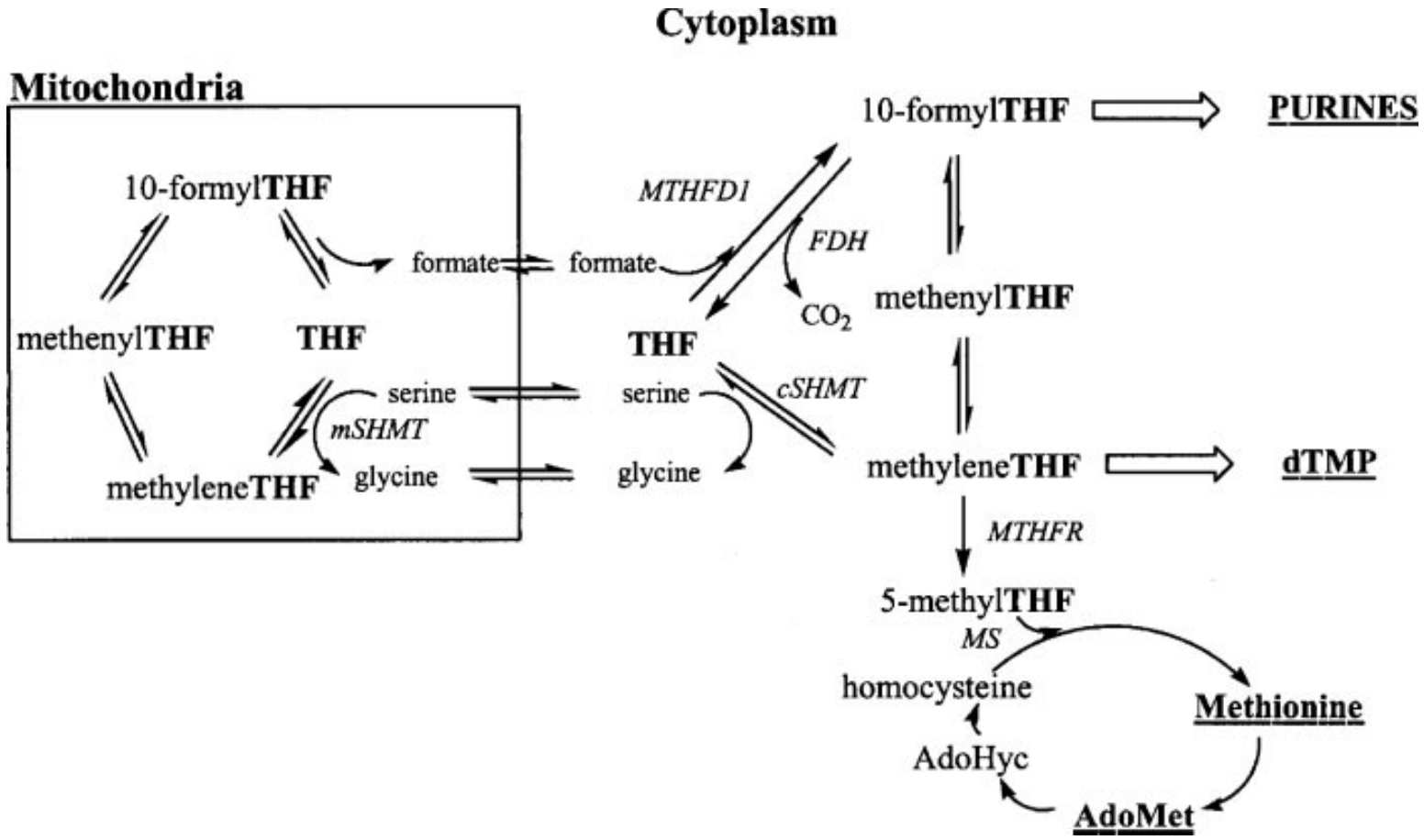
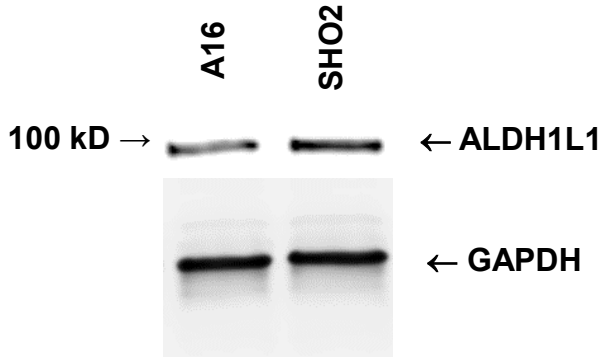
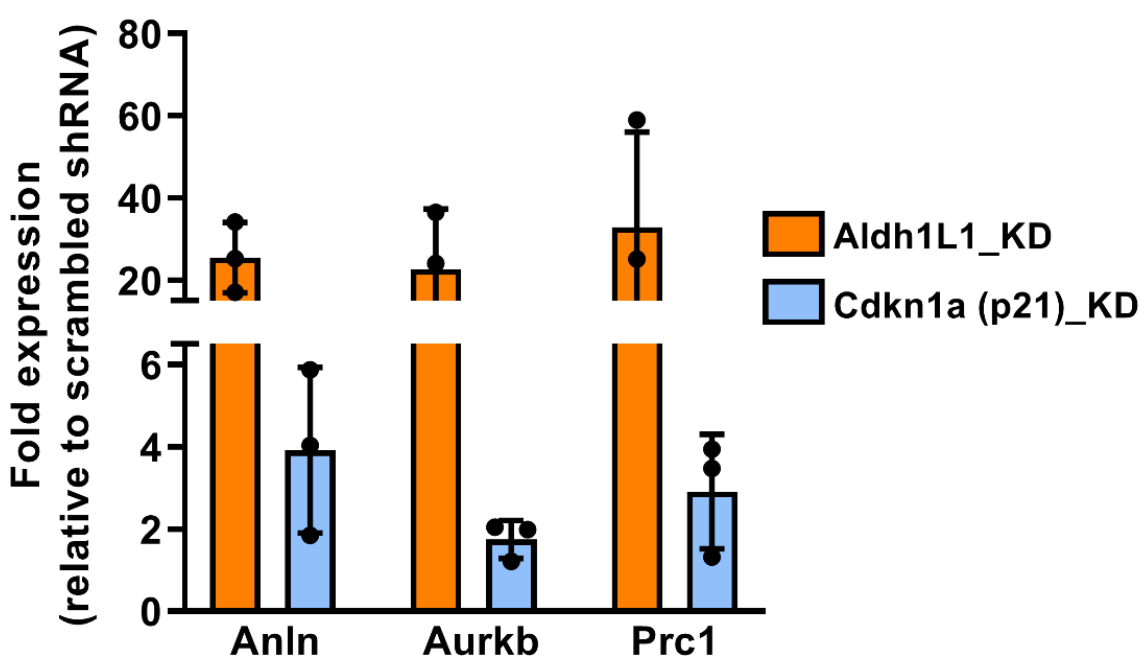
Aldh1L1 [Cytosolic 10-formyl tetrahydrofolate]

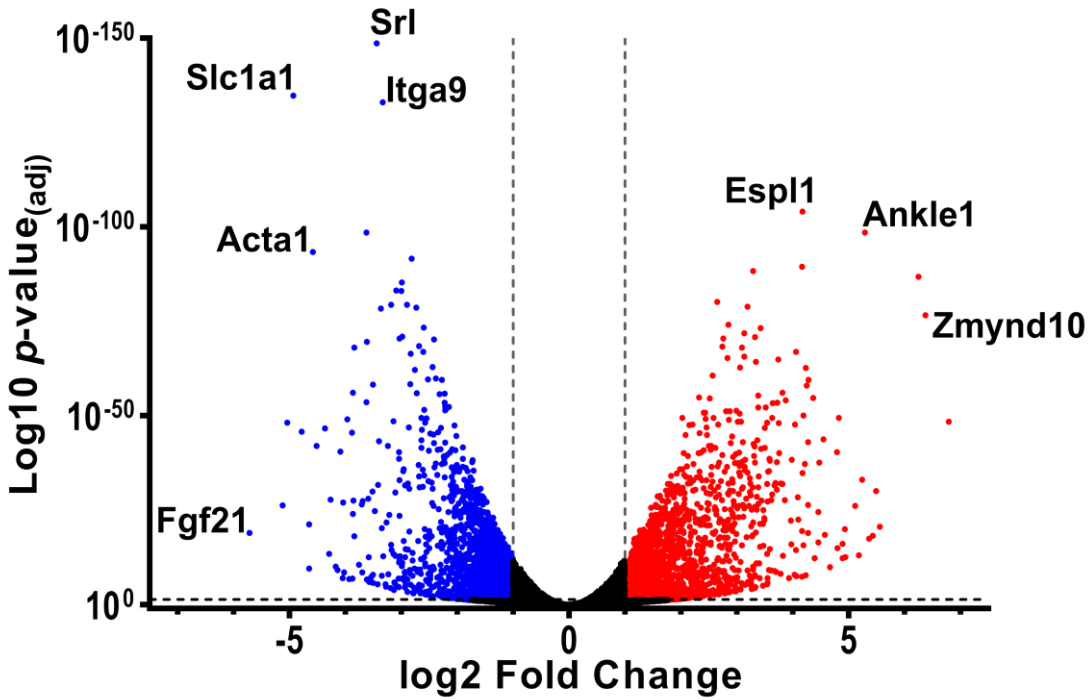




Anguera MC et al. (2006) JBC

Global overview of differentially expressed genes between Aldh1L1 and Cdkn1a-knocked down FCs:



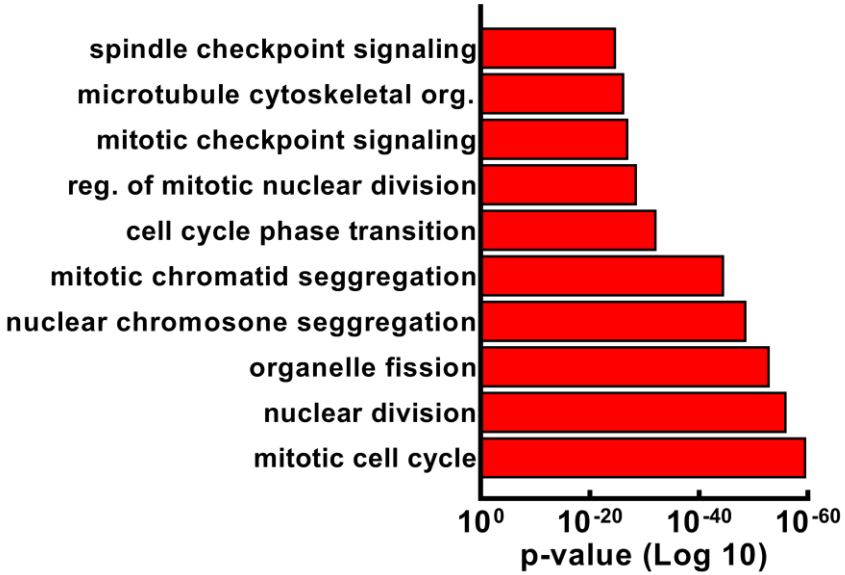


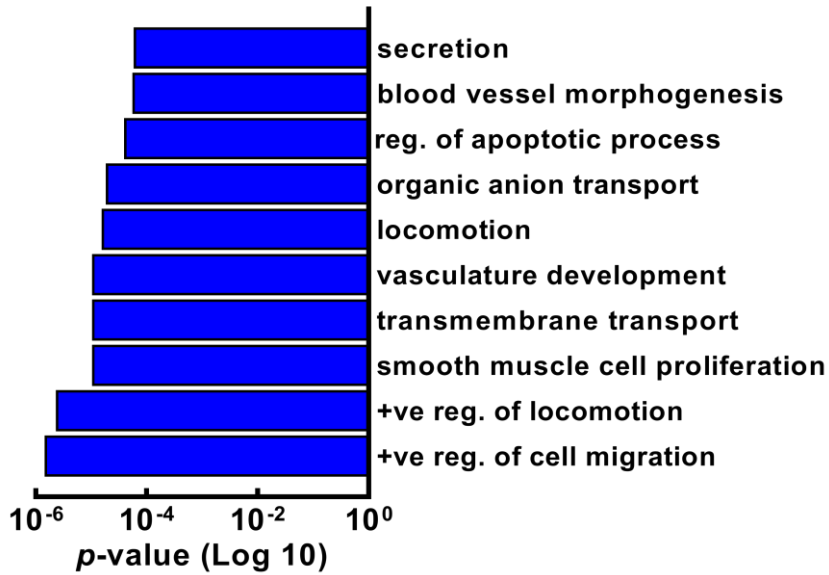
Adjusted p < 0.05 = 7275 DEGs

3564 upregulated genes
3711 downregulated genes

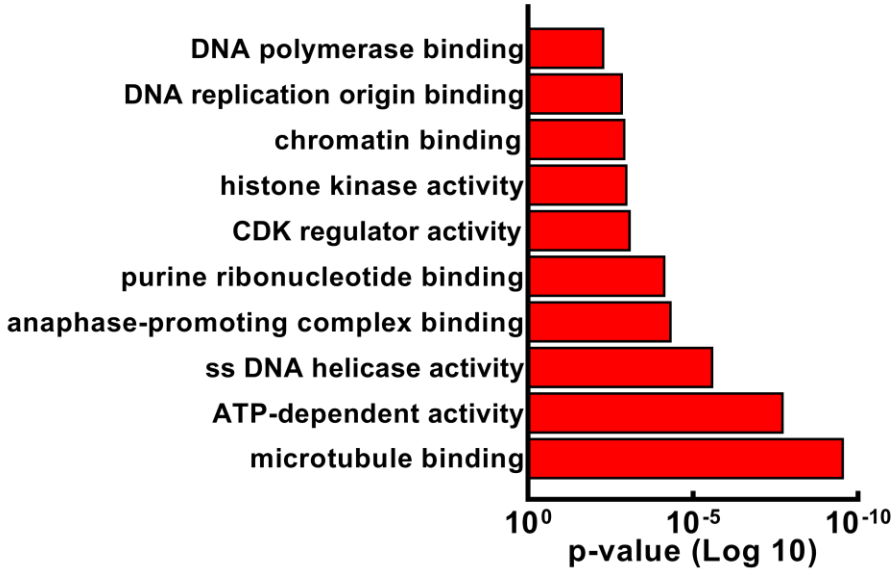
GO categorization of top 500 DEGS (upregulated and downregulated):

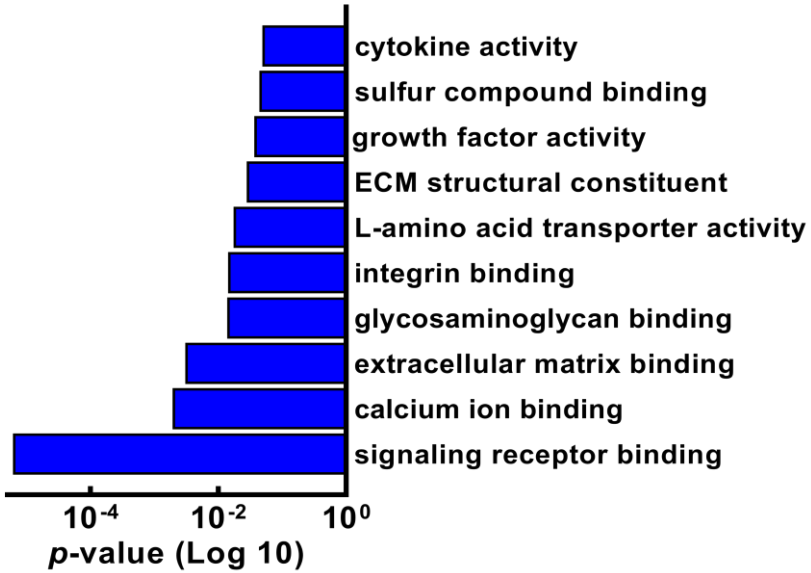
GO categories: Biological process





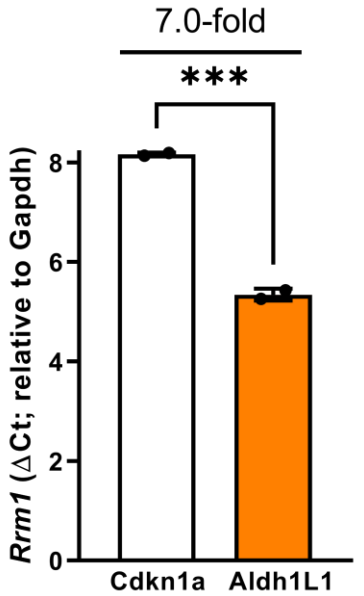
GO categories: Molecular function

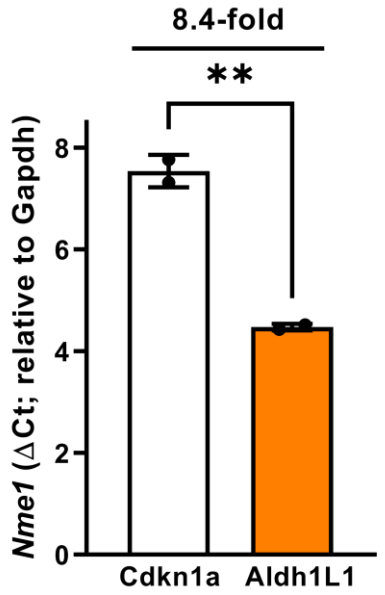




DEGs reveal probability of deeper alterations in transcriptional profile upon Aldh1l1 knock-down

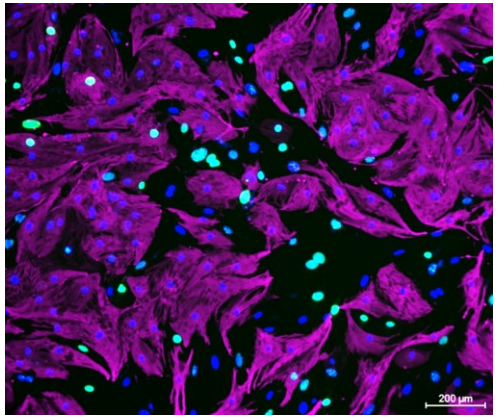
	Symbol	Description	log2FoldChange	padj
Cell cycle associated genes	Cdca5	cell division cycle associated 5	3.114277659	6.17E-32
	Cdca2	cell division cycle associated 2	3.264524807	1.39E-21
	Ccna1	cyclin A1	5.494152851	6.64E-31
	Cdc20	cell division cycle 20	4.282029944	7.81E-44
	Ccnb2	cyclin B2	3.722689178	1.42E-38
	Ccna2	cyclin A2	3.68319301	2.18E-32
	Ccnf	cyclin F	2.879716848	6.00E-31
	Espl1	extra spindle pole bodies 1_ separase	4.175648184	0.00
	Ankle1	ankyrin repeat and LEM domain containing 1	5.298763275	2.38E-99
	Brca1	breast cancer 1	3.098755827	1.65E-31
deoxyribonucleotide synthesis	Rrm1	ribonucleotide reductase M1	1.927140653	6.18E-22
	Rrm2	ribonucleotide reductase M2	3.079904743	3.51E-49
	Nme1	NME/NM23 nucleoside diphosphate kinase 1	2.332955246	1.04E-55
	Nme4	NME/NM23 nucleoside diphosphate kinase 4	1.6392776	7.74E-18

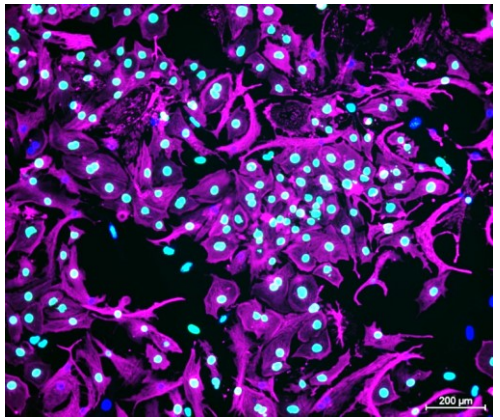




Expression levels of genes encoding key transcriptional factors implicated in stem cell like reprogramming might be altered in Aldh1L1 knockdown myocytes

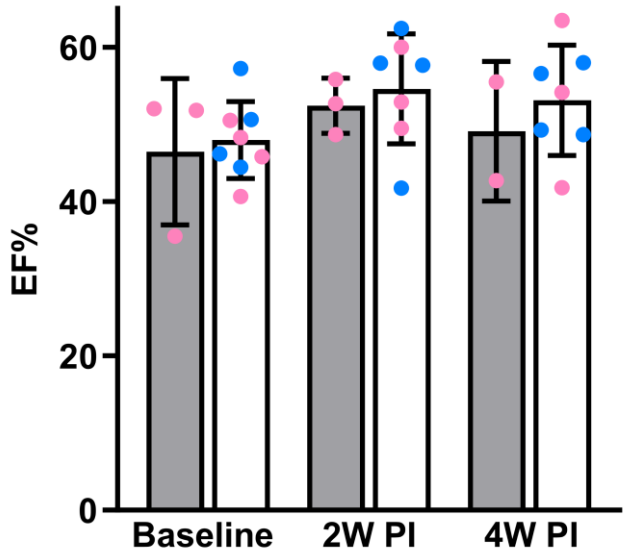
Symbol	Description	log2FoldChange	padj
T2	brachyury 2	3.070144977	4.81E-05
Pou3f2	POU domain_ class 3_ transcription factor 2	2.121046854	0.01462
Pou3f3	POU domain_ class 3_ transcription factor 3	2.702527883	0.00011
Sox4	SRY (sex determining region Y)-box 4	3.194603178	9.71E-80
Sox11	SRY (sex determining region Y)-box 11	2.994075068	3.95E-52
Sox12	SRY (sex determining region Y)-box 12	1.21365533	8.59E-08
Sall2	sal-like 2 (Drosophila)	0.765625547	3.70E-06
Nkx2-9	NK2 homeobox 9	3.58162903	6.39E-10
Mxd3	Max dimerization protein 3	3.580894979	3.54E-36
Msx1	msh homeobox 1	1.147897783	0.00653
Dlx5	distal-less homeobox 5	3.095907113	1.65E-06
Dlx6	distal-less homeobox 6	4.169585209	3.09E-08
Foxm1	forkhead box M1	2.934909953	9.82E-22

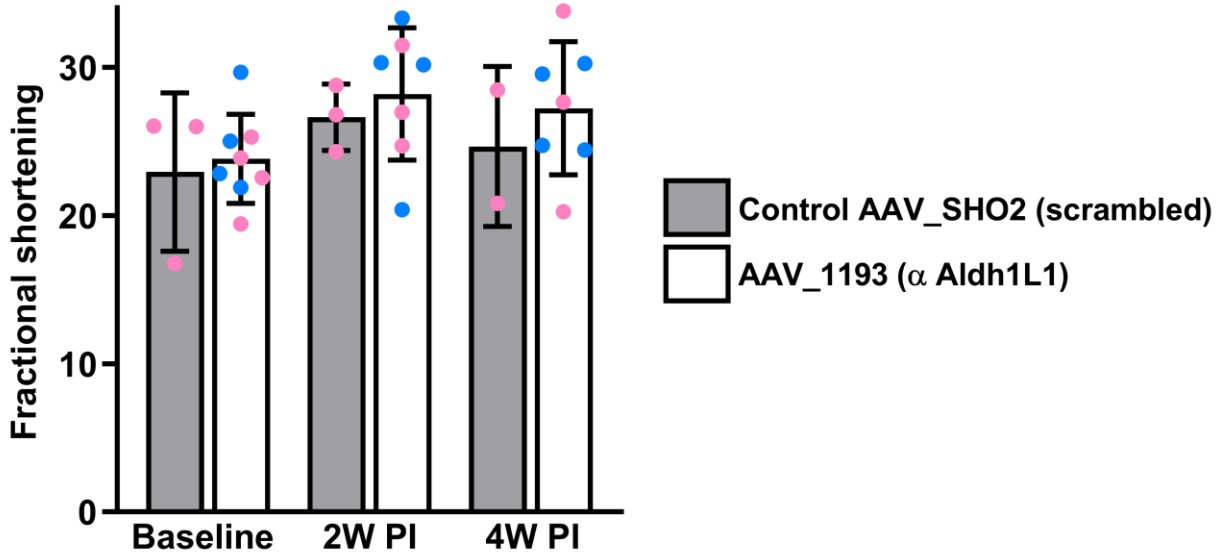




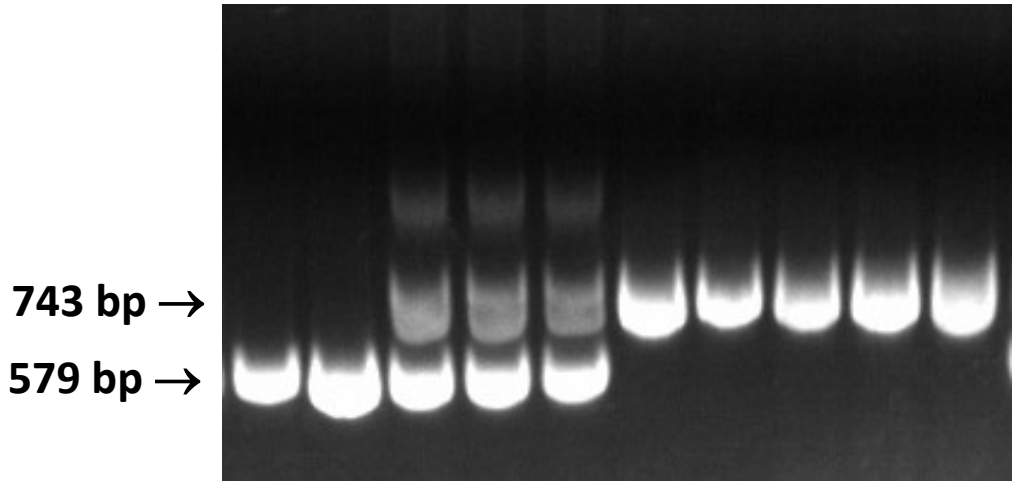
Pilot-analysis for cryoinjury model using Aldh1L2-KO mice

	Genotype	Nnt	Sex	AAV	Baseline		2-weeks PI		4-weeks PI	
	Aldh1L2				EF	FS	EF	FS	EF	FS
A301	-/-	+/-	F	SHO2	51.833589	25.986352	52.693528	26.78216		
A288	-/-	+/+	F	SHO2	35.532142	16.761085	48.681111	24.301924	42.708385	20.820596
A287	-/-	+/+	F	SHO2	52.010711	26.032684	55.813249	28.767777	55.512975	28.456123
A302	-/-	+/-	F	1193	40.62845	19.412923	59.979632	31.46509	54.12244	27.642623
A340	-/-	+/+	F	1193	50.536747	25.274308	52.906979	26.971424	63.434524	33.782281
A339	-/-	+/+	F	1193	45.775113	22.535987	49.456943	24.698779	41.766663	20.242484
A292	-/-	+/-	F	1193	48.281791	23.883766				
A343	-/-	+/+	M	1193	44.43528	21.884438	57.939031	30.310017	56.591338	29.535463
A337	-/-	+/+	M	1193	57.243786	29.644509	57.66025	30.160279	57.980793	30.253651
A341	-/-	+/+	M	1193	46.160619	22.812882	41.750432	20.386287	48.687058	24.42329
A344	-/-	+/+	M	1193	50.603307	25.000025	62.435348	33.294023	49.289804	24.714638



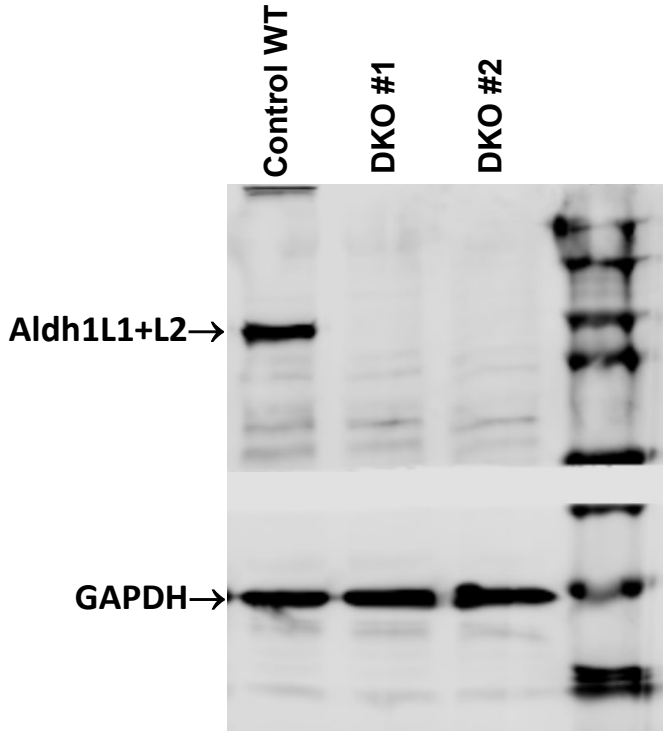
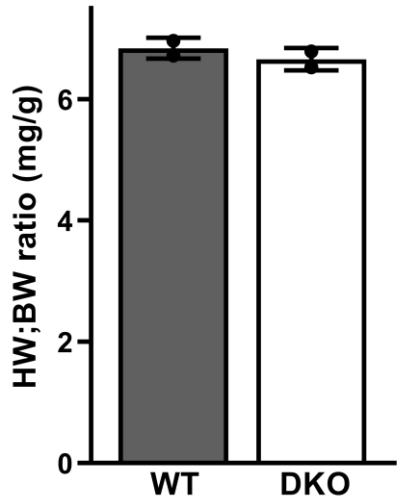


Genotyping for presence of *Nnt* mutant allele in mice:



WT allele: 579 bp
Mutant allele: 743 bp

Adopted and optimized from Nicholson *et al*. (2010) **Obesity 18**, 1902-1905.

Protocol optimized: include $MgCl_2$ at 2mM working concentration
annealing temp: 56°C
amplification cycles: 39

Generation of viable DKO mice lacking both Aldh1L1 and Aldh1L2 is feasible, and they are viable