SUPPLEMENTARY MATERIALS
to the article by D.O. Kuzmina, E.A. Zorin, A.S. Sulima, D.A. Romanyuk, M.L. Gordon,
A.I. Zhernakov, O.A. Kulaeva, G.A. Akhtemova, O.Y. Shtark, I.A. Tikhonovich, V.A. Zhukov
"Transcriptomic analysis of the symbiotic responsivity trait in pea (*Pisum sativum* L.)"

Table S1. *Sym* genes used for targeted expression analysis

Gene ID in the genome of *P. sativum* cv. Frisson	Gene name in *Medicago truncatula* or other legumes
Sym genes	
evm.TU.scaffold_1307.118	*COLD ACCLIMATION SPECIFIC* (*CAS31*)
evm.TU.contig_1206.43	*non-symbiotic Class 1 HAEMOGLOBIN 1* (*GLB1*)
evm.TU.contig_440.163	*ETHYLENE RESPONSE FACTOR REQUIRED FOR NODULATION2* (*ERN2*)
evm.TU.contig_121.402	*ETHYLENE RESPONSE FACTOR REQUIRED FOR NODULE DIFFERENTIATION* (*EFD*)
evm.TU.contig_770.90	*β-CAROTENE HYDROXYLASE* (*BCH1/BCH2*)
evm.TU.scaffold_284.499	*SYMBIOTIC REMORIN1* (*SymREM1*)
evm.TU.scaffold_5717.154	*BYPASS1* (*BPS1*)
evm.TU.scaffold_1707.235	*MATRIX METALLOENDOPROTEINASE LIKE* (*MMPL*)
evm.TU.contig_1536.159	*SERPIN* (*SER6*)
evm.TU.contig_3900.2	*LECTIN NUCLEOTIDE PHOSPHOHYDROLASE* (*LNP*)
evm.TU.scaffold_2490.81	*Rboh (respiratory burst oxidase homologues, NADPH oxidase)* (*RbohB*)
evm.TU.contig_396.88	*NODULIN 5* (*N5*)
evm.TU.contig_446.74	*MOLYBDATE TRANSPORTER TYPE 1.3*
evm.TU.scaffold_1736.200	*NODULE-SPECIFIC PLAT DOMAIN PROTEIN 2* (*NPD 1/2/3/4/5*)
evm.TU.scaffold_3991.14	*LEGHEMOGLOBIN* (*LB1/LB2/LB3*)
evm.TU.contig_1341.30	*MULTIDRUG AND TOXIC COMPOUND EXTRUSION 1* (*MATE1*)
evm.TU.scaffold_1753.165	*UREIDE PERMEASE* (*UPS1-1*)
evm.TU.scaffold_2585.47	*NODULE INCEPTION* (*NIN*)
evm.TU.contig_315.14	*DEFECTIVE IN Nitrogen Fixation2* (*DNF2*)
evm.TU.contig_1444.79	*VACUOLAR PROCESSING ENZYME* (*VPE*)
evm.TU.contig_4941.20	*NUCLEAR FACTOR YA1*
evm.TU.scaffold_540.545	*nodulin 22 in common bean*
evm.TU.contig_889.182	*NODULE PECTATE LYASE* (*NPL*)
evm.TU.scaffold_181.109	*ANNEXIN1* (*ANN1*)
evm.TU.contig_1310.46	*STATIONARY ENDOSYMBIONT NODULE 1* (*SEN1*)
evm.TU.contig_789.3	*STEAROYL-ACYL CARRIER PROTEIN DESATURASE ISOFORM C* (*SACPD-C*)
evm.TU.scaffold_2585.224	*CHALCONE REDUCTASE* (*CHR*)
evm.TU.scaffold_2406.181	*DELLA 1*
evm.TU.contig_2037.27	*EXOCYST70H4*
evm.TU.contig_516.59	*SYMRK INTERACTING PROTEIN 1* (*SIP1*)
evm.TU.contig_396.60	*DEFECTIVE IN Nitrogen Fixation1* (*DNF1*)
evm.TU.contig_1920.41	*KNOTTED-1 LIKE TAKE HOMEDOMAIN proteins* (*KNAT3/KNAT5/KNAT9/KNAT10*)
evm.TU.contig_274.62	*DELLA 2*
evm.TU.contig_1101.59	*FAIL IN ENLARGEMENT of infection CELLS* (*FEN1*)
evm.TU.contig_1281.359	*INTERACTING PROTEIN DMI 3*
evm.TU.contig_1514.45	*PHOSPHATE2 - LIKE*
evm.TU.scaffold_1858.574	*MOLYBDATE TRANSPORTER TYPE 1.2*
evm.TU.contig_655.139	*CALCIUM DEPENDANT PROTEIN KINASE 1* (*CDPK1*)
evm.TU.scaffold_1106.156	*SUCROSE SYNTHASE* (*SUS1/SUS3*)
AON genes	
evm.TU.contig_633.37	*NNC1*
evm.TU.scaffold_1481.314	*KLV2*
evm.TU.scaffold_1691.167	*CLAVATA2*
evm.TU.contig_606.3	*CRA2*
evm.TU.contig_379.74	*TML1*
evm.TU.scaffold_1481.305	*KLV1*
evm.TU.scaffold_2139.51	*SUNN*
evm.TU.contig_1493.156	*SYM1*
evm.TU.contig_1076.92	*CEP1*
evm.TU.contig_2358.4	*CORYNE*
evm.TU.scaffold_673.58	*CRE1*
evm.TU.scaffold_1654.89	*TML2*
evm.TU.contig_213.211	*CLE12*

Table S2. Top 10 up- and down-regulated genes in comparison of k-8274+Rh+AM with k-3358+Rh+AM

Gene ID in the genome of *P. sativum* cv. Frisson	Functional annotation	Log2 FoldChange	*p*-value
Differentially expressed genes in k-8274+Rh+AM as compared to k-3358+Rh+AM			
evm.TU.contig_1028.11	Protease inhibitor/seed storage/LTP family protein (Putative bifunctional inhibitor/plant lipid transfer protein/seed storage helical)	6.07	0.0323
evm.TU.scaffold_1034.33	Putative SOUL heme-binding protein (SOUL heme-binding family protein)	3.91	0.0004
evm.TU.contig_706.581	Myb-like transcription factor family protein (Putative transcription factor MYB-HB-like family)	3.28	0.0271
evm.TU.scaffold_1082.224	Rossmann-fold NAD(P)-binding domain protein	3.05	0.0039
evm.TU.contig_1296.15	Pentatricopeptide (PPR) repeat protein (Putative tetratricopeptide-like helical domain, DYW domain-containing protein)	1.85	0.0271
evm.TU.contig_1113.250	Haloacid dehalogenase-like hydrolase domain protein (Putative HAD hydrolase, subfamily IA)	1.79	0.0359
evm.TU.contig_1621.102	Expansin	1.73	0.0194
evm.TU.contig_947.147	Metallothionein-like protein	1.55	0.0074
evm.TU.contig_2637.4	Plectin/S10 N-terminal domain-containing protein	1.25	0.0291
evm.TU.contig_1332.50	FAD-binding berberine family protein (Putative tetrahydroberberine oxidase (EC 1.3.3.8))	1.04	0.0014
evm.TU.contig_910.72	Rubber elongation factor protein	–3.49	0.0002
evm.TU.scaffold_1169.303	Receptor-like kinase	–3.47	0.0384
evm.TU.scaffold_1691.492	Protein DETOXIFICATION (Multidrug and toxic compound extrusion protein)	–3.14	0.0039
evm.TU.contig_2092.1	NAD(P)-binding rossmann-fold protein (Putative farnesol dehydrogenase (NAD(+)) (EC 1.1.1.354))	–3.13	0.0291
evm.TU.scaffold_1267.79	Glutathione transferase (EC 2.5.1.18)	–2.71	0.0193
evm.TU.scaffold_1535.1460	GRP family	–1.74	0.0089
evm.TU.scaffold_1034.214	Late embryogenesis abundant protein (Putative Late embryogenesis abundant protein, LEA-14)	–1.71	0.0408
evm.TU.contig_697.245	Putative [Myosin heavy-chain] kinase transcription factor WD40-like family (EC 2.7.11.7) (Transducin/WD40 repeat protein)	–1.63	0.0024
evm.TU.contig_308.447	Putative thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese-related sulfurtransferase)	–1.57	0.0039

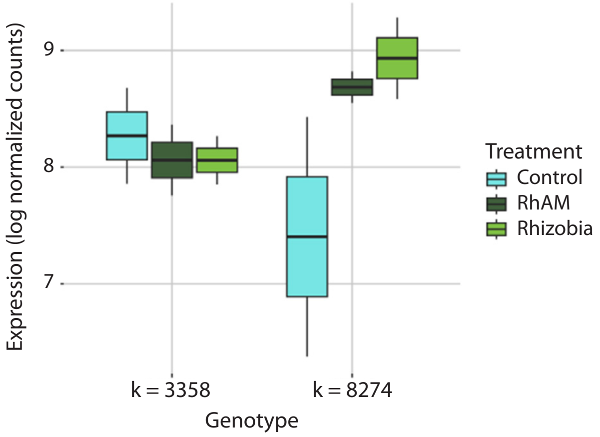

Fig. S1. Expression level of the marker gene *PsGLP2* across all samples.