**Complex molecular mechanisms underlying MYMIV-resistance in *Vigna mungo* revealed by comparative transcriptome profiling**

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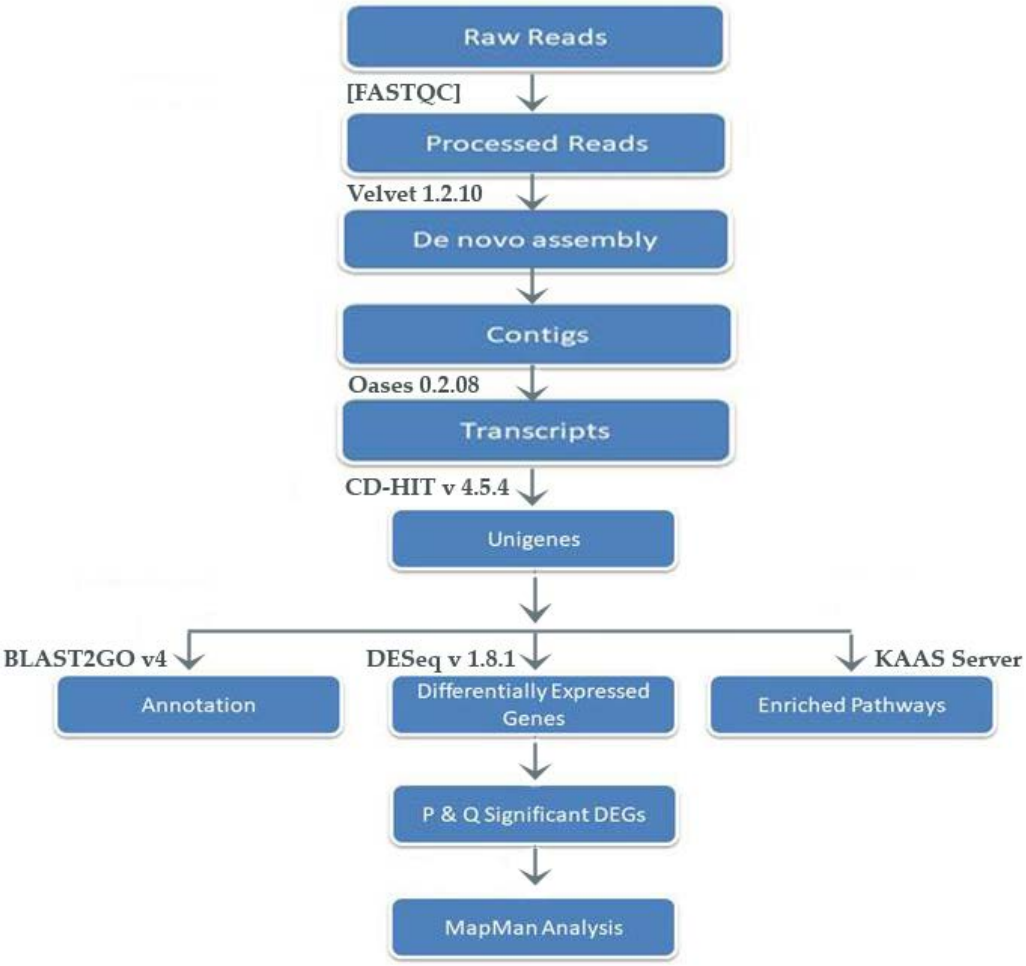
**Supplementary Figure S1:** NGS workflow blueprint for the RNA sequencing data.



**Supplementary Table S2: Primers list of transcripts used for qPCR analyses.** Sequence information and amplicon characteristics of primers of 15 candidate genes used for qPCR expression analyses.

| Sl. No. | Name | Sequence (5` to 3`) | | Amplicon Length (bp) |
|---|---|---|---|---|
| 1. | Calmodulin (CAM) | F | CGAAGAATGCCACAACATGA | 237 |
| | | R | CTACTCAGGGCGATTGAAC | |
| 2. | Heat shock protein 70 (HSP70) | F | TTCAAACCCTCCTTGGGACAC | 203 |
| | | R | GAATGAAAGCTGGCCAGAAG | |
| 3. | ABC transporter (ABC) | F | CAGGCCTATGTGACTCAAG | 180 |
| | | R | ACTCTCCTCTTCTGTCCTCC | |
| 4. | NAC transcription factor (NAC) | F | GTGGAGGGTGTGAAGGTTATC | 224 |
| | | R | CTCCGTCTCAGGTTCCCATGG | |
| 5. | Defensin (DEF) | F | GTGGCTCTGAGACTCACATG | 166 |
| | | R | CCGGTAAGCCTTCTCCACGC | |
| 6. | Argonaute (AGO) | F | GACGTTGTCTCTGCTGGCAG | 250 |
| | | R | ACACCTCCTCCTACATCAGC | |
| 7. | Ankyrin (ANK) | F | TACCACCCGTTGCACATAGC | 209 |
| | | R | GCAGGCAAGTACAACCCATC | |
| 8. | E3- Ubiquitin ligase(E3 UBL) | F | GTTTCGATATGCTTCAGGC | 139 |
| | | R | AGAGCTGCCTGAATGAAATG | |
| 9. | R-gene (NB-LRR) | F | CATGGGCTGGAACACCTCC | 236 |
| | | R | GCTCTCTATTCAGTGTCTTGAC | |
| 10. | Superoxide dismutase (SOD) | F | CCCTTGTCTGGGGAGGTTAT | 209 |
| | | R | GCACATCACACCATCCAAGGT | |
| 11. | WRKY transcription factor (WRKY33) | F | GATCACGAATCTCTCTCAGG | 238 |
| | | R | CGCTGGACCCCTCTAACAC | |
| 12. | Thioredoxin (TRX) | F | GAATCACTCCTCTGCGGTTC | 168 |
| | | R | TCCATAGCGGGAGAGATGAG | |
| 13. | Peroxidase (PER) | F | CTTGGCACAAAGCCTAGCTC | 164 |
| | | R | GAGCAGCCCAATATACTCGC | |
| 14. | Cysteine protease (CSP) | F | TCCTGCAAATTTGATAAAAGCA | 190 |
| | | R | ATGGCATGAGACACCACCA | |
| 15. | Pathogenesis related protein 1 (PR1) | F | CTGGCAAAGCCAAGAGTGAT | 248 |
| | | R | AGCTCTCACAATTATGCAGC | |