

Supplementary Information

Table S1. Correlation coefficient between SNP, InDel, SV, CNV and morphological indexes

	SNP		InDel		SV		CNV	
	Total SNPs	Intergenic region	Total InDels	Intergenic region	Total SVs	Intergenic region	Total CNVs	Intergenic region
Flower length	0.85	0.88	0.86	0.86	0.33	0.34	0.28	0.28
Flower width	0.96	0.96	0.95	0.95	0.72	0.71	0.63	0.63
Flower width/length	0.91	0.89	0.89	0.89	0.76	0.74	0.68	0.68
Calyx length	0.83	0.86	0.84	0.84	0.32	0.34	0.26	0.26
Calyx width	0.96	0.97	0.95	0.95	0.59	0.60	0.43	0.43
Calyx width/length	0.90	0.89	0.63	0.87	0.77	0.69	0.50	0.49
Sepal number	0.85	0.87	0.84	0.84	0.36	0.38	0.20	0.19
Petal number	0.95	0.96	0.94	0.95	0.71	0.71	0.58	0.58
Petaloid stamen number	0.96	0.97	0.95	0.95	0.51	0.52	0.49	0.49

Table S2. SNP annotations of six ornamental pomegranate varieties

SNP type	Single petal varieties			Double petal varieties		
	'Taiansan-baitian'	'Yichengdanban-fenhongtian'	'Zipi-tian'	'Luoyang-baimasi'	'Yichengfen-hongmudan'	'Taianhong-mudan'
Loss of starting codon	48	67	54	74	74	73
Acquisition of starting codon	346	370	404	487	506	515
Loss of ending codon	71	80	72	101	86	100
Acquisition of ending codon	287	323	310	403	398	441
Splicing site	45	62	55	93	85	94
Within 5K upstream of gene	6591	6458	6241	8150	8000	8396

Gene region	45058	49946	58079	66298	68695	68313
Region within 5K downstream of gene	6772	7655	6345	8285	8061	8325

Table S3. Correlation coefficient between different SNP types and morphological indexes

SNP type	Loss of Acquisition starting of starting		Loss of Acquisition ending of ending		Splicing site	Within 5K upstream of gene		Within 5K Gene region downstream of gene	
	codon	codon	codon	codon		of gene	region	m of gene	
Flower length	0.86	0.72	0.90	0.82	0.87	0.88	0.63	0.95	
Flower width	0.73	0.95	0.88	0.96	0.92	0.96	0.90	0.76	
Flower width/length	0.63	0.93	0.79	0.91	0.85	0.89	0.90	0.63	
Calyx length	0.84	0.70	0.90	0.80	0.86	0.87	0.60	0.95	
Calyx width	0.76	0.91	0.90	0.92	0.92	0.98	0.84	0.83	
Calyx width/length	0.57	0.91	0.74	0.84	0.80	0.90	0.87	0.60	
Sepal number	0.78	0.72	0.88	0.79	0.84	0.89	0.63	0.89	
Petal number	0.77	0.90	0.95	0.96	0.94	0.96	0.83	0.83	
Petaloid stamen number	0.81	0.91	0.95	0.93	0.95	0.97	0.86	0.85	

Table S4. InDel annotations of six ornamental pomegranate varieties

InDel type	Single petal varieties			Double petal varieties		
	'Taiansan- baitian'	'Yichengdanban- fenhongtian'	'Zipi- tian'	'Luoyang- baimasi'	'Yichengfen- hongmudan'	'Taianhong- mudan'
Within 5K upstream of gene	983	1022	999	1190	1243	1339
Gene region	10035	11339	10952	14646	14987	15291
Region within 5K downstream of gene	967	1010	955	1157	1146	1143
Exon region	3477	3933	4091	5085	5109	5226

Intron region	170	174	160	190	192	184
Pseudogene region	65	58	51	95	87	105

Table S5. Correlation coefficient between different InDel types and morphological indexes

InDel type	Region within 5K					Pseudogene region
	Within 5K upstream of gene	Gene region	downstream of gene	Exon region	Intron region	
Flower length	0.77	0.84	0.93	0.77	0.95	0.87
Flower width	0.96	0.94	0.90	0.94	0.75	0.95
Flower width/length	0.93	0.88	0.80	0.90	0.62	0.88
Calyx length	0.75	0.81	0.91	0.75	0.93	0.86
Calyx width	0.90	0.93	0.95	0.91	0.88	0.97
Calyx width/length	0.87	0.86	0.82	0.86	0.69	0.88
Sepal number	0.74	0.81	0.92	0.76	0.93	0.88
Petal number	0.95	0.92	0.91	0.91	0.77	0.97
Petaloid stamen number	0.88	0.94	0.96	0.93	0.86	0.94

Table S6. Statistics of SV type in six ornamental pomegranate varieties

Variety type	Variety name	Region within 5K					Total SV
		INS	DEL	INV	ITX	CTX	
Single petal variety	‘Taiansanbaitian’	0	4,860	8,713	3,905	11,761	29,239
Single petal variety	‘Yichengdanbanfenhongtian’	0	5,626	6,482	3,126	11,439	26,673
Single petal variety	‘Zipidian’	0	4,691	8,743	2,988	11,171	27,593
Double petal variety	‘Luoyangbaimasi’	0	4,869	8,557	4,237	10,719	28,382
Double petal variety	‘Yichengfenhongmudan’	0	6,024	8,273	3,135	10,970	28,402

Double petal variety	‘Taianhongmudan’	0	6,641	10,996	3,358	11,040	32,035
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Table S7. Statistics of CNV type in six ornamental pomegranate varieties							
Variety type	Variety name	Increased copy	Decreased copy	Total CNV			
Single petal variety	‘Taiansanbaitian’	4,504	5,361	9,865			
Single petal variety	‘Yichengdanbanfenhongtian’	5,391	5,931	11,322			
Single petal variety	‘Zipidian’	5,761	5,976	11,737			
Double petal variety	‘Luoyangbaimasi’	5,248	6,035	11,283			
Double petal variety	‘Yichengfenhongmudan’	5,745	6,172	11,917			
Double petal variety	‘Taianhongmudan’	6,111	6,282	12,393			

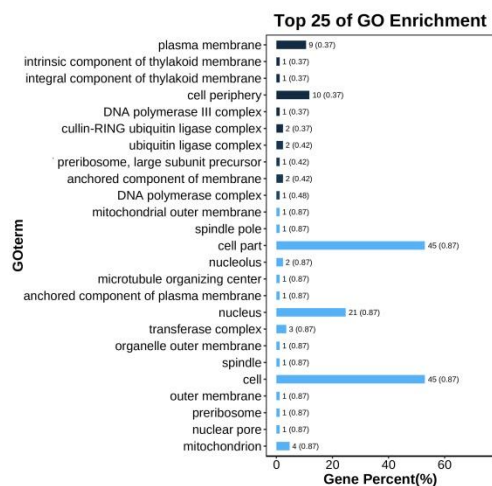


Figure S1. Enrichment map of GO cell components of variant genes between ‘Taiansanbaitian’ and ‘Luoyangbaimasi’

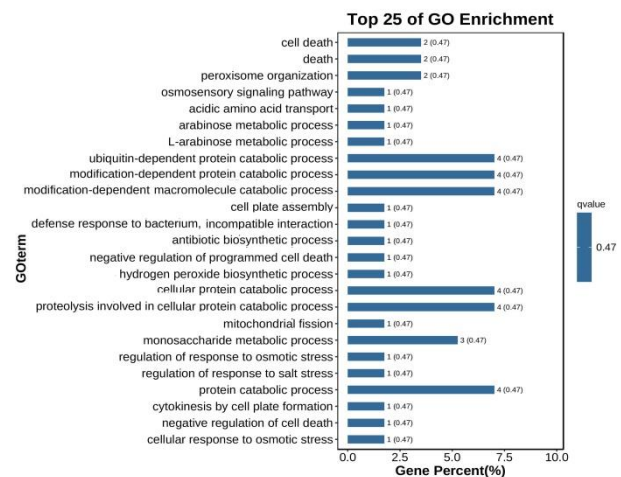


Figure S2. Enrichment map of GO biological process of variant genes between ‘Taiansanbaitian’ and ‘Luoyangbaimasi’

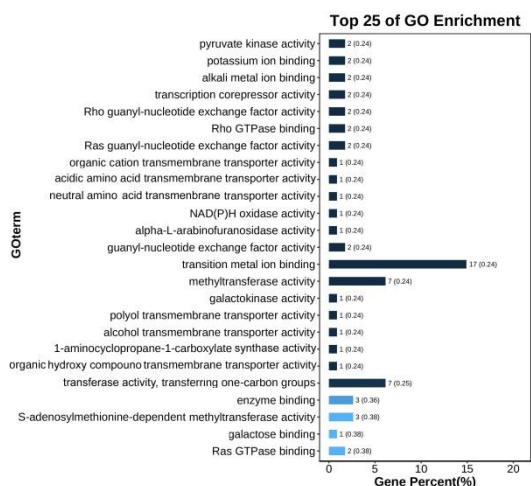


Figure S3. Enrichment map of GO molecular function of variant genes between 'Taiansanbaitian' and 'Luoyangbaimasi'

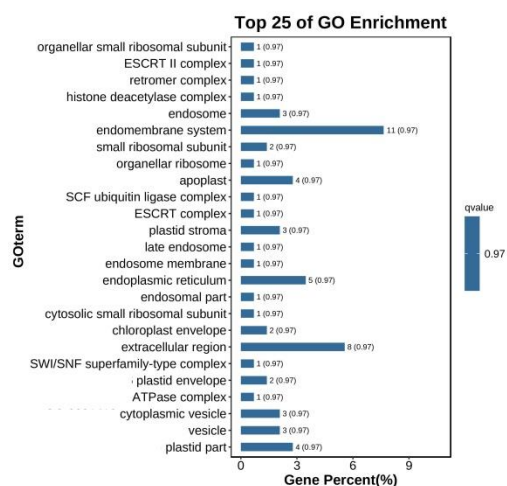


Figure S4. Enrichment map of GO cell components of variant genes between 'Yichengdanbanfenhongtian' and 'Yichengfenghongmudan'

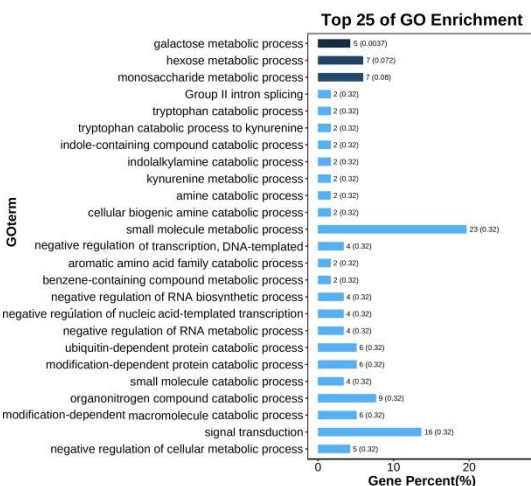


Figure S5. Enrichment map of GO biological process of variant genes between 'Yichengdanbanfenhongtian' and 'Yichengfenghongmudan'

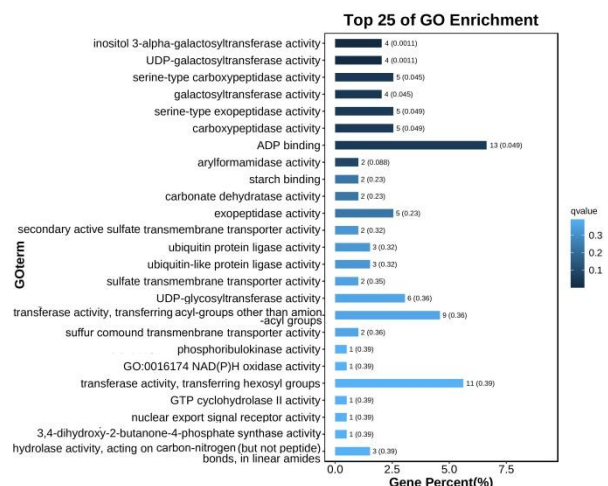


Figure S6. Enrichment map of GO molecular function of variant genes between 'Yichengdanbanfenhongtian' and 'Yichengfenghongmudan'

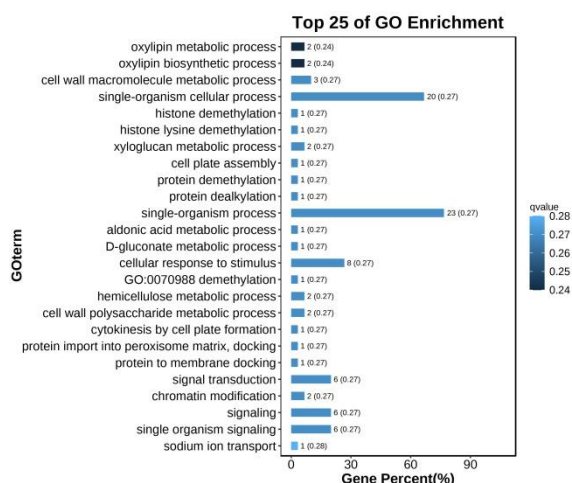
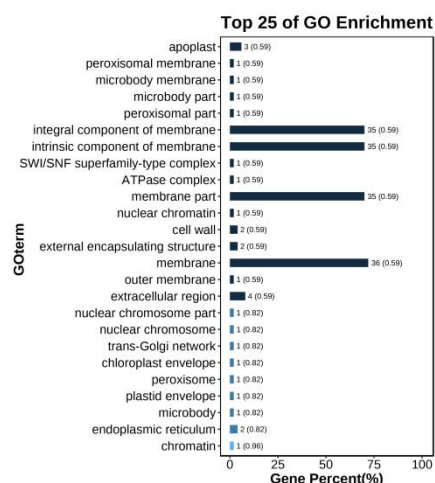


Figure S7. Enrichment map of GO cell components of variant genes between ‘Zipitian’ and ‘Taianhongmudan’ **Figure S8.** Enrichment map of GO biological process of variant genes between ‘Zipitian’ and ‘Taianhongmudan’

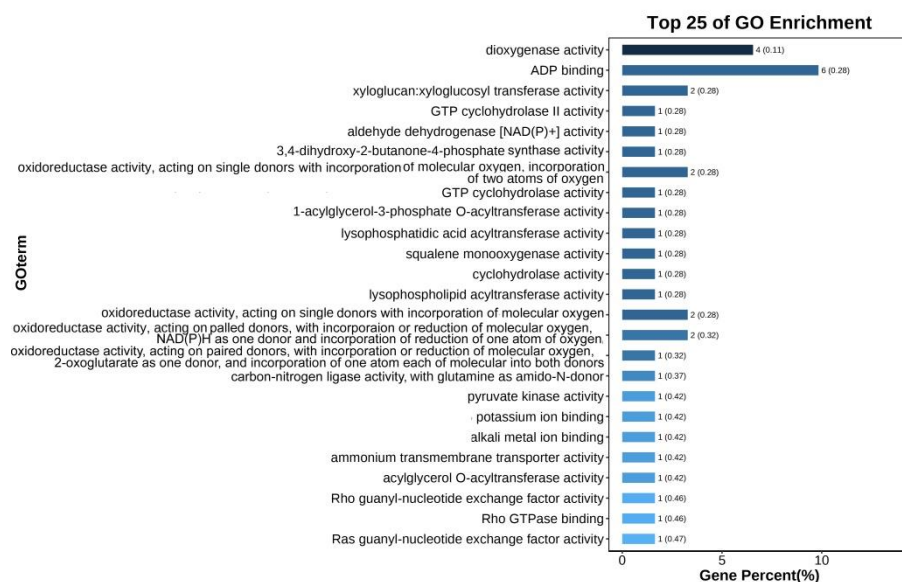


Figure S9. Enrichment map of GO molecular function of variant genes between ‘Zipitian’ and ‘Taianhongmudan’