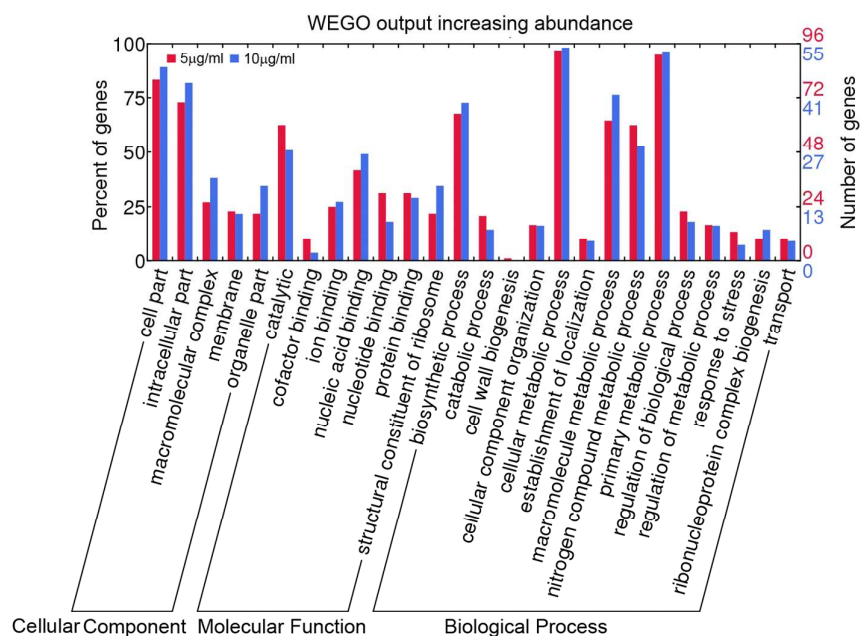
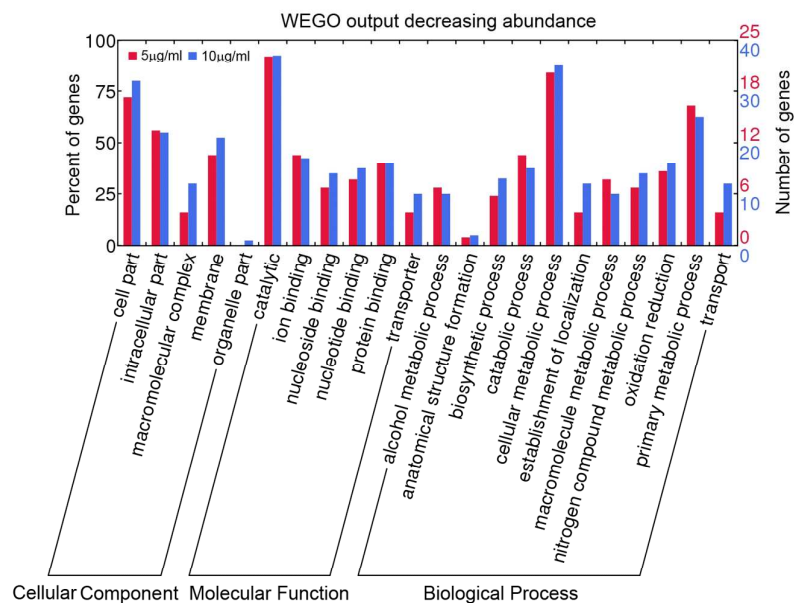


**Supplemental 4. SFigure1. Gene ontology categories for the differentially expressed proteins of *Aeromonas hydrophila* ATCC 7966 in oxytetracycline stress according to Wego analysis.** These proteins were classified into cellular component, molecular functions and biological processes. (A) and (B) Functional classification of the oxytetracycline-related (in both 5µg/ml and 10µg/ml OXY) differentially increasing and decreasing proteins, respectively.



A



B

Figure1