Top 30 of GO Enrichment urea carboxylase activity succinate-semialdehyde dehydrogenase [NAD(P)+] activity succinate-semialdehyde dehydrogenase (NAD+) activity peptide-transporting ATPase activity hydro-lyase activity host cell surface receptor binding -DNA ligase (ATP) activity -Gene\_number dihydrolipoyl dehydrogenase activity -• 2 androstan-3-alpha,17-beta-diol dehydrogenase activity allophanate hydrolase activity -3-hydroxypropionyl-CoA dehydratase activity -3-hydroxybutyryl-CoA dehydrogenase activity -2-hydroxy-3-oxopropionate reductase activity -GO\_domain chromosome biological\_process urea catabolic process cellular\_component streptomycin biosynthetic process molecular\_function short-chain fatty acid catabolic process q\_value pyruvate metabolic process nucleotide-excision repair -0.20 nitrogen utilization -0.15 negative regulation of sporulation resulting in formation of a cellula etc... negative regulation of fatty acid biosynthetic process -0.10 modulation by symbiont of microbe-associated molecular pattern-induced etc... -0.05 lagging strand elongation gamma-aminobutyric acid catabolic process -DNA ligation cellular response to alkalinity carnitine metabolic process carnitine catabolic process branched-chain amino acid catabolic process -5.0 10.0 12.5 7.5 Rich Factor