

Supplemental Material Table of Contents

Supplementary Figures

S1. Aging is associated with increased kidney CLCA1 expression in marmosets. Immunoblotting of kidney cortex of young and aged female marmosets showed increased expression of the 72 kDa fragment of CLCA1, probably the N-terminal fragment. A trend towards increase in the expression of the whole 130 kDa molecule was seen in the same animals.

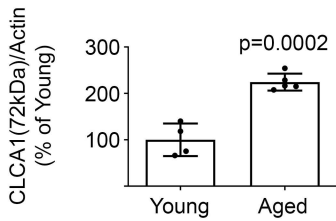
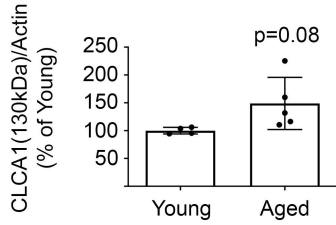
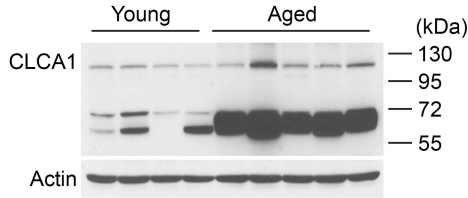
S2. Rapamycin abolished the increase in phosphorylation of p70S6 kinase in hCLCA1 overexpressing cells indicating inhibition of mTORC1.

Supplementary Tables

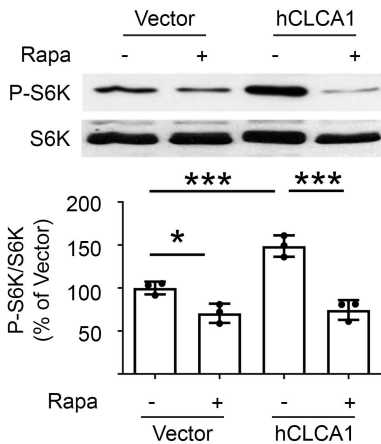
Table 1. List of mRNAs that were differentially regulated in renal cortex of aged mice.

Table 2. Top hits on RNA Seq and their possible functions.

Supplementary Figure S1



Supplementary Figure S2



Supplementary Table 1

List of mRNAs that were differentially regulated in renal cortex of aged mice

id	baseMean	baseMean2	Group	Group	Y	baseMean2	Group	Group	O	FC	Zowr1	log2FC_Zowr1	pval	geneName
Dsp	1833.02654	1833.02654	268	4383271		0.10520545				0.002038271	-2.815E-48	4.76E-44	D site albumin precursor binding protein	
Cndp2	18768.89938	29859.52537	7677	87339		0.257129691				-1.959431884	3.72E-25	3.39E-21	CNDP dipeptidase 2 (metalloproteinase M20 family) chloride channel accessory 1	
Claa1	418.327617	195.4522148	641	2030193		1.713665286				8.10E-20	4.92E-16		viopipe-like 2 (Drosophila)	
Ype2	682.6427859	307.7383851	507	547187		3.436513733				1.780945725	3.19E-18	1.46E-14	aryl hydrocarbon receptor nuclear translocator-like gene function protein, beta 2	
Amil	534.3858476	580.3858476	580	3858476		2.19388732				-1.452E-08	1.52E-08		nuclear factor, interleukin 3, regulated	
Glb2	2238.481135	3202.09596	1274	862675		0.398133361				-1.328676329	7.32E-16	2.25E-12		
Nli3	193.758882	41.84139841	345	750378		8.263356177				0.046727554	8.66E-15	2.55E-11		
Slc16a14	1951.855307	3170.863062	732	8475515		0.231119268				-2.113920552	1.39E-14	3.17E-11	solute carrier family 16 (monocarboxylic acid transporters), member 14	
Gm906	48.0132846	83.57120313	12	45527379		0.149307896				-2.746249171	2.55E-14	5.17E-11	predicted gene 308	
Tmem189	178.720272	301.725566	77	81949373		0.257011506				-1.955019588	4.29E-14	7.81E-11	transmembrane protein 169	
Ndrd1	55689.10339	32387.72184	78990	48493		2.438902165				1.286231887	8.44E-14	1.07E-10	N-myc downstream regulated gene 1	
Akr1c13	356.9862268	193.1849288	520	7515246		1.430621161				-1.430621161	1.14E-13	1.73E-10	aldo-keto reductase family 1, member C13	
Nuaf19	11940.37592	19677.27912	5203	4372722		0.278599077				-1.843737617	1.83E-13	2.56E-10	nucleoside diphosphate linked moiety X-type motif 19	
Pnt5	200.5901269	297.7277547	103	2904991		0.346829359				-1.52729816	1.87E-12	1.91E-09	aspartoacylase (aminocyclase) 3	
Acsm3	8521.756246	14920.21303	2123	299466		1.42310265				-2.812888368	2.35E-12	2.68E-09	acyl-CoA synthetase medium-chain family member 3	
Csaa	2942.984882	4288.492332	1597	477432		0.372503273				-1.424674992	4.80E-12	5.14E-09	cysteine sulfenic acid decarboxylase	
Cot10b	746.9477279	1069.59196	424	3037597		0.396869846				-1.333890903	7.86E-12	7.96E-09	comzyme C10B	
Gm953	578.456766	1105.95482	250	917126		0.228715598				-2.140250568	1.22E-11	1.13E-08	predicted gene 853	
Dio1	223.236307	357.912532	88	55636174		0.24742018				-2.014954202	1.24E-11	1.13E-08	deiodinase, iodothyronine, type I	
Gna14	318.5771489	450.9807839	186	5335139		0.413617432				-1.273631104	2.17E-11	1.88E-08	guanine nucleotide binding protein, alpha 14	
Cot15a1	561.942779	839.4688946	284	4166683		0.338805482				-1.561470877	3.07E-11	2.54E-08	collagen, type XV, alpha 1	
Fw3	41.38870721	12.6742344	70	72269398		5.868683278				2.525746177	3.37E-11	2.67E-08	flavininogen beta chain	
Cst3	344.438169	544.438169	138	117863		0.253689701				-1.378588693	3.82E-11	3.82E-08	carbohydrate (N-acetylglucosaminyl) sulfotransferase 7	
Tqb	326.873087	461.408878	192	3391994		0.416853776				-1.262386861	6.38E-11	4.65E-08	IRNA-VW synthesizing protein 3 homolog (S. cerevisiae)	
Osta	1175.047776	1803.655159	504	4403932		0.279677639				-1.838167826	8.02E-11	5.62E-08	NA	
Hsp90aa1	4623.501767	6336.637107	2911	366428		0.459522283				-1.217932723	3.03E-10	1.94E-07	heat shock protein 90, alpha (cytosolic), class A member 1	
Slc30a1	1771.815176	6242.672929	3118	850223		0.485462939				-1.042526192	3.05E-10	1.94E-07	solute carrier organic anion transporter family, member 3a1	
B4gat5	4034.772252	6426.691967	1642	852536		0.255629575				-1.967373337	3.08E-10	1.94E-07	UDP-Gal:beta(1-3)GalNAc beta 1,4-galactosyltransferase, polypeptide 5	
Fzrb	341.4334484	492.066649	190	7702918		0.387668376				-1.367105024	4.23E-10	2.57E-07	frizzled-related protein 2	
Ccdp1	1049.424182	1498.50862	690	2676818		0.490044831				-1.029104358	6.58E-10	3.87E-07	coiled-coil domain containing 91	
Mga2a	455.9402914	870.8608744	41	27494827		0.047400389				-1.686E-09	9.56E-07		major facilitator superfamily domain containing 2A	
Abs1a	286.7424263	513.0981726	172	328665		2.311535072				-1.203895831	2.04E-09	1.13E-06	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	
Oxct1	21110.75281	27891.88304	14329	62258		0.513756011				-0.960044725	4.37E-09	2.34E-06	3-oxoacid CoA transferase 1	
Gclm	3685.937386	4917.811895	2454	062877		0.499015198				-1.002844424	4.89E-09	2.55E-06	glutamate-cysteine liase, modifier subunit	
Tlcc2	93.12675788	138.8447953	47	40872044		0.341451189				-1.550248738	5.64E-09	2.84E-06	TLC domain containing 2	
Gpc3	910.38745	486.99207	1353	28182		2.898825482				1.535466226	5.77E-09	1.84E-06	glypican 3	
Aops	8510.957798	13114.91678	3908	398821		0.297049865				-1.747057927	6.44E-09	3.09E-06	alkylglycerone phosphate synthase	
Tmco3	1158.986446	1615.991442	701	9814501		0.434396762				-1.202914745	7.18E-09	3.35E-06	transmembrane and coiled-coil domains 3	
Camd1	143.237489	67.0715332	219	4043646		3.271199481				-1.709819739	1.42E-08	6.32E-06	CLB and Sushi motifs domains 1	
Cd6	108.7293301	58.53189045	159	6266787		2.721569223				-1.444438972	2.04E-08	8.83E-06	chemokine (C-C motif) ligand 6	
Absc1	1971.332128	3371.925632	2450	611103		0.893252532				0.915433403	2.45E-08	1.01E-05	ATP-binding cassette, sub-family A (ABC1), member 1	
Slc16a9	4049.367191	5348.25285	2750	192998		0.51149484				-0.959612963	2.45E-08	1.01E-05	solute carrier family 16 (monocarboxylic acid transporters), member 9	
Atp1a	31129.32621	49223.52069	13035	13173		0.264815124				-1.016426287	2.97E-08	1.20E-05	ATPase, class VI, type 11A	
Itd4	349.2278072	538.5088446	159	9487698		0.297022704				-1.751354784	3.17E-08	1.26E-05	interleukin 34	
31145C21R1k	133.4878179	76.8787479	76	8787479		0.393828454				-1.393828454	3.30E-08	1.27E-05	RIKEN cDNA 31145C21R1k gene	
Hsd1b2	1072.02048	1399.452911	744	608048		0.532070813				-0.91039829	5.17E-08	1.91E-05	interferon-related developmental regulator 2	
Ilh11hdh	827.6300654	1083.506139	511	7539916		0.527688742				-0.92224089	5.44E-08	1.91E-05	histone cluster 1, H4h	
9030619P08Rk	167.0246702	285.6471323	148	40202807		0.169448118				-2.561095552	5.56E-08	1.91E-05	lymphocyte antigen 6 complex pseudogene	
Ces2b	124.074298	271.895435	30	25314295		0.13884247				-2.848479157	5.57E-08	1.91E-05	carboxylesterase 2B	
Cnv45	607.256928	1144.37707	155	7772357		2.852189257				1.407183757	8.45E-08	1.91E-05	cardiomyopathy-associated 5	
Fnh1b	4661.950777	2967.207716	6356	693838		2.142315081				1.09917068	8.56E-08	1.91E-05	folate hydrolase 1	
Hnf1b	5497.863626	7926.427145	3069	300106		0.387223657				-1.3688781	7.63E-08	2.53E-05	HNF1b homeobox B	
Smpn2f	505.264284	6554.455073	3548	4073495		0.541322422				-0.885439948	8.07E-08	2.63E-05	serine (or cysteine) peptidase inhibitor, clade F, member 2	
Cnv45	607.256928	1144.37707	155	7772357		2.852189257				1.407183757	8.45E-08	1.91E-05	male enzyme 1, NAD(P)-dependent, cytosolic	
Mogat1	1209.531887	1664.688809	754	3749656		0.561627554				-1.141898905	1.01E-07	3.13E-05	monoglycerol O-acyltransferase 1	
Dusp9	132.4164147	187.1092329	77	72359659		0.415391562				-1.267456183	1.19E-07	3.62E-05	dual specificity phosphatase 9	
Pk3	839.6521456	1165.472545	513	8317468		0.440878465				-1.181547085	1.24E-07	3.71E-05	pyruvate dehydrogenase kinase, isoenzyme 3	
Sued1	601.1074849	1123.563156	490	6397734		0.436681971				-1.195345127	1.76E-07	5.03E-05	sushi domain containing 3	
Gpc2b	9559.99228	1414.37707	1727	8787479		0.251745044				-1.507397999	1.87E-07	5.99E-05	UDP-glucuronosyltransferase 2 family, polypeptide B3B	
Ucp2	2362.02101	35302.45324	11221	58879		0.317869943				-1.653491491	1.81E-07	5.09E-05	kidney expressed gene 1	
Pde3b	31.019101	510.235747	951	8024673		0.809498252				2.25E-07	6.20E-05		phosphodiesterase 3B, cGMP-inhibited	
Amacr	3263.207055	4695.102236	1831	311874		0.390047284				-1.588290629	2.31E-07	6.28E-05	alpha-methylacyl-CoA racemase	
Smpn2f	505.264284	6554.455073	3548	4073495		0.541322422				-1.148140478	2.52E-07	6.76E-05	spermatogenesis associated, sperm-rich 2-like	
Gm1534b	344.438169	544.438169	138	117863		0.253689701				-1.378588693	2.78E-07	2.95E-05	predicted gene 853	
Cv56e1	190.489342	770.5983821	410	3635043		0.53252578				-0.909076728	2.85E-07	7.29E-05	cytochrome b-561	
0610012H03Rk	1151.195007	2773.840372	1450	549643		0.521810409				-0.938223027	2.88E-07	7.29E-05	NA	
Cot1a1	468.921889	653.519914	284	1234658		0.434738696				-1.20171321	3.14E-07	7.83E-05	collagen, type I, alpha 1	
Ces1	1435.84289	187.8028938	95	8051633		0.502516383				-0.988510091	3.14E-07	7.83E-05	carboxylesterase 1	
Cor	6093.837473	7757.699694	4429	975251		0.571042374				-0.808330293	3.58E-07	8.63E-05	P450 (cytochrome) oxidoreductase	
Cd3a1	682.616583	960.2785711	404	9447455		0.421695076				-1.245727917	3.60E-07	8.63E-05	collagen, type II, alpha 1	
Reep5	1640.305997	2096.744775	1184	333719		0.5647002				-0.824442952	3.81E-07	9.03E-05	receptor accessory protein 5	
Vwat1	153.627237	432.617279	43	2163081		0.453208681								

Tnfrsf12a	251.8152088	330.2468148	173.3836028	0.525012188	-0.92957718	9.58E-06	0.001196184	tumor necrosis factor receptor superfamily, member 12a
Mpv17l	643.7069371	971.138287	316.275568	0.329135009	-1.603248694	1.03E-05	0.001274313	Mpv17 transgene, kidney disease mutant-like
Sema4q	597.0269941	1171.337339	702.7218586	0.599531242	-0.737130832	1.06E-05	0.001309924	sema domain, immunoglobulin domain (D1), transmembrane domain (TM) and short cytoplasmic domain. (semaforin) 4G
Sexn1	2408.926542	3974.12127	1934.536634	0.84555968	-0.77145515	1.13E-05	0.001346115	sexn domain
Pl4ka	4985.68973	6150.926292	3820.453167	0.621118346	-0.687059213	1.21E-05	0.001469428	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
Adams1	1740.789903	2164.802724	1316.77082	0.602866549	-0.717222419	1.27E-05	0.00153251	a disintegrin-like and metalloprotease (resolysin type) with thrombospondin type 1 motif, 1
B3gatl5	1014.822234	1347.15521	686.6952377	0.511636235	-0.966898954	1.29E-05	0.001469954	UDP-Gal beta1:3GalNAc beta 1-3-galactosyltransferase, polypeptide 5
Km5b	453.827055	502.933857	262.168016	0.426168016	-1.23052772	1.43E-05	0.00160121	potassium channel, beta 5
181006419Rik	537.4070224	1047.800035	627.8049921	0.599159743	-0.738874041	1.46E-05	0.001707086	NA
Hbecf	280.425025	362.0289871	198.8210628	0.549185479	-0.864634164	1.46E-05	0.001707086	heparin-binding EGF-like growth factor
Sct22a12	22703.6449	27882.5029	17524.78889	0.628522732	-0.669963171	1.49E-05	0.001728265	solute carrier family 22 (organic anion/cation transporter), member 12
Spin8	141.4284491	187.8537327	90.0031656	0.505729454	-0.983260291	1.58E-05	0.001820596	serine peptidase inhibitor, Kazal type 8
Serpinf2	1056.95245	1369.39387	573.021103	0.714461459	0.80208831	1.61E-05	0.001846171	serine (or cysteine) peptidase inhibitor, clade E, member 2
Hspd1	6576.95165	8090.320883	5073.58575	0.627840993	-0.671406855	1.63E-05	0.001846171	heat shock protein 1 (chaperonin)
Asergl1	198.428361	117.5139202	279.345752	2.377129036	1.249202018	1.64E-05	0.001846171	asparaginase like 1
Sct26a6	123.678518	167.1205884	80.2144749	0.480111088	-1.055859947	1.64E-05	0.001846171	solute carrier family 26, member 6
Elavl1	1238.12872	1517.854424	940.3929194	0.619554092	-0.696987848	1.73E-05	0.001928328	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, vesel1-like 1) citron
Cit	365.5173889	504.5804242	226.4543554	0.448797348	-1.15569434	1.77E-05	0.001955563	NA
1500011B03Rik	115.7388224	75.67614015	155.8015047	2.058792961	1.04179855	1.79E-05	0.001955563	RIKEN cDNA 1500011B03 gene
Ph1r	8167.09347	10118.28176	6215.916929	0.614323451	-0.702925191	1.79E-05	0.001955563	parathyroid hormone 1 receptor
Lag3	7583.283156	9530.588778	5175.97735	0.543091167	-0.880733988	1.79E-05	0.001955563	leucine aminopeptidase 3
Azn1l	3223.87912	3971.380007	2478.399203	0.62355222	-0.881417243	1.93E-05	0.002092886	antimycin inhibitor 1
Unc13c	90.92146462	124.058553	57.7890739	0.465826781	-1.102135111	1.95E-05	0.00209342	unc-13 homolog C (C. elegans)
Tsk1	1466.100395	1811.379508	1120.821283	0.618766679	-0.692532586	1.95E-05	0.00209342	thiamine pyrophosphatase
Fam55c	704.2304122	959.1181373	449.347451	0.468436796	-1.039898007	2.01E-05	0.002145345	NA
Uchl1	1553.389175	2233.987167	853.9387652	0.673835662	-1.33138864	2.03E-05	0.002150559	3-hydroxybutyrate dehydrogenase, type 1
Ect2	70.3603625	100.533734	40.2598909	0.40056522	-1.320251858	2.05E-05	0.002154306	ect2 oncogene
Pxovyl1	142.5171427	188.360256	96.67402951	0.513240062	-0.96239407	2.11E-05	0.002204969	prenylcysteine oxidase 1 like
Pag9l	1903.758528	2345.795918	1461.721138	0.623123745	-0.682490301	2.13E-05	0.002217337	progesterin and adipon receptor family member IX
Hes6	676.5940737	846.8939367	506.2882107	0.597813495	-0.742326251	2.20E-05	0.002275881	hair and enhancer of split 6
Fhcl1	125.3072039	335.844168	168.0456982	0.623532728	1.02537228	2.23E-05	0.002297234	proline 5-hydroxylase
Sh3bp2	363.4554178	585.8884306	314.0224051	0.240689385	-2.054701571	2.54E-05	0.00259676	SH3 domain binding protein 2
Tmem189	2598.9031	3318.327251	1879.478949	0.566393489	-0.820123414	2.56E-05	0.002601825	transmembrane protein 189
Prr15l	1056.563023	1318.244143	812.8819035	0.616638875	-0.697499911	2.60E-05	0.002609439	proline rich 15-like
Uchl1	145.321855	195.635488	82.6233719	0.46221618	-1.602816	2.63E-05	0.002609439	transglutaminase 1, K polypeptide
D1H2P2880E	596.1088355	1113.214034	679.0038332	0.609949132	-0.712339165	2.61E-05	0.002609439	NA
Glt1	2367.327706	3054.350023	1680.30539	0.550135177	-0.86214194	2.71E-05	0.0026955	galactosidase, beta 1
Apln	154.2493916	204.879766	103.620665	0.505760296	-0.983474131	2.72E-05	0.002697609	apelin
A464131	1115.552696	1380.205274	850.9001183	0.616520284	-0.697821153	2.84E-05	0.00279287	expressed sequence A464131
At2g243	425.937249	673.240041	278.629817	1.72602373	0.78451917	2.87E-05	0.002807234	AT2g243.2-like transposon, ubiquitous transmembrane protein 176B
Tmem176b	8620.215414	10682.28941	6558.144422	0.613926582	-0.703861957	2.92E-05	0.002814768	NA
4931417G12Rik	39.12046329	58.38181851	19.85910806	0.340159121	-1.555719322	3.01E-05	0.002844429	NA
Cxd12	2958.39882	2287.044171	3629.757169	1.587097918	0.66639114	3.36E-05	0.003201515	chemokine (C-X-C motif) ligand 12
Sct22a6	2800.309086	473.2353009	67.38289109	0.184649885	-2.437134662	3.40E-05	0.003227796	solute carrier family 22 (organic cation transporter), member 26
Pxov1	1983.98425	2603.84025	1603.84025	0.510733816	0.645705	3.42E-05	0.003219314	proctin and adipon receptor family member VII
1700021F05Rik	403.943838	513.5128163	306.3748613	0.59625654	-0.745102358	3.46E-05	0.003246927	RIKEN cDNA 1700021F05 gene
Cadm2	33.23991567	15.85224457	51.60758677	3.255538138	1.70289604	3.47E-05	0.003246927	cell adhesion molecule 2
Bcl6b	122.7173387	183.1976277	82.23704959	0.503910815	-0.988759783	3.59E-05	0.003340394	B cell CLL/lymphoma 6, member B
Uchl1	1781.932929	2233.987167	853.9387652	0.673835662	-1.16539412	3.65E-05	0.003375928	Uchl1, beta 2
Amp19	1829.83298	2238.946887	1240.71897	0.634546787	-0.656199008	3.67E-05	0.003375928	cAMP-regulated phosphoprotein 19
Mat2a	7669.189865	9663.749771	5564.629959	0.583929789	-0.776133194	3.72E-05	0.003404722	methionine adenosyltransferase II, alpha
Sypl2	1485.081658	1970.038911	1000.125125	0.507687887	-0.679843082	3.79E-05	0.003454743	synaptophysin-like 2
Acln1a7	707.0700961	914.64223	472.9830401	0.792919309	1.329448366	3.87E-05	0.003495425	aldehyde dehydrogenase family 1, subfamily A7
Cd88	4038.115711	5294.163676	4680.926685	0.488290397	-1.004707807	3.93E-05	0.003508911	CD88 antigen
Sepl1	10118.41294	52829.30799	27407.5179	0.518793809	-0.946768832	3.91E-05	0.003508911	selenoprotein P, plasma, 1
Wsp1	128.4619998	186.8623263	70.0607326	0.37480377	-1.141503866	4.02E-05	0.003573104	WNT1 inducible signaling pathway protein 1
Sw12	170.5026974	223.7390087	117.2683386	0.524112326	-0.932027282	4.07E-05	0.003602847	synovialtannin XII
Cntn6	4540.93868	5953.78822	3259.162396	0.621619396	-0.738109369	4.21E-05	0.003704883	CKL1-like MARVEL transmembrane domain containing 6
1300022Q09Rik	228.077061	354.2952363	161.8601759	0.456851121	-1.130204	4.25E-05	0.003724205	NA
Apol2	523.0743219	626.8281259	1019.320491	1.626156206	0.701465847	4.29E-05	0.003737425	adipator protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2
2610528J11Rik	910.6790961	1122.474235	698.8839573	0.622628062	-0.883557495	4.36E-05	0.003785022	RIKEN cDNA 2610528J11 gene
Mefm1	313.7406059	395.655266	231.8256443	0.885927891	-0.71204894	4.45E-05	0.003844853	meis1m, alk1 cell differentiation regulator-like
Tm6d7	614.494266	834.240041	365.2781636	0.64476538	-0.749812692	4.57E-05	0.003925186	ribonucleic protein 47
Dnaaj4	539.3559941	685.3703558	393.3416323	0.573911067	-0.8011099	4.65E-05	0.003975201	DnaJ4 heat shock protein family (Hsp40), member A4
Ccrn4l	277.4183276	358.1259951	196.71066	0.549277804	-0.864392101	4.77E-05	0.004059974	NA
Rm2a	1118.725523	1888.23832	349.213215	1.184941721	-2.443857374	5.13E-05	0.004351902	ring finger protein 24
Uchl1	614.0882168	834.240041	365.2781636	0.621619396	-0.738109369	5.24E-05	0.004424011	stimulated by retinoic acid gene 6
Tmem176a	6463.348372	8135.844751	4790.851994	0.588587532	-0.764000905	5.30E-05	0.004455006	transmembrane protein 176A
Rhhb1l	1804.771576	1970.577714	2529.965438	2.343476904	1.228650676	5.40E-05	0.004515686	Rho-related BTB domain containing 1
Skiv2l	1928.43836	2189.826914	1395.049805	0.637059393	-0.650002123	5.72E-05	0.00475938	superkiller viralicidal activity 2-like 2 (S. cerevisiae)
Sct4a2	539.0418186	670.1033689	407.1324963	0.606896781	-0.720477214	5.77E-05	0.004779851	solute carrier family 41, member C12
Hf2p2	125.3072039	335.844168	168.0456982	0.623532728	1.02537228	5.83E-05	0.004819726	interferon regulator 1, binding protein 2
Pnc1a	4888.74586	5578.304676	3599.092262	0.645184187	-0.632712015	5.92E-05	0.004841295	protease, serine 8 (proteinase)
Uros	317.2630566	398.3046076	236.2214037	0.593067213	-0.753732478	5.97E-05	0.00485327	uroporphyrinogen III synthase
Eci3	2332.752119	2960.001435	1705.502903	0.5761831	-0.795400749	6.22E-05	0.005026831	enoyl-Coenzyme A delta isomerase 3
Uchl1	680.9295181	834.240041	365.2781636	0.621619396	-0.738109369	6.24E-05	0.005026831	aldehyde dehydrogenase family 1, subfamily A1
Gm1653	36.43608021	58.81804758	13.95411284	0.236833963	-2.078912138	6.28E-05	0.005041226	predicted gene 1653
Csf1r	804.3075935	1075.633879	532.9813078	0.495504389	-1.013030259	6.43E-05	0.005137377	colony stimulating factor 1 receptor
Tnfrsf121	8858.253452	10732.57282	6983.934079	0.650723195	-0.619884115	6.62E-05	0.005242626	tumor necrosis factor receptor superfamily, member 21
Akr1c12	1121.5486974	149.4189103	193.6784938	3.919117782	1.970528931	6.93E-05	0.005436893	aldo-keto reductase family 1, member C12
Nr2f1	404.0882168	513.844751	252.913215	0.523984673	-1.210572884	7.24E-05	0.005477756	nucleic acid dephosphorylation (NAD) motif 8
Fbxo36	336.9514435	420.960647	252.913215	0.600838665	-0.734950438	7.29E-05	0.005570905	F-box protein 36
Pcdhga2	56.14083916	32.6382763	79.6785068	2.440653042	1.287267419	7.36E-05	0.005704995	protocadherin gamma subfamily A, 2
Tubat1	516.4402804	638.						

Emp44	1400.650878	1883.599574	1117.702202	0.663876513	-0.591031182	0.000205295	0.01234751	endoplasmic reticulum protein 44
Arhgap27	844.944239	1025.49273	864.394078	0.647876584	-0.626209078	0.000210485	0.012618	Rho GTPase activating protein 27
Nghn1	5893.652374	7222.518348	4694.7884	0.645551675	-0.631395511	0.000213047	0.012713688	neuronal glycerol-ester hydrolase 1
Sicd15	596.827464	629.83712	420.840112	0.639012294	-0.639012294	0.000213474	0.012713688	solute carrier family 8 (neurotransmitter transporter), member 15
Myc5a	1292.212669	1909.85475	678.5705878	0.35604528	-1.48986738	0.000215451	0.012728361	myosin Va
Pecr	4859.236651	6549.357367	3237.225936	0.494282089	-1.016590388	0.000221821	0.013124906	peroxisomal trans-2-enoyl-CoA reductase
Aph1c1	185.562971	234.394809	136.712333	0.583337612	-0.777596998	0.000224589	0.013245688	hect
Nctd1	2125.323817	3725.323817	157.941424	1.505234234	0.589999258	0.000225743	0.01329254	neuropathological cellular transforming gene 1
Pxh1	6296.063714	8793.945948	3748.18148	0.42678168	-1.226878369	0.000232554	0.013627202	alcohol dehydrogenase 1 (class 1)
Rares2	341.5768394	259.1586898	423.9949799	1.636043791	0.710213164	0.000240799	0.014065156	retinoic acid receptor responder (tazarotene induced)
Mcd2	2178.682606	2813.042117	1740.323095	0.666014177	-0.586375208	0.000241587	0.014180657	multiple coagulation factor deficiency 2
Holo2	212.0146306	286.087873	177.941424	0.593598211	-0.75251426	0.000242081	0.014197974	indoleamine 2,3-dioxygenase 2
Csrl1	428.93969	1225.82372	1882.91507	1.54225157	0.62592148	0.000242763	0.01423889	cellular receptor of 15-oxo- Δ^2 -steroid genes 1
Selenb2	358.589775	362.734165	159.9841784	0.441051668	-1.189000421	0.000249583	0.01439368	selenium binding protein 2
Sic6a9	442.3047613	563.6714775	320.9380451	0.569307038	-0.812599748	0.000253065	0.014548424	solute carrier family 6 (neurotransmitter transporter, glycine), member 9
1500001M20Rk	420.039175	417.5296845	252.5421456	1.711805638	0.777596998	0.000257049	0.014676071	NA
Fa1	554.29877	6753.663138	4354.918616	0.644823191	-0.633024464	0.000257701	0.014676071	fatty acid CoA reductase 1
C3	948.0470663	509.9184193	1386.175713	2.71842644	1.44277179	0.000262641	0.014953814	complement component 3
Trpv4	2272.244693	2789.342376	1755.147011	0.629233265	-0.66833152	0.000264685	0.014933814	transient receptor potential cation channel, subfamily V, member 4
Sf6aanc2	2282.25973	2720.63259	1803.88687	0.663039499	-0.592232736	0.000269071	0.015134434	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetylglucosaminide alpha-2,6-sialyltransferase 2
Mlx	797.618195	963.9846073	631.386178	0.6503924	-0.610348965	0.00027075	0.015135413	MAX-like protein X
H2-Cst10	473.623386	355.6116088	592.095484	1.68748747	0.73732894	0.000271169	0.01521696	NA
Thsd4	270.012688	180.9718937	359.0606439	1.984068557	0.98461477	0.000276272	0.015349963	thrombospondin, type 1, domain containing 4
Tmem117	250.493271	312.7189917	188.2675504	0.602034272	-0.732082478	0.000278864	0.015395695	transmembrane protein 117
Cns711	180.0824976	192.8566662	106.306329	0.546028904	-0.872951829	0.000278785	0.015395695	centrosomal protein 57-like 1
hars1	474.04168532	371.2712725	642.14168532	0.63861725	-0.63861725	0.00028027	0.01540464	homocystadine adenylylase 1
Drd1	2704.61984	3251.305182	2157.334498	0.662611302	-0.590133007	0.000283189	0.015700464	discosoma domain receptor family 3
Cy2a5	5189.929816	2801.451398	7578.408234	2.705172126	1.435720393	0.000287251	0.015700464	cytochrome P450, family 2, subfamily A, polypeptide 5
Osmr	610.043573	477.5428854	742.5440293	1.554926378	0.636846274	0.00028775	0.015700464	oncostatin M receptor
Tiam2	253.5834741	180.7186189	326.4503312	1.80642217	0.85134337	0.000291183	0.015840232	T cell lymphoma invasion and metastasis 2
Ap2k1	428.93969	1171.7874	883.9351698	0.654131621	-0.21932929	0.000292928	0.016215195	apoptosis kinase 2
Lass5	548.8497624	670.6007051	427.0988198	0.636899006	-0.650884088	0.000295906	0.015954437	NA
Abcc4	3447.513235	1625.778876	5069.247594	3.118042478	1.640640582	0.000305192	0.016389317	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
Fuc2	737.010638	937.789563	550.261713	0.950594138	-0.759791057	0.000305771	0.016389317	fucosidase, alpha-L-2, plasma
Rnq1p1	252.108242	287.127685	687.231689	0.687231689	-0.598727228	0.000306739	0.016391513	reticulon 4 interacting protein 1
Sic3a1	2835.543334	3453.672527	2211.414141	0.640307998	-0.643162064	0.000315652	0.016770951	solute carrier family 33 (anion/cation transporter), member 1
Lgr4	7884.658124	6059.091611	9710.224636	1.602857526	0.680403153	0.000329021	0.017427505	leucine-rich repeat-containing G-protein-coupled receptor 4
Idp1	261.603672	338.109349	185.0979951	0.547500995	-0.86920064	0.000343842	0.018058133	isopentenyl-diphosphate delta isomerase
Slit1	1578.285909	1946.134738	1210.437083	0.621969826	-0.680583053	0.000359491	0.018354463	stress-induced phosphoprotein 1
Lpl	2045.33319	2374.98171	1255.89466	0.43691717	-1.19446743	0.000356824	0.019212095	lipoprotein lipase
Tmem125	312.1042444	390.0540221	234.1630868	0.600345081	-0.736128398	0.000363923	0.018948941	transmembrane protein 125
Znf830	575.9157169	698.4877064	453.3437275	0.649036087	-0.6236294	0.00038076	0.019546386	zinc finger protein 830
H2af	1322.707244	1672.401011	1113.014327	0.655519146	-0.58744274	0.000382283	0.019546386	H2A histone family, member J
Mycv	299.841133	116.0490416	327.633245	0.776392976	1.474992536	0.000386881	0.019745733	myelocytomatosis oncogene
Lchd	1987.619478	1987.619478	9871.949478	0.53693342	-0.60039076	0.00039076	0.019837162	lactate dehydrogenase D
Them4	482.8658242	587.9260691	377.8056154	0.642807354	-0.637990605	0.000397893	0.020142209	thioesterase superfamily member 4
Aplnr	77.35480062	110.4422305	44.2673072	0.400819238	-1.318978339	0.000405315	0.020461103	apelin receptor
Sac2b3	1876.691001	2365.964079	1387.417924	0.588407011	-0.770297427	0.000407143	0.020496652	SEC23 homolog B, COP11 coat complex component
Rit1	2101.1211	2484.98545	48.920284795	-0.92178523	-0.92178523	0.000413245	0.020496652	DD61 and C14orf138-interacting protein 1
Gen3	50.91923645	198.7430677	103.216612	0.519473018	-0.944879278	0.00042408	0.021040397	GAT3 protein-like 3
Rdh16	3666.343384	2767.638763	4565.048006	1.649437805	0.72194378	0.000431145	0.021409235	retinol dehydrogenase 16
Pdgfra	2657.706534	317.510728	197.912054	0.623342946	-0.681190183	0.000448472	0.022089053	platelet-derived growth factor, D polypeptide
Rabqta	916.593765	1108.786884	378.288263	0.665324947	-0.587868964	0.000451225	0.022166238	Rab geranyltransferase, a subunit
Sic182	428.93969	335.241363	522.1358175	1.557431554	0.639244354	0.000462199	0.022296333	solute carrier family 1 (renal glycerol phosphate transporter), member 2
Ncd1	295.576372	365.5675372	225.9477371	0.618073855	-0.694148855	0.00046926	0.022396333	neurofilament, differentiation and control 1
Cmi1	3527.958004	4527.95395	2215.162057	0.489219211	-1.031447038	0.000467767	0.022729332	NA
Znf2	2242.911051	2729.054194	1756.767908	0.64372747	-0.635477439	0.000472563	0.022834631	zinc and zinc finger 2
Mtp	1196.284262	1287.24404	117.284448	0.64481656	-0.711828363	0.000473938	0.022834631	microsomal triphosphatid phosphatase
Cy6	2451.643438	3589.735247	1313.551629	0.365918904	-1.450044538	0.000475521	0.02286517	cytochrome P450, family 5
Irf5	1169.190606	1428.454589	909.9266238	0.637000736	-0.650633057	0.000482701	0.023149341	interferon regulatory factor 5
Akr1c14	212.938393	4539.55951	1124.938393	0.24280783	-0.000267434	0.000482824	0.024008224	alko-keto reductase family 1, member C14
Ucd32	2008.42821	2409.744886	1599.30765	0.683939211	-0.590876397	0.000513694	0.024325597	UDP glycosyltransferase 3 family, polypeptide A2
Fam163a	2832.296192	3524.1284	174.007152	0.645739952	-1.041746982	0.000526624	0.024325597	family with sequence similarity 163, member A
Plod2	741.822528	931.1015514	552.5435045	0.593429904	-0.75280465	0.000516572	0.024325597	procollagenase 2, α -oxoalate 5-dioxygenase 2
BCO2B6585	3238.943893	3917.315526	254.572626	0.652123181	-0.616783592	0.000529924	0.024890035	cDNA sequence BCO2B585
Alz2a4	274.5854476	350.259796	198.9110992	0.567895892	-0.816301617	0.00053855	0.025213019	NA
Sic4a1	385.619205	481.321205	385.619205	0.651193862	-0.598638367	0.000548154	0.025213019	solute carrier family 46, member 1
Pncr1	1746.85922	1236.751768	2588.960076	1.524095827	0.927840397	0.000573291	0.026525193	proline-rich nuclear receptor coactivator 1
C8a	247.3954793	391.5251895	103.265789	0.263752555	-1.922743026	0.000592151	0.027389231	complement component 8, alpha polypeptide
Mrc1	165.3321949	119.7224818	210.941908	1.761923949	0.8117151654	0.000638079	0.029364503	mannose receptor, C type 1
Hox9b	373.4557315	453.5078203	293.4037726	0.648859374	-0.628239594	0.000670519	0.030102339	homeobox A9
Pih2b2	624.2892936	747.2892936	162.7879329	0.627879329	-0.70229329	0.000674721	0.030102339	pyrimidin nucleoside phosphatase 2
Oim1	268.9659763	108.1429135	339.7897392	1.714878083	0.778106013	0.00070121	0.031867442	olfactomedin-like 1
Mttf3a	3295.641975	4185.974264	2405.3561036	0.574610036	-0.999434978	0.00070546	0.032075398	methyltransferase like 7B
Akr1c18	41.64818972	81.8890178	1.472816339	0.017434698	-5.841894779	0.000714477	0.032320972	alko-keto reductase family 1, member C18
Rit129	20.27929177	20.27929177	0.302937204	-1.723385841	-1.723385841	0.000714452	0.032436555	NA
Glc	7961.514671	10959.17607	4963.853269	0.45234037	-1.142069633	0.000728524	0.032663101	glutamate-cysteine lyase, catalytic subunit
Hlf2bp	141.2802518	90.0707947	0.48660663	-1.039172117	0.000730745	0.000730745	0.032663101	heat shock transcription factor 2 binding protein
2610029101Rk	861.8776565	204.9317017	122.9416113	0.600260677	-0.736338934	0.000731263	0.032663101	NA
Fmo4	798.975959	574.8137101	1022.961875	1.7792088	0.93123855	0.000743104	0.033011375	flavin containing monooxygenase 4
Ras2	86.1739618	112.5420249	69.80589866	0.531409477	-0.912104137	0.00075941	0.033428731	ras protein p21
Cntn1	318.1122466	245.6729301	390.5515631	1.589721598	0.668774134	0.000771682	0.033805601	centrin, centrosomal protein
Dna11	1456.453336	1886.54738	1046.542446	-0.85073014	0.00077328	0.00		

Supplementary Table 2

(Top hits on RNA Seq and their possible functions)

Gene Symbol	Gene Name	Gene Ontology: Biological Process	Gene Ontology: Molecular Function	InterPro	KEGG Pathways
Dtp	D site albumin promoter binding protein(Dtp)	GO:0001889-liver development, GO:0006331-transcription, DNA-templated, GO:0006350-regulation of transcription, DNA-templated, GO:0006357-regulation of transcription from RNA polymerase II promoter	GO:0009777-RNA polymerase II regulatory region sequence-specific DNA binding	IPR04827-Basic-leucine zipper domain	
Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)(Cndp2)	GO:0006508-proteolysis, GO:0008152-metabolic process, GO:0043171-peptide catabolic process	GO:004160-carboxypeptidase activity, GO:0008233-peptidase activity, GO:0008237-metallopeptidase activity	IPR01261-ArgE/DapE/ACY1ICPQ2/lecS, conserved site	mmu03330-Arginine and proline metabolism, mmu03040-Histidine metabolism
Cica1	chloride channel/accessory 1(Cica1)	GO:0005509-proteolysis, GO:0006810-transport, GO:0006811-ion transport, GO:0006819-calcium ion transport, GO:0006821-chloride transport, GO:0071456-cellular response to hypoxia	GO:0005229-intracellular calcium-activated chloride channel activity, GO:0008237-metallopeptidase activity, GO:0016787-hydrolase activity, GO:0046872-metal ion binding	IPR02039-von Willebrand factor, type A, IPR004127-Calcium-activated chloride channel protein, IPR013642-Chloride channel/calcium-activated	mmu04024-Neurin secretion, mmu04972-Pancreatic secretion
Ypel2	ypppe-like 2 (Drosophila)(Ypel2)		GO:0046872-metal ion binding	IPR04810-Ypppe-like protein	
Arntl	aryl hydrocarbon receptor nuclear translocator-like(Arntl)	GO:0000960-protein import into nucleus, translocation, GO:0006351-transcription, DNA-templated, GO:0007293-epigenomeogenesis, GO:0007623-circadian rhythm, GO:0032007-negative regulation of TOR signaling	GO:0009796-transcription regulatory region sequence-specific DNA binding, GO:0000982-transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	IPR00014-PAS domain, IPR01087-Nuclear translocator, IPR01810-PAC motif, IPR01598-Myo-type, basic helix-helix (bHLH) domain, IPR013767-PAS fold	mmu04710-Circadian rhythm, mmu04728-Dopaminergic synapse
Gjb2	gap junction protein, beta 2(Gjb2)	GO:0007154-cell communication, GO:0007267-cell-cell signaling, GO:0007656-sensory perception of sound, GO:0016264-gap junction assembly	GO:0005243-gap junction channel activity, GO:0005515-protein binding	IPR00500-Connexin, IPR02268-Gap junction beta-2 protein (Cx26), IPR013062-Connexin, N-terminal, IPR019670-Gap junction protein, cysteine-rich domain	
Nr1h3	nuclear factor, interleukin 3, regulated(Nr1h3)	GO:000122-negative regulation of transcription from RNA polymerase II promoter, GO:0006351-transcription, DNA-templated, GO:0006350-regulation of transcription, DNA-templated	GO:0009777-RNA polymerase II regulatory region sequence-specific DNA binding, GO:0009797-RNA polymerase II core promoter sequence-specific DNA binding, GO:0001078-transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	IPR04827-Basic-leucine zipper domain, IPR01033-Vertebrate interleukin-3 regulated transcription factor, IPR016743-Transcription factor, basic leucine zipper, L68P4	
Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14(Slc16a14)	GO:0006810-transport, GO:0050885-transmembrane transport	GO:0006028-monoanionic acid transmembrane transporter activity, GO:0015293-symporter activity	IPR011701-Major facilitator superfamily, IPR020840-Major facilitator superfamily domain	
Gm908	predicted gene 908(Gm908)			IPR008978-Galactose-binding domain-like	

Note: 1) Gene annotation were performed using DAVID (<https://david.ncifcrf.gov/>), Huang DW, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID Bioinformatics Resources. *Nature Protoc.* 2009;4(1):44-57.
2) InterPro: Classification of protein families. <https://www.ebi.ac.uk/interpro/>
3) KEGG: Kyoto Encyclopedia of Genes and Genomes. <https://www.genome.jp/kegg/>