

Table 1 Suppl. Top 10 pathway annotations of all identified proteins. We identified 4419 differentially expressed proteins in all, and the top 10 pathways were ranked by the percentage.

Pathway	Number and percentage of proteins	Pathway ID
Metabolic pathways	1486 (33.63 %)	ko01100
Biosynthesis of secondary metabolites	836 (18.92 %)	ko01110
Microbial metabolism in diverse environments	446 (10.09 %)	ko01120
Ribosome	243 (5.50 %)	ko03010
Plant-pathogen interaction	199 (4.50 %)	ko04626
Spliceosome	197 (4.46 %)	ko03040
Starch and sucrose metabolism	180 (4.07 %)	ko00500
Protein processing in endoplasmic reticulum	179 (4.05 %)	ko04141
Phenylpropanoid biosynthesis	141 (3.19 %)	ko00940
Oxidative phosphorylation	130 (2.94 %)	ko00190

Table 2 Suppl. Detailed information related to *Turnip mosaic virus* (TuMV) long distance movement and resistance. The *red colour* represents up-regulated genes and the *green colour* represents down-regulated genes.

Acc. No.	Gene	<i>A. thaliana</i>	E-value	<i>Arabidopsis thaliana</i> annotations
M4DAE0	<i>Bra013450</i>	AT4G20260	4.00E-58	ATPCAP1; DREPP
M4CQV4	<i>Bra020155</i>	AT3G43810	2E-81	CAM7; calcium ion binding
M4DR27	<i>Bra018970</i>	AT1G52410	0	TSA1; calcium ion binding
M4EEJ7	<i>Bra027209</i>	AT3G15730	0	PLDALPHA1; calcium ion binding
M4CUW7	<i>Bra008012</i>	AT1G72150	9.00E-177	PATL1; transporter
M4CBG7	<i>Bra001547</i>	AT3G14310	0	ATPME3
M4DZA0	<i>Bra021847</i>	AT2G33380	1E-109	RD20; calcium ion binding
M4EDL7	<i>Bra026877</i>	AT1G13870	4E-155	DRL1; calmodulin binding
M4D3W8	<i>Bra011172</i>	AT4G30190	0	PMA2
M4CH44	<i>Bra003527</i>	AT1G59870	0	PEN3 ; defense response by callose deposition in cell wall
M4FA40	<i>Bra037954</i>	AT1G54020	4E-173	myrosinase-associated protein
M4CSX3	<i>Bra007315</i>	AT3G57260	1E-128	PR2
M4CWS0	<i>Bra008667</i>	AT5G15870	0	glucan endo-1,3-beta-D-glucosidase activity
M4D4Y0	<i>Bra011537</i>	AT4G34480	0	glucan endo-1,3-beta-D-glucosidase activity
M4EIB1	<i>Bra028526</i>	AT5G42100	0	glucan endo-1,3-beta-D-glucosidase/ hydrolase
M4ET74	<i>Bra032004</i>	AT3G03250	0	UGP (UDP-glucose pyrophosphorylase)
M4C781	<i>Bra005917</i>	AT5G06870	1E-115	PGIP2
M4CKN6	<i>Bra004771</i>	AT2G43570	2E-110	chitinase, putative
M4CB73	<i>Bra001453</i>	AT3G12500	1E-95	PR3;chitinase
M4CHU1	<i>Bra003774</i>	AT1G75030	2E-46	ATLP-3
M4EAC2	<i>Bra025730</i>	AT1G19320	4E-83	pathogenesis-related thaumatin family protein
Q8H6J9	<i>Bra001122</i>	AT3G04720	1E-51	PR4;chitin binding
M4EVA1	<i>Bra032734</i>	AT4G13770	0	CYP83A1(CYTOCHROME P450 83A1)
M4DR26	<i>Bra018969</i>	AT1G52400	0	BGLU18 (BETA GLUCOSIDASE 18)
M4FAI0	<i>Bra038094</i>	AT5G26000	3E-161	TGG1 (THIOGLUCOSIDE GLUCOHYDROLASE 1)
M4C9J6	<i>Bra000875</i>	AT2G02930	7E-103	ATGSTF3 (GLUTATHIONE S-TRANSFERASE F3)
M4EZ33	<i>Bra034076</i>	AT3G09640	3E-131	APX2; L-ascorbate peroxidase
M4DBB4	<i>Bra013774</i>	AT4G24190	0	HSP90.7
G1EIL9	<i>Bra000703</i>	AT4G10250	2E-89	ATHSP22.0

Table 3 Suppl. Primer sequences used in reverse transcription PCR.

Gene ID	Forward primers 5'-3'	Reverse primers 5'-3'
Actin	CTCAGTCCAAAAGAGGTATTCT	GTAGAATGTGTGATGCCAGATC
Bra018970	CGACTGATAAGAACACTA	TAAGACCATTGAGATGAG
Bra037954	GACTCCGCTACTATACTTG	TGTAATCATCGTTCCAGTT
Bra005917	AACAAGTGCTTGTGTGGT	TAAGTTTAGATAAAGATCGGTTGC
Bra001547	CGGAGAATAGTAATAAGAGGTAT	TTGCGGTAATAATAGTTGTTG
Bra013774	ATTCATTAACTTCCCTATCAACCT	GCTGACTCGTCTTCCTCA
Bra028526	TCTCATTCTCTCTGGTGT	GTAGTTGATGCCAATGGA
Bra034076	ATAAGGCTTCCACAAGAG	TCAGCGTAGGATAAGATG
Bra001453	GTTATGGAGTGATTACGAATATC	TATCCGATCTTGGACCTT
Bra018969	ATTCTACCACGACCTCAT	AACCACTGTATTCATCTTCTA
Bra032004	GTCGGTTATTGAAGTTCGTGAT	GCCATACTTGTTGTTGAGGTT
Bra000703	GTGGCATAGAGTTGAGAG	TTGTGAGGTTAATAGTGAGAA
Bra011172	AGAGGATGAAGAACTACACTA	CCAGATGAGAGCAATGAG
Bra003774	CGAGGAAGTTCAAGAACG	CCAGCACAAAGTGAAGGTA
Bra038094	TCCTCAAGCACTACAAGA	TCCAGTTCGTTACATTAGC
Bra003527	TGATGAGTTGATGCTGATG	ACCTTGTGAGAGTTGCTA
Bra020155	ATGGCGAGGAAGATGAAG	CCGTTCTGGTCCTTATCA
Bra004771	GAGACTTATTGGCTACAC	AACATTAGTGGTCCAGTA
Bra026877	ACCGCAACCAGAACTATG	ATCTATCAACATCCGACCTAAG
Bra013450	GAGATTGTTGAAGAGACTAAG	CTTCTTCTCCTCCTCCTT
Bra007315	ACGGTAGATTACGGATG	AGAGGAGATTGCTTGCTTA
Bra035347	TGCCTTCTACAATAATCTAA	AATGCTTCACTCTATCAC
Bra008667	ATTATGGTCAACGAAGAG	TATCGGTAATAACTGTATCC
Bra027209	CATCAACGCTCTTCACTT	CACCACAACATACACTCTAA
Bra001122	TTGTTGGTGTGCTATGT	AGGATTGTAGAAATGGTAAGT
Bra021847	TTGCCATCACCCTATTG	CCTTCCTTCGGTATCATAG
Bra032734	ATTCTCTATGGCACTCAA	CTCATCAATAATCTCCTGTATA
Bra000875	GAAGAGGAGGCTAAGTTA	TAGGAATGTGGTGAAGAT
Bra025730	TTGCCCTAGAGCGTATAG	GATGGAGTAATTAGCATTGGT
Bra011537	GAGGAGGAGCAGGAAGTA	GAAGATTAGGGACACAACAAAG

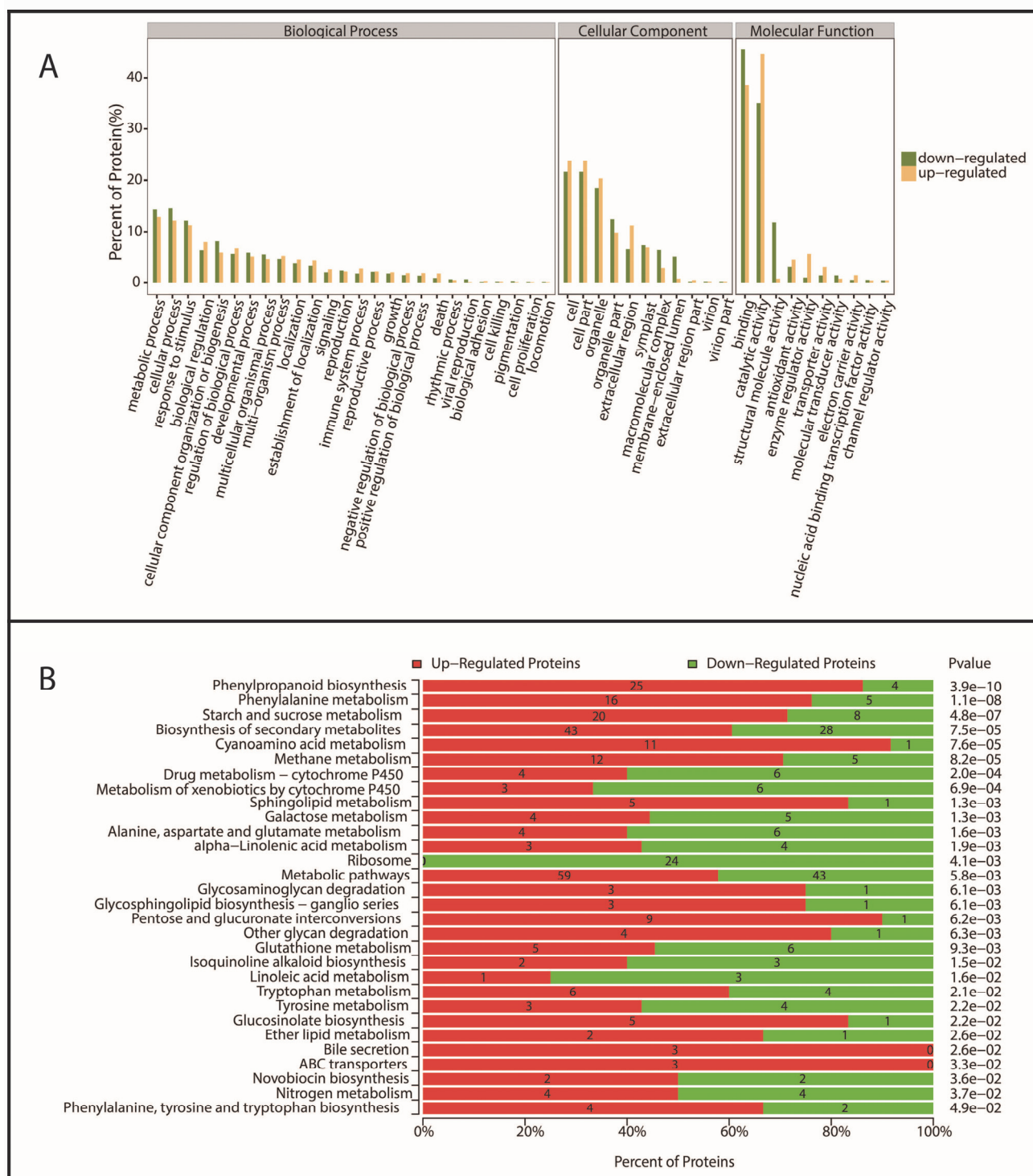


Fig. 1. Suppl. GO comparison and pathway enrichment of TuMV-7/control. *A* - GO comparison, *B* - pathway enrichment.

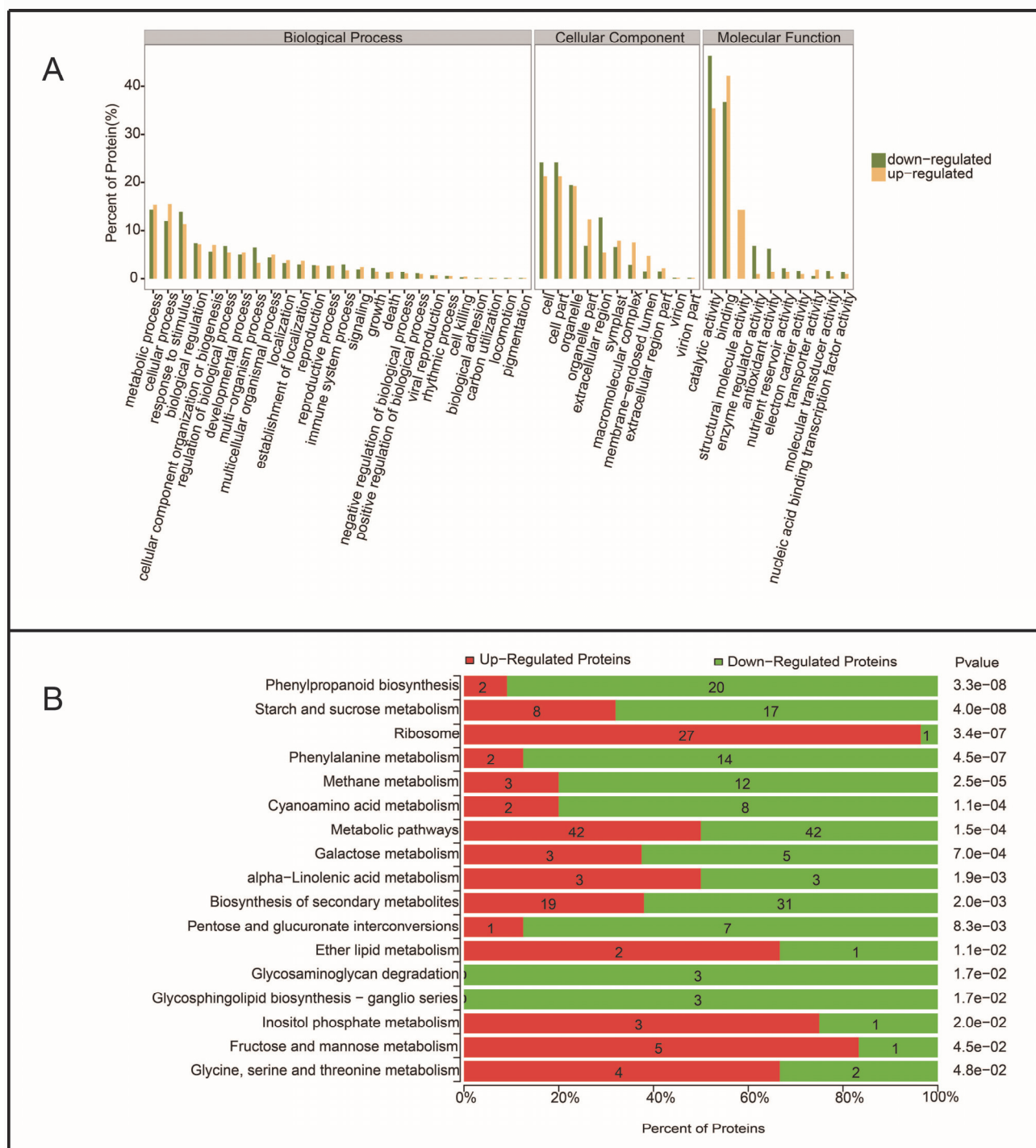


Fig. 2. Suppl. GO comparison and pathway enrichment of TuMV-14/TuMV-7. *A* - GO comparison, *B* - pathway enrichment.

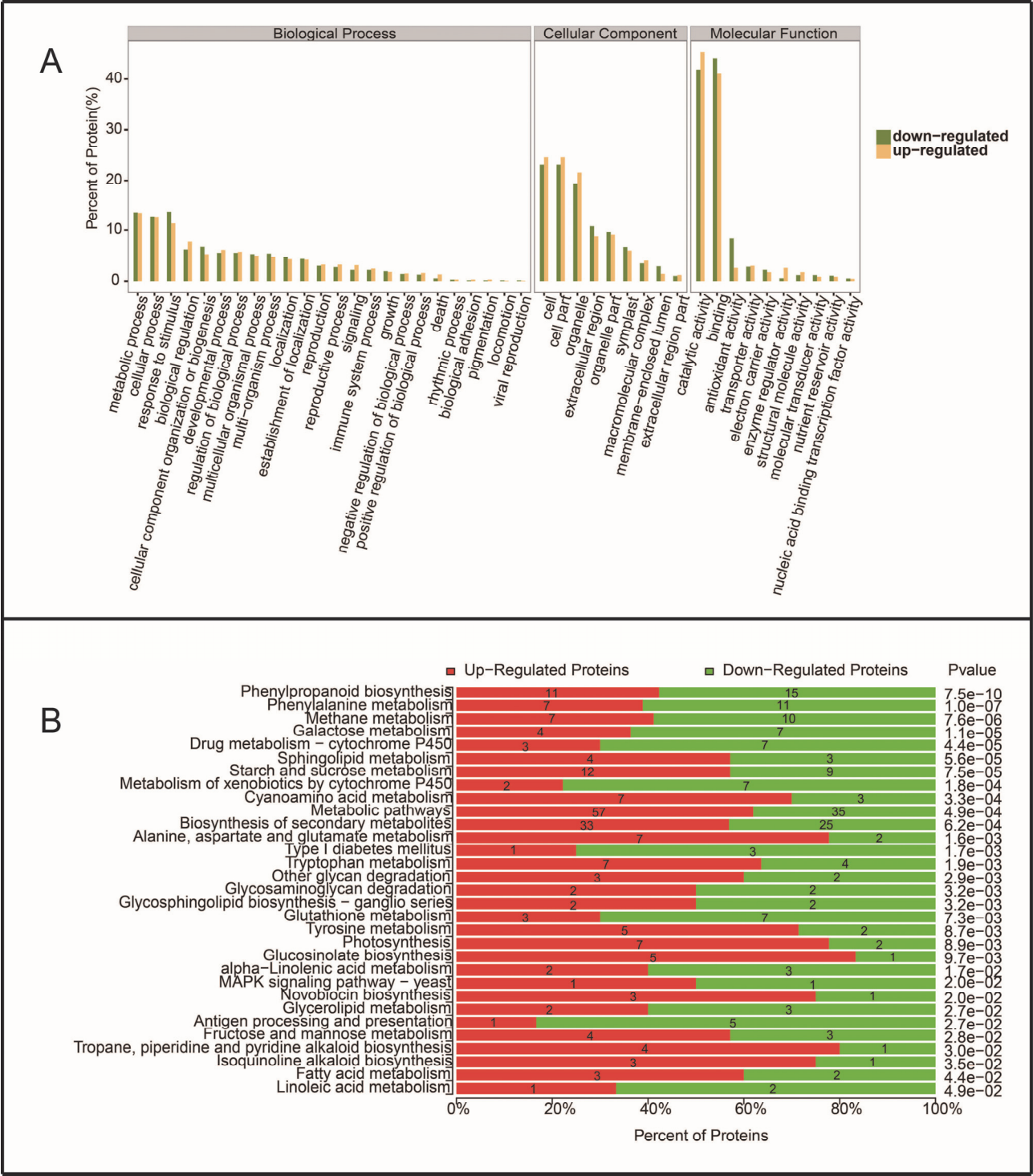


Fig. 3. Suppl. GO comparison and pathway enrichment of TuMV-14/control. *A* - GO comparison, *B* - pathway enrichment.

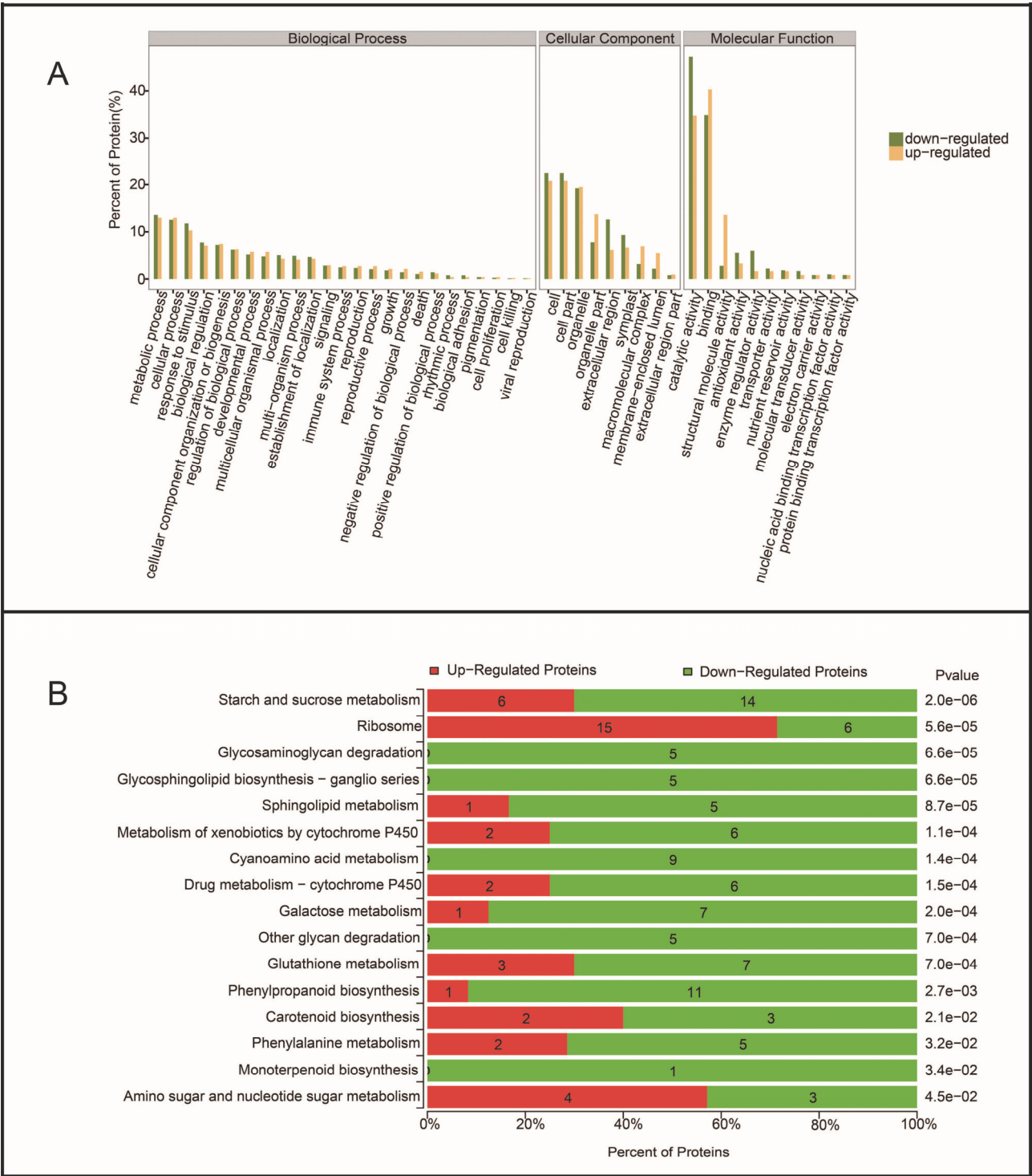


Fig. 4. Suppl. GO comparison and pathway enrichment of TuMV-21/TuMV-7. *A* - GO comparison, *B* - pathway enrichment.

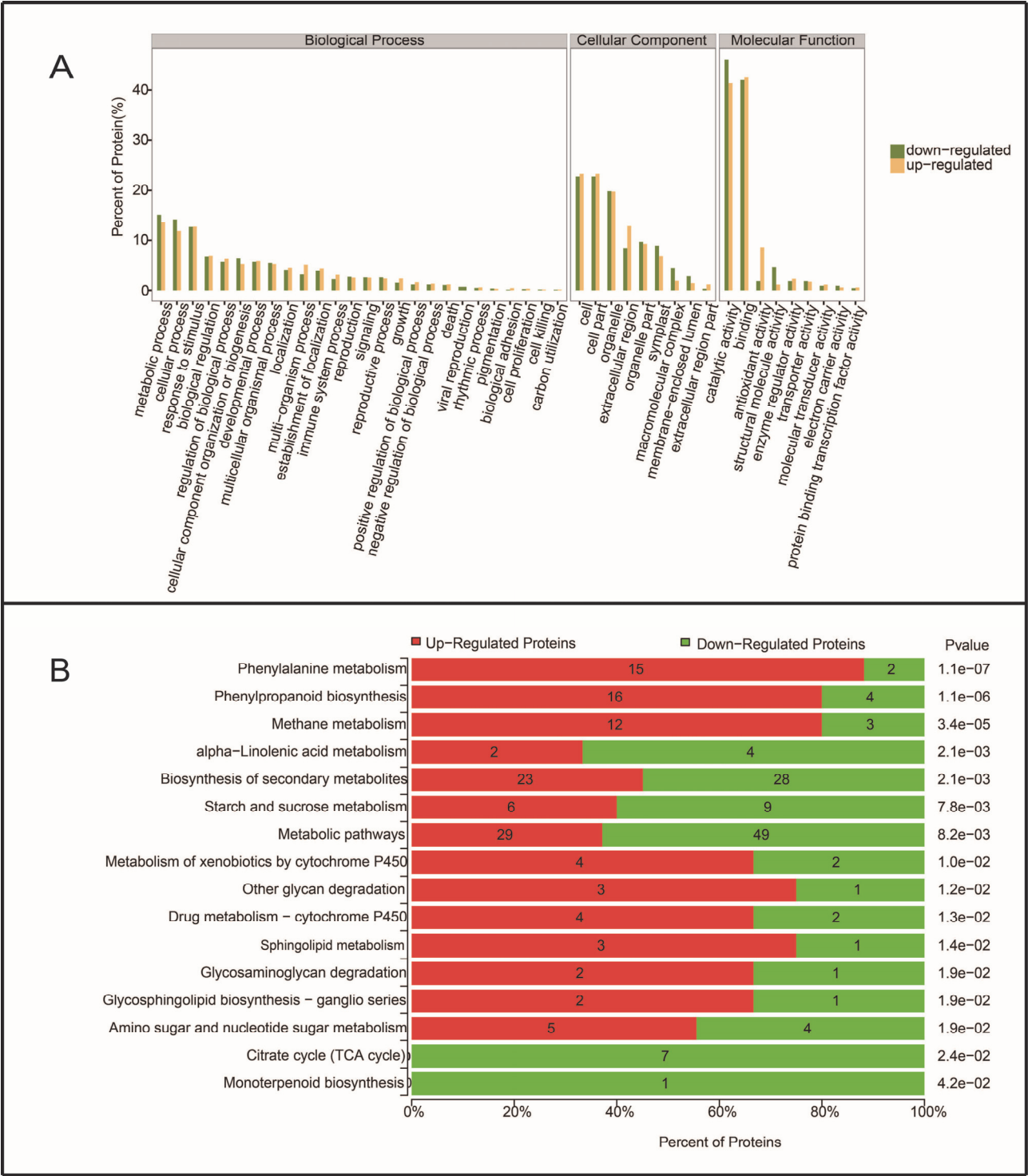


Fig. 5. Suppl. GO comparison and pathway enrichment of TuMV-21/TuMV-14. *A* - GO comparison, *B* - pathway enrichment.

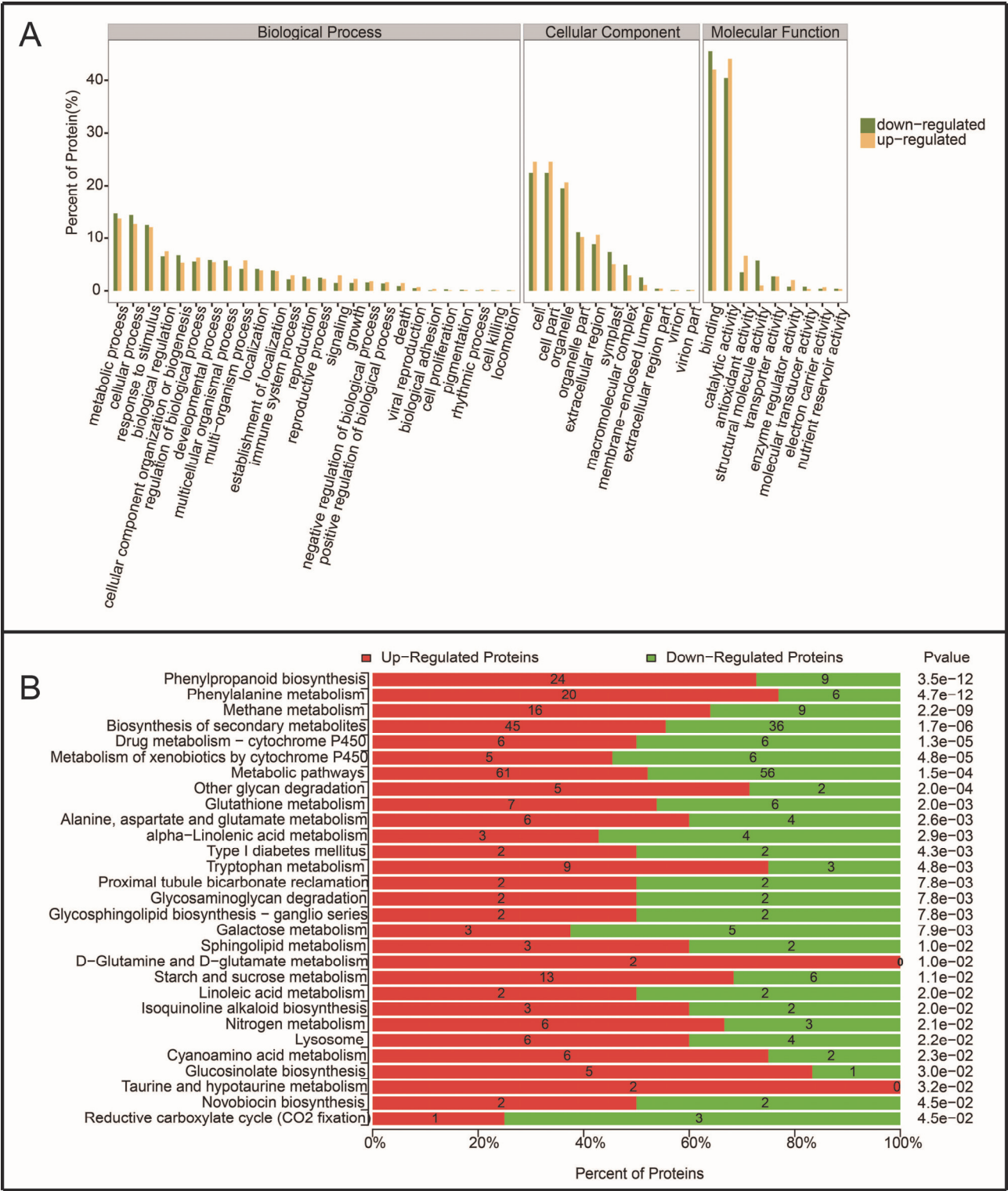


Fig. 6. Suppl. GO comparison and pathway enrichment of TuMV-21/control. *A* - GO comparison, *B* - pathway enrichment.