Insertion of a knockout-first cassette in *Ampd1* gene leads to neonatal death by disruption of neighboring genes expression

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Supplementary Information

Gene	Chr/Strand	Start/End	RNA seq		RT-PCR	
			Value of WT	p-adjust	Value of WT	p-value
Man1a2	3/-	100562208/100685503	18.07% ±2.30%	9.070E-53	24.37% ±2.19%	0.0001
Ptgfrn	3/-	101040232/101110278	100.33% ±5.80%	1	107.37% ±23.93%	0.7776
Igsf3	3/+	101377125/101463060	101.78% ±4.13%	1	103.57% ±19.44%	0.8723
Atp1a1	3/-	101576219/101604603	113.65% ±0.79%	1	115.33% ±14.01%	0.4038
Casq2	3/+	102086415/102146514	84.78% ±7.41%	1	$80.17\% \pm 16.35\%$	0.4416
Csde1	3/+	103020546/103058189	101.64% ±7.75%	1	$86.48\% \pm 10.34\%$	0.1547
Nras	3/+	103058339/103067914	63.63% ±5.43%	3.314E-04	50.85% ±5.53%	0.0037
Ampd1	3/+	103074014/103099714	0.16% ±0.04%	6.089E-38	0.11% ±0.16%	0.0003

Supplementary Table 1: Differentially expressed genes identified by RNA sequencing and RT-PCR verification.

In RNA sequencing, muscle tissue come from E18.5 WT mice (n=3) and $Ampd1^{tm1a/tm1a}$ mice (n=3). The P-values were adjusted using the Benjamini and Hochberg's approach for controlling the false discovery rate. Another group of E18.5 WT mice (n=5) and $Ampd1^{tm1a/tm1a}$ mice (n=5) muscle were used for RT-PCR. Two-tailed Student's *t* test was used to determine the significance of differences, mean ±SEM.

Allele	Primer	Sequence(5'-3')	Product size(bp)	
	WT-F	tgggctgacagctgcagttagca	WT:354bp tm1a/+:354bp & 410bp	
$Ampd1^{tm1a}$	loxP-F	gagatggcgcaacgcaattaat		
	Tm1a-R ccaagaaaaagacagcacaggagacc		- tm1a/tm1a:410bp	
A non d 1tmlc	Tm1c-F:	ggcaactcccttttaccaca	WT:352bp	
Ampai	Tm1c-R	tttccctgatctccaaccag	tm1c/tm1c:516bp	
A pap d 1 ^{tm1d}	Tm1d-F	ggcaactcccttttaccaca	WT:1090bp	
Атрат	Tm1d-R	ggtaacacgcatgacaggtg	tm1d/tm1d:400bp	

Supplementary Table 2: Genotyping primers and PCR products size of different *Ampd1* mice.









Supplementary Figure 1: Nucleotide levels in the brain, the heart and the liver of E18.5 mice. There is no genotypic difference in the nucleotide levels of the brain (a), the heart (b), the liver (c) and the lung (d) in E18.5 $Ampd1^{tm1a/tm1a}$ mice. n=5/each genotype, mean ± SEM.



Supplementary Figure 2: RNA level of different genes, which located between *Ampd1* and *Man1a2*, in the lung of *Ampd1*^{tm1a/tm1a} mice. Man1a2 expression level was significantly decreased to $42.69\% \pm 3.52\%$ in lung of *Ampd1*^{tm1a/tm1a} mice, but the expression of genes located between *Man1a2* and *Ampd1* (*Ptgfrn, lgsf3, Atp1a2, Casq2, Csde1* and *Nras*) did not change in lung (n=5/each genotype, mean ± SEM. As compared with WT, **P<0.01, two-way ANNOVA followed with Bonferroni's multiple comparisons test).



Supplementary Figure 3: Potential long range interactions between *Ampd1* and *Man1a2* gene. Hi-C results hosted in WashU Epigenome Browser indicated probable long range interaction between *Ampd1* and *Man1a2* in (a) human H1 embryonic stem cell or (b) mouse embryonic stem cell. Purple arc represented Long range interaction.