

Table S3. Functional categories enriched in the group of mRNAs with concentration under mainly degradational control (p-value < 0.07). For each category, the associated genes are listed according to the number of comparisons (one or two) in which the degradational control is present.

Functional category	Two comparisons	One comparison
Fatty acid biosynthesis	-	<i>accA, acpP, fabF, fabG, fabI, fabR, fabZ, lipA</i>
Purine nucleotide biosynthesis	-	<i>adk, atpE, atpF, atpH, flil, guaA, guaB, kdpB, purA, purB, purC, purD, purF, purM, purN, purT</i>
Amino acid biosynthesis		
- Val/Leu/Ile	<i>leuB, leuC</i>	<i>asd, ilvB, ilvC, ilvD, ilvE, ilvN</i>
- His	<i>hisB, hisH, hisJ</i>	<i>hisD, hisI</i>
- Arg	-	<i>argA, argC, argE, argF, argG, carB</i>
- Cys/Met	-	<i>cysH, cysI, cysJ, cysK, iscS, metB, metC, metE, metJ, mmuM, mtn</i>
- Ser/Gly	-	<i>serA, serC, glyA, sdaA</i>
- Asp/Asn/Thr/Lys	<i>aspC</i>	<i>asd, asnA, asnB, dapA, dapD, thrA, thrB</i>