

**ST15.** Classification of transposable elements detected in the *L. stagnalis* genome assembly.

Consensus classification	1 <sup>st</sup> de novo library (all consensus sequences)	2 <sup>nd</sup> de novo library (FLC consensus sequences)
Consensus sequences	5085	2643
Class I TEs	2428 (47.75%)	1517 (57.40%)
Class II TEs	1799 (35.38%)	774 (29.28%)
TEs unassigned to a class	1 (0.02%)	1 (0.04%)
PH (gene match)	181 (3.56%)	105 (3.97%)
noCat (no annotation, within Class I)	246 (4.83%)	14 (0.53%)
Chimeric (annotated, other classification)	631 (12.41%)	232 (8.78%)