Supplem Table 2. Proteins which activity in acetate cultures might be compromised in the *cobB* mutant.

Protein	Protein residue and experimental evidence	References
Fructose-1,6-bisphosphatase class 1 (Fbp)	• K269: highly conserved. Belongs to catalytic site. • Site specific mutation K269A reduces 20-fold the affinity of the enzyme for its substrate and decreases 500-fold affinity for the competitive inhibitor fructose 2,6-bisphosphate • Higher acetylation of this residue in the Δ*cobB* mutant might affect gluconeogenesis.	(el-Maghrabi *et al*, 1992)
RNA polymerase sigma subunit (RpoD)	• K557: belongs to an helix-turn helix domain responsible for the interaction with the -35 box of gene promoters. • It is not clear if this residue interacts directly with the DNA backbone, but the abundance of positively charged amino acids in this domain, suggests that it may play a role in the fine tuning of transcription initiation in *E. coli*.	(Paget & Helmann, 2003)
Ribosome-associated inhibitor A protein (Rai)	• K87: belongs a protein region that blocks the P-site (peptidyl-tRNA site) of the ribosome. • Regulates translation in stationary phase in *E. coli*. It can block the dimer formation of 70S, decreasing the translation rate. This protein has two different regions that block the A-site (aminoacyl-tRNA site) and P-site (peptidyl-tRNA site) of the ribosome blocking translation. Both regions are particularly enriched with positively charged amino acids.	(Agafonov *et al*, 1999; Maki *et al*, 2000).
Long chain fatty acid CoA ligase (FadD)	• K543. • When it is acetylated in its active site, as occurs on Acs, acyl-CoA synthase activity is abolished. • The acetylation ratio was 35-fold higher in the *cobB* mutant than in the *patZ* mutant (not in all replicates). • Regulation of FadD by lysine acetylation has also been described in other organisms like *Rhodopseudomonas palustris*.	(Crosby *et al*, 2010)
Glyceraldehyde-3-phosphate dehydrogenase (GapA)	• K184: necessary for NAD^+ binding and activity. • It was found to be more acetylated only in the *cobB* mutant. • The activity of this protein is essential under glycolitic and gluconeogenic conditions.	(Kuhn *et al*, 2014) (Seta *et al*, 1997)