

Table S1. Significant GO terms of DEGs in the biological process category for *cr-osvp1* vs. NIP.

GO term	GO term annotation	p-value
GO:0005975	carbohydrate metabolic process	0.000452629
GO:0006270	DNA replication initiation	0.00127223
GO:0044723	single-organism carbohydrate metabolic process	0.00137605
GO:0016052	carbohydrate catabolic process	0.001798276
GO:0000272	polysaccharide catabolic process	0.002449886
GO:0006261	DNA-dependent DNA replication	0.002449886
GO:1901615	organic hydroxy compound metabolic process	0.002449886
GO:0055086	nucleobase-containing small molecule metabolic process	0.004657742
GO:0034637	cellular carbohydrate biosynthetic process	0.005137597
GO:0009116	nucleoside metabolic process	0.005277327
GO:1901657	glycosyl compound metabolic process	0.005277327
GO:0015074	DNA integration	0.00598867
GO:0030001	metal ion transport	0.007471242
GO:0009117	nucleotide metabolic process	0.008187998
GO:0000041	transition metal ion transport	0.00925773
GO:0009119	ribonucleoside metabolic process	0.00925773
GO:0006163	purine nucleotide metabolic process	0.010985615
GO:0016051	carbohydrate biosynthetic process	0.012620134
GO:0019693	ribose phosphate metabolic process	0.012620134
GO:0006753	nucleoside phosphate metabolic process	0.013294646
GO:0006457	protein folding	0.013299071
GO:0009150	purine ribonucleotide metabolic process	0.014918978
GO:0009259	ribonucleotide metabolic process	0.014918978
GO:0072521	purine-containing compound metabolic process	0.016464951
GO:0030243	cellulose metabolic process	0.017575992
GO:0030244	cellulose biosynthetic process	0.017575992
GO:0005976	polysaccharide metabolic process	0.02020563
GO:0006260	DNA replication	0.0227723
GO:0042254	ribosome biogenesis	0.026961064
GO:0044262	cellular carbohydrate metabolic process	0.030103584
GO:0006812	cation transport	0.030588976
GO:0005984	disaccharide metabolic process	0.031189821
GO:0010035	response to inorganic substance	0.032249542
GO:0019637	organophosphate metabolic process	0.033753798
GO:0005992	trehalose biosynthetic process	0.03424044
GO:0034470	ncRNA processing	0.034987032
GO:1901135	carbohydrate derivative metabolic process	0.039011051
GO:0006720	isoprenoid metabolic process	0.039286061
GO:0008299	isoprenoid biosynthetic process	0.039286061
GO:0005991	trehalose metabolic process	0.043139143
GO:0033865	nucleoside bisphosphate metabolic process	0.044216301
GO:0033875	ribonucleoside bisphosphate metabolic process	0.044216301
GO:0034032	purine nucleoside bisphosphate metabolic process	0.044216301
GO:0022613	ribonucleoprotein complex biogenesis	0.044338193
GO:0009628	response to abiotic stimulus	0.04769147

Table S2. Significant GO terms of DEGs in the cellular component category for *cr-osvpI* vs. NIP.

GO term	GO term annotation	<i>p</i> -value
GO:0005759	mitochondrial matrix	0.089307
GO:0030529	intracellular ribonucleoprotein complex	0.170143
GO:1990904	ribonucleoprotein complex	0.170143
GO:0030684	preribosome	0.176018
GO:0005840	ribosome	0.262134
GO:0005634	nucleus	0.297766
GO:0005576	extracellular region	0.331895
GO:0043228	non-membrane-bounded organelle	0.353844
GO:0043232	intracellular non-membrane-bounded organelle	0.353844
GO:0015629	actin cytoskeleton	0.390035
GO:0044429	mitochondrial part	0.42238

Table S3. Significant GO terms of DEGs in molecular function category for *cr-osvp1* vs. NIP.

GO term	GO term annotation	p-value
GO:0051087	chaperone binding	5.86E-05
GO:0016160	amylase activity	0.000128886
GO:0016829	lyase activity	0.001108157
GO:0004866	endopeptidase inhibitor activity	0.001733896
GO:0030414	peptidase inhibitor activity	0.001733896
GO:0061134	peptidase regulator activity	0.001733896
GO:0061135	endopeptidase regulator activity	0.001733896
GO:0016161	beta-amylase activity	0.002306814
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	0.005358568
GO:0016759	cellulose synthase activity	0.007989119
GO:0016760	cellulose synthase (UDP-forming) activity	0.007989119
GO:0003887	DNA-directed DNA polymerase activity	0.00880899
GO:0046915	transition metal ion transmembrane transporter activity	0.00880899
GO:0016830	carbon-carbon lyase activity	0.00884685
GO:0046983	protein dimerization activity	0.009577294
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.010286441
GO:0034061	DNA polymerase activity	0.014227469
GO:0060589	nucleoside-triphosphatase regulator activity	0.014993334
GO:0035251	UDP-glucosyltransferase activity	0.017664701
GO:0008081	phosphoric diester hydrolase activity	0.019128854
GO:0046527	glucosyltransferase activity	0.020919177
GO:0004869	cysteine-type endopeptidase inhibitor activity	0.021499904
GO:0030234	enzyme regulator activity	0.022071204
GO:0098772	molecular function regulator	0.028154195
GO:0051082	unfolded protein binding	0.029405228
GO:0034062	5'-3' RNA polymerase activity	0.029795088
GO:0097747	RNA polymerase activity	0.029795088
GO:0001071	nucleic acid binding transcription factor activity	0.030440817
GO:0003700	transcription factor activity, sequence-specific DNA binding	0.030440817
GO:0016836	hydro-lyase activity	0.040843535
GO:0016717	oxidoreductase activity	0.042310743
GO:0004857	enzyme inhibitor activity	0.04253225
GO:0005506	iron ion binding	0.044436051
GO:0003682	chromatin binding	0.048061222

Table S4. Significant GO terms of DEGs in the biological process category for *cr-sdr4* vs. NIP.

GO term	GO term annotation	<i>p</i> -value
GO:0034637	cellular carbohydrate biosynthetic process	5.26E-06
GO:0016051	carbohydrate biosynthetic process	8.04E-06
GO:0005975	carbohydrate metabolic process	2.40E-05
GO:0044262	cellular carbohydrate metabolic process	2.78E-05
GO:0044723	single-organism carbohydrate metabolic process	5.52E-05
GO:0005976	polysaccharide metabolic process	0.00011
GO:0006518	peptide metabolic process	0.00011
GO:0043603	cellular amide metabolic process	0.000127
GO:0015074	DNA integration	0.000217
GO:1901566	organonitrogen compound biosynthetic process	0.000257
GO:0043604	amide biosynthetic process	0.000454
GO:0030243	cellulose metabolic process	0.000456
GO:0030244	cellulose biosynthetic process	0.000456
GO:0043043	peptide biosynthetic process	0.000535
GO:0046351	disaccharide biosynthetic process	0.000551
GO:0005992	trehalose biosynthetic process	0.000652
GO:0006412	translation	0.000728
GO:0006073	cellular glucan metabolic process	0.001014
GO:0044042	glucan metabolic process	0.001014
GO:0044264	cellular polysaccharide metabolic process	0.001014
GO:0005991	trehalose metabolic process	0.001231
GO:0044711	single-organism biosynthetic process	0.001759
GO:0000271	polysaccharide biosynthetic process	0.002136
GO:0009250	glucan biosynthetic process	0.002136
GO:0033692	cellular polysaccharide biosynthetic process	0.002136
GO:0051273	beta-glucan metabolic process	0.002136
GO:0051274	beta-glucan biosynthetic process	0.002136
GO:0055086	nucleobase-containing small molecule metabolic process	0.002577
GO:0005984	disaccharide metabolic process	0.002974
GO:0016052	carbohydrate catabolic process	0.003347
GO:0009312	oligosaccharide biosynthetic process	0.004678
GO:0019693	ribose phosphate metabolic process	0.006543
GO:0006753	nucleoside phosphate metabolic process	0.007568
GO:0016485	protein processing	0.007917
GO:0051604	protein maturation	0.007917
GO:0019637	organophosphate metabolic process	0.007967
GO:0009451	RNA modification	0.008398
GO:0009117	nucleotide metabolic process	0.010853
GO:0009311	oligosaccharide metabolic process	0.013382
GO:0007186	G-protein coupled receptor signaling pathway	0.013419
GO:0010035	response to inorganic substance	0.013419
GO:0006457	protein folding	0.014095

GO:1901615	organic hydroxy compound metabolic process	0.016426
GO:0009150	purine ribonucleotide metabolic process	0.01793
GO:0009259	ribonucleotide metabolic process	0.01793
GO:0006163	purine nucleotide metabolic process	0.018101
GO:0009141	nucleoside triphosphate metabolic process	0.020519
GO:0022613	ribonucleoprotein complex biogenesis	0.020739
GO:0009116	nucleoside metabolic process	0.021504
GO:1901657	glycosyl compound metabolic process	0.021504
GO:0006732	coenzyme metabolic process	0.021919
GO:0019362	pyridine nucleotide metabolic process	0.023367
GO:0046496	nicotinamide nucleotide metabolic process	0.023367
GO:0006091	generation of precursor metabolites and energy	0.024557
GO:0006090	pyruvate metabolic process	0.025808
GO:0044724	single-organism carbohydrate catabolic process	0.026949
GO:0072524	pyridine-containing compound metabolic process	0.029434
GO:0000272	polysaccharide catabolic process	0.029802
GO:0009144	purine nucleoside triphosphate metabolic process	0.030463
GO:0009199	ribonucleoside triphosphate metabolic process	0.030463
GO:0009205	purine ribonucleoside triphosphate metabolic process	0.030463
GO:0009123	nucleoside monophosphate metabolic process	0.030827
GO:0009126	purine nucleoside monophosphate metabolic process	0.030827
GO:0009161	ribonucleoside monophosphate metabolic process	0.030827
GO:0009167	purine ribonucleoside monophosphate metabolic process	0.030827
GO:0044712	single-organism catabolic process	0.031106
GO:0072521	purine-containing compound metabolic process	0.031429
GO:0006733	oxidoreduction coenzyme metabolic process	0.036617
GO:0006298	mismatch repair	0.037715
GO:0009628	response to abiotic stimulus	0.037715
GO:0006096	glycolytic process	0.041382
GO:0006165	nucleoside diphosphate phosphorylation	0.041382
GO:0006757	ATP generation from ADP	0.041382
GO:0009132	nucleoside diphosphate metabolic process	0.041382
GO:0009135	purine nucleoside diphosphate metabolic process	0.041382
GO:0009179	purine ribonucleoside diphosphate metabolic process	0.041382
GO:0009185	ribonucleoside diphosphate metabolic process	0.041382
GO:0042254	ribosome biogenesis	0.041382
GO:0046031	ADP metabolic process	0.041382
GO:0046939	nucleotide phosphorylation	0.041382
GO:0006396	RNA processing	0.042445
GO:0006720	isoprenoid metabolic process	0.044673
GO:0008299	isoprenoid biosynthetic process	0.044673
GO:0046034	ATP metabolic process	0.04527
GO:0043414	macromolecule methylation	0.049958

Table S5. Significant GO terms of DEGs in the cellular component category for *cr-sdr4* vs. NIP.

GO term	GO term annotation	<i>p</i> -value
GO:0030529	intracellular ribonucleoprotein complex	3.98E-07
GO:1990904	ribonucleoprotein complex	3.98E-07
GO:0005840	ribosome	2.00E-06
GO:0043228	non-membrane-bounded organelle	0.001144667
GO:0043232	intracellular non-membrane-bounded organelle	0.001144667
GO:0044444	cytoplasmic part	0.001708308
GO:0005737	cytoplasm	0.007058281
GO:1905368	peptidase complex	0.020354979

Table S6. Significant GO terms of DEGs in molecular function category for *cr-sdr4* vs. NIP.

GO term	GO term annotation	p-value
GO:0003735	structural constituent of ribosome	4.24E-07
GO:0005198	structural molecule activity	5.86E-06
GO:0016759	cellulose synthase activity	7.68E-05
GO:0016760	cellulose synthase (UDP-forming) activity	7.68E-05
GO:0003924	GTPase activity	0.000160535
GO:0035251	UDP-glucosyltransferase activity	0.0007405
GO:0046527	glucosyltransferase activity	0.001083178
GO:0016853	isomerase activity	0.002571872
GO:0019001	guanyl nucleotide binding	0.00848005
GO:0016160	amylase activity	0.008727637
GO:0001883	purine nucleoside binding	0.009998755
GO:0005525	GTP binding	0.009998755
GO:0032549	ribonucleoside binding	0.009998755
GO:0032550	purine ribonucleoside binding	0.009998755
GO:0032561	guanyl ribonucleotide binding	0.009998755
GO:0001882	nucleoside binding	0.011547629
GO:0008194	UDP-glycosyltransferase activity	0.012901332
GO:0016860	intramolecular oxidoreductase activity	0.013341918
GO:0004525	ribonuclease III activity	0.016338449
GO:0032296	double-stranded RNA-specific ribonuclease activity	0.016338449
GO:0008094	DNA-dependent ATPase activity	0.029647611
GO:0016161	beta-amylase activity	0.029647611
GO:0016891	endoribonuclease activity, producing 5'-phosphomonoesters	0.029647611
GO:0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	0.029647611
GO:0017111	nucleoside-triphosphatase activity	0.031092319
GO:0016667	oxidoreductase activity, acting on a sulfur group of donors	0.033158498
GO:0030983	mismatched DNA binding	0.037536005
GO:0008233	peptidase activity	0.038296778
GO:0004521	endoribonuclease activity	0.044420813
GO:0016462	pyrophosphatase activity	0.048551111