**Table S3.** Statistical summary of data generated from de novo transcriptome sequencing of wheat mutant (M3), parent (P3) and mutant exposed to HS (M3H) using Illumina HiSeq 4000.

|  |  |
| --- | --- |
| De novo Transcriptome Assembly Statistics | |
| Total trinity ’genes' | 3,05,537 |
| Total trinity transcripts | 5,88,788 |
| Percent GC | 49.06 |
| Stats Based on All Transcripts Contigs | |
| Contig N10 | 3,464 |
| Contig N20 | 2,587 |
| Contig N30 | 2,065 |
| Contig N40 | 1,678 |
| Contig N50 | 1,349 |
| Median Contig length | 496 |
| Average Contig | 836.88 |
| Total assembled bases | 49,27,44,700 |
| Stats based on Only Longest Isoform per Gene | |
| Contig N10 | 3,118 |
| Contig N20 | 2,202 |
| Contig N30 | 1,626 |
| Contig N40 | 1,175 |
| Contig N50 | 835 |
| Median Contig length | 355 |
| Average Contig | 603.8 |
| Total assembled bases | 18,44,83,645 |

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