

Table 1 Suppl. Primer sequences for reverse transcription quantitative PCR.

Gene	Primer 1	Primer 2	Size [bp]
BraA03002010	GTTTACTGCTCACCCTACTC	GACTCCTCGTATGTTGTTGT	279
BraA03004735	ATTCACCGACCAGATTCCAT	AGTTTCCTTGCAGCTCAACC	212
BraA01001489	ACCATTTACATCGTCCTCTT	ATATCATCAGCTAACCCATT	129
BraA05004043	TATTACGGTCGTGGTCTAT	GATCCCAAACCTGCCTACAGA	288
BraA10001834	GCGTACATTGTTCTTCTTAT	TAGCATTTCCCTCTGTATCA	146
BraA04003128	GCAGAGTCGCCTGAGAAGAT	AAGTCGCAGTAGCATTGGT	185

Table 2. Suppl. Overview data of the sequencing process. Q20, Q30 - the proportion of base number with a quality higher than 20 (30) clean reads from the total base number.

Sample name	Raw reads	Clean reads	Clean bases	Error rate [%]	Q20 [%]	Q30 [%]	GC content [%]
TXC1_4	83359228	78057322	11.71G	0.02	97.44	93.27	45.94
TXC2_4	65840692	64050906	9.61G	0.02	97.03	92.38	45.92
TXC1_10	69762934	67286532	10.09G	0.02	96.81	91.96	45.96
TXC2_10	69468022	66935102	10.04G	0.02	96.94	92.23	46.01
TXC1_16	83893300	80644946	12.1G	0.02	97.06	92.47	45.77
TXC2_16	83989492	80827814	12.12G	0.02	96.90	92.12	45.74
TXC1_45	84507390	81321814	12.2G	0.02	96.85	91.97	50.47
TXC2_45	76511728	73155288	10.97G	0.02	97.1	92.47	50.15
TSF1_4	76585812	72939848	10.94G	0.02	97.41	93.21	46.19
TSF2_4	73083044	70483456	10.57G	0.02	96.88	92.09	46.17
TSF1_10	71491216	68969258	10.35G	0.02	97.35	93.14	45.84
TSF2_10	65933852	64118824	9.62G	0.02	96.88	92.13	45.86
TSF1_16	71008094	68784416	10.32G	0.02	96.73	91.81	45.67
TSF2_16	71547510	69540370	10.43G	0.02	97.15	92.68	45.59
TSF1_45	80128512	77300976	11.6G	0.02	96.33	90.96	49.59
TSF2_45	69703518	67027528	10.05G	0.02	96.95	92.25	48.90
TCK1_4	74843988	71594314	10.74G	0.02	97.00	92.36	45.19
TCK2_4	62329920	60192510	9.03G	0.02	96.85	92.08	45.35
TCK1_10	77826318	74701408	11.21G	0.01	97.69	93.95	46.22
TCK2_10	71625608	69803470	10.47G	0.02	97.37	93.30	46.26
TCK1_16	74702214	72505232	10.88G	0.02	97.36	93.28	46.22
TCK2_16	87386444	85058774	12.76G	0.01	97.47	93.51	46.23
TCK1_45	68714930	65722848	9.86G	0.02	95.45	89.11	45.47
TCK2_45	66195436	62860626	9.43G	0.02	95.60	89.42	45.79

Table 3 Suppl. The significantly enriched *Gene ontology* (GO) terms of differentially expressed genes (DEGs, $P \leq 0.05$). SF - Shifang isolate, XC - Xichang isolate.

	GO accession	GO terms	DEG item	Corrected P-value
Molecular function	GO:0003824	catalytic activity	1703	9.09E-12
SF vs. XC	GO:0016762	xyloglucan:xyloglucosyl transferase activity	22	2.00E-08
4 dpi	GO:0016740	transferase activity	773	5.11E-08
	GO:0005509	calcium ion binding	80	1.41E-07
	GO:0016491	oxidoreductase activity	389	3.29E-07
	GO:0016757	transferase activity, transferring glycosyl groups	143	9.04E-07
	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	65	2.03E-04
	GO:0048037	cofactor binding	135	2.19E-04
	GO:0016832	aldehyde-lyase activity	14	5.55E-04

	<i>GO</i> accession	<i>GO</i> terms	DEG item	Corrected <i>P</i> -value
	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	70	7.66E-04
Molecular function	GO:0003735	structural constituent of ribosome	292	5.23E-53
SF vs. XC	GO:0005198	structural molecule activity	380	1.10E-36
10 dpi	GO:0004298	threonine-type endopeptidase activity	22	4.68E-06
	GO:0070003	threonine-type peptidase activity	22	4.68E-06
	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	38	5.07E-05
	GO:0003942	N-acetyl-gamma-glutamyl-phosphate reductase activity	9	9.18E-05
	GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	29	1.67E-04
	GO:0016757	transferase activity, transferring glycosyl groups	173	7.38E-04
	GO:0016866	intramolecular transferase activity	26	7.44E-04
	GO:0051287	NAD binding	45	1.78E-03
Molecular function	GO:0003735	structural constituent of ribosome	159	4.03E-25
SF vs. XC	GO:0005198	structural molecule activity	187	7.66E-14
16 dpi	GO:0016740	transferase activity	529	3.05E-05
	GO:0005509	calcium ion binding	56	5.46E-04
	GO:0004672	protein kinase activity	191	9.71E-04
	GO:0016773	phosphotransferase activity, alcohol group as acceptor	218	9.76E-04
	GO:0031683	G-protein beta/gamma-subunit complex binding	16	2.05E-03
	GO:0016301	kinase activity	223	2.56E-03
	GO:0016762	xyloglucan:xyloglucosyl transferase activity	13	2.79E-03
	GO:0032403	protein complex binding	41	1.21E-02
Molecular function	GO:0003735	structural constituent of ribosome	238	2.02E-11
SF vs. XC	GO:0003777	microtubule motor activity	54	6.33E-09
45 dpi	GO:0008017	microtubule binding	80	1.29E-07
	GO:0001071	nucleic acid binding transcription factor activity	332	1.47E-07
	GO:0003700	transcription factor activity, sequence-specific DNA binding	332	1.47E-07
	GO:0005198	structural molecule activity	338	1.53E-06
	GO:0015631	tubulin binding	87	6.83E-06
	GO:0003774	motor activity	71	1.00E-05
	GO:0008092	cytoskeletal protein binding	167	2.24E-05
	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	208	2.27E-04
Cellular component	GO:0031012	extracellular matrix	34	1.59E-08
SF vs. XC	GO:0005578	proteinaceous extracellular matrix	31	2.00E-08
4 dpi	GO:0048046	apoplast	22	2.00E-08
	GO:0005618	cell wall	49	5.40E-07
	GO:0030312	external encapsulating structure	60	7.56E-06
	GO:0009521	photosystem	48	1.99E-03
	GO:0044421	extracellular region part	45	2.84E-03
	GO:0009579	thylakoid	55	3.75E-03
	GO:0034357	photosynthetic membrane	50	4.42E-03
	GO:0005576	extracellular region	155	3.81E-02
Cellular component	GO:0005840	ribosome	290	5.23E-53
SF vs. XC	GO:0030529	ribonucleoprotein complex	327	1.37E-35
10 dpi	GO:0044444	cytoplasmic part	624	3.03E-31
	GO:0005737	cytoplasm	732	3.93E-29
	GO:0043232	intracellular non-membrane-bounded organelle	398	2.16E-23
	GO:0043228	non-membrane-bounded organelle	400	6.33E-22
	GO:0032991	macromolecular complex	774	3.58E-16
	GO:0005622	intracellular	1213	5.27E-11
	GO:0044424	intracellular part	1179	6.20E-11

	<i>GO</i> accession	<i>GO</i> terms	DEG item	Corrected <i>P</i> -value
	GO:0005623	cell	1312	2.87E-10
Cellular component	GO:0005840	ribosome	159	5.23E-53
SF vs. XC	GO:0030529	ribonucleoprotein complex	178	1.37E-35
16 dpi	GO:0043232	intracellular non-membrane-bounded organelle	208	3.03E-31
	GO:0043228	non-membrane-bounded organelle	209	3.93E-29
	GO:0044444	cytoplasmic part	290	2.16E-23
	GO:0005737	cytoplasm	338	6.33E-22
	GO:0031012	extracellular matrix	23	3.58E-16
	GO:0048046	apoplast	13	5.27E-11
	GO:0005578	proteinaceous extracellular matrix	21	6.20E-11
	GO:0005853	eukaryotic translation elongation factor 1 complex	5	1.74E-02
Cellular component	GO:0005840	ribosome	159	5.23E-53
SF vs. XC	GO:0043232	intracellular non-membrane-bounded organelle	178	1.37E-35
45 dpi	GO:0043228	non-membrane-bounded organelle	208	3.03E-31
	GO:0030529	ribonucleoprotein complex	209	3.93E-29
	GO:0030117	membrane coat	290	2.16E-23
	GO:0048475	coated membrane	338	6.33E-22
	GO:0043229	intracellular organelle	23	3.58E-16
	GO:0043226	organelle	13	5.27E-11
	GO:0000145	exocyst	21	6.20E-11
	GO:0044424	intracellular part	1058	8.15E-03
Biological process	GO:0005975	carbohydrate metabolic process	254	4.95E-11
SF vs. XC	GO:0006073	cellular glucan metabolic process	46	3.59E-09
4 dpi	GO:0044042	glucan metabolic process	46	3.59E-09
	GO:0044264	cellular polysaccharide metabolic process	50	7.02E-09
	GO:0005976	polysaccharide metabolic process	58	1.15E-08
	GO:0044262	cellular carbohydrate metabolic process	68	6.84E-08
	GO:0055114	oxidation-reduction process	368	3.11E-06
	GO:0016310	phosphorylation	286	1.62E-05
	GO:0044710	single-organism metabolic process	727	1.62E-05
	GO:0044723	single-organism carbohydrate metabolic process	111	3.29E-05
Biological process	GO:0006412	translation	353	1.71E-38
SF vs. XC	GO:0043043	peptide biosynthetic process	356	3.10E-37
10 dpi	GO:0043604	amide biosynthetic process	365	1.27E-36
	GO:0006518	peptide metabolic process	362	3.57E-35
	GO:1901566	organonitrogen compound biosynthetic process	540	4.21E-34
	GO:0043603	cellular amide metabolic process	375	3.23E-33
	GO:1901564	organonitrogen compound metabolic process	644	4.02E-30
	GO:0009058	biosynthetic process	1313	7.17E-19
	GO:1901576	organic substance biosynthetic process	1258	1.44E-17
	GO:0044249	cellular biosynthetic process	1225	1.39E-16
Biological process	GO:0006412	translation	182	5.79E-17
SF vs. XC	GO:0044267	cellular protein metabolic process	455	1.21E-16
16 dpi	GO:0043043	peptide biosynthetic process	183	1.87E-16
	GO:0043604	amide biosynthetic process	186	1.30E-15
	GO:0006518	peptide metabolic process	184	6.38E-15
	GO:0043603	cellular amide metabolic process	192	1.49E-14
	GO:1901566	organonitrogen compound biosynthetic process	259	5.94E-12
	GO:0019538	protein metabolic process	507	2.51E-11
	GO:1901564	organonitrogen compound metabolic process	306	3.87E-10
	GO:0055114	oxidation-reduction process	346	4.44E-10
Biological process	GO:0008152	metabolic process	3378	1.01E-10
SF vs. XC	GO:0009059	macromolecule biosynthetic process	1254	1.79E-10
45 dpi	GO:0034645	cellular macromolecule biosynthetic process	1239	2.79E-10

<i>GO</i> accession	<i>GO</i> terms	DEG item	Corrected <i>P</i> -value
GO:0051641	cellular localization	445	1.03E-09
GO:0051649	establishment of localization in cell	427	1.03E-09
GO:0009058	biosynthetic process	1589	1.66E-09
GO:0008150	biological process	4365	1.66E-09
GO:0044271	cellular nitrogen compound biosynthetic process	1198	6.33E-09
GO:0046907	intracellular transport	371	1.84E-08
GO:1901576	organic substance biosynthetic process	1516	2.13E-08

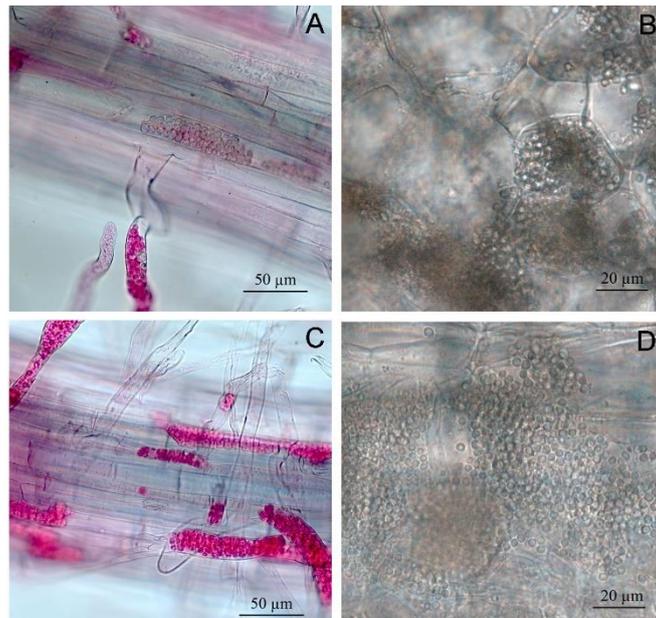


Fig. 1 Suppl. *Brassica rapa* L. cv. T1-45 inoculated with the Shifang or Xichuang isolate of *Plasmodiophora brassicae*. The ultrastructure of small spheroid galls was determined on a bare-handed section after 4 days post inoculation (dpi, A), 10 dpi (B), 16 dpi (C), and 45dpi (D).