Supplementary Materials

Molecular Biology of the Cell

Sakato-Antoku and King

Supplemental Material for

Developmental Changes in Ciliary Composition during Gametogenesis in *Chlamydomonas*

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Supplemental Table S1

Global Analysis of Mass Spectrometry Data for Vegetative and Gametic Cilia

Sample	Proteins Present in all 3 Replicates	Proteins Unique to Sample* A Samples	Proteins Unique to Sample B Samples	Proteins Unique to Sample C Samples
1. CC124 V M&M†	978	574	565	571
2. CC124 V Axo	750	310	327	318
3. CC124 G M&M	1355	821	868	850
4. CC124 G Axo	840	290	281	285
5. CC125 V M&M	947	576	586	564
6. CC125 V Axo	744	309	309	306
7. CC125 G M&M	1004	592	580	606
8. CC125 G Axo	757	297	287	298

† V, vegetative; G, gametic; M&M, membrane plus matrix; Axo, axoneme.

* For example, for Sample A of CC124 vegetative cilia, 574 proteins out of the 978 identified in the membrane plus matrix fraction were exclusively present in that fraction, while 310 proteins out of the 750 identified were only found in the axonemal fraction.

Supplemental Table S2 Legend

Abundance Data for Vegetative and Gametic Cilia Samples

This table provides the mass spectrometric abundance data (normalized total spectral counts) for all replicates (labeled A-C) of each fractionated cilia sample (labeled 1-8). Samples 1A-C = membrane/matrix vegetative CC124 mating type *minus*, 2A-C = axoneme vegetative CC124 mating type *minus*; 3A-C = membrane/matrix gametic CC124 mating type *minus*, 4A-C axoneme gametic CC124 mating type *minus*; 5A-C = membrane/matrix vegetative CC125 mating type *plus*, 6A-C = axoneme vegetative CC125 mating type *plus*; 7A-C = membrane/matrix gametic CC125 mating type *plus*, 8A-C axoneme gametic CC125 mating type *plus*. Additional tabs provide lists of proteins (Cre#s) present only in axoneme and membrane plus matrix fractions (*.xlsx format).

Supplemental Table S3

Proteins that Exhibit a ≥5-fold Change in Abundance between CC124 (mating type *minus*) Vegetative and Gametic Cilia Samples

Vegetative Cilia > Gametic Cilia	
Cre#	**Description**
Cre01.g003950	PAS domain
Cre01.g004124	PAS domain
Cre01.g014050	Zinc finger protein P48ZNF
Cre01.g033000	FAP334
Cre01.g044900	PhoD-like phosphatase
Cre01.g050050	Guanidino-acetate N-methyl transferase
Cre01.g052000	NTPase with CobW (metal chaperone) domain
Cre01.g054550	Toll receptor homology domain
Cre02.g090050	FAP170
Cre02.g092900	GMP synthetase
Cre02.g105400	Cell division cycle protein 14
Cre02.g110950	IFT dynein intermediate chain DIC5 (FAP133, WDR34)
Cre02.g143400	3’,5’-cNMP phosphodiesterase
Cre03.g143887	Arginyl tRNA synthetase
Cre03.g152550	WD repeat protein
Cre03.g187450	Ribose-5-phosphate isomerase
Cre03.g196550	Antibiotic biosynthesis monooxygenase
Cre03.g204601	Adenosine kinase
Cre05.g233050	FAP162
Cre05.g233800	Glycyl tRNA synthetase
Cre05.g241637	IFT46
Cre06.g251200	IFT43
Cre06.g275250	No obvious domains
Cre06.g278167	DUF5522 superfamily
Cre06.g278169	GHMP (sugar) kinase family C-terminal domain
Cre06.g286600	DUF4205 domain
Cre06.g298950	Queuosine salvage protein family
Cre07.g326900	No obvious domains
Cre07.g328850	NimA-related kinase
Cre07.g329700	Proteasome subunit P45
Cre07.g344150	Queuosine salvage protein family
Cre08.g361200	Outer dynein arm assembly factor ODA10
Cre08.g361950	FAP153 (PAS domain)

Gametic Cilia > Vegetative Cilia	
Cre#	**Description**
Cre01.g001678	S/T kinase
Cre01.g002500	Chlamyopsin 1
Cre01.g040750	No obvious domains
Cre01.g055420	Protein phosphatase 2A regulatory subunit
Cre02.g076350	Vacuolar ATP synthase subunit B
Cre02.g087950	Methionyl tRNA synthetase
Cre02.g097650	Proteasome regulatory complex subunit RPN6
Cre02.g098450	eIF2 γ subunit
Cre02.g113200	Glutamine synthetase
Cre03.g152150	Zinc finger protein
Cre03.g189950	HOP1 heat shock protein chaperone
Cre03.g206750	Tubby C-terminal domain-like
Cre05.g245950	Dynamin-related GTPase
Cre06.g263250	Alanine-rich low complexity
Cre06.g298350	FAP224
Cre07.g317150	Dual specificity protein phosphatase
Cre07.g339050	Cofilin
Cre07.g353700	Armadillo repeats
Cre09.g387171	Nucleotide rhamnose synthase/epimerase-reductase
Cre09.g393506	Hydroxylamine reductase
Cre09.g393650	N-terminal GAF domain and C-terminal kinase domain
Cre09.g394200	FAP102
Cre09.g400850	Carbohydrate binding and C-terminal polycystin cation channel domains
Cre10.g434750	Acetohydroxy acid isomeroreductase
Cre10.g459200	P-type ATPase/cation transporter
Cre10.g461250	Vesicle fusing ATPase (NSF)
Cre11.g469800	Contains DUF1399 domain
Cre11.g478156	AP-1 complex β-1 subunit
Cre12.g484150	S/T protein phosphatase 6 regulatory subunit 3
Cre12.g497300	Rhodanase-like Ca^{2+}-sensing receptor
Cre12.g503600	Leucine-rich repeat protein
Cre12.g507750	Protein kinase with N-terminal ankyrin repeats
Cre12.g530650	Glutamine synthetase

Cre08.g362050	FAP49 (PAS domain)
Cre08.g382100	S/T kinase
Cre09.g387912	FAP139
Cre09.g401700	TPR repeats
Cre10.g423300	Bleomycin hydrolase
Cre10.g428664	IFT dynein intermediate chain DIC6 (FAP163, WDR60)
Cre10.g432450	Ankyrin repeats
Cre10.g433600	Methylene tetrahydrofolate reductase
Cre10.g437100	DUF383 domain
Cre11.g467611	Bestrophin chloride channel
Cre12.g484500	Ankyrin repeats
Cre12.g489250	Formin-related
Cre12.g514650	S/T kinase (NimA-related) with IFT57-like C-terminal domain
Cre12.g541550	SYLF domain – lipid binding module
Cre12.g559300	Armadillo repeats
Cre13.g567500	Alanine/glycine/proline-rich
Cre14.g609202	Zinc metallopeptidase
Cre15.g641451	Transmembrane protein
Cre16.g654800	Ankyrin repeats
Cre16.g680250	No obvious domains, signal peptide
Cre16.g680300	Phosphatidylcholine-sterol O-acyltransferase
Cre17.g708100	Hypoxanthine phosphoribosyl transferase
Cre17.g718900	FAP88
Cre17.g738050	Aggregation protein AGG4
Cre17.g742300	FAP179
Cre17.g746697	FAP249

Cre13.g604650	Methionyl aminopeptidase
Cre14.g612000	S/T kinase ULK4
Cre14.g617050	Armadillo repeats
Cre16.g651750	Isoleucyl tRNA synthetase
Cre16.g652100	Methionine aminopeptidase
Cre16.g662951	Heterokaryon incompatibility/ankyrin repeat protein
Cre16.g676200	Guanylate-binding protein
Cre16.g689647	Argonaute-like protein
Cre17.g696250	eIF4G
Cre17.g708300	Proteasome regulatory subunit RPN12
Cre17.g725200	ABC transporter

Supplemental Table S4

Proteins that Exhibit a ≥5-fold Change in Abundance between CC125 (mating type *plus*) Vegetative and Gametic Cilia Samples

Vegetative Cilia > Gametic Cilia	
Cre#	**Description**
Cre02.g094350	Importin α 1b
Cre02.g108450	FAP280
Cre03.g156850	Sphingomyelin phosphodiesterase-related
Cre03.g177200	CELF family RNA binding
Cre03.g198000	Protein phosphatase 2C
Cre03.g199759	Oxysterol binding protein
Cre06.g293900	UBX domain protein 11
Cre06.g302800	S/T kinase
Cre06.g304150	Heterokaryon incompatibility/ankyrin repeat protein
Cre08.g362050	FAP49
Cre08.g362100	FAP154
Cre09.g399030	4-hydroxyphenyl pyruvate dioxygenase
Cre11.g467611	Bestrophin chloride channel
Cre11.g467770	Phosphoglycerate kinase
Cre12.g489250	Formin-related
Cre12.g495250	FAP31
Cre12.g553900	cNMP-gated K^+ channel
Cre12.g554800	Phosphoribulokinase
Cre16.g674700	ADP-ribosyl dinitrogen reductase
Cre16.g693601	Hydroxyproline-rich pherophorin
Cre17.g706250	Kinesin light chain 2
Cre17.g725200	ABC transporter-like
Cre17.g728700	MAP kinase kinase kinase STE11

Gametic Cilia > Vegetative Cilia	
Cre#	**Description**
Cre01.g003376	DnaJ homolog
Cre02.g110350	Synaptogamin-related
Cre02.g113200	Glutamine synthetase
Cre03.g156750	T complex protein 1 ε subunit
Cre03.g161550	FAP55 (prefoldin domain)
Cre03.g166450	No obvious domains
Cre05.g239450	Atypical dual specificity phosphatase
Cre06.g250200	S-adenosylmethionine synthetase
Cre06.g278125	MyTH4 and ERM plasma membrane binding domain plus C-terminal kinesin motor domain
Cre07.g322550	FAP240
Cre07.g336200	Ubiquitin carboxyl terminal hydrolase USP7
Cre07.g339050	Cofilin
Cre09.g389282	FAP114
Cre09.g397200	T complex protein 1 ζ subunit
Cre10.g439100	T complex protein 1 α subunit
Cre10.g443250	T complex protein 1 γ subunit
Cre11.g467547	tRNA synthetase-related
Cre11.g469800	Contains DUF1399 domain
Cre11.g479250	RAN GTPase-activating (RANGAP1)
Cre12.g484150	S/T protein phosphatase 6 regulatory subunit 3
Cre12.g497450	Toll-like receptor
Cre12.g502700	Coiled coil protein
Cre12.g506400	No obvious domains
Cre12.g515350	Polycystin cation channel with RCC1 domain
Cre12.g528850	Outer arm dynein LC3
Cre12.g532950	Ionotropic glutamate receptor
Cre12.g560350	NIMA-related kinase 2
Cre13.g602400	Kinesin (Kin8 family)
Cre13.g604050	Superficially similar to GPCRs with pectate lyase repeats
Cre14.g618776	No obvious domains
Cre15.g635600	FAP357
Cre16.g652100	Methionine aminopeptidase
Cre16.g655750	Tektin