Supplementary Table 4: Significantly regulated phosphorylation events in ΔPrkC and ΔPrpC strains. Details of phosphorylation sites with significantly changing SILAC ratios in Δ*prkC* and Δ*prpC* strains compared to WT. T290 on PrkC is a known substrate of the phosphatase PrpC (internal positive control).

No.	**Gene Name**	**Position**	**Localization Probability**	**PEP Score**	**SILAC ratio in Δ*prkC* (Log$_2$ scale)**	**SILAC ratio in Δ*prpC* (Log$_2$ scale)**	**Description**
1	*citM*	S182	1	1.63E-13	-2.45182	0.439527	2-oxoglutarate dehydrogenase component E2
2	*jofD*	S365	0.509	1.24E-31	-2.18683	-1.13958	30S ribosomal protein S1 homolog
3	*yabS*	T88	1	8.35E-192	-1.54057	0.235825	Uncharacterized protein
4	*ykwC*	S281	0.998	7.69E-23	-1.15752	2.917978	Uncharacterized oxidoreductase
5	*thiA*	S565	1	5.77E-81	-1.09944	-0.0718	Thiamine biosynthesis protein
6	*yabS*	T90	1	8.35E-192	-1.04965	-0.14854	Uncharacterized protein yabS
7	*ahpF*	S49	0.958	1.53E-33	-1.03892	-0.77889	Alkyl hydroperoxide reductase - NADH dehydrogenase
8	*cotB*	S253	0.883	8.65E-07	1.973082	5.353034	Spore coat protein B
9	*gapA*	S282	0.976	2.45E-91	1.200391	1.711156	Glyceraldehyde-3-phosphate dehydrogenase 1
10	*ptkA*	Y228	0.773	0.00011	1.125995	1.561541	Tyrosine-protein kinase
11	*prkC*	T290	1	1.31E-71	-0.81333	3.544522	Serine/threonine -protein kinase (Positive Control)
12	*patA*	T388	1	5.03E-05	0.128373	3.188502	Putative aminotransferase A
13	*ymfM*	S69	1	6.18E-88	-0.26271	2.575126	Uncharacterized membrane protein
14	*rplN*	T6	1	0.0006	0.193166	1.001053	50S ribosomal protein L14
15	*phoD*	S545	0.908	0.001854	0.6382483	-2.597943	Alkaline phosphatase D
16	*glmM*	S98	0.5	3.11E-17	-0.6031706	-2.45766	Phosphoglucosamine mutase
17	*ptsH*	T20	0.972	9.63E-07	0.07748499	-2.009252	Histidine-containing phosphocarrier protein HPr