

Supplementary Table 2. Molecular features of the main proteins downregulated in CECs from *Dhps*^{Δepi} mice.

Proteins	Fold change (<i>Dhps</i> ^{Δepi} / <i>Dhps</i> ^{fl/fl})	nnnnn AAAUGU nnnnn sequence in mRNA ^a	Number of diprolyl motifs	Number of diglycyl motifs
AL1A7	0.4796	UCAAG AAAUUU UGAGG GCCUU AAAUGC GCAGA GUUCA GAUGUCUGGAAA UGG GAGAG AAAUGG GUGA UUU AAAAUGCCAAAC GUAUAG AAUGUGAAAUG AAGA UU	1	4
AL1B1	0.4829	CGGGC GAUGU GGAUC GGGC AAAUCUG AUUU UUUG AAAUGU UGUGG	1	3
AL3A2	0.8292	GAAGG AAUCU UAGCA UGAGC AAAGU GAACU GCAGG AAAUGC UGCCA CUUAC GAUGU UGAUC AGAAG AAUUU UGGA GUG AAAAUGU AGACG UUCAU AAUGA CCGUG CUACU AAAUGC UUAAC UUCAC GAUGU ACUGC GAGCC AAUCU CCGCA CGAGAA CAUGU CACAC AAGUUG AAUGU UUUGU CAAGG AAUUU ACUU UUAUUG AAUGU AUAGC AAUUU CAAUGU GAAC AAAAU AAAUGU AUUUC	1	5
AL3B2	0.8408	AGCCA GAUGU CUGCU AACAC AAUUU GACUA GAAUCA GAUGU GGAA UUCUG GAUGU UUUCUG A AUGU ACCCG CAGGC GAUGU AUACC CUAUU AAAUGA CCUCA	1	6
AL9A1	0.8292	GUAAG AAAAGU GGCCU CAUGG GAUGU CCGCU GGGGC AAUCU CCUCU UUCAU AAAUGA GGUUG AACUA UAAUGU CAGCC UUUG AAAUGU GCACA GAGAA UAUGU AGACC	1	6
ALDH2	0.5703	UCCUG AAAUGU CUCCG CAGGAG AAUGU GUAUG CUAU AGAUGU CAGGG CGUCC GAUGU GCAGG GCAGC AAAUGA GCAAU	1	3
GSTA4	0.5284	GAUUG CAUGU AUGCA	1	0

		AUGACAAAUGCCAAUU		
GSTK1	0.7578	AGUAUAAAUGCCAUGC GGCUGGAAUGUCCACA CCUGCAAAUAUGGGGC AACCUACAUGUUAUUU	2	0
GSTM1	0.3868	UGAGAAAUGAAGCUC	0	0
GSTM2	0.4796	UGGAGGAAUGUACUAG	0	0
GSTM3	0.4862	AAGAGUAUGUCAUGG UGAGAAAUGAAGCUC	0	0
GSTM5	0.6070	GCCCAAAUGUCAUCC GCACAACAUGUGUGGU	0	0
GSTO1	0.4474	UACUUAAAUCUCUACC UCAGCAAAUGCUGUUU AAGAAAAAUGUCAAGU UCAUUAAAUCUCUUAU	2	1
GSTP1	0.4632	GCGGCAAAUAUGUCAC CCGGAAACAUGUGAACC	1	1
GSTT2	0.6551	CAAGAAAUGUUACCA	1	0
GSTT3	0.5743	CUGCAAAUCUUUGAG UAUAUACAUGUAUAUA	2	0
K1C16	0.3922	CCUGGAAAUGCAGAUU GACGUCAAUGUGGAGA CGCAGAGAUGUGGAGG GGGACUAAUGUUUUGC	1	11
K2C6A	0.2284	CAGUGCAAUGUGUGGA AGAGCAAAUAUGAAGA AGACUAAAUAUGAGGA CUCAUGAAUGUCAAGC GUCCCAGAUGUCAUGG	1	15
K2C79	0.5175	CCUCUCAAAUGUGGAGA CAGACCAAUGUGUCUG AGACCAAAUAUGAAGA ACUAAAAAUGAGAUCG GGCUCAAAUCUACUCA	1	13
LANCL1	0.6328	CUCCACAAUGUGUUUG	1	0
MPTX	0.0877	GUGGAAAUAUAGGAGAA UACAUGUUCUAU CCCACAAAUCUCCUG GGGGGAAAUUUUGAUG CUAUGAAAUAUAAGUC UGUUAAAAUGAUAUGUG CAUU CAAAGAAAUGAGCAUC	0	2
S26A3	0.3208	AGGCAAAUGAUCGAA ACAGAAAUGACUCGU UUGGCUAAUGUUGGAA UUUUUAGAUGUCCAUC AAUACAAAUGGAGGAC AUCGGGAAUGUCAGGU	2	2

*Substitutions are indicated in red.