The Alphaproteobacterium *Caulobacter crescentus* displays a dimorphic life cycle where daughter cells after cellular division have differing morphology. To create differentiated daughter cells *C. crescentus* uses complex regulatory networks and asymmetrical distribution of cellular structures, making it a model organism for studying intracellular signaling and subcellular protein localization in bacteria. With increased whole genome sequencing it is becoming evident that the developmental signaling systems discovered in *C. crescentus* are conserved in whole or part in other Alphaproteobacteria, suggesting a conserved physiology among a large group of bacteria. Yet, the degree of conservation between organisms is unknown. Utilizing the fact that many regulatory genes are essential in *C. crescentus*, the essential genome of a closely related bacterium *Brevundimonas subvibrioides* was determined by saturating transposon mutagenesis (>1,000,000 mutants) followed by high-throughput sequencing of insertions. The results showed several differences between the organisms, including two key developmental regulators essential in *C. crescentus* that are non-essential in *B. subvibrioides* (GcrA and DivK), suggesting a change in operation. Mutants of these regulators display developmental defects, and in the case of *divK* the phenotypes are opposite of those displayed by a conditional *divK C. crescentus* mutant. These results suggest that genes conserved across large evolutionary distances can have important changes in operation across short evolutionary distances.