

Supplemental Table S1.

Datasets used to validate microarray detection of upregulation transcripts and the strategy of flagellar gene identification based on upregulation during flagellar regeneration.

Within each category, entries in bold type indicate at least 75% up-regulation at either 30 or 45 min after initiation of flagellar regeneration. Plain text indicates genes classified as not up-regulated according to this same criterion. Within each list, entries are sorted in increasing order of up-regulation at t=30 min.

I. Genes known to be upregulated during flagellar regeneration.

Gene-list consists of the strongly up-regulated genes from the RT-PCR analysis of Li et al. (2004, Table S4), plus 20 Chlamydomonas genes (as indicated in the table) whose up-regulation has been reported in the literature based on Northern blot analysis.

<u>Gene ID</u>		<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
167398	DLC5	-20.88%	-15.26%	-11.58%
168923	PF6	-5.69%	34.6%	-30.05%
158670		-4.1%	16.43%	7.14%
159590		-1.86%	-27.63%	-1.13%
165162	ODA5	-0.4%	-11.64%	2.73%
169516	DHC2	1.63%	4.81%	-7.89%
159662	FA1	10.92%	0.2%	-0.61%
157246		19.49%	20.12%	27.04%
157793		23.53%	26.8%	6.53%
163484		24.01%	15.86%	-4.08%
169293		25.39%	9.84%	-16.11%
165004		25.85%	31.32%	5.78%
168565		30.25%	-4.18%	-14.56%
153422		31.21%	6.02%	-6.38%
169882		41.2%	13.25%	9.73%
153053		47.19%	23.29%	-1.24%
159155		54.96%	27.24%	-13.87%
158615		60.01%	40.31%	8.66%
158194	FLA10	61.09%	45.16%	0.6%
158033		71.88%	66.67%	-8.88%
163664		74.46%	23.13%	1.15%
157052	MBO2	76.19%	40.82%	-5.26%
153708	LF4	81.06%	27.19%	12.12%
163277		91.26%	41.44%	-14.82%
165115		91.7%	79.72%	11.98%
166736	IDA7	92.65%	42.85%	3.51%
164264		100%	22.26%	-23.52%
167776		110.06%	37.1%	33.84%
156043		116.06%	48.75%	9.94%
164149		117.95%	77.94%	6.19%
166131	PF20	118.52%	43.45%	31.97%
157798	ODA3	127.93%	33.57%	1%
164561		129.22%	93.45%	24.46%
158863		134.99%	49.99%	-2.5%
162279	RSP3	143.86%	56.65%	6.06%
171911		153.4%	43.84%	-9.11%
163193		161.35%	80.24%	-6.28%
154393	IFT52	168.36%	81.09%	5.86%
164100	ODA6	170.31%	81%	4.73%

153853		196.25%	75.98%	7.61%
159749		212.19%	180.48%	37.7%
153658		220.27%	157.04%	-1.71%
161253		221.12%	27.38%	2.99%
156948	IFT57	232.55%	56.82%	19%
171602		302.64%	147.04%	109.3%
159247		334.95%	35.71%	-20.73%
164620	TUA1	345.71%	192.45%	114.43%
171096	PF16	367.77%	123.03%	-4.21%
160297		371.12%	219.34%	83.35%
157967	RSP4	382.67%	240.87%	30.47%
165606		389.99%	208.84%	67.13%
170055	TUB2	418.67%	214.58%	97.42%
171102		431.1%	197.22%	16.93%
168339		443.1%	126.61%	-7.46%
160952	ODA-DC3	676.09%	213.18%	43.84%
162703		724.23%	436.64%	87.7%

II. Genes known to NOT be upregulated during flagellar regeneration.
Gene list consists of the genes identified by Li et al. (2004, Table S4) as not being up-regulated according to RT-PCR, as well as four Chlamydomonas genes (as indicated in table) known by Northern analysis not to be up-regulated, as found in the literature.

<u>Gene ID</u>	<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
158239	-45.89%	-46.98%	-24.85%
166667	-41.33%	-47.33%	-47.79%
171242	-39.75%	-9.63%	105.39%
171299	-35.25%	-27.41%	-33.95%
158560	-27.97%	-35.55%	29.5%
168391 RBCS2	-25.38%	-32.96%	-1.52%
162000	-21.88%	-37.58%	56.8%
169942	-21.45%	-24.52%	-18.7%
158402	-19.33%	-26.86%	5.77%
165846	-19.08%	2.27%	-16.83%
161792	-18.1%	-27.43%	-22.81%
165904 CRY1	-18.1%	-51.04%	-3.18%
165247 Cblp	-17.46%	-50.04%	-21.45%
162224	-16.43%	-32.88%	-2.81%
156229	-16.27%	-2.31%	-18.13%
162018	-16.06%	-21.6%	-21.05%
165072 ALD	-13.38%	-58.89%	-37.67%
165102	-12.77%	-8.36%	-3.96%
154013	-12.36%	-10.5%	30.87%
168343	-10.34%	-10.97%	12.15%
162907	-10.07%	40.77%	-23.24%
156671	-7.83%	-22.75%	3.93%
157385	-7.8%	-9.36%	-18.8%
159566	-7.57%	-25.11%	37.68%
162058	-7.21%	-4.31%	-0.47%
168715	-6.38%	-14.89%	-5.41%
155468	-5.1%	25.83%	2.75%
155925	-5.1%	26.12%	9.2%
161779	-4.58%	-19.44%	17.62%
165569	-4.24%	13.55%	-5.78%
166774	-3.69%	-20.98%	15.43%
163738	-3.54%	-12.68%	-10.14%
155451	-3.06%	-7.51%	8.34%
171166	-1.98%	2.02%	-12.48%
167803	-1.66%	-1.66%	-4.38%
167053	0%	-12.03%	9.74%
156530	0.43%	-13.81%	73.01%
154789	0.55%	1.07%	13.04%
156598	1.28%	13.94%	-3.15%
155817	2.39%	-41.05%	2.15%
164517	3.45%	22.26%	2.58%
157943	4.57%	7.35%	-3.54%
168286	6.17%	9.26%	-6.48%
153859	6.34%	-19%	28.05%
171684	10.76%	8.41%	4.88%
155464	13.31%	-21.39%	-21.49%
166044	14.63%	15.19%	1.14%
160951	16.88%	19.13%	-1.15%
164610	19.07%	-5.11%	1.39%

164333	19.68%	5.51%	6.29%
168283	20%	2.97%	-6.13%
164774	20.01%	18.47%	21.39%
159111	28%	18.85%	23.4%
164526	56.59%	16.79%	5.31%

III. Genes whose products are known to localize to flagella.

Gene-list consists of Chlamydomonas proteins shown to localize to flagella either by immunofluorescence or by Western blot analysis.

<u>Gene ID</u>		<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
167398	DLC5	-20.88%	-15.26%	-11.58%
168923	PF6	-5.69%	34.6%	-30.05%
171599	DHC11	-3.27%	4.97%	-10.14%
161759	DHC3	-2.89%	-8.67%	-1.45%
162594	DHC4	-1.1%	11.69%	5.29%
165162	ODA5	-0.4%	-11.64%	2.73%
169516	DHC1b	1.63%	4.81%	-7.89%
171127	DHC2	5%	1.88%	-6.26%
161758	DHC3	5.47%	11.53%	-3.66%
163907	DHC6	6.62%	12.65%	2.7%
162407	DHC5	9.2%	7.97%	2.43%
169338	FMG1b	11.36%	16.8%	5.48%
158922	IDA2	15.01%	4.81%	-5.95%
168520	ODA11	17.18%	9.41%	1.96%
154251	MST1	27.86%	34.42%	9.6%
153556	DHC1	28.78%	12.12%	12.87%
161325	DHC7	33.96%	16.82%	5.39%
157469	ODA2	34.33%	14.93%	7.46%
168243	IFT140	40.74%	38.52%	3.7%
160289	ODA4	43.92%	22.11%	-0.94%
158273	DLC4	51.77%	13.04%	1.35%
157911	IFT172	59.1%	44.48%	-4.07%
158194	FLA10	61.09%	45.16%	0.6%
157405	FLA8	66.96%	21.54%	2.66%
160144	PP1a	70.3%	23.89%	-9.21%
168012	FLA3	72.02%	28.37%	7.19%
155416	RSP2	76.14%	40.91%	5.6%
157052	MBO2	76.19%	40.82%	-5.26%
169254	IFT88	77.32%	30.59%	-5.96%
166736	IDA7	92.65%	42.85%	3.51%
159022	IFT81	106.16%	35.44%	-7.71%
168881	Tektin	108.69%	73.91%	8.98%
166131	PF20	118.52%	43.45%	31.97%
157798	ODA3	127.93%	33.57%	1%
156307	D1bLIC	133.23%	23.69%	10.76%
162279	RSP3	143.86%	56.65%	6.06%
164295	ODA12	159.93%	88.85%	15.33%
171226	Tctex1	164.74%	45.98%	-8.08%
169383	IDA4	165.46%	54.52%	26.03%
154393	IFT52	168.36%	81.09%	5.86%
164100	ODA6	170.31%	81%	4.73%
156214	IFT20	183.92%	37.02%	-1.71%
155586	PF2	207.12%	129.09%	-3.74%
164979	IFT72	221.01%	104.7%	30.23%
156948	IFT57	232.55%	56.82%	19%
167565	KLP1	248.19%	90.7%	-0.66%
170981	FAP2	248.61%	81.67%	-9.67%
169795	DLC7a	251.48%	142.96%	15.57%
159281	FLA14	265.12%	128.04%	36.99%
170694	RIB43	270.91%	119%	0.63%
171680	ODA9	289.52%	139.73%	23.18%

164307	DLC3	316.27%	133.37%	-5.76%
168602	DLC1	337.65%	246.55%	26.75%
171096	PF16	367.77%	123.03%	-4.21%
168675	RIB72	377.18%	152.45%	26.45%
157967	RSP4	382.67%	240.87%	30.47%
164722	ODA13	430.58%	330.93%	40.97%
169971	DLC7b	464.3%	333.2%	71.19%
160952	ODA15	676.09%	213.18%	43.84%

IV. Genes whose products localize to other organelles

Gene list consists of two sub-lists, A. lists proteins that localize to chloroplast, B lists proteins that localize to nucleus.

A. Chloroplast-localized proteins

<u>Gene ID</u>		<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
158611	psbW	-57.02%	-82.3%	-59.07%
160286	THYL	-37.96%	-51.07%	-27.46%
169972	petM	-32.22%	-36.25%	6.46%
165812	petC	-26.4%	-45.99%	-19.2%
154244	petN	-18.48%	-58.55%	-36.81%
156157	pgk	-12.17%	-43.54%	-19.05%
165989	rbcS2	-3.31%	-51.55%	5.28%
159627	cema	-1.81%	-14.54%	8.18%
154594	minE2	4.49%	3.7%	0.16%
169504	met1	4.98%	2.99%	11.25%

B. Nuclear-localized proteins

<u>Gene ID</u>		<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
157840	HFO1	-23.77%	-7.05%	-6.4%
169457	PSR1	-12.66%	2.39%	9.04%
164461	NUP98	-4.85%	-9.7%	-4.38%
163504	NUP155	-1.62%	8.14%	-0.66%
169614	TOP2	1.44%	8.69%	-2.94%
170696	TOP1	5.65%	14.31%	-7.34%
162123	POLA2	7.98%	-4.2%	-5.48%
161483	TFIIA	15.74%	-15.66%	23.88%
152784	Hon1	21.87%	40.62%	28.9%
157278	PCNA	30.77%	1.44%	35.81%

V. Random genes

Gene list was generated by a random number generator, without any information concerning gene identity. Entries sorted by gene ID.

<u>Gene ID</u>	<u>30 min</u>	<u>45 min</u>	<u>120 min</u>
152963	-31.45%	-29.29%	-34.06%
153085	6.76%	-13.5%	-3.39%
155554	-5.96%	4.65%	56.97%
156681	-1.98%	-22.83%	8.41%
157184	-9.64%	-7.2%	14.74%
157482	0.39%	4.88%	9.75%
158830	-13.7%	-0.96%	-1.94%
159026	36.24%	-2.73%	21.38%
159393	-31.94%	-30.87%	35.62%
159414	-5.94%	-19.13%	9.89%
160388	11.17%	-11.16%	3.45%
160518	-4%	16%	-14.7%
162564	-8.42%	-19.22%	0.6%
164658	-8.9%	-17%	29.08%
165045	0.15%	8.92%	12.03%
167309	4.27%	-37.77%	-23.03%
167940	34.43%	-18.57%	21.57%
170062	-4.16%	-8.05%	-8.13%
170932	15.57%	7.53%	2.49%
171282	-4.24%	-10.2%	0.56%
171962	23.77%	-11.69%	16.86%