Supplementary Table 1. Cultures of *Pseudo-nitzschia* spp. used in the present study (nb: the collection references of the strains have also been added to enable comparisons with other studies). (A) stands for strains isolated in the Atlantic and (EC) for strains from the English Channel.

Species	**Collection reference**	**Name present study**	**Collection date**	**Station**	**GPS Coordinates (approximative)**
P. australis	P1D2	Pa1	28/03/14	Anse de Dinan, Camaret-sur-Mer (A)	48.225679; -4.563602
P. australis	P3B2	Pa2	04/04/14	Môle St Anne, Plouzané (A)	48.358573; -4.551193
P.australis	IFR-PAU-010	Pa3	14/07/15	Ouessant (A)	48.449511; -5.108088
P. fraudulenta	PNfra2	Pf1	24/08/11	Cabourg (EC)	49.302888; -0.103549
P. fraudulenta	PNfra31	Pf2	11/07/11	COMOR 41(EC)	49.414444; -0.408889
P. pungens	PNpun47	Pp1	24/08/11	Cabourg (EC)	49.302888; -0.103549
P. pungens	PNpun102	Pp2	21/08/12	Luc sur Mer (EC)	49.320109; -0.351193

Supplementary Table 2. Reference transcriptomes statistics

	Samples	**Transcripts**	**Total length**	**Annotated**	**Considered for DE analyses**	**Mean coverage per transcript****	**Considered for clustering**
P. australis	35*	99,935	75,394,910	38,919	32,371	26-74-345	20,663
P. fraudulenta	12	50,449	43,415,564	17,265	16,045	64-375-1343	2,057
P. pungens	22	65,902	46,434,497	20,737	20,535	37-145-685	3,390
Interspecific	69	6,557	Pa :16,840,898 Pf :19,994,148 Pp :16,412,818	4,151	6,557	394-877-1,951	2,325

*For computing reasons, only 18 samples (2 replicates per strain and per condition) were used to obtain the reference transcriptome.

**First quartile, Median, and Third quartile of the mean coverage per transcripts considered for DE analyses, respectively.

Supplementary Table 3: Transcriptome wide genetic distances between strains

Species	Strains	Number of SNPs	Pairwise genetic distance
P. australis	Pa1, Pa2	14,878	$3.00\ 10^{-4}$
	Pa1, Pa3	15,283	$3.08\ 10^{-4}$
	Pa2, Pa3	14,655	$2.95\ 10^{-4}$
P. fraudulenta	Pf1, Pf2	24,132	$4.77\ 10^{-4}$
P. pungens	Pp1, Pp2	103,723	$2.07\ 10^{-3}$

Supplementary Table 4. DA biosynthesis (dab) gene cluster in the three reference transcriptomes

Species	*dab* gene	Identifier in reference transcriptome	Blastn e-value
P. australis	*dabA*	comp50001_c0_seq1	0.0
	dabB	comp42388_c0_seq2	6e-125
	dabC	comp12082_c0_seq1	0.0
	dabD	comp40532_c0_seq1	0.0
P. pungens	*dabA*	comp74256_c0_seq1	2e-43
	dabB	NA	
	dabC	NA	
	dabD	comp49085_c0_seq1	8e-177
P. fraudulenta	*dabA*	NA	
	dabB	NA	
	dabC	NA	
	dabD	comp60317_c0_seq1	6e-93

Supplementary Table 5: For each expression profile (Cluster), Gene ontology categories (GO) identified as over-represented. Fisher Exact tests FDR corrected q-values, the proportion of transcripts belonging to the cluster, the number of transcripts in the GO category, and the name of the GO category are indicated.

Cluster	GO	q_value	Prop_DE	Size	name
Pa_C1	GO:0005929	4,52E-28	0,89	251	cilium
Pa_C1	GO:0005575	1,68E-15	0,70	774	cellular_component
Pa_C1	GO:0005813	3,61E-12	0,79	237	centrosome
Pa_C1	GO:0036064	1,32E-09	0,98	50	ciliary basal body
Pa_C1	GO:0005089	4,37E-09	0,96	53	Rho guanyl-nucleotide exchange factor activity
Pa_C1	GO:0031252	6,89E-09	0,96	52	cell leading edge
Pa_C1	GO:0031235	2,17E-08	1,00	38	intrinsic component of the cytoplasmic side of the plasma membrane
Pa_C1	GO:0051056	3,75E-08	1,00	37	regulation of small GTPase mediated signal transduction
Pa_C1	GO:0031143	6,29E-08	1,00	36	pseudopodium
Pa_C1	GO:0006909	4,07E-07	0,88	72	phagocytosis

Pa_C1	GO:0001726	2,64E-06	0,93	44	ruffle
Pa_C1	GO:0016849	3,14E-06	0,84	81	phosphorus-oxygen lyase activity
Pa_C1	GO:0016477	6,97E-06	0,89	54	cell migration
Pa_C1	GO:0030041	9,38E-06	0,97	32	actin filament polymerization
Pa_C1	GO:0035091	1,82E-05	0,86	59	phosphatidylinositol binding
Pa_C1	GO:0030027	3,75E-05	0,89	46	lamellipodium
Pa_C1	GO:0006869	4,50E-05	0,81	80	lipid transport
Pa_C1	GO:0045335	4,59E-05	0,77	114	phagocytic vesicle
Pa_C1	GO:0005272	4,63E-05	1,00	23	sodium channel activity
Pa_C1	GO:0007224	1,34E-04	0,91	35	smoothened signaling pathway
Pa_C1	GO:0006511	2,05E-04	0,71	188	ubiquitin-dependent protein catabolic process
Pa_C1	GO:0005769	2,47E-04	0,79	78	early endosome
Pa_C1	GO:0015629	3,20E-04	0,83	58	actin cytoskeleton
Pa_C1	GO:0031410	3,79E-04	0,68	273	cytoplasmic vesicle
Pa_C1	GO:0030175	4,73E-04	0,91	32	filopodium
Pa_C1	GO:0006915	8,20E-04	0,72	143	apoptotic process
Pa_C1	GO:0003950	9,00E-04	1,00	17	NAD+ ADP-ribosyltransferase activity
Pa_C1	GO:0030833	9,00E-04	0,95	22	regulation of actin filament polymerization
Pa_C1	GO:0032391	9,00E-04	1,00	17	photoreceptor connecting cilium
Pa_C1	GO:0042981	9,84E-04	0,79	67	regulation of apoptotic process
Pa_C1	GO:0031589	1,02E-03	0,90	30	cell-substrate adhesion
Pa_C1	GO:0007283	1,11E-03	0,73	122	spermatogenesis
Pa_C1	GO:0043025	1,35E-03	0,76	87	neuronal cell body
Pa_C1	GO:0000922	1,39E-03	0,78	72	spindle pole
Pa_C1	GO:0055037	1,40E-03	0,88	33	recycling endosome
Pa_C1	GO:0006996	1,44E-03	0,82	50	organelle organization
Pa_C1	GO:0048870	1,44E-03	0,82	50	cell motility
Pa_C1	GO:0005814	1,62E-03	0,80	56	centriole
Pa_C1	GO:0007507	1,69E-03	0,80	59	heart development
Pa_C1	GO:0042626	1,74E-03	0,74	106	ATPase activity, coupled to transmembrane movement of substances
Pa_C1	GO:0006897	1,85E-03	0,73	117	endocytosis
Pa_C1	GO:0022604	2,44E-03	1,00	15	regulation of cell morphogenesis
Pa_C1	GO:0030154	2,70E-03	0,69	175	cell differentiation
Pa_C1	GO:0045121	2,82E-03	0,81	48	membrane raft
Pa_C1	GO:0007368	2,96E-03	0,80	51	determination of left/right symmetry
Pa_C1	GO:0005911	3,36E-03	0,83	41	cell-cell junction
Pa_C1	GO:0030425	3,43E-03	0,74	92	dendrite
Pa_C1	GO:0097190	4,02E-03	1,00	14	apoptotic signaling pathway
Pa_C1	GO:0000278	4,36E-03	0,76	68	mitotic cell cycle
Pa_C1	GO:0007399	4,65E-03	0,73	102	nervous system development
Pa_C1	GO:0042470	5,19E-03	0,81	43	melanosome
Pa_C1	GO:0008543	5,28E-03	0,88	26	fibroblast growth factor receptor signaling pathway
Pa_C1	GO:0031234	5,70E-03	0,91	22	extrinsic component of cytoplasmic side of plasma membrane
Pa_C1	GO:0002102	6,42E-03	1,00	13	podosome
Pa_C1	GO:0005227	6,42E-03	1,00	13	calcium activated cation channel activity
Pa_C1	GO:0046578	6,42E-03	1,00	13	regulation of Ras protein signal transduction
Pa_C1	GO:0046956	6,42E-03	1,00	13	positive phototaxis
Pa_C1	GO:0048013	6,42E-03	1,00	13	ephrin receptor signaling pathway
Pa_C1	GO:0005875	6,99E-03	0,81	42	microtubule associated complex
Pa_C1	GO:0007186	7,35E-03	0,80	45	G-protein coupled receptor signaling pathway
Pa_C1	GO:0048812	7,59E-03	0,88	25	neuron projection morphogenesis
Pa_C1	GO:0031288	8,43E-03	0,83	35	sorocarp morphogenesis
Pa_C1	GO:0032587	8,43E-03	0,83	35	ruffle membrane
Pa_C1	GO:0005765	9,12E-03	0,70	118	lysosomal membrane
Pa_C1	GO:0005516	9,29E-03	0,68	163	calmodulin binding
Pa_C1	GO:0008360	1,04E-02	0,77	53	regulation of cell shape
Pa_C1	GO:0007160	1,05E-02	1,00	12	cell-matrix adhesion
Pa_C1	GO:0045010	1,05E-02	1,00	12	actin nucleation
Pa_C1	GO:0006661	1,12E-02	0,88	24	phosphatidylinositol biosynthetic process
Pa_C1	GO:0016337	1,12E-02	0,88	24	single organismal cell-cell adhesion
Pa_C1	GO:0019954	1,31E-02	0,90	20	asexual reproduction
Pa_C1	GO:0035082	1,31E-02	0,90	20	axoneme assembly
Pa_C1	GO:0000776	1,31E-02	0,73	78	kinetochore
Pa_C1	GO:0007169	1,31E-02	0,94	16	transmembrane receptor protein tyrosine kinase signaling pathway

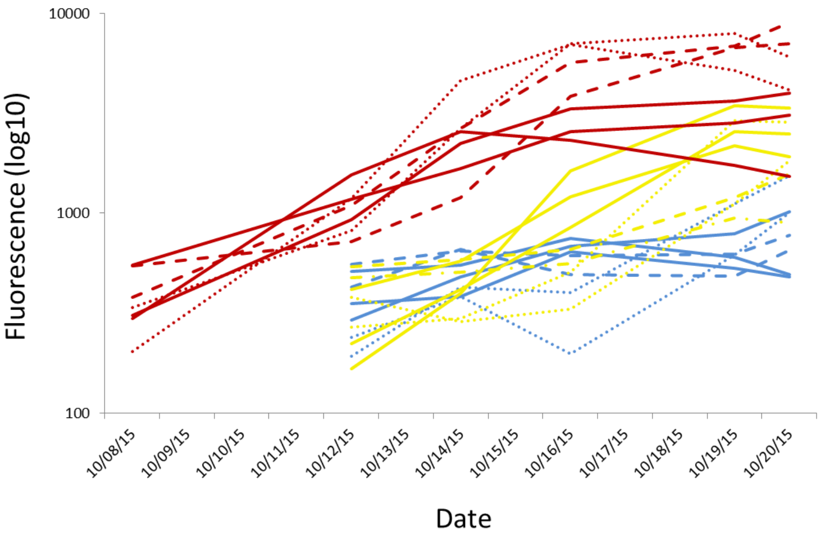
Pa_C1	GO:0014065	1,31E-02	0,94	16	phosphatidylinositol 3-kinase signaling
Pa_C1	GO:0032433	1,31E-02	0,94	16	filopodium tip
Pa_C1	GO:0048194	1,31E-02	0,94	16	Golgi vesicle budding
Pa_C1	GO:0014069	1,33E-02	0,85	27	postsynaptic density
Pa_C1	GO:0017016	1,69E-02	1,00	11	Ras GTPase binding
Pa_C1	GO:0032009	1,69E-02	1,00	11	early phagosome
Pa_C1	GO:0050680	1,69E-02	1,00	11	negative regulation of epithelial cell proliferation
Pa_C1	GO:0051371	1,69E-02	1,00	11	muscle alpha-actinin binding
Pa_C1	GO:0090630	1,69E-02	1,00	11	activation of GTPase activity
Pa_C1	GO:0007015	1,75E-02	0,76	54	actin filament organization
Pa_C1	GO:0000902	1,81E-02	0,79	42	cell morphogenesis
Pa_C1	GO:0071963	1,88E-02	0,89	19	establishment or maintenance of cell polarity regulating cell shape
Pa_C1	GO:0005547	2,03E-02	0,93	15	phosphatidylinositol-3,4,5-trisphosphate binding
Pa_C1	GO:0000151	2,06E-02	0,74	62	ubiquitin ligase complex
Pa_C1	GO:0006886	2,28E-02	0,65	219	intracellular protein transport
Pa_C1	GO:0019901	2,32E-02	0,70	100	protein kinase binding
Pa_C1	GO:0015031	2,55E-02	0,61	638	protein transport
Pa_C1	GO:0043409	2,72E-02	1,00	10	negative regulation of MAPK cascade
Pa_C1	GO:0045762	2,72E-02	1,00	10	positive regulation of adenylate cyclase activity
Pa_C1	GO:1903506	2,72E-02	1,00	10	regulation of nucleic acid-templated transcription
Pa_C1	GO:0004114	2,78E-02	0,89	18	3',5'-cyclic-nucleotide phosphodiesterase activity
Pa_C1	GO:0005876	2,90E-02	0,82	28	spindle microtubule
Pa_C1	GO:0043066	2,90E-02	0,69	112	negative regulation of apoptotic process
Pa_C1	GO:0000038	2,97E-02	0,93	14	very long-chain fatty acid metabolic process
Pa_C1	GO:0000910	2,97E-02	0,93	14	cytokinesis
Pa_C1	GO:0001570	2,97E-02	0,93	14	vasculogenesis
Pa_C1	GO:0030032	2,97E-02	0,93	14	lamellipodium assembly
Pa_C1	GO:0030426	2,97E-02	0,81	31	growth cone
Pa_C1	GO:0031648	2,97E-02	0,93	14	protein destabilization
Pa_C1	GO:0005086	3,05E-02	0,79	34	ARF guanyl-nucleotide exchange factor activity
Pa_C1	GO:0005543	3,05E-02	0,77	43	phospholipid binding
Pa_C1	GO:0030670	3,05E-02	0,79	34	phagocytic vesicle membrane
Pa_C1	GO:0031175	3,07E-02	0,78	37	neuron projection development
Pa_C1	GO:0006892	3,25E-02	0,86	21	post-Golgi vesicle-mediated transport
Pa_C1	GO:0005546	3,70E-02	0,83	24	phosphatidylinositol-4,5-bisphosphate binding
Pa_C1	GO:0031901	3,70E-02	0,75	51	early endosome membrane
Pa_C1	GO:0007067	3,97E-02	0,63	294	mitotic nuclear division
Pa_C1	GO:0019722	3,97E-02	0,81	27	calcium-mediated signaling
Pa_C1	GO:0001578	4,06E-02	1,00	9	microtubule bundle formation
Pa_C1	GO:0006635	4,06E-02	0,73	59	fatty acid beta-oxidation
Pa_C1	GO:0006972	4,06E-02	0,77	39	hyperosmotic response
Pa_C1	GO:0012506	4,06E-02	1,00	9	vesicle membrane
Pa_C1	GO:0030660	4,06E-02	1,00	9	Golgi-associated vesicle membrane
Pa_C1	GO:0070260	4,06E-02	1,00	9	5'-tyrosyl-DNA phosphodiesterase activity
Pa_C1	GO:0090004	4,06E-02	1,00	9	positive regulation of establishment of protein localization to plasma membrane
Pa_C1	GO:0032403	4,16E-02	0,72	67	protein complex binding
Pa_C1	GO:0034220	4,16E-02	0,72	67	ion transmembrane transport
Pa_C1	GO:0044281	4,77E-02	0,65	178	small molecule metabolic process
Pa_C2	GO:0003723	7,78E-39	0,21	797	RNA binding
Pa_C2	GO:0008652	7,41E-11	0,25	157	cellular amino acid biosynthetic process
Pa_C2	GO:0044822	2,37E-10	0,18	356	poly(A) RNA binding
Pa_C2	GO:0006413	3,72E-09	0,28	95	translational initiation
Pa_C2	GO:0005666	3,52E-06	0,44	25	DNA-directed RNA polymerase III complex
Pa_C2	GO:0005622	2,31E-05	0,12	685	intracellular
Pa_C2	GO:0042128	3,21E-05	0,50	16	nitrate assimilation
Pa_C2	GO:0006526	6,47E-05	0,54	13	arginine biosynthetic process
Pa_C2	GO:0006541	6,47E-05	0,31	39	glutamine metabolic process
Pa_C2	GO:0000027	7,33E-05	0,28	46	ribosomal large subunit assembly
Pa_C2	GO:0022626	2,31E-04	0,25	51	cytosolic ribosome
Pa_C2	GO:0006164	7,13E-04	0,39	18	purine nucleotide biosynthetic process
Pa_C2	GO:0006807	7,14E-04	0,28	36	nitrogen compound metabolic process
Pa_C2	GO:0000028	1,97E-03	0,33	21	ribosomal small subunit assembly
Pa_C2	GO:0051539	2,26E-03	0,16	125	4 iron, 4 sulfur cluster binding
Pa_C2	GO:0006221	3,23E-03	0,35	17	pyrimidine nucleotide biosynthetic process
Pa_C2	GO:0080008	3,23E-03	0,30	23	Cul4-RING E3 ubiquitin ligase complex

Pa_C2	GO:0000049	3,90E-03	0,19	69	tRNA binding
Pa_C2	GO:0006096	4,19E-03	0,17	96	glycolytic process
Pa_C2	GO:0017183	4,89E-03	0,38	13	peptidyl-diphthamide biosynthetic process from peptidyl-histidine
Pa_C2	GO:0000287	6,56E-03	0,12	252	magnesium ion binding
Pa_C2	GO:0003924	1,19E-02	0,13	177	GTPase activity
Pa_C2	GO:0005743	1,44E-02	0,11	378	mitochondrial inner membrane
Pa_C2	GO:0006099	1,79E-02	0,18	56	tricarboxylic acid cycle
Pa_C2	GO:0043022	2,27E-02	0,20	41	ribosome binding
Pa_C2	GO:0006417	4,49E-02	0,14	84	regulation of translation
Pa_C2	GO:0051607	4,73E-02	0,18	38	defense response to virus
Pa_C2	GO:0003746	4,80E-02	0,17	47	translation elongation factor activity
Pa_C2	GO:0000184	4,92E-02	0,20	30	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Pa_C3	GO:0009507	3,36E-03	0,05	589	chloroplast
Pa_C3	GO:0005506	2,41E-02	0,07	187	iron ion binding
Pa_C4	GO:0031012	9,78E-07	0,28	25	extracellular matrix
Pa_C4	GO:0043565	1,68E-04	0,08	109	sequence-specific DNA binding
Pa_C4	GO:0007219	1,99E-03	0,11	46	Notch signaling pathway
Pa_C4	GO:0005615	1,72E-02	0,04	283	extracellular space
Pa_C4	GO:0045454	1,92E-02	0,05	117	cell redox homeostasis
Pa_C4	GO:0007399	3,49E-02	0,05	102	nervous system development
Pa_C4	GO:0009986	3,49E-02	0,05	101	cell surface
Pa_C5	GO:0009579	1,97E-59	0,36	176	thylakoid
Pa_C5	GO:0055114	3,57E-08	0,05	1365	oxidation-reduction process
Pa_C5	GO:0006782	2,92E-04	0,25	20	protoporphyrinogen IX biosynthetic process
Pa_C5	GO:0034599	9,58E-04	0,15	41	cellular response to oxidative stress
Pa_C5	GO:0015995	1,01E-03	0,19	27	chlorophyll biosynthetic process
Pa_C5	GO:0045454	3,47E-03	0,08	117	cell redox homeostasis
Pa_C5	GO:0000413	7,19E-03	0,07	107	protein peptidyl-prolyl isomerization
Pa_C5	GO:0006096	1,38E-02	0,07	96	glycolytic process
Pa_C5	GO:0008652	1,91E-02	0,06	157	cellular amino acid biosynthetic process
Pa_C5	GO:0008483	3,00E-02	0,08	63	transaminase activity
Pa_C6	GO:0015074	1,58E-10	0,42	24	DNA integration
Pa_C6	GO:0009536	9,00E-09	0,06	514	plastid
Pa_C6	GO:0006098	1,50E-04	0,16	37	pentose-phosphate shunt
Pa_C6	GO:0042597	2,98E-04	0,14	42	periplasmic space
Pa_C6	GO:0003824	2,44E-03	0,03	1071	catalytic activity
Pa_C6	GO:0008652	1,27E-02	0,05	157	cellular amino acid biosynthetic process
Pa_C6	GO:0016829	3,08E-02	0,03	344	lyase activity
Pa_C6	GO:0006633	3,60E-02	0,04	156	fatty acid biosynthetic process
Pp_C1	GO:0009765	4,79E-08	0,29	48	photosynthesis, light harvesting
Pp_C1	GO:0005578	5,13E-04	0,38	13	proteinaceous extracellular matrix
Pp_C1	GO:0004674	2,43E-03	0,08	262	protein serine/threonine kinase activity
Pp_C1	GO:0060271	1,30E-02	0,19	27	cilium morphogenesis
Pp_C1	GO:0008283	2,95E-02	0,15	34	cell proliferation
Pp_C1	GO:0006952	3,15E-02	0,12	49	defense response
Pp_C1	GO:0005615	4,73E-02	0,08	106	extracellular space
Pp_C2	GO:0009279	5,71E-06	0,50	16	cell outer membrane
Pp_C2	GO:0006099	3,00E-05	0,28	36	tricarboxylic acid cycle
Pp_C2	GO:0042597	3,00E-05	0,28	36	periplasmic space
Pp_C2	GO:0016987	5,13E-05	0,41	17	sigma factor activity
Pp_C2	GO:0016620	2,64E-04	0,27	30	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
Pp_C2	GO:0016829	2,64E-04	0,11	200	lyase activity
Pp_C2	GO:0003824	4,70E-04	0,07	628	catalytic activity
Pp_C2	GO:0019843	4,70E-04	0,19	53	rRNA binding
Pp_C2	GO:0051536	3,37E-03	0,11	124	iron-sulfur cluster binding
Pp_C2	GO:0006865	6,89E-03	0,17	41	amino acid transport
Pp_C2	GO:0018298	3,75E-02	0,11	72	protein-chromophore linkage
Pp_C2	GO:0008652	3,79E-02	0,09	136	cellular amino acid biosynthetic process
Pp_C2	GO:0006814	4,64E-02	0,15	34	sodium ion transport
Pp_C3	GO:0004672	2,56E-04	0,07	296	protein kinase activity
Pp_C3	GO:0023014	7,89E-04	0,19	32	signal transduction by protein phosphorylation
Pp_C3	GO:0005615	2,09E-02	0,08	106	extracellular space
Pp_C3	GO:0005575	2,71E-02	0,05	245	cellular_component
Pp_C3	GO:0071555	2,90E-02	0,10	49	cell wall organization

Pp_C3	GO:0016042	3,15E-02	0,10	51	lipid catabolic process
Pp_C3	GO:0070062	4,65E-02	0,05	187	extracellular exosome
Pp_C3	GO:0045944	4,65E-02	0,07	83	positive regulation of transcription from RNA polymerase II promoter
Pp_C4	GO:0005730	1,58E-11	0,10	238	nucleolus
Pp_C4	GO:0003723	1,92E-03	0,04	465	RNA binding
Pp_C5	GO:0030076	1,32E-05	0,16	38	light-harvesting complex
Pp_C5	GO:0005576	1,10E-02	0,03	185	extracellular region
Pp_C5	GO:0007049	1,75E-02	0,03	208	cell cycle
Pf_C1	GO:0005730	3,38E-40	0,36	223	nucleolus
Pf_C1	GO:0030529	3,79E-28	0,32	198	intracellular ribonucleoprotein complex
Pf_C1	GO:0000027	2,41E-06	0,53	17	ribosomal large subunit assembly
Pf_C1	GO:0003676	1,35E-04	0,13	303	nucleic acid binding
Pf_C1	GO:0019740	1,00E-03	0,50	10	nitrogen utilization
Pf_C1	GO:0030490	1,00E-03	0,50	10	maturation of SSU-rRNA
Pf_C1	GO:0006807	2,79E-03	0,33	18	nitrogen compound metabolic process
Pf_C1	GO:0004527	2,31E-02	0,18	44	exonuclease activity
Pf_C2	GO:0009536	3,40E-07	0,12	472	plastid
Pf_C2	GO:0016853	6,84E-04	0,12	197	isomerase activity
Pf_C2	GO:0015074	4,91E-03	0,24	29	DNA integration
Pf_C2	GO:0006855	1,60E-02	0,20	30	drug transmembrane transport
Pf_C2	GO:0006629	1,88E-02	0,09	237	lipid metabolic process

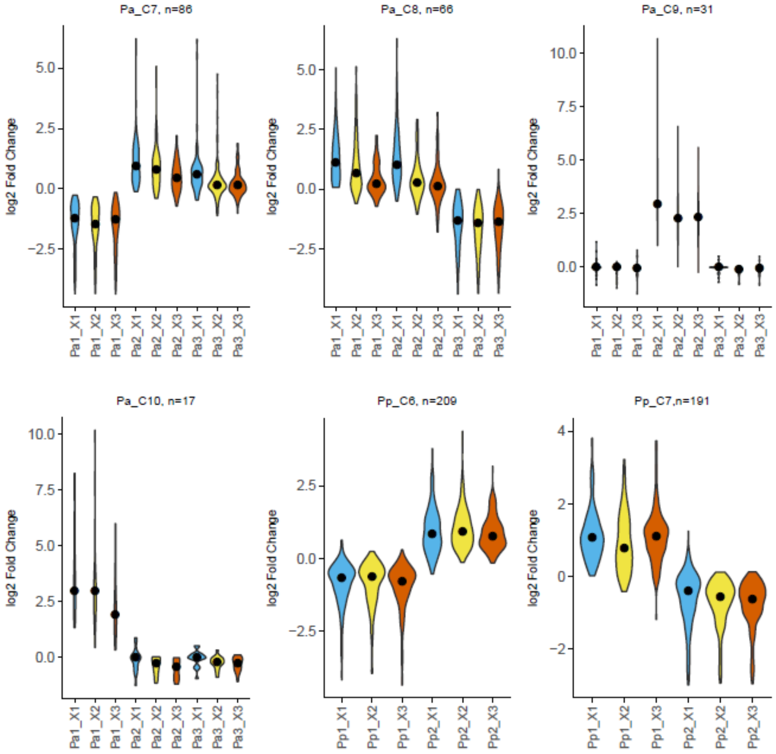
Supplementary Figures

Supplementary Figure 1



Supplementary figure 1: Growth kinetics. Growth curves of the seven strains in the three media. Growth is quantified using chlorophyll fluorescence (ex: 440/40, em: 680/20). Data from the media X1, X2, and X3 are in blue, yellow and red, respectively. *P. autralis*, *P. pungens*, and *P. fraudulenta* strains are in full, dashed and dotted lines, respectively.

Supplementary Figure 2



Supplementary figure 2: Small *P. australis* and *P. pungens* strain specific expression clusters. Expression profiles, across strains and media, of 4 *P. australis* (Pa_C7-10) and 2 *P. pungens* (Pp_C6-7) clusters of transcripts. Expression is indicated using violin plots (rotated kernel density plots) based on the log2 fold change of the median expression in the category of interest over the median expression considering all samples (see methods). Black dots indicate median log2 fold change. Blue, Yellow and Red report to X1, X2, and X3 media, respectively. The number of transcripts belonging to each cluster is indicated.