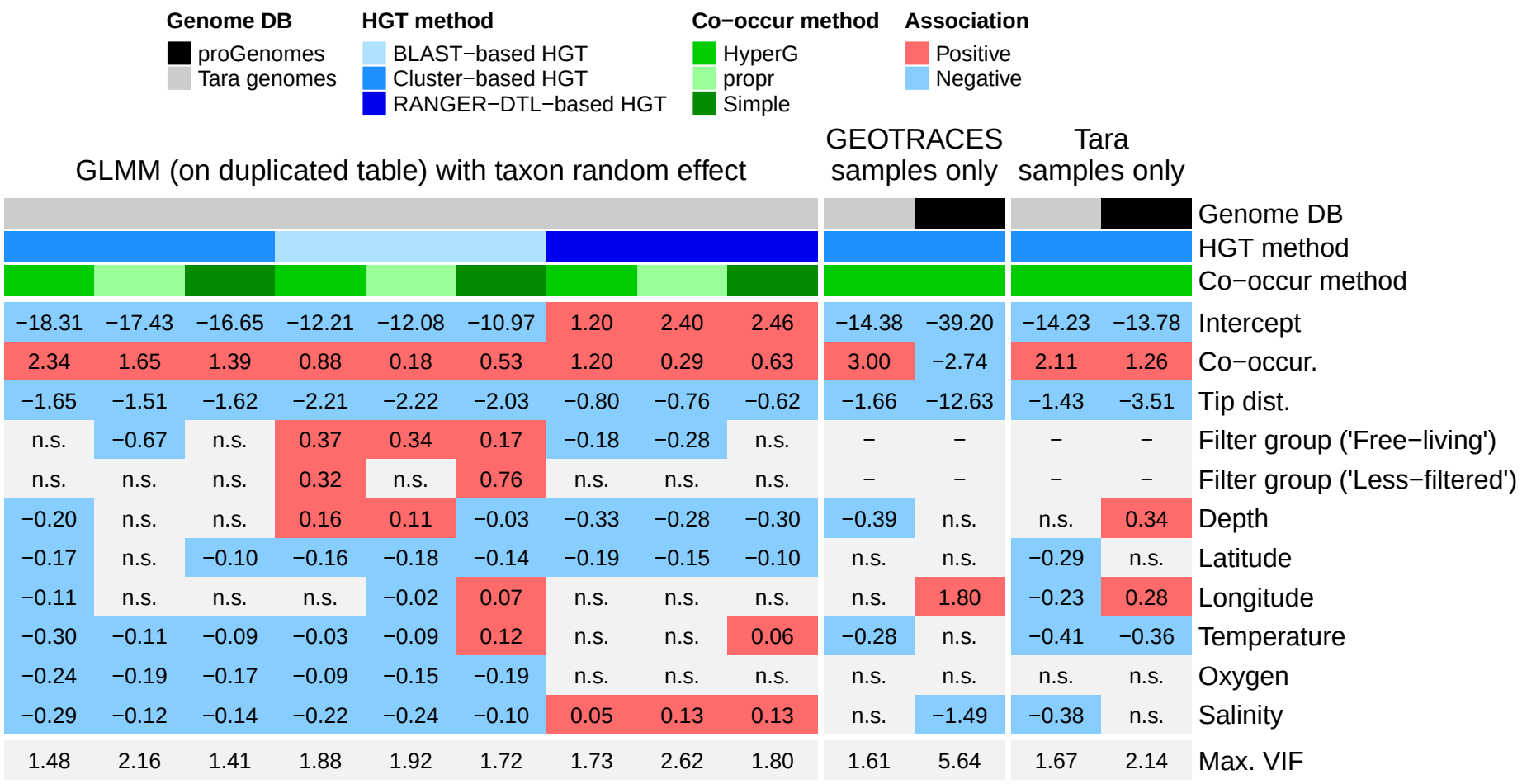
Genome DB
proGenomes
Tara genomes
HGT method
BLAST−based HGT
Cluster−based HGT
RANGER−DTL−based HGT
Co−occur method
HyperG
propr
Simple
Association
Positive
Negative
GLMM (on duplicated table) with taxon random effect
GEOTRACES samples only
Tara samples only
Genome DB
HGT method
Co−occur method
−18.31 −17.43 −16.65 −12.21 −12.08 −10.97 1.20 2.40 2.46 −14.38 −39.20 −14.23 −13.78 Intercept
2.34 1.65 1.39 0.88 0.18 0.53 1.20 0.29 0.63 3.00 −2.74 2.11 1.26 Co−occur.
−1.65 −1.51 −1.62 −2.21 −2.22 −2.03 −0.80 −0.76 −0.62 −1.66 −12.63 −1.43 −3.51 Tip dist.
n.s. −0.67 n.s. 0.37 0.34 0.17 −0.18 −0.28 n.s. – – – – Filter group ('Free−living')
n.s. n.s. n.s. 0.32 n.s. 0.76 n.s. n.s. n.s. – – – – Filter group ('Less−filtered')
−0.20 n.s. n.s. 0.16 0.11 −0.03 −0.33 −0.28 −0.30 −0.39 n.s. n.s. 0.34 Depth
−0.17 n.s. −0.10 −0.16 −0.18 −0.14 −0.19 −0.15 −0.10 n.s. n.s. −0.29 n.s. Latitude
−0.11 n.s. n.s. n.s. −0.02 0.07 n.s. n.s. n.s. n.s. 1.80 −0.23 0.28 Longitude
−0.30 −0.11 −0.09 −0.03 −0.09 0.12 n.s. n.s. 0.06 −0.28 n.s. −0.41 −0.36 Temperature
−0.24 −0.19 −0.17 −0.09 −0.15 −0.19 n.s. n.s. n.s. n.s. n.s. n.s. n.s. Oxygen
−0.29 −0.12 −0.14 −0.22 −0.24 −0.10 0.05 0.13 0.13 n.s. −1.49 −0.38 n.s. Salinity
1.48 2.16 1.41 1.88 1.92 1.72 1.73 2.62 1.80 1.61 5.64 1.67 2.14 Max. VIF