

Table S3. General information about the metatranscriptomes collected in this study. # Contigs is the number of sequences after the reads were assembled. The balance of % sequences remaining after the sum of bacterial and eukaryotic are archaeal+viral (data from MG-RAST).

Sample	Sample information	Date collected	# Contigs	Average length of contigs (bp)	% bacterial contigs	% eukaryotic contigs	% of all contigs assigned to nitrogen metabolism
4550	5 <i>Undinula</i> individuals from net	6 Aug, 2013	8,812	225	31.95	67.53	0.44
4569	10 copepods from experiment	8 Aug, 2013	31,673	273	97.23	2.74	0.66
4570	10 copepods from experiment	8 Aug, 2013	33,894	279	96.95	2.99	0.90
4646	10 <i>Undinula</i> from experiment	9 Aug, 2013	22,809	285	86.45	13.52	0.59
4647	10 <i>Undinula</i> from experiment	9 Aug, 2013	11,432	244	74.85	25.13	0.70
4648	10 <i>Undinula</i> from experiment	9 Aug, 2013	20,316	267	83.22	16.76	0.69