

Table 1 Global statistics of the Chinese treeshrew genome (Adopted from Fan Y. et. al. 2013)

	Insert size (bp)	Total data (Gb)	Sequence coverage (X)
(a) Sequencing			
	170–800	187.09	58.47
Paired-end library	2–40000	66.36	20.74
	Total	253.45	79.20
	N50 (Kb)	Longest (Kb)	Size (Gb)
(b) Assembly			
Contig	22	188	2.72
Scaffold	3656	19270	2.86
	Number	Total length (Mb)	Percentage of genome
(c) Annotation			
Repeats	4843686	1001.9	35.01
Genes	22063	743.4	25.98
CDS	166392	31.0	1.08