

Additional Table S4 Comparison analyses on the gene annotations involved in MEP/MVA/ginsenoside biosynthesis-related pathways between our assembled RNA-seq dataset and two published reference genomes and one Pacbio transcriptome of *P. ginseng*.

Pathway	Enzyme	Our-assembled	Iso-seq	IPGA	Renamed
MEP	DXR	14	4	–	9
	DXS	59	20	1	43
	IspD	8	1	1	7
	IspE	6	7	–	23
	IspF	10	4	–	2
	IspG	14	6	2	6
	IspH	11	4	2	4
	AACT	20	12	–	29
MVA	HMGR	34	15	1	34
	HMGS	23	5	1	7
	MVD	2	5	–	8
	MVK	13	3	–	9
	PMK	30	125	14	37
	FPS	15	3	1	16
Skeleton	GGR	33	12	1	27
	IDI	6	2	–	5
	SS	13	3	2	7
	AS	18	5	–	34
Saponin	DS	7	3	1	4
	SE	22	6	–	18
	GT	260	27	9	65
	P450	221	66	8	151

Note: The annotation threshold was set as the identity $\geq$ 90% and gene transcription abundance (TPM) $\geq$ 1. “–” means not to be annotated.

The reference transcriptomic data of Iso-seq (Jo et al. Genes 2017, 8, 228), genomic data of IPGA (Xu et al. GigaScience, 2017, 6, 1–15) and Renamed (Kim et al. Plant Biotechnology Journal, 2018, 1–14) were cited in the table.