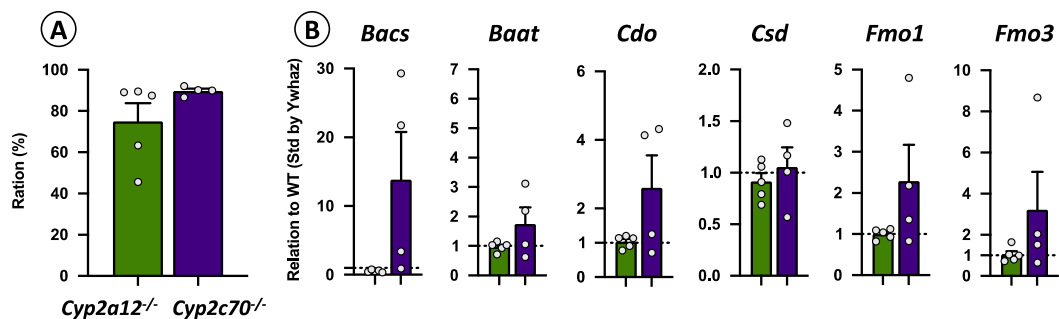


**Supplementary Table S1.** Evaluation stability and ranking of 14 candidate reference genes evaluated by geNorm and Bestkeeper algorithms.

Reference Gene	Accession number	geNorm		SD	BestKeeper	
		M Value	Rank		Coefficient of correlation	Rank
<i>Ywhaz</i> *	NM_011740	0.205	1	0.99	0.981	1
<i>B2m</i> *	NM_009735	0.205	1	>1	0.983	
<i>Hpt1</i> *	NM_013556	0.234	3	>1	0.973	
<i>Tbp</i> *	NM_013684	0.250	4	0.98	0.978	2
<i>Pgk1</i> *	NM_008828	0.273	5	>1	0.984	
<i>Atp5f</i> *	NM_009725	0.283	6	>1	0.976	
<i>Ppia</i> *	NM_008907	0.289	7	>1	0.981	
<i>Tfrc</i> *	NM_011638	0.301	8	0.96	0.963	3
<i>Actb</i> *	NM_007393	0.318	9	>1	0.969	
<i>Gusb</i> *	NM_010368	0.328	10	>1	0.965	
<i>Gapdh</i> *	NM_008084	0.343	11	>1	0.911	
<i>Rps18</i> *	NM_011296	0.364	12	>1	0.954	
<i>Rplp1</i> *	NM_018853	0.407	13	>1	0.925	
<i>18SrRNA</i>	X56974	0.429	14	0.80	0.908	4

\* Mouse Housekeeping Gene Primer Set, Takara Bio, Inc. Abbreviation of gene: *18SrRNA*, 18S ribosomal RNA; *Actb*, actin; *bata*, *Atp5f1*, ATP synthase peripheral stalk-membrane subunit b; *B2m*, beta-2 microglobulin; *Gapdh*,



KO (n=5) and *Cyp2c70* KO (n=4) mice. The mRNA level is expressed in the relation to the WT group after standardization by *Ywhaz*. All data are presented as the mean  $\pm$  standard error.