Analysis scripts are available at: https://github.com/immanuelazn/saanich_denitrification_SI072

SUPPLEMENTARY FIGURES

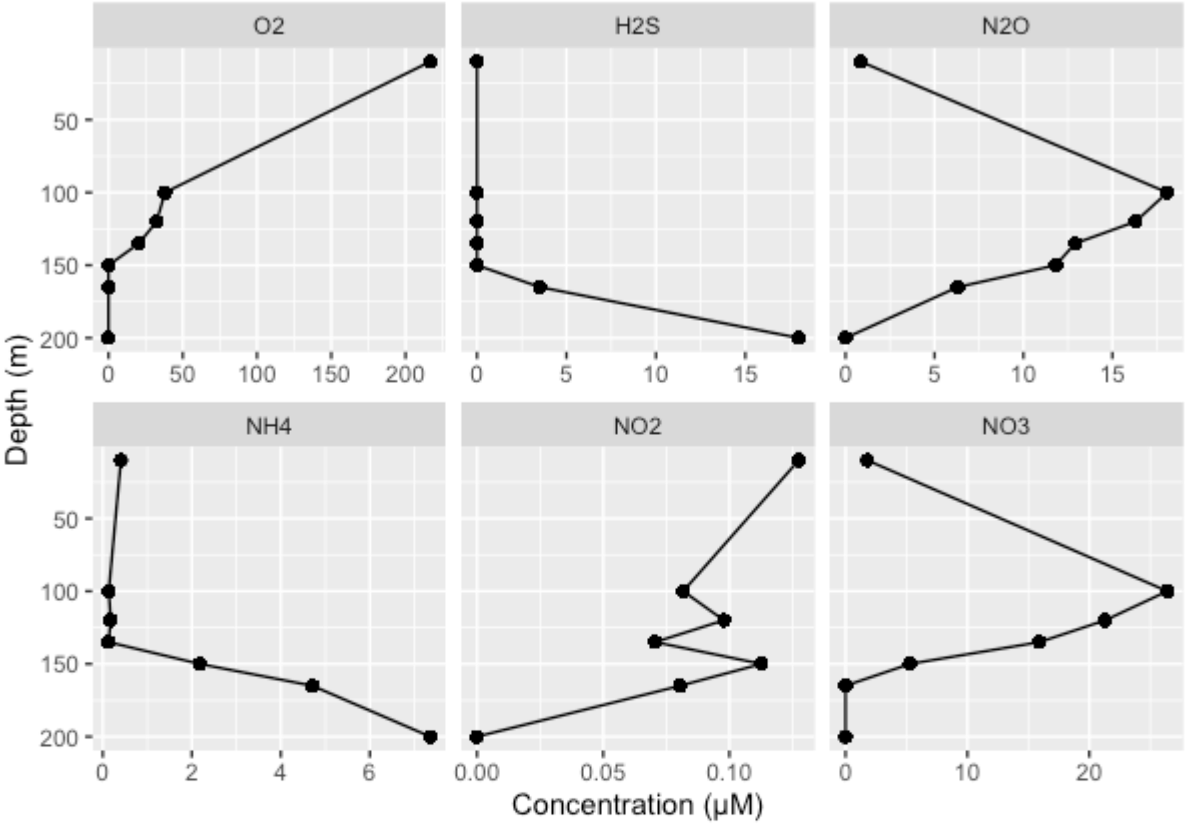

Figure S1. Nutrient concentrations measured across varying depths of the Saanich Inlet. [H_2S], [N_2O], [NH_4], and [NO_2] represent the mean concentration at the given depths of the Saanich Inlet. [O_2] was measured with conductivity, temperature, and depth (CTD) instrumentation. [O_2] decreases with depth while [NH_4] appears to increase past 150 m. [N_2O] and [NO_3^-] peak at a midway depth of approximately 100m. [NO_2^-] decreases until a fluctuation point between 100-150 m, after which it continues to decrease.

Gene product	**Metabolic reaction**	**$\Delta_f G^\circ$ (kcal/mol)**
NarI	$NO_3^- \rightarrow NO_2^-$	-69.334
NapA	$NO_3^- \rightarrow NO_2^-$	-74.12053
NirK	$NO_2^- \rightarrow NO$	-45.3
NorB	$NO \rightarrow N_2O$	8.969482
NosZ	$N_2O \rightarrow N_2$	34.26947

Table S1. Standard Gibbs free energy formation for each gene analyzed in the Denitrification pathway.

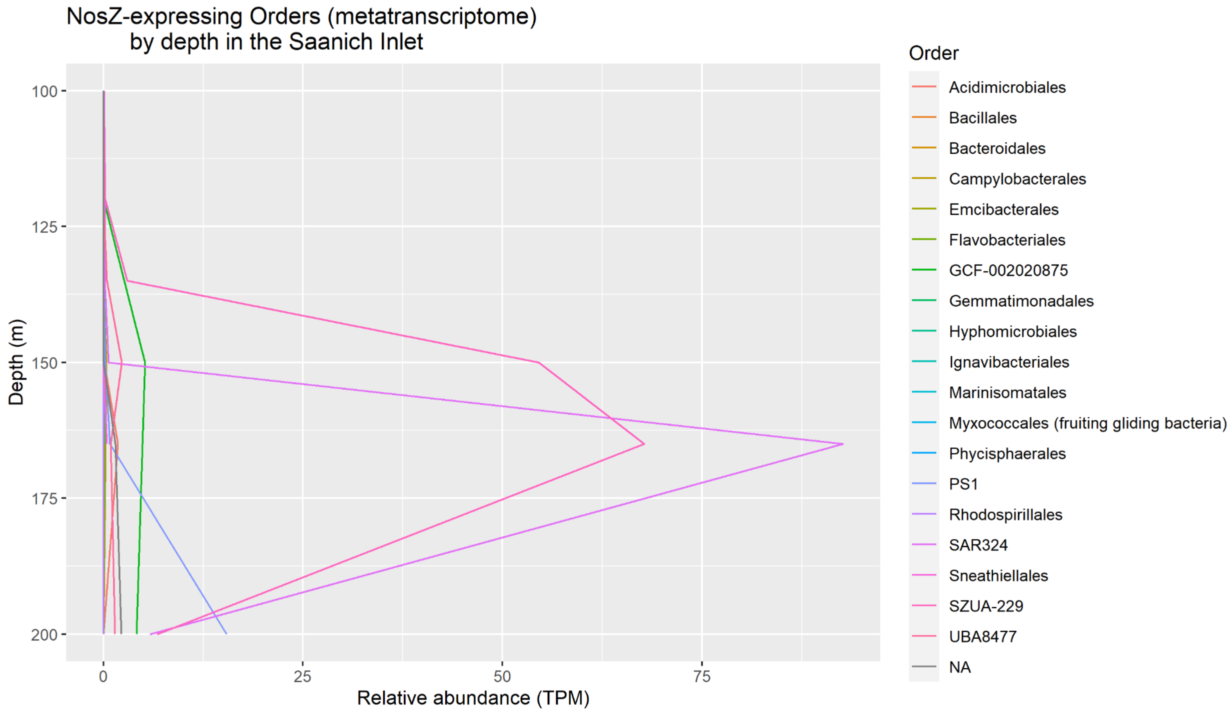

Figure S2. SAR234 and SZUA-299 dominate *nosZ* expression at 165 m. Figure depicting metatranscriptomic data for *nosZ* resolved to the order level.

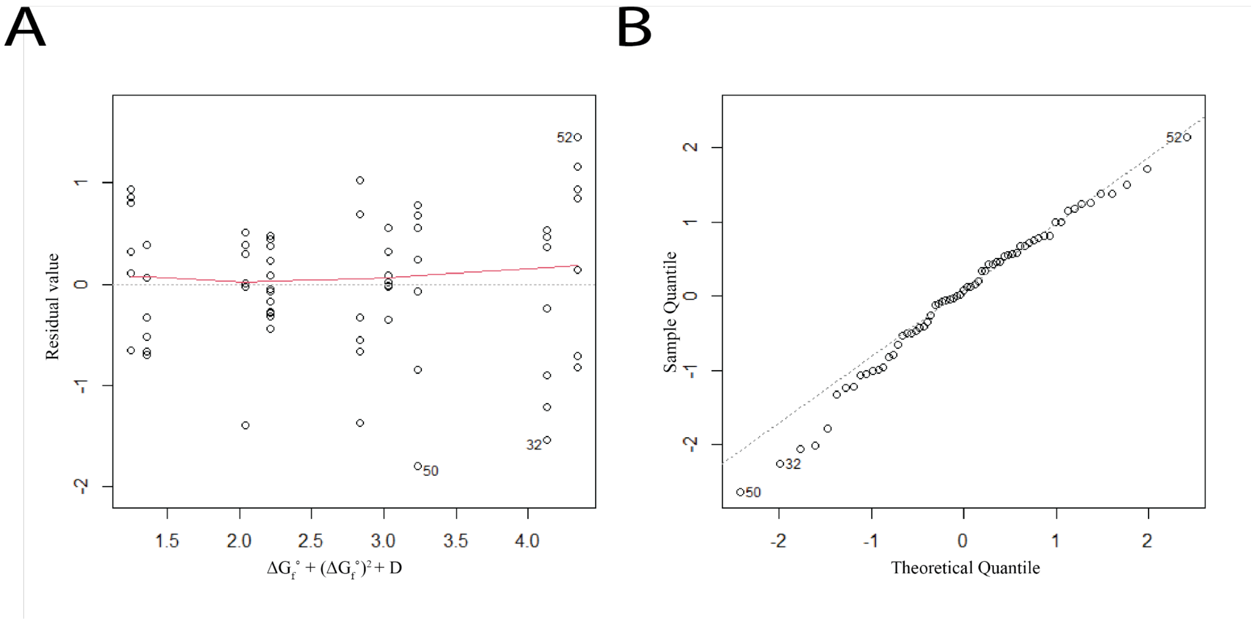

Figure S3. Diagnostic plots of the regression model between standard Gibbs free energy of reaction and Shannon diversity. A. Residuals compared to predictors. B. Quantile-quantile plot. Predictor variables exhibit a minor left skew.