

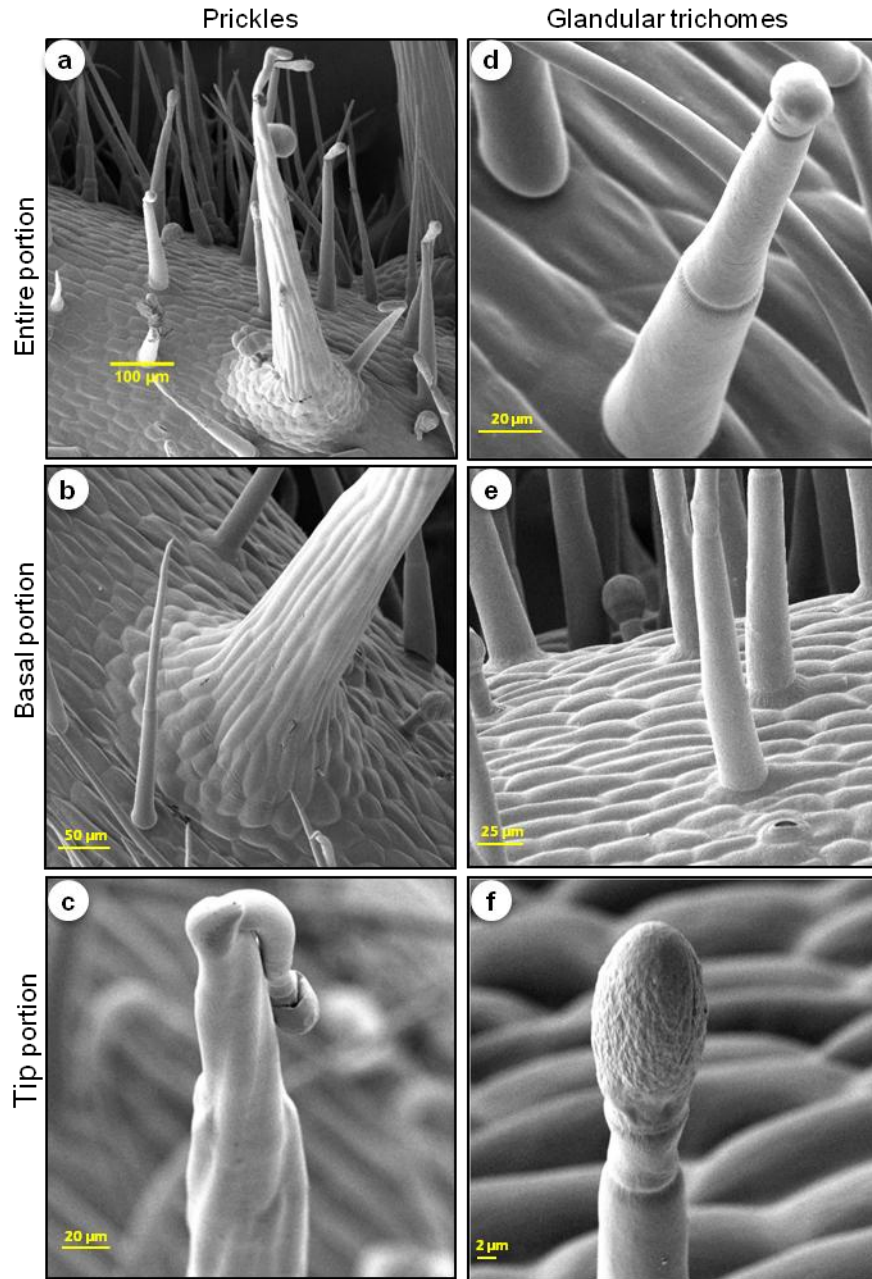
Transcriptome analysis provides insight into prickly development and its link to defense and secondary metabolism in *Solanum viarum* Dunal

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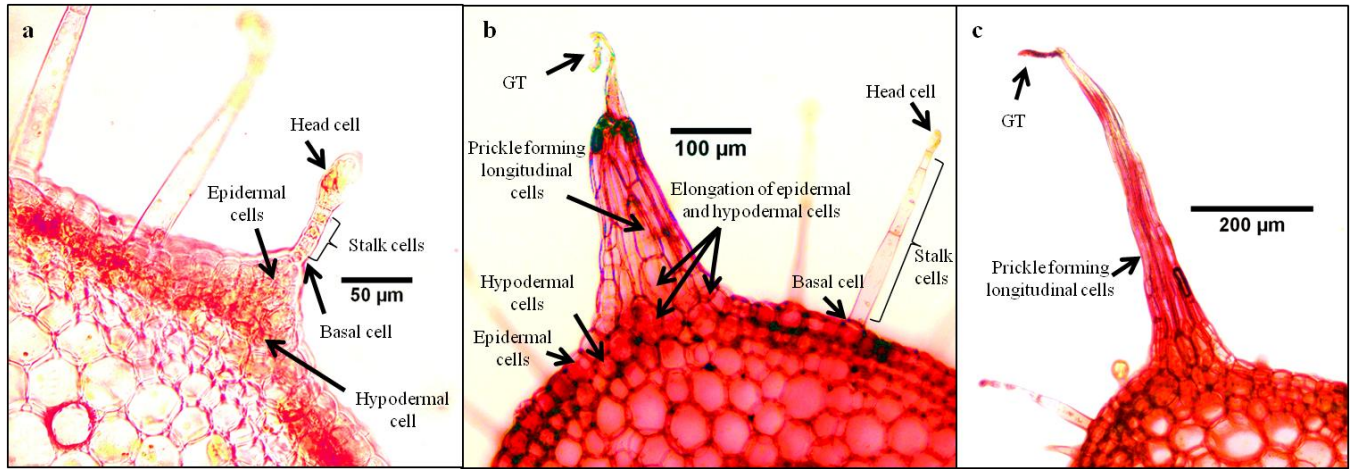
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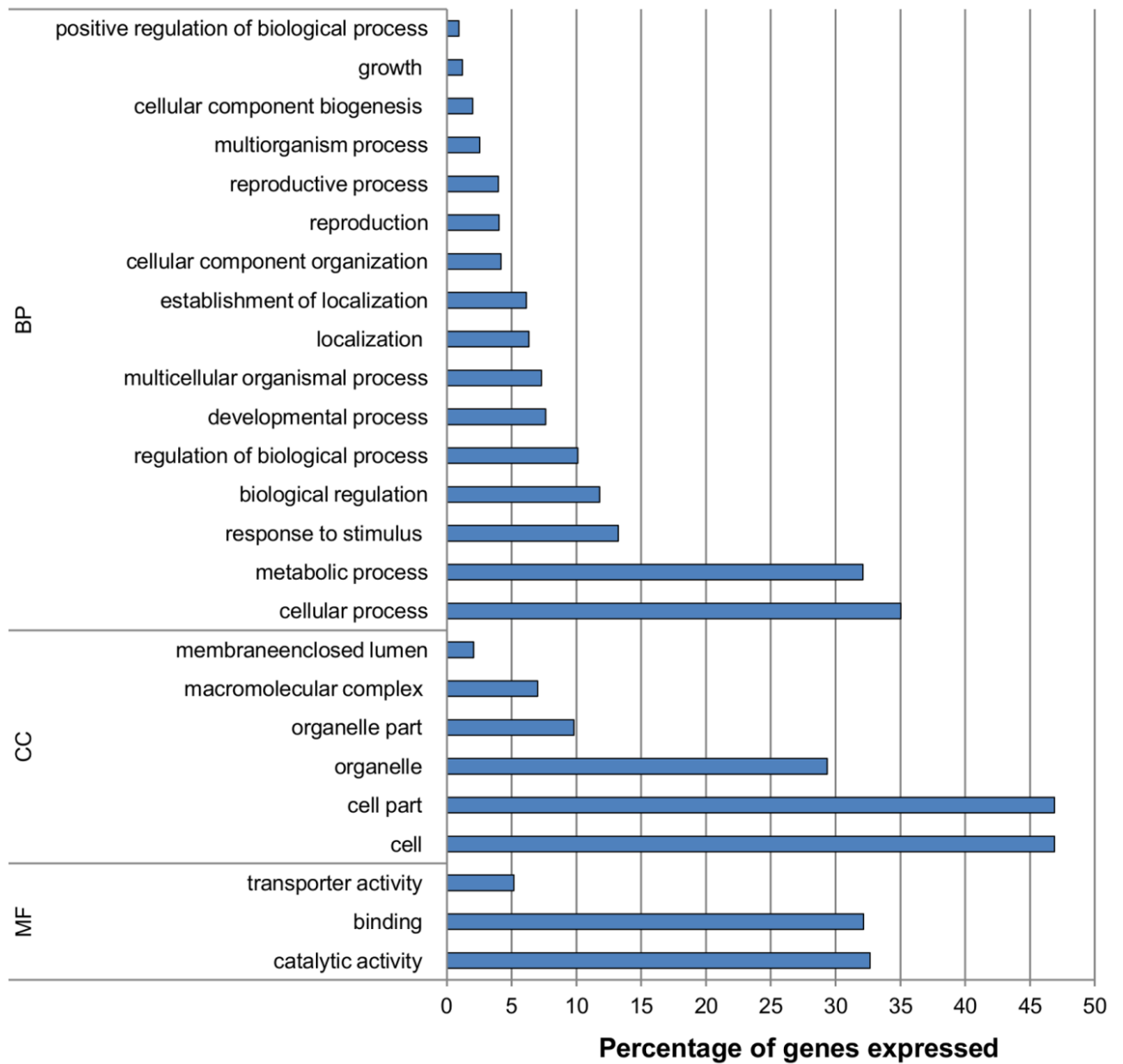
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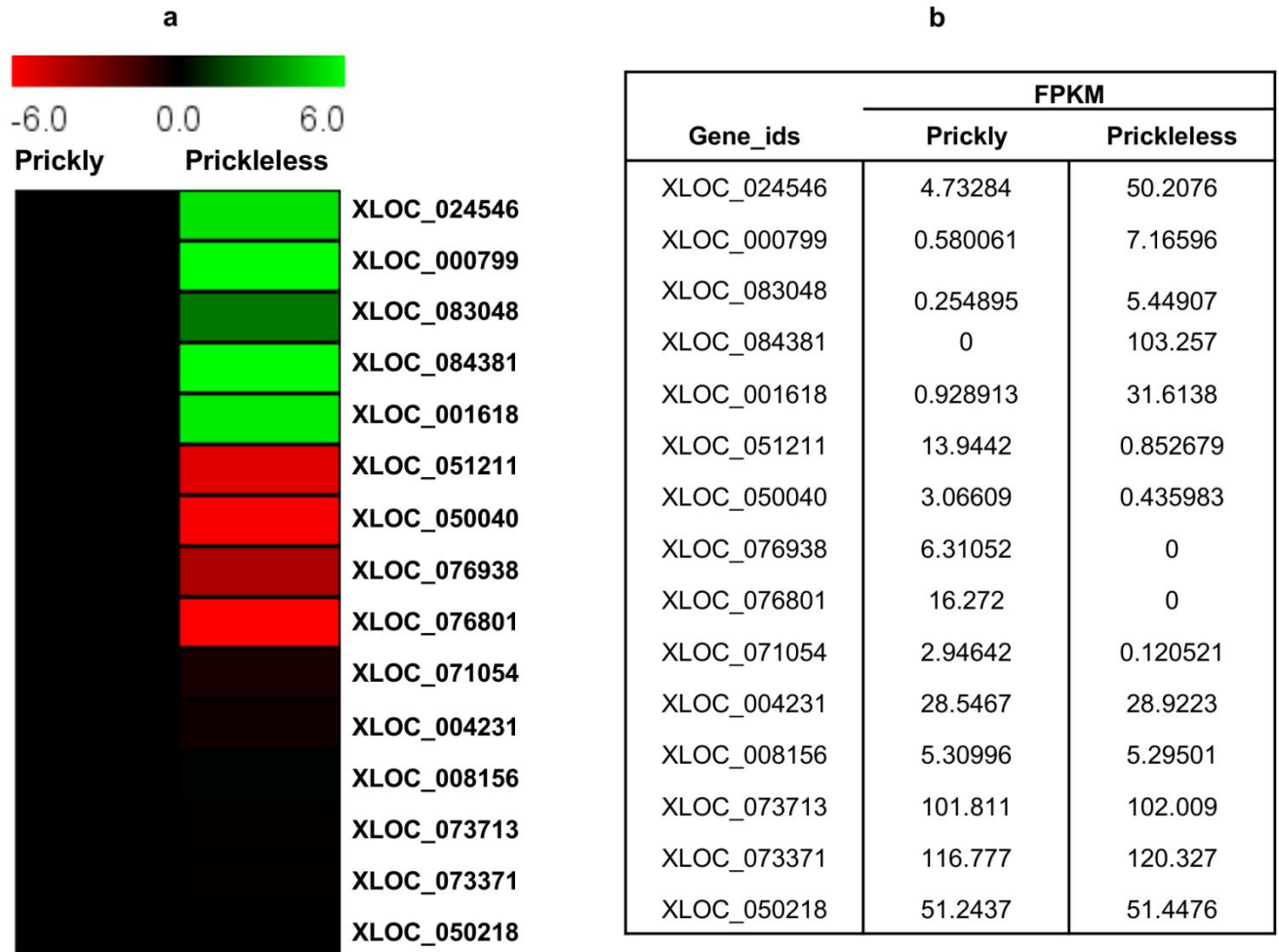
Supplementary Figure S1. Morphological similarity and differences between glandular prickle and glandular trichome of *S. viarum*. (a) Complete prickly hair. (b) Basal portion of prickly hair. (c) Tip portion of prickly hair showing GT attached to prickly hair. (d) Multicellular glandular trichome. (e) Base of trichomes. (f) Head of GTs.



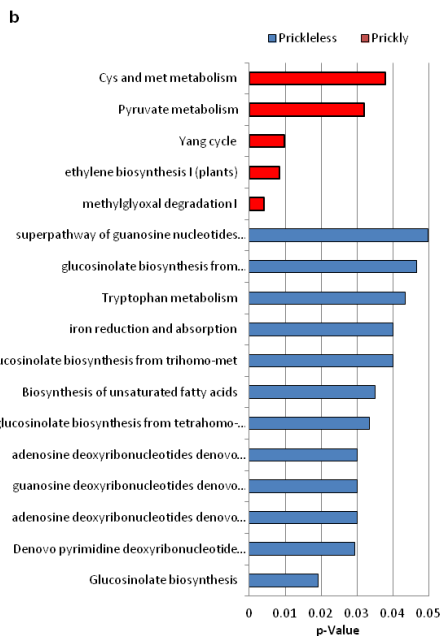
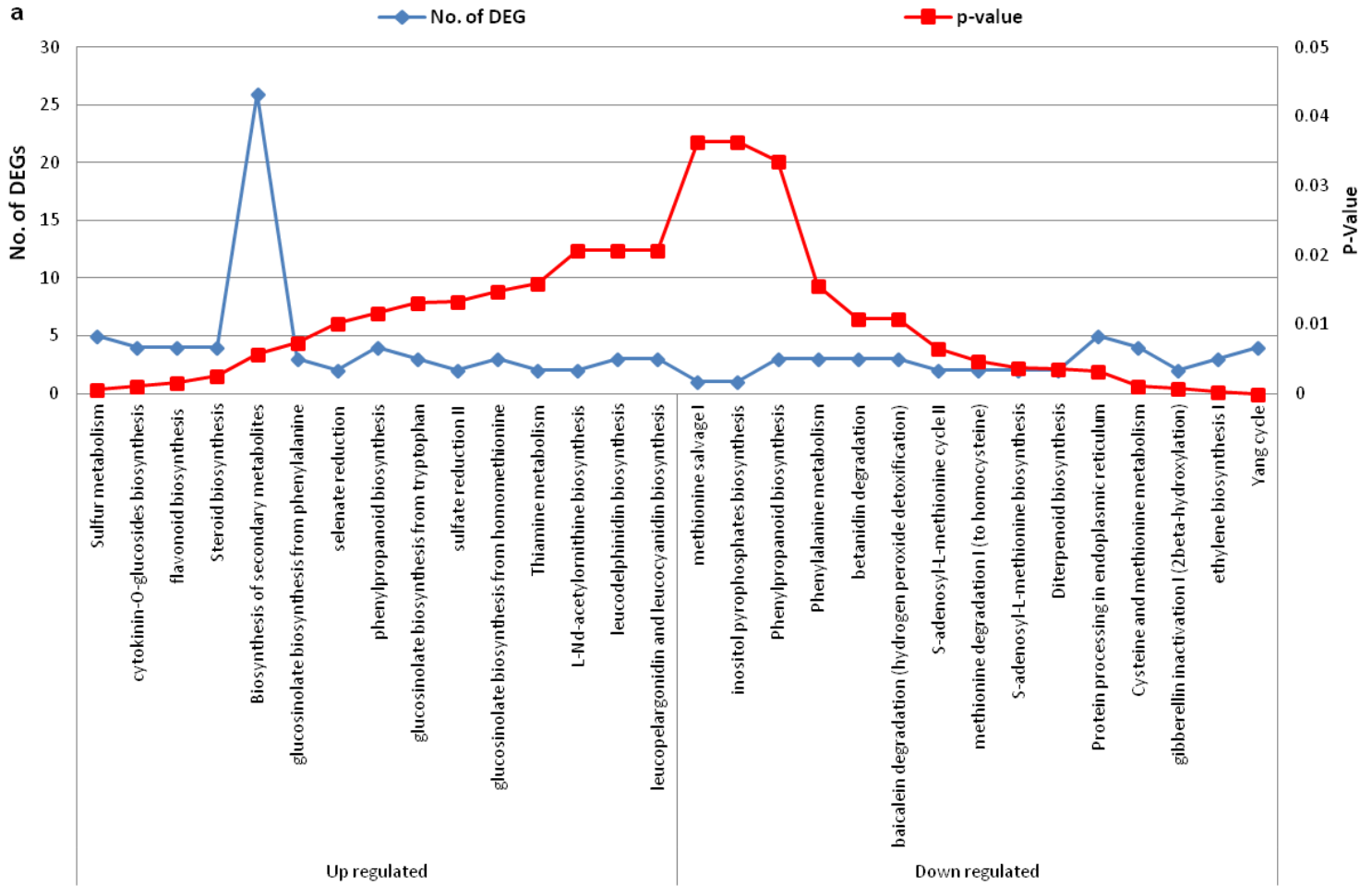
Supplementary Figure S2. T. S. of prickly stem showing different stages of prickles development in *S. viarum*. (a) Initiation of prickles formation beneath the basal cell of GT. (b) Developing prickly stem with GT attached to the tip. (c) Mature prickly stem with GT attached to the tip.



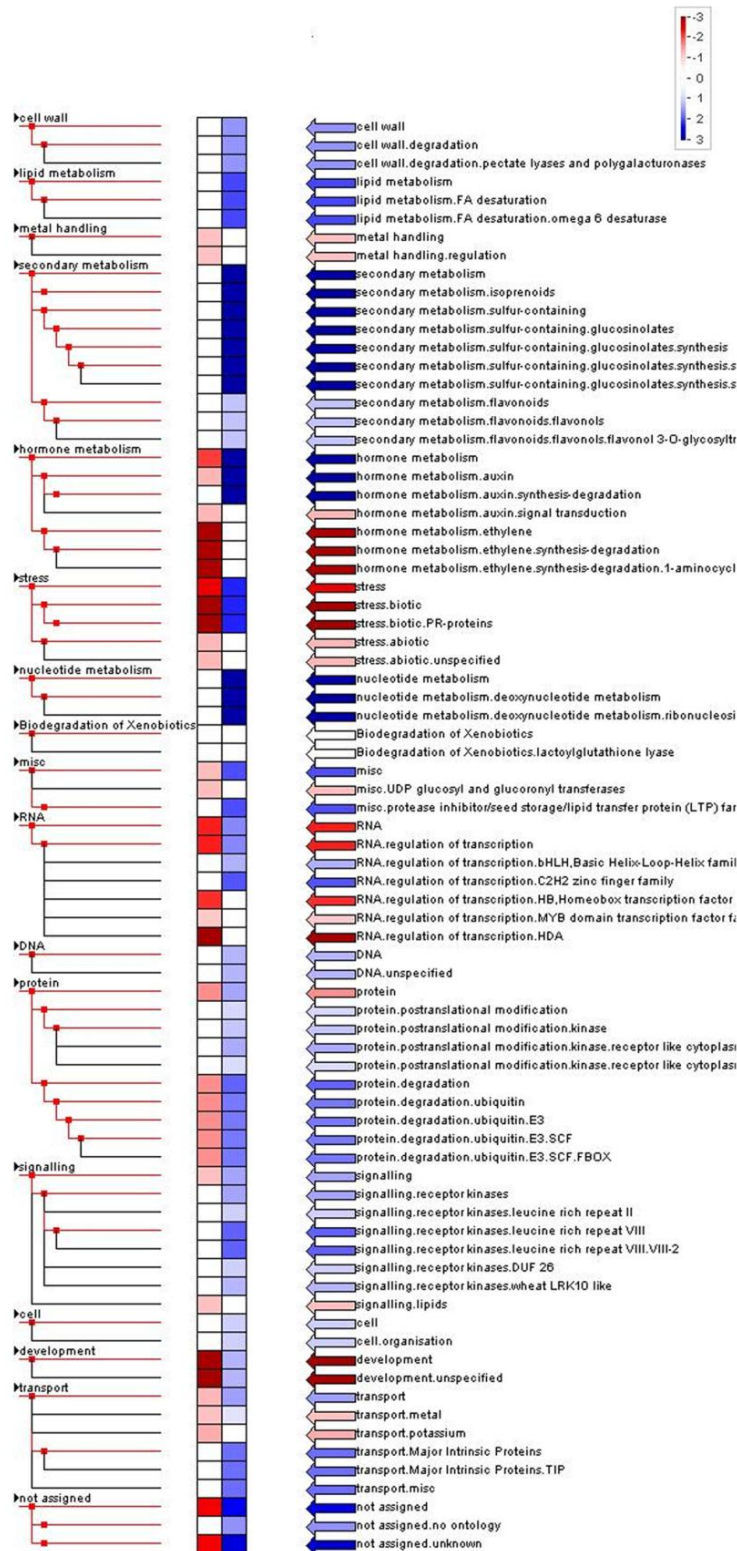
Supplementary Figure S3. Functional categorization of genes expressed in the epidermis of *S. viarum* through GO analysis.



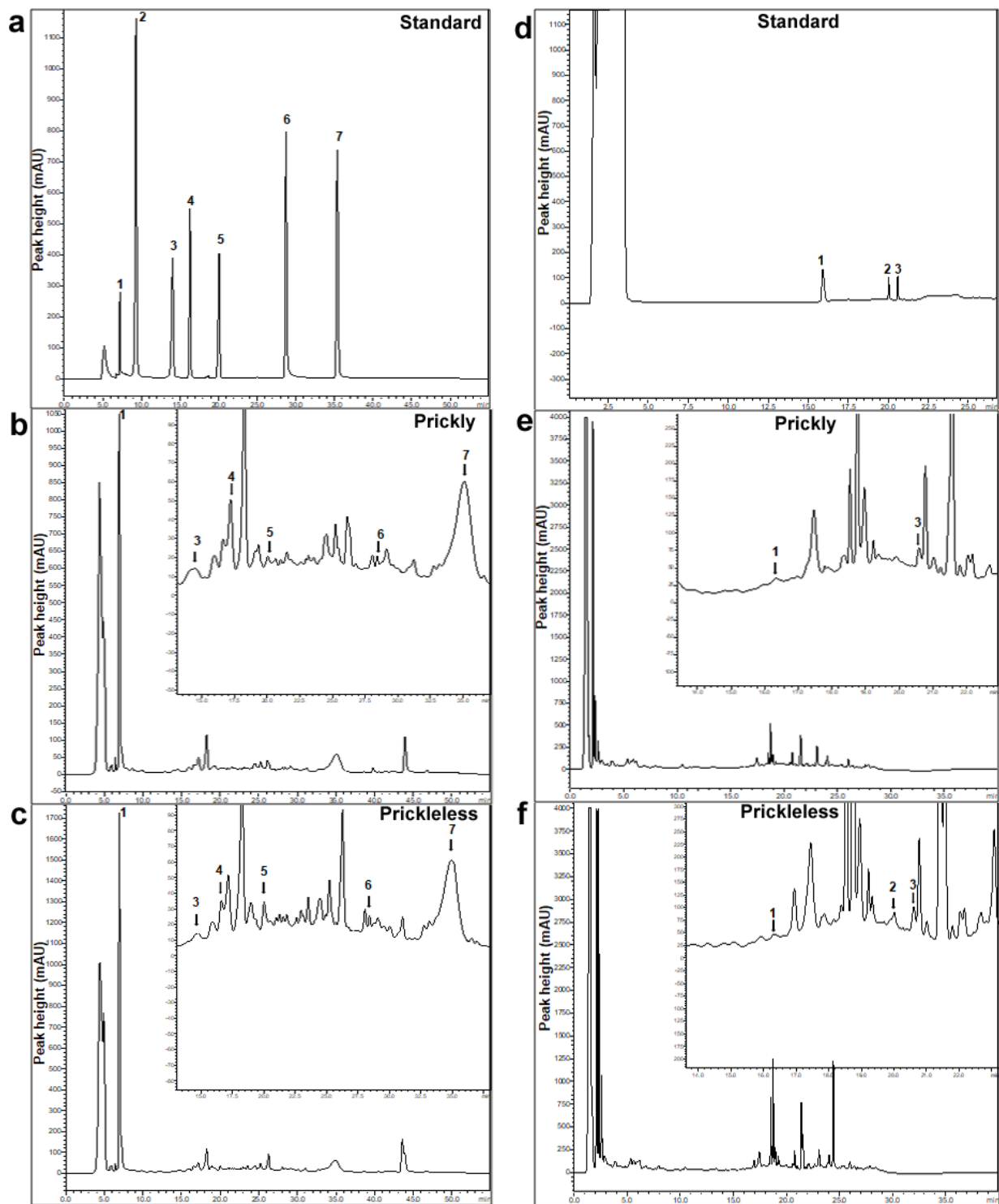
Supplementary Figure S4. qRT-PCR of some randomly selected highly up-regulated, down-regulated and similarly expressed genes for validation of transcriptome data of *S. viarum*. (a) Relative expression pattern analyzed through qRT-PCR. (b) FPKM based digital gene expression pattern analyzed through RNA-seq.



Supplementary Figure S5. Metabolic pathways altered in prickless mutant of *S. viarum*. (a) Top 15 up and 15 down regulated pathways. (b) Uniquely expressed genes enriched to metabolic pathways significantly altered in prickly and prickless mutant. Pathways with p-value ≤ 0.05 were considered statistically significant.



Supplementary Figure S7. PageMan analysis of uniquely expressed genes in epidermis of prickly or prickless mutant of *S. viarum*.



Supplementary Figure S8. HPLC chromatogram of the standard and crude extract of prickly and prickless *S. viarum*. a-c) phenolics and flavonoid [gallic acid -1, chlorogenic acid -2, caffeic acid-3, rutin-4, ferulic acid-4, quercetin-6, kaempferol-7. (d-f) alkaloid [α -solanine-1, solanidine-2, solasodine-3].

Supplementary Table S1. Summary of the transcriptome sequencing, *de novo* assembly and annotation of *S. viarum*.

	Prickly		Prickleless	
	R1	R2	R1	R2
No. Of Reads	18175222	15851932	17096127	13586099
No. of HQ reads	17444985 (95.98%)	15153863 (95.60%)	16429445 (96.10%)	12992487 (95.63%)
No. of Contigs	150880		142861	
Largest Contig (bp)	59569		46421	
Smallest contig(bp)	201		201	
Average Length (bp)	1126.75		1117.51	
GC%	46.11%		46.70%	
NR Annotated transcript	73189		70970	
No. of transcripts after clustering	156926			
Largest Contig	59569			
Smallest contig	201			
Average Length	1110.9			
GC%	39.30%			
TAIR Annotated transcripts	62975			
TAIR Unannotated transcripts	93951			
Tomato Annotated transcripts	67752			
Tomato Unannotated transcripts	89174			

Supplementary Table S4. List of the top 15 up and 15 down-regulated genes in epidermis of prickly vs. prickless mutant of *S. viarum*.

Gene_Ids	Prickly vs. Prickleless (fold change)	p-value	Plant GD ID	Description	TAIR10 Ids	Tomato Ids
XLOC_064742	-5.118538307	0.00005	YCX91_PHAAO	Uncharacterized protein ORF91	NA	NA
XLOC_079911	-4.697050957	0.00005	NA	NA	NA	NA
XLOC_066158	-4.656741736	0.00005	YCF1A_MARPO	Putative membrane protein ycf1 N-terminal part; AltName: ORF 1068;	NA	NA
XLOC_071054	-4.611606642	0.00005	C5XHE6_SORBI	Putative uncharacterized protein Sb03g011550	NA	NA
XLOC_065300	-4.596655786	0.00005	Q40502_TOBAC	Extensin	NA	NA
XLOC_051211	-4.031518631	0.00005	B9HID6_POPTR	DEFORMED ROOTS AND LEAVES 1 family protein	AT1G13870.1	Solyc08g008250.1.1
XLOC_076801	-4.024319679	0.00005	F6HF70_VITVI	Putative uncharacterized protein	AT2G03440.1	Solyc04g005480.1.1
XLOC_067196	-3.927747592	0.00015	F6HH27_VITVI	Putative uncharacterized protein	AT3G22440.1	Solyc11g071340.1.1
XLOC_062280	-3.897727126	0.00035	Q0MX19_ARAH Y	Leucine rich protein	NA	NA
XLOC_085802	-3.82662512	0.00005	E3W9P7_TOBA C	Putative PR-10 type pathogenesis-related protein	AT1G70890.1	Solyc04g007010.2.1
XLOC_065725	-3.796462781	0.00005	B3VI97_SOLDE	Putative disease resistance protein CC-NBS-LRR (Fragment)	AT3G14460.1	Solyc08g007630.1.1
XLOC_051029	-3.684004197	0.0001	Q93YD2_TOBA C	Putative translocation transactivator	NA	Solyc08g044450.1.1
XLOC_042610	-3.682356673	0.00005	Q39467_CAPAN	Sn-2 protein (MLP-like protein 34)	AT5G28010.1	Solyc04g007770.2.1
XLOC_024732	-3.652715931	0.00005	D7LTE8_ARAL L	Amino acid transporter, putative	NA	NA
XLOC_038231	-3.596861021	0.00005	E7D4U5_TOBA C	Cysteine protease	AT5G45890.1	Solyc02g076910.2.1
XLOC_084381	6.690095778	0.00005	F2CZR9_HORV D	Predicted protein (Uncharacterized protein)	NA	NA
XLOC_007885	6.004369091	0.00005	B9GNI9_POPTR	Uncharacterized protein	AT5G48850.1	Solyc06g007970.2.1
XLOC_031857	5.987186837	0.00005	B9S545_RICCO	Putative uncharacterized protein	AT5G48850.1	Solyc06g007970.2.1
XLOC_002160	5.647052243	0.00095	B3SP99_CAPAN	Fatty acid desaturase	AT3G12120.2	Solyc01g006430.2.1
XLOC_085535	5.481334466	0.00005	PRS2_SOLTU	Pathogenesis-related protein STH-2	NA	Solyc09g091000.2.1

XLOC_023238	5.201494901	0.00005	A5BSN3_VITVI	Putative uncharacterized protein	AT1G22400.1	Solyc04g074330.2.1
XLOC_005604	5.10395771	0.00005	Q9LM08_CAPA N	Pepper esterase	AT5G62180.1	Solyc06g035520.2.1
XLOC_001618	5.088867165	0.00005	B9HUS6_POPTR	Homocysteine S-methyltransferase 3 family protein	AT3G63250.1	Solyc09g082460.2.1
XLOC_034413	5.07700713	0.0002	B9RP37_RICCO	Putative uncharacterized protein	NA	NA
XLOC_018784	4.961102747	0.0003	A2Q1J3_MEDT R	DUF506 family protein	AT1G12030.1	Solyc11g012120.1.1
XLOC_015461	4.911130691	0.00005	D7MJF9_ARAL L	Putative uncharacterized protein	NA	NA
XLOC_030037	4.709704193	0.00005	D5KXD2_SOLL C	Beta caryophyllene/humulene synthase (Caryophyllene/alpha- humulene synthase)	AT3G14540.1	Solyc06g059930.2.1
XLOC_019256	4.564999303	0.00005	C6TGT6_SOYB N	Uncharacterized protein	AT3G63030.1	Solyc06g084400.2.1
XLOC_022696	4.457186326	0.00005	B9TIC7_RICCO	Cytochrome P450, putative (EC 1.14.13.76) (Fragment)	NA	NA
XLOC_083048	4.418035045	0.0002	P93789_SOLTU	UDP-galactose:solanidine galactosyltransferase	AT2G36790.1	Solyc07g043490.1.1

Supplementary Table S6. List of the primers used for qRT-PCR analysis.

Selected primers used for transcriptome data validation				
Sl. No.	Gene Ids	Primer Sequence 5' to 3'		
		Forward		Reverse
1	XLOC_024546	CCATTCCACCAGCCCATCT		CGCCACATCGTTGTTTG
2	XLOC_000799	CAAAAAATGAGCACGTGAGAAAA		CGCCCCAAGCTAACTTCTT
3	XLOC_083048	CCAGCCTACCATTGATGACGA		TGGCAGTGTGAAGCTCTCA
4	XLOC_084381	GGAAAGCCGGTGA CTCTCAA		TCGTCTGCTCTGCTTCGTTT
5	XLOC_001618	AGGCAACTCTTCAGGGATTT		TCTCTACGCTTCTTTTGAGCA
6	XLOC_051211	TGTTTGGCTAGAGCAGCAGG		ACGGTTCCTCTCTCACGA
7	XLOC_050040	GCTTCATTGCGTGCTTGTTG		TATCGCCTTATCTTCACCATTCC
8	XLOC_076938	CGAAAGGAGATAGAGAAGATGGAAGA		CCTTTTCTAACTCCACCGTGTGT
9	XLOC_076801	CGGTTGTTGTGGTGGTAGA		ATTCGTCGGAAAAGCAGAG
10	XLOC_071054	TCAGGCATTGAGTTTGTGTA		CTCGGGCATTGTTGTTTTAC
11	XLOC_004231	TGCGAAGCAGAGACCATAACAGT		GGAGGACCCAGAACGGAATT
12	XLOC_008156	GGTGATTCTTGGTCTCCTTTCC		CACGCTAAGGAGGCTGCAA
13	XLOC_073713	GCATTCAACCCATCAGAGCAA		TTGTCTTCCCACCACTCTGTGA
14	XLOC_073371	CGGCTGTGGTGGTAAAGAG		TCTGGCAGGGCGTGATCT
15	XLOC_050218	CCACAGCGGGCAACAGTAA		TCTCCGTGGTGGTTTTTAGGTT
Selected primers used for the expression analysis of transcription factors				
Sl. No.	Gene Ids	Gene names	Forward	Reverse
1	XLOC_067399	REM	TTGAAGCTGAATGGACATCG	CCCAATTGCACATTATGATCC
2	XLOC_040694	MSM1	TGGACTCATTGTTTTTCTGCTACTG	CCCTTTCTGACTGCGTCTTGT
3	XLOC_050040	C2C2-CO-like	GCTTCATTGCGTGCTTGTTG	TATCGCCTTATCTTCACCATTCC
4	XLOC_051211	DRL1	TGTTTGGCTAGAGCAGCAGG	ACGGTTCCTCTCTCACGA
5	XLOC_027183	Homeobox	TCTTCCATCTAGCTCGCCTG	TGCTAAAGAGTTGGGTGTTCC
6	XLOC_075558	R2R3-MYB	ATGTGGTCATATTCCTCTGGTTG	GGACCTCTCTCAATCCA ACTCT
7	XLOC_035637	HAP2	GACGAATGGAAGCATCAACGA	TGCATACATCAGACTGCACAAC
Selected primers used for expression analysis of secondary metabolite pathways				
1	XLOC_009213	FLS1	ATTTGTGAGCCCCTTCCAC	TTGCACCCATTTTTCTCCA
2	XLOC_034589	CHS	GAAGGTCGAAGCCCAAGAA	GCCAAGCCAAGTCCAAAAT
3	XLOC_084597	CFI	TTCCATGTCCCATCAAAGGT	TGAAGTGGTGGTGGATGAAA
4	XLOC_025921	COMT	CAAAAAGCGTGGTTGGAGTT	TTTTGGTTCTTCCACGCAAT
5	XLOC_052049	4CL	GGCAAGGTCTCTCCACTTTCAG	TGAGGAAACAGACCGGTATGG