

Supplementary figures and tables

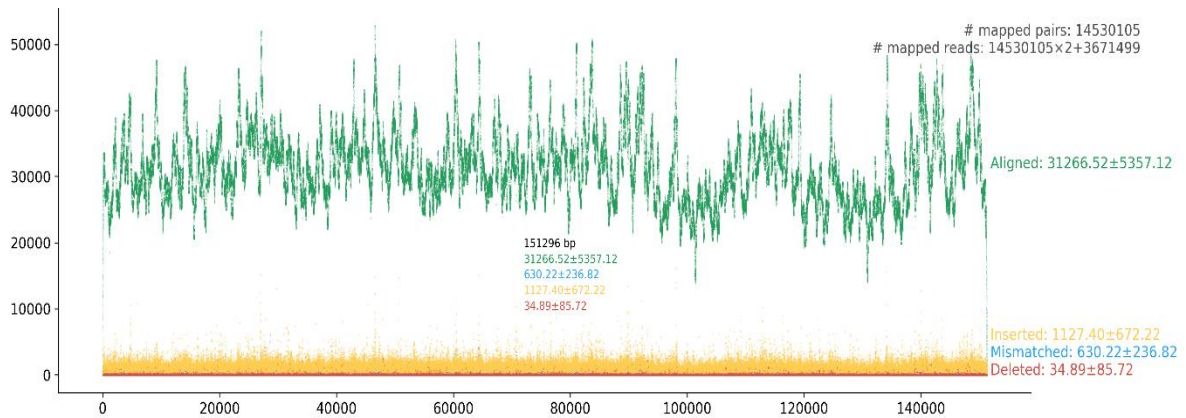


Figure S1 Read coverage of the assembled genome. The paired-end (PE) reads were remapped to the assembled genome. The number aligned bases and the polymorphic sites were counted from the mapping result.

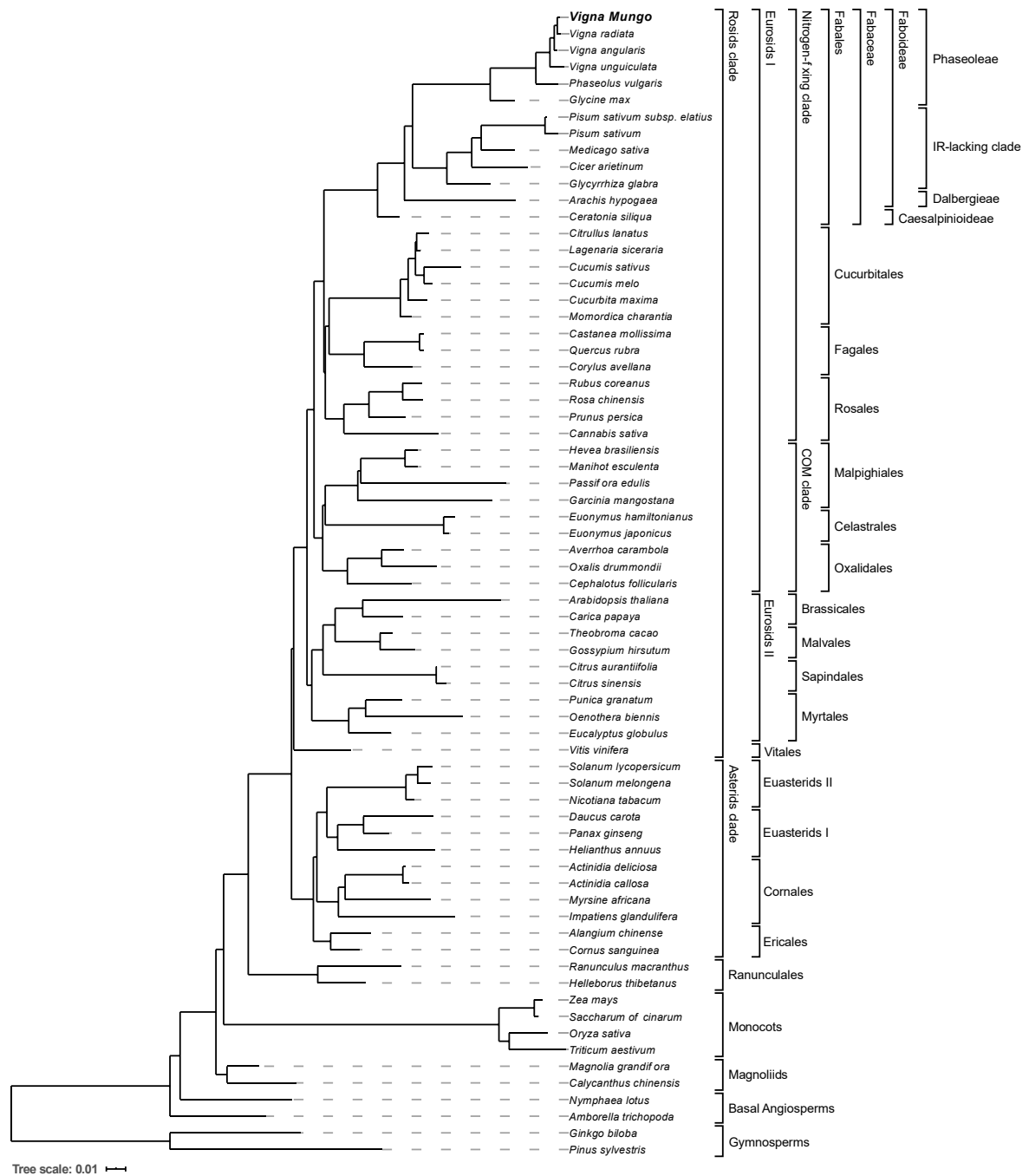


Figure S2 Phylogenetic tree of 69 plant species. The tree was calculated from the connected sequence of the 38 orthologous proteins.

P.vulgaris	ATGAGTATATTGAAAAACGATCAAAAGAAGTACTGATATATTCTATAACAGAGT--CA	57
V.angularis	ATGAATATTTTTAAAAAAGATCAAAAGAAGTATTGATCTATTCTATAACAGGGTCTCGA	60
V.Mungo	ATGAATATTTTTAAAAAAGATCAAAAGAAGTACTGATCTATTCTATAACAGGGTCTCGA	60
V.radiata	ATGAATATTTTTAAAAAAGATCAAAAGAAGTACTGATCTATTCTATAACAGGGTCTCGA	60
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P.vulgaris	AAAATAAGCAATATCTTTTCAGCCTTGATCATTTTTTTAGGTTCTTGGGGTTATTGTTG	117
V.angularis	AAAATAAGCAATATCTTTTCAGCCTTTATCATTTTTGTTAGGTTCTTGGGGTTATTGTTG	120
V.Mungo	AAAATAAGCAATATCTTTTCAGCCTTTATCATTTTTGTTAGGTTCTTGGGGTTATTGTTG	120
V.radiata	AAAATAAGCAATATCTTTTCAGCCTTTATCATTTTTTTAGGTTCTTGGGGTTATTGTTG	120
	***** ***** ***** ***** *****	
P.vulgaris	GTTGCAATTTCCAGTTATCTCGGTATGGATCTTTTCCTTTTTCTGAGGAAATTAGTAAT	177
V.angularis	GTTGGAATTTCCAGTTATCTCGGTATGGATCTTTTCCTTTTTCTGAGGAAATTAGTAAA	180
V.Mungo	GTTGCAATTTCCAGTTATCTCGGTATGGATCTTTTCCTTTTTCTGAGGAAATTAGTAAT	180
V.radiata	GTTGCAATTTCCAGTTATCTCGGTATGGATCTTTTCCTTTTTCTGAGGAAATTAGTAAT	180
	*** *****	
P.vulgaris	TTCCCATTTATTCCACAAGGGGCCACGATGGCTTTTTATGGAATTGGGGTCTCTTTATT	237
V.angularis	TTTCCATTTATTCCACAAGGGGCCACGATGGCTTTTTATGGAATTGGGGTCTCTTTATT	240
V.Mungo	TTTCCATTTATTCCACAAGGGGCCACGATGGCTTTTTATGGAATTGGGGTCTCTTTATT	240
V.radiata	TTTCCATTTATTCCACAAGGGGCCACGATGGCTTTTTATGGAATTGGGGTCTCTTTATT	240
	** *****	
P.vulgaris	AGTTTTTATTTGTGGTGGATTCTTTTGTGGAATATAGGTGGTGGTTTTGATATCTTCGAT	297
V.angularis	AGTTTTTATTTGTGGTGGATTATTTTGTGGGATATAGGCGGTGGTTTTGATATCTTCGAT	300
V.Mungo	AGTTTTTATTTGTGGTGGATTATTTTGTGGGATATAGGCGGTGGTTTTGATATCTTCGAT	300
V.radiata	AGTTTTTATTTGTGGTGGATTATTTTGTGGGATATAGGCGGTGGTTTTGATATCTTCGAT	300
	***** ***** ***** *****	
P.vulgaris	AAAAAAAATA--AAAAAGTATGTTTTATTCGTTGGGGATTTCCTGGAAAAAATCGTCGT	354
V.angularis	AAAAAAAAGAAAAAAGAGTATGTTTTCTTCGTTGGGGATTTCCTGGAAAAAATCGTCGT	360
V.Mungo	AAAAAAAAGAAAAAAGAGTATGTTTTCTTCGTTGGGGATTTCCTGGAAAAAATCGTCGT	360
V.radiata	AAAAAAAAGAAAAAAGAGTATGTTTTCTTCGTTGGGGATTTCCTGGAAAAAATCGTCGT	360
	***** * ***** ***** ***** *****	
P.vulgaris	ATTATTCTCAAAATACCTATGAACGAGATTCAATCTATCAGAATAATAGCAGGAGTTCAA	414
V.angularis	ATTATTAATAAAATACCTATGAACGATATTCAATCTATCAGAATAATAACAGGAGTTCAA	420
V.Mungo	ATTATTATAAAATACCTATGAACGATATTCAATCTATCAGAATAATAACAGGAGTTCAA	420
V.radiata	ATTCTTATAAAATACCTATGAACGATATTCAATCTATCAGAATAATAACAGGAGTTCAA	420
	*** ** ***** ***** ***** *****	
P.vulgaris	GAACGAGGTATTTTGACTCGTACCCTTACTTATGAGAGTATCGTTTATATGGAACAATA	474
V.angularis	GAACGAGGTATTTTACTCGTACTCTTACTTATGAGAGTATCGTTTATATGGAACAATA	480
V.Mungo	GAACGAGGTCTTTTACTCGTACTCTTACTTATGAGAGTATCGTTTATATGGAACAATA	480
V.radiata	GAACGAGGTATTTTACTCGTACTCTTACTTATGAGAGTATCGTTTATATGGAACAATA	480
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P.vulgaris	GAACAGGGGTTTATTACCTTGACTCGTATTGAAGATAATTTGACTCCGCCAGAAATTGCA	534
V.angularis	GAACAGGGGTTTATTCCTTGACTCGTATTGAAGATAATTTGACTCCACCAGAAATTGCA	540
V.Mungo	GAACAGGGGTTTATTCCTTGACTCGTATTGAAGATAATTTGACTCCACCAGAAATTGCA	540
V.radiata	GAACAGGGGTTTATTCCTTGACTCGTATTGAAGATAATTTGACTCCACCAGAAATTGCA	540
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P.vulgaris	AATAAGCTGGCGAATTAGCTTTTTTTTTAGGTGTACCACTTCTGTATTGA	585
V.angularis	AATAGAGCTGGCGAATTAGCTTTTTTTTTAGGTGTACCGCTTCTGTATTGA	591
V.Mungo	AATAGAGCTGGCGAATTAGCTTTTTTTTTAGGTGTACCGCTTCTGTATTGA	591
V.radiata	AATAGAGCTGGCGAATTAGCTTTTTTTTTAGGTGTACCGCTTCTGTATTGA	591
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Figure S3 Edited sites on *ycf4*. Sequence of *ycf4* from three *Vigna* species, which have this gene in their cp genomes, and *P. vulgaris* are aligned and three edited sites are marked with pink bars.

Table S1 Orthologous genes calculated from the chloroplast genome of twelve legume species with OrthoFinder program.

[illegible]

[illegible]