Responses to Reviewer #1's Comments

※ Reviewer's comments in *italic* black; Our responses were made in blue; Our changes were made in red.

Dear, **Reviewer#1**,
We thank Reviewer #1 for the careful and constructive evaluation of our manuscript. The comments and suggestions have been highly valuable in improving both the clarity and rigor of the study. We have carefully considered each point and revised the manuscript accordingly. Our detailed, point-by-point responses are provided below. We hope that these revisions adequately address the concerns raised.

Reviewer comments and our responses	Page and line number for change (track-changes file)
1) I am not a specialist in genomics approaches but (or maybe because of that) I find that the Methods section lack literature references (with doi) for applied protocols, bioinformatics tools/pipelines and used databases. Hopefully, other reviewers more proficient in the field may assess whether the used methodology is sound. → We appreciate this comment. In response, we have added appropriate literature references (including DOIs) to each key step of the Methods section, including DNA quality verification (Desjardins and Condlin, 2010), library preparation (Klindworth et al., 2013), sequencing (Kozich et al., 2013), database (Sayers et al., 2021, Quast et al., 2013) and taxonomic analysis (Edgar, 2010). By explicitly linking each step of the workflow to established protocols and databases, we aim to provide a more robust methodological foundation and improve the clarity and credibility of the analytical procedures.	(Page 4) line 98–111
2) This said, the main and critical caveat of this work is, in my opinion, that the conclusions are not supported by the data and the interpretation of the results is sometimes way too speculative. → We thank the reviewer for this insightful comment. To strengthen the linkage between nutrient dynamics and genomic observations, we added depth-resolved vertical profiles (0–1000 m) of NO_3^-, PO_4^{3-}, and NO_3^-: PO_4^{3-} ratio, along with monthly NO_3^-–PO_4^{3-} scatter plots, prior to the genomic results (Section 3.1; Figure 2). These additions provide a quantitative nutrient context that frames the subsequent genomic analyses within a nutrient–genomic linkage framework. In addition, we revised the description of N-reducing genes and associated taxa to more precisely reflect that our results represent functional potential rather than direct measurements of N-loss rates. This clarification ensures that the interpretation remains consistent with the scope of gene-based analyses. Together, these revisions improve the clarity, structure, and interpretability of the manuscript by explicitly connecting nutrient distributions with genomic patterns while avoiding overinterpretation of gene-based results.	(Page 5–6) line 128–149 & (Page 11) line 249–252

3)The authors base their conclusions in a series of numbers (percentages of N-reducing genes and associated bacterial communities) which do not give sufficient quantitative information. → We agree that the original description did not clearly convey how the reported proportions were defined. We have therefore revised the text to explicitly clarify the basis of these calculations. Specifically, the proportion of N-reducing genes is now defined as the fraction of nitrate (N)-reduction genes relative to the total N-transformation gene pool (including ammonification, nitrification, and denitrification pathways). In parallel, the proportion of N-reducing taxa is now defined as the fraction of OTUs affiliated with known N-reduction lineages relative to the total detected bacterial taxa at the order level. These clarifications have been incorporated into the Results section and figure legends to ensure that the quantitative framework is transparent and that the interpretation of gene- and taxa-based proportions is unambiguous.	(Page 8–10) line 186–190, 195–197, 206–216
4) Throughout the manuscript, the authors state that they found « high » abundances of N-reducing genes; but high compared to what? → We thank the reviewer for this helpful comment. To improve clarity, we replaced qualitative expressions (e.g., “high”) with quantitative, pattern-based descriptions (e.g., “progressively increased with depth, reaching a maximum at…”), thereby more explicitly conveying the depth- and time-resolved variability in gene and taxa proportions in accordance with the purpose of the figures. Regarding comparisons with other regions, we note that directly comparable estimates of N-reducing gene or taxa proportions under fully oxic conditions are currently lacking due to differences in sampling design, temporal coverage, and analytical methods. Instead, we revised the Discussion to incorporate studies that explicitly report the presence of N-reducing genes in oxic marine environments and used these as a basis for contextual comparison. This approach allows us to situate our results within the broader framework of oxic N cycling while avoiding inappropriate numerical comparisons.	(Page 10–11) line 227–243, line 250–272
5) And how can we know that the obtained percentages are « enough » to explain the observed N:P ratios? → We thank the reviewer for this insightful comment. While our study does not directly quantify N-loss rates, previous studies have shown positive relationships between functional gene abundance and process rates, supporting the ecological relevance of gene-based metrics. In this context, our results suggest that N-reducing genes and affiliated taxa may represent a functionally relevant component of N cycling in the EJS. Although directly comparable abundance or ratio-based estimates from other oxic systems are limited, we incorporated studies demonstrating the presence of N-reducing genes under oxic conditions to provide context. Building on this, our study provides a depth-resolved and seasonally integrated baseline of N-reduction potential across the oxic water column of the EJS.	(Page 11) line 249–272

6) Moreover, seasonal and vertical variability is presented without really assessing the reasons and consequences of this variability. → We agree that the previous version did not sufficiently address the drivers and implications of the observed seasonal and vertical variability. In the revised manuscript, we explicitly link these patterns to physical and biogeochemical controls by describing how seasonal stratification and mixing regulate nutrient supply, particle production and export, and subsequent remineralization processes. We further clarify that particle-associated microenvironments can support nitrate reduction under oxygenated conditions, providing a mechanistic basis for the observed variability (e.g., Wolgast et al., 1998; Yamagishi et al., 2005; Cram et al., 2015). Importantly, while our primary objective is to assess whether N-reducing genes and their affiliated taxa are broadly and consistently distributed across space and time, we acknowledge that seasonal and vertical variability can influence these patterns and have incorporated this aspect into the Discussion, linking the observed variability to the development of N:P imbalances. These revisions strengthen the manuscript by providing a clearer mechanistic framework linking environmental variability to internal nitrogen loss and its role in maintaining low $NO_3^-:PO_4^{3-}$ ratios in the EJS.	(Page 12) line 295–316
7) Nutrient data collected during the cruises are exploited only superficially although they should be at the center of their study. In the current version, all nutrient data have been merged to produce a unique value of $NO_3:PO_4$ ratio which is not presented in the results section but in the introduction. I strongly suggest to present the nutrient profiles for each cruise to explore seasonal and vertical variability in the same way as the genomics data. This may allow to compare the variability between nutrients and genomics data which may help assessing the role of N-reducing pathways in N loss in the water column. The Results and Discussion section reads more like a literature review of the factors that may drive N:P ratios in the study area and I found that the results are not discussed enough. → We thank the reviewer for this constructive comment and agree that nutrient data were not sufficiently integrated into the Results in the previous version. In the revised manuscript, we reorganized the Results and Discussion to place nutrient data at the center of the analysis. Cruise-resolved vertical profiles of NO_3^-, PO_4^{3-}, and $NO_3^-:PO_4^{3-}$ ratio are now presented in Figure 2 and Section 3.1 using the same depth framework as the genomic dataset. In this section, we describe the key seasonal and vertical features of nutrient distributions to provide the environmental background for the genomic results. The genomic data are then interpreted within this framework, allowing direct comparison of variability between nutrient and genomic patterns. We also revised the Discussion to reduce descriptive content and focus on interpreting the results. These changes establish a clearer nutrient–genomic linkage and strengthen the overall interpretation of nitrogen-reducing processes in the water column.	(Page 5–6) line 128–149

8) Moreover, there are a number of inconsistencies in the arguments given. For instance, the first part of the section claims that external phosphorus inputs are insufficient to explain low N:P ratios but later on, the authors state that N-enriched atmospheric deposition is responsible for high N:P ratios in surface waters. Again, presenting nutrient profiles will be very useful to understand whether N:P ratios are indeed higher in the surface that in deeper waters. → We thank the reviewer for this comment and agree that the previous version did not clearly distinguish processes across depth and timescales, which may have led to confusion. In the revised manuscript, we explicitly separate two independent aspects of the study. The evaluation of phosphorus sources (Section 3.4) assesses whether enhanced P supply can explain the low N:P ratios, which we find unlikely, and Sections 3.1 → 3.4 have been reorganized to provide a clearer progression toward this conclusion. In contrast, the discussion of implications addresses how N:P ratios may be influenced by different processes operating on distinct timescales. These two components therefore address different questions and are not intended to provide alternative explanations for the same observation. We further distinguish short- and long-term processes operating at different depths. Newly added cruise-resolved vertical profiles of NO_3^-, PO_4^{3-}, and NO_3^-:PO_4^{3-} show that surface waters exhibit relatively higher and more variable N:P ratios, whereas deeper waters maintain persistently low values. This vertical structure supports our interpretation that atmospheric N deposition may act as a short-term surface forcing, while long-term processes such as reduced ventilation and deoxygenation may enhance nitrogen loss at depth. These processes are therefore not contradictory but represent scale-dependent forcing operating in different parts of the water column. By incorporating the observed vertical structure, the revised manuscript provides a more robust and internally consistent framework for interpreting the mechanisms and implications of low N:P ratios in the East Sea.	(Page 5–6) line 128–149 & (Page 13–14) line 332–374
Specific comments and our responses	Page and line number for change (track-changes file)
9) Lines 57-59. If low N:P ratios are a known feature of the EJA, I suggest the authors refer to literature data in the introduction and present their own data in the results section in a more detailed way. → We thank the reviewer for this helpful suggestion. In the revised manuscript, we have incorporated literature-based estimates of NO_3^-:PO_4^{3-} ratios in the East/Japan Sea to clearly contextualize the long-standing observation of low N:P values and to better link these findings to the central message of our study. In addition, we introduced new depth-resolved profiles of NO_3^-, PO_4^{3-}, and NO_3^-:PO_4^{3-} ratios from the 2021 observations (Fig. 2), providing a detailed nutrient background prior to the genomic analysis. These revisions strengthen the data-driven framework of the manuscript and more clearly position our results as contributing mechanistic insight into the persistently low NO_3^-:PO_4^{3-} signature of the system.	(Page 3) line 60–68 & (Page 6) Figure 2

10) Lines 64-66. Since genomics-based techniques are experiences rapid advances, the authors may want to cite more recent references. → We appreciate this suggestion and have revised the manuscript accordingly. We added four recent references to better position our approach within current frameworks linking microbial communities to biogeochemical (nitrogen) cycling, and to clarify both the interpretative basis and limitations of inferring functional potential from 16S rRNA gene data. These additions strengthen the conceptual grounding and transparency of our analysis.	(Page 3) line 76–78
11) Line 81. I guess it was filters and not filtered samples that were frozen and used for DNA extraction. Line 83. Same comment as above. → Thank you for the referee for pointing out this wording issue. We have revised the text to clarify that the membrane filters, rather than the filtered seawater samples, were frozen and used for DNA extraction.	(Page 4) line 93–96
12) As said before, the results and discussion section is awkward. Indeed, only 3.2. sub-section is properly results and a bit of light discussion. Sub-section 3,1 reads more like a literature review. → We thank the reviewer for this constructive comment and have substantially revised the structure of the Results and Discussion sections. In the revised manuscript, Section 3.1 has been reorganized to present depth-resolved NO_3^-, PO_4^{3-}, and NO_3^-:PO_4^{3-} profiles from the 2021 observations, providing a data-driven nutrient background rather than a literature-based overview. The Results are now clearly separated from broader contextual discussion, and the manuscript has been restructured to emphasize direct interpretation of the observational and genomic data. These changes ensure that the Results section is centered on our dataset and that subsequent discussion builds explicitly on these findings.	(Page 5) Line 128–149
13) Lines 139-140. Please, add references for the selected biomarker genes. → We have added appropriate references supporting the use of the selected biomarker genes for the corresponding N transformation pathways. These genes have been widely used and validated in previous studies, and the added references clarify their established relevance. This revision strengthens the methodological foundation and improves the robustness of our interpretations.	(Page 7) line 179
14) Figure 2. Is there a possibility of adding error bars? → We thank the reviewer for this helpful suggestion. Error bars can typically be derived from (i) biological or technical replicates, (ii) variability within defined depth bins, or (iii) pipeline-based uncertainty estimates. However, the present dataset represents single observations at each cruise-depth point during the 2021, and replicate measurements are not available. In addition, our objective is to illustrate the vertical and spatiotemporal consistency of nitrate-reduction–associated gene proportions rather than to quantify variability within grouped samples. Pipeline-related uncertainties are already well constrained in previous studies and referenced in the Methods. Therefore, instead of adding error bars, we have clarified the nature of the data and its interpretation in the figure caption and main text.	(Page 8) line 190

15) Line 169. Aren't some of these orders (e.g. Alteromonadales, Pseudomonadales) ubiquitous in the ocean? → We agree that several of the identified taxa are widely distributed in marine environments. Our interpretation, however, is not based on their regional specificity but on their functional potential and consistent co-occurrence with nitrate-reduction–associated genes throughout the water column. To clarify this point, we revised the manuscript to explicitly avoid implying regional uniqueness and instead frame these taxa within a broader ecological context. Previous studies show that many of these heterotrophic groups are commonly associated with sinking particles and organic-matter-rich microenvironments, where localized oxygen depletion can occur even in otherwise oxic waters. Such particle-associated micro-niches have been identified as sites where nitrate reduction and denitrification can proceed under suboxic conditions, providing a plausible mechanism linking the observed taxa and gene distributions to N-reducing processes in the water column. This revision strengthens the mechanistic basis of our interpretation without relying on taxonomic uniqueness.	(Page 10) line 230–243
16) Line 178-179. The statement that proportions of 37.7% of N-reducing genes and 20.0% of taxa indicate the potential for bacterially mediated N loss is not very convincing. How these numbers compare with other regions? → We appreciate the referee's suggestion to place our findings in broader quantitative context. Direct numerical comparison remains inherently limited because nitrate-reduction pathways have been predominantly studied in anoxic environments (e.g., sediments and OMZs), and depth- and temporally resolved observations from fully oxygenated water columns are still scarce. In addition, differences in analytical approaches and gene normalization across studies further constrain direct comparisons on a common quantitative basis. Nevertheless, following the reviewer's suggestion, we have expanded the discussion to include studies reporting nitrate-reduction–associated genes (e.g., *nar* and *nir*) and their affiliated taxa in oxic open-ocean environments, thereby providing a relevant comparative context for our observations. Importantly, we clarify that our analysis does not infer N removal rates, but instead characterizes the depth- and time-integrated distribution of nitrate-reduction–associated functional potential. This distinction is now explicitly stated to avoid overinterpreting gene-based metrics as rate-based processes.	(Page 10–11) line 249–272

Responses to Reviewer #2's Comments

※ Reviewer's comments in *italic* black; Our responses were made in blue; Our changes were made in red.

Dear, **Reviewer#2**,

We sincerely thank Reviewer #2 for the careful evaluation and constructive comments. The reviewer's suggestions have significantly improved the clarity and precision of the manuscript, particularly by prompting us to refine ambiguous statements, better articulate the unresolved aspects of N:P regulation in the East/Japan Sea, and incorporate additional supporting evidence and literature. These revisions have helped us strengthen the logical flow of the Results and Discussion and present our conclusions more clearly. We have revised the manuscript accordingly and address each comment in detail below.

Reviewer comments and our responses	Page and line number for change (track-changes file)
1) Overall, the paper is well written and clear. However, I think that the evidence given in the manuscript does not justify the conclusion. First, the water column in the EJS is well oxygenated (Fig. 1B). So, even a proposed reduction in 20 M O_2 will not make the deep ocean anoxic. Therefore, the proposed dual-scale feedback seems to be irrelevant to the EJS. →Thank you for this insightful comment. We agree that the East/Japan Sea remains well oxygenated and that a reduction of ~20 μM O_2 would not lead to the development of anoxic conditions. We recognize that our previous wording may have overstated this aspect and caused confusion regarding the relevance of the proposed dual-scale framework. To address this, we have revised the manuscript to explicitly frame the longer-timescale component in terms of progressive deoxygenation rather than anoxia. Specifically, we now clarify that climate-driven surface warming reduces water density, suppresses deep-water formation, and weakens ventilation, allowing continuous biological remineralization to gradually consume oxygen at depth. This revision makes clear that the proposed mechanism operates entirely within an oxic system. In addition, we reorganized the section to clearly distinguish short-term surface forcing from longer-term subsurface responses, and refined the final paragraph to explicitly summarize the dual-timescale framework and its implications. In particular, we now clarify how surface N enrichment and subsurface nitrate reduction act in opposite directions, potentially amplifying vertical NO_3^-:PO_4^{3-} gradients over time. These revisions directly address the reviewer's concern by clarifying that the proposed feedback does not rely on the development of anoxic conditions, but instead reflects gradual shifts in the balance of the reactive N inventory under ongoing deoxygenation.	(Page 15) line 405–420

2) The author also mentions in the abstract that low $NO_3:PO_4$ in the well-oxygenated EJS is a “long-standing biogeochemical enigma”. This is the first time I have heard of this interesting enigma, and I would like to understand more about how past studies have approached it. The authors only provide a general statement (“Much of our current understanding of marine N cycling ...” LN 50). It is missing to understand what has been done until today. →Thank you for this important comment. We agree that the previous version did not sufficiently contextualize the “long-standing biogeochemical enigma” of low NO_3^{-}:PO_4^{3-} ratios in the EJS within the framework of prior studies, which may have limited the reader’s ability to understand how this problem has been approached and why it remains unresolved. To address this, we have substantially revised the Introduction to provide a more structured and explicit synthesis of prior work. Specifically, we now summarize that previous studies consistently reported N:P ratios below the Redfield ratio throughout much of the water column, indicating persistent N limitation, and proposed several explanations, including physical circulation and remineralization processes (Kim and Kim, 2013), lateral inputs from the East China Sea (Lee et al., 2009), and the possibility of denitrification (Yanagi, 2002). We further clarify that substantial denitrification is difficult to reconcile with the well-oxygenated conditions of the basin, leaving the mechanism responsible for maintaining low NO_3^{-}:PO_4^{3-} ratios unresolved. Importantly, we now explicitly distinguish between established findings and remaining uncertainties, thereby reframing the persistence of low NO_3^{-}:PO_4^{3-} ratios under oxic conditions as a clearly defined and unresolved biogeochemical problem. In doing so, the revised text directly links prior hypotheses to their limitations and more clearly positions our genomic analysis as a targeted and testable approach to address this gap. As a result, the manuscript now provides a more coherent and complete research context, enabling readers to understand both the progression of previous work and the specific contribution of the present study. These revisions directly address the reviewer’s concern by clarifying what has been done to date and how our study advances beyond existing explanations.	(Page 3) line 60–68

3) P-balance: The riverine P balance has not been sufficiently analyzed. I would like to get more quantitative information about the riverine input – when was the dam constructed? What is the NO_3:PO_4 in the CDW? What do you mean by "confined to surface layers"? It is possible that the low NO_3:PO_4 is due to past influx? I would like more quantitative information on the long-term NO_3:PO_4 balance for the EJS. →Thank you for this constructive comment. We have revised the manuscript to provide clearer and more quantitative constraints on riverine phosphorus inputs in the EJS. First, we now specify that the Nakdong River estuarine barrage was constructed in 1990 and include its mean discharge (~0.0004 Sv), demonstrating negligible basin-scale input. Second, we added quantitative information on CDW, which exhibits high DIN:DIP ratios (50–100 near the source, decreasing offshore; Lee et al., 2009). Third, we clarify that Changjiang-derived freshwater forms a buoyant plume confined to the upper mixed layer due to density stratification, limiting its vertical influence (Tseng et al., 2014). Together, these constraints indicate that riverine and CDW inputs—being surface-confined, seasonally variable, and N-enriched—cannot sustain a basin-wide, depth-coherent low NO_3^-:PO_4^{3-} signal, even via past transport to deeper waters. We also clarify that the long-term NO_3^-:PO_4^{3-} balance of the EJS is introduced in the Introduction as the framework for evaluating these mechanisms.	(Page 13–14) line 330–372
4) Furthermore, what about the release of P from anoxic sediment? →Thank you for this insightful comment. We have now explicitly addressed the potential role of sedimentary P release in the revised manuscript to ensure that all plausible P sources are systematically evaluated. While phosphorus release from anoxic sediments can occur under reducing conditions, we clarify that this mechanism is unlikely to exert a significant influence on the water-column nutrient budget of the EJS. Sediment studies in the EJS indicate that phosphorus is predominantly retained through burial and adsorption processes, and that phosphate released during early diagenesis is efficiently scavenged by iron oxides under largely oxic conditions (Cha et al., 2005). Importantly, this constrains both the magnitude and vertical reach of sediment-derived phosphorus fluxes, making them insufficient to influence basin-scale NO_3^-:PO_4^{3-} stoichiometry across the full water column. This clarification has been incorporated into Section 3.4, where sedimentary phosphorus release is evaluated alongside other external and internal sources within a consistent basin-scale framework. These revisions directly address the reviewer's concern by demonstrating that sedimentary phosphorus inputs are unlikely to account for the observed NO_3^-:PO_4^{3-} patterns in the EJS.	(Page 14) line 366–372

5) I am not so familiar with the sequencing protocol, so I am unable to evaluate it. However, to gain more quantitative intuition into the significance of the N-reducing genes, it would be beneficial to compare them with other locations. Perhaps other studies showed the relationship between N-reducing genes and rates? →Thank you for this constructive comment. We understand that the reviewer is seeking a clearer quantitative context for interpreting the significance of N-reducing genes, including comparison with other environments and their relationship to process rates. To address this, we first clarify that the gene abundance and taxonomic composition data used in this study are based on relative, rather than absolute, measurements and therefore do not provide direct quantitative estimates of nitrogen loss rates. This limitation has now been explicitly stated in the Materials and Methods section, and the manuscript has been revised to avoid direct interpretation in terms of rates. To provide a more quantitative and comparative context, we have expanded the Discussion to incorporate previous studies that (i) report positive relationships between functional gene abundance and process rates across diverse ecosystems (Rocca et al., 2015), and (ii) document the widespread presence of nitrate-reduction genes (e.g., *nir*, *nar*) and affiliated taxa in oxic marine environments, including particle-associated and fully oxygenated systems (e.g., Li et al., 2018; Wan et al., 2023; Broman et al., 2021). Importantly, we emphasize that these studies do not establish direct rate equivalence, but collectively indicate that nitrate-reduction potential can represent a non-negligible component of nitrogen cycling under oxic conditions. Within this constrained framework, the relatively high and vertically persistent proportions observed in the EJS suggest an elevated and integrated reservoir of nitrate-reduction potential compared to typical oxic systems. We also explicitly acknowledge the limitations of cross-system comparisons due to differences in normalization, sequencing depth, and ecosystem structure, and therefore avoid direct numerical comparisons. Instead, we frame our results as providing a depth-resolved baseline for nitrate-reduction potential within a single, well-characterized system. Together, these revisions directly address the reviewer's request by providing a clearer quantitative and comparative context, while maintaining a conservative interpretation grounded in the limitations of the data.	(Page 10) line 230–243 & (Page 11) Line 249–272

6) Is it possible to plot NO_3:PO_4 vs. depth? →Thank you for this helpful suggestion, which we have incorporated in the revised manuscript. Using the full observational dataset collected over five cruises in 2021 (surface to 1000 m), we now present depth-resolved NO_3^-, PO_4^{3-}, and NO_3^-:PO_4^{3-} profiles in Figure 2, plotted at the same vertical resolution as the genomic data and described in a newly added Section 3.1. This addition enables direct comparison between nutrient structure and genomic patterns and establishes a clearer observational framework for interpreting N:P variability. The results consistently show higher and more variable NO_3^-:PO_4^{3-} ratios in surface waters and persistently lower ratios at depth, reproducing the characteristic low N:P signature of the East/Japan Sea across the study period. While this vertical structure cannot be directly attributed to a specific forcing, it provides an important observational constraint for our dual-timescale interpretation. Specifically, it is consistent with short-term surface forcing elevating NO_3^-:PO_4^{3-} ratios and longer-term deoxygenation reducing deep-water ratios. We have incorporated this observation into Section 3.5 to more explicitly frame how these processes may act together to strengthen the vertical contrast under future forcing scenarios. Together, these revisions establish a more coherent linkage between nutrient observations and nitrate-reduction–associated processes, strengthening the overall interpretative framework of the study.	(Page 5–6) Line 128–149
Minor comments and our responses	Page and line number for change (track-changes file)
7) line 35 - > cite Tyrell 'The relative influences of nitrogen and phosphorus on oceanic primary production' (1999) → We have now cited Tyrrell (1999) in the Discussion and incorporated it to frame our interpretation of N:P regulation in terms of the balance between nitrogen fixation and denitrification controlling the oceanic nitrogen inventory.	(Page2) line 36
8) Line 50 -> cite Martiny et al., 'Strong latitudinal patterns in the elemental ratios of marine plankton and organic matter', 2013. → We have incorporated Martiny et al. (2013) at this point to support and contextualize the statement, highlighting that while the global NO_3^-:PO_4^{3-} ratio approximates the Redfield ratio, substantial regional variability in marine N:P stoichiometry is well documented.	(Page 3) line 51

9) Line 50: What do you mean by "circulation terminates"? → We thank the reviewer for pointing out this ambiguity. In the revised manuscript, we replaced the phrase "circulation terminates" with a more precise description, stating that this region represents the terminal part of the global overturning circulation and contains relatively old deep waters. We further clarify that the lower oxygen concentrations reflect the cumulative effect of respiratory oxygen consumption along the circulation pathway.	(Page 3) line 53–54
10) Line 60: "Much of our current understanding of marine N cycling..." is it a general statement or is it specific to the EJS? → We thank the reviewer for this helpful comment. Our intention was to refer to the broader development of research on microbial nitrogen cycling processes rather than a region-specific context. In the revised manuscript, we have clarified this by removing ambiguous wording and refining the sentence to explicitly describe a general marine context, thereby improving both precision and readability.	(Page 3) line 71–72