GEM: Acidobacteriota

Pathway Features (y-axis, top to bottom):
- Mu-like prophage protein gp36
- Uncharacterized conserved protein, DUF1284 domain
- Uncharacterized protein, contains phage Mu head morphogenesis gpF-like domain
- Thiosulfate dehydrogenase TsdA, contains C-terminal cytochrome c domain
- Bifunctional DNA-binding transcriptional regulator of stationary/sporulation/toxin gene expression and antitoxin component of the YhaV-PrlF toxin-antitoxin module
- Flp pilus assembly protein, pilin Flp
- Mu-like prophage protein gp29
- Mu-like prophage FluMu protein gp28
- DNA-binding response regulator, ActR/RegA family, consists of REC and Fis-type HTH domains
- Uncharacterized phage-associated protein, contains DUF4065 domain
- Tagatose-1,6-bisphosphate aldolase non-catalytic subunit AgaZ/GatZ
- Mu-like prophage tail sheath protein gpL
- ABC-type microcin C transport system, duplicated ATPase component YejF
- Pectin methylesterase and related acyl-CoA thioesterases
- Uncharacterized conserved protein involved in copper resistance

Direction: ● Positive   ● Negative

x-axis: LASSO Coefficient (Absolute) Value
y-axis: Pathway Features