

**Supplementary Table S1:** Statistical results of the GO overrepresentation test of the comparison between the Ctrl and HTX groups

**GO molecular function complete**

GO molecular function complete	#	#	expected	fold enrichment	+/-	raw <i>p</i> -value	FDR
enoyl-CoA hydratase activity	10	2	.01	> 100	+	$1.71 \times 10^{-5}$	$2.79 \times 10^{-2}$
structural constituent of ribosome	168	4	.09	44.56	+	$1.48 \times 10^{-6}$	$7.26 \times 10^{-3}$
RNA binding	1655	7	.88	7.92	+	$5.42 \times 10^{-6}$	$1.33 \times 10^{-2}$

**GO biological process complete**

GO biological process complete	#	#	expected	fold enrichment	+/-	raw <i>p</i> -value	FDR
cytoplasmic translation	124	4	.07	60.38	+	$4.54 \times 10^{-7}$	$7.11 \times 10^{-3}$
translation	377	5	.20	24.82	+	$9.00 \times 10^{-7}$	$7.06 \times 10^{-3}$
peptide biosynthetic process	404	5	.22	23.16	+	$1.26 \times 10^{-6}$	$6.59 \times 10^{-3}$
peptide metabolic process	538	5	.29	17.40	+	$5.06 \times 10^{-6}$	$1.59 \times 10^{-2}$
amide biosynthetic process	520	5	.28	18.00	+	$4.29 \times 10^{-6}$	$1.68 \times 10^{-2}$

**GO cellular component complete**

GO cellular component complete	#	#	expected	fold enrichment	+/-	raw <i>p</i> -value	FDR
polysomal ribosome	32	2	.02	> 100	+	$1.44 \times 10^{-4}$	$4.20 \times 10^{-2}$
ribosome	226	4	.12	33.13	+	$4.70 \times 10^{-6}$	$2.40 \times 10^{-3}$
ribonucleoprotein complex	687	5	.37	13.62	+	$1.65 \times 10^{-5}$	$6.72 \times 10^{-3}$
cytosolic large ribosomal subunit	58	3	.03	96.81	+	$4.01 \times 10^{-6}$	$2.73 \times 10^{-3}$
cytosolic ribosome	104	4	.06	71.99	+	$2.29 \times 10^{-7}$	$4.68 \times 10^{-4}$
large ribosomal subunit	113	3	.06	49.69	+	$2.78 \times 10^{-5}$	$9.45 \times 10^{-3}$
ribosomal subunit	187	4	.10	40.04	+	$2.25 \times 10^{-6}$	$2.29 \times 10^{-3}$