Additional file 6. The 100 most expressed genes of the *C. striatus* stigma with style transcriptome

Gene	FPKM	Longest isoform	Length (bp)	Sequence Description	InterProScan (PFAM)	GO terms	Mean similarity (%)
c48578_g1	15380.77	*c48578_g1_i1*	804	NA	IPR006501	F:pectinesterase activity; F:enzyme inhibitor activity	NA
c50936_g1	12242.09	*c50936_g1_i9*	997	proline-rich protein 4-like	no IPS match	NA	NA
c52888_g1	10478.76	*c52888_g1_i6*	1921	l-ascorbate oxidase-like	IPR011707; IPR011706; IPR001117	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process	72.24
c51372_g2	9746.66	*c51372_g2_i1*	1161	1-aminocyclopropane-1-carboxylate oxidase	IPR005123; IPR026992	P:oxidation-reduction process; F:oxidoreductase activity	92.40
c19588_g1	9687.56	*c19588_g1_i1*	208	NA	no IPS match	NA	NA
c48712_g1	8535.12	*c48712_g1_i2*	773	pollen ole e 1 allergen and extensin family	no IPS match	NA	64.65
c51468_g2	7286.2	*c51468_g2_i1*	1050	lipid transfer	IPR016140	NA	73.30
c48699_g2	7201.71	*c48699_g2_i2*	1035	fasciclin-like arabinogalactan protein 3-like	no IPS match	NA	71.55
c52392_g6	7038.02	*c52392_g6_i1*	365	pectinesterase inhibitor domain	IPR000070	C:cell wall; P:cell wall modification; F:pectinesterase activity	66.55
c90467_g1	6788.62	*c90467_g1_i1*	569	NA	no IPS match	NA	NA
c50936_g2	6738.06	*c50936_g2_i1*	177	repetitive proline-rich cell wall protein 1-like	no IPS match	NA	66.56
c50110_g2	6484.17	*c50110_g2_i1*	2534	tonoplast intrinsic	no IPS match	NA	91.70
c46921_g3	6476.23	*c46921_g3_i1*	2136	senescence-associated	no IPS match	NA	88.90
c48255_g4	6332.68	*c48255_g4_i1*	350	NA	no IPS match	NA	NA
c16527_g1	5646.63	*c16527_g1_i1*	178	NA	no IPS match	NA	NA
c45810_g2	5446.95	*c45810_g2_i3*	799	NA	no IPS match	NA	NA
c47271_g2	4948.52	*c47271_g2_i3*	833	plant invertase pectin methylesterase inhibitor	IPR006501	F:pectinesterase activity; F:enzyme inhibitor activity	58.40
c47242_g1	4940.39	*c47242_g1_i1*	670	NA	no IPS match	NA	NA
c48578_g2	4883.16	*c48578_g2_i1*	1020	hypothetical ENH_00061390	no IPS match	NA	78.00

c45963_g2	4459.43	*c45963_g2_i3*	1085	kda proline-rich	IPR027923	NA	89.55
c43040_g1	4441.74	*c43040_g1_i1*	695	NA	no IPS match	NA	NA
c42721_g1	4312.93	*c42721_g1_i2*	338	cold dehydrin	no IPS match	NA	74.25
c46311_g1	4214.36	*c46311_g1_i1*	1705	s-like ribonuclease	IPR001568	F:ribonuclease T2 activity; F:RNA binding	48.80
c42336_g1	4193.27	*c42336_g1_i1*	944	invertase inhibitor-like	IPR006501	F:enzyme inhibitor activity; F:pectinesterase activity	73.40
c46687_g1	4079.14	*c46687_g1_i2*	894	uncharacterized LOC100305719	IPR003496	P:response to stress	74.00
c75788_g1	4034.93	*c75788_g1_i1*	1025	p21 family	IPR001938	NA	87.05
c48812_g1	3930.24	*c48812_g1_i3*	1260	NA	no IPS match	NA	NA
c51659_g1	3779.05	*c51659_g1_i1*	590	NA	no IPS match	NA	NA
c50501_g2	3754.39	*c50501_g2_i2*	2312	pectinesterase inhibitor-like	IPR000070; IPR006501	F:pectinesterase activity; P:cell wall modification; C:cell wall; F:enzyme inhibitor activity	74.15
c90364_g1	3627.86	*c90364_g1_i1*	517	NA	no IPS match	NA	NA
c45961_g1	3489.33	*c45961_g1_i1*	667	NA	no IPS match	NA	NA
c52061_g1	3421.89	*c52061_g1_i2*	1057	pectinesterase inhibitor 28-like	IPR000070	C:cell wall; P:cell wall modification; F:pectinesterase activity	84.85
c22143_g1	3230.07	*c22143_g1_i1*	865	mlp-like protein 28	IPR000916	P:defense response; P:response to biotic stimulus	68.60
c75794_g1	3125.87	*c75794_g1_i1*	680	NA	no IPS match	NA	NA
c51219_g2	2960.16	*c51219_g2_i2*	1617	s-adenosylmethionine decarboxylase	no IPS match	NA	85.95
c50488_g7	2936.95	*c50488_g7_i1*	1269	major intrinsic protein family transporter	IPR000425	P:transport; C:membrane; F:transporter activity	94.25
c48144_g1	2933.95	*c48144_g1_i7*	733	ubiquitin-like	no IPS match	NA	99.50
c40350_g1	2790.6	*c40350_g1_i1*	275	NA	no IPS match	NA	NA
c52392_g5	2773.69	*c52392_g5_i1*	1056	pectinesterase inhibitor	IPR000070	P:cell wall modification; C:cell wall; F:pectinesterase activity	71.15
c51003_g1	2753.36	*c51003_g1_i1*	729	xyloglucan endotransglucosylase	IPR010713	P:cellular glucan metabolic process; F:xyloglucan:xyloglucosyl transferase activity; C:cell wall; C:apoplast	92.90
c51003_g2	2654.02	*c51003_g2_i1*	617	endo-xyloglucan transferase	IPR000757	P:carbohydrate metabolic process; F:hydrolase activity, hydrolyzing O-glycosyl compounds	94.40

c50255_g2	2653.13	*c50255_g2_i1*	315	ubiquitin-like partial	IPR000626	F:protein binding	99.50
c42538_g1	2644.45	*c42538_g1_i1*	809	dehydrin b	IPR000167	P:response to stress; P:response to water stimulus	55.55
c46921_g1	2601.19	*c46921_g1_i1*	1781	senescence-associated partial	no IPS match	NA	83.55
c46492_g1	2463.08	*c46492_g1_i1*	856	21 kda protein	no IPS match	NA	84.45
c46038_g1	2437.19	*c46038_g1_i3*	467	late embryogenesis abundant protein family	no IPS match	NA	87.50
c46271_g2	2429.47	*c46271_g2_i1*	375	cytochrome b-c1 complex subunit 8-like	IPR020101	C:respiratory chain; C:mitochondrial inner membrane; P:electron transport chain	85.80
c52202_g1	2416.04	*c52202_g1_i1*	609	pectate lyase-like	IPR002022	-	83.50
c49613_g1	2376.49	*c49613_g1_i2*	1570	polygalacturonase-like	IPR000743	P:carbohydrate metabolic process; F:polygalacturonase activity	80.80
c44507_g1	2363.77	*c44507_g1_i2*	598	b12d protein	IPR010530	NA	89.30
c52982_g1	2355.48	*c52982_g1_i1*	2274	atpase plasma membrane-type	IPR008250; IPR023214	F:nucleotide binding; F:metal ion binding	93.15
c1249_g1	2352.19	*c1249_g1_i1*	485	cell wall	no IPS match	NA	70.17
c35223_g1	2349.05	*c35223_g1_i1*	1392	gdsl esterase lipase at5g33370-like	IPR001087	P:lipid metabolic process; F:hydrolase activity, acting on ester bonds	88.20
c39168_g1	2346.25	*c39168_g1_i1*	230	hypothetical PHAVU_011G150500g	no IPS match	NA	88.00
c48584_g3	2327.12	*c48584_g3_i1*	443	protein ralf-like 9-like	IPR008801	NA	58.25
c50298_g1	2302.94	*c50298_g1_i3*	515	pectinesterase ppme1	no IPS match	NA	76.05
c47149_g2	2266.48	*c47149_g2_i2*	905	lipid transfer protein precursor	no IPS match	NA	75.80
c47764_g3	2184.35	*c47764_g3_i1*	652	acid beta-fructofuranosidase	IPR013189	NA	92.70
c44734_g1	2184.03	*c44734_g1_i3*	3141	cell wall-associated hydrolase	no IPS match	NA	82.00
c41993_g1	2152.52	*c41993_g1_i1*	790	cell wall	no IPS match	NA	61.28
c52221_g1	2147.31	*c52221_g1_i4*	679	NA	no IPS match	NA	
c39797_g1	2137.55	*c39797_g1_i1*	868	mlp-like protein 423-like	IPR000916	P:response to biotic stimulus; P:defense response	83.55
c46440_g2	2129.59	*c46440_g2_i1*	471	arabinogalactan peptide 16-like	no IPS match	NA	83.39
c46355_g1	2075.15	*c46355_g1_i1*	785	NA	IPR015157	NA	NA

c49376_g2	2039.82	*c49376_g2_i2*	492	late embryogenesis abundant protein 1-like	no IPS match	-	77.45
c52202_g2	2013.73	*c52202_g2_i2*	943	pectate lyase-like	IPR007524; IPR002022	F:pectate lyase activity	75.85
c49407_g1	2006.4	*c49407_g1_i1*	974	stem 28 kda glycoprotein	no IPS match	NA	82.00
c46921_g2	2002.22	*c46921_g2_i1*	2594	rrna intron-encoded homing endonuclease	no IPS match	NA	76.80
c31965_g1	1962.53	*c31965_g1_i1*	790	ekn protein	no IPS match	NA	66.00
c45615_g2	1943.6	*c45615_g2_i3*	883	ribulose- -bisphosphate carboxylase oxygenase small subunit	IPR000894; IPR024680	NA	90.05
c48699_g1	1942.53	*c48699_g1_i1*	623	NA	no IPS match	NA	
c40016_g1	1932.13	*c40016_g1_i1*	808	non-specific lipid-transfer protein 2-like	IPR016140	NA	86.00
c35211_g1	1925.86	*c35211_g1_i1*	738	leguminosin group485 secreted peptide	no IPS match	NA	64.75
c51694_g1	1922.15	*c51694_g1_i4*	1636	pectinesterase pectinesterase inhibitor	IPR000070; IPR006501	F:pectinesterase activity; C:cell wall; P:cell wall modification; F:enzyme inhibitor activity	72.85
c51082_g2	1885.87	*c51082_g2_i3*	2125	pectinesterase inhibitor 45-like	IPR006501; IPR000070	F:pectinesterase activity; F:enzyme inhibitor activity; P:cell wall modification; C:cell wall	73.85
c52392_g2	1880.4	*c52392_g2_i1*	762	pectinesterase inhibitor 21-like	IPR006501	F:enzyme inhibitor activity; F:pectinesterase activity	72.60
c49201_g4	1877.53	*c49201_g4_i2*	325	calmodulin	IPR002048	F:calcium ion binding	100.00
c52376_g4	1869.32	*c52376_g4_i3*	1855	alpha tubulin 1	no IPS match	NA	99.00
c52177_g1	1868.51	*c52177_g1_i1*	2100	sucrose transport	no IPS match	NA	79.90
c48584_g2	1846.64	*c48584_g2_i1*	1344	microtubule organization 1 family	IPR008801	NA	82.10
c41972_g2	1777.82	*c41972_g2_i1*	444	probable pectate lyase 3-like	no IPS match	NA	79.40
c51841_g1	1712.04	*c51841_g1_i1*	2865	beta-galactosidase 13-like	IPR001944; IPR000922; IPR006104	P:carbohydrate metabolic process; F:hydrolase activity, hydrolyzing O-glycosyl compounds; F:carbohydrate binding	82.65
c47409_g1	1711.14	*c47409_g1_i3*	900	protein ralf-like 19-like	IPR008801	NA	74.35
c33197_g1	1703.12	*c33197_g1_i1*	1118	phosphate-responsive 1 family	IPR006766	NA	62.55

c35308_g1	1693.61	*c35308_g1_i1*	199	NA	no IPS match	NA	NA
c50150_g2	1658.2	*c50150_g2_i1*	1506	Lipoxygenase	IPR013819	F:metal ion binding; P:oxidation-reduction process; F:oxidoreductase activity	88.15
c20413_g1	1627.37	*c20413_g1_i1*	386	NA	no IPS match	NA	NA
c51808_g2	1625.43	*c51808_g2_i2*	218	sphingolipid delta -desaturase des1-like	no IPS match	NA	95.90
c76225_g1	1624.68	*c76225_g1_i1*	686	cysteine proteinase inhibitor	no IPS match	NA	88.85
c51857_g1	1621.74	*c51857_g1_i1*	893	adp-ribosylation factor 2-like	no IPS match	NA	98.60
c50488_g3	1617.34	*c50488_g3_i1*	180	aquaporin protein 7	no IPS match	NA	93.00
c48268_g1	1605.12	*c48268_g1_i1*	522	polcalcin nic t 1-like	no IPS match	NA	92.90
c49048_g1	1578.23	*c49048_g1_i1*	824	NA	no IPS match	NA	NA
c42408_g1	1556.53	*c42408_g1_i1*	505	arabinogalactan peptide 23-like	no IPS match	NA	66.33
c44616_g1	1555.27	*c44616_g1_i1*	882	linoleate 9s-lipoxygenase-like	IPR013819	F:metal ion binding; F:oxidoreductase activity; P:oxidation-reduction process	89.25
c50673_g2	1548.65	*c50673_g2_i2*	373	NA	no IPS match	NA	NA
c45131_g1	1517.41	*c45131_g1_i1*	578	nucleolar protein 58-like	no IPS match	NA	79.20
c47465_g2	1510.38	*c47465_g2_i1*	684	uncharacterized LOC101515237	no IPS match	NA	59.25
c39091_g2	1510.04	*c39091_g2_i1*	659	pollen-specific protein c13-like	no IPS match	NA	77.10
c38416_g1	1480.9	*c38416_g1_i1*	722	NA	no IPS match	NA	NA

FPKM- Fragments Per Kilobase of target transcript length per Million reads mapped

Mean similarity- the average similarity of the putative *C. striatus* protein and the 20 most similar proteins at NCBI

NA- not available

IPS- InterProScan