

**Table S4: Overview of sequencing results for metagenomic analysis of wastewater samples collected from the one Belgian WWTP on three time points in 2024.** The table includes the total number of bases, median read quality, and median read length for each sample. The yellow rows represent the Nanotrap method in combination with the QIAamp RNeasy PowerFecal Pro Kit, the green rows the precipitation method in combination with the QIAamp RNeasy PowerFecal Pro Kit and the orange rows the ZymoPURE Water DNA/RNA Kit.

Sample	Median read length	Median read quality	Number of Reads
T2-NANO-RN	704	22.7	675 160
T2-PREC-RN	1140	25	5 441 584
T2-ZYMO	966	20.8	10 676 774
T2-spike-NANO-RN	947	21.3	8 711 354
T2-spike-PREC-RN	936	22.7	9 011 679
T2-spike-ZYMO	968	21.7	4 328 245
T4-NANO-RN	804	22.2	3 743 533
T4-PREC-RN	1021	22.3	8 113 889
T4-ZYMO	1306	23	4 825 660
T4-spike-NANO-RN	1140	24.3	3 791 983
T4-spike-PREC-RN	880	22.7	5 777 901
T4-spike-ZYMO	972	22.7	5 490 452
T5-NANO-RN	639	20.5	981 301
T5-PREC-RN	1 591	24	5 711 045
T5-ZYMO	1 025	22.8	4 527 015
T5-spike-NANO-RN	743	21.8	5 865 344
T5-spike-PREC-RN	810	20.9	6 595 992
T5-spike-ZYMO	1 695	21.9	5 072 539