**Table S2. Pairwise counts of differentially expressed features between aerated and non-aerated experimental treatments**. Numbers represent transcripts with significant differential expression in a log2 fold change scale after passing an FDR of 1% in edgeR and DEseq2. Each treatment included three replicates. Experimental conditions were: aerated, negative control (AC) and non-aerated, negative control (NC). These comparisons exclude non-aerated treatments with oil and dispersant (OO and OD) to determine transcripts expressed in hypoxic conditions.

|  |  |  |  |
| --- | --- | --- | --- |
| **Method/Features** | **Treatments** | **AC - Aerated** | **NC – Non Aerated** |
| edgeR genes | AC | - | 0 |
|  | NC | 0 | - |
|  |  |  |  |
| edgeR isoforms | AC | - | 0 |
|  | NC | 0 | - |
|  |  |  |  |
| DEseq2 genes | AC | - | 26 |
|  | NC | 26 | - |
|  |  |  |  |
| DEseq2 isoforms | AC | - | 33 |
|  | NC | 33 | - |