

1

2 Table S2. Summary of the miRNA reads generated from miRNA-seq analysis

Sample	Raw reads	Reads to be aligned	Reads aligned to TAIR9
P- WT	7,728,824	6,314,349 (81.70%)	5,171,403(81.90%)
P- <i>hps8</i>	15,872,004	13,516,271 (85.16%)	10,694,969(79.13%)
P+ WT	4,843,536	4,031,581 (83.24%)	3,429,963(85.08%)
P+ <i>hps8</i>	8,468,540	7,972,229 (94.14)	6,596,527(82.74%)
Total	83,350,440	68,320,744 (81.97%)	48,737,211(71.34%)