

Supplementary Table 3

Apollo tracks from genomics, transcriptomics and proteomics data

| Category | Apollo tracks | Description |
|-----------------|------------------------------------|---|
| Maker pipeline | Maker | Maker gene predictions |
| | Augustus | Ab-initio gene predictions |
| | SNAP | Ab-initio gene predictions |
| | Repeatmasker | Repeat annotations |
| | Repeatrunner | Repeat annotations |
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| NCBI v100 | Genes | NCBI predicted protein coding genes |
| | ncRNA | NCBI predicted noncoding RNA |
| | Pseudogenes | NCBI Predicted pseudogenes |
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| Transcriptomics | Adult | RNAseq from adult psyllid tissue. Mapped reads and coverage plot |
| | Egg | RNAseq from adult egg tissue. Mapped reads and coverage plot |
| | Nymph | RNAseq from adult nymph tissue. Mapped reads and coverage plot |
| | Healthy adult and nymph | Data from Vyas 2015. Mapped reads and coverage plot |
| | CLas infected adult and nymph | Data from Vyas 2015. Mapped reads and coverage plot |
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| Proteomics | Expressed protein tags (ePSTs) | Peptides from mass spectrometry (MS) proteomics data from whole adult psyllid and percoll gradient fraction (Ramsey 2015) |
| | Reverse-translated peptides (RTPs) | Peptides from mass spectrometry (MS) proteomics data from whole adult psyllid and percoll gradient fraction (Ramsey 2015) |
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| Genomics | Paired-end DNaseq reads | Mapped reads and coverage plot |