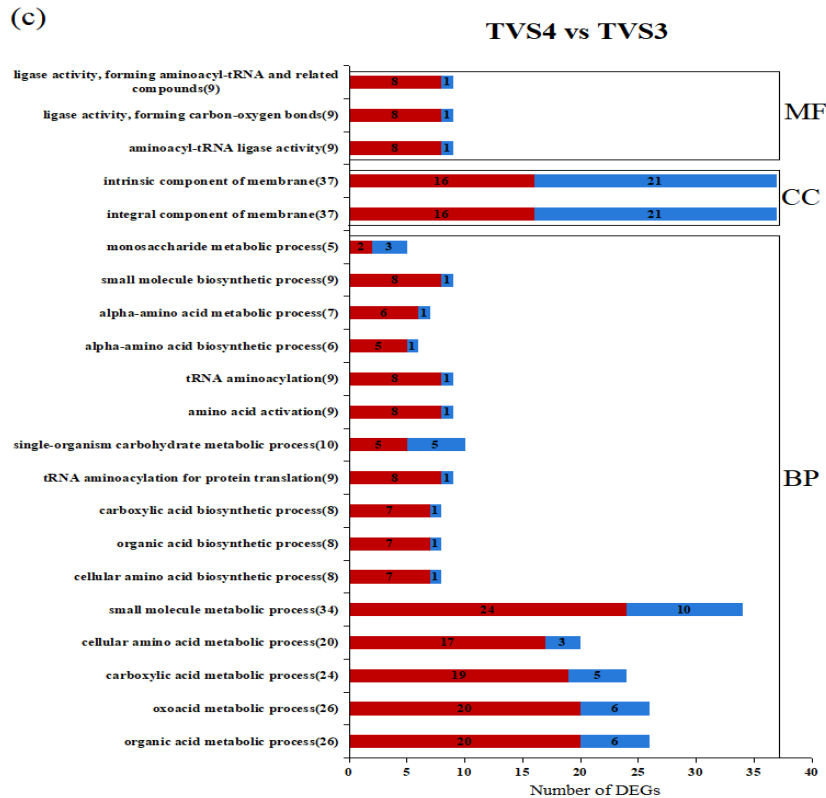
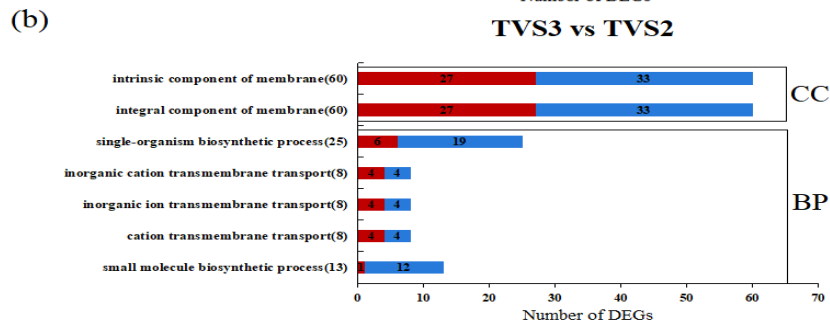
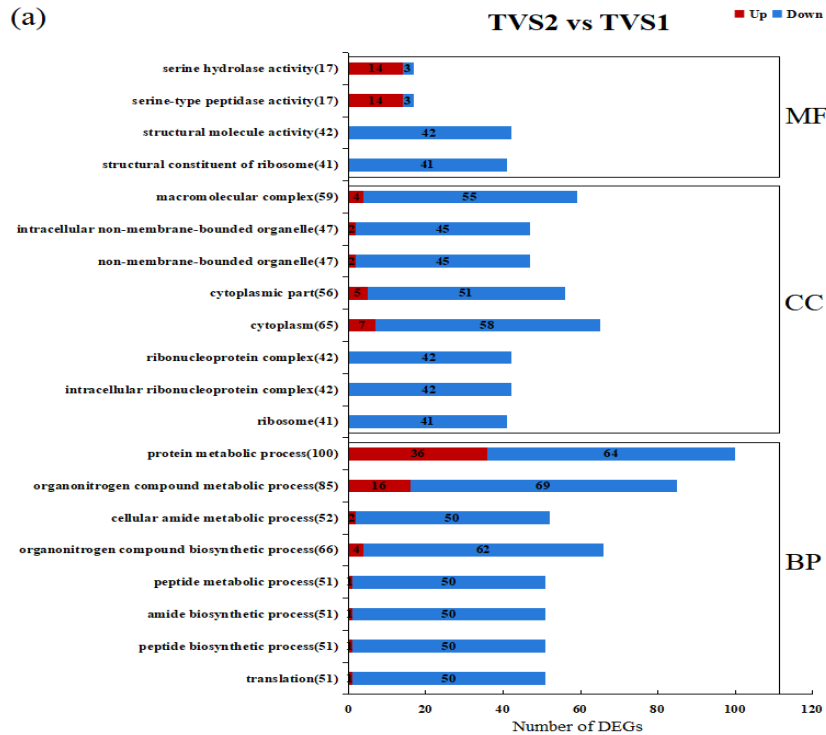
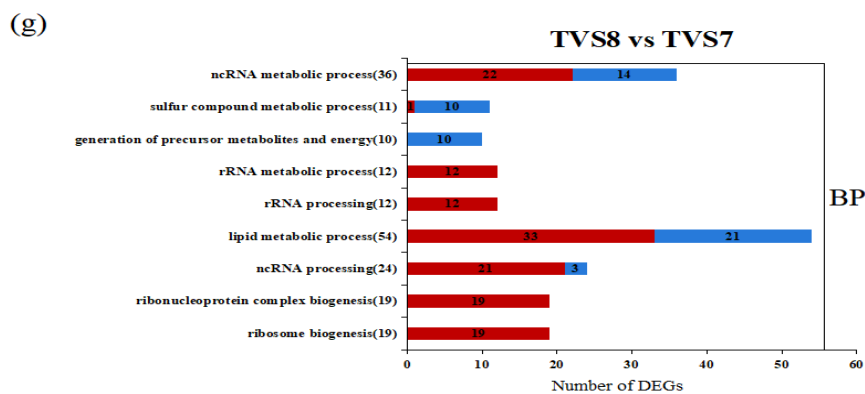
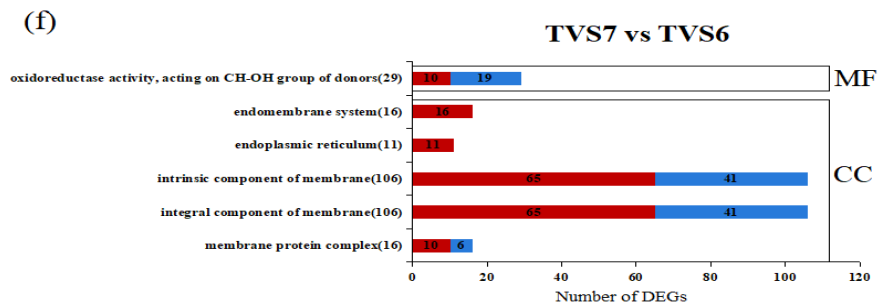
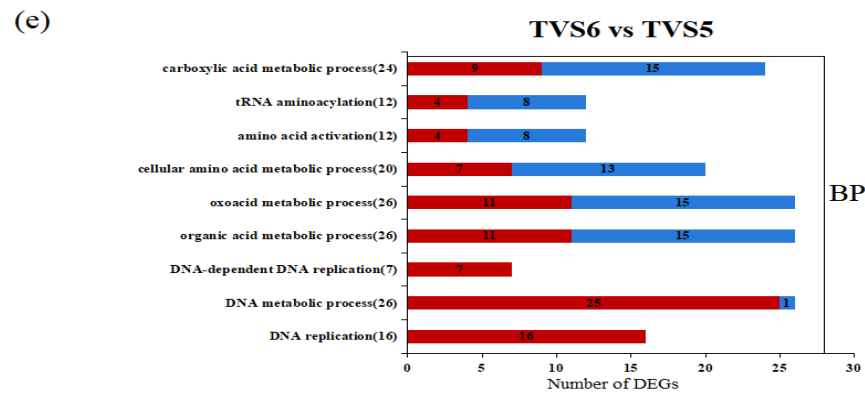
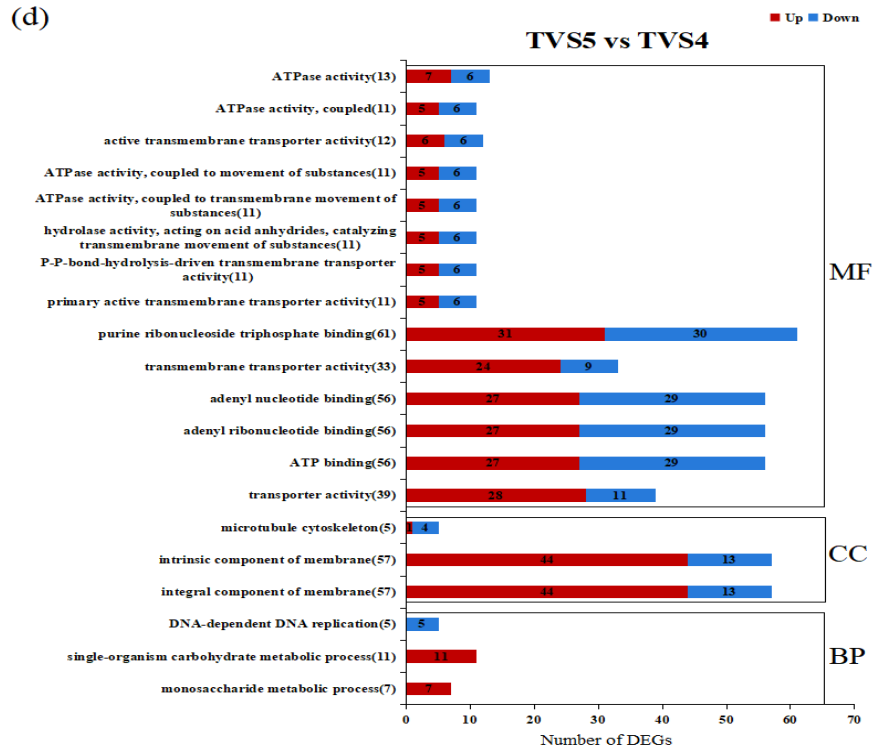
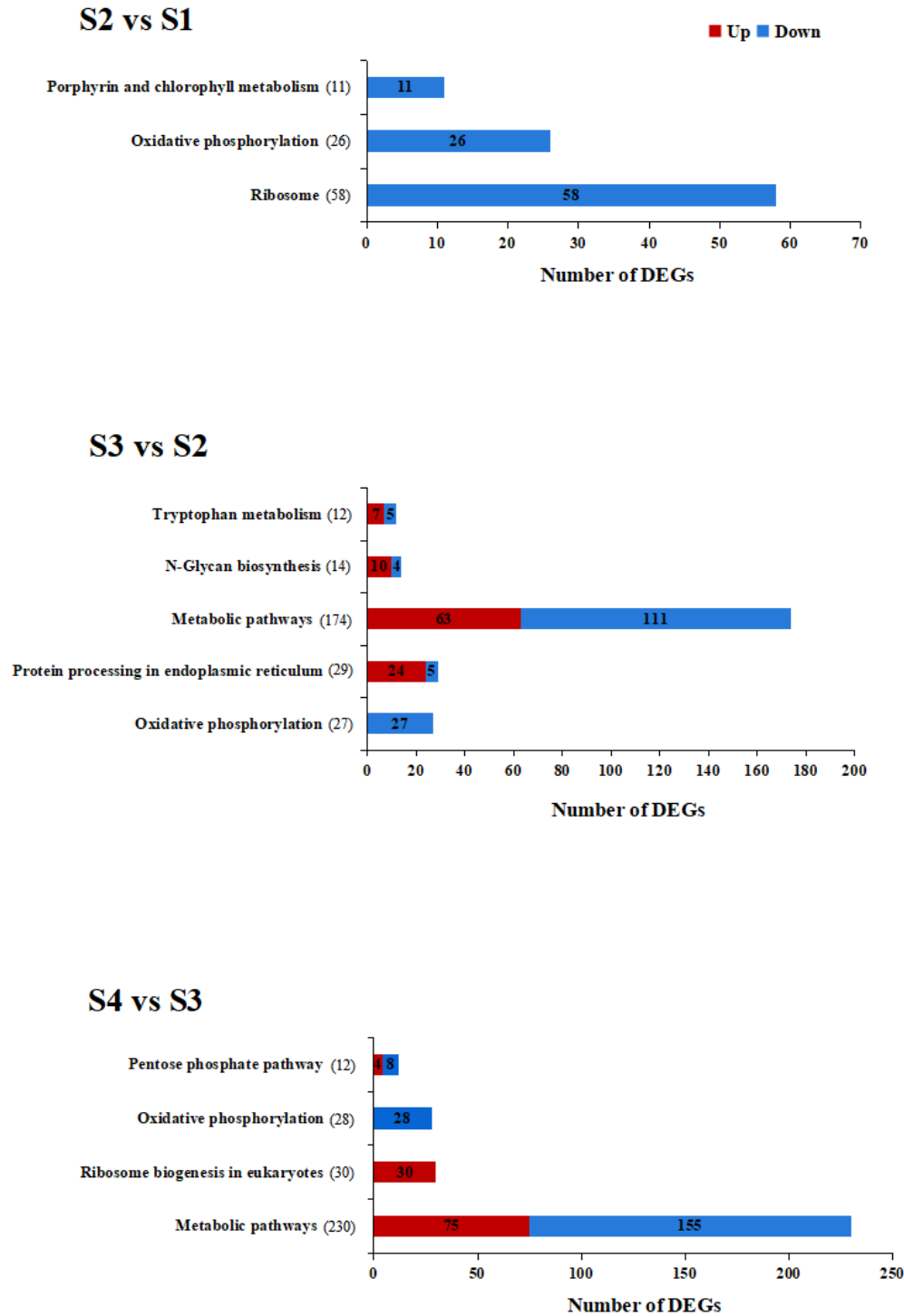


**Fig. S1 GO functional classification of DEGs among samples of adjacent stages.** (a), (b) and (c) represent functional classification of DEGs between S2 vs S1, S3 vs S2 and S4 vs S3, respectively. The bars represent significantly enriched GO terms ( $P < 0.05$ ), and the numbers beside terms indicates the number of DEGs for each term. The number in the center of red and blue bars represents the number of up-regulated and down-regulated DEGs in the term, respectively. Because the picture is too big, we splited it into 2 parts to see it more clearly.



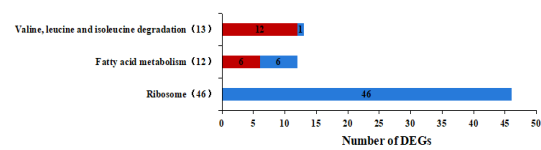


**Fig. S2 GO functional classification of DEGs between adjacent sampling time points.** (a), (b), (c), (d), (e), (f) and (g) represent GO functional classification of DEGs between TVS2 vs TVS1, TVS3 vs TVS2, TVS4 vs TVS3, TVS5 vs TVS4, TVS6 vs TVS5, TVS7 vs TVS6 and TVS8 vs TVS7, respectively. The bars represented significantly enriched GO terms ( $P < 0.05$ ), and the number beside each term indicates the number of DEGs in the term. The number in the center of the red and blue bars represents the number of up-regulated and down-regulated DEGs in the term, respectively. Because the picture is too big, we splited it into 2 parts to see it more clearly.

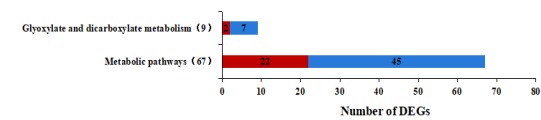


**Fig. S3 KEGG functional classification of DEGs between adjacent stages.** The bars represent significantly enriched KEGG pathways ( $P < 0.05$ ), and the number beside the term indicates the number of DEGs included in the pathway. The number in the center of red and blue bars represents up-regulated and down-regulated DEGs, respectively.

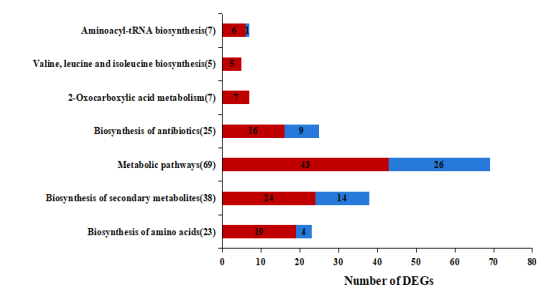
#### TVS2 vs TVS1



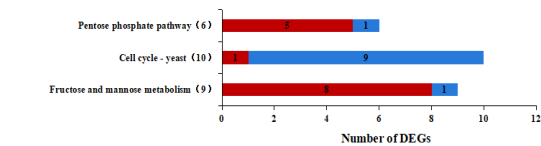
#### TVS3 vs TVS2



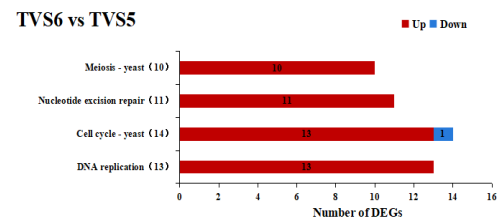
#### TVS4 vs TVS3



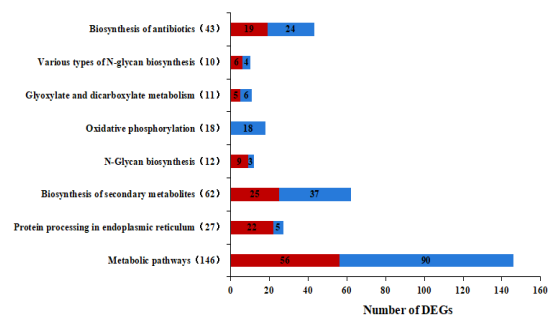
#### TVS5 vs TVS4



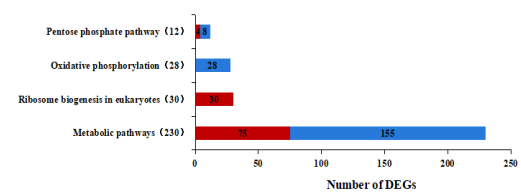
#### TVS6 vs TVS5



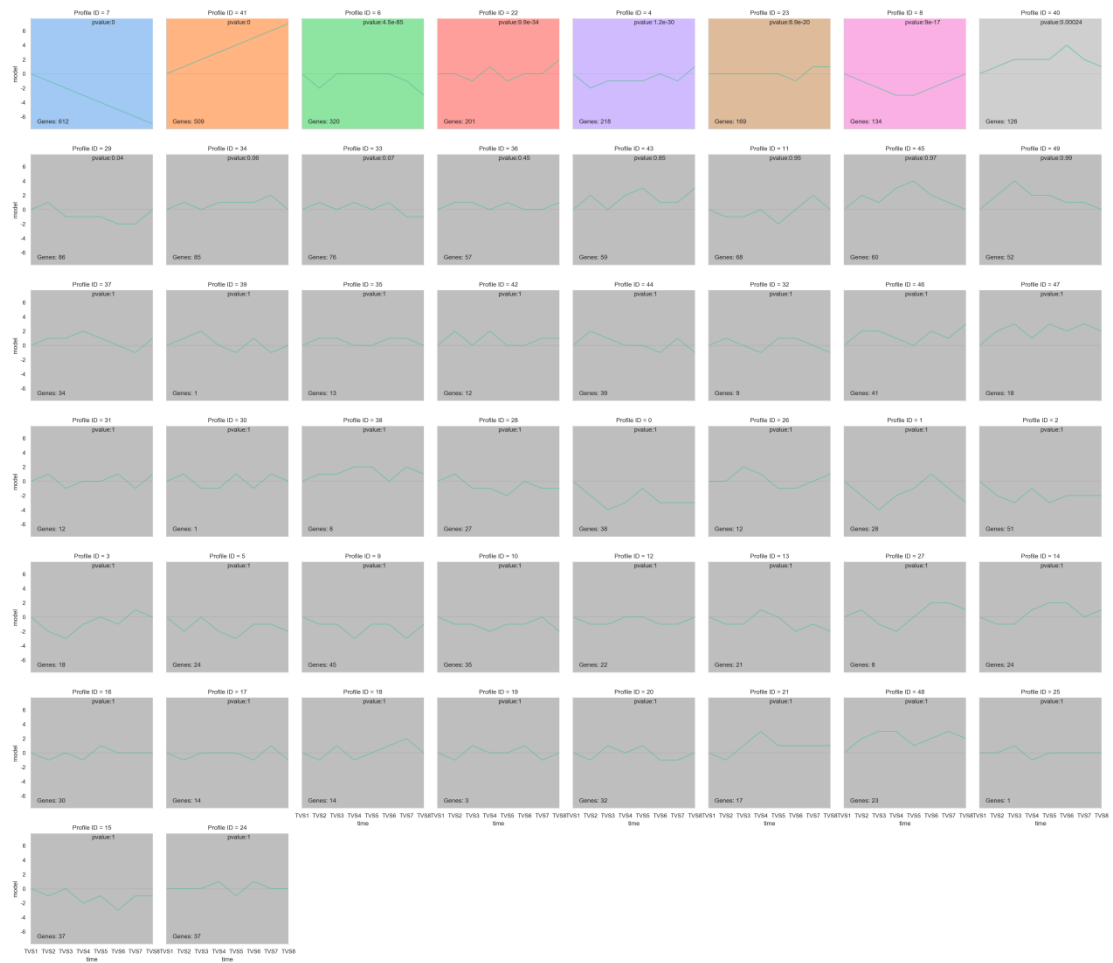
#### TVS7 vs TVS6



#### TVS8 vs TVS7



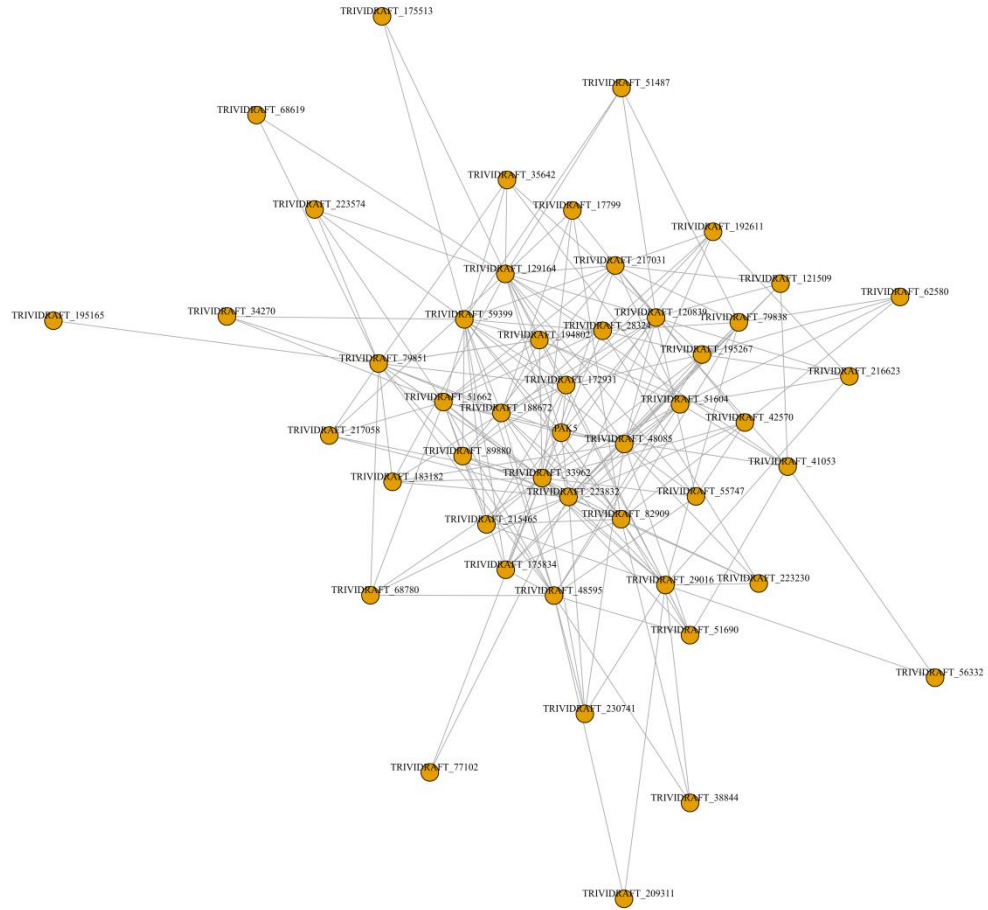
**Fig. S4 KEGG functional classification of DEGs among the samples of adjacent time points.** The bars represent significantly enriched KEGG pathways ( $P < 0.05$ ), and the number beside the term indicates the number of DEGs included in the pathway. The number in the center of red and blue bars represents up-regulated and down-regulated DEGs, respectively.



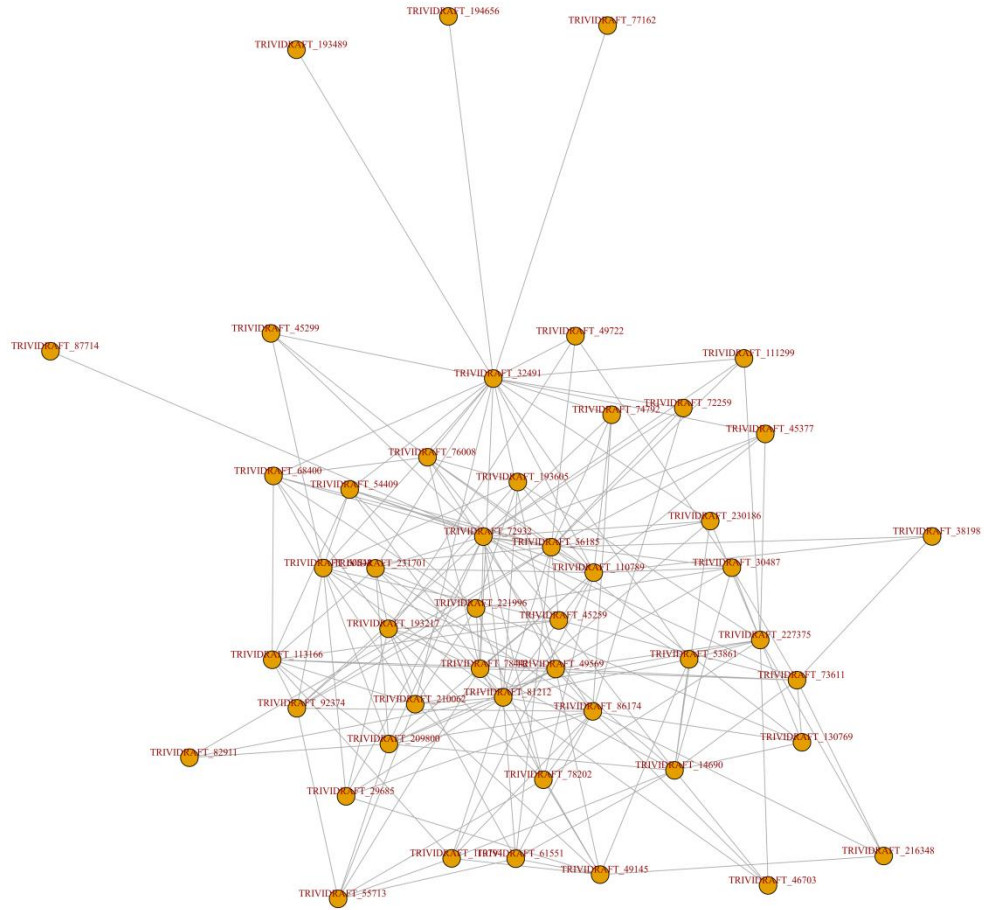
**Fig. S5 Summary Plot of all DEGs STC classification.**



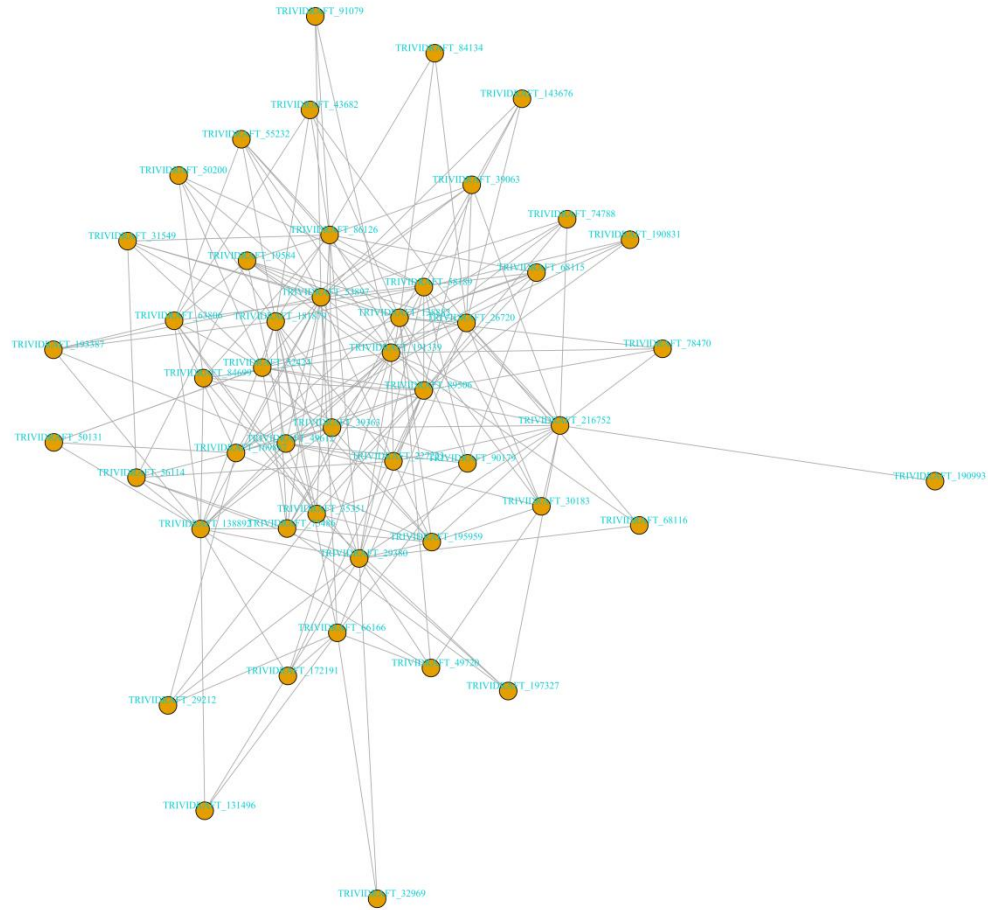
## black\_Hub\_network



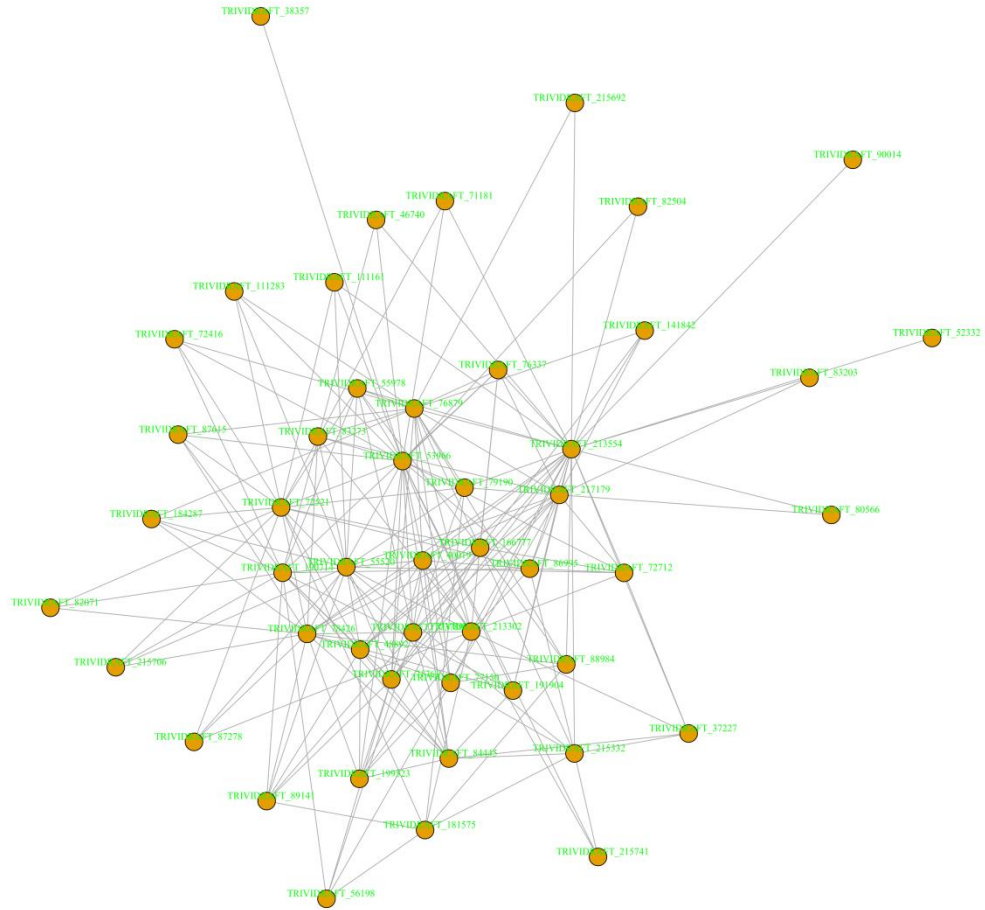
**dark red\_Hub\_network**



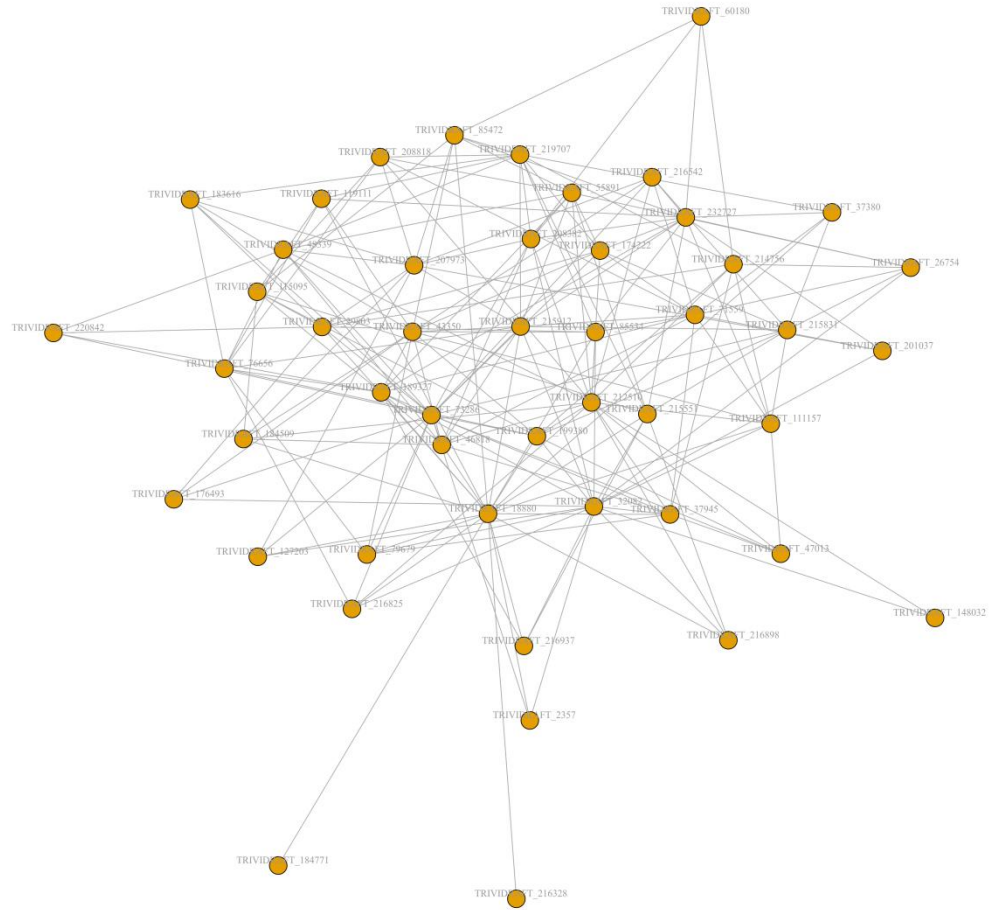
## dark turquoise\_Hub\_network



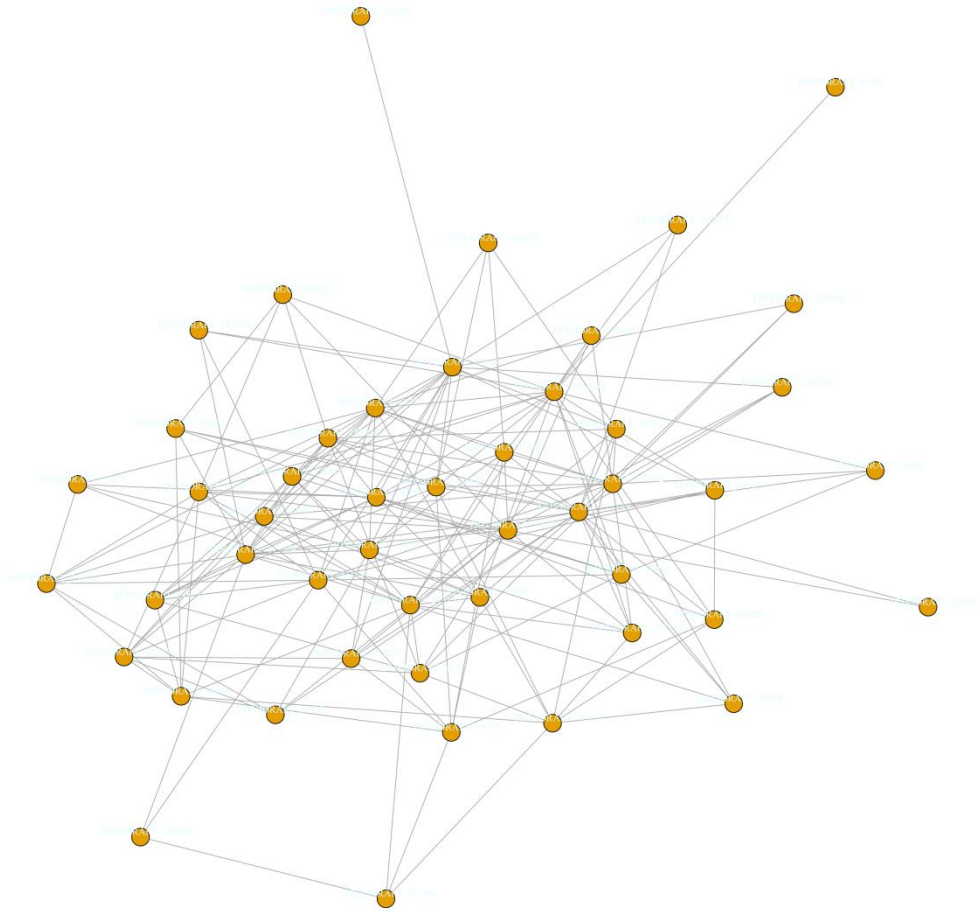
**green\_Hub\_network**



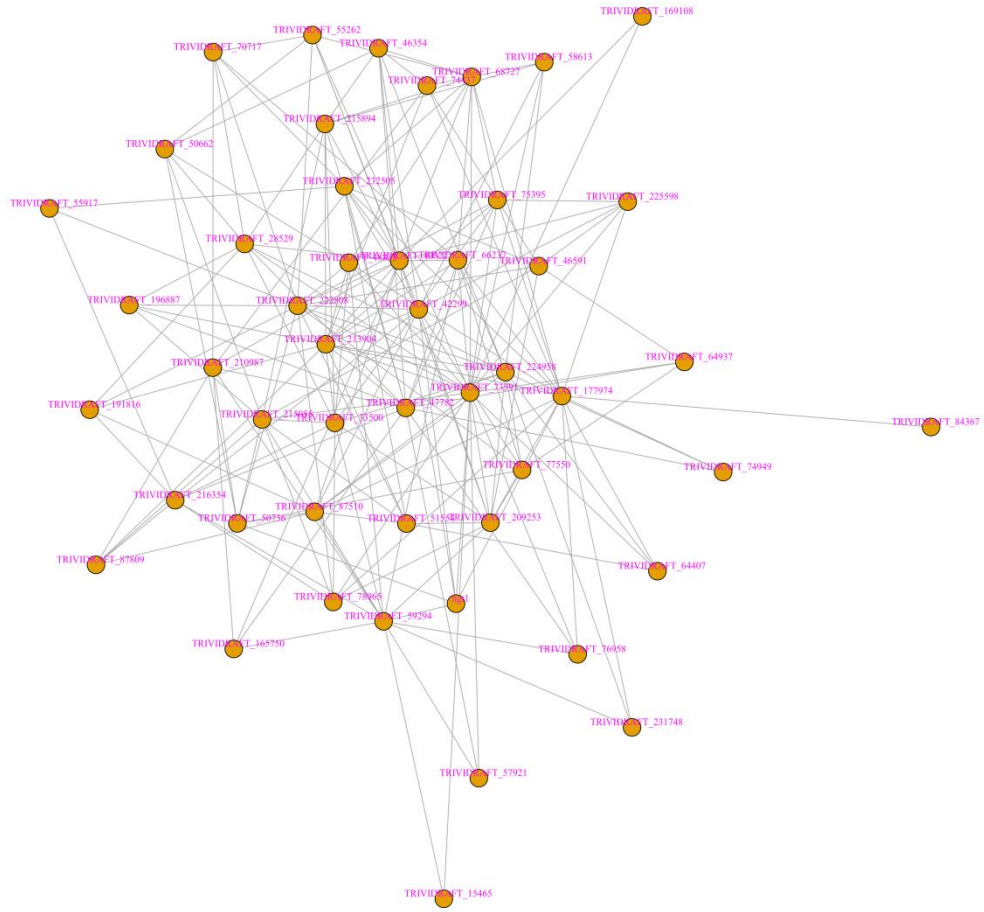
**grey60\_Hub\_network**



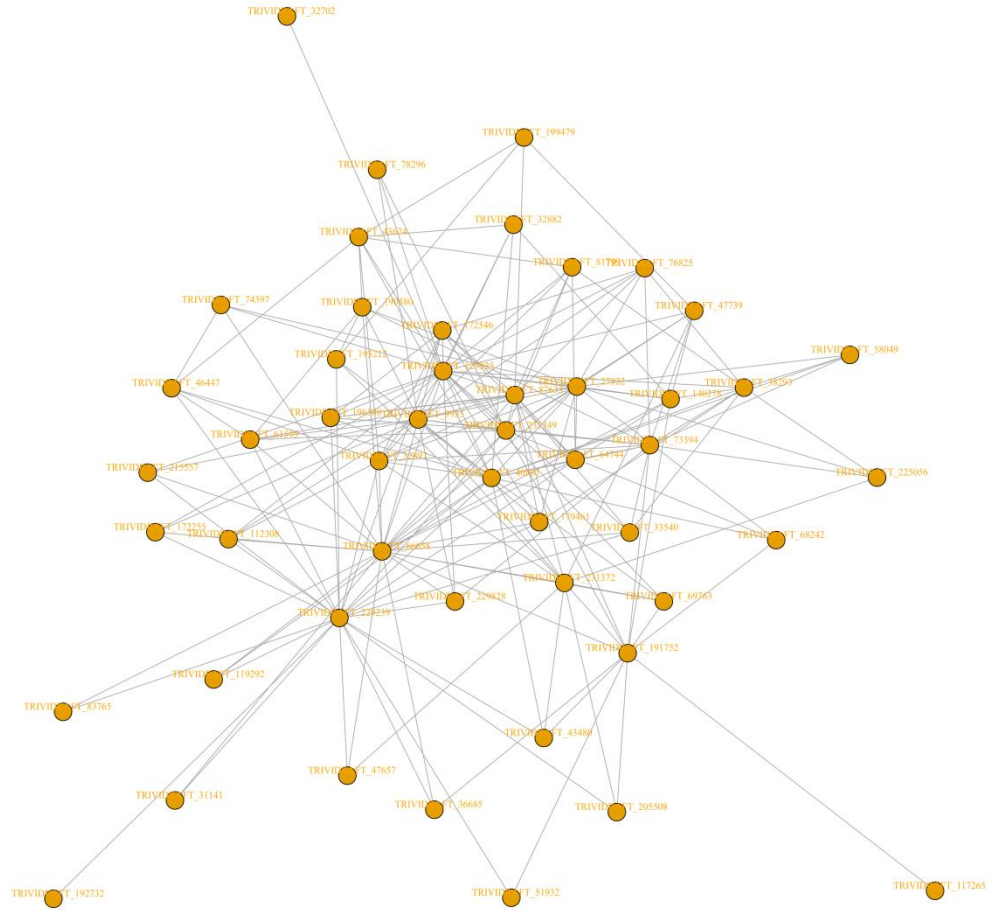
light cyan\_Hub\_network



## magenta\_Hub\_network

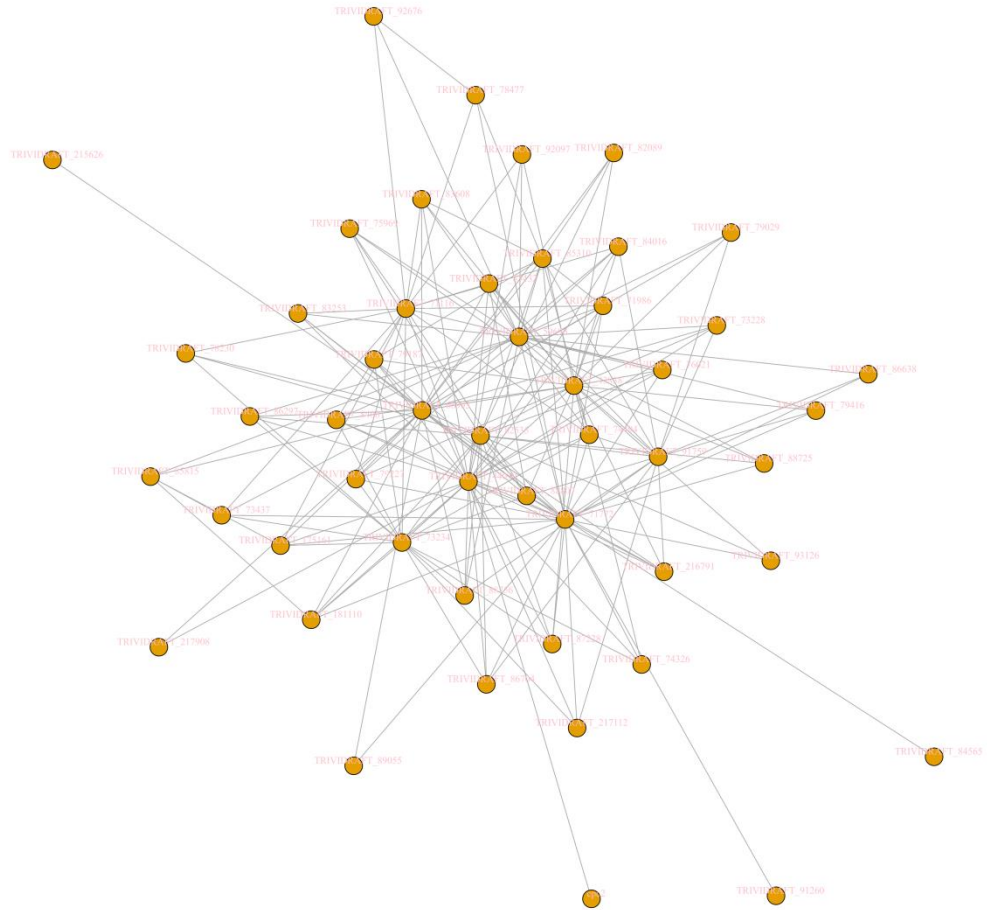


## orange\_Hub\_network

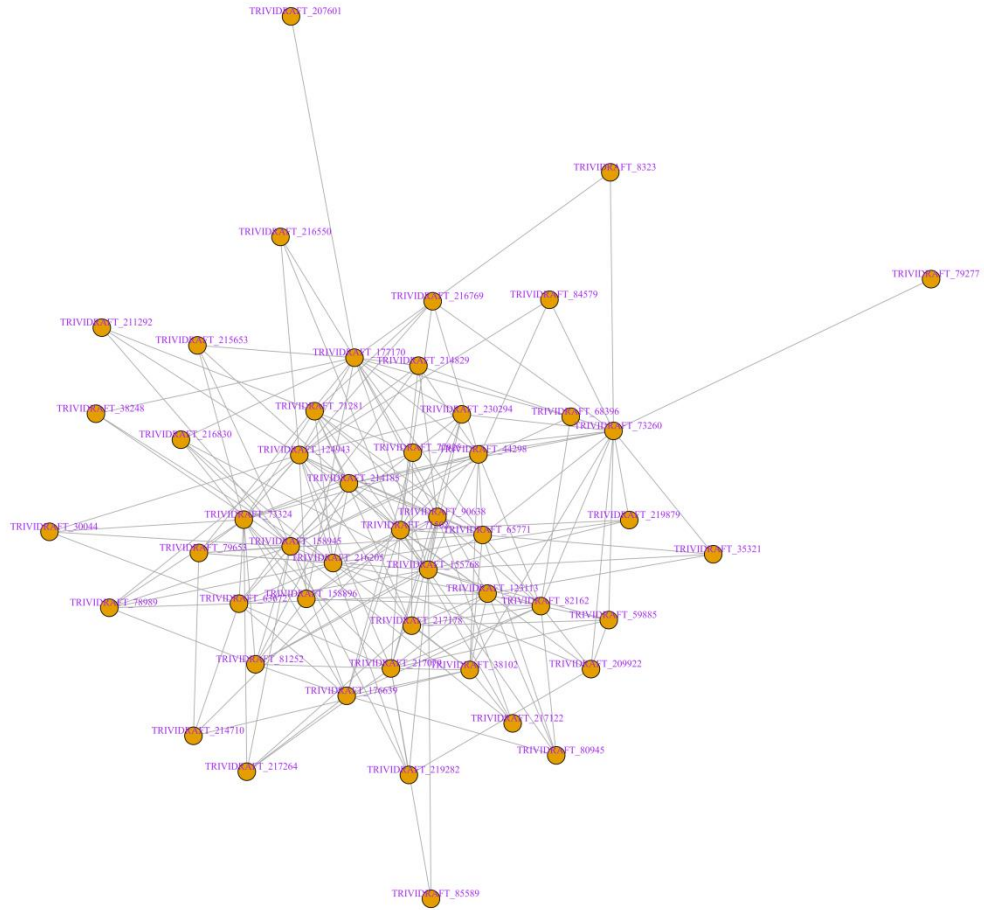




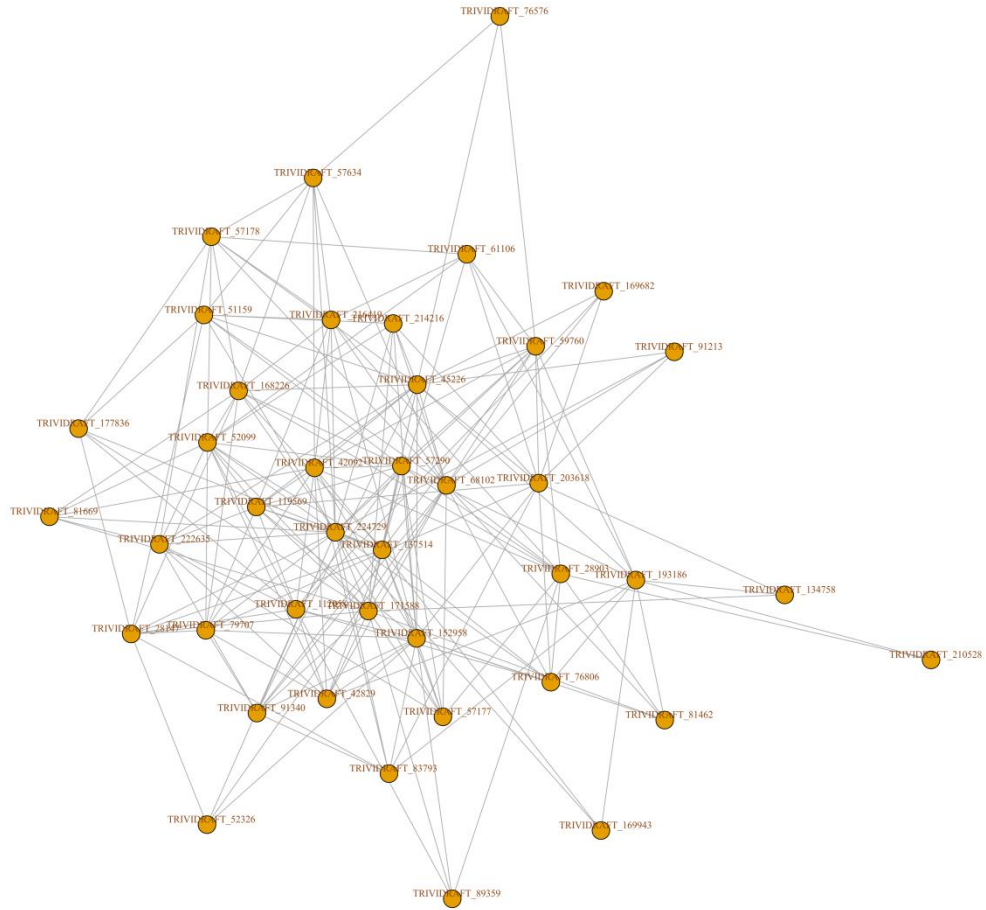
## pink\_Hub\_network



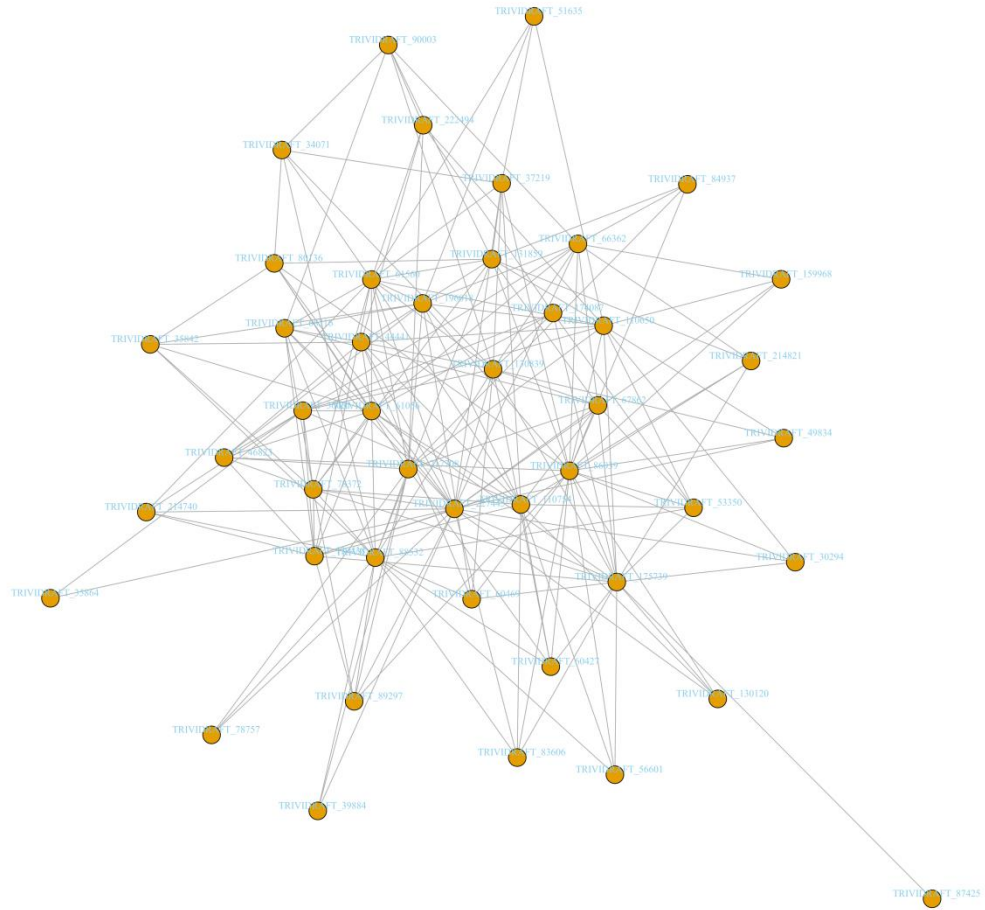
**purple\_Hub\_network**



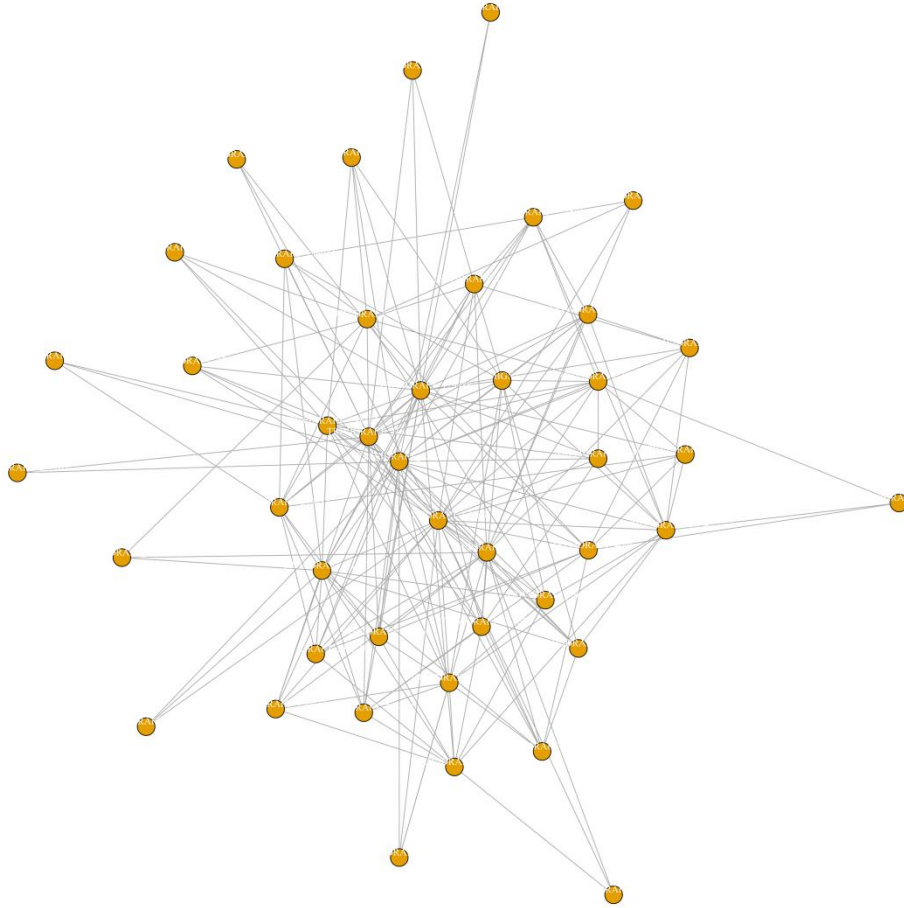
## saddle brown\_Hub\_network



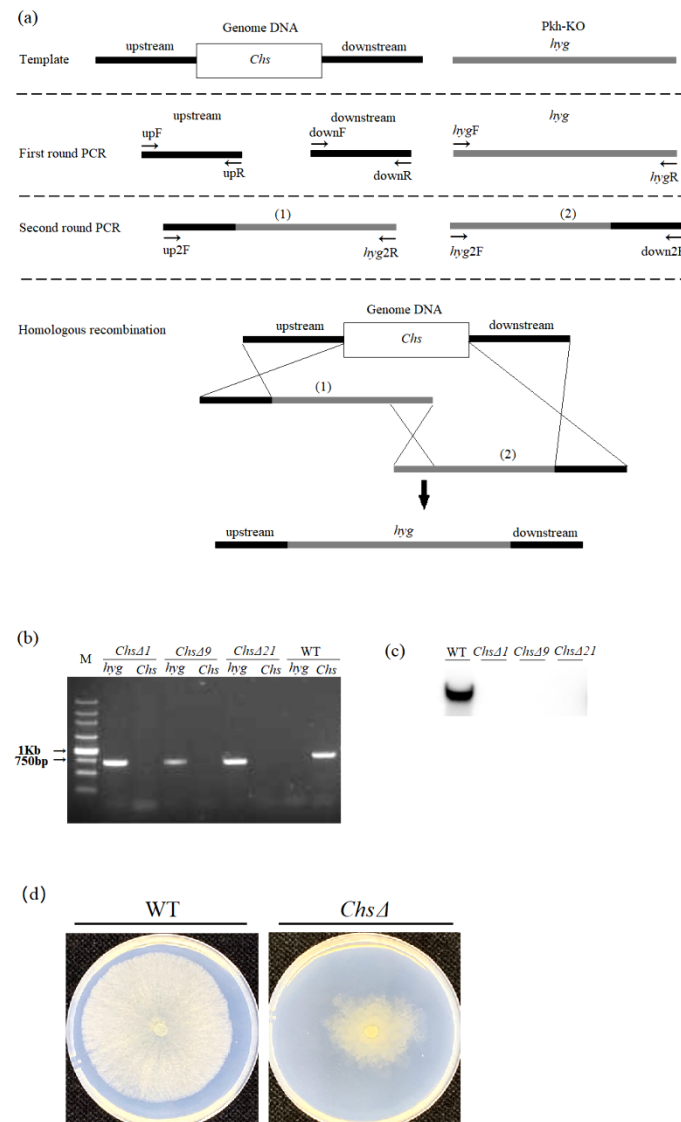
## sky blue\_Hub\_network



**white\_Hub\_network**



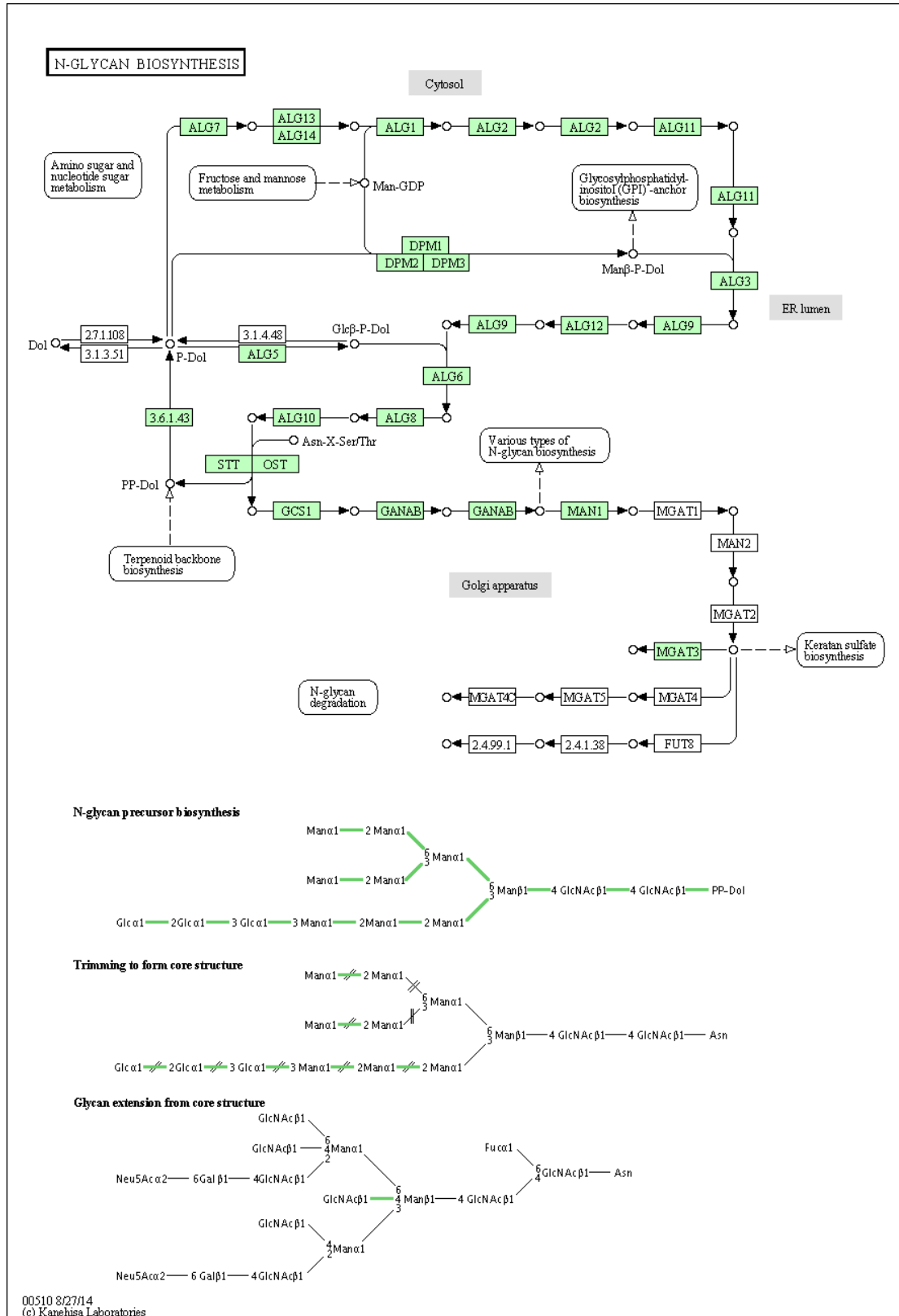
**Fig. S6 Protein-protein interaction (PPI) network of genes in the black, dark red, dark turquoise, green, grey60, light cyan, magenta, orange, pink, purple, saddle brown, sky blue and white modules.**



**Fig. S7 Construction of chitin synthase gene (TRIVIDRAFT\_90152) deletion mutants and the effect on phenotypes of the *T. virens* GV29-8**

(a) Chitin synthase gene (TRIVIDRAFT\_90152) deleting strategy. The *Chs* gene of *T.virens* GV29-8 was knocked out by split-PCR strategy. The split-marker cassettes were developed using fusion PCR, and involved two rounds of PCR. First round PCR: the upstream and downstream homologous fragments of *Chs* were amplified using primers upF/upR and downF/downR with the genome DNA of *T.virens* GV29-8 as template, respectively. Fragment of the hygromycin gene was amplified with the plasmid pKH-KO as template, and *hygF/hygR* as primer. Second round PCR: the upstream homologous fragment of *Chs* gene and the *hyg* gene fragment from the first round of PCR products were simultaneously used as templates, and the final fragment (1) was amplified by using the primer up2F/hyg2R, which contained the upstream homologous region of the *Chs* gene and two thirds of the hygromycin

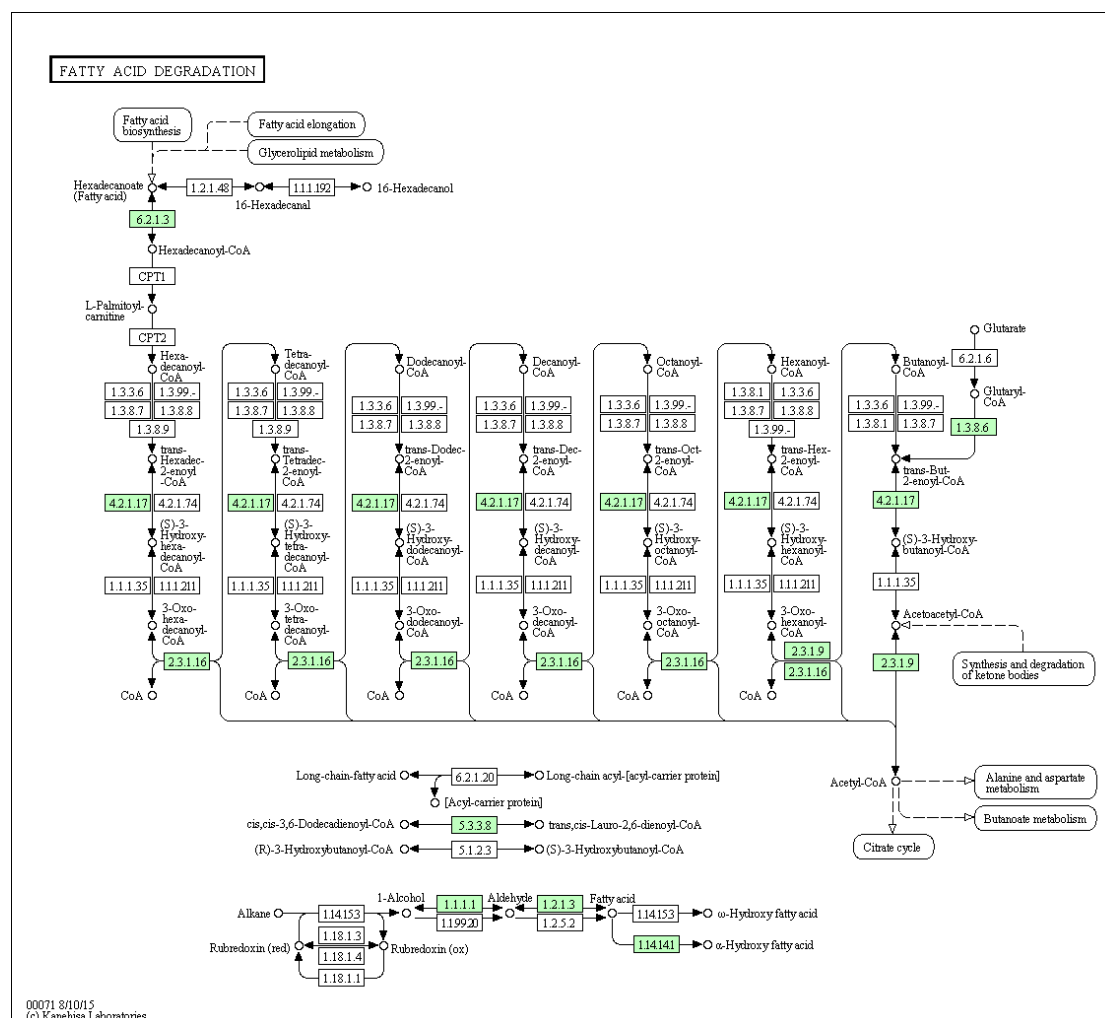




**Fig. S9 N-Glycan biosynthesis pathway (tre00510).** DEGs in N-Glycan biosynthesis pathway: 3.6.1.43: dolichyldiphosphatase (25792540); DMP1: dolichol-phosphate mannosyltransferase (25798517); ALG5: dolichyl-phosphate beta-glucosyltransferase (25795393); OST: oligosaccharyltransferase complex subunit alpha (25786852/25787193/25798795); MAN1: mannosyl-oligosaccharide alpha-1,2-mannosidase (25798667/



25789754/25795445); STT: dolichyl-diphosphooligosaccharide-protein glycosyltransferase (25797749); ALG1: beta-1,4-mannosyltransferase (25795163); GCS1: mannosyl-oligosaccharide glucosidase (25793447); DPM3: dolichol-phosphate mannosyltransferase subunit 3 (25799030), beta-1,4-N-acetylglucosaminyltransferase (25793326). The green box represents a specific gene or enzyme in *Trichoderma Reesei* and does not indicate up-regulation or down-regulation of the gene.

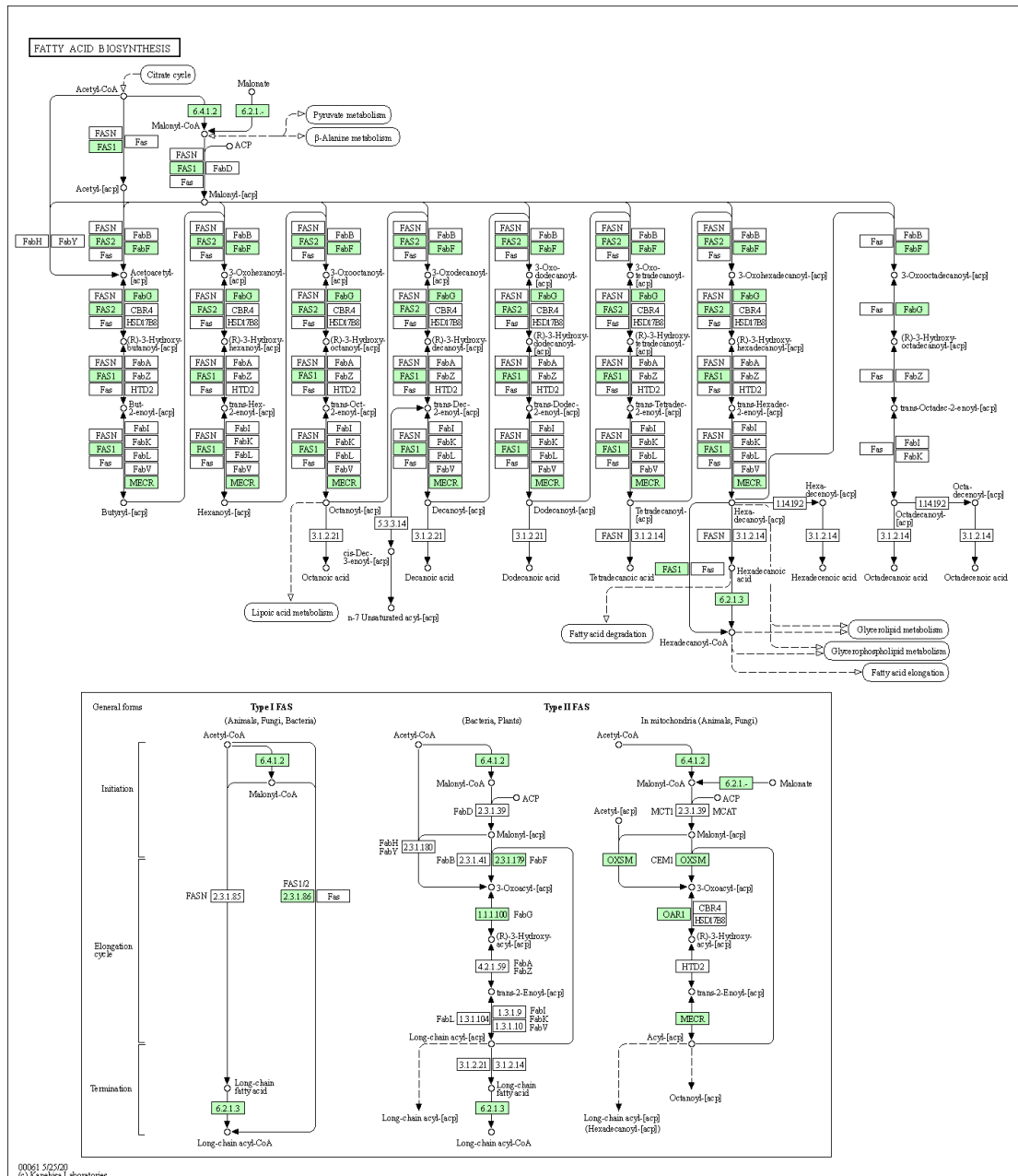


DEGs in fatty acid degradation pathway: 4.2.1.17: enoyl-CoA hydratase (25798760); 2.3.1.9: acetyl-CoA C-acetyltransferase (25788734/25797542); 5.3.3.8: Delta3-Delta2-enoyl-CoA isomerase (25795747); 1.1.1.1: alcohol dehydrogenase, propanol-preferring (25793381); 1.3.8.7: acyl-CoA dehydrogenase (25788983).

0	1	2	3	4	5	6
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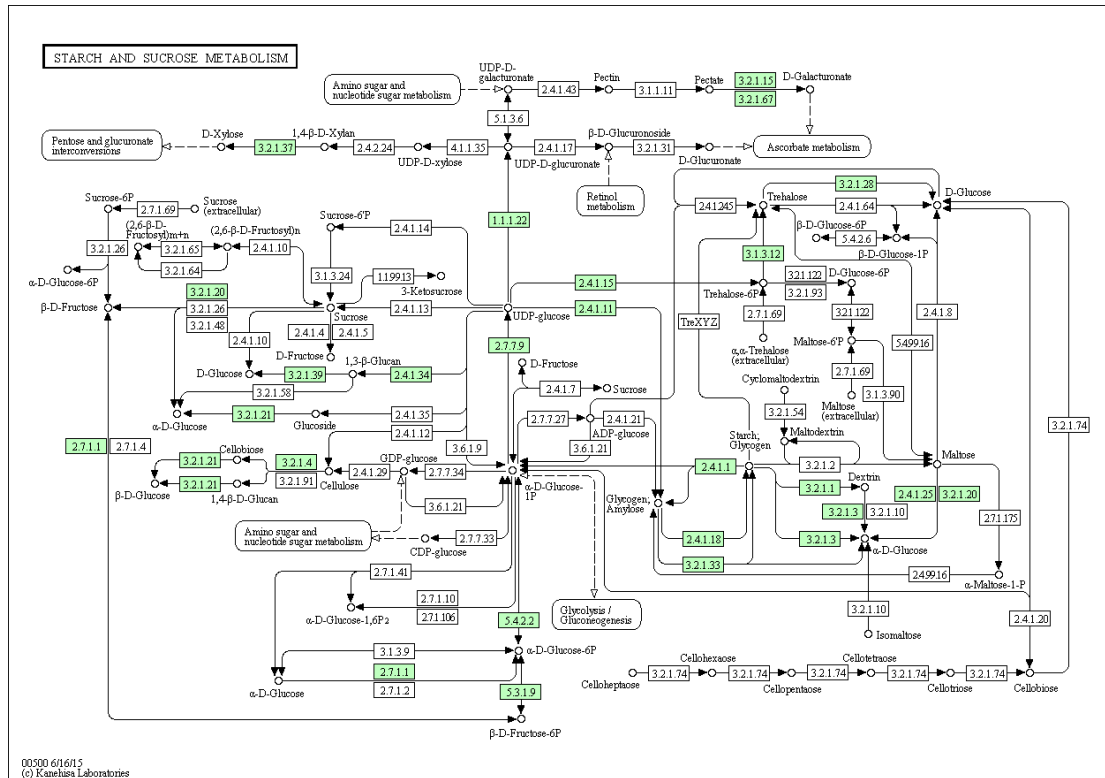


2



DEGs in fatty acid biosynthesis pathway: 6.4.1.2: acetyl-CoA carboxylase (25798001); 2.3.1.86: fatty acid synthase subunit beta, fungi type (25788772); 2.3.1.179: 3-oxoacyl-[acyl-carrier-protein] synthase II (25798380); 1.1.1.100: 3-oxoacyl-[acyl-carrier protein] reductase (25792427); 6.2.1.3: long-chain acyl-CoA synthetase (25798208).

**Fig. S10 Fatty acid metabolic pathway(fatty acid degradation(tre00071), biosynthesis of unsaturated fatty acid (tre01040) and fatty acid biosynthesis pathway (tre00061) ). The green box represents a specific gene or enzyme in *Trichoderma Reesei* and does not indicate up-regulation or down-regulation of the gene.**



**Fig. S11 Starch and sucrose metabolism pathway (tre00500).** DEGs in starch and sucrose metabolism pathway: 3.2.1.39: glucan endo-1,3-beta-D-glucosidase (25786810); 3.2.1.21: beta-glucosidase (25797680); 3.2.1.28: alpha,alpha-trehalase (25794082); 5.4.2.2: phosphoglucomutase (25798750). The green box represents a specific gene or enzyme in *Trichoderma Reesei* and does not indicate up-regulation or down-regulation of the gene.

