

Table S5. Phosphopeptides showing significant changes in wheat after infection by *Septoria tritici*

Sequence	Accession	Protein	Ratio infected/control					
			Sevin			Stakado		
			3 dai	7 dai	11dai	3 dai	7 dai	11dai
Signaling process								
DEHDEDpTDEDEEEEEEEK	BJ275521	Ankyrin repeat domain protein 17 isoform 1	15.06	50.01			1.66	
ITAAQVLEHPWLHDpSK	DR741624	Calcium-dependent protein kinase 7	12.86		1.59		1.89	1.64
pSQESVGLTGDGTGK	TC457254	Protein kinase NPH1-1	1.54	50.53	0.44			
SAATAWGSPSDApSDAEGDAGHGR	CV762209	Pherophorin-C1 protein				0.31	1.80	0.62
FLTASGpTFK	CA694214	Protein kinase ZmMEK1				0.41		
HVDApSDDDDVVK	BG604433	Pleckstrin homology domain containing protein						1.90
IAPLPDTEGpSAPGHVSTVVK	TC410926	Receptor-like kinase						2.81
RApSLSGAAALGAGALQK	TC439304	RPT2-like protein	0.54		0.58			
VEDLWEVAQPQLpSPSEK	TC370389	SNF1-related protein kinase regulatory subunit gamma 1	5.98					
SDpSVVIDEVELQQHQR	CA660480	Src homology-3 domain protein 3				0.65	0.60	
TPpSFSELNEILLGQEHLK	TC449684	DENN (AEX-3) domain-containing protein-like	0.62		0.65			
Transport								
KPPEDTpSPPIVGEGLVIDEWK	CA736971	27 k vesicle-associated membrane protein	9.42				1.52	
SFIIEpSDDDDDEEDPAHR	BQ241431	Amino acid transporter				0.18	0.52	
pYSEHQPIGTAAQGGGADEK	CA692290	PIP1;3 protein	9.20	34.88		0.64		
pTLHGLQAPEPASHTLFNDK	BJ227308	Plasma membrane ATPase			2.07	0.42		
LGSSApSFGR	TC385048	Plasma membrane intrinsic protein			1.75			
EIAAPHGpSIMGVGR	TC423348	Sugar transporter		0.56				
GGGQSALGSALGLMpSR	TC423348	Sugar transporter		34.04	34.03		1.90	
GGGQSALGpSALGLMSR	TC423348	Sugar transporter					1.73	22.72
GGGQSALGpSALGLMpSR	TC423348	Sugar transporter					2.24	
GGGQpSALGSALGLMpSR	TC423348	Sugar transporter					2.07	
GGGQSALGpSALGLmSR	TC423348	Sugar transporter		0.59				
GGGQpSALGpSALGLMSR	TC423348	Sugar transporter	0.28	0.56				
STLFPNFGpSMFVAEQQQAQ	TC423348	Sugar transporter				2.28		
STLFPNFGSMFpSVAEQQQAQ	TC423348	Sugar transporter	1.50		2.19			
QMQAGMSSMpSFk	TC371555	TOM (Target of myb1)-like protein					1.85	0.35
RpPSGIQQLLAAEQEAQQIVNAAR	CA594105	Vacuolar ATPase subunit G					0.33	1.73
Biological regulation								
EEGEIpSESEEQIK	TC403079	Chromodomain-helicase-DNA-binding protein						1.68
GGGDTSFSTpSLPVLPEK	TC389520	Acute myeloid leukemia protein 1-like		0.53				

EAApSPAPADGSAPAK	TC389456	HMG-I/Y protein HMGa-like	0.54	0.68				
KVEADSTINPpTPPPVEVK	TC390629	Methyl binding domain protein MBD109		0.50			1.85	
QEDAEDAEEpSGDHADAEEAK	TC390629	Methyl binding domain protein MBD109		33.99	0.50		1.69	
DEDDpSGGEEEEEGEEHEK	TC370869	Alfalfa zinc finger protein-like	3.51	50.83				1.54
YDNDNDGHpSPR	CJ656504	Alfalfa zinc finger protein-like						1.98
pSPNATPAK	TC378754	BRI1-KD interacting protein 105		0.68				
EEAEApSEMEQEASGK	TC408268	BRI1-KD interacting protein 135						1.74
AIEAAGGpSPR	TC454885	WRKY35-like protein						1.53
GEEDGDGpSDVGDGAPPAAPHR	BG908374	ZF-HD homeobox protein				3.48	0.38	
ANpSSSLPNsYGGGGR	CK201783	Alternative splicing regulator		1.57	0.61			
IWQYGDVEpSDEEDQAPGGR	CK163910	RNA binding protein Rp120				0.58	3.29	9.46
HGGEDpSDEPEEEPEEQIEVEGDGDGDGR	TC397506	RNA recognition motif family protein					4.72	7.27
ALQESLNTEpSPPR	TC384395	LIM domain-containing protein	4.52	50.55	50.72			
INFPSAASSLQDLSATGNpSPLHPSAGR	TC440813	Arm repeat-containing protein						1.74
Protein folding								
AkpTLDVPHAlDISK	TC381714	Calmodulin-binding heat-shock protein		0.68				
ElpSDEDEDEK	GD186640	Heat shock protein 80					3.03	10.02
ElpSDEDEEEK	CA671116	Heat shock protein 90					1.78	3.78
EPEHDPENDDpSPEDENEEDFDNR	CJ933354	Peptidyl-prolyl cis-trans isomerase					4.98	4.19
Response to stress								
VDALHSGGIGVVAPPpSPSQR	TC429879	Dehydration responsive element-binding protein 1	1.78	3.40	34.10			
FYDEPQGYGMHAGPpSPPR	TC458788	LigA					4.67	
RAPpSGGADAIGQMFQGPpELWTK	CK198030	Stress-induced protein sti1			2.43			
IAASQAAVAAlQPSpSPR	CK208110	Universal stress protein						1.55
Primary metabolic process								
AHGTAVGLPSSDDMGnpSEVGHNALGAGR	TC368880	Phosphoglycerate mutase	1.92			1.61	0.57	11.58
pSFDEQSWSDLShR	TC451647	Alkaline invertase					2.18	
GGMpTSHAAVVAR	TC415232	Orthophosphate dikinase		50.75				
ATGAFILpTASHNPGGPTEDFGIK	TC373718	Phosphoglucomutase				0.53		0.65
DVpSEQFDEFPLAYNK	CA648206	Protein kinase					1.61	
FEFEPVDPtIDK	TC461954	Ribulose biphosphate carboxylase large chain				0.61	0.54	0.60
IPMFGpSTDATQVINEVEEVKK	CK215513	Ribulose biphosphate carboxylase small chain	0.47	0.50		0.38	1.58	
VPGVPAASpSmGGGDSLSDpSLR	CV763920	Sucrose-phosphate synthase					0.36	0.45
VPGVPAASpSMGGGDSLSDpSLR	CV763920	Sucrose-phosphate synthase		30.26	0.03			
VPGVPAASpSMGGGDSLpSDSLR	CV763920	Sucrose-phosphate synthase		30.26	50.03			
IAAQSSDpSPR	TC389412	UDP-N-acetylglucosamine pyrophosphorylase				1.64		
QVAHAPQELNpSPR	BE411978	Asparagine synthase	10.00	34.47	0.51			

VdpSEGVMcGANFK	TC385268	Asparagine synthase				1.64		0.69
YTQDpSDDpSDTESHR	TC384837	Eukaryotic translation initiation factor					0.62	1.50
pSPTGSTTSALLQQYELHQQQVR	TC396045	Topoisomerase-like protein			16.81		1.55	33.95
Cellular component organization								
TVETTADDTEGTpSK	TC384644	Hyphal wall protein 1-like		50.58	50.64			
EMPLPVpSPGADYMSHR	CA502135	KH domain containing protein	13.00	50.63	0.32			34.29
EASNVEDpSPR	TC393311	Myosin heavy chain-like	0.63	0.68	0.68			
KApSPPPQSVVLHVDHLR	CA716965	Ser/Arg-related nuclear matrix protein	13.05	0.51		0.51		
GRpSPAFNALAATFENSAR	CA644276	Villin 2	0.66		1.63	0.60	0.63	
ADTDAVAGEDQGApSENEAER	TC448038	Plectin-like protein					1.97	
pTPTGSGYLGR	CK205332	Transformer-SR ribonucleoprotein					0.66	15.39
GQDPQGmpSPGPGGR	DR731822	Heterogeneous nuclear ribonucleoprotein A2/B1				0.53	2.27	2.10
VVPSTGMAANpSPPSR	TC374890	AT-hook motif nuclear localized protein					1.81	
DDpSDEDDDLHER	CJ781661	DNA-dependent protein kinase						1.78
NDDQEDpSVTVGGTR	TC398351	Nuclear matrix constituent protein				0.64		1.66
NDDQEDpSVpTVGGTR	TC398351	Nuclear matrix constituent protein						1.87
Growth and development								
SGPTGDASGFAPsVEK	TC418760	IgE autoantigen-like	0.50		0.40			
Unknown								
pSAAGAGFLDDDDDEGDLHSHR	TC455092	AGAP006340-PA	1.60					
EDSHATEIYNDHQpSDSADVQNVDR	TC405479	Chromosome chr1 scaffold_46	1.85	0.50	0.69			
pTISESMDELTSQR	CD889063	Chromosome chr1 scaffold_5			0.69			
DAAAGYDpSDDANANAR	TC437438	Chromosome chr14 scaffold_26			50.62			
YPAHTALApTDEEEASET	CJ846803	Chromosome chr17 scaffold_16						1.56
AApSADDLTLPKD	TC406559	Chromosome chr18 scaffold_1				1.52		
VQSGVMpTAETGTYR	TC384916	Chromosome chr3 scaffold_8	1.51	1.56				
FSTQLAAVGApTAR	TC389022	Chromosome chr6 scaffold_3	7.32	0.53	0.63			
RDDNDEpSYGMAR	TC405552	Chromosome chr6 scaffold_3				0.59	1.59	1.67
RDDNDEpSYGmAR	TC405552	Chromosome chr6 scaffold_3			50.38			
HNVPNNDVPDESIEGPPpSDEEGEALAK	CK154232	Chromosome chr7 scaffold_42						5.77
SLESDAADNpSDEEDTR	BQ294942	Chromosome chr7 scaffold_42				0.39		2.10
SLESDAADNpSDEEDTRR	BQ294942	Chromosome chr7 scaffold_42			3.54			
STLAANpSPAAR	TC410891	Chromosome chr8 scaffold_68	0.68	50.51	0.49			
AADSDAANVSpSPR	TC386795	Chromosome chr9 scaffold_33	3.24	50.46				
DHPEPDDDSpSEQETGTFK	CA605418	Chromosome chr9 scaffold_7					0.29	0.45
DDHHQAAASDNPPSIPTATpSPLATTATSK	TC383200	Predicted protein				4.54	6.78	
AAAEHWGpSPAAAAAFDADLVR	TC395764	Expressed protein				14.88	0.51	

ApSLGGDDDLLAHHK	CA610545	Expressed protein	0.53	0.51			1.73
VSpSPHADDEVIPEEAAEK	CJ730168	Gene 11-1 protein		0.51	0.23	1.55	
VVASSVESpSDAGR	TC412973	H0311C03.6 protein	3.06	50.47			
VVASSVESpSSDAGR	TC412973	H0311C03.6 protein	3.16	50.50			
HQHDVQSPDPpSPMLDK	TC375311	Os01g0139200 protein		33.98			
GGDpSWDEPFSSAAAAAAGGGGGR	TC441838	Os01g0139200 protein					0.34
MAADHAADAEAPApSAED	CK165439	Os04g0103300 protein					0.54 1.55
TLAAADDEDpTGGEENEGAQDVADR	TC447034	Os05g0151400 protein					0.27
DYVAQPLPLpTPAYAEQ GK	CN011061	Os05g0583100 protein	7.24			1.55	0.53
GGKPINPNDPVENPEAFSSVVAPpSPNR	TC392922	Os08g0526400 protein	0.57		21.90		
KPAAGpSEGGGFNLGGLFAK	BE418735	PE-PGRS family protein					0.24 0.68
NSIpSDDEEHDMTEDATDAQSGK	CK161991	Putative uncharacterized protein		0.70			
SpSPDDYTGGGSYNK	TC370657	Putative uncharacterized protein				0.46	

The present ratios were calculated by TMT-127/TMT-126 for 3 dai, TMT-129/TMT-128 for 7 dai, TMT-131/TMT-130 for 11 dai from at least two biological replications. Capital letters in the peptide sequence indicate amino acids, and lower case m and c indicate oxidation of Met and carbamidomethyl Cys, respectively. Lower case p indicates phosphorylation of Ser, Thr or Tyr that follows. Peptides marked in yellow were identified in both wheat cultivars Sevin and Stakado. Accession numbers are from TaGI wheat gene index Release 12.0.