

Experiment	Condition	Sample	Size	Number of Reads	Read Length
Analysis of the transcriptome from Fe-repleted, Fe-limited and Fe-deprived Chlamydomonas cells grown in TAP and minimal media	WT strain 2137	SRR402019	2.1	8.67	70
	Fe-repleted TAP	SRR402020	2.2	9.38	70
	WT strain 2137	SRR402021	2.3	9.85	70
	Fe-deficient TAP	SRR402022	2.2	9.33	70
		SRR402023	2.2	9.20	70
	WT strain 2137	SRR402024	2.3	9.63	70
	Fe-limited TAP	SRR402025	2.3	9.62	70
		SRR402026	2.0	8.51	70
	WT strain 2137	SRR402027	5.4	11.00	200
	Fe-repleted	SRR402028	6.0	19.23	100
	Minimal Medium	SRR402029	7.2	14.64	200
		SRR402030	8.5	27.13	100
	WT strain 2137	SRR402031	6.2	12.70	200
	Fe-deficient	SRR402032	6.8	21.58	100
	Minimal Medium	SRR402033	6.7	13.68	200
		SRR402034	7.9	25.32	100
		SRR402035	4.8	9.87	200
		SRR402036	6.6	21.04	100
	SRR402037	6.7	13.80	200	
	SRR402038	8.6	27.60	100	
Impact of oxidative stress on the transcriptome	WT strain 2137	SRR394058	8.0	30.27	76
	t=0 of H <sub>2</sub> O <sub>2</sub> treatment	SRR394059	39.48	21.04	76
	WT strain 2137	SRR394060	8.8	33.03	76
	t=0.5 of H <sub>2</sub> O <sub>2</sub> treatment	SRR394061	8.1	30.54	76
	WT strain 2137	SRR394062	8.3	31.28	76
	SRR394063	13.0	47.92	76	
Singlet oxygen acclimation	WT strain 4A+	SRR363977	0.91	5.4	36
		SRR363978	0.93	5.26	36
Different TAP recipes	Recipe1	SRR074357	1.3	6.52	35
	Recipe2	SRR074358	1.4	7.00	35
Analysis of the transcriptome from Cu-deficient and Cu-sufficient wild type and crr1 mutant cells grown in TAP and minimal media	WT strain 2137 Copper deficient cells grown in TAP medium	SRR096493	0.61	4.38	17
		SRR096494	0.44	3.13	17
		SRR096495	2.00	7.45	70
		SRR096496	1.30	6.70	35
		SRR096497	1.30	6.65	35
		SRR096498	0.75	4.47	33
		SRR096499	0.72	4.26	33
	WT strain 2137 Copper deficient cells grown in TAP medium	SRR096500	0.70	3.79	33
		SRR096501	0.92	5.01	33
		SRR096502	0.60	4.26	17
		SRR096503	0.57	3.80	17
		SRR096504	1.8	6.68	70
		SRR096505	1.3	6.73	35
		SRR096506	1.4	7.03	35
	Crr1:crr1 strain Cu-deficient	SRR096507	0.78	4.64	33
		SRR096508	0.80	4.67	33
		SRR096509	0.90	4.88	33
	Crr1:crr1 strain Cu-deficient	SRR096510	0.90	4.89	33
		SRR096511	0.34	2.44	17
		SRR096512	0.68	4.87	17
WT strain 2137 Cu-deficient Min	SRR096513	1.50	7.43	35	
	SRR096514	1.40	6.83	35	
	SRR096515	1.3	6.66	35	
WT strain 2137 Cu-sufficient Min	SRR096516	1.4	7.13	35	
	SRR096517	3.4	11.49	100	
	SRR096518	3.9	13.26	100	
Global changes following N-deprivation	WT strain cw15 Nitrogen repletion	SRR096519	3.6	12.40	100
		SRR096520	3.6	12.25	100
	WT strain cw15 Nitrogen deprivation	SRR066643	4.30	16.90	75
Analysis of the transcriptome from S-deprived Chlamydomonas cells	WT strain D66 Sulfur repleted	SRR066644	4.70	18.30	75
		SRR066645	4.50	17.81	75
		SRR066646	4.50	17.66	75
		SRR066647	4.60	17.87	75
	WT strain D66 Sulfur deprived	SRR066648	3.90	15.22	75
		SRR039669	1.4	6.91	35
		SRR039670	1.4	6.89	35
		SRR039671	1.2	6.33	35
	ArsI1 mutant Sulfur repleted	SRR039672	1.2	5.91	35
		SRR039673	1.3	6.74	35
		SRR039674	1.2	6.10	35
		SRR039675	1.4	7.22	35
		SRR039676	0.77	4.22	33
ArsI1 mutant Sulfur deprived	SRR039677	0.77	4.26	33	
	SRR039678	0.84	4.52	33	
	SRR039679	0.89	4.80	33	