

Table S1. Three-way ANOVA results from the comparison of relative expression levels of feeding treatment in *D. rhizophagus*.

	<i>df</i>	<i>AACT</i>		<i>HMGS</i>		<i>HMGR</i>		<i>MK</i>		<i>PMK</i>		<i>MDPC</i>		<i>IPPI</i>		<i>GPPS/FPPS</i>		<i>GGPPS</i>	
		<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>
Sex (S)	1	18.71	<0.001	71.52	<0.001	26.08	<0.001	31.07	<0.001	175.83	<0.001	27.39	<0.001	42.40	<0.001	7.71	0.008	0.20	0.65
Condition (C)	1	0.59	0.45	2.18	0.15	1.90	0.17	26.56	<0.001	2.31	0.14	23.82	<0.001	12.49	0.001	32.33	<0.001	9.96	0.003
Time (t)	1	18.64	<0.001	1.07	0.31	0.042	0.84	8.96	0.005	18.73	<0.001	1.74	0.19	1.87	0.18	5.74	0.021	2.08	0.16
S*C	1	0.93	0.34	0.95	0.33	3.29	0.077	0.72	0.400	12.04	0.001	4.86	0.033	7.47	0.009	1.11	0.29	1.53	0.22
S*t	1	0.003	0.96	2.82	0.10	0.32	0.57	3.15	0.084	13.78	<0.001	9.18	0.004	3.95	0.054	4.77	0.035	5.31	0.026
C*t	1	0.93	0.34	0.69	0.41	0.76	0.39	3.24	0.079	11.51	0.002	11.62	0.002	0.19	0.66	2.40	0.13	5.10	0.029
S*C*t	1	0.006	0.94	1.77	0.19	0.13	0.72	0.85	0.36	17.72	<0.001	23.11	<0.001	2.20	0.14	7.98	0.007	1.22	0.28

Bold fonts indicate significant difference.

Table S2. Two-way ANOVA results from the comparison of relative expression levels of JH III treatment in *D. rhizophagus*.

	<i>df</i>	<i>AACT</i>		<i>HMGS</i>		<i>HMGR</i>		<i>MK</i>		<i>PMK</i>		<i>MDPC</i>		<i>IPPI</i>		<i>GPPS/FPPS</i>		<i>GGPPS</i>	
		<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>
Sex (S)	1	0.76	0.39	1.09	0.31	17.73	<0.001	67.89	<0.001	2.15	0.16	5.56	0.029	0.30	0.59	4.69	0.043	0.81	0.38
Time (t)	1	0.23	0.64	8.36	0.009	17.77	<0.001	5.17	0.034	88.42	<0.001	3.33	0.083	0.34	0.57	0.66	0.42	7.09	0.015
S*t	1	9.29	0.006	11.21	0.003	22.51	<0.001	98.87	<0.001	0.049	0.83	2.95	0.10	4.62	0.044	9.58	0.006	4.13	0.056

Bold fonts indicate significant difference.

Table S3. Tukey's test comparisons for JH III treatment in *D. rhizophagus*.

<i>AACT</i>							<i>MDPC</i>						
Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050	Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050
Sex	Males vs. Females	0.285	2	1.229	0.395	No	Sex	Males vs. Females	2.57	2	3.336	0.029	Yes
Time	8.000 vs. 24.000	0.157	2	0.676	0.638	No	Time	8.000 vs. 24.000	1.99	2	2.582	0.083	No
Time within Males	8.000 vs. 24.000	1.157	2	3.527	0.022	Yes	Time within Males	8.000 vs. 24.000	0.118	2	0.108	0.94	No
Time within Females	8.000 vs. 24.000	0.844	2	2.571	0.084	No	Time within Females	8.000 vs. 24.000	3.862	2	3.544	0.021	Yes
Sex within 8	Males vs. Females	0.715	2	2.18	0.139	No	Sex within 8	Males vs. Females	0.698	2	0.641	0.655	No
Sex within 24	Males vs. Females	1.285	2	3.918	0.012	Yes	Sex within 24	Males vs. Females	4.442	2	4.076	0.009	Yes
<i>HMGS</i>							<i>IPPI</i>						
Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050	Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050
Sex	Males vs. Females	0.533	2	1.477	0.309	No	Sex	Males vs. Females	0.359	2	0.775	0.59	No
Time	8.000 vs. 24.000	1.476	2	4.089	0.009	Yes	Time	8.000 vs. 24.000	0.38	2	0.819	0.569	No
Time within Males	8.000 vs. 24.000	3.185	2	6.239	<0.001	Yes	Time within Males	8.000 vs. 24.000	1.029	2	1.571	0.28	No
Time within Females	8.000 vs. 24.000	0.233	2	0.457	0.75	No	Time within Females	8.000 vs. 24.000	1.788	2	2.73	0.068	No
Sex within 8	Males vs. Females	1.176	2	2.303	0.119	No	Sex within 8	Males vs. Females	1.05	2	1.602	0.271	No
Sex within 24	Males vs. Females	2.243	2	4.392	0.006	Yes	Sex within 24	Males vs. Females	1.768	2	2.698	0.071	No
<i>HMGR</i>							<i>GPSS/FPSS</i>						
Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050	Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050
Sex	Males vs. Females	0.461	2	5.956	<0.001	Yes	Sex	Males vs. Females	0.116	2	3.064	0.043	Yes
Time	8.000 vs. 24.000	0.461	2	5.962	<0.001	Yes	Time	8.000 vs. 24.000	0.0437	2	1.151	0.425	No
Time within Males	8.000 vs. 24.000	0.98	2	8.96	<0.001	Yes	Time within Males	8.000 vs. 24.000	0.122	2	2.28	0.123	No
Time within Females	8.000 vs. 24.000	0.0579	2	0.529	0.712	No	Time within Females	8.000 vs. 24.000	0.21	2	3.909	0.012	Yes
Sex within 8	Males vs. Females	0.98	2	8.956	<0.001	Yes	Sex within 8	Males vs. Females	0.0498	2	0.928	0.519	No
Sex within 24	Males vs. Females	0.0584	2	0.533	0.71	No	Sex within 24	Males vs. Females	0.282	2	5.261	0.002	Yes
<i>MK</i>							<i>GGPSS</i>						
Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050	Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050
Sex	Males vs. Females	0.471	2	11.653	<0.001	Yes	Sex	Males vs. Females	0.528	2	1.276	0.378	No
Time	8.000 vs. 24.000	0.13	2	3.216	0.034	Yes	Time	8.000 vs. 24.000	1.558	2	3.765	0.015	Yes
Time within Males	8.000 vs. 24.000	0.439	2	7.669	<0.001	Yes	Time within Males	8.000 vs. 24.000	2.746	2	4.695	0.004	Yes
Time within Females	8.000 vs. 24.000	0.699	2	12.218	<0.001	Yes	Time within Females	8.000 vs. 24.000	0.369	2	0.63	0.661	No
Sex within 8	Males vs. Females	0.0975	2	1.704	0.243	No	Sex within 8	Males vs. Females	1.716	2	2.934	0.051	No
Sex within 24	Males vs. Females	1.04	2	18.183	<0.001	Yes	Sex within 24	Males vs. Females	0.661	2	1.13	0.434	No
<i>PMK</i>													
Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050	Comparisons for factor	Comparison	Diff of Means	p	q	P	P<0.050
Sex	Males vs. Females	0.0878	2	2.072	0.159	No	Sex	Males vs. Females	0.0878	2	2.072	0.159	No
Time	8.000 vs. 24.000	0.564	2	13.298	<0.001	Yes	Time	8.000 vs. 24.000	0.564	2	13.298	<0.001	Yes
Time within Males	8.000 vs. 24.000	0.55	2	9.181	<0.001	Yes	Time within Males	8.000 vs. 24.000	0.55	2	9.181	<0.001	Yes
Time within Females	8.000 vs. 24.000	0.577	2	9.626	<0.001	Yes	Time within Females	8.000 vs. 24.000	0.577	2	9.626	<0.001	Yes
Sex within 8	Males vs. Females	0.101	2	1.688	0.247	No	Sex within 8	Males vs. Females	0.101	2	1.688	0.247	No
Sex within 24	Males vs. Females	0.0745	2	1.243	0.39	No	Sex within 24	Males vs. Females	0.0745	2	1.243	0.39	No

Table S4. Tukey's test comparisons for feeding treatment in *D. rhizophagus*.

AACT

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	1.826	2	6.118	<0.001	Yes
Condition	Paired vs. Solitary	0.325	2	1.087	0.447	No
Time	8.000 vs. 24.000	1.822	2	6.105	<0.001	Yes
Condition within Males	Paired vs. Solitary	0.732	2	1.733	0.228	No
Condition within Females	Paired vs. Solitary	0.0826	2	0.196	0.891	No
Sex within Solitary	Males vs. Females	1.419	2	3.362	0.022	Yes
Sex within Paired	Males vs. Females	2.233	2	5.29	<0.001	Yes
Time within Males	8.000 vs. 24.000	1.799	2	4.262	0.005	Yes
Time within Females	8.000 vs. 24.000	1.846	2	4.372	0.004	Yes
Sex within 8	Males vs. Females	1.849	2	4.381	0.004	Yes
Sex within 24	Males vs. Females	1.803	2	4.271	0.005	Yes
Time within Solitary	8.000 vs. 24.000	1.414	2	3.35	0.023	Yes
Time within Paired	8.000 vs. 24.000	2.23	2	5.284	<0.001	Yes
Condition within 8	Paired vs. Solitary	0.0836	2	0.198	0.889	No
Condition within 24	Paired vs. Solitary	0.733	2	1.736	0.227	No

HMGS

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	5.604	2	11.96	<0.001	Yes
Condition	Paired vs. Solitary	0.978	2	2.088	0.148	No
Time	8.000 vs. 24.000	0.686	2	1.464	0.307	No
Condition within Males	Paired vs. Solitary	1.626	2	2.453	0.091	No
Condition within Females	Paired vs. Solitary	0.331	2	0.5	0.726	No
Sex within Solitary	Males vs. Females	4.957	2	7.48	<0.001	Yes
Sex within Paired	Males vs. Females	6.251	2	9.434	<0.001	Yes
Time within Males	8.000 vs. 24.000	1.799	2	2.715	0.062	No
Time within Females	8.000 vs. 24.000	0.428	2	0.645	0.651	No
Sex within 8	Males vs. Females	6.718	2	10.137	<0.001	Yes
Sex within 24	Males vs. Females	4.491	2	6.777	<0.001	Yes
Time within Solitary	8.000 vs. 24.000	0.132	2	0.199	0.889	No
Time within Paired	8.000 vs. 24.000	1.24	2	1.871	0.193	No
Condition within 8	Paired vs. Solitary	1.532	2	2.312	0.11	No
Condition within 24	Paired vs. Solitary	0.424	2	0.64	0.653	No

HMGR

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	4.029	2	7.223	<0.001	Yes
Condition	Paired vs. Solitary	1.089	2	1.952	0.175	No
Time	8.000 vs. 24.000	0.162	2	0.291	0.838	No
Condition within Males	Paired vs. Solitary	2.519	2	3.194	0.03	Yes
Condition within Females	Paired vs. Solitary	0.342	2	0.433	0.761	No
Sex within Solitary	Males vs. Females	2.598	2	3.294	0.025	Yes
Sex within Paired	Males vs. Females	5.459	2	6.921	<0.001	Yes
Time within Males	8.000 vs. 24.000	0.608	2	0.771	0.589	No
Time within Females	8.000 vs. 24.000	0.284	2	0.36	0.801	No
Sex within 8	Males vs. Females	4.475	2	5.673	<0.001	Yes
Sex within 24	Males vs. Females	3.583	2	4.542	0.003	Yes
Time within Solitary	8.000 vs. 24.000	0.849	2	1.076	0.451	No
Time within Paired	8.000 vs. 24.000	0.525	2	0.665	0.641	No
Condition within 8	Paired vs. Solitary	0.402	2	0.51	0.721	No
Condition within 24	Paired vs. Solitary	1.776	2	2.251	0.119	No

MK

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	0.8	2	7.883	<0.001	Yes
Condition	Paired vs. Solitary	0.739	2	7.288	<0.001	Yes
Time	8.000 vs. 24.000	0.429	2	4.233	0.005	Yes
Condition within Males	Paired vs. Solitary	0.861	2	6.004	<0.001	Yes
Condition within Females	Paired vs. Solitary	0.617	2	4.303	0.004	Yes
Sex within Solitary	Males vs. Females	0.678	2	4.724	0.002	Yes
Sex within Paired	Males vs. Females	0.922	2	6.425	<0.001	Yes
Time within Males	8.000 vs. 24.000	0.684	2	4.767	0.002	Yes
Time within Females	8.000 vs. 24.000	0.175	2	1.219	0.394	No
Sex within 8	Males vs. Females	1.054	2	7.349	<0.001	Yes
Sex within 24	Males vs. Females	0.545	2	3.8	0.011	Yes
Time within Solitary	8.000 vs. 24.000	0.171	2	1.193	0.404	No
Time within Paired	8.000 vs. 24.000	0.688	2	4.794	0.002	Yes
Condition within 8	Paired vs. Solitary	0.998	2	6.954	<0.001	Yes
Condition within 24	Paired vs. Solitary	0.481	2	3.353	0.023	Yes

PMK

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	4.16	2	18.75	<0.001	Yes
Condition	Solitary vs. Paired	0.477	2	2.15	0.136	No
Time	8.000 vs. 24.000	1.358	2	6.12	<0.001	Yes
Sex within Solitary-8h	Males vs. Females	7.733	2	17.43	<0.001	Yes
Sex within Paired-8h	Males vs. Females	2.915	2	6.57	<0.001	Yes
Condition within Males-8	Solitary vs. Paired	3.951	2	8.90	<0.001	Yes
Sex within 24	Males vs. Females	2.995	2	9.55	<0.001	Yes

MDPC

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	0.837	2	7.401	<0.001	Yes
Condition	Solitary vs. Paired	0.781	2	6.903	<0.001	Yes
Time	8.000 vs. 24.000	0.211	2	1.866	0.195	NO
Sex within Paired-8h	Males vs. Females	2.444	2	10.8	<0.001	Yes
Condition within Males-8	Solitary vs. Paired	2.448	2	10.82	<0.001	Yes

IPPI

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	1.575	2	9.209	<0.001	Yes
Condition	Paired vs. Solitary	0.855	2	4.999	0.001	Yes
Time	8.000 vs. 24.000	0.331	2	1.932	0.18	No
Condition within Males	Paired vs. Solitary	1.517	2	6.269	<0.001	Yes
Condition within Females	Paired vs. Solitary	0.194	2	0.801	0.574	No
Sex within Solitary	Males vs. Females	0.914	2	3.778	0.011	Yes
Sex within Paired	Males vs. Females	2.237	2	9.246	<0.001	Yes
Time within Males	8.000 vs. 24.000	0.812	2	3.354	0.023	Yes
Time within Females	8.000 vs. 24.000	0.15	2	0.622	0.663	No
Sex within 8	Males vs. Females	2.056	2	8.5	<0.001	Yes
Sex within 24	Males vs. Females	1.094	2	4.524	0.003	Yes
Time within Solitary	8.000 vs. 24.000	0.223	2	0.921	0.519	No
Time within Paired	8.000 vs. 24.000	0.438	2	1.811	0.208	No
Condition within 8	Paired vs. Solitary	0.963	2	3.98	0.008	Yes
Condition within 24	Paired vs. Solitary	0.748	2	3.09	0.035	Yes

GPSS/FPPS

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	0.246	2	3.926	0.008	Yes
Condition	Solitary vs. Paired	0.504	2	8.041	<0.001	Yes
Time	8.000 vs. 24.000	0.212	2	3.389	0.021	Yes
Sex within Paired-8h	Males vs. Females	0.783	2	6.251	<0.001	Yes
Condition within Males-8	Solitary vs. Paired	0.71	2	5.668	<0.001	Yes
Condition within 24 h	Solitary vs. Paired	0.641	2	7.236	<0.001	Yes

GGPPS

Comparisons for factor	Comparison	Diff of Means	p		P	P<0.050
			p	q		
Sex	Males vs. Females	0.103	2	0.636	0.655	No
Condition	Paired vs. Solitary	0.72	2	4.463	0.003	Yes
Time	8.000 vs. 24.000	0.329	2	2.039	0.157	No
Condition within Males	Paired vs. Solitary	0.438	2	1.919	0.183	No
Condition within Females	Paired vs. Solitary	1.002	2	4.393	0.004	Yes
Sex within Solitary	Males vs. Females	0.385	2	1.687	0.24	No
Sex within Paired	Males vs. Females	0.18	2	0.787	0.581	No
Time within Males	8.000 vs. 24.000	0.197	2	0.864	0.545	No
Time within Females	8.000 vs. 24.000	0.855	2	3.747	0.012	Yes
Sex within 8	Males vs. Females	0.423	2	1.855	0.197	No
Sex within 24	Males vs. Females	0.629	2	2.755	0.059	No
Time within Solitary	8.000 vs. 24.000	0.187	2	0.818	0.567	No
Time within Paired	8.000 vs. 24.000	0.844	2	3.701	0.013	Yes
Condition within 8	Paired vs. Solitary	1.236	2	5.415	<0.001	Yes
Condition within 24	Paired vs. Solitary	0.205	2	0.897	0.53	No

Table S5. Primers designed for cloning and RT-qPCR analysis of MVA pathway genes in *D. rhizophagus*.

Gene	Primers sequences (5' → 3')	Location of amplicon & Amplicon length (bp)	Application	Annealing temperature (°C) & Extension time (s)
<i>AACT</i>	F GGC GAA TGC CTC CAC TTT G	834-893 60 bp	RT-qPCR (Assay ID. AI6RPRP)	60 °C / 60 s
	R GCC GCT CTT GTG GTT AAA ATC AG			
	P CCG CAG CTC CGT CAT T			
<i>HMGS</i>	F TGT TAC CAG CTT TAC TGC CAG AAG	667-733 67 bp	RT-qPCR (Assay ID. AI70NXX)	“
	R CAA ACG ACT CAA TAC TCA CAG GCT			
	P CTG CAA CAG CTT TTC C			
<i>HMGR</i>	F CCA AGC TCC TTG AAA ACT TAC CTT TT	1382-1480 99 bp	RT-qPCR (Assay ID. AI89L35)	“
	R CCA CTG GTA TTG GCA TGT ATC CA			
	P CAC GCA CCC ATG ACC AA			
<i>MK</i>	F GGT GTG TAC TTT TGG CAA TAT GGT	762-862 101 bp	RT-qPCR (Assay ID. AIAA09Y)	“
	R GCA CTT TGC TAT TTA CGA GCA GTA A			
	P CCG TCG TTC ATC TCT C			
<i>PMK</i>	F ACT TGG AGT GAT GAA ATC AGA AAG GG	220-287 68 bp	RT-qPCR (Assay ID. AIBJZF6)	“
	R GCC GCT GAT TTG CAA GCT			
	P CCG GGC TAC TTT TGC A			
<i>MDPC</i>	F GAC AGG GTT CTG GAA GTG CAT	413-476 64 bp	RT-qPCR (Assay ID. AICSXME)	“
	R TCA CCC TTG TGC CAT TGC A			
	P CCA ACC ACC ATA AAT AC			
<i>IPPI</i>	F AGA CAG CAT TCC CAT TGA CAG TAT TAA	432-520 89 bp	RT-qPCR (Assay ID. AID1VSM)	“
	R TT			
	P CGA TCT CAT GCT CGC CAT ATT TG			
<i>GPPS/FPFS</i>	F GCC AAA ACG ATC CTG ATG GAA ATG	910-978 69 bp	RT-qPCR (Assay ID. AIFATYU)	“
	R GCC GAA GCA ATC CAG AAA ATC G			
	P TTG AAT CTG GAA AAA CTG			
<i>GGPPS</i>	F CAC CTG TCC CTC TGA GGA AGA	417-491 75 bp	RT-qPCR (Assay ID. AIGJR42)	“
	R CTG ATG GCC AGC ATG AAC AAC			
	P CCG CCC GTT TTT CGA G			
<i>CYP4G55v1</i>	F GACTATGCAATGGCTGTGATGAAG	688-768 81 bp	RT-qPCR (Assay ID. AIS065U) [40]	“
	R GATGTAGTCGGAGTAAAGCCAGATT			
	P CTGTGCGACATTCTC			
<i>AACT</i>	F AAC ATT TAG ACT CAG CTA TTG GG	1340 bp	cDNA cloning	61 °C / 80 s
	R ACA ACT ACT CGA ACA TGA ACG C			
<i>HMGS</i>	F ATG AGT GCC TGG CCT GAA GAT GTG	1374 bp	cDNA cloning	66 °C / 85 s
	R CTA TGA GTG GCC GTT GGT GAT CAT			
<i>HMGR</i>	F1 GGA ATA ACT TGG ATA TTC TCA TCT G	500 bp	cDNA cloning	60 °C / 35 s
	R1 GTG TCT CTA CCA GTG TAT CTA AAG	1155 bp		58 °C / 75 s
	F2 GCT CAA TTC GCT CTT AAT GGG G			
	R2 AGC TCT ACA TCC TCT ATT AGT GC	991 bp		60 °C / 60 s
	F3 GCT TCT GGA TGG TCG TGA GTT GTA			
	R3 TAA GGT AGT GGA TCG GTT GTG C	400 bp		60 °C / 35 s
	F4 ATA GGT GGA TTC AAC GCT CAT GCT G			
	R4 GCT ACA TTT TTA AGC ATT GTC TTG GC			
<i>MK</i>	F GCA AAC TTT AAC TAC CAA GCA GTG	1350 bp	cDNA cloning	64 °C / 85 s
	R TTA ATC AAC TCT AAC CCC TGG AC			
<i>PMK</i>	F GCG AAA TTA AGA ATC AGT AAT ACC T	511 bp	cDNA cloning	62 °C / 40 s
	R AAA TCG TCT AGG TCG CAT TCG	550 bp		62 °C / 40 s
	F CTG GTA AAG ACT TCA TTT GTG AG			
R CTA TAT TGT GCC GCC ACC AAA GG				
<i>MDPC</i>	F ATT CCT AAA GTA GCG AGT TGT G	1200 bp	cDNA cloning	61 °C / 75 s
	R GCA CCG TTC ATC AGT TTG ACT TCA			
<i>IPPI</i>	F GTT TAT CAG TGG ACC ATT GTG CTG	1100 bp	cDNA cloning	59 °C / 65 s
	R GTT CTT AAA CAT AGA TGA CTA GCA G			
<i>GPPS/FPFS</i>	F ATG TTT TCG ATG AAA ATG TGC CGC	1290 bp	cDNA cloning	63 °C / 80 s
	R TCC CTA AGG AGC TTC TAA CAC TCG			
<i>GGPPS</i>	F ACC ACA AAA CCT TTC CCA AAT T	1000 bp	cDNA cloning	56 °C / 60 s
	R TTC CTG GAA TTA TTA CAA GAA CTT			

*F: Forward, R: Reverse, P: TaqMan™ Probe.

Table S6. Minimum Information for Publication of Quantitative Real-Time PCR Experiments (MIQE) checklist.

Item to check	Details
Experimental design	
Definition of experimental and control groups	yes, included in the manuscript
Number within each group	yes, included in the manuscript
Assay carried out by the core or investigator's laboratory?	yes, all experiments were performed in our laboratory
Acknowledgment of authors' contributions	yes, included in the manuscript
Sample	
Description	yes, included in the manuscript
Volume/mass of sample processed	yes, included in the manuscript
Microdissection or macrodissection	yes, included in the manuscript
Processing procedure	yes, included in the manuscript
If frozen, how and how quickly?	this does not apply
If fixed, with what and how quickly?	this does not apply
Sample storage conditions and duration (especially for FFPEb samples)	this does not apply
Nucleic acid extraction	
Procedure and/or instrumentation	yes, we followed the manufacturer's protocol without modification
Name of kit and details of any modifications	yes, included in the manuscript. We used a commercial RiboPure™ kit (Ambion by Life Technologies, Cat. No. AM1924)
Source of additional reagents used	this does not apply, as we did not use any other additional reagent
Details of DNase or RNase treatment	we did not perform DNase or RNase treatment
Contamination assessment (DNA or RNA)	this was evaluated by means of A ₂₆₀ /A ₂₈₀ absorbance
Nucleic acid quantification	
Instrument and method	yes, this is included in the manuscript
Purity (A ₂₆₀ /A ₂₈₀)	yes, this was evaluated
Yield	yes, we described the yield estimation in the manuscript
RNA integrity: method/instrument	yes, we described the yield estimation in the manuscript
RIN/RQI or C _q of 3' and 5' transcripts	this was not evaluated
Electrophoresis traces	yes, included in the manuscript
Inhibition testing (C _q dilutions, spike, or other)	this was not evaluated
Reverse transcription	
Complete reaction conditions	yes, we followed all manufacturer's protocols with no single modification
Amount of RNA and reaction volume	yes, included in the manuscript
Priming oligonucleotide (if using GSP) and concentration	this does not apply
Reverse transcriptase and concentration	the information is not provided by the manufacturer
Temperature and time	we followed manufacturer's protocol: 37°C for 60 minutes and 95°C for 5 minutes
Manufacturer of reagents and catalogue numbers	yes, included in the manuscript. We used a commercial High Capacity RNA to cDNA kit (Applied Biosystems, USA; Cat. No. 4387406)
C _q s with and without reverse transcription	this was not evaluated
Storage conditions of cDNA	yes, included in the manuscript
qPCR target information	
Gene symbol	yes, included in the manuscript
Sequence accession number	yes, included in the manuscript
Location of amplicon	yes, included in the supplementary data
Amplicon length	yes, included in the supplementary data
In silico specificity screen (BLAST, and so on)	yes, this was done by the manufacturer (Applied Biosystems)
Pseudogenes, retropseudogenes, or other homologs?	does not apply
Sequence alignment	yes, this was done by the manufacturer (Applied Biosystems)
Secondary structure analysis of amplicon	yes, this was done by the manufacturer (Applied Biosystems)
Location of each primer by exon or intron (if applicable)	does not apply
What splice variants are targeted?	does not apply
qPCR oligonucleotides	
Primer sequences	yes, included in the supplementary data
RTPrimerDB identification number	does not apply
Probe sequences	yes, included in the supplementary data
Location and identity of any modifications	does not apply
Manufacturer of oligonucleotides	yes, included in the manuscript

Purification method	the information provided by the manufacturer indicates that oligonucleotides are purified via Transgenomic Wave HPLC. The method is proprietary
qPCR protocol	
Complete reaction conditions	yes, included in the manuscript
Reaction volume and amount of cDNA/DNA	yes, included in the manuscript
Primer, (probe), Mg ²⁺ , and dNTP concentrations	yes, concentration of the primers and probe are in the manuscript; however, the concentration of the master mix is not provided by the manufacturer
Polymerase identity and concentration	AmpliAq Gold® DNA polymerase, UP; dNTPs with dUTP; ROX™ passive reference; optimized buffer components.
Buffer/kit identity and manufacturer	this is included along with the PCR master mix II (Cat No. 4427788), but the information is not provided by the manufacturer
Exact chemical composition of the buffer	this is included along with the PCR master mix II (Cat No. 4427788), but the information is not provided by the manufacturer
Additives (SYBR Green I, DMSO, and so forth)	does not apply
Manufacturer of plates/tubes and catalog number	only 48-well plates were used (MicroAmp™, Cat. No.4375816) and optical adhesive film (MicroAmp™, Cat. No. 4375928) (Applied Biosystems, USA)
Complete thermocycling parameters	yes, included in the manuscript
Reaction setup (manual/robotic)	manual
Manufacturer of qPCR instrument	yes, included in the manuscript
qPCR validation	
Evidence of optimization (from gradients)	yes, available upon request
Specificity (gel, sequence, melt, or digest)	yes, this is described in the manuscript
For SYBR Green I, C _q of the NTC	does not apply
Calibration curves with slope and y intercept	yes, available upon request
PCR efficiency calculated from slope	yes, available upon request
CIs for PCR efficiency or SE	yes, available upon request
r ² of calibration curve	yes, this is described in the manuscript
Linear dynamic range	yes, they are available upon request
C _q variation at LOD	this does not apply
CIs throughout range	yes, available upon request
Evidence for LOD	this does not apply
If multiplex, efficiency and LOD of each assay	this does not apply
Data analysis	
qPCR analysis program (source, version)	yes, included in the manuscript.
Method of C _q determination	C _q is determined by the StepOne™ Software v2.3 in the geometric phase where the standard deviation between replicates is minor
Outlier identification and disposition	Outliers were automatically identified by the qPCR instrument software. Once this, they were eliminated from the analysis. However, when only one out of three group replicates were eliminated, the remaining two were subsequently used in the analysis
Results for NTCs	yes, this was not reported
Justification of number and choice of reference genes	does not apply
Description of normalization method	yes, included in the manuscript
Number and concordance of biological replicates	yes, included in the manuscript
Number and stage (reverse transcription or qPCR) of technical replicates	yes, included in the manuscript
Repeatability (intraassay variation)	yes, we estimated this as SD for the C _q variance and are available upon request
Reproducibility (interassay variation, CV)	does not apply
Power analysis	this was not evaluated
Statistical methods for results significance	yes, included in the manuscript
Software (source, version)	yes, included in the manuscript. The program used for the analysis was SigmaStat v. 3.5.
C _q or raw data submission with RDML	this was not reported