

Supplementary materials

Table S1 Overview of protein identification

Order number	Total spectra	Spectra	Peptide	Unique peptide	Protein
16C1369A-1	82970	25183	20844	18348	2769
16C1369A-2	83893	24955	20653	18181	2823
16C1369A-3	82005	24350	20311	17893	3289
16C1369B-1	84636	25352	20306	17907	2571
16C1369B-2	84668	25391	20279	17848	2587
16C1369B-3	84044	25621	20440	18006	2756
Total	502216	150852	29056	26108	4909

Table S3 Summary of RNA sequencing and assembly

Sample Name	Clean Reads	Genome Map Rate	Unique genes
16C1369A-1	47179448	89.07%	25168
16C1369A-2	39567516	88.84%	24941
16C1369A-3	45583918	88.47%	25035
16C1369B-1	46992664	87.75%	25454
16C1369B-2	43014098	87.38%	25176
16C1369B-3	41683754	88.76%	25221

Table S10. Primers used in this study.

Gene name	Gene ID	Forward sequence (5'→3')	Reverse sequence (5'→3')
ACOS5	Capana02g003302	CCAGCTGAATTAGAGGGGATCC	CTCGTTTATAATGTGCAGCGGT
PKSA	Capana01g003460	GGTGATCAACTGAAGGAGACCA	CCCCATTCTTCACCACCATCTT
PKSB	Capana08g002676	GGGCAGTTCATCCAGGTGG	TGTGATTCCAGGACCAAATGCA
MS2	Capana03g003125	AGGAAGTCAGTGGAGCAAGC	CCTTAGCCCTGGAATGTGGA
TKPR1	Capana05g000665	ACCAACTTGCCTCACTTCTATCA	TCGTCAAACATCTCTCAATGGAC
TKPR1	Capana01g002831	ACAGAAGGTTGGGGTTTGTTC	CTATGTGCCATGTCTTCCCTT
CYP704B	Capana01g002203	GAATACAATTGGGGCTCTGATGC	CCCAGGCACCAACTTGAATTTAT
ABCG26	Capana07g002406	AAGGGCTGGAATGGTTGCTT	ACCAACAGTGTCAAATGAAGGTG
AMS	Capana08g000254	AGACTGGTGGATTGTGAGGATC	CTAGCCATTTCAGACCAACCTCT
TDF1	Capana04g001901	AGTACACAGCTACTCCCTTCT	GGCTGCTTTTCTCAACTTCAG
ATXR6	Capana03g001971	CCGTGAAGCTGATGATGGAGAT	CTCGGCTTTCACCATTAAACGTC
A7	Capana07g001721	AGAAACTCACACGCGAATGTTG	GCGTTCAGAGATGGGGAAACTA
ACA9	Capana03g000026	CCCCTCTTCTCTGGTGTATAGG	GGTGTCTTTGGAAGTGGGATGA
4CL3	Capana03g001733	CAAAAGGATGATGCTGCAGGG	TGGCTCTCAGTCTTTCTCAG
GATL4	Capana01g003063	TTTGCAGGAAACATCAAGGCAG	TAACGCAACTCTGGATGAACGA
ARO1	Capana08g002699	CCAAGCACCTAGTACCACATGT	CGTGAGCCTCTGGACTGATAAA
AGL62	Trans_newGene_14655	AGCGGAGAAGAAGAAGAAAGAGA	GATCCTCAGCTCCAAATCTTGC
FAS1	Capana06g000774	TGGCATTGATCAAGTCCCTGGAA	ATGAGCAGCAGATTTCAAGTGGT
LAP3	Capana03g003177	TACCTGGCTAGATTGATGGGGA	ATGGAAGGGTGGCAATATGGTT
PG2	Capana11g001305	AATGTCATTGTTCGAACCACCG	TATCAGCTTCATAGACCCGCAC
TA29	Capana02g001969	ATGTCCACGCAACAGTCCAT	CTTCTCTCGCTGCTCTGAC
TA1	Capana04g001989	AGTTGGGCATTACGGGATT	TGGCCAGTCACAAAACCAGA
UBI-3	AY486137.1	CACATGTACAAGACTGACAGGGCCA	AGACCCGTTCTTGTGACAACCCAC

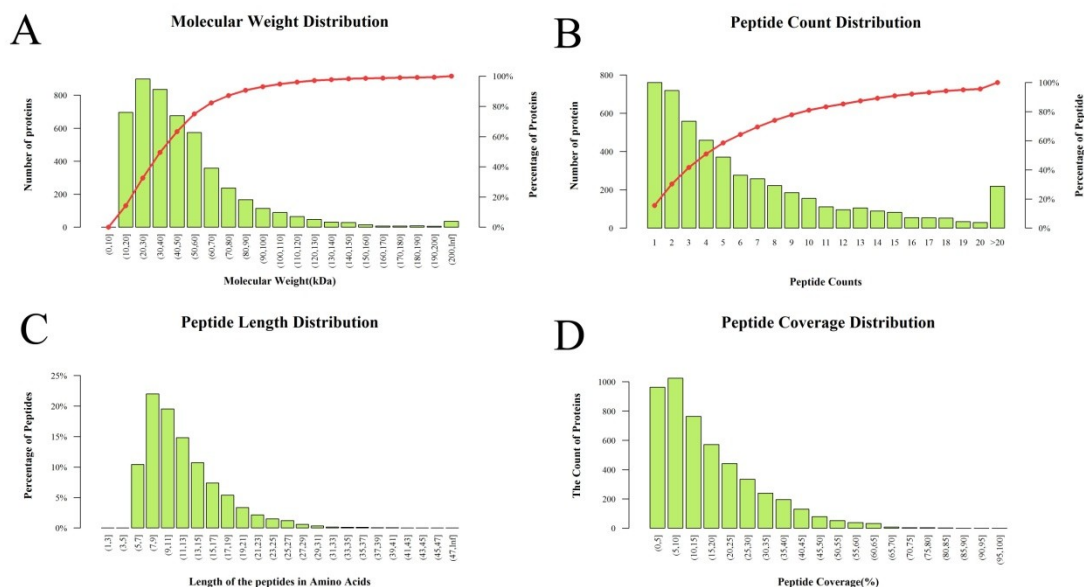


Figure S1. Summary of the label-free proteome. A: Molecular weights distribution of identified proteins; B: Number of peptides that match to unique proteins; C: Length distribution of identified peptides; D: Distribution of coverage of the proteins by the identified peptides.

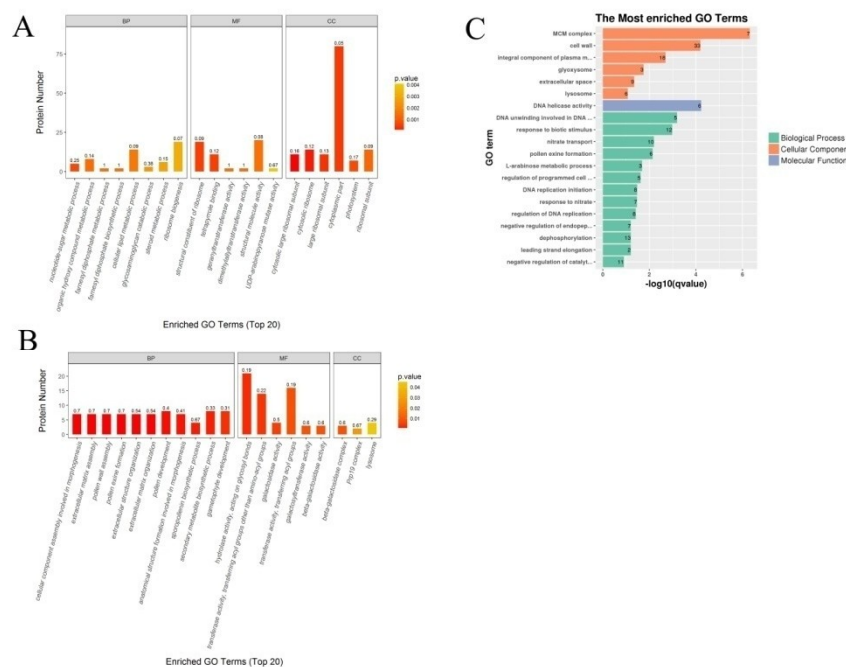


Figure S2. GO functional classification based on DEPs and DEGs. A:GO functional classification based on the 182 DEPs in the proteome; B:GO functional classification based on the 492 DEPs (presence/absence proteins) in the proteome; C: GO functional classification based on the 1069 DEGs in the transcriptome.

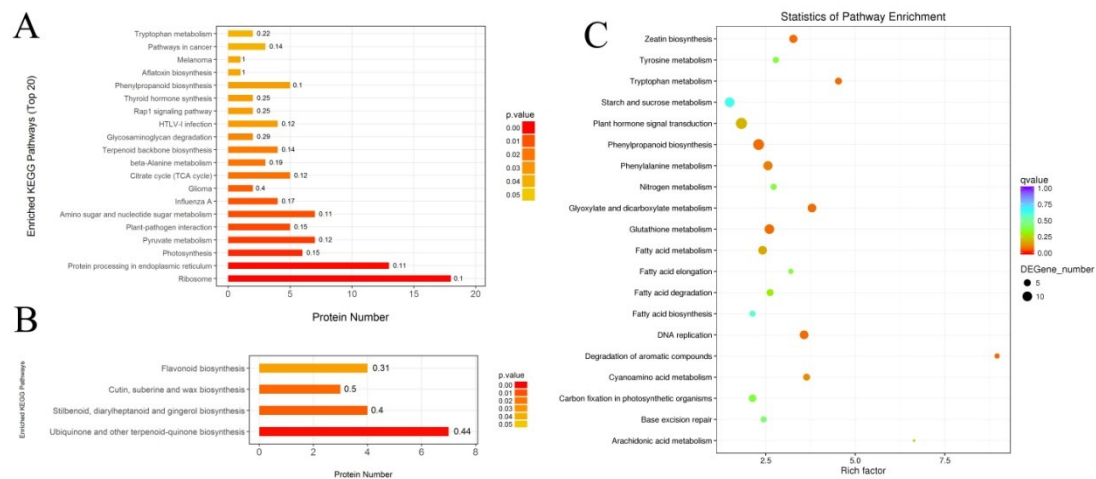


Figure S3. KEGG pathways associated with DEPs and DEGs. A: KEGG pathways associated with the 182 DEPs in the proteome; B: KEGG pathways associated with the 492 DEPs (presence/absence proteins) in the proteome; C: KEGG pathways associated with the 1069 DEGs in the transcriptome.