

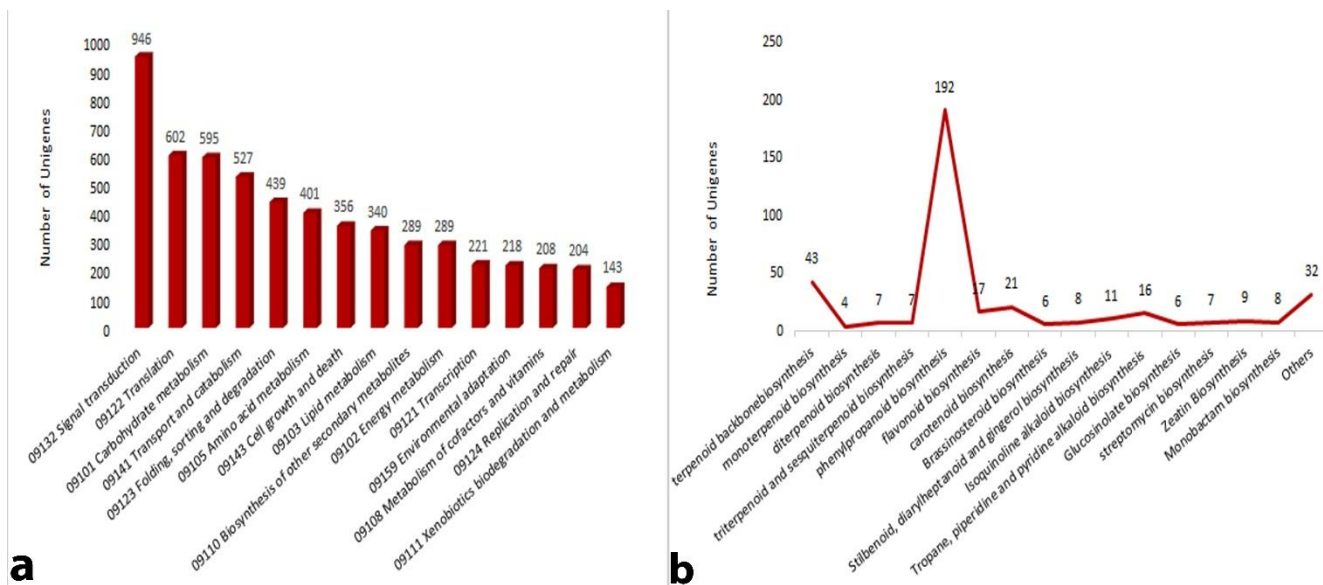


Figure S1: The top 15 largest KEGG pathways

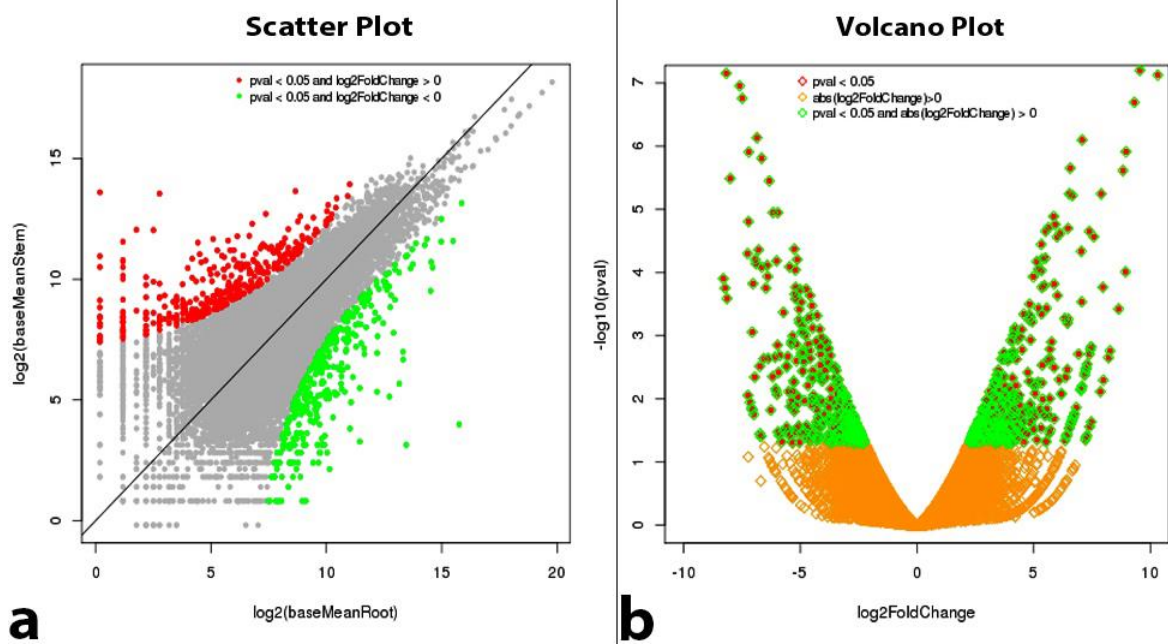


Figure S2: a) Scatter plot for normalized values obtained through DESeq basemean values of all differentially expressed genes in Root-vs-Stem. Each dot indicates one gene. The dots above the black diagonal line indicate up-regulated genes and below this line are down-regulated genes. Where red dots represent significantly upregulated genes with $P\text{-value} < 0.05$ and $\log_2\text{FC} > 0$ and green dots represents significantly downregulated genes with $P\text{-value} < 0.05$ and $\log_2\text{FC} < 0$. The horizontal coordinates represent the $\log_2(\text{basemean})$ values of Root and the vertical coordinates the Stem $\log_2(\text{basemean})$ values.

b) Volcano plots of the distribution of gene expression for Root-Vs-Stem samples. DESeq was performed to show the differentially expressed genes. Red, green, and orange correspond to genes with $p\text{-value} < 0.05$, absolute $\log_2\text{FC} < 0$ and ($p\text{-value} < 0.05$ and absolute $\log_2\text{FC} > 0$) respectively.

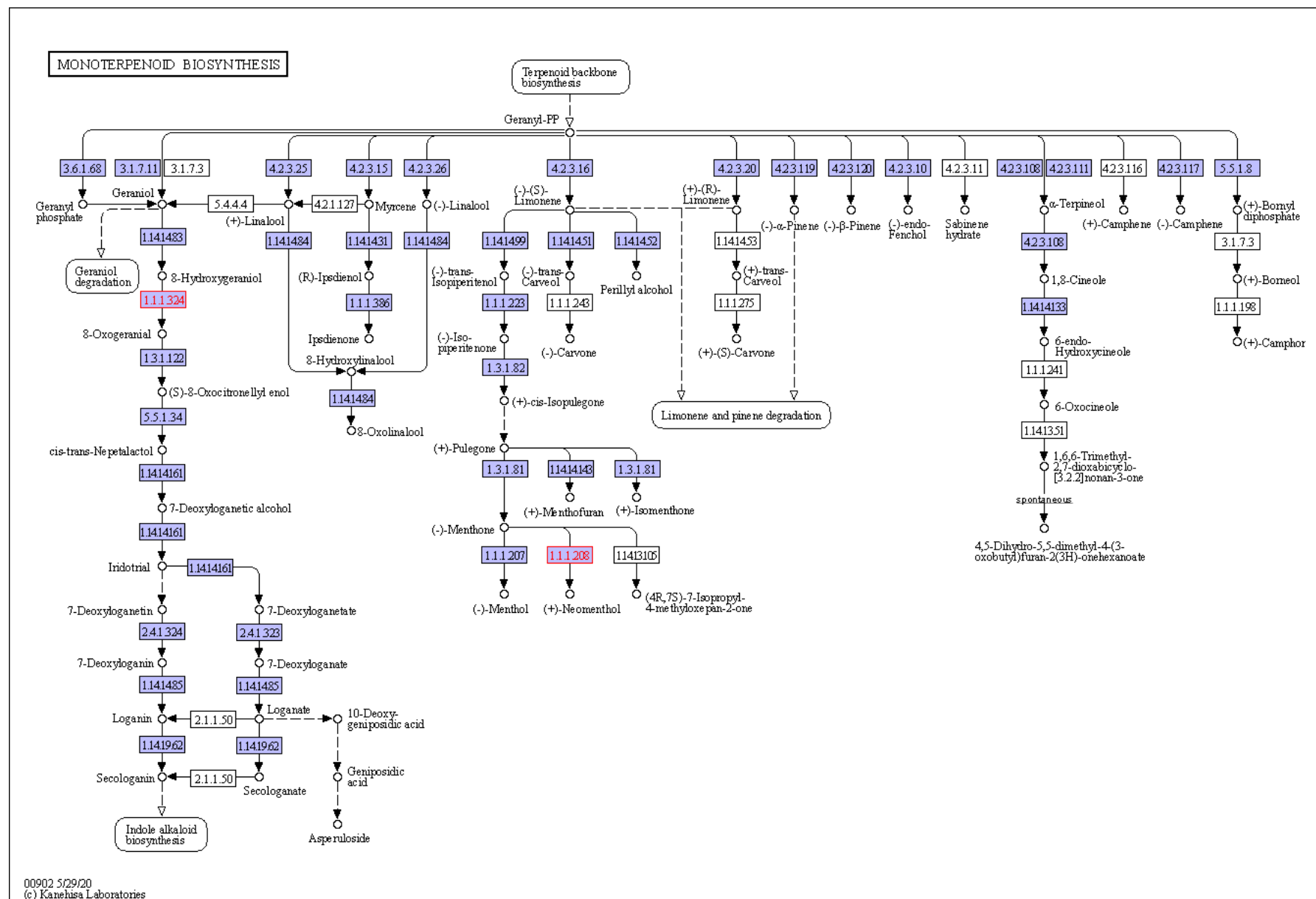
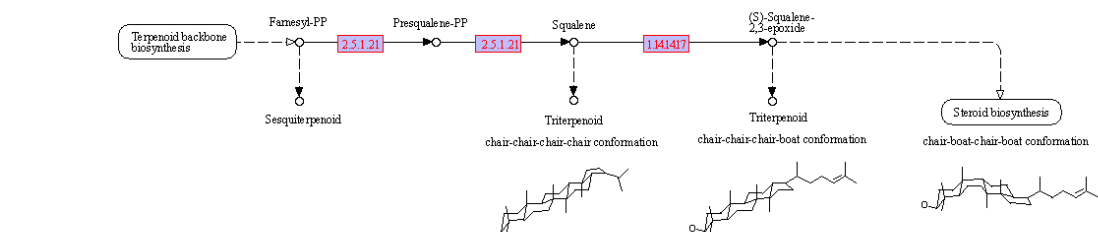
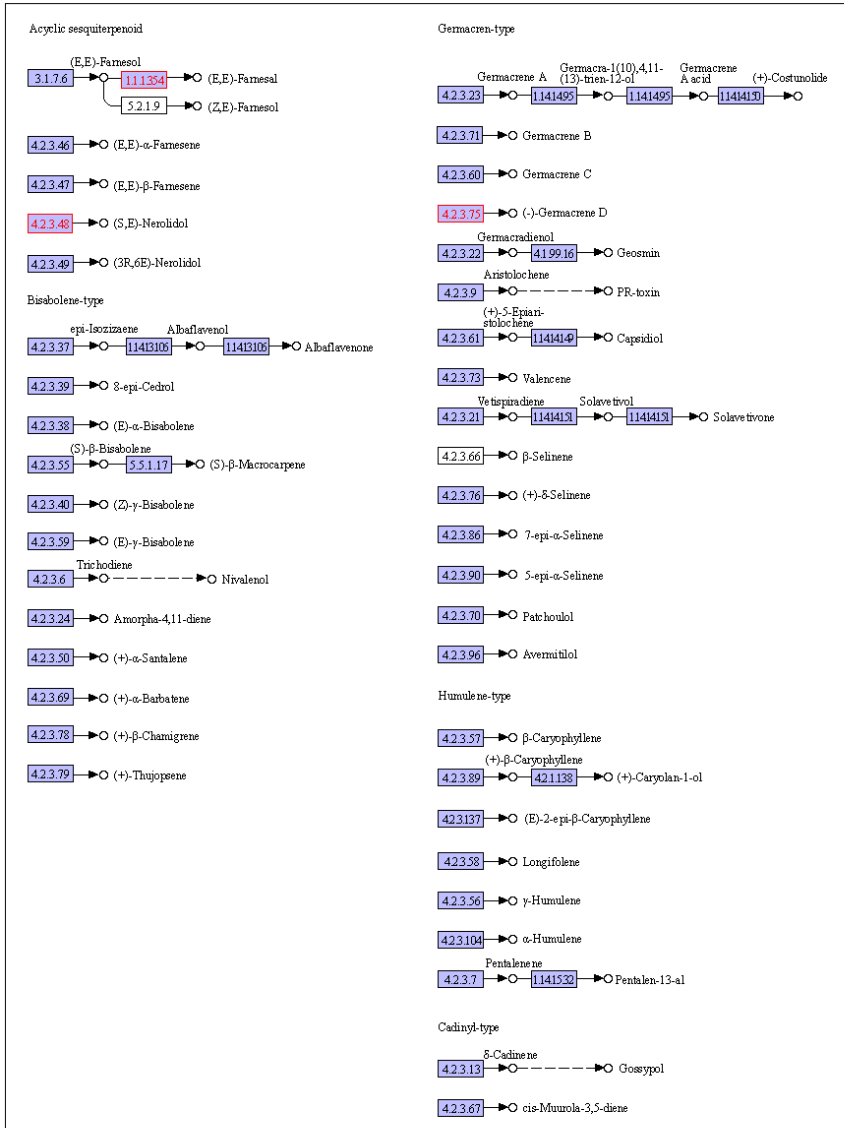


Figure S6. The color-coded map corresponds to map ko00902 in the KEGG database. (<https://www.kegg.jp/kegg/pathway.html>) The Red-color box represents the unigenes encoding key enzyme involved in Monoterpenoid Biosynthesis pathway in *O. turpethum*.

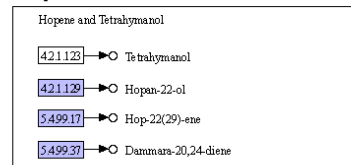
SESQUITERPENOID AND TRITERPENOID BIOSYNTHESIS



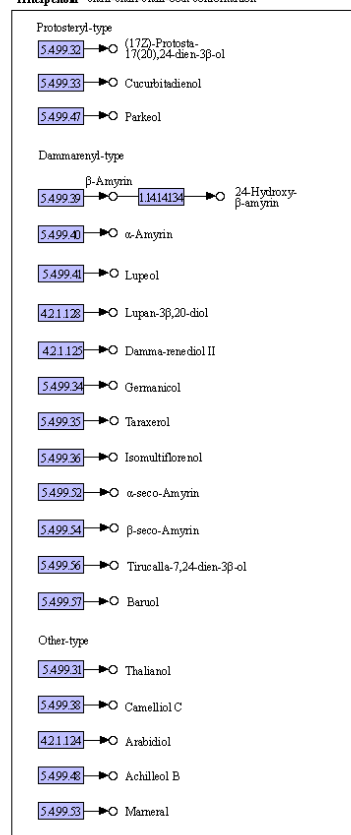
Sesquiterpenoid



Triterpenoid chair-chair-chair-chair conformation



Triterpenoid chair-chair-chair-boat conformation



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(c) Kanehisa Laboratories

Figure S8. The color-coded map corresponds to map ko00909 in the KEGG database. (<https://www.kegg.jp/kegg/pathway.html>) The Red-color box represents the unigenes encoding key enzyme involved in Sesquiterpenoid and triterpenoid Biosynthesis pathway in *O. turpethum*.

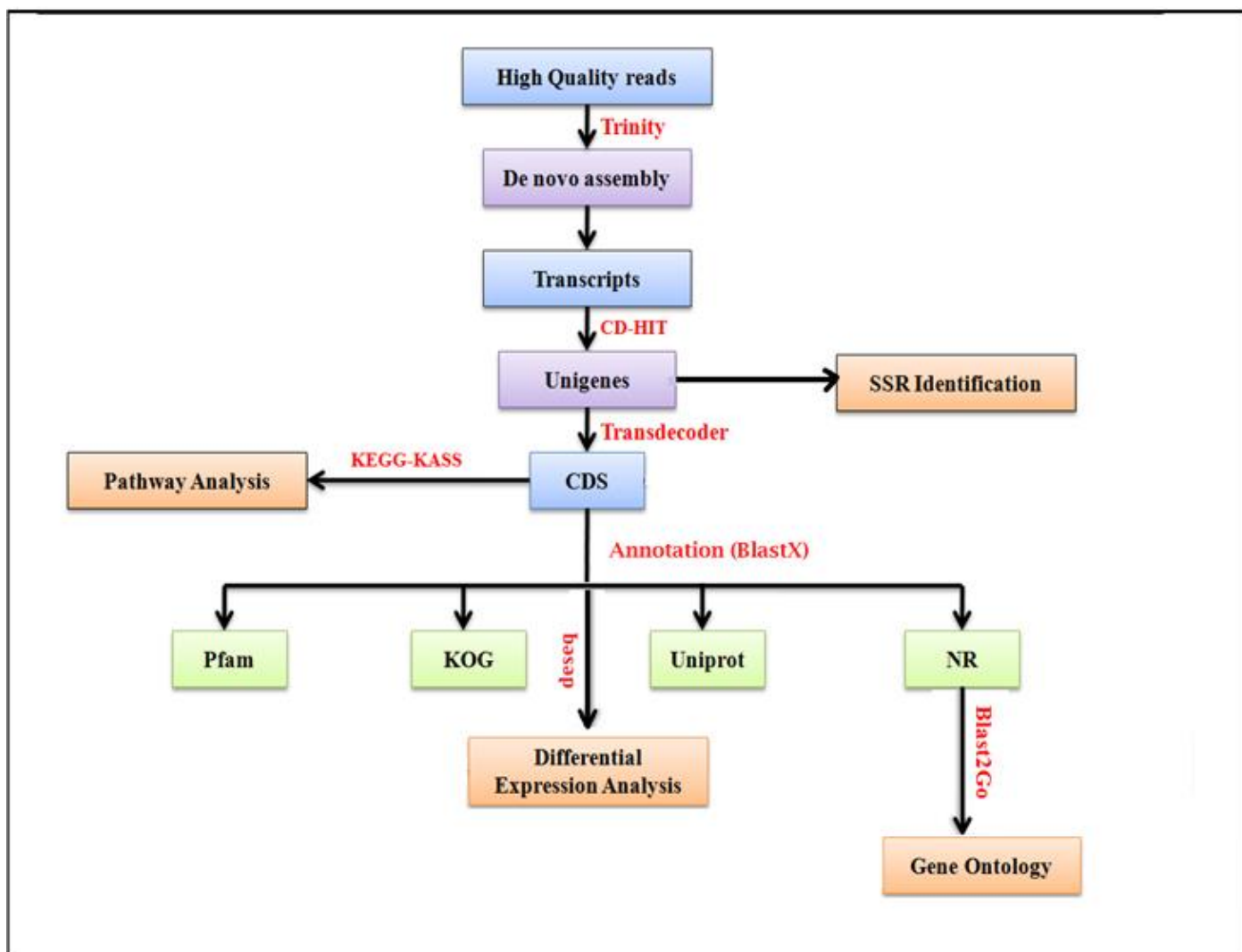


Figure S9. Workflow for Illumina Sequencing de novo Assembly, Annotation and other Bioinformatics Analysis carried out in the Root- Stem Transcriptome of *O. turpethum*.