

Table 2 Statistical analysis of SSR repeat types in transcriptome sequences of *Glehnia littoralis*

Repeat type	Number	Proportion (%)	Frequency (%)	Average distance (kb)	Total length (bp)	Average length (bp)
Mononucleotide	5766	39.98	7.31	16.99	70 858	12
Dinucleotide	5910	40.98	7.50	16.58	86 300	15
Trinucleotide	2529	17.54	3.21	38.74	43 128	17
Tetranucleotide	145	1.01	0.18	675.75	3 024	21
Pentanucleotide	42	0.29	0.05	2 332.95	1 125	27
Hexanucleotide	29	0.20	0.04	3 378.76	1 032	36