

**Supplemental Table S1.** Alignments of transcripts with NR, SWISS-PROT, TREMBL, CDD, PRAM and COG data

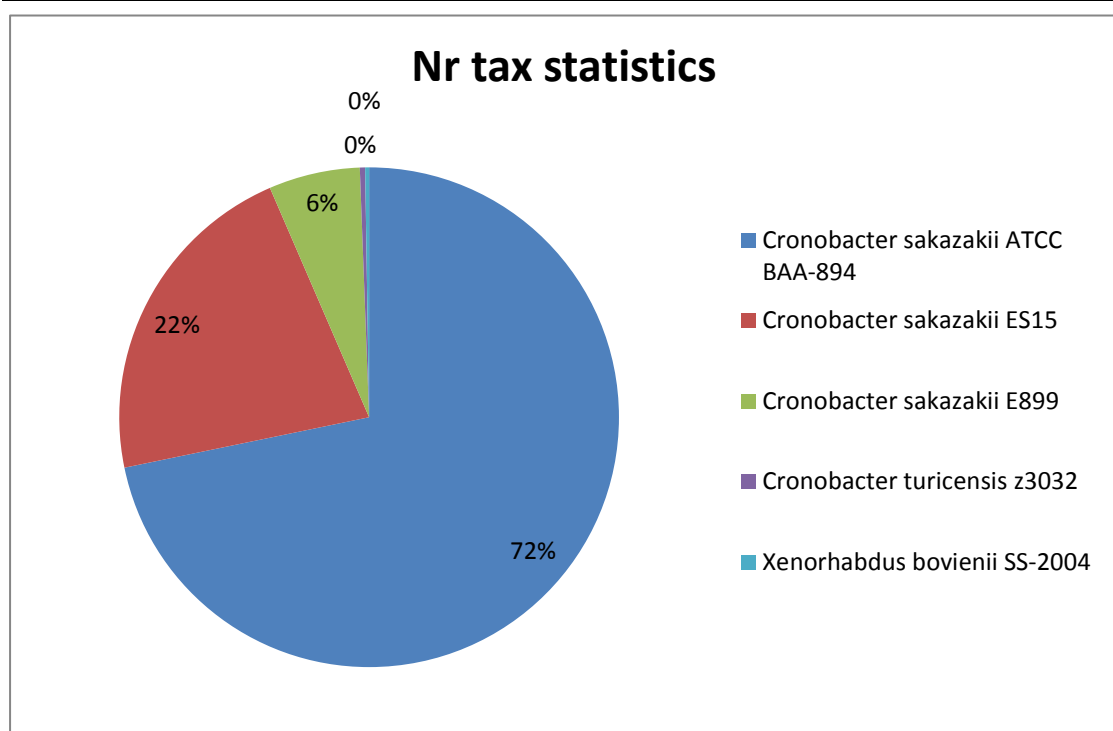
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<b>Num</b>	<b>NR</b>	<b>SWISS-PROT</b>	<b>TREMBL</b>	<b>CDD</b>	<b>PFAM</b>	<b>COG</b>
<b>4408</b>	2382	1757	2979	1631	1283	736
<b>100%</b>	54.04%	39.86%	67.58%	37.00%	29.11%	16.70%

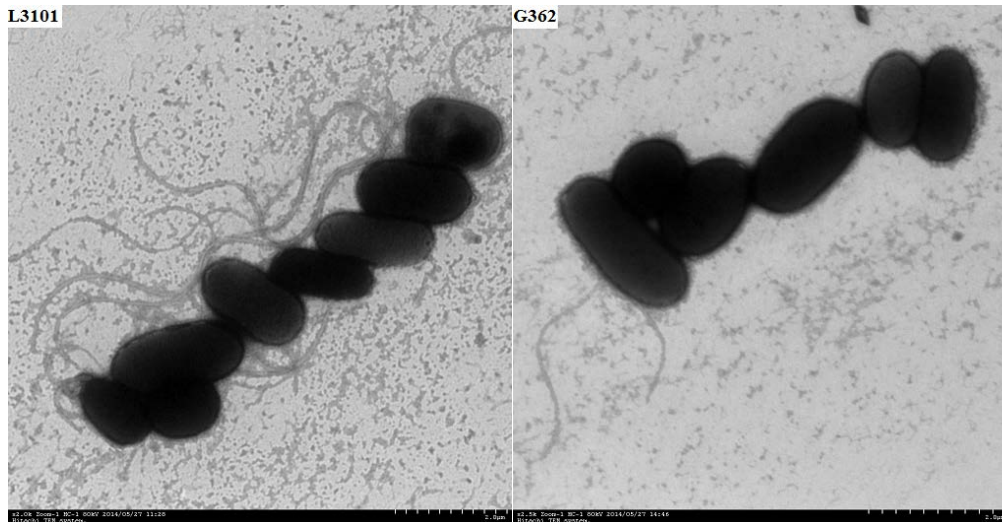
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**Supplemental Table S2.** Highest five pathway using analysis of Kyoto Encyclopedia of Gene and Genomes (KEGG)

Pathway	Refgene num
Ko02010, ABC transporters	185
ko02020, Two-component system	131
ko00230, Purine metabolism	77
ko00240, Pyrimidine metabolism	63
ko03010, Ribosome	59



**Supplemental Figure S1.** Alignment of transcripts with close species in NR data.



**Supplemental Figure S2.** Flagella biosynthesis of *Cronobacter* G362 and L3101 under 37°C for 16 h using transmission electron microscopy.