

Supplementary table-1: List of down regulated genes in ATP9A knock-down cells

No	Gene symbol	Gene name	Fold differences	P value
1	CORO1A	coronin, actin binding protein, 1A	-2	3,46E-05
2	ATP9A	ATPase, class II, type 9A	-2,72	3,45E-04
3	ICK	intestinal cell (MAK-like) kinase	-3,11	6,24E-04
4	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	-2,64	1,05E-03
5	PLCXD1	phosphatidylinositol-specific phospholipase C, X domain 1	-2,11	1,92E-03
6	MAPT	microtubule-associated protein tau	-2,03	2,26E-03
7	DLX1	distal-less homeobox 1	-2,07	2,90E-03
8	IL17D	interleukin 17D	-2	3,04E-03
9	RBP4	retinol binding protein 4, plasma	-2,12	3,05E-03
10	OAF		-2,14	3,19E-03
11	GPAM	Glycerol 3 phosphate Acyl transferase mitochondrial	-2,73	3,44E-03
12	SLC22A7	Solute carrier family 22 member 7	-2,41	3,49E-03
13	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	-2,78	4,16E-03
14	PAQR8	progesterin and adipoQ receptor family member VIII	-2,39	4,32E-03
15	NR1H4	nuclear receptor subfamily 1, group H, member 4	-2,62	4,67E-03
16	ATP6V0E2	ATPase, H ⁺ transporting V0 subunit e2	-2,23	4,72E-03
17	TMEM41A	transmembrane protein 41A	-2,09	5,20E-03
18	SLC25A1	solute carrier family 25	-2,47	5,53E-03
19	CPN2	carboxypeptidase N, polypeptide 2	-2,41	5,78E-03
20	SLC6A10P	solute carrier family 6 MEMBER 10	-2,17	5,84E-03
21	CERK	ceramide kinase	-2,04	6,26E-03
22	HOXD1	homeobox D1	-3,08	8,96E-03
23	THG1L	tRNA-histidine guanylyltransferase 1-like	-2,05	9,29E-03
24	GNG7	guanine nucleotide binding protein (G protein), gamma 7	-2,13	9,82E-03
25	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	-2,25	9,83E-03
26	AIF1L	allograft inflammatory factor 1-like	-2,28	9,84E-03
27	PANX2	pannexin 2	-2,27	0,011
28	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	-2,16	0,011
29	ERBB3	erb-b2 receptor tyrosine kinase 3	-2,14	0,015

30	ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-2,03	0,018
31	LOC401720		-2,28	0,019
32	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-2,08	0,02
33	FAM83D	family with sequence similarity 83, member D	-2,14	0,02
34	C9orf58		-2,21	0,02
35	LOC100134081	allograft inflammatory factor 1-like	-2,15	0,024
36	KANK4	KN motif and ankyrin repeat domains 4	-2,74	0,024
37	C2orf82		-2,04	0,025
38	PNPLA7	patatin-like phospholipase domain containing 7	-2,04	0,025
39	HEY1	hes-related family bHLH transcription factor with YRPW motif 1	-2,31	0,027
40	C9orf140		-2,16	0,029
41	PCSK9	proprotein convertase subtilisin/kexin type 9	-2,97	0,029
42	KLHL14	kelch-like family member 14	-2,37	0,03
43	HADH	hydroxyacyl-CoA dehydrogenase	-2,19	0,033
44	S100A9	S100 calcium binding protein A9	-2,97	0,036
45	SP5	Sp5 transcription factor	-2,04	0,036
46	MACROD1	MACRO domain containing	-2,09	0,036
47	ANKRD38	KN motif and ankyrin repeat domains 4	-3,08	0,039
48	PRELID1	PRELI domain containing 1	-2,05	0,043
49	LOC100132863	high mobility group box 1 pseudogene 37	-2,1	0,044
50	CENPM	centromere protein M	-2,05	0,047

Supplementary table-1: : List of genes that are significantly ≥ 2 fold downregulated in *ATP9A* depleted HepG2 cells as compared to controls. HepG2 cells were transduced with the sh*ATP9A* #33, #34 or sh-control. 72 hours after transduction, cells were harvested for RNA isolation. RNA from *ATP9A* knock-down and control cells was labeled with cRNA labeling kit for Illumina BeadArrays (Ambion) and hybridized with Ref8v3. Genes are presented in the order of their significance.