

ST12. Summary statistics of the Nanopore-sequenced cDNA libraries used to annotate the genome of *L.stagnalis* (raw vs NaS-corrected reads).

	# mapped reads / total read number	Avg. % of mapped reads	# reads > 1 kb	Avg. identity percent	Avg. number of exons per alignment	% GT/AC	% GC/AG
Nanopore reads (sample 1)	105,718 / 179,614	58.86%	75,499	85.68%	3.50	78.27%	10.00%
Nanopore reads (sample 2)	65,859 / 138,868	47.43%	98,273	85.42%	3.71	80.14%	9.92%
NaS reads (sample 1)	123,374	98.58%	49,587	99.69%	4.92	95.96%	2.36%
NaS reads (sample 2)	81,383	93.32%	41,484	99.65%	4.98	95.95%	2.40%