Table S1 Statistic correlation coefficients of biological replicates using to assemble sequences

Sample	test	Correlation	*P*-value
S1	R1-vs-R2	0.9932625	2.20E-16
	R1-vs-R3	0.9843602	2.20E-16
	R2-vs-R3	0.982757	2.20E-16
S2	R1-vs-R3	0.9408083	2.20E-16
S3	R1-vs-R2	0.9940531	2.20E-16
	R1-vs-R3	0.9920043	2.20E-16
	R2-vs-R3	0.991774	2.20E-16
P1	R1-vs-R2	0.9832744	2.20E-16
P2	R2-vs-R3	0.9834377	2.20E-16
P3	R1-vs-R2	0.9850565	2.20E-16
	R1-vs-R3	0.9296429	2.20E-16
	R2-vs-R3	0.9445614	2.20E-16
Ck	R1-vs-R2	0.9357648	2.20E-16
	R1-vs-R3	0.9659491	2.20E-16
	R2-vs-R3	0.9887152	2.20E-16

Note: Ck: resistant wheat N9134 exempt from pathogen stress; S1, S2 and S3: N9134 infected with stripe rust pathogen CYR 31 at 1, 2 and 3 dpi, respectively; P1, P2 and P3: N9134 infected with powdery mildew pathogen E09 at 1, 2 and 3 dpi, respectively.

7 D E O & K 6 D U D F W H U Q] Q R W R Q W H R L P R O R J L F D O L J H Q H V L V Q G X F H G E \ V W U L S H U X V W S D W K R J H Q D Q G S R Z G H U \

GO.ID	Term	Annotated Unigenes	Bgt stress only DEGs			Overlapped DEGs			Pst stress only DEGs		
			Significant	Expected	KS	Significant	Expected	KS	Significant	Expected	KS
GO:0043581	mycelium development				H			(			(
GO:0006278	RNA-dependent DNA replication				(			(			(
GO:0006310	DNA recombination				(			(			(
GO:0009405	pathogenesis				(			(			(
GO:0055114	oxidation-reduction process				(			(			(
GO:0015074	DNA integration				(			(			(
GO:0036180	filamentous growth of a population of un...				(			(			(
GO:0036170	filamentous growth of a population of un...				(			(			(
GO:0006805	xenobiotic metabolic process				(			(			(
GO:0080167	response to karrikin				(						
GO:0009751	response to salicylic acid stimulus				(						
GO:0035690	cellular response to drug				(			(			(
GO:0009737	response to abscisic acid stimulus				(						
GO:0015706	nitrate transport				(						
GO:0010167	response to nitrate				(						
GO:0071216	cellular response to biotic stimulus				(			(			(
GO:0006956	complement activation				(			(			(
GO:0009725	response to hormone stimulus				(						
GO:0006695	cholesterol biosynthetic process				(			(			(
GO:0044283	small molecule biosynthetic process				(						
GO:0009723	response to ethylene stimulus				(						
GO:0009628	response to abiotic stimulus				(						
GO:0009813	flavonoid biosynthetic process				(						

GO:0010264	myo-inositol hexakisphosphate biosynthet...	(		
GO:0006415	translational termination	(	(	(
GO:0006614	SRP-dependent cotranslational protein ta...	(	(	(
GO:0044249	cellular biosynthetic process	(		
GO:0009755	hormone-mediated signaling pathway	(		
GO:0006979	response to oxidative stress	(		
GO:0006863	purine nucleobase transport	(		
GO:0010363	regulation of plant-type hypersensitive ...	(		
GO:0010200	response to chitin	(		
GO:0046148	pigment biosynthetic process	(		
GO:0002679	respiratory burst involved in defense re...	(		
GO:0009620	response to fungus	(		
GO:0080052	response to histidine	(		
GO:0080053	response to phenylalanine	(		
GO:0009611	response to wounding	(		
GO:0080009	mRNA methylation	(	(	(
GO:0017187	peptidyl-glutamic acid carboxylation	(	(	(
GO:0006414	translational elongation	(	(	(
GO:0042430	indole-containing compound metabolicpro..	(		
GO:0006612	protein targeting to membrane	(		
GO:0015804	neutral amino acid transport	(		
GO:0009624	response to nematode	(		
GO:0044281	small molecule metabolic process	(		
GO:0019083	viral transcription	(	(	(
GO:0042538	hyperosmotic salinity response	(		
GO:0006552	leucine catabolic process	(		

GO:0000184	nuclear-transcribed mRNA catabolic proce..	(	(	(
GO:0006526	arginine biosynthetic process	(		
GO:0042631	cellular response to water deprivation	(		
GO:0009863	salicylic acid mediated signaling pathwa...	(		
GO:0043201	response to leucine	(		

GO:0030476	**ascospore wall assembly**	25	1	3.14	0.00034	4	0.33	0.04099	4	0.55	0.05656
GO:0043496	**regulation of protein homodimerization a...**	11	8	1.38	0.00034	0	0.79	9.50E-05	0	1.31	0.0002
GO:0044409	**entry into host**	78	13	9.79	0.00036	0	2.36	0.00033	1	3.93	0.00034
GO:0010114	**response to red light**	551	115	69.14	0.00037	3	37.99	3.80E-11	35	63.1	2.80E-12
GO:0006413	**translational initiation**	1253	101	157.23	0.00037	55	16.71	0.00406	74	27.75	0.00032
GO:0031505	**fungal-type cell wall organization**	104	11	13.05	0.00038	0	3.15	0.00013	3	5.24	1.90E-05
GO:0042938	**dipeptide transport**	139	40	17.44	0.00038	9	4.21	0.65779	11	7	0.6592
GO:0006103	**2-oxoglutarate metabolic process**	86	19	10.79	0.00041	4	2.61	0.00734	6	4.33	0.00576
GO:0051502	**diterpene phytoalexin biosynthetic proce...**	75	25	9.41	0.00042	2	2.27	0.06904	3	3.78	0.07837
GO:0006891	**intra-Golgi vesicle-mediated transport**	284	54	35.64	0.00044	5	8.61	0.01918	10	14.3	0.03401
GO:0009987	**cellular process**	45474	5883	5706.1	0.00045	1430	1378.74	0.01375	2370	2290.05	0.00462
GO:0052746	**inositol phosphorylation**	9	7	1.13	0.00046	0	0.27	0.5797	0	0.45	0.61507
GO:0016114	**terpenoid biosynthetic process**	1265	240	158.73	0.00048	66	38.35	0.09471	100	63.7	0.05177
GO:0000041	**transition metal ion transport**	1452	253	182.2	0.00049	56	44.02	0.30982	79	73.12	0.40997
GO:0030447	**filamentous growth**	355	44	44.55	0.00055	9	10.76	0.00014	1	3.22	9.70E-05
GO:0030448	**hyphal growth**	64	8	8.03	0.00055	0	1.94	0.00015	14	17.88	0.00027
GO:0006696	**ergosterol biosynthetic process**	27	3	3.39	0.00056	2	0.82	5.80E-05	2	1.36	0.00011
GO:0009753	**response to jasmonic acid stimulus**	2460	429	308.68	0.00061	108	74.59	0.1923	161	123.88	0.17187
GO:0051591	**response to cAMP**	86	6	10.79	0.00067	0	2.61	3.80E-05	0	4.33	0.00018
GO:0007118	**budding cell apical bud growth**	11	0	1.38	0.00068	0	0.33	0.00017	0	0.55	0.00024
GO:0010183	**pollen tube guidance**	61	17	7.65	0.0007	2	1.85	0.1031	3	3.07	0.14081
GO:0051262	**protein tetramerization**	246	41	30.87	0.00075	15	7.46	0.00097	23	12.39	0.00018
GO:0019878	**lysine biosynthetic process via aminoadi...**	19	0	2.38	0.00077	0	0.73	2.40E-05	0	1.21	5.70E-05
GO:0019373	**epoxygenase P450 pathway**	24	1	3.01	0.00077	0	0.58	0.00022	0	0.96	0.00031
GO:0010035	**response to inorganic substance**	7436	1228	933.07	0.00083	150	83.14	0.02452	492	374.47	0.01069
GO:0006790	**sulfur compound metabolic process**	2742	467	344.07	0.00083	348	225.45	0.00725	197	138.09	0.05135

GO:0000727	**double-strand break repair via break-ind...**	6	0	0.75	0.00085	0	0.18	0.00016	0	0.3	0.00024
GO:0010099	**regulation of photomorphogenesis**	86	28	10.79	0.00085	8	2.61	0.46987	10	4.33	0.41732
GO:0010324	**membrane invagination**	132	9	16.56	0.00086	1	4	0.10736	3	6.65	0.11838
GO:0006690	**icosanoid metabolic process**	143	29	17.94	0.00088	5	4.34	0.10015	8	7.2	0.1506
GO:0044182	**filamentous growth of a population of un...**	272	38	34.13	0.00092	0	3	0.00026	3	4.99	0.00011
GO:0044011	**single-species biofilm formation on inan...**	99	10	12.42	0.00092	8	8.25	0.00054	13	13.7	0.00154
GO:0016101	**diterpenoid metabolic process**	528	119	66.25	0.00096	109	53.73	0.01457	167	89.24	0.03966
GO:0008299	**isoprenoid biosynthetic process**	1772	342	222.35	0.00096	26	16.01	0.08673	33	26.59	0.1687
GO:0019344	**cysteine biosynthetic process**	831	155	104.27	0.001	55	25.2	0.08786	65	41.85	0.22009
GO:0019252	**starch biosynthetic process**	491	97	61.61	0.00534	56	14.89	0.00076	74	24.73	3.50E-05
GO:0006897	**endocytosis**	1244	83	156.1	0.0665	12	37.72	7.80E-05	38	62.65	6.20E-05
GO:0030307	**positive regulation of cell growth**	109	10	13.68	0.00172	2	3.3	4.60E-05	3	5.49	6.70E-05
GO:0045471	**response to ethanol**	147	17	18.45	0.003	4	4.46	9.00E-05	7	7.4	7.80E-05
GO:0070374	**positive regulation of ERK1 and ERK cas...**	17	2	2.13	0.01851	0	0.52	0.00207	2	0.86	8.50E-05
GO:0006450	**regulation of translational fidelity**	70	5	8.78	0.00296	0	2.12	0.0001	2	3.53	9.50E-05
GO:0010204	**defense response signaling pathway, resi...**	331	26	41.53	0.00369	6	10.04	6.90E-05	13	16.67	0.0001
GO:0032007	**negative regulation of TOR signaling cas...**	11	1	1.38	0.00308	0	0.33	0.00086	1	0.55	0.00011
GO:0090304	**nucleic acid metabolic process**	19234	2080	2413.49	0.07559	486	583.16	0.34502	910	968.62	0.00011
GO:0032506	**cytokinetic process**	175	21	21.96	0.0056	1	5.31	0.00144	10	8.81	0.00013
GO:0009792	**embryo development ending in birth or eg...**	1646	141	206.54	0.35607	17	49.91	0.00027	53	82.89	0.00014
GO:0019067	**viral assembly, maturation, egress, and...**	74	6	9.29	0.00397	1	2.24	0.00015	3	3.73	0.00015
GO:0042738	**exogenous drug catabolic process**	26	0	3.26	0.00217	0	0.79	7.30E-05	0	1.31	0.00017
GO:0061178	**regulation of insulin secretion involved...**	19	1	2.38	0.00152	0	0.58	0.00348	0	0.96	0.0002
GO:0051046	**regulation of secretion**	312	32	39.15	0.00229	2	9.46	0.03258	7	15.71	0.0002
GO:0030435	**sporulation resulting in formation of a ...**	130	8	16.31	0.04477	1	3.94	0.00028	2	6.55	0.00021
GO:0010244	**response to low fluence blue light stimu...**	20	7	2.51	0.00116	1	0.61	0.0008	2	1.01	0.00023

GO:0006283	**transcription-coupled nucleotide-excisio...**	77	1	9.66	0.00146	0	2.33	0.00014	0	3.88	0.00027
GO:0042760	**very long-chain fatty acid catabolic pro...**	12	0	1.51	0.00109	0	0.36	0.00017	0	0.6	0.00028
GO:0000023	**maltose metabolic process**	496	86	62.24	0.08399	52	15.04	0.00229	68	24.98	0.00029
GO:0001914	**regulation of T cell mediated cytotoxici...**	8	2	1	0.00131	2	0.24	0.00021	2	0.4	0.00032
GO:0034418	**urate biosynthetic process**	13	0	1.63	0.00101	0	0.39	0.00022	0	0.65	0.00033
GO:0043603	**cellular amide metabolic process**	466	65	58.47	0.00658	19	14.13	0.00072	31	23.47	0.00034
GO:0019288	**isopentenyl diphosphate biosynthetic pro...**	634	112	79.55	0.02345	49	19.22	0.04131	80	31.93	0.00035
GO:0016045	**detection of bacterium**	540	38	67.76	0.0107	10	16.37	0.00029	20	27.19	0.00036
GO:0030449	**regulation of complement activation**	27	3	3.39	0.00132	0	0.82	0.00017	0	1.36	0.00038
GO:0007596	**blood coagulation**	427	38	53.58	0.02328	5	12.95	7.50E-05	8	21.5	0.00038
GO:0042364	**water-soluble vitamin biosynthetic proce...**	167	30	20.96	0.01138	10	5.06	0.00515	16	8.41	0.00041
GO:1901700	**response to oxygen-containing compound**	10514	1780	1319.3	0.03053	480	318.78	0.00146	703	529.48	0.00042
GO:0001403	**invasive growth in response to glucose l...**	6	1	0.75	0.00141	0	0.18	0.00031	0	0.3	0.00044
GO:0006144	**purine nucleobase metabolic process**	109	11	13.68	0.00153	5	3.3	0.00085	7	5.49	0.00044
GO:0006418	**tRNA aminoacylation for protein translat...**	245	18	30.74	0.00332	1	7.43	0.00112	8	12.34	0.00045
GO:0000011	**vacuole inheritance**	21	1	2.64	0.00197	0	0.64	0.00031	0	1.06	0.00051
GO:0048732	**gland development**	216	15	27.1	0.02019	4	6.55	0.00493	5	10.88	0.00052
GO:0034446	**substrate adhesion-dependent cell spread...**	41	4	5.14	0.0097	1	1.24	0.00021	1	2.06	0.00057
GO:0070989	**oxidative demethylation**	36	1	4.52	0.00533	0	1.09	0.00029	0	1.81	0.00063
GO:0060627	**regulation of vesicle-mediated transport**	305	27	38.27	0.00876	3	9.25	0.0073	7	15.36	0.00065
GO:0043967	**histone H4 acetylation**	108	9	13.55	0.00298	1	3.27	0.00068	3	5.44	0.00071
GO:0000750	**pheromone-dependent signal transduction...**	7	0	0.88	0.00189	0	0.21	0.00055	0	0.35	0.00075
GO:0009658	**chloroplast organization**	619	107	77.67	0.04995	43	18.77	0.12431	77	31.17	0.00076
GO:0048313	**Golgi inheritance**	18	1	2.26	0.01186	0	0.55	0.00281	1	0.91	0.00077
GO:0006370	**7-methylguanosine mRNA capping**	63	0	7.91	0.00327	0	1.91	0.00044	0	3.17	0.00078
GO:0033129	**positive regulation of histone phosphory...**	6	1	0.75	0.02623	0	0.18	0.00943	1	0.3	0.00078

GO:0045038	**protein import into chloroplast thylakoi...**	15	4	1.88	0.49237	4	0.45	0.17554	8	0.76	0.00078
GO:0006890	**retrograde vesicle-mediated transport, G...**	119	19	14.93	0.00158	3	3.61	0.00055	4	5.99	0.00079
GO:0018279	**protein N-linked glycosylation via aspar...**	179	17	22.46	0.00116	2	5.43	0.00027	4	9.01	0.00084
GO:0030466	**chromatin silencing at silent mating-typ...**	10	0	1.25	0.0021	0	0.3	0.00062	0	0.5	0.00086
GO:0035066	**positive regulation of histone acetylati...**	10	2	1.25	0.01588	0	0.3	0.00579	1	0.5	0.00086
GO:0000082	**G1/S transition of mitotic cell cycle**	437	28	54.84	0.01177	3	13.25	0.0002	6	22.01	0.00088
GO:0019265	**glycine biosynthetic process, by transam...**	15	1	1.88	0.00512	1	0.45	0.00051	1	0.76	0.0009
GO:0001666	**response to hypoxia**	637	100	79.93	0.01894	34	19.31	0.00028	45	32.08	0.00092
GO:0000075	**cell cycle checkpoint**	594	34	74.54	0.01572	3	18.01	0.00028	11	29.91	0.00093
GO:0031425	**chloroplast RNA processing**	353	18	44.29	0.00277	0	10.7	0.00041	2	17.78	0.00094
GO:0042221	**response to chemical stimulus**	17001	2719	2133.3	0.00131	693	515.46	0.0003	1052	856.16	0.04557
GO:0006357	**regulation of transcription from RNA pol...**	1097	86	137.65	0.01648	19	33.26	0.00038	36	55.24	0.00155
GO:0052548	**regulation of endopeptidase activity**	325	42	40.78	0.00927	8	9.85	0.00054	8	16.37	0.00627
GO:0030437	**ascospore formation**	60	3	7.53	0.00164	0	1.82	0.00058	0	3.02	0.00105
GO:0009436	**glyoxylate catabolic process**	13	1	1.63	0.00582	1	0.39	0.0007	1	0.65	0.00118
GO:1901069	**guanosine-containing compound catabolic ...**	777	57	97.5	0.09556	7	23.56	0.00078	23	39.13	0.00108
GO:0060628	**regulation of ER to Golgi vesicle-mediat...**	10	2	1.25	0.00394	0	0.3	0.0008	0	0.5	0.00123
GO:0007107	**membrane addition at site of cytokinesis**	9	0	1.13	0.00257	0	0.27	0.00081	0	0.45	0.0011
GO:0045033	**peroxisome inheritance**	9	0	1.13	0.00257	0	0.27	0.00081	0	0.45	0.0011
GO:0031099	**regeneration**	123	10	15.43	0.01279	2	3.73	0.00084	4	6.19	0.00247
GO:0051298	**centrosome duplication**	142	10	17.82	0.02957	2	4.31	0.00095	2	7.15	0.0035
GO:0008298	**intracellular mRNA localization**	78	5	9.79	0.00285	0	2.36	0.00097	1	3.93	0.00184
GO:0051666	**actin cortical patch localization**	8	1	1	0.00575	0	0.24	0.00099	0	0.4	0.00149
GO:0006706	**steroid catabolic process**	31	1	3.89	0.00389	0	0.94	0.001	0	1.56	0.00196

on) Unigenes induced by stripe rust pathogen and powdery mildew pathogen.

***Bgt* stress only DEGs**			**Overlapped DEGs**			***Pst* stress only DEGs**		
Significant	**Expected**	**KS**	**Significant**	**Expected**	**KS**	**Significant**	**Expected**	**KS**
27	245.79	8.00E-24						

GO:0080043	**quercetin 3-O-glucosyltransferase activi...**	238	58	28.54	0.00021	16	6.75	0.34981	18	11.27	0.53262
GO:0042936	**dipeptide transporter activity**	139	40	16.67	0.00022	9	3.94	0.66493	11	6.58	0.68335
GO:0016165	**lipoxygenase activity**	65	24	7.79	0.00028	4	1.84	0.69968	4	3.08	0.72289
GO:0043008	**ATP-dependent protein binding**	24	2	2.88	0.00029	0	0.68	0.00117	0	1.14	0.00179
GO:0016410	**N-acyltransferase activity**	352	62	42.2	0.0003	16	9.98	0.00303	27	16.66	0.00725
GO:0016616	**oxidoreductase activity, acting on the C...**	775	131	92.92	0.0003	38	21.98	0.00739	51	36.69	0.01841
GO:0030976	**thiamine pyrophosphate binding**	38	8	4.56	0.00031	1	1.08	8.90E-05	1	1.8	0.00017
GO:0042937	**tripeptide transporter activity**	137	39	16.43	0.00033	9	3.89	0.6496	11	6.49	0.68857
GO:0016413	**O-acetyltransferase activity**	65	20	7.79	0.00036	4	1.84	0.21728	5	3.08	0.23227
GO:0043424	**protein histidine kinase binding**	81	24	9.71	0.00044	7	2.3	0.04365	8	3.83	0.06613
GO:0004100	**chitin synthase activity**	23	0	2.76	0.00052	0	0.65	9.30E-05	0	1.09	0.00016
GO:0008236	**serine-type peptidase activity**	587	72	70.38	0.00062	11	16.65	0.00113	17	27.79	0.0033
GO:0016780	**phosphotransferase activity, for other s...**	34	5	4.08	0.00067	3	0.96	0.00182	3	1.61	0.0002
GO:0008374	**O-acyltransferase activity**	308	79	36.93	0.00071	22	8.74	0.00374	25	14.58	0.00799
GO:0004523	**ribonuclease H activity**	270	0	32.37	0.00074	0	7.66	1.10E-05	0	12.78	3.80E-05
GO:0004672	**protein kinase activity**	5613	640	672.99	0.00078	124	159.22	1.40E-05	201	265.73	0.00095
GO:0036201	**ent-isokaurene C2-hydroxylase activity**	84	25	10.07	0.00078	7	2.38	0.00865	8	3.98	0.01971
GO:0005315	**inorganic phosphate transmembrane transp**	29	12	3.48	0.00081	6	0.82	0.01645	6	1.37	0.0289
GO:0052638	**indole-3-butyrate beta-glucosyltransfera...**	51	17	6.11	0.00081	5	1.45	0.06666	6	2.41	0.0623
GO:0072341	**modified amino acid binding**	132	26	15.83	0.00085	8	3.74	0.00784	9	6.25	0.0166
GO:0005338	**nucleotide-sugar transmembrane transport.**	55	17	6.59	0.00087	2	1.56	0.00033	5	2.6	0.00021
GO:0003735	**structural constituent of ribosome**	1291	138	154.79	0.00271	16	36.62	5.00E-07	56	61.12	2.00E-09
GO:0034875	**caffeine oxidase activity**	21	0	2.52	0.00168	0	0.6	9.00E-05	0	0.99	0.00018
GO:0019199	**transmembrane receptor protein kinase ac...**	584	64	70.02	0.00181	10	16.57	7.70E-05	17	27.65	0.00018
GO:0004591	**oxoglutarate dehydrogenase (succinyl-tra...**	12	4	1.44	0.00124	0	0.34	0.00032	0	0.57	0.00045
GO:0016491	**oxidoreductase activity**	5531	934	663.16	0.00145	268	156.89	0.00309	363	261.84	0.00056

GO:0043559	**insulin binding**	11	1	1.32	0.01426

Table S4 Characterization of annotated Go term (Cellular component) Unigenes induced by stripe rust pathogen and powdery mildew pathogen.

GO.ID	Term	Annotated unigenes	*Bgt* stress only DEGs			overlapped DEGs			*Pst* stress only DEGs		
			Significant	Expected	KS	Significant	Expected	KS	Significant	Expected	KS
GO:0009536	plastid	14615	2117	1865.41	2.50E-13	648	453.69	0.01134	1022	755.09	2.50E-13
GO:0016021	integral to membrane	5054	814	645.08	5.60E-13	212	156.89	1.30E-05	314	261.12	1.90E-05
GO:0009535	chloroplast thylakoid membrane	911	212	116.28	4.20E-10	98	28.28	1.20E-05	130	47.07	1.40E-07
GO:0016023	cytoplasmic membrane-bounded vesicle	9940	1418	1268.71	1.10E-09	324	308.56	1.10E-09	486	513.56	1.90E-08
GO:0044428	nudear part	8973	1311	1145.28	3.40E-09	305	278.54	0.00087	567	463.6	7.10E-05
GO:0044446	intracellular organelle part	19487	2897	2487.26	3.70E-09	742	604.93	1.80E-05	1283	1006.81	
GO:0005759	mitochondrial matrix	618	82	78.88							

GO:0005886	**plasma membrane**	12757	1830	1628.26	0.00018	405	396.01	0.51917	670	659.1	0.52861
GO:0009705	**plant-type vacuole membrane**	520	113	66.37	0.0002	37	16.14	0.18382	52	26.87	0.08504
GO:0031298	**replication fork protection complex**	8	0	1.02	0.00028	0	0.25	5.00E-05	0	0.41	7.70E-05
GO:0005773	**vacuole**	5028	803	641.76	0.0004	217	156.08	0.14006	318	259.78	0.15262
GO:0030479	**actin cortical patch**	27	1	3.45	0.00041	0	0.84	4.00E-05	0	1.39	7.40E-05
GO:0044425	**membrane part**	8459	1266	1079.68	0.00044	301	262.59	0.00705	461	437.04	0.03737
GO:0005934	**cellular bud tip**	25	1	3.19	0.00045	0	0.78	9.80E-05	0	1.29	0.00015
GO:0005615	**extracellular space**	481	58	61.39	0.00046	9	14.93	1.10E-06	14	24.85	1.10E-05
GO:0009570	**chloroplast stroma**	2232	400	284.89	0.00048	173	69.29	0.00168	260	115.32	7.80E-07
GO:0030126	**COPI vesicle coat**	107	22	13.66	0.00052	2	3.32	0.00024	2	5.53	0.00052
GO:0000775	**chromosome, centromeric region**	227	17	28.97	0.00058	3	7.05	0.00077	5	11.73	8.80E-05
GO:0000178	**exosome (RNase complex)**	35	5	4.47	0.00061	1	1.09	0.00036	1	1.81	0.00058
GO:0005782	**peroxisomal matrix**	123	18	15.7	0.00075	4	3.82	0.00349	8	6.35	0.00245
GO:0022625	**cytosolic large ribosomal subunit**	634	56	80.92	0.14578	2	19.68	0.00031	24	32.76	1.00E-05
GO:0022627	**cytosolic small ribosomal subunit**	396	46	50.54	0.01224	2	12.29	9.60E-05	8	20.46	0.00018
GO:0033588	**Elongator holoenzyme complex**	10	1	1.28	0.00644	0	0.31	0.00202	1	0.52	0.00025
GO:0042645	**mitochondrial nucleoid**	98	12	12.51	0.02617	5	3.04	0.00084	8	5.06	0.00036
GO:0005811	**lipid particle**	364	33	46.46	0.00711	1	11.3	7.80E-05	4	18.81	0.00046
GO:0031965	**nuclear membrane**	168	15	21.44	0.00449	1	5.22	0.0006	4	8.68	0.00049
GO:0019028	**viral capsid**	22	5	2.81	0.00182	0	0.68	0.00029	0	1.14	0.00056
GO:0030139	**endocytic vesicle**	271		34.59							

GO:0009277	**fungal-type cell wall**	193	25	24.63	0.00251	0	5.99	0.00073	0	9.97	0.00205
GO:0030136	**clathrin-coated vesicle**	348	50	44.42	0.05338	7	10.8	0.00075	12	17.98	0.002
GO:0030127	**COPII vesicle coat**	28	3	3.57	0.00459	0	0.87	0.00076	0	1.45	0.00128
GO:0030496	**midbody**	231	19	29.48	0.03794	7	7.17	0.00082	11	11.93	0.00134
GO:0030134	**ER to Golgi transport vesicle**	68	10	8.68	0.00455	0	2.11	0.00087	0	3.51	0.00137
GO:0030445	**yeast-form cell wall**	85	12	10.85	0.00196	0	2.64	0.00097	0	4.39	0.00179

Table S5 Significant KEGG pathway of Stimulus-Specific Responses to *Pst* versus *Bgt* directly.

KEGG pathway	Correct-p value		
	1 dpi	2 dpi	3 dpi
ko00360 Phenylalanine metabolism	2.02E-09	1(0.78)	1
ko03010 Ribosome	3.59E-08	1(2.43)	1(1.98)
ko00940 Phenylpropanoid biosynthesis	2.38E-07	1(0.84)	0.5222380
ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	0.0005789	1(0.84)	1(2.58)
ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.0119933	1(0.7)	0.5003830
ko00910 Nitrogen metabolism	0.0336965	1	0.2145717
ko00941 Flavonoid biosynthesis	0.2339049	1	0.0712646
ko00904 Diterpenoid biosynthesis	0.2650820	0.0002160	1
ko00592 alpha-Linolenic acid metabolism	1(0.57)	0.0021489	0.0012211
ko00280 Valine, leucine and isoleucine degradation	1(0.64)	0.0028822	0.3054773
ko00402 Benzoxazinoid biosynthesis	–	0.0036764	0.0236634
ko00196 Photosynthesis - antenna proteins	1(4.61)	0.0136544	1
ko00906 Carotenoid biosynthesis	–	0.0467859	0.0494775
ko00195 Photosynthesis	1(3.32)	0.0860785	0.0281121
ko00591 Linoleic acid metabolism	1(0.56)	0.2615313	0.0082961
ko00710 Carbon fixation in photosynthetic organisms	1(1.21)	0.6822167	0.0579076

Table S6. Specific KEGG pathway of DEGs caused by distinct pathogen and corresponding disturbed enzymes

KEGG pathway	Stress	Related enzymes and K number
ko03020 RNA polymerase	Bgt	RPA1(K02999), RPA2(K03002), RPB1(K03006), RPC1(K03018), RPC37(K14721)
ko03030 DNA replication	Bgt	DpoI(K02335), RFA1(K07466), RFA2/4(K10739), RNAseH2A(K10743)
ko03420 Nucleotide excision repair	Bgt	DpoI(K02335), RBX1(K03868), DDB2(K10140), XPC(K10838), XPG(K10846),RPA(K07466,K10739)
ko03430Mismatch repair	Bgt	RPA(RFA1 K07466, RFA2 K10739)
ko03450 Non-homologous end-joining	Bgt	Ku80(K10885), Rad50(K10866) and Mre11(K10865)
ko02010 ABC transporters	Bgt	ABCB1(K05658)
ko00780 Biotin metabolism	Bgt	biotin synthase bioB (K01012)
ko00785 Lipoic acid metabolism	Bgt	lipoyl(octanoyl) transferase lipB (K03801)
ko00510 N-Glycan biosynthesis	Bgt	ALG7 (K01001), dolichyldiphosphatase (K07252), STT(K07151), OST(K12666, K12670), MAN1(K01230), MGAT1(K00726), MGAT2(K00736), MGAT3(K00737)
ko00062 Fatty acid elongation in mitochondria	Bgt	MECR (K07512)
ko00430 Taurine and hypotaurine metabolism	Bgt	GAD(K01580), ggt (K00681), ADO (K10712)
ko00603Glycosphingolipid biosynthesis - globoseries	Pst	galA(K07407)
ko00531Glycosaminoglycan degradation	Pst	HGSNAT(K10532)
ko04140Regulation of autophagy	Pst	ATP1(K08269), VPS15(K08333)
ko00232Caffeine metabolism	Pst	urate oxidase(K00365)

Table S7. The top 1% up and

T19_Unigene_BMK.65657	3	2	1	6	5*	4*	Arabidopsis thaliana	UDP-glycosyltransferase 75D1	flavonoid biosynthetic process
T16_Unigene_BMK.66660	5	3	1	2	6*	4	Brachypodium distachyon	UDP-glycosyltransferase 73C1-like	flavonol biosynthetic process
T7_Unigene_BMK.55212	4*	2	1	6	3	5*	Aegilops tauschii	Linalool synthase, chloroplastic	isoprenoid biosynthetic process
T19_Unigene_BMK.32541	5	2	1	3	4	6*	Swertia mussotii	Geraniol 8-hydroxylase	diterpenoid biosynthetic process
T4_Unigene_BMK.31253	3	1	2	4	6*	5*	Mus musculus	Serine/arginine repetitive matrix protein 2	cellular macromolecule biosynthetic process
T19_Unigene_BMK.63278	4	1	2	3	6*	5*	Arabidopsis thaliana	Probable isoaspartyl peptidase/L-asparaginase 2	autophagic cell death
T10_Unigene_BMK.40836	6*	1	3	2	5	4	Hordeum vulgare	predicted protein	oxidation-reduction process
T19_Unigene_BMK.36612	6*	2	1	3	5	4	Aegilops tauschii	putative Cytochrome P450 71D11	oxidation-reduction process
T4_Unigene_BMK.36102	6*	1	2	4	5	3	Aegilops tauschii	hypothetical protein F775_52192	oxidation-reduction process
T7_Unigene_BMK.35938	3	2	1*	4	6	5	Brassica rapa subsp. chinensis	ribulose 1,5-bisphosphate carboxylase/oxygenase	oxidation-reduction process
T10_Unigene_BMK.79471	4	6	5	1*	2*	3	Aegilops tauschii	Putative flavin-containing monooxygenase 1	oxidation-reduction process
T10_Unigene_BMK.39391	2	6	3	1*	4	5	Oryza sativa	Laccase-19	oxidation-reduction process
T10_Unigene_BMK.2939	4	5	6	1*	4*	3	Triticum aestivum	class III peroxidase	oxidation-reduction process
T10_Unigene_BMK.78990	4	5	6	1*	2	3	Oryza sativa	Ent-isokaurene C2-hydroxylase	oxidation-reduction process
T19_Unigene_BMK.38731	1	5	3*	2	6	4	Aegilops tauschii	Cytochrome P450 71D7	oxidation-reduction process
T10_Unigene_BMK.9714	3	5	6	1*	2	4	Triticum urartu	Cytochrome P450 71D18	oxidation-reduction process
T10_Unigene_BMK.77447	3	5	6	1*	2	4	Triticum urartu	Cytochrome P450 99A2	oxidation-reduction process
T13_Unigene_BMK.10824	4	5	6	1*	2*	3	Triticum urartu	Peroxidase	oxidation-reduction process
T10_Unigene_BMK.64805	4	5	6	2	1*	3*	Glarea lozoyensis	putative fumarate reductase	oxidation-reduction process
T19_Unigene_BMK.50234	4	1	2	3	6*	5	Aegilops tauschii	Nitrate reductase (NAD(P)H)	oxidation-reduction process
T16_Unigene_BMK.30983	4	5	6	2	1*	3*	Mycobacterium tuberculosis	Putative monooxygenase Rv1533	oxidation-reduction process
T13_Unigene_BMK.85907	4	5	6	3	1*	2	Blumeria graminis	catalase/peroxidase	oxidation-reduction process
T19_Unigene_BMK.39009	3	6*	2	1	4	5*	Triticum urartu	Hyoscyamine 6-dioxygenase	oxidation-reduction process
T10_Unigene_BMK.73994	4	5	6	1*	2	3	Triticum urartu	3β-hydroxysteroid-dehydrogenase/decarboxylase isoform 1	oxidation-reduction process
T4_Unigene_BMK.49818	1*	2	3	5	4	6	Pgt	hypothetical protein PGTG_06207	oxidation-reduction process
T10_Unigene_BMK.8063	2	4	5	1*	6	3	Aspv	RNA replication protein	oxidation-reduction process
T10_Unigene_BMK.4777	2	4	5	1*	6	3	Apple stem pitting virus	RNA replication protein	oxidation-reduction process
T10_Unigene_BMK.3559	2	4	5	1*	6	3	Apple stem pitting virus	RNA replication protein	oxidation-reduction process; mRNA methylation
T13_Unigene_BMK.46461	1	5*	6	4	2	3	Hordeum vulgare	predicted protein	tricarboxylic acid cycle
T13_Unigene_BMK.34608	1	4	5	6*	2	3	Triticum aestivum	isocitrate lyase	tricarboxylic acid cycle
T13_Unigene_BMK.46459	1	4	6*	5	2	3	Zea mays	Malate synthase, glyoxysomal	tricarboxylic acid cycle

T13_Unigene_BMK.34608	1	4	5*	6*	2	3	Triticum aestivum	isocitrate lyase	tricarboxylic acid cycle
T19_Unigene_BMK.64560	6*	2	1	3	4	5*	Aegilops tauschii	Putative UDP-glucosyltransferase	response to karrikin
T16_Unigene_BMK.16938	2	5	6*	3	1	4	Arabidopsis thaliana	Probable galactinol-sucrose galactosyltransferase 6	response to karrikin
T19_Unigene_BMK.52305	3	1	2	6*	2	5*	Homo sapiens	Serine/arginine repetitive matrix protein 1	response to karrikin
T10_Unigene_BMK.42975	4	5	6	1*	2	3	Aegilops tauschii	Luminal-binding protein	cellular response to antibiotic
T13_Unigene_BMK.49119	4	5	6	1*	2	3*	Botryotinia fuckeliana	elongation factor 1-alpha	cellular response to drug
T16_Unigene_BMK.86937	3*	2	1	4	5*	6*	Triticum aestivum	chalcone synthase	response to jasmonic acid stimulus
T1_Unigene_BMK.41264	1	2	3	5	4	6*	Triticum aestivum	MYB-related protein	response to hormone stimulus
T19_Unigene_BMK.62625	3	1	2	4	6*	5*	Oryza sativa	Putative calmodulin-like protein 2	hyperosmotic salinity response
T10_Unigene_BMK.9898	1	6*	4	3	2	5	Triticum urartu	Cold shock protein CS66	response to stimulus
T13_Unigene_BMK.44172	1	6*	5	3	2	4	Arabidopsis thaliana	BTB/POZ and TAZ domain-containing protein 2	response to stimulus
T10_Unigene_BMK.10044	4	5	6	2	1*	3	Marssonina brunnea f. sp. &apos	chalcone and stilbene synthase domain-containing protein	response to stimulus
T19_Unigene_BMK.48456	3	2	1	4	6	5*	Arabidopsis thaliana	UDP-glycosyltransferase 90A2	response to stimulus
T10_Unigene_BMK.68445	4	5	6	2	1*	3	Sclerotinia sclerotiorum	enolase	filamentous growth of apop…to biotic stimulus
T16_Unigene_BMK.30394	5	6	4	2*	1*	3*	Sclerotinia sclerotiorum	hypothetical protein SS1G_03130	Signal transduction mechanisms
T10_Unigene_BMK.72147	3	6	4	1*	2	5	Arabidopsis thaliana	Benzoate--CoA ligase, peroxisomal	GA mediated signaling pathway
T10_Unigene_BMK.62784	4	5	6	3	1*	2	Eutypa lata	putative replicase readthrough protein	binding (GO:0005488)
T1_Unigene_BMK.22881	1*	2	3	5	6	4	Pgt	hypothetical protein PGTG_04611	protein binding
T4_Unigene_BMK.24386	1*	2	3	5	4	6	Pgt	hypothetical protein PGTG_04693	biological regulation
T1_Unigene_BMK.39163	1	2	3	6	4	5*	Triticum aestivum	MYB-related protein	regulation of protein homodimerization activity
T10_Unigene_BMK.4959	3	5	4	1*	2	6	Arabidopsis thaliana	Putative transcription factor bHLH041	regulation of transcription
T4_Unigene_BMK.16776	1*	2	3	5	6	4	Medicago truncatula	hypothetical protein MTR_7g109740	regulation of cellular process
T19_Unigene_BMK.62039	5*	3*	1	2	4*	6*	Aegilops tauschii	hypothetical protein F775_20874	cellular process
T16_Unigene_BMK.82348	4	6	5	1*	2	3	Hordeum vulgare	predicted protein	RNA processing
T19_Unigene_BMK.58369	4	1	2	3	5	6*	Arabidopsis thaliana	F-box only protein 13	RNA metabolic process
T16_Unigene_BMK.71879	4	5	6	3	1*	2*	Eutypa lata	putative replicase readthrough protein	metabolic process
T19_Unigene_BMK.61704	4	2	1	3	6	5*	Triticum urartu	(E)-beta-farnesene synthase	metabolic process
T4_Unigene_BMK.1295	2	3	1*	4	6	5	Brachypodium distachyon	PREDICTED: UDP-glycosyltransferase 89B1-like	metabolic process
T7_Unigene_BMK.49453	5	1	2	3	6*	4	Castanea crenata	Agglutinin	protein catabolic process
T19_Unigene_BMK.22212	4	1	2	5	3	6*	Synechococcus	ATP-dependent Clp protease adapter protein	protein catabolic process
T19_Unigene_BMK.60696	4*	2	1	5	6*	3*	Clarkia breweri	Benzyl alcohol O-benzoyltransferase	macromolecule metabolic process

T13_Unigene_BMK.22137	4	5	6	3	1*	2*	Eutypa lata	putative replicase readthrough protein	macromolecule metabolic process
T19_Unigene_BMK.55835	4	1	2	3	6	5*	Clarkia breweri	Salicylate O-methyltransferase	lipid metabolic process
T10_Unigene_BMK.42111	3	4	2*	1	5	6	Blastocladiella emersonii	apocytochrome b	electron transport chain
T10_Unigene_BMK.37883	4	2*	3*	1	5	6	Lingulodinium polyedrum	cytochrome c oxidase subunit I	electron transport chain
T4_Unigene_BMK.35276	3	1	2	4	5*	6*	Triticum urartu	Bidirectional sugar transporter SWEET2b	carbohydrate transport
T10_Unigene_BMK.2206	2	4	5	1*	6	3	Aspv	Capsid protein	transport
T19_Unigene_BMK.68629	4*	2	1	3	5*	6*	Triticum aestivum	boron transporter 2	borate transmembrane transport
T10_Unigene_BMK.63925	4	5	6	1*	2	3	Blumeria graminis	plasma membrane H+-ATPase	mycelium development
T19_Unigene_BMK.52800	2	6	5*	4	1	3	Aegilops tauschii	hypothetical protein F775_28626	developmental process
T19_Unigene_BMK.63651	6*	2	3	5	1	4	Brachypodium distachyon	pyruvate kinase isozyme G, chloroplastic-like	phosphorylation
T7_Unigene_BMK.36614	6*	2	1	5	4	3	Aegilops tauschii	Profilin	actin cytoskeleton organization
T13_Unigene_BMK.45944	4	5	6	1*	2	3	Aegilops tauschii	delta-cadinene synthase isozyme XC14	terpene synthase activity
T19_Unigene_BMK.67352	2	3	1	4	5	6*	Petunia hybrida	Flavonoid 3'-monooxygenase	monooxygenase activity
T19_Unigene_BMK.54041	3*	2*	1	4	5*	6*	Hordeum vulgare	Low molecular mass early light-inducible protein HV90	chloroplast membrane
T13_Unigene_BMK.67646	2	6*	1	4	3*	5	Hordeum vulgare	Low molecular mass early light-inducible protein HV90	chloroplast membrane
T16_Unigene_BMK.90713	2	6	5*	4	1	3	Arabidopsis thaliana	Lysine-rich arabinogalactan protein 19	unknown
T10_Unigene_BMK.70553	2	5	6*	4	1	3	Aegilops tauschii		

T4_Unigene_BMK.40145	4	2	1	3	6*	5	Hordeum vulgare	predicted protein	unknown
T4_Unigene_BMK.27233	1	3	2	4	6*	5*	Brachypodium distachyon	uncharacterized protein LOC100821901	unknown
T4_Unigene_BMK.11511	4	1	2	6	3	5*	Brachypodium distachyon	uncharacterized protein LOC100841361	unknown
T1_Unigene_BMK.25312	1*	2	3	5	6	4	-	NS	unknown
T4_Unigene_BMK.360	1*	2	3	4	6	5	-	NS	unknown
T4_Unigene_BMK.2196	1*	2	3	6	5	4	-	NS	unknown
T16_Unigene_BMK.9085	4	5	6	3*	1*	2*	-	NS	unknown
T16_Unigene_BMK.30030	4	5	6	2*	1*	3*	-	NS	unknown
T16_Unigene_BMK.30281	4	5	6	3*	1*	2*	-	NS	unknown
T13_Unigene_BMK.81987	4	5	6	3*	1*	2*	-	NS	unknown
T19_Unigene_BMK.48960	6*	1	2	3	5*	4*	-	NS	unknown
T10_Unigene_BMK.9590	4	5	6	2	1*	3*	-	NS	unknown
T19_Unigene_BMK.63301	1	2	3	5	4*	6	-	NS	unknown
T16_Unigene_BMK.30338	4	5	6	3	1	2*	-	NS	unknown

Note: S1, S2 and S3 mean N9134 infected with stripe rust pathogen CYR 31 at 1, 2 and 3 dpi, respectively; P1, P2 and P3 represent N9134 infected with powdery mildew pathogen E09 at 1, 2 and 3 dpi respectively. The gene expression level was ranked from high to low at all treatments, and marked from 1 to 6. Pink cell indicated the unigene was up regulated at relative treatment comparing with non inoculation control, while grey cell means down regulation conversely.

Table S8 PCR primers used for Q-PCR amplification with cDNAs and PCR with gDNA

Primer	Forward primer sequence	Reverse primer sequence
T4.38637	5-TGGGAGACGTTCGACCTGCTGT-3	5-ATCGGCGAGGTGGTGTTGTTGT-3
T10.2939	5-GATCATGGCGGTCGTGAAGG-3	5-GCACTCGGACCAGGTGCTGT-3
T13.48786	5-TGCAGGCTTCATTCCAATCT-3	5-TAGAAGCTACGCCGTCACAT-3
T16.15561	5-TGAGCGGTACTGCTAGAATGGA-3	5-AGTCGAGCCGGGTGGTTTGT-3
T16.9085	5-TGAGACTCGGTTATGACAGTAGGAAG-3	5-ACAGGGTAGAAACCCCGTATTTGC-3
T19.26915	5-TCTTCTCGCAGCAGCGTCAC-3	5-GTCGTCCGAGCAGCATTCCA-3
T7.8064	5-GATGATGGATCCGTGGAGAT-3	5-AGAGGAGAAAGATGGGAGCA-3
T16.9260	5-GATGCAACCCACTTGGTCTT-3	5-ACCTCAACACCTCCATGAGC-3

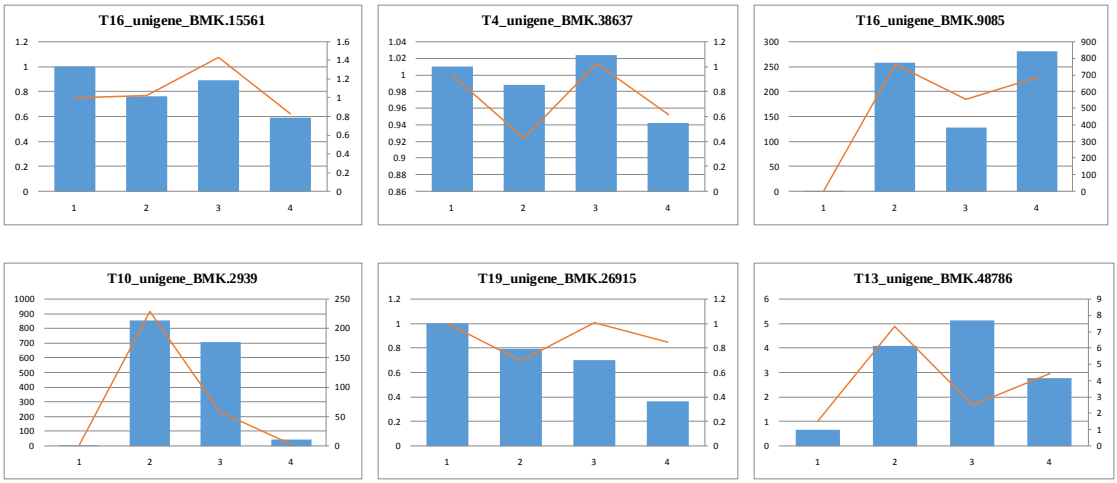
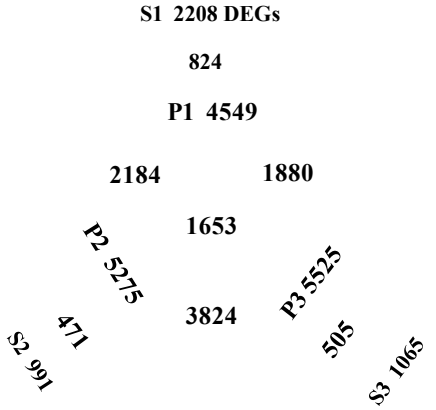


Figure S1. Evaluate the reliability of RNA-Seq with qRT-PCR. Bar graph showed the result of gene expression checked with qRT-PCR, while line graph represent the results of RNA-Seq. The unigenes name was given on the top of each chart.

Figure S2. M A Scatter plot analysis of gene expression quantity variability. The effect of different factors and time points on signal variation was analyzed: powdery mildew stress (top panel) and stripe rust stress (bottom panel) at 1 dpi (left), 2 dpi (middle) and 3 dpi (right) respectively. Green signals represent differentially expressed genes and Red signals are false DEGs. X axle is the value of log2 (RPKM) and represents gene expression level. Y axle is the value of log2(FC) and measure variant of expression quantity among test samples.


S1 2208 DEGs
824
P1 4549
2184
1880
1653
P2 5275
P3 5525
3824
471
505
S2 991
S3 1065

Pst *Bgt*

Bgt