

Supplementary Materials: Smilansky *et al.*

Table S1. Top 10 BLASTn hits of the *Perkinsea* PPC and NAG01a-c probes. Top 10 BLASTn hits of the (A) PPC_P1 probe and (B) NAG01a-c_P1 probe against NCBI nr database (checked November 2020). The top hits were the corresponding PPC or NAG01a-c *Perkinsus* sequences (highlighted in grey), with the remaining hits showing a reduced query coverage/percentage identity

A. Top 10 BLAST hits for PPC probe

Description	Total score	Query coverage	E-value	Percentage identity	Accession no.
<i>Accessions:</i> MF103770.1; MF103771.1; KY679209.1 - KY679301.1; KP122566.1 - KP122569.1; EF675616.1	42.1	100%	0.14	100%	<i>See Description</i>
<i>Comamonas thiooxydans</i> strain QYY chromosome, complete genome	36.2	85%	8.7	100%	CP053920.1
<i>Podospora comata</i> strain T genome assembly, chromosome: 6	36.2	85%	8.7	100%	LR026969.1
<i>Comamonas thiooxydans</i> strain CNB-1 substr. CNB-2 chromosome, complete genome	36.2	85%	8.7	100%	CP001220.2
<i>Haloarcula hispanica</i> N601 plasmid pHH406, complete sequence	36.2	85%	8.7	100%	CP006887.1
<i>Comamonas thiooxydans</i> strain ZDHYF418 chromosome, complete genome	36.2	85%	8.7	100%	CP063057.1
<i>Streptomyces</i> sp. SCUT-3 chromosome, complete genome	36.2	85%	8.7	100%	CP046907.1
<i>Haloarcula hispanica</i> ATCC 33960 plasmid pHH400, complete sequence	36.2	85%	8.7	100%	CP002923.1
PREDICTED: <i>Esox lucius</i> interferon-related developmental regulator 2 (ifrd2), transcript variant X2, mRNA	34.2	80%	34	100%	XM_010895846.3
PREDICTED: <i>Esox lucius</i> interferon-related developmental regulator 2 (ifrd2), transcript variant X1, mRNA	34.2	80%	34	100%	XM_010895845.3

B. Top 10 BLAST hits for NAG01a-c probe

Description	Total score	Query coverage	E-value	Percentage identity	Accession no.
Accessions: MH009692.1; KP122529.1; KP122530.1; KP122544.1; KP122558.1 - KP122565.1; KP122570.1 - KP122639.1; KP122642.1 - KP122724.1; KP122726.1; KP122728.1 - KP122738.1; KP122740.1; KP122742.1 - KP122747.1; JX471030.1 - JX471032.1; JX471023.1; JX471024.1; FJ410727.1; FJ410723.1; FJ410700.1; FJ410512.1	46.1	100%	0.013	100%	See Description
Accessions: MH023176.1; MH022915.1; MH009782.1; MH009666.1; MH009655.1; MH009169.1; MH009123.1; MH008709.1; MH008586.1; KP122545.1 - KP122550.1; KP122552.1 KP122557.1; AB996680.1; AB996658.1; GU067813.1; FJ410549.1; EF196787.1; DQ244038.1	42.1	91%	0.21	100%	See Description
Accessions: JN547327.1; FJ410785.1; FJ410767.1; FJ410742.1; FJ410730.1; FJ410726.1; FJ410687.1; FJ410674.1; EF196788.1; AY919735.1	40.1	86%	0.83	100%	See Description
Accessions: MH009023.1; KP122739.1; KP122727.1; KP122725.1; KP122641.1; KP122640.1; KP122551.1	38.2	82-100%	3.3	95.65-100%	See Description
<i>Cyanothece</i> sp. PCC 7424, complete genome	38.2	82%	3.3	100%	CP001291.1
PREDICTED: <i>Anarrhichthys ocellatus</i> lon peptidase 2, peroxisomal (lonp2), transcript variant X2, mRNA	36.2	78%	13	100%	XM_031874384.1
PREDICTED: <i>Anarrhichthys ocellatus</i> lon peptidase 2, peroxisomal (lonp2), transcript variant X1, mRNA	36.2	78%	13	100%	XM_031874383.1
PREDICTED: <i>Marmota flaviventris</i> olfactory receptor 6M1 (LOC114088773), mRNA	36.2	78%	13	100%	XM_027930480.1
Uncultured eukaryote isolate P578 small subunit ribosomal RNA gene, partial sequence	36.2	78%	13	100%	MH009066.1
PREDICTED: <i>Marmota marmota marmota</i> olfactory receptor 6M1 (LOC107145971), mRNA	36.2	78%	13	100%	XM_015490031.1