Supplemental Table S2. Significance and slope of the fit of the phylogenetic generalized least squares (PGLS) models between the reference GTA genes and putative head-completion protein in *Sphingomonadales*. Statistically significant associations (p-value <0.05) are highlighted in orange.

| Reference GTA gene | p-value  | Slope   |
|--------------------|----------|---------|
| g2                 | 0.82086  | -0.03579|
| g3                 | 0.59683  | 0.08254 |
| g4                 | 0.40305  | 0.13635 |
| g5                 | 0.21417  | 0.15219 |
| g6                 | 0.01450  | 0.41291 |
| g8                 | 0.83146  | 0.03253 |
| g10                | 0.50256  | 0.17411 |
| g11                | 0.00004  | 0.10553 |
| g12                | 0.03593  | 0.25124 |
| g13                | 0.85847  | 0.02868 |
| g14                | 0.00170  | 0.59603 |
| g15                | 0.00002  | 0.13779 |