



**Fig. S1 Coregenome phylogeny of *Aeromonas hydrophila* GSH8-2 among publicly available 108 strains (updated at 2018/10/29).** Using the complete genome sequence of GSH8-2 (4,962,478 bp), bwa-read mapping analysis identified 48.95% of the full genome as core-genome sequence and a total of 491,764 single nucleotide variations (SNVs) were identified, excluding prophages and repeated regions.