

Table S4. Summary of Illumina reads collected for each individual. Shown are the total number of reads obtained for each individual, retained reads after filtering out low quality scores, total reads mapped to the *Helicoverpa zea* reference genome, and the mean sequencing depth.

Sample ID	Total PE Reads	Filtered PE Reads	Mapped Reads	Mean sequence depth (×)
B1	66,745,362	55,600,073	25,856,243	23.20
C1	46,778,103	37,872,611	18,701,181	16.77
D1	36,901,929	30,932,529	14,965,749	13.43
D2	39,279,497	31,755,375	16,842,162	15.11
D3	56,513,308	47,456,576	24,214,897	21.72
E1	46,111,320	38,826,792	19,755,879	17.72
E3	27,045,423	22,790,570	11,657,375	10.46
F2	43,250,346	36,592,604	19,233,797	17.26
G2	21,228,969	17,772,582	8,876,363	7.96
H1	43,282,524	36,602,796	18,937,097	16.99