

## SUPPLEMENTARY MATERIALS

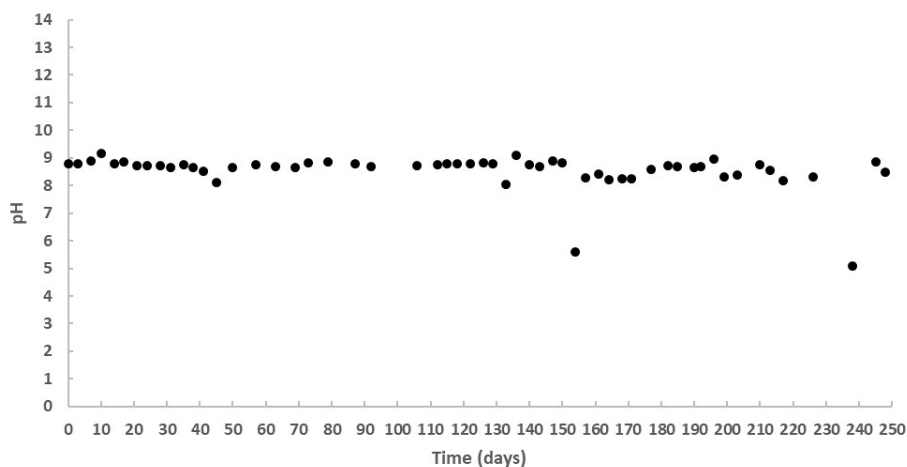


Figure S1. Values of pH measured in the outlet along reactor operation.

| Functional Group | Bacterial genera                 | Phase I | Phase II | Phase III | Phase IV | Phase V | Phase VI | Phase VII | Phase VIII | Phase IX |
|------------------|----------------------------------|---------|----------|-----------|----------|---------|----------|-----------|------------|----------|
|                  |                                  | d0      | d14      | d36       | d63      | d90     | d122     | d168      | d199       | d248     |
| AOB              | <i>Nitrosomonas</i>              | 1.6     | 1.9      | 0.0       | 0.0      | 0.0     | 0.6      | 1.2       | 1.2        | 1.2      |
| NOB              | <i>Nitrospira</i>                | 1.0     | 3.1      | 0.0       | 0.0      | 0.0     | 1.0      | 0.0       | 0.0        | 0.6      |
| NOB              | <i>Nitrobacter</i>               | 0.0     | 0.0      | 0.0       | 0.0      | 0.0     | 0.0      | 0.3       | 0.3        | 0.4      |
| Anammox          | <i>Candidatus Kuenenia</i>       | 0.2     | 0.1      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| PAO              | <i>Tetrasphaera</i>              | 0.7     | 0.3      | 0.0       | 0.0      | 0.0     | 0.9      | 0.6       | 0.6        | 0.7      |
| PAO              | <i>Gemmatimonas</i>              | 2.2     | 2.4      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.3      |
| PAO              | <i>Candidatus Accumulibacter</i> | 0.5     | 0.0      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| PAO              | <i>Dechloromonas</i>             | 0.0     | 0.5      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| GAO, DNB         | <i>Defluviicoccus</i>            | 0.0     | 0.0      | 0.0       | 0.0      | 0.0     | 0.1      | 0.3       | 0.4        | 2.9      |
| DNB              | <i>Nitratireductor</i>           | 0.0     | 0.0      | 0.0       | 0.0      | 0.0     | 0.2      | 0.2       | 0.3        | 0.2      |
| DNB              | <i>Denitratisoma</i>             | 0.0     | 1.5      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| DNB              | <i>Azoarcus</i>                  | 0.3     | 0.6      | 0.0       | 0.0      | 0.0     | 0.7      | 0.6       | 0.3        | 1.0      |
| DNB              | <i>Ralstonia</i>                 | 0.1     | 0.1      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| DNB              | <i>Lysobacter</i>                | 0.0     | 0.7      | 73.8      | 48.7     | 8.5     | 15.7     | 15.4      | 10.1       | 1.8      |
| DNB              | <i>Pseudofulvimonas</i>          | 0.0     | 0.0      | 0.0       | 0.0      | 1.8     | 6.7      | 3.5       | 3.5        | 3.2      |
| DNB              | <i>Hydrogenophaga</i>            | 0.2     | 0.0      | 0.0       | 0.0      | 0.0     | 1.5      | 0.6       | 1.1        | 1.8      |
| DNB              | <i>Phaeodactylibacter</i>        | 0.2     | 0.3      | 0.0       | 0.0      | 3.7     | 0.9      | 0         | 0          | 0        |
| EPS              | <i>Chryseobacterium</i>          | 1.4     | 0.9      | 0.0       | 0.0      | 3.0     | 4.5      | 2.2       | 2.8        | 5.1      |
| EPS              | <i>Flavobacterium</i>            | 3.2     | 2.1      | 0.0       | 0.0      | 0.0     | 0.2      | 0.6       | 0.8        | 1.3      |
| EPS              | <i>Acidovorax</i>                | 0.6     | 0.7      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.0      |
| DNB, EPS         | <i>Devosia</i>                   | 0.0     | 0.0      | 0.0       | 0.0      | 0.0     | 0.0      | 0.0       | 0.0        | 0.3      |
| DNB, EPS         | <i>Pseudoxanthomonas</i>         | 1.7     | 1.8      | 0.0       | 0.0      | 0.0     | 4.7      | 2.2       | 0.7        | 0.5      |
| DNB, EPS         | <i>Denitromonas</i>              | 0.0     | 0.0      | 0.0       | 0.0      | 0.0     | 0.1      | 0.2       | 0.1        | 0.1      |
| DNB, EPS         | <i>Thauera</i>                   | 7.6     | 10.8     | 0.0       | 0.0      | 0.0     | 1.7      | 0.3       | 0.2        | 0.1      |
| DNB, EPS         | <i>Paracoccus</i>                | 1.3     | 1.3      | 0.0       | 0.0      | 0.0     | 7.2      | 6.5       | 3.8        | 1.5      |
| PAO, EPS         | <i>Rhodocyclus</i>               | 0.0     | 0.2      | 0.0       | 49.7     | 60.2    | 1.8      | 27.2      | 28.4       | 22.1     |

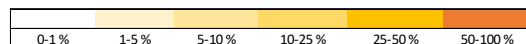


Figure S2. Heatmap with the relative abundance of bacterial genera in the AGS biomass with putative functional roles associated with one or more well-known metabolic activities, namely nitrogen removal (AOB, NOB, Anammox), phosphate removal (PAO), glycogen-accumulating organisms (GAO), denitrifying bacteria (DNB), and extracellular polymeric substances (EPS) producers.