1	Gcnt3	-1.349801273
1430984_at	antizyme inhibitor 1	Enc1	-1.346528444
1453488_at	RIKEN cDNA 4930458D05 gene	Azin1	-1.346135849
1424367_a_at	homer homolog 2 (Drosophila)	4930458D05Rik	-1.34589319
1448117_at	kit ligand	Homer2	-1.344712561
1435815_at	leucine zipper, down-regulated in cancer 1	Kitl	-1.343923883
1416237_at	myelin protein zero-like 2	Ldoc1	-1.343075559
1415856_at	embigin	Mpzl2	-1.339648721
1431686_a_at	glia maturation factor, beta	Emb	-1.33798393
1421821_at	low density lipoprotein receptor	Gmfb	-1.323122488
1434553_at	transmembrane protein 56	Ldlr	-1.320258918
1421943_at	transforming growth factor alpha	Tmem56	-1.320046658
1429700_at	RIKEN cDNA 3110040M04 gene	Tgfa	-1.318052585
1421830_at	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1	3110040M04Rik	-1.317545207
1426664_x_at	solute carrier family 45, member 3	Ak4	-1.317088958
1449422_at	cadherin 4	Slc45a3	-1.315704215
1448752_at	carbonic anhydrase 2	Cdh4	-1.314204203
1457867_at	sphingosine-1-phosphate phosphatase 2	Car2	-1.314191463
1421440_at	similar to wingless related MMTV integration site 8b; wingless related MMTV integration site 8b	Sgpp2	-1.313681091
1423635_at	bone morphogenetic protein 2	Wnt8b	-1.312005078
1455887_at	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glycosyltransferase)	Bmp2	-1.31117644
1437128_a_at	RIKEN cDNA A630033E08 gene	Alg8	-1.310608839
1429013_at	MAP7 domain containing 2	Zfp945	-1.308565386
1450194_a_at	myeloblastosis oncogene	Mtap7d2	-1.307742765
1415874_at	sprouty homolog 1 (Drosophila); similar to sprouty 1	Myb	-1.307002458
1438343_at	RIKEN cDNA 0610037L13 gene	Spry1	-1.304973111
1450061_at	ectodermal-neural cortex 1	0610037L13Rik	-1.30390992
1436988_at	isthmin 1 homolog (zebrafish)	Enc1	-1.303816608
		lsm1	-1.301800907

1429106_at	RIKEN cDNA 4921509J17 gene	4921509J17Rik	-1.300471378
1427679_at	large tumor suppressor	Lats1	-1.297636721
1440867_at	sprouty homolog 4 (Drosophila)	Spry4	-1.294435182
1448227_at	growth factor receptor bound protein 7	Grb7	-1.291492971
1418153_at	laminin, alpha 1	Lama1	-1.291465414
1434709_at	neuron-glia-CAM-related cell adhesion molecule	Nrcam	-1.291262541
1437244_at	similar to growth arrest-specific 2 like 3; growth arrest-specific 2 like 3	Gas2l3	-1.287549248
1417689_a_at	PDZK1 interacting protein 1	Pdzk1ip1	-1.284390698
1415855_at	kit ligand	Kitl	-1.283595843
1419593_at	similar to Greb1 protein	Greb1	-1.283477431
1422733_at	four jointed box 1 (Drosophila)	Fjx1	-1.283457783
1419254_at	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase	Mthfd2	-1.278053741
1447073_at	thyroid hormone receptor interactor 12	Trip12	-1.277506688
1421105_at	jagged 1	Jag1	-1.276352235
1419465_at	naked cuticle 2 homolog (Drosophila)	Nkd2	-1.27567014
1434766_at	protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	-1.274574925
1440882_at	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	Lrp8	-1.273914066
1444901_at	---	NA	-1.271537331
1447925_at	RIKEN cDNA D630033A02 gene	D630033A02Rik	-1.269792696
1422087_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Myc1l	-1.268455026
1456397_at	cadherin 4	Cdh4	-1.267258499
1437199_at	protocadherin gamma subfamily B, 7	Dusp5	-1.266533859
1450440_at	glial cell line derived neurotrophic factor family receptor alpha 1	Gfra1	-1.266300915
1419250_a_at	PFTAIRE protein kinase 1	Cdk14	-1.265832791
1453201_at	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	Rassf10	-1.265001803
1420795_at	fibroblast growth factor 9	Fgf9	-1.264797175
1427778_at	defensin beta 8	Defb8	-1.264507417
1457648_x_at	family with sequence similarity 20, member C	Fam20c	-1.263798592
1455080_at	protein phosphatase 1, regulatory (inhibitor) subunit 16B	Ppp1r16b	-1.262269583
1421829_at	predicted gene 13639; similar to adenylate kinase 4; adenylate kinase 3-like 1	Ak4	-1.261772168
1415801_at	gap junction protein, alpha 1	Gja1	-1.260220198
1460258_at	leukocyte cell derived chemotaxin 1	Lect1	-1.26000842
1452811_at	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase; similar to 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	Atic	-1.259508187
AFFX-TransRecMurr/X57	transferrin receptor	Tfrc	-1.257000815
1419633_at	UNC homeobox	Uncx	-1.256480188
1425746_at	RIKEN cDNA D730039F16 gene	D730039F16Rik	-1.251530269
1418108_at	rotectin 2	Rtkn2	-1.249613284
1422299_a_at	serine/threonine/tyrosine interacting-like 1	Styx1	-1.247363876
1420005_s_at	bone morphogenetic protein 15	Bmp15	-1.245679066
1438784_at	B-cell leukemia/lymphoma 11B	Bcl11b	-1.243471516
1454714_x_at	predicted gene 7669; predicted gene 5207; predicted gene 9252; predicted gene 8096; predicted gene 13337; predicted gene 9210; predicted gene 8341; predicted gene 5847; predicted gene 7901; predicted gene 9347; predicted gene, EG627427; similar to 3-phosphoglycerate dehydrogenase; 3-phosphoglycerate dehydrogenase	Phgdh	-1.243439993
1448183_a_at	hypoxia inducible factor 1, alpha subunit	Hif1a	-1.24209123
1436584_at	sprouty homolog 2 (Drosophila)	Spry2	-1.239344661
1420965_a_at	ectodermal-neural cortex 1	Enc1	-1.238328884
1436656_at	cDNA sequence BC062109	NA	-1.237471032
1429239_a_at	STAR-related lipid transfer (START) domain containing 4	Stard4	-1.23744132
1417028_a_at	tripartite motif-containing 2	Trim2	-1.236735789
1433787_at	NEL-like 1 (chicken)	Nell1	-1.229013509
1453612_at	NIMA (never in mitosis gene a)-related expressed kinase 1	Nek1	-1.228405385
1439716_at	piwi-like homolog 4 (Drosophila)	Piwil4	-1.227858642
1439015_at	glial cell line derived neurotrophic factor family receptor alpha 1	Gfra1	-1.227800664
1433579_at	transmembrane protein 30B	Tmem30b	-1.224727562
1418966_a_at	discoidin, CUB and LCCL domain containing 1	Dcbld1	-1.224591639
1415673_at	phosphoserine phosphatase	Psph	-1.224330342
1420816_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	-1.222067258
1421816_at	similar to Glutathione reductase, mitochondrial precursor (GR) (GRase); glutathione reductase	Gsr	-1.220965791
1426560_a_at	nephronectin	Npnt	-1.215847455
1422552_at	reprimin, TP53 dependent G2 arrest mediator candidate	Rprm	-1.212050117
1431430_s_at	similar to mouse RING finger 1; tripartite motif-containing 59	Trim59	-1.210831666
1449293_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	-1.207800163
1421268_at	UDP-glucose ceramide glucosyltransferase	Ugcg	-1.206690191
1418102_at	hairy and enhancer of split 1 (Drosophila)	Hes1	-1.206034446
1423291_s_at	hypoxia up-regulated 1	Hyou1	-1.204636967
1422021_at	sprouty homolog 4 (Drosophila)	Spry4	-1.193404256
1452315_at	kinesin family member 11	Kif11	-1.190638445
1441632_at	RIKEN cDNA C130079B09 gene	C130079B09Rik	-1.187508804
1448348_at	cell cycle associated protein 1	Caprin1	-1.18624827
1452427_s_at	protein tyrosine phosphatase-like A domain containing 1	Ptplad1	-1.185037571

Supplemental Table 3: mRNA transcripts upregulated in *Ilk<sup>-UB</sup>* kidneys (p<0.003)

Probe ID	Gene Name	Gene Symbol	Fold Change
1455625_at	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf10	2.435240921
1424923_at	serine (or cysteine) peptidase inhibitor, clade A, member 3G	Serpina3g	2.169109205
1418930_at	chemokine (C-X-C motif) ligand 10; similar to Small inducible cytokine B10 precursor (CXCL10) (Interferon-gamma-induced protein CRG-2) (Gamma-IP10) (IP-10) (C7)	Cxcl10	2.093562828
1419135_at	lymphotoxin B	Ltb	2.089585405
1449254_at	secreted phosphoprotein 1	Spp1	2.083494347
1424409_at	claudin 23	Cldn23	2.08167134
1436094_at	VGF nerve growth factor inducible	Vgf	1.927429218
1440916_at	RIKEN cDNA 2510049J12 gene	2510049J12Rik	1.831515812
1422557_s_at	metallothionein 1	Mt1	1.785723465
1418714_at	dual specificity phosphatase 8	Dusp8	1.73978671
1427975_at	RAS-like, family 10, member A	Rasl10a	1.725595252
1417381_at	complement component 1, q subcomponent, alpha polypeptide	C1qa	1.671182229
1449401_at	complement component 1, q subcomponent, C chain	C1qc	1.622632894
1417063_at	complement component 1, q subcomponent, beta polypeptide	C1qb	1.608649553
1417156_at	keratin 19	Krt19	1.60225823
1437029_at	tachykinin receptor 3	Tacr3	1.597848833
1450792_at	TYRO protein tyrosine kinase binding protein	Tyrobp	1.571933919
1421375_a_at	S100 calcium binding protein A6 (calcyclin)	S100a6	1.569716603
1437726_x_at	complement component 1, q subcomponent, beta polypeptide	C1qb	1.568838004
1442082_at	complement component 3a receptor 1	C3ar1	1.568596503
1424754_at	membrane-spanning 4-domains, subfamily A, member 7	Ms4a7	1.564037229
1422903_at	lymphocyte antigen 86	Ly86	1.549701842
1417428_at	guanine nucleotide binding protein (G protein), gamma 3	Gng3	1.532411077
1420697_at	solute carrier family 15, member 3	Slc15a3	1.526725665
1427618_at	cadherin 9	Cdh9	1.522242671
1438512_at	cDNA sequence BC048679	BC048679	1.515935157
1447726_at	rippy2 homolog (zebrafish)	Rippy2	1.503715
1419482_at	complement component 3a receptor 1	C3ar1	1.501249724
1418677_at	actinin alpha 3	Actn3	1.484010064
1447825_x_at	protocadherin 8	Pcdh8	1.482882082
1457508_at	RIKEN cDNA C430003N24 gene	C430003N24Rik	1.481848478
1417051_at	protocadherin 8	Pcdh8	1.478866687
1448591_at	cathepsin S	Ctss	1.476825264
1424208_at	prostaglandin E receptor 4 (subtype EP4)	Ptger4	1.468653
1440803_x_at	tachykinin receptor 3	Tacr3	1.467626844
1422029_at	chemokine (C-C motif) ligand 20	Ccl20	1.466336995
1437868_at	family with sequence similarity 46, member A	Fam46a	1.455306129
1449009_at	T-cell specific GTPase 2; T-cell specific GTPase	Gm12185	1.452761547
1448931_at	coagulation factor II (thrombin) receptor-like 1	F2rl1	1.444142734
1419708_at	wingless-related MMTV integration site 6	Wnt6	1.435609414
1419282_at	chemokine (C-C motif) ligand 12; similar to monocyte chemoattractant protein-5	Ccl12	1.426576232
1449195_s_at	chemokine (C-X-C motif) ligand 16	Cxcl16	1.4264928
1455748_at	predicted gene, ENSMUSG00000056252; dynein light chain Tctex-type 1D; dynein light chain Tctex-type 1; dynein light chain Tctex-type 1E; similar to tctex-1 protein	Dynl1d	1.424880281
1460700_at	similar to Stat3B; signal transducer and activator of transcription 3	Stat3	1.423204562
1423691_x_at	predicted gene 5604; keratin 8	Krt8	1.41366422
1426587_a_at	similar to Stat3B; signal transducer and activator of transcription 3	Stat3	1.409272685
1419561_at	chemokine (C-C motif) ligand 3	Ccl3	1.408225595
1418340_at	Fc receptor, IgE, high affinity I, gamma polypeptide	Fcer1g	1.407166846
1455607_at	R-spondin 3 homolog ( <i>Xenopus laevis</i> )	Rspo3	1.406194293
1432466_a_at	apolipoprotein E	ApoE	1.402598646
1435980_x_at	wingless-related MMTV integration site 6	Wnt6	1.400987077
1448620_at	Fc receptor, IgG, low affinity III	Fcgr3	1.398229753
1456890_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Ddx58	1.396360924
1444009_at	Ras association (RalGDS/AF-6) domain family member 4	Rassf4	1.395041538
1418588_at	neurensin 1	Nrsn1	1.392367249
1435989_x_at	predicted gene 5604; keratin 8	Krt8	1.385732813
1460259_s_at	chloride channel calcium activated 1	Clca1	1.384285435
1429315_at	synaptotagmin XI; similar to synaptotagmin XI	Syt11	1.380814728
1420647_a_at	predicted gene 5604; keratin 8	Krt8	1.373543432
1448891_at	Fc receptor-like S, scavenger receptor	Fcrls	1.360485832
1449363_at	activating transcription factor 3	Atf3	1.355898772
1435138_at	family with sequence similarity 155, member A	Fam155a	1.354953846
1439170_at	---	NA	1.353757105
1419209_at	chemokine (C-X-C motif) ligand 1	Cxcl1	1.353328995
1427076_at	macrophage expressed gene 1	Mpeg1	1.349928888
1435190_at	cell adhesion molecule with homology to L1CAM	Chl1	1.3468365
1457235_at	low density lipoprotein-related protein 1B (deleted in tumors)	Lrp1b	1.346108831
1418674_at	oncostatin M receptor	Osmr	1.335420587
1425214_at	pyrimidinergic receptor P2Y, G-protein coupled, 6	P2ry6	1.334171317
1445288_at	---	NA	1.334008751

1445176_a_at	synaptotagmin XI; similar to synaptotagmin XI	Syt11	1.320045652
1418726_a_at	troponin T2, cardiac	Tnnt2	1.316556328
1418762_at	CD55 antigen	Cd55	1.314500849
1428983_at	scleraxis	Scx	1.308945983
1445445_s_at	prostaglandin E receptor 1 (subtype EP1)	Ptger1	1.300103036
1439622_at	Ras association (RalGDS/AF-6) domain family member 4	Rassf4	1.29837223
1448694_at	Jun oncogene	Jun	1.29803647
1418283_at	claudin 4	Cldn4	1.297992533
1421840_at	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	1.293755998
1450019_at	similar to chemokine receptor CX3CR1; chemokine (C-X3-C) receptor 1	Cx3cr1	1.290647509
1423754_at	interferon induced transmembrane protein 3	Ifitm3	1.289122842
1457799_at	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	Kcns3	1.286409999
1455471_at	canopy 1 homolog (zebrafish)	Cnpy1	1.285106939
	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	1.283317182
1425519_a_at	membrane associated guanylate kinase, WW and PDZ domain containing 1	Magi1	1.280680488
1440071_at	synaptotagmin XI; similar to synaptotagmin XI	Syt11	1.280509023
1449264_at	soluble carrier family 26, member 7	Slc26a7	1.279947717
1436279_at	3-hydroxybutyrate dehydrogenase, type 2	Bdh2	1.278282732
1453011_at	golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	1.275808062
1460535_at	RIKEN cDNA 2610035D17 gene	2610035D17Rik	1.275043031
1453261_at	carboxymethylenebutenolidase-like (Pseudomonas)	Cmb1	1.27477708
1451322_at	similar to creatine kinase, brain; predicted gene 12892; creatine kinase, brain	Ckb	1.274324471
1455106_a_at	5-hydroxytryptamine (serotonin) receptor 2B	Htr2b	1.270615681
1422125_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Ddx58	1.268284713
1436562_at	synaptotagmin XI; similar to synaptotagmin XI	Syt11	1.266673225
1429314_at	cDNA sequence BC031353	BC031353	1.265514895
1436033_at	RIKEN cDNA A830082K12 gene	A830082K12Rik	1.260606239
1458470_at	calbindin 1	Calb1	1.259780877
1456934_at	transmembrane protease, serine 2	Tmprss2	1.257913133
1449369_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.25543227
1416926_at	RIKEN cDNA A930001N09 gene	A930001N09Rik	1.254014494
1454967_at	integrin alpha 4	Itga4	1.253683459
1457376_at	mannosidase 1, alpha	Man1a	1.253351195
1417110_at	transmembrane protease, serine 2	Tmprss2	1.250335157
1458347_s_at	reticulon 1	Rtn1	1.24517565
1430788_at	RIKEN cDNA 4930525G20 gene	4930525G20Rik	1.243775403
1438346_at	potassium inwardly-rectifying channel, subfamily J, member 16	Kcnj16	1.242963728
1436163_at	expressed sequence C77545	C77545	1.23958173
1449654_s_at	Jun oncogene	Jun	1.237079359
1417409_at	serine peptidase inhibitor, Kazal type 2	Spink2	1.234649819
1454710_at	synuclein, gamma	Sncg	1.231662238
1417788_at	RIKEN cDNA 1810028F09 gene	1810028F09Rik	1.230985216
1430027_at	abhydrolase domain containing 4	Abhd4	1.2219681
1416315_at	maternally expressed 3	Meg3	1.221531392
1452183_a_at	similar to Stat3B; signal transducer and activator of transcription 3	Stat3	1.220743854
1459961_a_at	RIKEN cDNA E130002L11 gene	E130002L11Rik	1.219977598
1444965_at	N-myc downstream regulated gene 4	Ndr4	1.216154305
1436188_a_at	secernin 1	Scrn1	1.215763492
1439500_at	disabled homolog 2 (Drosophila)	Dab2	1.215581074
1420498_a_at	N-myc downstream regulated gene 4	Ndr4	1.212201945
1426615_s_at	transcobalamin 2	Tcn2	1.203953742
1448200_at			

Supplemental Table 4: Gene ontology analysis of biological process terms enriched in genes downregulated in *Ilk*<sup>-/-UB</sup> kidneys

ID	Name	P-value	Genes in Test Set	Hit Count in Genome	Genes in Test Set
GO:0009887	organ morphogenesis	6.22E-08	26	885	UNCX HES1 GCNT3 MYO7A POU3F4 SOX8 GJA1 FGF9 FGF1 CXCR4 BMP2 LAMA1 BCL11B JAG1 AT1C HIF1A SOSTDC1 WNT11 CA2 ETV4 ETV5 ALDH1A1 FAM20C SPRY1 SPRY2 WNT8B
GO:0051094	positive regulation of developmental process	1.66E-07	24	781	HES1 CAPRIN1 SOX8 GJA1 NRCAM CHRNA7 FGF9 FGF1 NPNT CXCR4 BTC NEL1 LRP8 BMP2 KITLG JAG1 MYB HIF1A CA2 CDH4 ETV5 FAM20C SPRY1 ILK
GO:2000026	regulation of multicellular organismal development	9.87E-07	29	1249	HES1 CAPRIN1 SOX8 GJA1 NRCAM CHRNA7 FGF9 FGF1 CXCR4 YWHAG NEL1 LRP8 BMP2 LAMA1 KITLG BCL11B JAG1 MYB HIF1A WNT11 LECT1 CA2 ETV4 CDH4 ETV5 FAM20C SPRY1 WNT8B ILK
GO:0002009	morphogenesis of an epithelium	1.39E-06	17	406	HES1 SOX8 GJA1 FGF1 NPNT CXCR4 BMP2 LAMA1 JAG1 HIF1A WNT11 CA2 ETV4 ETV5 ALDH1A1 FREM2 ILK
GO:0060429	epithelium development	1.88E-06	21	665	HES1 SOX8 GJA1 FGF1 NPNT CXCR4 ROS1 BMP2 LAMA1 BCL11B JAG1 HIF1A WNT11 LECT1 CA2 ETV4 ETV5 ALDH1A1 FREM2 LATS1 ILK
GO:0035295	tube development	2.25E-06	18	478	HES1 SOX8 GJA1 FGF9 FGF1 NPNT CXCR4 ARG2 BMP2 LAMA1 JAG1 HIF1A WNT11 ETV4 ETV5 SPRY1 SPRY2 ILK
GO:0048729	tissue morphogenesis	8.51E-06	18	520	HES1 GCNT3 SOX8 GJA1 FGF1 NPNT CXCR4 BMP2 LAMA1 JAG1 HIF1A WNT11 CA2 ETV4 ETV5 ALDH1A1 FREM2 ILK
GO:0045597	positive regulation of cell differentiation	3.64E-05	18	571	HES1 CAPRIN1 SOX8 NRCAM NPNT CXCR4 BTC NEL1 BMP2 KITLG JAG1 MYB HIF1A CA2 CDH4 ETV5 FAM20C ILK
GO:0035239	tube morphogenesis	4.56E-05	14	331	HES1 SOX8 GJA1 FGF1 NPNT CXCR4 BMP2 LAMA1 HIF1A WNT11 ETV4 ETV5 SPRY2 ILK
GO:0001657	ureteric bud development	5.85E-05	9	108	HES1 SOX8 FGF1 NPNT ARG2 BMP2 WNT11 SPRY1 ILK
GO:0007423	sensory organ development	1.58E-04	16	491	HES1 MYO7A POU3F4 SOX8 GJA1 FGF9 CXCL14 BMP2 LAMA1 BCL11B JAG1 HIF1A ALDH1A1 FREM2 SPRY2 WNT8B
GO:0060562	epithelial tube morphogenesis	2.51E-04	12	266	HES1 SOX8 GJA1 FGF1 NPNT BMP2 LAMA1 HIF1A WNT11 ETV4 ETV5 ILK
GO:0072001	renal system development	2.61E-04	12	267	HES1 GCNT3 SOX8 FGF1 NPNT ARG2 BMP2 JAG1 WNT11 CA2 SPRY1 ILK
GO:0045595	regulation of cell differentiation	3.63E-04	24	1157	UNCX HES1 CAPRIN1 SOX8 NRCAM FGF9 NPNT CXCR4 YWHAG BTC NEL1 LRP8 BMP2 KITLG BCL11B JAG1 MYB HIF1A CA2 CDH4 ETV5 FAM20C WNT8B ILK
GO:0048754	branching morphogenesis of a tube	3.67E-04	10	176	SOX8 FGF1 NPNT CXCR4 BMP2 LAMA1 ETV4 ETV5 SPRY2 ILK
GO:0048839	inner ear development	3.87E-04	10	177	HES1 MYO7A POU3F4 FGF9 CXCL14 BMP2 JAG1 FREM2 SPRY2 WNT8B
GO:0010627	regulation of intracellular protein kinase cascade	4.68E-04	19	753	HES1 PTPLAD1 SPRY4 GJA1 CHRNA7 DUSP5 FGF9 FGF1 NPNT CXCR4 ROS1 BMP2 KITLG WNT11 SPRY1 SPRY2 ILK TRIM59 TGFA
GO:0030182	neuron differentiation	7.29E-04	23	1112	HES1 CAPRIN1 MYO7A POU3F4 SOX8 GJA1 NRCAM CXCR4 YWHAG LRP8 BMP2 LAMA1 BCL11B JAG1 GFRA1 HIF1A WNT11 ETV4 CDH4 ETV5 PHGDH WNT8B ILK
GO:0050769	positive regulation of neurogenesis	7.94E-04	9	146	HES1 CAPRIN1 SOX8 CXCR4 BMP2 HIF1A CDH4 ETV5 ILK
GO:0042127	regulation of cell proliferation	7.98E-04	25	1300	HES1 LDOC1 SOX8 GJA1 CHRNA7 FGF9 FGF1 BTC NEL1 IRS2 RTKN2 BMP2 KITLG BCL11B JAG1 SKP2 HIF1A WNT11 LECT1 ETV4 ETV5 SPRY1 SPRY2 ILK TGFA
GO:0060675	ureteric bud morphogenesis	8.57E-04	7	73	HES1 SOX8 FGF1 NPNT BMP2 WNT11 ILK
GO:0001655	urogenital system development	1.26E-03	12	309	HES1 GCNT3 SOX8 FGF1 NPNT ARG2 BMP2 JAG1 WNT11 CA2 SPRY1 ILK
GO:0001649	osteoblast differentiation	1.32E-03	9	155	SOX8 GJA1 FGF9 NPNT NEL1 BMP2 WNT11 FAM20C ILK
GO:0043583	ear development	1.51E-03	10	205	HES1 MYO7A POU3F4 FGF9 CXCL14 BMP2 JAG1 FREM2 SPRY2 WNT8B
GO:0051960	regulation of nervous system development	2.09E-03	15	522	HES1 CAPRIN1 SOX8 NRCAM CXCR4 YWHAG LRP8 BMP2 BCL11B JAG1 HIF1A CDH4 ETV5 WNT8B ILK

GO:0032268	regulation of cellular protein metabolic process	2.09E-03	25	1369	HES1 CAPRIN1 PIWIL4 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 GMFB CXCR4 YWHAG NELL1 LRP8 BMP2 KITLG MYB WNT11 HYOU1 SPRY1 SPRY2 GRB7 LAT S1 ILK NKD2 TGFA
GO:0051174	regulation of phosphorus metabolic process	2.15E-03	25	1371	HES1 ARHGAP26 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 NPNT GMFB CXCR4 YWHAG LDLR IRS2 LRP8 BMP2 KITLG WNT11 ALDH1A1 FAM20C HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0001763	morphogenesis of a branching structure	2.53E-03	10	217	SOX8 FGF1 NPNT CXCR4 BMP2 LAMA1 ETV4 ETV5 SPRY2 ILK
GO:0048699	generation of neurons	2.75E-03	23	1200	HES1 CAPRIN1 MYO7A POU3F4 SOX8 GJA1 NRCAM CXCR4 YWHAG LRP8 BMP2 LAMA1 BCL11B JAG1 GFRA1 HIF1A WNT11 ETV4 CDH4 ETV5 PHGDH WNT8B ILK
GO:0050767	regulation of neurogenesis	2.81E-03	14	464	HES1 CAPRIN1 SOX8 NRCAM CXCR4 YWHAG LRP8 BMP2 BCL11B JAG1 HIF1A CDH4 ETV5 ILK
GO:0043549	regulation of kinase activity	2.84E-03	17	686	PTPLAD1 SPRY4 CHRNA7 DUSP5 GMFB CXCR4 YWHAG IRS2 LRP8 KITLG WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0033673	negative regulation of kinase activity	3.31E-03	9	173	SPRY4 DUSP5 GMFB YWHAG IRS2 SPRY1 SPRY2 LATS1 ILK
GO:0042325	regulation of phosphorylation	3.39E-03	20	944	HES1 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 GMFB CXCR4 YWHAG IRS2 LRP8 BMP2 KITLG WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0060485	mesenchyme development	3.47E-03	9	174	HES1 SOX8 GJA1 FGF9 BMP2 KITLG JAG1 HIF1A WNT11
GO:0007243	intracellular protein kinase cascade	3.56E-03	20	947	HES1 PTPLAD1 SPRY4 GJA1 CHRNA7 DUSP5 FGF9 FGF1 NPNT CXCR4 ROS1 IRS2 BMP2 KITLG WNT11 SPRY1 SPRY2 ILK TRIM59 TGFA
GO:0051338	regulation of transferase activity	4.29E-03	17	707	PTPLAD1 SPRY4 CHRNA7 DUSP5 GMFB CXCR4 YWHAG IRS2 LRP8 KITLG WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0001932	regulation of protein phosphorylation	5.14E-03	19	883	HES1 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 GMFB CXCR4 YWHAG LRP8 BMP2 KITLG WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0010720	positive regulation of cell development	5.27E-03	9	183	HES1 CAPRIN1 SOX8 CXCR4 BMP2 HIF1A CDH4 ETV5 ILK
GO:0006468	protein phosphorylation	5.37E-03	24	1344	HES1 CDK14 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 GMFB CXCR4 YWHAG ROS1 NEK1 LRP8 BMP2 KITLG PRKAA2 WNT11 FAM20C HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0051348	negative regulation of transferase activity	5.51E-03	9	184	SPRY4 DUSP5 GMFB YWHAG IRS2 SPRY1 SPRY2 LATS1 ILK
GO:0061138	morphogenesis of a branching epithelium	5.76E-03	9	185	SOX8 FGF1 NPNT CXCR4 BMP2 LAMA1 ETV4 ETV5 ILK
GO:0019220	regulation of phosphate metabolic process	6.43E-03	24	1358	HES1 ARHGAP26 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 NPNT GMFB CXCR4 YWHAG LDLR IRS2 LRP8 BMP2 KITLG WNT11 ALDH1A1 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0045859	regulation of protein kinase activity	7.14E-03	16	654	PTPLAD1 SPRY4 CHRNA7 DUSP5 GMFB CXCR4 YWHAG LRP8 KITLG WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0022008	neurogenesis	7.20E-03	23	1270	HES1 CAPRIN1 MYO7A POU3F4 SOX8 GJA1 NRCAM CXCR4 YWHAG LRP8 BMP2 LAMA1 BCL11B JAG1 GFRA1 HIF1A WNT11 ETV4 CDH4 ETV5 PHGDH WNT8B ILK
GO:0043408	regulation of MAPK cascade	7.22E-03	14	503	PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF9 NPNT CXCR4 ROS1 BMP2 KITLG SPRY1 SPRY2 ILK TGFA
GO:0022603	regulation of anatomical structure morphogenesis	7.58E-03	16	657	HES1 CAPRIN1 SOX8 GJA1 NRCAM CHRNA7 FGF1 LRP8 BMP2 HIF1A LECT1 ETV4 CDH4 ETV5 SPRY1 ILK
GO:0001503	ossification	1.04E-02	11	314	SOX8 GJA1 FGF9 NPNT NELL1 BMP2 HIF1A WNT11 LECT1 FAM20C ILK
GO:0014015	positive regulation of gliogenesis	1.16E-02	5	40	HES1 SOX8 CXCR4 BMP2 ETV5
GO:0045168	cell-cell signaling involved in cell fate commitment	1.32E-02	5	41	HES1 SOX8 FGF1 BMP2 SPRY1
GO:0010740	positive regulation of intracellular protein kinase cascade	1.32E-02	14	530	HES1 PTPLAD1 GJA1 CHRNA7 FGF9 FGF1 NPNT CXCR4 BMP2 KITLG WNT11 SPRY2 ILK TGFA
GO:0045664	regulation of neuron differentiation	1.41E-02	12	390	HES1 CAPRIN1 SOX8 NRCAM YWHAG LRP8 BMP2 BCL11B JAG1 CDH4 ETV5 ILK



GO:0007167	enzyme linked receptor protein signaling pathway	1.42E-02	19	947	HES1 FGF9 FGF1 NPNT ROS1 BTC IRS2 BMP2 GFRA1 HIF1A PRKAA2 SOSTDC1 LECT1 FAM20C SPRY1 SPRY2 GRB7 ILK TGFA
GO:0006469	negative regulation of protein kinase activity	1.92E-02	8	162	SPRY4 DUSP5 GMFB YWHAG SPRY1 SPRY2 LATS1 ILK
GO:0048514	blood vessel morphogenesis	1.96E-02	13	474	HES1 GJA1 NRCAM CHRNA7 FGF9 FGF1 CXCR4 LAMA1 JAG1 HIF1A WNT11 LECT1 TGFA
GO:0043405	regulation of MAP kinase activity	1.97E-02	10	273	PTPLAD1 SPRY4 CHRNA7 DUSP5 CXCR4 KITLG SPRY1 SPRY2 ILK TGFA
GO:0030278	regulation of ossification	2.98E-02	8	172	GJA1 NPNT NELL1 BMP2 HIF1A LECT1 FAM20C ILK
GO:0060284	regulation of cell development	3.44E-02	14	577	HES1 CAPRIN1 SOX8 NRCAM CXCR4 YWHAG LRP8 BMP2 BCL11B JAG1 HIF1A CDH4 ETV5 ILK
GO:0031399	regulation of protein modification process	3.49E-02	20	1103	HES1 PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF1 GMFB CXCR4 YWHAG LRP8 BMP2 KITLG MYB WNT11 HYOU1 SPRY1 SPRY2 LATS1 ILK TGFA
GO:0000165	MAPK cascade	3.51E-02	14	578	PTPLAD1 SPRY4 CHRNA7 DUSP5 FGF9 NPNT CXCR4 ROS1 BMP2 KITLG SPRY1 SPRY2 ILK TGFA
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	4.15E-02	15	668	FGF9 FGF1 ROS1 BTC IRS2 BMP2 GFRA1 HIF1A PRKAA2 LECT1 FAM20C SPRY1 SPRY2 GRB7 TGFA
GO:0000904	cell morphogenesis involved in differentiation	4.77E-02	16	761	HES1 CAPRIN1 MYO7A GJA1 NRCAM CXCR4 LRP8 BMP2 LAMA1 BCL11B GFRA1 HIF1A LECT1 ETV4 CDH4 ILK



GO:0019199	transmembrane receptor protein kinase activity	0.0438951	76	184	Acvr1 Acvr1b Acvr1c Acvr2a Acvr2b Acvr1 Alk Amhr2 Axl Bmpr1a Bmpr1b Bmpr2 Csf1r Ddr1 Ddr2 Efemp1 Egfr Eng Epha1 Epha10 Epha2 Epha3 Epha4 Epha5 Epha6 Epha7 Epha8 Ephb1 Ephb2 Ephb3 Ephb4 Ephb6 Erbb2 Erbb3 Erbb4 Fgfr1 Fgfr2 Fgfr3 Fgfr4 Fgfr1 Fit1 Fit3 Fit4 Hmcrn1 Igf1r Igf1 Igf10 Insr Insr Irs1 Kdr Kil Ltk Lyc6g6a Mer Met Mst1 Musk Nrg2 Nrp1 Ntrk1 Ntrk2 Ntrk3 Pdgrfa Pdgrfb Ptk7 Ret Ror1 Ror2 Ros1 Ryk Tek Tgfb1 Tgfb2 Tgfb3 Tie1 Tyro3
GO:0001848	complement binding	0.0415488	7	16	C1qbp C3ar1 C5ar1 Cd46 Cd93 Cfh Serping1
GO:0008081	phosphoric diester hydrolase activity	0.0399154	74	155	Acap1 Adora1 Apex1 Cnp Enpp1 Enpp2 Enpp3 Enpp6 Gde1 Gdpd1 Gdpd2 Gdpd3 Gdpd5 Gpcpd1 Gpld1 Hmox1 Htr2b Mef2b Mppe1 Pde10a Pde11a Pde1a Pde1b Pde1c Pde2a Pde3a Pde3b Pde4a Pde4b Pde4d Pde5a Pde6a Pde6b Pde6c Pde6d Pde6g Pde6h Pde7a Pde7b Pde8a Pde8b Pde9a Pcb1 Pcb2 Pcb3 Pcb4 Pcd1 Pcd3 Pcd4 Pce1 Pcg1 Pcg2 Pch1 Pch2 Pcl1 Pcl2 Pcxd1 Pcxd2 Pcxd3 Pcz1 Pld1 Pld2 Pld3 Pld4 Pld6 Smpd1 Smpd2 Smpd3 Smpd4 Smpd3a Smpd3b Tdp1 Tdp2 Tulp2
GO:0031491	nucleosome binding	0.0437812	8	16	Hmgb2 Mum1 Noc2 Rcc1 Rdh11 Rnf4 Smarca1 Smarca5
GO:0005275	amine transmembrane transporter activity	0.0450061	89	179	AU018091 Abcc1 Ager Anxa11 Atp2a2 Casp8 Cflar Ctns Fadd Fas Fgf1 Nat3 Pdpn Pdzd8 S100a11 S100a6 S100b Serinc1 Slc13a3 Slc15a4 Slc16a2 Slc17a6 Slc18a2 Slc18a3 Slc1a1 Slc1a2 Slc1a3 Slc1a4 Slc1a5 Slc1a6 Slc22a1 Slc22a16 Slc22a2 Slc22a21 Slc22a3 Slc22a4 Slc22a5 Slc22a8 Slc25a12 Slc25a13 Slc25a22 Slc25a26 Slc32a1 Slc36a1 Slc36a2 Slc38a1 Slc38a2 Slc38a3 Slc38a4 Slc38a5 Slc3a2 Slc43a1 Slc43a2 Slc44a1 Slc5a7 Slc6a1 Slc6a11 Slc6a12 Slc6a13 Slc6a14 Slc6a19 Slc6a2 Slc6a20a Slc6a20b Slc6a3 Slc6a4 Slc6a5 Slc6a6 Slc6a7 Slc6a8 Slc6a9 Slc7a1 Slc7a10 Slc7a11 Slc7a12 Slc7a13 Slc7a14 Slc7a15 Slc7a2 Slc7a3 Slc7a4 Slc7a5 Slc7a6 Slc7a7 Slc7a8 Slc7a9 Slc10a5 Slc10a41 Trt
GO:0051864	histone demethylase activity (H3-K36 specific)	0.0462897	9	23	2410016006Rik 4921501E09Rik Jhdm1d Jmjd5 Kdm2a Kdm2b Kdm4a Pfh8 Trps1
GO:0005262	calcium channel activity	0.0452083	67	130	Cacna1a Cacna1b Cacna1c Cacna1d Cacna1e Cacna1f Cacna1g Cacna1h Cacna1s Cacna2d1 Cacna2d2 Cacna2d3 Cacna2d4 Cacnb1 Cacnb2 Cacnb3 Cacnb4 Cacng1 Cacng2 Cacng3 Cacng4 Cacng5 Cacng6 Cacng7 Cacng8 Catsper1 Catsper2 Catsper3 Fgf2 Gpm6a Grin1 Grin2a Grin2b Grin3a Grin3b Grm7 Htr2b Itpr1 Itpr2 Itpr3 Orai1 Pkd1 Pkd2 Ryr1 Ryr2 Ryr3 Slc24a2 Tmem37 Tpcn1 Tpcn2 Tpr1 Tprc1 Tprc2 Tprc3 Tprc4 Tprc5 Tprc6 Tprc7 Trpm2 Trpm4 Trpm6 Trpm7 Trpm8 Trpv1 Trpv2 Trpv4 Trpv6
GO:0016410	N-acyltransferase activity	0.0446548	85	180	1700019G17Rik Aanat Acnat2 Alas1 Alas2 Arhgap4 Atat1 Baat Cdy Cited2 Clock Cml1 Cml2 Cml3 Cml5 Crebbp Csrp2bp Elp3 Ep300 Epc1 Gdf1 Glyat1 Glyat2 Gm12372 Taf9 Gnpat1 Gtf3c4 Hat1 Hgsnat Hyal1 Nat6 Ing3 Kat2a Kat2b Kat5 Keg1 Lass2 Lass3 Lass4 Lass5 Lass6 Med24 Mettl8 Mgea5 Myst1 Myst2 Myst3 Myst4 Naa10 Naa11 Naa15 Naa20 Naa30 Naa40 Naa50 Nags Nat1 Nat10 Nat14 Nat15 Nat2 Nat3 Nat6 Nat8 Nat9 Ncoa1 Ncoa2 Ncoa3 Nmt1 Nmt2 Ogt Pogk Tad1 Sat1 Sat2 Sat1 Supt7 Tada1 Tada2a Tada3 Taf1 Taf12 Taf5 Taf5l Taf6 Taf9 Tadn4a Usp22
GO:0009975	cyclase activity	0.0462787	28	47	Adcy1 Adcy10 Adcy2 Adcy3 Adcy4 Adcy5 Adcy6 Adcy7 Adcy8 Adcy9 Dak Gm13880 Trappc6b Gucy1a2 Gucy1a3 Gucy1b3 Gucy2c Gucy2e Gucy2g Magi2 Npr1 Npr2 Rcl1 Rtcd1 Thtpa Trappc3 Trappc5 Trappc6a Trappc6b
GO:0005242	inward rectifier potassium channel activity	0.0455169	17	33	Kcnh2 Kcnh7 Kcnj1 Kcnj10 Kcnj11 Kcnj12 Kcnj13 Kcnj14 Kcnj15 Kcnj16 Kcnj2 Kcnj3 Kcnj4 Kcnj5 Kcnj6 Kcnj8 Kcnj9
GO:0019887	protein kinase regulator activity	0.0499115	79	191	1190002H23Rik 2310007A19Rik 4930435E12Rik 4932431P20Rik Hmgb11 Hmgb1 Hmgb11 A830018L16Rik Abi1 Agap2 Ahsg Ak5 Als2 Angpt4 Ankrd54 Apc Cables1 Cables2 Cabyr Camk2n1 Camk2n2 Casp3 Cend1 Cene1 Cne2 Cnci Cny Cnd24a Cdk5r1 Cdk5r2 Cdkn1a Cdkn1b Cdkn1c Cdkn2a Cdkn2b Cdkn2c Cks1b Cks2 Csnk2b Dnajc3 Efcab10 Elp3 Elp4 Erbb3 Fgf13 Fgfr1op Ghr Gm2710 Hmgb11 Hmgb1 Gm6531 Hexim1 Hexim2 Hmgb1 Ibtk Ikbkap Kat2b Kidins220 Mapk8ip2 Nckap1 Nos2 P2rx7 Pki Pki Pki Pki Prkar1a Prkar1b Prkar2a Prkar2b Prkarip1 Rapgef3 Rapgef4 Ropn1 Ropn1 Sh3bp5 Spa17 Taok1 Tom11 Trib1 Trib2 Trib3 Wnk1 Wnt11
GO:0004725	protein tyrosine phosphatase activity	0.0494356	97	222	2410017P09Rik 5530400B01Rik Dusp8 Acp1 Cdc14a Cdc14b Cdc25a Cdc25b Cdc25c Cdkn3 Dnajc6 Dusp1 Dusp10 Dusp11 Dusp12 Dusp13 Dusp14 Dusp15 Dusp16 Dusp18 Dusp19 Dusp2 Dusp21 Dusp22 Dusp23 Dusp26 Dusp28 Dusp3 Dusp4 Dusp5 Dusp6 Dusp7 Dusp8 Dusp9 Epm2a Eya1 Eya2 Eya3 Eya4 Gm13363 Ptp4a1 LOC100504120 Ssh2 Map2k1 Mdp1 Mtm1 Mtmr1 Mtmr14 Mtmr2 Mtmr3 Mtmr4 Mtmr6 Mtmr7 Pten Ptp4a1 Ptp4a2 Ptp4a3 Ptpdc1 Ptpmt1 Ptpn1 Ptpn11 Ptpn12 Ptpn13 Ptpn14 Ptpn18 Ptpn2 Ptpn20 Ptpn21 Ptpn22 Ptpn23 Ptpn3 Ptpn4 Ptpn5 Ptpn6 Ptpn9 Ptpn10 Ptpn11 Ptpn12 Ptpn13 Ptpn14 Ptpn15 Ptpn16 Ptpn17 Ptpn18 Ptpn19 Ptpn20 Ptpn21 Ptpn22 Ptpn23 Ptpn24 Ptpn25 Ptpn26 Ptpn27 Ptpn28 Ptpn29 Ptpn30 Ptpn31 Ptpn32 Ptpn33 Ptpn34 Ptpn35 Ptpn36 Ptpn37 Ptpn38 Ptpn39 Ptpn40 Ptpn41 Ptpn42 Ptpn43 Ptpn44 Ptpn45 Ptpn46 Ptpn47 Ptpn48 Ptpn49 Ptpn50 Ptpn51 Ptpn52 Ptpn53 Ptpn54 Ptpn55 Ptpn56 Ptpn57 Ptpn58 Ptpn59 Ptpn60 Ptpn61 Ptpn62 Ptpn63 Ptpn64 Ptpn65 Ptpn66 Ptpn67 Ptpn68 Ptpn69 Ptpn70 Ptpn71 Ptpn72 Ptpn73 Ptpn74 Ptpn75 Ptpn76 Ptpn77 Ptpn78 Ptpn79 Ptpn80 Ptpn81 Ptpn82 Ptpn83 Ptpn84 Ptpn85 Ptpn86 Ptpn87 Ptpn88 Ptpn89 Ptpn90 Ptpn91 Ptpn92 Ptpn93 Ptpn94 Ptpn95 Ptpn96 Ptpn97 Ptpn98 Ptpn99 Ptpn100 Ptpn101 Ptpn102 Ptpn103 Ptpn104 Ptpn105 Ptpn106 Ptpn107 Ptpn108 Ptpn109 Ptpn110 Ptpn111 Ptpn112 Ptpn113 Ptpn114 Ptpn115 Ptpn116 Ptpn117 Ptpn118 Ptpn119 Ptpn120 Ptpn121 Ptpn122 Ptpn123 Ptpn124 Ptpn125 Ptpn126 Ptpn127 Ptpn128 Ptpn129 Ptpn130 Ptpn131 Ptpn132 Ptpn133 Ptpn134 Ptpn135 Ptpn136 Ptpn137 Ptpn138 Ptpn139 Ptpn140 Ptpn141 Ptpn142 Ptpn143 Ptpn144 Ptpn145 Ptpn146 Ptpn147 Ptpn148 Ptpn149 Ptpn150 Ptpn151 Ptpn152 Ptpn153 Ptpn154 Ptpn155 Ptpn156 Ptpn157 Ptpn158 Ptpn159 Ptpn160 Ptpn161 Ptpn162 Ptpn163 Ptpn164 Ptpn165 Ptpn166 Ptpn167 Ptpn168 Ptpn169 Ptpn170 Ptpn171 Ptpn172 Ptpn173 Ptpn174 Ptpn175 Ptpn176 Ptpn177 Ptpn178 Ptpn179 Ptpn180 Ptpn181 Ptpn182 Ptpn183 Ptpn184 Ptpn185 Ptpn186 Ptpn187 Ptpn188 Ptpn189 Ptpn190 Ptpn191 Ptpn192 Ptpn193 Ptpn194 Ptpn195 Ptpn196 Ptpn197 Ptpn198 Ptpn199 Ptpn200 Ptpn201 Ptpn202 Ptpn203 Ptpn204 Ptpn205 Ptpn206 Ptpn207 Ptpn208 Ptpn209 Ptpn210 Ptpn211 Ptpn212 Ptpn213 Ptpn214 Ptpn215 Ptpn216 Ptpn217 Ptpn218 Ptpn219 Ptpn220 Ptpn221 Ptpn222 Ptpn223 Ptpn224 Ptpn225 Ptpn226 Ptpn227 Ptpn228 Ptpn229 Ptpn230 Ptpn231 Ptpn232 Ptpn233 Ptpn234 Ptpn235 Ptpn236 Ptpn237 Ptpn238 Ptpn239 Ptpn240 Ptpn241 Ptpn242 Ptpn243 Ptpn244 Ptpn245 Ptpn246 Ptpn247 Ptpn248 Ptpn249 Ptpn250 Ptpn251 Ptpn252 Ptpn253 Ptpn254 Ptpn255 Ptpn256 Ptpn257 Ptpn258 Ptpn259 Ptpn260 Ptpn261 Ptpn262 Ptpn263 Ptpn264 Ptpn265 Ptpn266 Ptpn267 Ptpn268 Ptpn269 Ptpn270 Ptpn271 Ptpn272 Ptpn273 Ptpn274 Ptpn275 Ptpn276 Ptpn277 Ptpn278 Ptpn279 Ptpn280 Ptpn281 Ptpn282 Ptpn283 Ptpn284 Ptpn285 Ptpn286 Ptpn287 Ptpn288 Ptpn289 Ptpn290 Ptpn291 Ptpn292 Ptpn293 Ptpn294 Ptpn295 Ptpn296 Ptpn297 Ptpn298 Ptpn299 Ptpn300 Ptpn301 Ptpn302 Ptpn303 Ptpn304 Ptpn305 Ptpn306 Ptpn307 Ptpn308 Ptpn309 Ptpn310 Ptpn311 Ptpn312 Ptpn313 Ptpn314 Ptpn315 Ptpn316 Ptpn317 Ptpn318 Ptpn319 Ptpn320 Ptpn321 Ptpn322 Ptpn323 Ptpn324 Ptpn325 Ptpn326 Ptpn327 Ptpn328 Ptpn329 Ptpn330 Ptpn331 Ptpn332 Ptpn333 Ptpn334 Ptpn335 Ptpn336 Ptpn337 Ptpn338 Ptpn339 Ptpn340 Ptpn341 Ptpn342 Ptpn343 Ptpn344 Ptpn345 Ptpn346 Ptpn347 Ptpn348 Ptpn349 Ptpn350 Ptpn351 Ptpn352 Ptpn353 Ptpn354 Ptpn355 Ptpn356 Ptpn357 Ptpn358 Ptpn359 Ptpn360 Ptpn361 Ptpn362 Ptpn363 Ptpn364 Ptpn365 Ptpn366 Ptpn367 Ptpn368 Ptpn369 Ptpn370 Ptpn371 Ptpn372 Ptpn373 Ptpn374 Ptpn375 Ptpn376 Ptpn377 Ptpn378 Ptpn379 Ptpn380 Ptpn381 Ptpn382 Ptpn383 Ptpn384 Ptpn385 Ptpn386 Ptpn387 Ptpn388 Ptpn389 Ptpn390 Ptpn391 Ptpn392 Ptpn393 Ptpn394 Ptpn395 Ptpn396 Ptpn397 Ptpn398 Ptpn399 Ptpn400 Ptpn401 Ptpn402 Ptpn403 Ptpn404 Ptpn405 Ptpn406 Ptpn407 Ptpn408 Ptpn409 Ptpn410 Ptpn411 Ptpn412 Ptpn413 Ptpn414 Ptpn415 Ptpn416 Ptpn417 Ptpn418 Ptpn419 Ptpn420 Ptpn421 Ptpn422 Ptpn423 Ptpn424 Ptpn425 Ptpn426 Ptpn427 Ptpn428 Ptpn429 Ptpn430 Ptpn431 Ptpn432 Ptpn433 Ptpn434 Ptpn435 Ptpn436 Ptpn437 Ptpn438 Ptpn439 Ptpn440 Ptpn441 Ptpn442 Ptpn443 Ptpn444 Ptpn445 Ptpn446 Ptpn447 Ptpn448 Ptpn449 Ptpn450 Ptpn451 Ptpn452 Ptpn453 Ptpn454 Ptpn455 Ptpn456 Ptpn457 Ptpn458 Ptpn459 Ptpn460 Ptpn461 Ptpn462 Ptpn463 Ptpn464 Ptpn465 Ptpn466 Ptpn467 Ptpn468 Ptpn469 Ptpn470 Ptpn471 Ptpn472 Ptpn473 Ptpn474 Ptpn475 Ptpn476 Ptpn477 Ptpn478 Ptpn479 Ptpn480 Ptpn481 Ptpn482 Ptpn483 Ptpn484 Ptpn485 Ptpn486 Ptpn487 Ptpn488 Ptpn489 Ptpn490 Ptpn491 Ptpn492 Ptpn493 Ptpn494 Ptpn495 Ptpn496 Ptpn497 Ptpn498 Ptpn499 Ptpn500 Ptpn501 Ptpn502 Ptpn503 Ptpn504 Ptpn505 Ptpn506 Ptpn507 Ptpn508 Ptpn509 Ptpn510 Ptpn511 Ptpn512 Ptpn513 Ptpn514 Ptpn515 Ptpn516 Ptpn517 Ptpn518 Ptpn519 Ptpn520 Ptpn521 Ptpn522 Ptpn523 Ptpn524 Ptpn525 Ptpn526 Ptpn527 Ptpn528 Ptpn529 Ptpn530 Ptpn531 Ptpn532 Ptpn533 Ptpn534 Ptpn535 Ptpn536 Ptpn537 Ptpn538 Ptpn539 Ptpn540 Ptpn541 Ptpn542 Ptpn543 Ptpn544 Ptpn545 Ptpn546 Ptpn547 Ptpn548 Ptpn549 Ptpn550 Ptpn551 Ptpn552 Ptpn553 Ptpn554 Ptpn555 Ptpn556 Ptpn557 Ptpn558 Ptpn559 Ptpn560 Ptpn561 Ptpn562 Ptpn563 Ptpn564 Ptpn565 Ptpn566 Ptpn567 Ptpn568 Ptpn569 Ptpn570 Ptpn571 Ptpn572 Ptpn573 Ptpn574 Ptpn575 Ptpn576 Ptpn577 Ptpn578 Ptpn579 Ptpn580 Ptpn581 Ptpn582 Ptpn583 Ptpn584 Ptpn585 Ptpn586 Ptpn587 Ptpn588 Ptpn589 Ptpn590 Ptpn591 Ptpn592 Ptpn593 Ptpn594 Ptpn595 Ptpn596 Ptpn597 Ptpn598 Ptpn599 Ptpn600 Ptpn601 Ptpn602 Ptpn603 Ptpn604 Ptpn605 Ptpn606 Ptpn607 Ptpn608 Ptpn609 Ptpn610 Ptpn611 Ptpn612 Ptpn613 Ptpn614 Ptpn615 Ptpn616 Ptpn617 Ptpn618 Ptpn619 Ptpn620 Ptpn621 Ptpn622 Ptpn623 Ptpn624 Ptpn625 Ptpn626 Ptpn627 Ptpn628 Ptpn629 Ptpn630 Ptpn631 Ptpn632 Ptpn633 Ptpn634 Ptpn635 Ptpn636 Ptpn637 Ptpn638 Ptpn639 Ptpn640 Ptpn641 Ptpn642 Ptpn643 Ptpn644 Ptpn645 Ptpn646 Ptpn647 Ptpn648 Ptpn649 Ptpn650 Ptpn651 Ptpn652 Ptpn653 Ptpn654 Ptpn655 Ptpn656 Ptpn657 Ptpn658 Ptpn659 Ptpn660 Ptpn661 Ptpn662 Ptpn663 Ptpn664 Ptpn665 Ptpn666 Ptpn667 Ptpn668 Ptpn669 Ptpn670 Ptpn671 Ptpn672 Ptpn673 Ptpn674 Ptpn675 Ptpn676 Ptpn677 Ptpn678 Ptpn679 Ptpn680 Ptpn681 Ptpn682 Ptpn683 Ptpn684 Ptpn685 Ptpn686 Ptpn687 Ptpn688 Ptpn689 Ptpn690 Ptpn691 Ptpn692 Ptpn693 Ptpn694 Ptpn695 Ptpn696 Ptpn697 Ptpn698 Ptpn699 Ptpn700 Ptpn701 Ptpn702 Ptpn703 Ptpn704 Ptpn705 Ptpn706 Ptpn707 Ptpn708 Ptpn709 Ptpn710 Ptpn711 Ptpn712 Ptpn713 Ptpn714 Ptpn715 Ptpn716 Ptpn717 Ptpn718 Ptpn719 Ptpn720 Ptpn721 Ptpn722 Ptpn723 Ptpn724 Ptpn725 Ptpn726 Ptpn727 Ptpn728 Ptpn729 Ptpn730 Ptpn731 Ptpn732 Ptpn733 Ptpn734 Ptpn735 Ptpn736 Ptpn737 Ptpn738 Ptpn739 Ptpn740 Ptpn741 Ptpn742 Ptpn743 Ptpn744 Ptpn745 Ptpn746 Ptpn747 Ptpn748 Ptpn749 Ptpn750 Ptpn751 Ptpn752 Ptpn753 Ptpn754 Ptpn755 Ptpn756 Ptpn757 Ptpn758 Ptpn759 Ptpn760 Ptpn761 Ptpn762 Ptpn763 Ptpn764 Ptpn765 Ptpn766 Ptpn767 Ptpn768 Ptpn769 Ptpn770 Ptpn771 Ptpn772 Ptpn773 Ptpn774 Ptpn775 Ptpn776 Ptpn777 Ptpn778 Ptpn779 Ptpn780 Ptpn781 Ptpn782 Ptpn783 Ptpn784 Ptpn785 Ptpn786 Ptpn787 Ptpn788 Ptpn789 Ptpn790 Ptpn791 Ptpn792 Ptpn793 Ptpn794 Ptpn795 Ptpn796 Ptpn797 Ptpn798 Ptpn799 Ptpn800 Ptpn801 Ptpn802 Ptpn803 Ptpn804 Ptpn805 Ptpn806 Ptpn807 Ptpn808 Ptpn809 Ptpn810 Ptpn811 Ptpn812 Ptpn813 Ptpn814 Ptpn815 Ptpn816 Ptpn817 Ptpn818 Ptpn819 Ptpn820 Ptpn821 Ptpn822 Ptpn823 Ptpn824 Ptpn825 Ptpn826 Ptpn827 Ptpn828 Ptpn829 Ptpn830 Ptpn831 Ptpn832 Ptpn833 Ptpn834 Ptpn835 Ptpn836 Ptpn837 Ptpn838 Ptpn839 Ptpn840 Ptpn841 Ptpn842 Ptpn843 Ptpn844 Ptpn845 Ptpn846 Ptpn847 Ptpn848 Ptpn849 Ptpn850 Ptpn851 Ptpn852 Ptpn853 Ptpn854 Ptpn855 Ptpn856 Ptpn857 Ptpn858 Ptpn859 Ptpn860 Ptpn861 Ptpn862 Ptpn863 Ptpn864 Ptpn865 Ptpn866 Ptpn867 Ptpn868 Ptpn869 Ptpn870 Ptpn871 Ptpn872 Ptpn873 Ptpn874 Ptpn875 Ptpn876 Ptpn877 Ptpn878 Ptpn879 Ptpn880 Ptpn881 Ptpn882 Ptpn883 Ptpn884 Ptpn885 Ptpn886 Ptpn887 Ptpn888 Ptpn889 Ptpn890 Ptpn891 Ptpn892 Ptpn893 Ptpn894 Ptpn895 Ptpn896 Ptpn897 Ptpn898 Ptpn899 Ptpn900 Ptpn901 Ptpn902 Ptpn903 Ptpn904 Ptpn905 Ptpn906 Ptpn907 Ptpn908 Ptpn909 Ptpn910 Ptpn911 Ptpn912 Ptpn913 Ptpn914 Ptpn915 Ptpn916 Ptpn917 Ptpn918 Ptpn919 Ptpn920 Ptpn921 Ptpn922 Ptpn923 Ptpn924 Ptpn925 Ptpn926 Ptpn927 Ptpn928 Ptpn929 Ptpn930 Ptpn931 Ptpn932 Ptpn933 Ptpn934 Ptpn935 Ptpn936 Ptpn937 Ptpn938 Ptpn939 Ptpn940 Ptpn941 Ptpn942 Ptpn943 Ptpn944 Ptpn945 Ptpn946 Ptpn947 Ptpn948 Ptpn949 Ptpn950 Ptpn951 Ptpn952 Ptpn953 Ptpn954 Ptpn955 Ptpn956 Ptpn957 Ptpn958 Ptpn959 Ptpn960 Ptpn961 Ptpn962 Ptpn963 Ptpn964 Ptpn965 Ptpn966 Ptpn967 Ptpn968 Ptpn969 Ptpn970 Ptpn971 Ptpn972 Ptpn973 Ptpn974 Ptpn975 Ptpn976 Ptpn977 Ptpn978 Ptpn979 Ptpn980 Ptpn981 Ptpn982 Ptpn983 Ptpn984 Ptpn985 Ptpn986 Ptpn987 Ptpn988 Ptpn989 Ptpn990 Ptpn991 Ptpn992 Ptpn993 Ptpn994 Ptpn995 Ptpn996 Ptpn997 Ptpn998 Ptpn999 Ptpn1000