



**Supplemental Figure 1:** Figure with the YGS results of *T. californica*. The plot shows the distribution of scaffolds in relation to the proportion of valid-single copy unmatched sequences when either (A) the XY-GS or (B) the ZW-GS were used. *T. californica* assembled genome has 393,963 scaffolds, a total length of 593,066,717 and a N50 of 2,408. XY-GS showed only 160 scaffolds  $\geq 70\%$  unmatched *k*-mers totaling 47,799 bp while with the ZW-GS analysis, 7,260 scaffolds have  $\geq 70\%$  unmatched *k*-mers corresponding to 3,594,618 bp of the genome. YGS clearly shows a ZW system in *T. californica* in accordance with the known karyotype<sup>3</sup>.

