***Supplementary materials***

**Comparative transcriptome analysis of onion in response to infection by *Alternaria porri* (Ellis) Cifferi**

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**1 Supplementary Data**

Supplementary Excel S1. All differentially expressed genes in both genotype along with their functional annotation

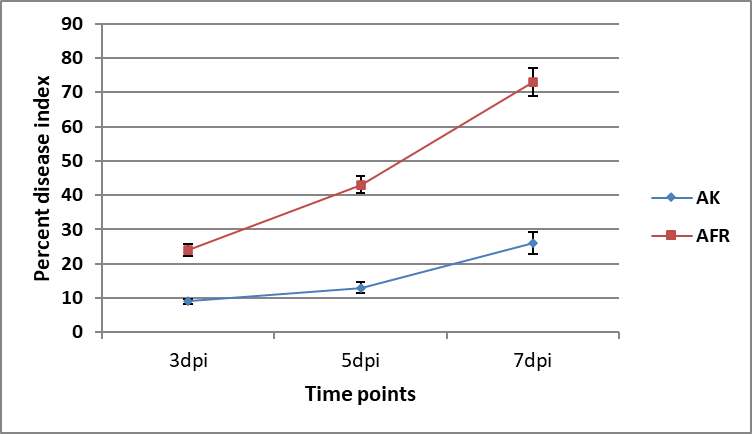
Supplementary Excel S2. PRGdb analysis

Zip folder 1: Statistical analysis for qRT-PCR of selected DEGs after PB infection in onion genotypes

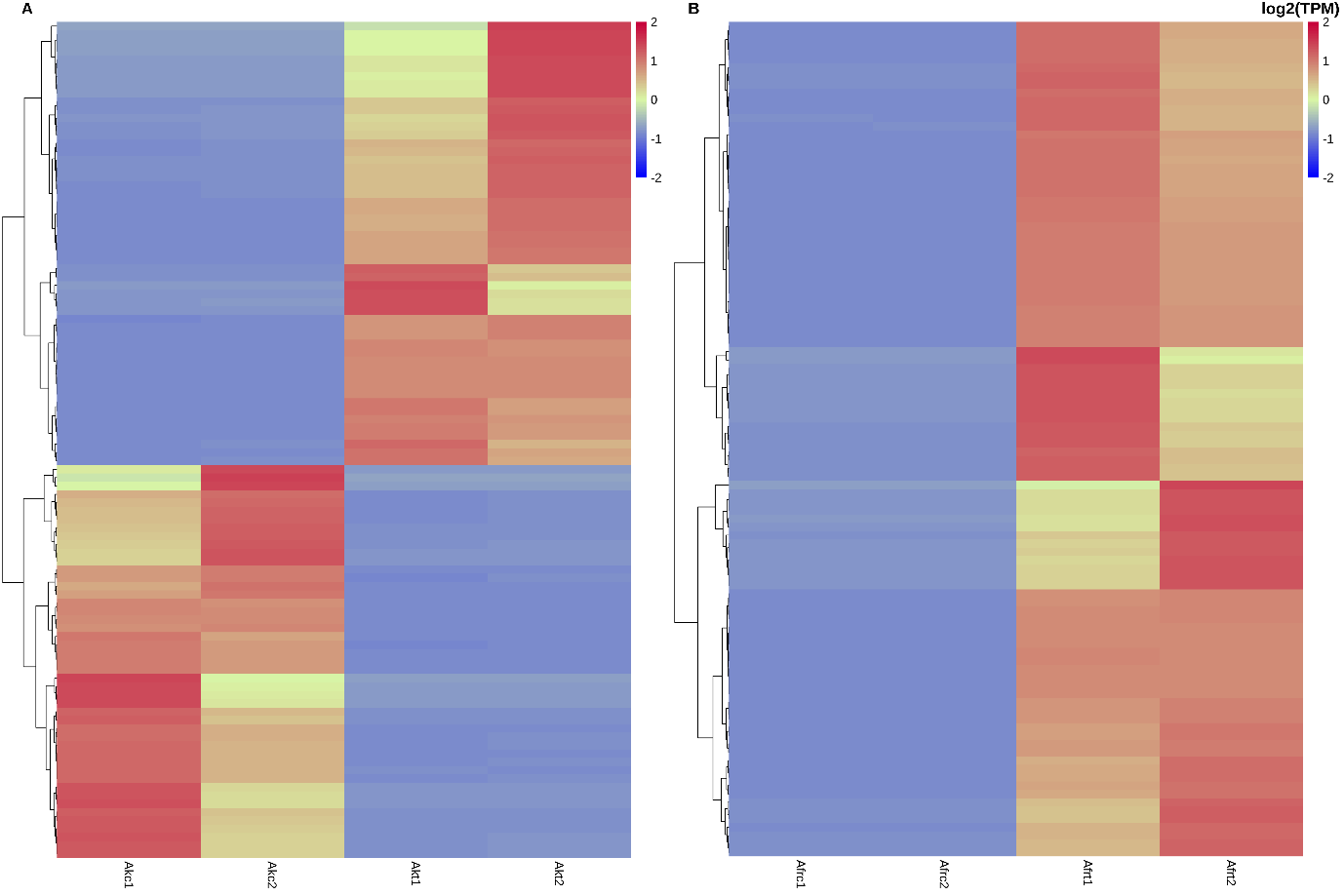
Zip folder 2: Statistical analysis for enzyme activities after PB infection in onion genotypes

**2** **Supplementary Figures and Tables**

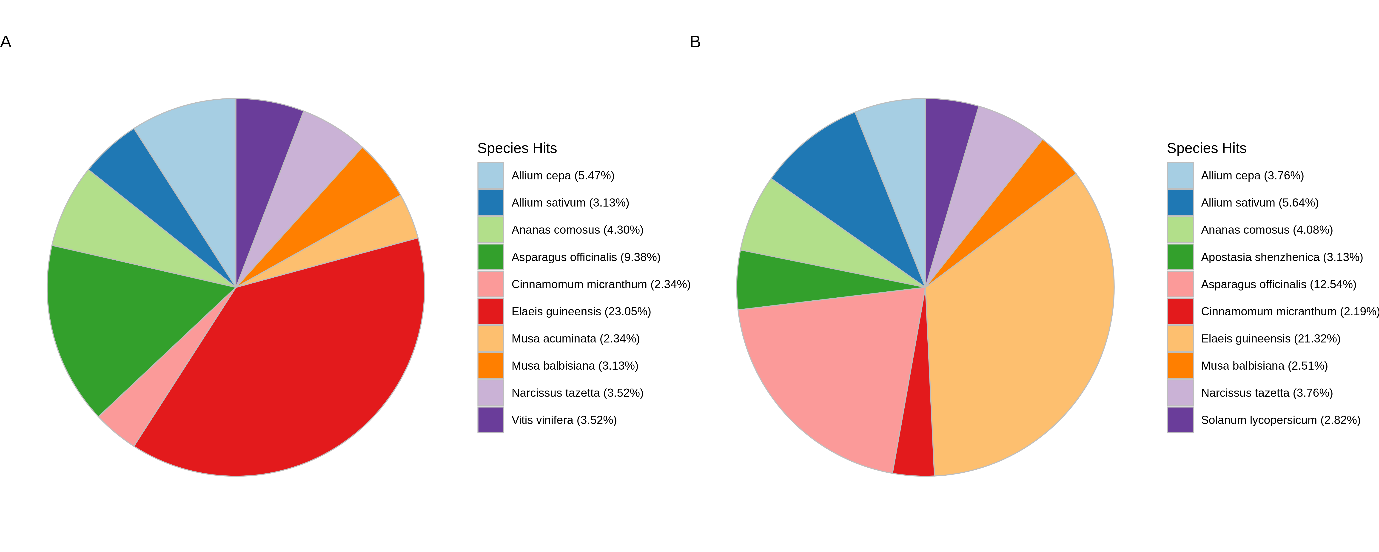
**2.1 Supplementary Figures**



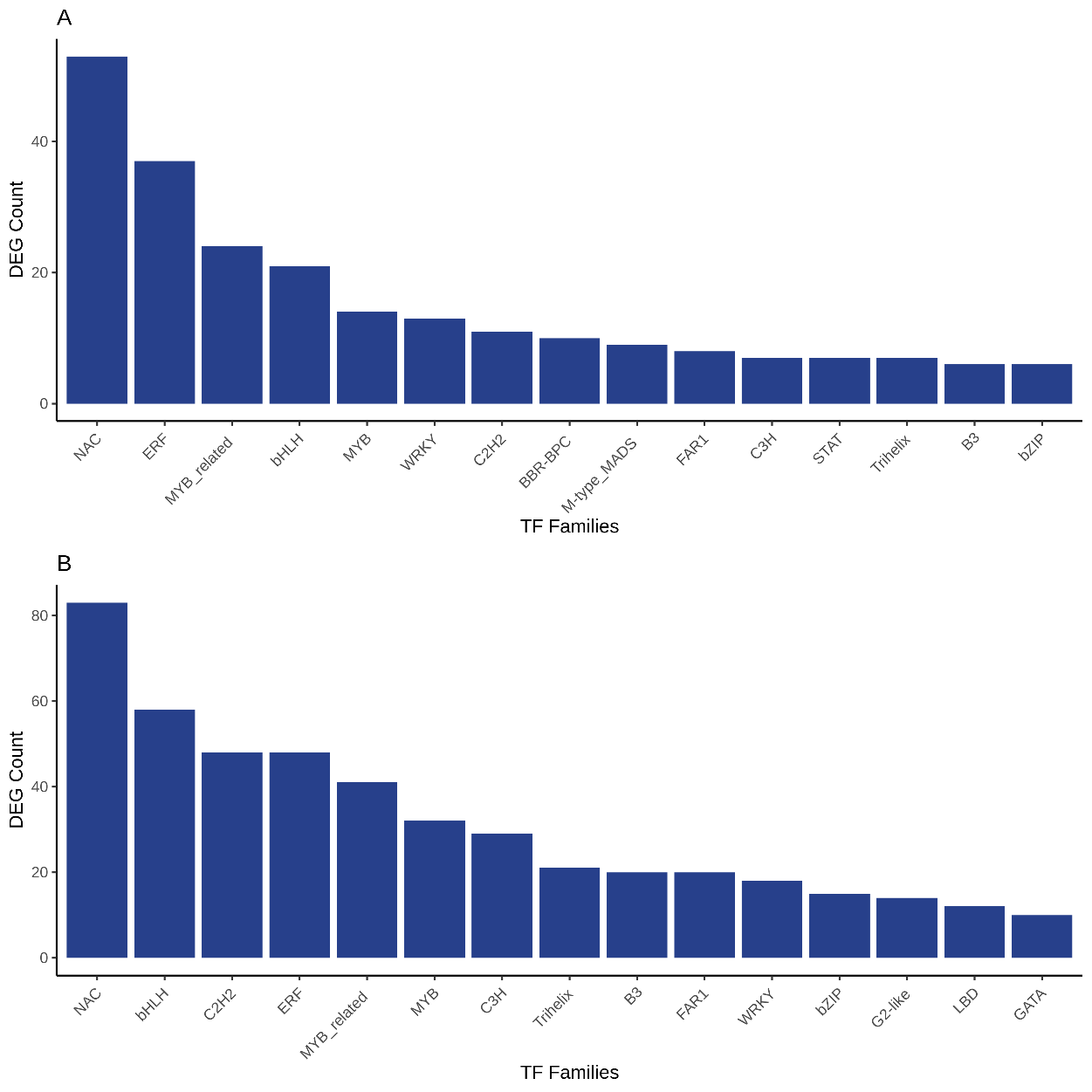
**Supplementary Figure S1.** Disease severity index of AK and AFR after *A. porri* inoculation at three time points



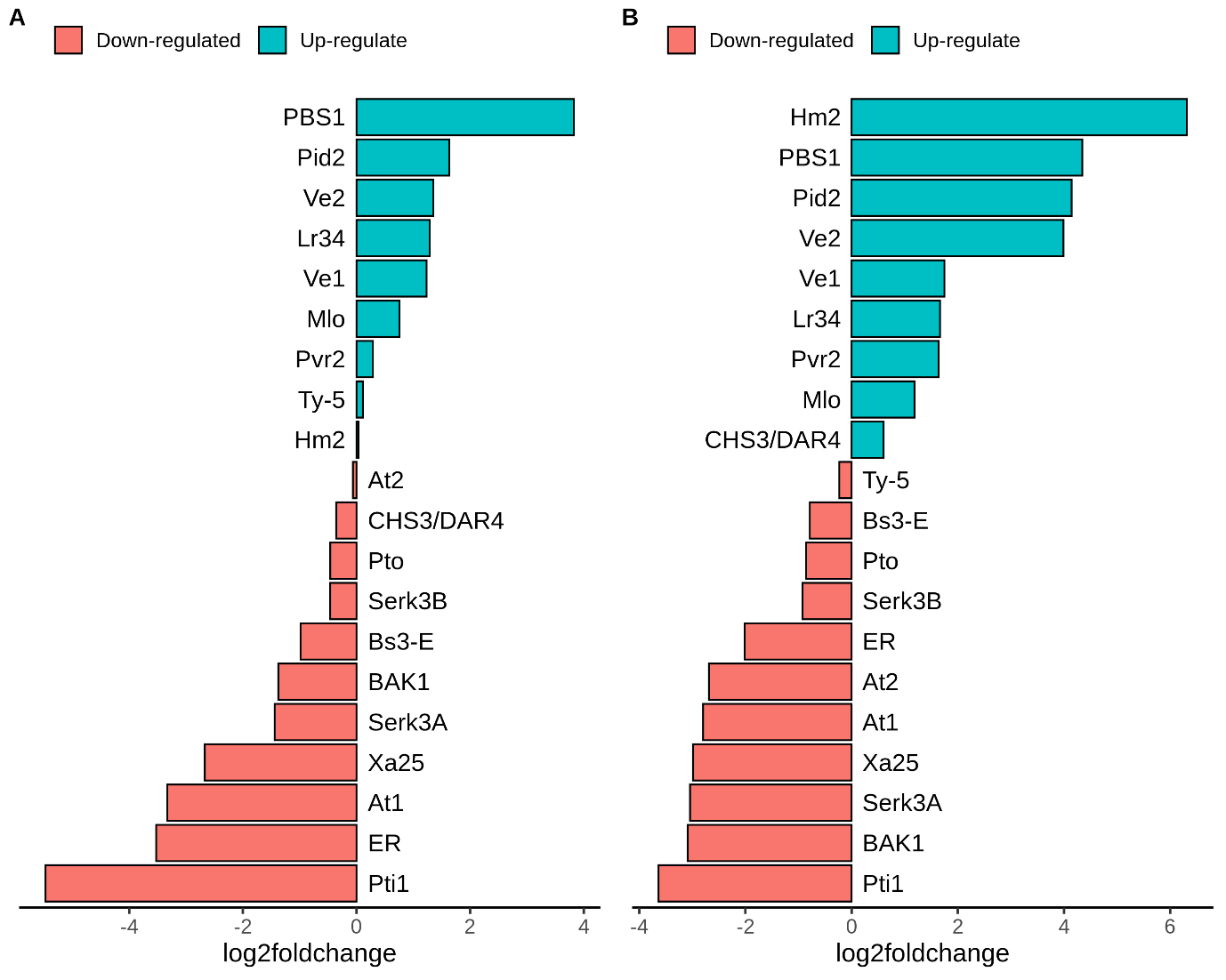
**Supplementary Figure S2.** Differential expression pattern showed by top 100 significantly expressed transcripts in onion genotypes A. Arka Kalyan and B. Agrifound rose in response to purple blotch infection



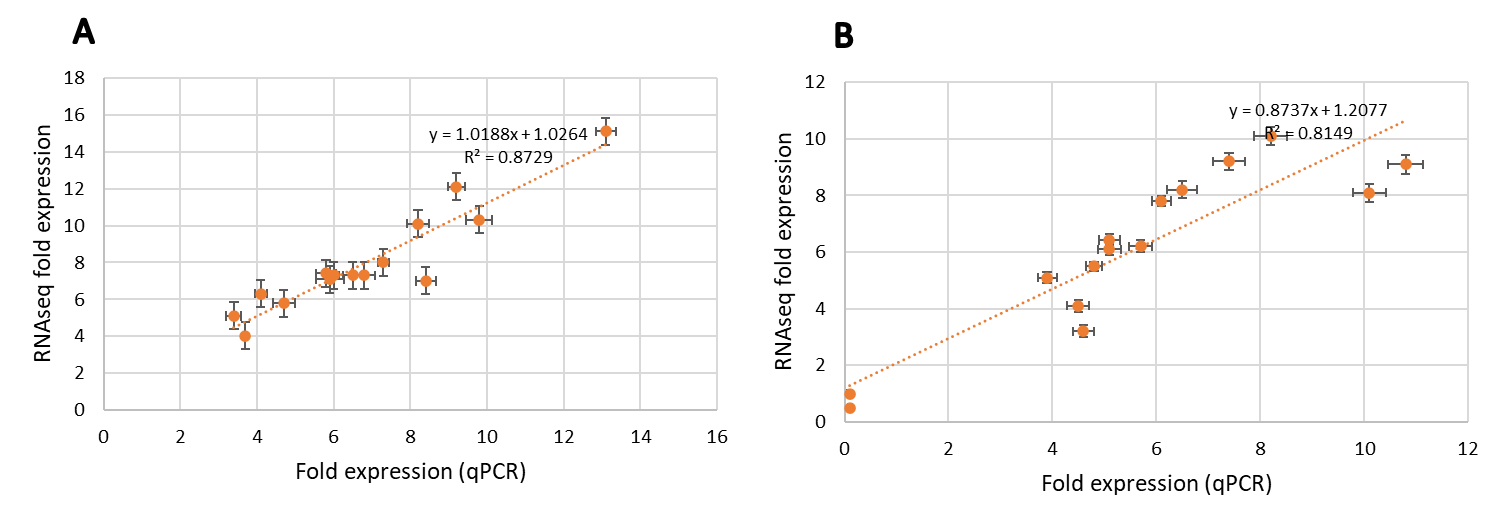
**Supplementary Figure S3.** Species hit distribution of transcripts expressed in onion genotypes; A. Arka Kalyan and B. Agrifound rose



**Supplementary Figure S4.** Transcription factor distribution of transcripts expressed in onion genotypes A. Arka Kalyan and B. Agrifound rose in response to purple blotch infection. X axis represents TF families and Y axis showed DEG count for each TF family.



**Supplementary Figure S5.** PRGdb analysis of transcripts expressed in onion genotypes; A. Arka Kalyan and B. Agrifound rose



**Supplementary Figure S6.** Validation of RNA-Seq data using qPCR. A good correlation of 15 differentially expressed genes between RNA-Seq and qPCR data of Arka Kalyan (A) and Agrifound rose (B) after infection of Purple blotch

**2.1 Supplementary Tables**

**Supplementary Table 1: List of primers used for validation of RNAseq data**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **No.** | **Name** | **Sequence (5'->3')** | **Length**  **(bp)** | **Product**  **(bp)** | **Efficiency (%)** |
| 1 | MYB\_F | ACAAAGGAGTTGGGGGTTTTG | 21 | 227 | 102.4 |
| MYB\_R | AGAGCGAACAGACAACGACA | 20 |
| 2 | ERF\_F | CAAAGCGACAACAGGGGAC | 19 | 198 | 97.2 |
| ERF\_R | GACTAGAAACGGGGTGAGGG | 20 |
| 3 | LOX\_F | CTGTTCCCCATACTCGCTCA | 20 | 220 | 96.5 |
| LOX\_R | AAGGTACTCCAGCGCAAGAA | 20 |
| 4 | PEROX\_F | CAGTCCGTCCTAATCTCCCC | 20 | 247 | 104.3 |
| PEROX\_R | ACAACCTCGGTCCACTTGAT | 20 |
| 5 | GST\_F | ACAAACGCACACACGAGAAT | 20 | 230 | 103.2 |
| GST\_R | GACGAGGTAAAGCTGCCAAA | 20 |
| 6 | PR4\_F | AGTTGTTGCATCGTATGGGC | 20 | 240 | 96.7 |
| PR4\_R | GCTCCAGTTCCTTGGTTTGT | 20 |
| 7 | PR3\_F | CATGCCCTGCCAATGGATTT | 20 | 223 | 98.4 |
| PR3\_R | TAATCGGGTGGGTTGCCTTG | 20 |
| 8 | PR5\_F | GCCCATGCCTTATCCCATGT | 20 | 182 | 102.8 |
| PR5\_R | TAATAACCCACAAGCGGCGA | 20 |
| 9 | BTB/POZ\_F | TGCCGTAGACCCAAAACTTGA | 21 | 233 | 97.3 |
| BTB/POZ\_R | GACGGAGTGGCATTAGCTCG | 20 |
| 10 | Ankyrin\_F | GTCAACTACAGCACCCACCA | 20 | 209 | 99.4 |
| Ankyrin\_R | TGGTGAAGGGAACATCTCCG | 20 |
| 11 | ACS\_F | TCTCCACTCAAACGCAGCAT | 20 | 175 | 95.2 |
| ACS\_R | ATCCAGCAAAACAAACCCGC | 20 |
| 12 | NCED\_F | GCATCATCGTAGGCTGCTCT | 20 | 220 | 103.6 |
| NCED\_R | ACGAGTTCAGGCGATTTGGA | 20 |
| 13 | NAC\_F | TCCGACTCCGTTCGTAAACA | 20 | 229 | 96.3 |
| NAC\_R | CCCGGTGTCATCACTAACCA | 20 |
| 14 | PGIP\_F | TACAATCCCAGAAGCGGTCG | 20 | 184 | 98.2 |
| PGIP\_R | AAGGGAGGTGAGGTTAGCGA | 20 |
| 15 | PR1\_F | TAACCGACTTTGCCCACACA | 20 | 180 | 101.3 |
| PR1\_F | TTCACTCCGGTGGTCCCTAT | 20 |
| 16 | *AcAct*\_F | GCACCAAGAGCAGTATTC | 18 | 183 | 100.3 |
| AcAct\_R | CCAAATCTTCTCCATGTCA | 19 |

**Supplementary Table S2: Sequencing and data QC of RNAseq of AK and AFR in response to PB**

