Suplimentary content

Table S1. DNA primer list for Realtime-qPCR validation

Gene	Primer sequence (5′-3′)
CHI1A	F: CTTCCGAGGAACTCGTTGAC R: CAGCTTCAGCATCACCGTAA
CHI2A	F: ACAATGATCTTGCCCCTGAC R: CTGGTGGGAATGTTTCGTCT
CHI3A2	F: TGACGCCATATCACCAAGAA R: GAAGCCCATTTGAGGAGACA
CHI3B	F: GAGCATTCGTTCTGTGCGTA R: TGGATTCTTCCCACTTCCTG
CHI4A	F: TGCACAGTATGGGGTTCAGA R: GCCTCTACCACATTGGCATT
CHS11	F: TCGTGTGCTTGTCGTTTGTT R: GGGTTTTCAACTGGCAGAGG
CHS13	F: GAAGCGATACATGCACCTGA R: TGCGTGATCTTTGACTTTGG
CHS14	F: GGGTCACCAATAGCGAACAT R: GGGGACATTCTGTCGTGTCT
UGT2	F: TCCAAATGAAGCCAAAGACC R: CCTTTGTCATCTTCCCCGTA
UGT74B1	F: ACAAGGCAGTCCCAAATGAC R: TCTCCAGATCAGGGATGACC

Table S2. Details of sample collected

No.	Origin	Cultivar	Library	Tissue	No. sample
1	Thailand	TLBYT	L1	Leave	3
2	Thailand	TLBYT	T1	Stem	3
3	Thailand	TLBYT	C1	Tube	3
4	Thailand	TLCNX	C2	Tube	3
5	Thailand	TLDB	C3	Tube	3
6	Viet Nam	NA	C4	Tube	3
7	Viet Nam	SL	L5	Leave	3
8	Viet Nam	SL	T5	Stem	3
9	Viet Nam	SL	C5	Tube	3

Table S3. Transcriptomic filtered database. Order from 1-5 denotes the cultivars order: TLBYT, TLCNX, DB, NgheAn, SonLa; L denotes leaf sample, C denotes tuber sample, T denotes stem sample

Sample	Length	Reads	Bases	Q20 (%)	Q30 (%)	GC (%)
L1	148.33	56079458	8318322428	98.2	94.79	48.48
L5	148.54	61201140	9090616733	98.42	95.22	48.16
C1	147.55	60740762	8962580433	98.24	95.09	46.11
C2	147.51	60944258	8989723588	98.16	94.97	46.24
C3	147.59	59723918	8814927352	98.19	95.03	45.94
C4	147.51	61445068	9063619908	98.42	95.36	45.3
C5	147.44	60760138	8958463050	98.29	95.2	45.75
T1	147.49	61266174	9036362369	98.42	95.38	48.72
T5	147.79	59744308	8829797465	98.62	95.84	51.89

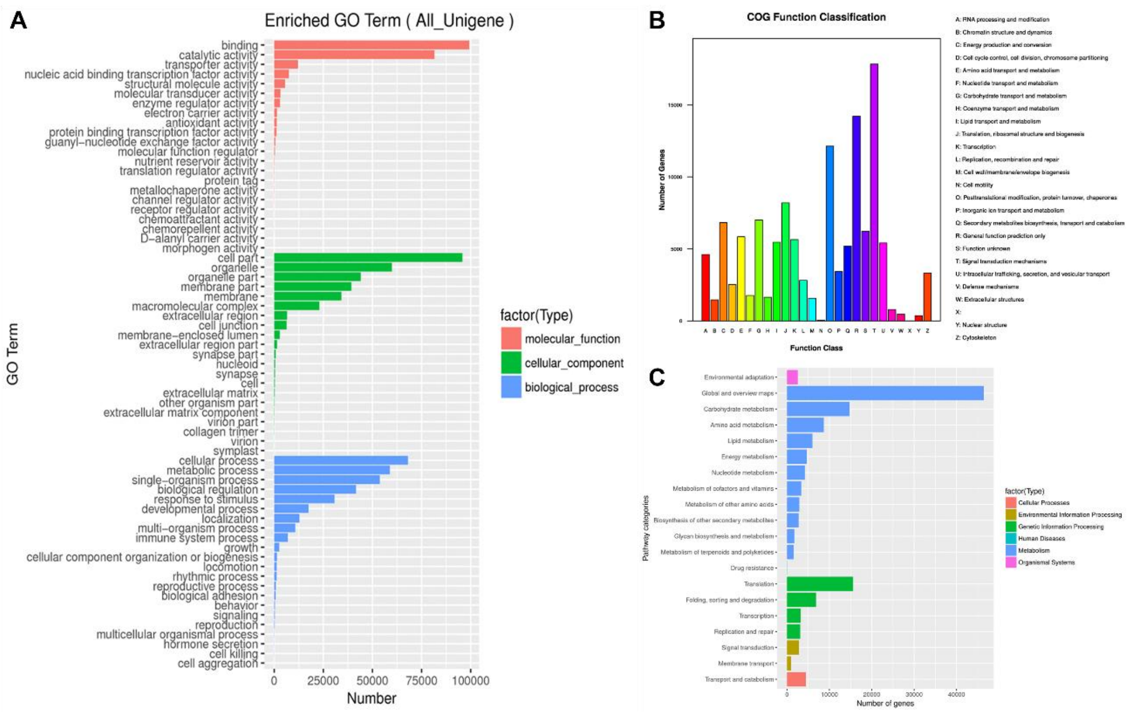

Fig S1: ***Pueraria mirifica*** **transcriptome annotation results by GO, COG, and KEGG analysis. (a) Histogram presentation of Gene ontology (GO) classification of *P. mirifica* transcriptome, all unigenes were assigned to three main categories of cellular function, (b) COG classification of *P. mirifica* unigenes into 25 groups, the capital letters of the X – axis mention the COG categories as listed on the right of histogram, (c) KEGG classification represents the DEGs distribution into five major metabolic categories: Cellular process, Environmental information process, Genetic information process, Metabolism, Organism system.**