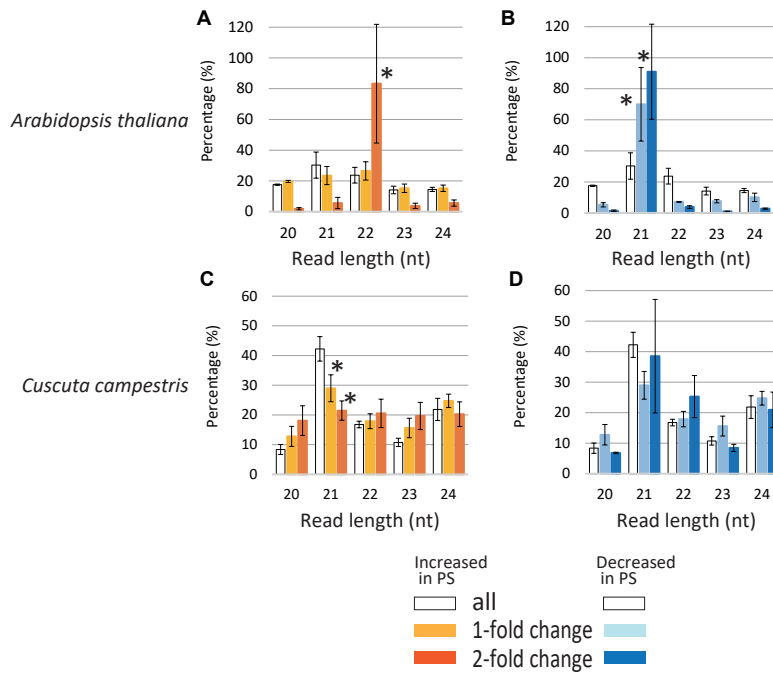Supplementary Figure S1. Enrichment of specific length of sRNA reads in parasitic stems. (A) Read length distribution of all ATPS ShortStack-loci (SS-loci) (white), SS-loci associated with the same reference gene of which reads per million (RPM) exhibited increase compared to ATNS (pale orange), and SS-loci of which RPM exhibited more than 2-fold increase compared to ATNS (deep orange). (B) Read length distribution of all ATPS SS-loci (white), SS-loci associated with the same reference gene of which RPM exhibited decrease compared to ATNS (pale blue), and were greater than SS-loci associated with the same reference gene of which RPM exhibited more than 2-fold decrease compared to ATNS (deep blue). (C) Read length distribution of all CCPS SS-loci (white), SS-loci associated with the same reference gene of which RPM exhibited increase compared to CCNS (pale orange), and SS-loci associated with the same reference gene of which RPM exhibited more than 2-fold increase compared to CCNS (deep orange). (D) Read length distribution of all CCPS SS-loci (white), SS-loci associated with the same reference geneof which RPM exhibited decrease compared to CCNS (pale blue), and SS-loci associated with the same reference gene of which RPM exhibited more than 2-fold decrease compared to CCNS (deep blue). Values indicate means and standard deviations of two (panel A, B) and three (panel C, D) replicates, respectively. Asterisk; significant difference ($p<0.05$).