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Correction

Probe design for simultaneous, targeted capture of diverse metagenomic targets

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A local blast database used to disambiguate reads that mapped to the bacterial genomes used to validate the sepsis probe set contained mislabeled sequences. As a result, 80,130 of the 44,343,116 (0.18%) reads were assigned to the incorrect on-target taxa. This misassignment has no qualitative impacts on the described findings; it merely slightly adjusts the specific fold enrichment for each genus in Figure 5 and for each region in Figure 6. The authors apologize for any confusion that it has caused. Figures 5 and 6 have been corrected online.

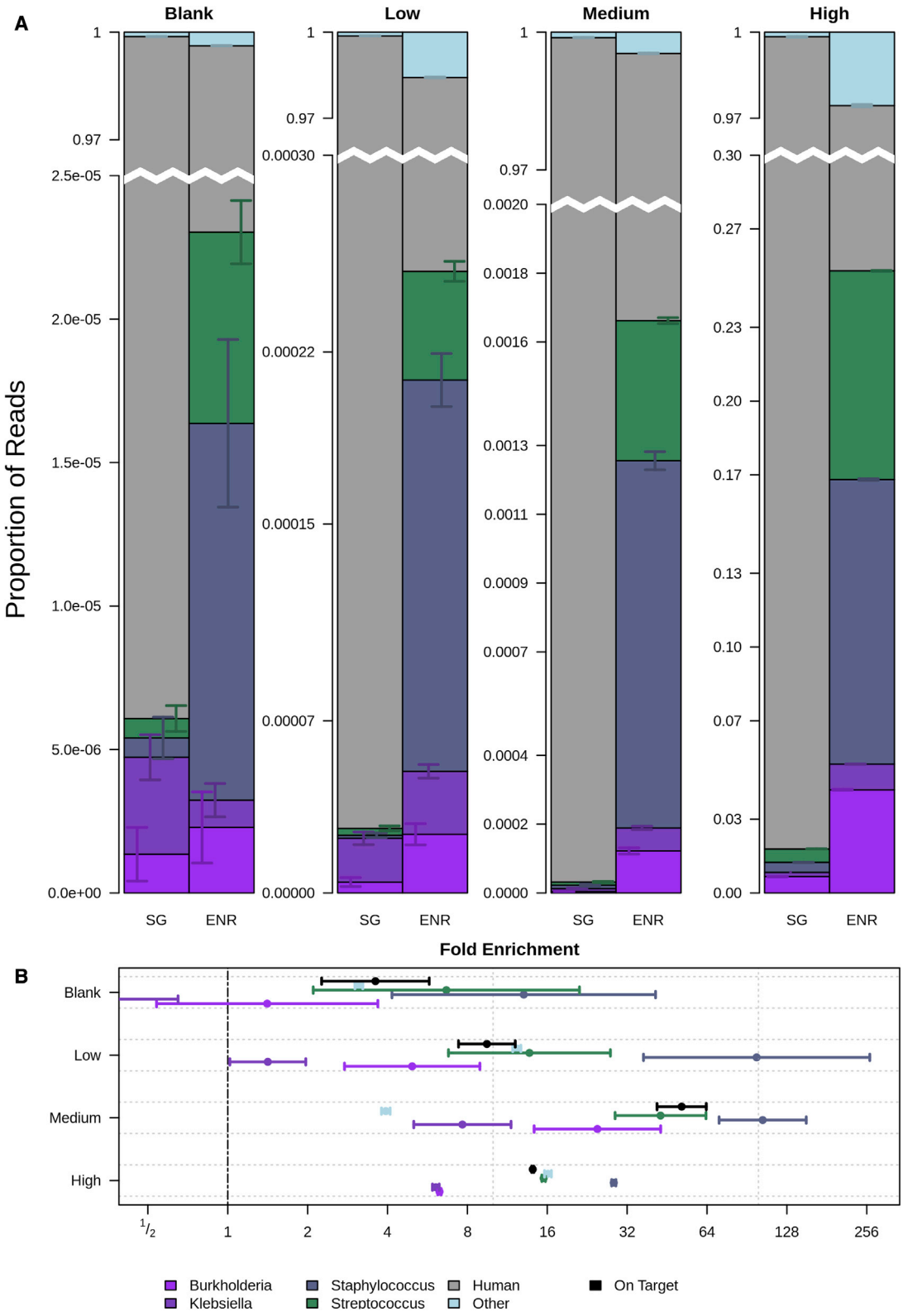

Figure 5. Fold enrichment of on-target sepsis reads (original)

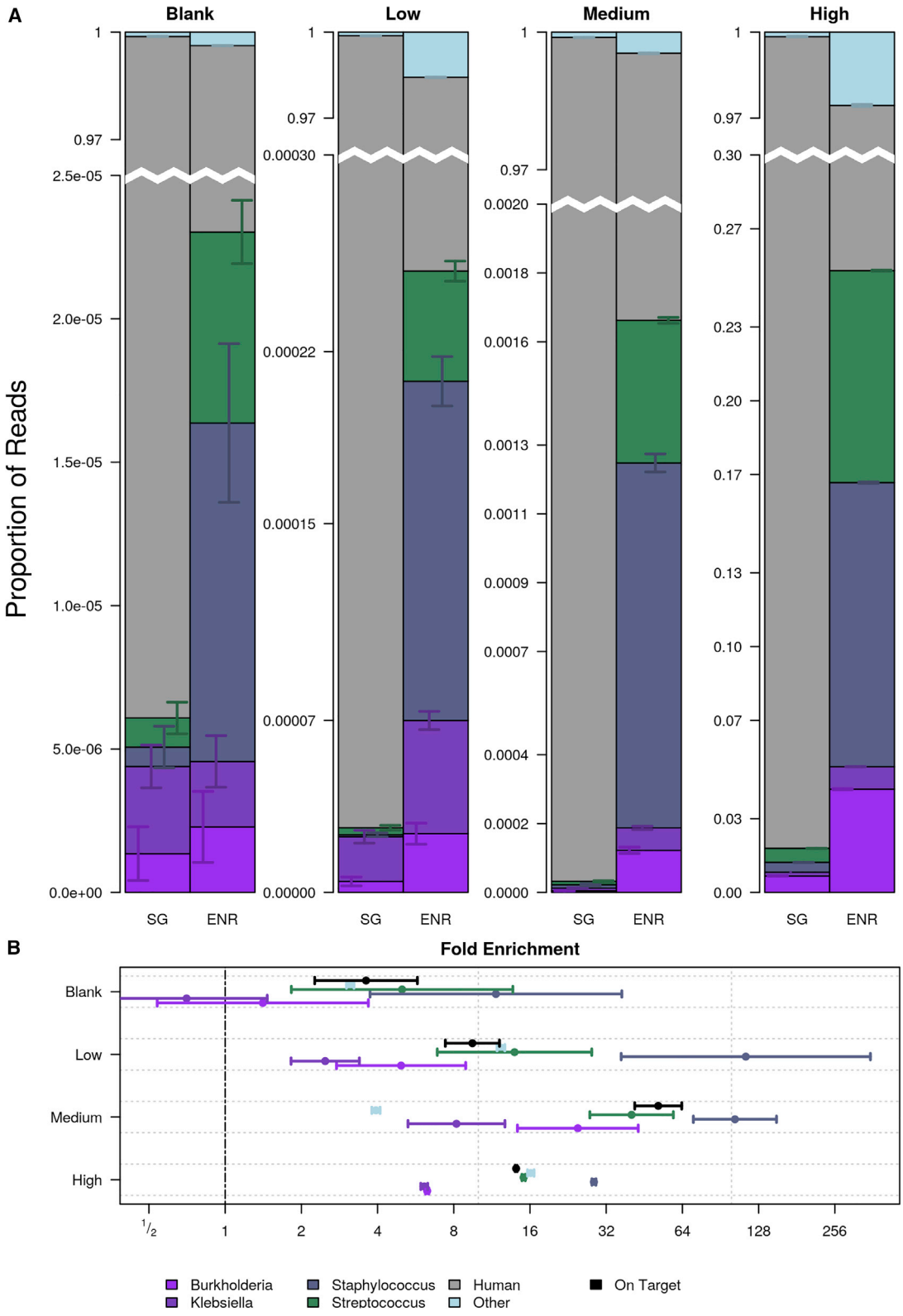

Figure 5. Fold enrichment of on-target sepsis reads (corrected)

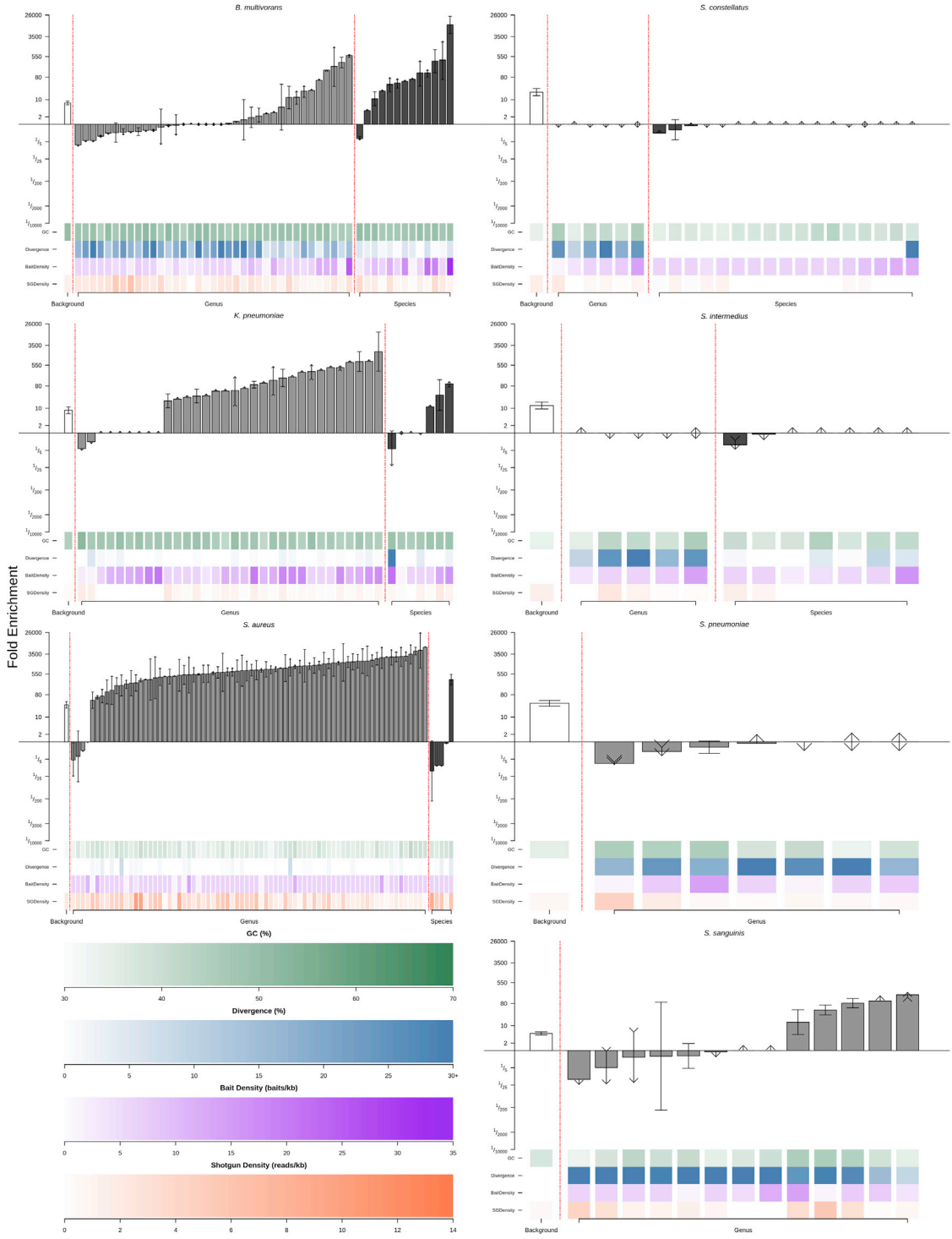

Figure 6. The fold enrichment within regions targeted by the sepsis probe set for each spiked strain (original)

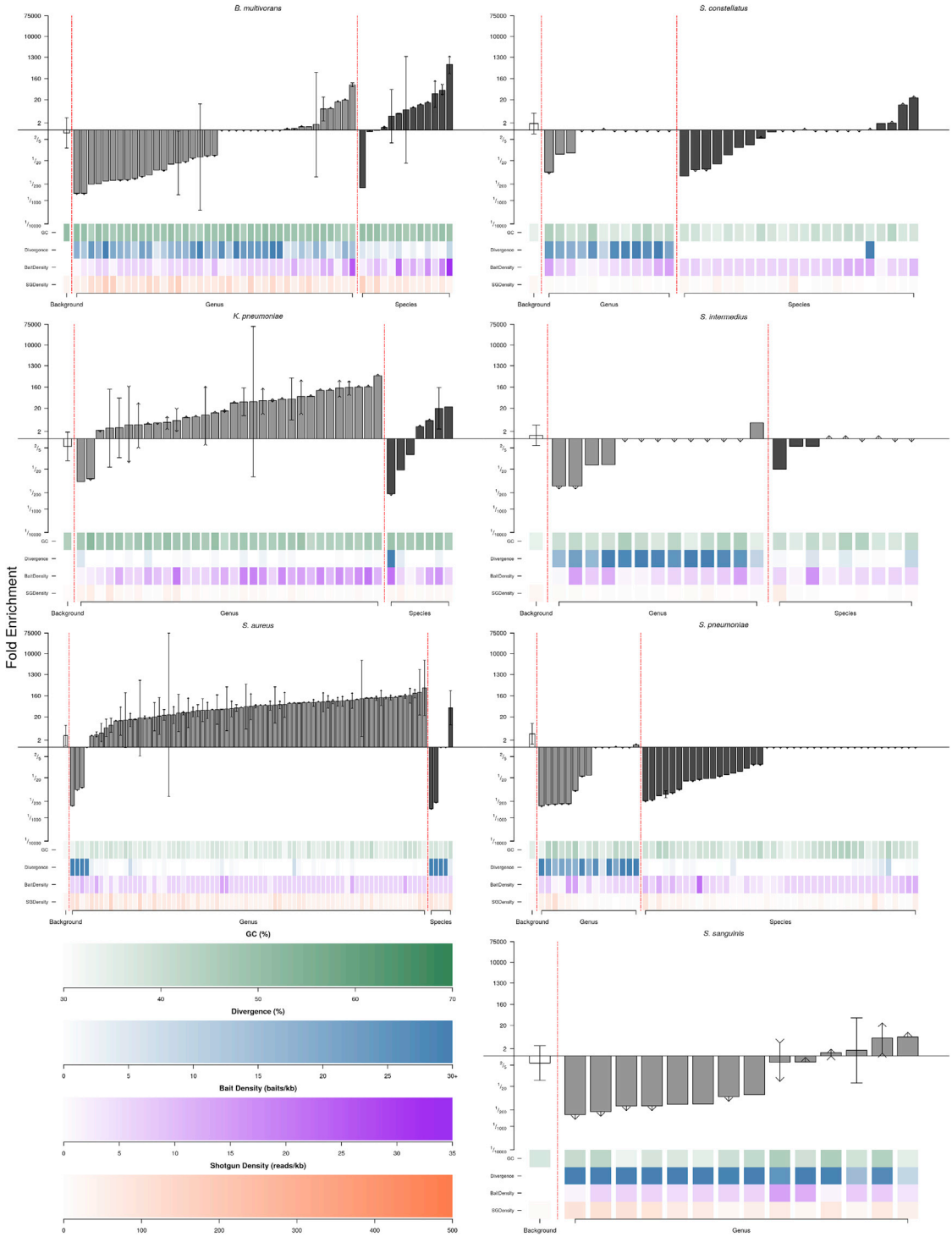

Figure 6. The fold enrichment within regions targeted by the sepsis probe set for each spiked strain (corrected)