Table S1: Number of raw reads (in million) obtained for each biological replicate and numbers and percentages of reads that passed the different filtering steps: trimming, mapping and counting. R1 and R2 refer to forward and reverse sequencing of the reads.

Samples	Raw reads	Trimmed reads	Mapped reads	Assigned reads
Female1	R1: 76.24	75.50 (99.02%)	69.66 (92.26%)	61.46 (86.5%)
	R2: 76.24			
Female2	R1: 64.59	64.00 (99.07%)	58.89 (92.01%)	52.85 (88.2%)
	R2: 64.59			
Female3	R1: 68.13	67.46 (99.02%)	62.33 (92.39%)	55.36 (87.1%)
	R2: 68.13			
Female4	R1: 73.42	72.75 (99.10%)	67.37 (92.61%)	59.14 (86.1%)
	R2: 73.42			
Male1	R1: 138.22	137.20 (99.26%)	128.21 (93.45%)	110.56 (84.4%)
	R2: 138.22			
Male2	R1: 126.44	125.57 (99.31%)	117.96 (93.94%)	102.48 (85.0%)
	R2: 126.44			
Male3	R1: 143.63	142.39 (99.13%)	133.41 (93.7%)	116.50 (85.8%)
	R2: 143.63			
Male4	R1: 106.43	104.50 (98.19%)	980.83 (93.86%)	83.73 (83.1%)
	R2: 106.43			