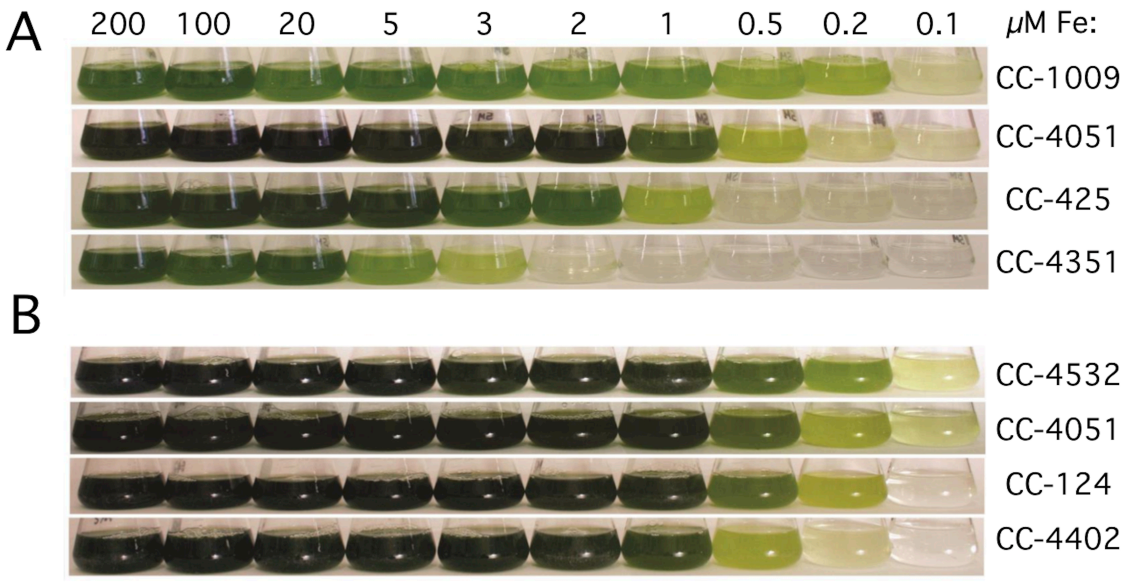
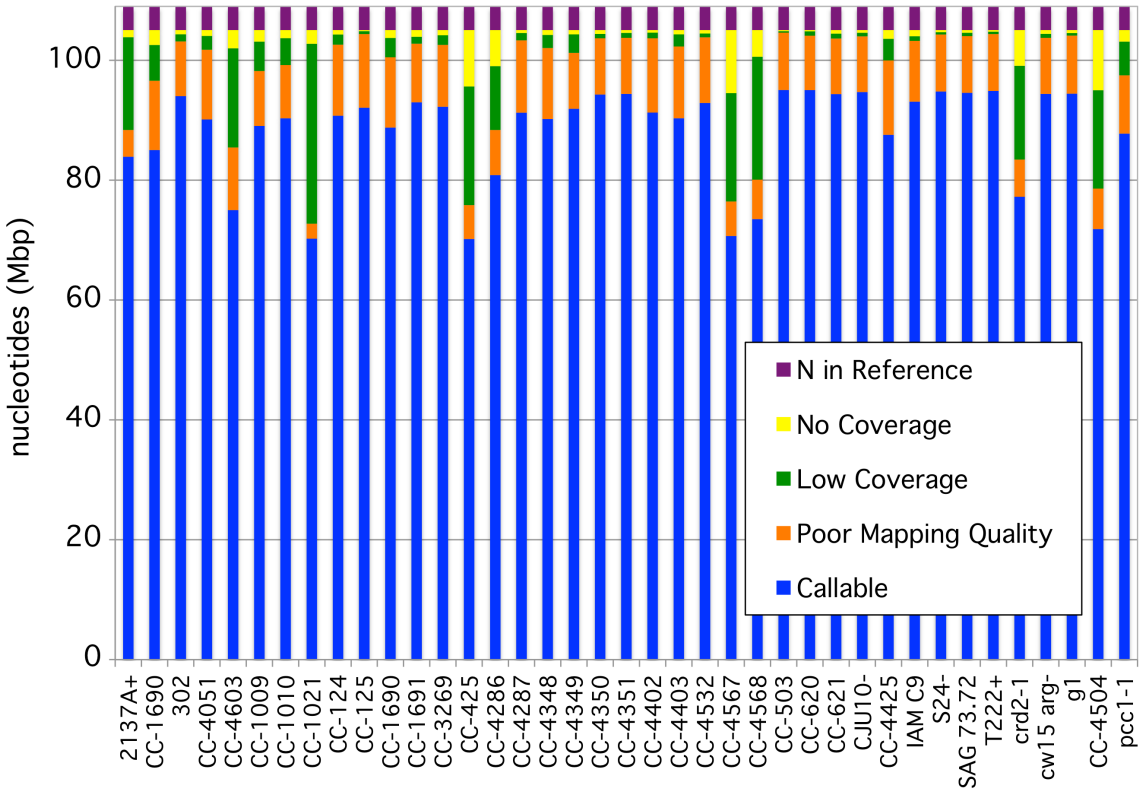


Supplemental Figure 1. Growth Phenotype of Iron Limitation on Additional Wild Type Strains

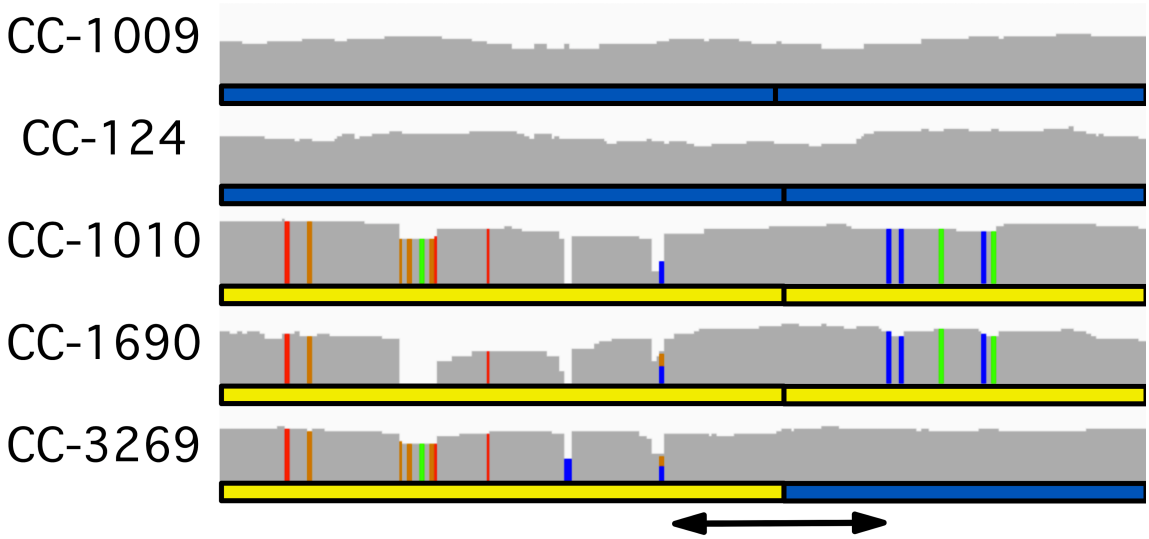
The indicated strains were inoculated to a density of 1 x 10^4 cells / mL in 100 mL cultures of TAP medium containing iron concentrations ranging from 0.1 to 200 μM.

(**A**) A first batch of cultures was photographed after 4 d of growth.

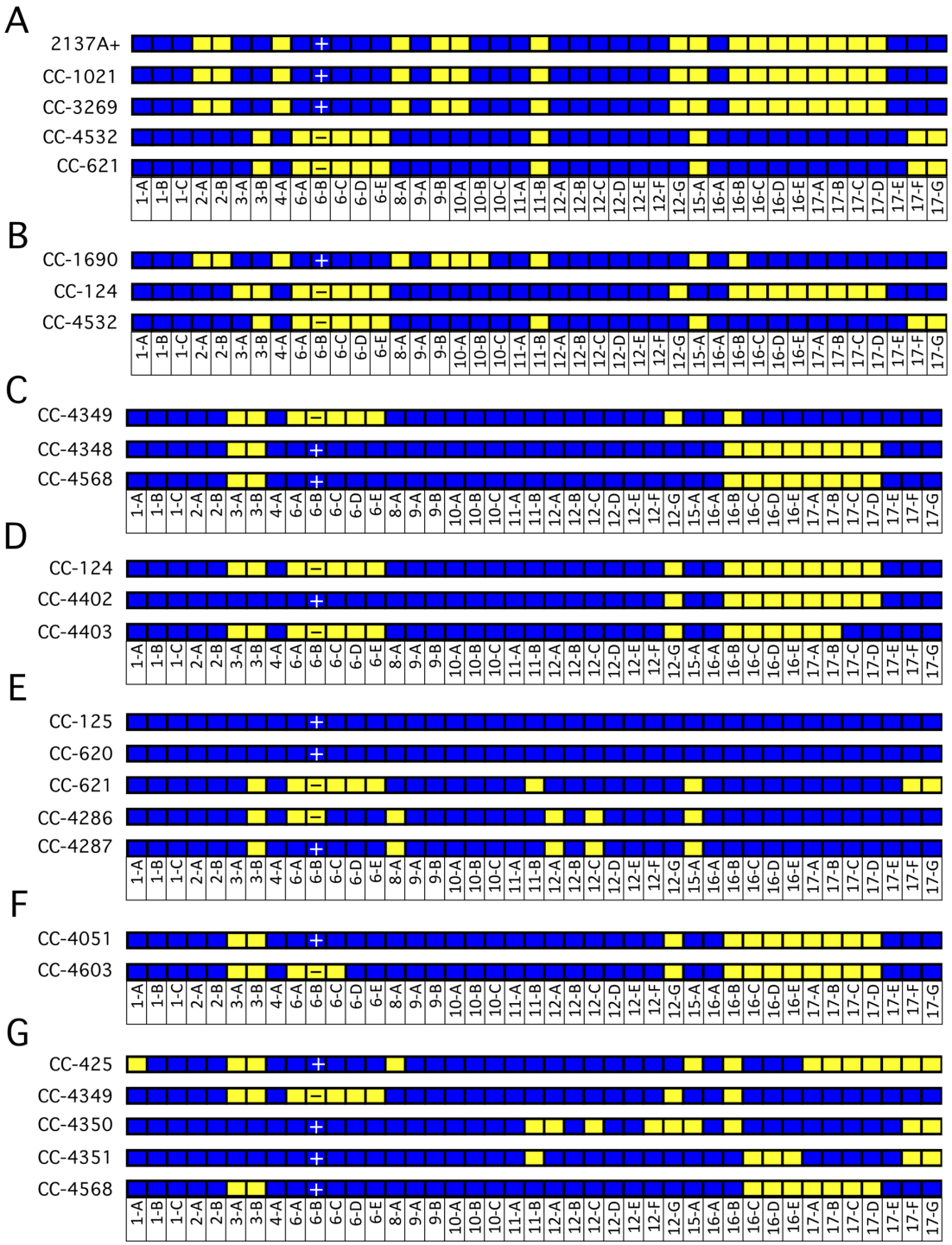
(**B**) A second batch of cultures was photographed after 5 d of growth.



Supplemental Figure 2. Callable Loci
The quality of the base calls for each of the 109 million total nucleotides in the *C. reinhardtii* genome were categorized and plotted by GATK CallableLoci for each strain. Callable loci were those base calls that were based on four or more quality control-passing reads. The remaining reads were evaluated by the software to be uncallable due to insufficient coverage, low mapping quality, or a lack of sequence information in the reference genome.



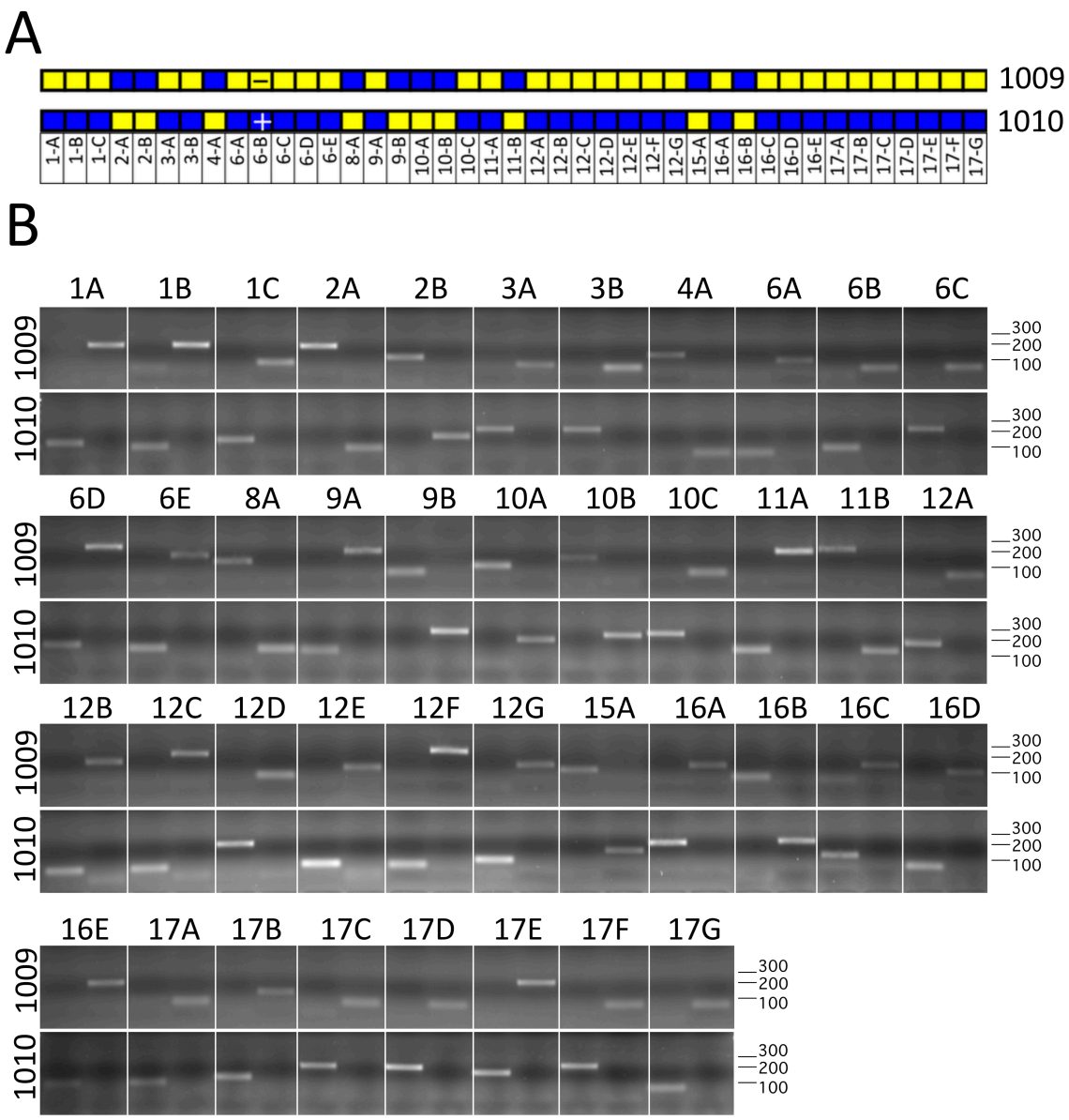
Supplemental Figure 3. Evidence for Recombination Between Haplotypes
Nucleotides the same as reference (i.e. haplotype 1) are gray. SNVs relative to reference are color-coded: green = A, blue = C, brown = G, red = T. Regions that were identified as haplotype 2 based on their pattern of SNVs are indicated by a yellow box below the alignment. Haplotype 1 regions are indicated by a blue box. The double-headed arrow indicates the 52-bp region that is the likely site of a meiotic recombination event in the cross that produced CC-3269.



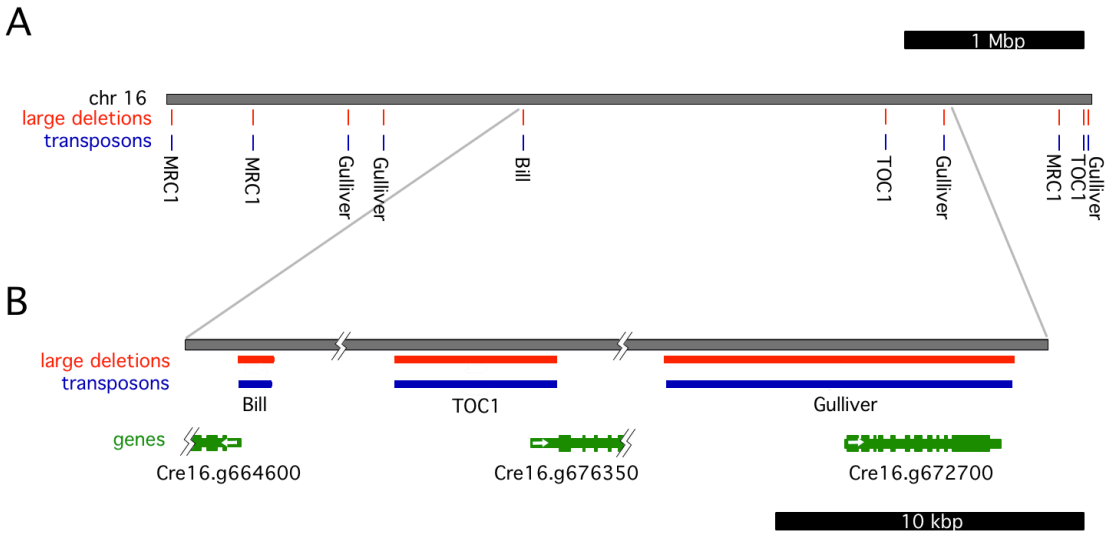
Supplemental Figure 4. Comparison of Haplotype Patterns for Selected Strains

Subsets of strains from Figure 5 are presented separately for easier comparison. Blue indicates haplotype 1, and yellow indicates haplotype 2. The mating locus is depicted with + or –.

(**A**) Strain 2137. Comparison of three examples of strain 2137 compared to CC-4532.
(**B**) CC-4532 cannot result from a cross of CC-124 and CC-1690.
(**C**) CC-4349 cannot be the parental strain of CC-4348.
(**D**) CC-124 backcrossed strains. CC-4402 and CC-4403 remain distinct from CC-124, despite 10 backcrosses to that strain.
(**E**) CC-4246 and CC4287. The parents of these two strains are not as reported, and remain to be identified.
(**F**) CC-4051 and CC-4603. These two strains are nearly isogenic. They differ in haplotype only in those blocks that include, or are adjacent to, the mating locus.
(**G**) *cw15* mutant strains. Five different *cw15* strains have dramatically different haplotypes.



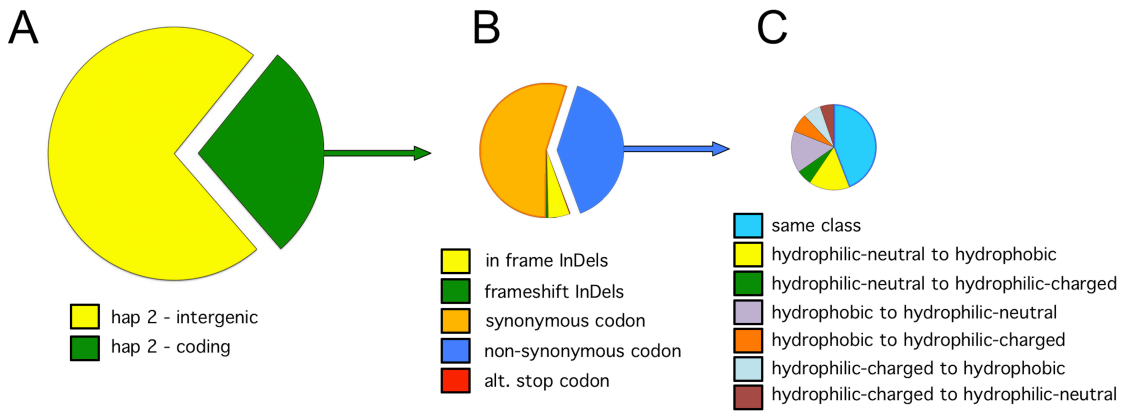
Supplemental Figure 5. Allele-Specific Amplification to Identify Haplotype
Allele-specific amplification primers were designed to amplify a product in one haplotype, but not the other, for all 41 defined haplotype blocks (Table 2). The sequences of all 82 primer pairs are included in Supplemental Dataset 6.
(**A**) Strains CC-1009 and CC-1010 have alternate haplotypes in all 41 regions.
(**B**) Haplotype scoring by analytical gel electrophoresis. DNA from CC-1009 and CC-1010 was subjected to PCR amplification with all 82 primer pairs, and scored by analytical gel electrophoresis. In each panel, the haplotype 1 specific product is on the left, and the haplotype 2 product is on the right. The position of 100, 200, and 300 bp markers is indicated to the right of each panel.



Supplemental Figure 6. Examples of Transposon Position Jumping in Chromosome 16

(**A**) Transposons in Chromosome 16. The position of 10 transposons identified in the reference sequence in chromosome 16 are depicted in blue. Large deletions (greater than 40 bp) identified by sequencing the standard laboratory strains are depicted in red. The scale bar indicates 1 Mbp.

(**B**) An expanded view of three transposons. The scale bar indicates 10 kbp. An additional track in green indicates the loci of genes likely to be affected by these transposons.



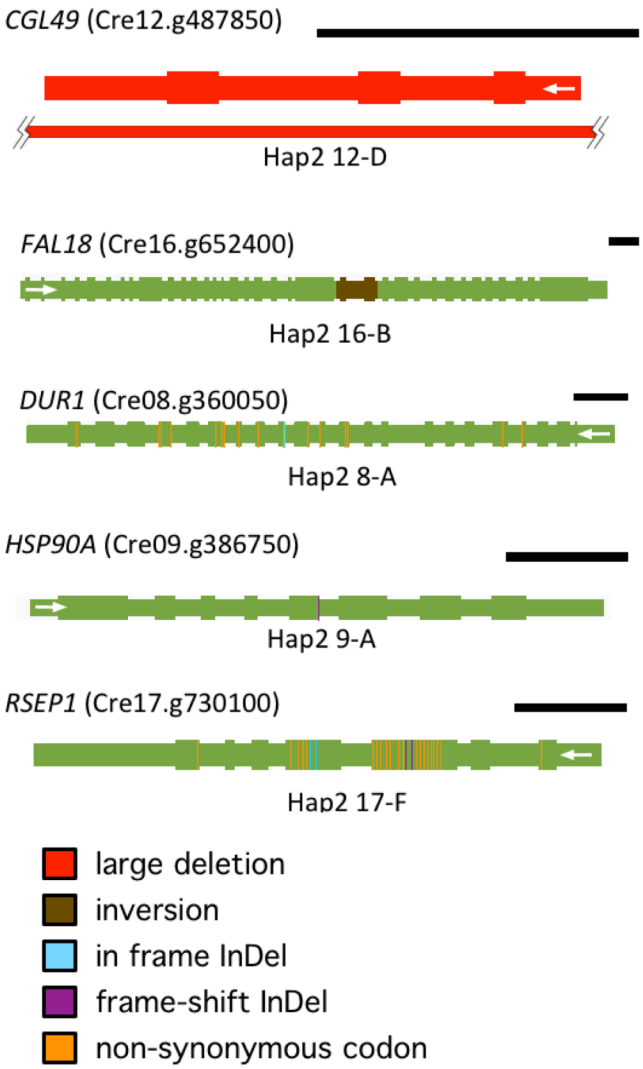
Supplemental Figure 7. Predicted Effects of Haplotype 2 Variants on Gene Models

The likely effect of the haplotype 2 SNVs and small InDels on the gene models was predicted computationally. Each class of variant is presented in a proportionately size pie chart.

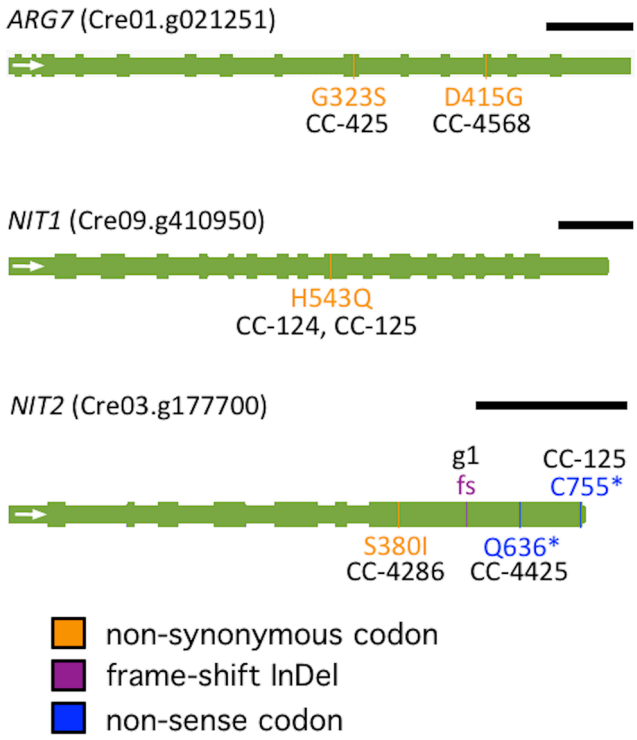
(**A**) All haplotype 2 variants. 164,606 out of 592,554 haplotype 2 small variants were localized within coding regions.

(**B**) Coding region-localized variants. These were classified based on their predicted effect on the relevant gene model.

(**C**) Non-synonymous codon changes. The 64,685 non-synonymous codon changes are further subdivided based on the predicted change to the encoded amino acid.

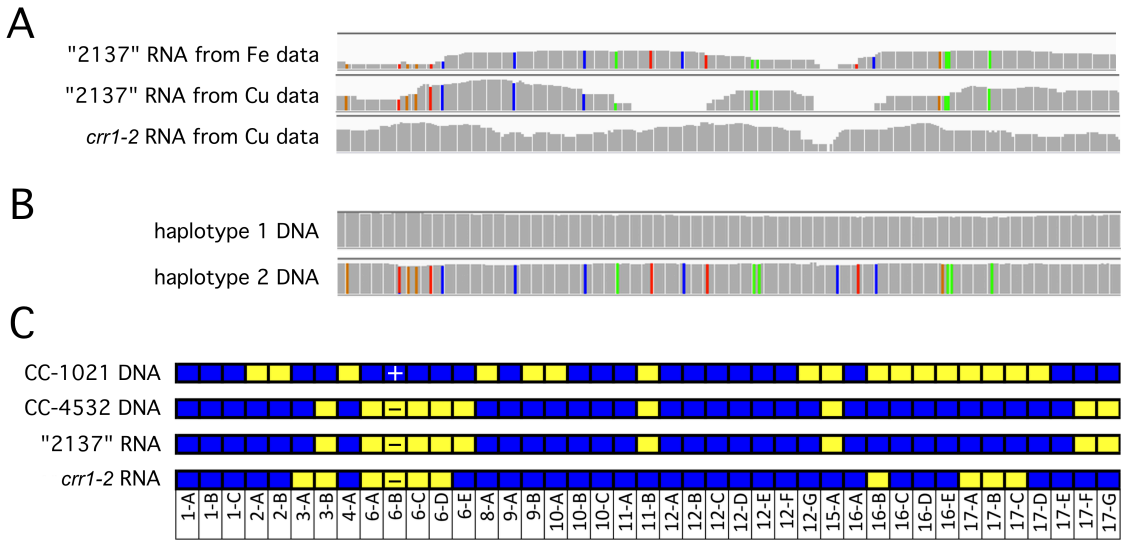


Supplemental Figure 8. Variants in Genes Attributable to Haplotype 2
The predicted effects of haplotype 2 variants on gene models are color coded according to the legend, and a black scale bar representing 1 kbp of DNA is included for each.



Supplemental Figure 9. Laboratory-Originated Mutations in Commonly Studied Genes

Presented here are mutations that we identified in three commonly studied genes. A black scale bar indicating 1 kbp of DNA is included for each gene. Mutations are color coded according to the legend, and an example strain that carries the mutation is indicated for each variant.



Supplemental Figure 10. Determining Haplotype from RNA-seq Data Identifies Mislabeled "2137" Strain

Reads from RNA-seq experiments performed by this group in 2007 were realigned to the reference genome in order to identify the haplotypes of the strains used in those experiments.

(**A**) A representative region of chromosome 17 from 4,359,642 to 4,359,871 that has a distinctive pattern of SNVs between the two haplotypes. The coverage of RNA-seq reads to the *SDR28* locus is shown for the indicated experiments. Nucleotides the same as reference (i.e. haplotype 1) are gray. SNVs are color-coded: green = A, blue = C, brown = G, red = T. "2137" RNA from Fe data indicates reads from an RNA-seq study in a strain that was believed to be 2137 that was grown in limiting iron (Urzica et al., 2012). "2137" RNA from Cu data indicates reads from an independent RNA-seq study performed with the same strain grown in limiting copper (Castruita et al., 2011). *crr1-2* RNA from Cu data indicates reads from the same copper study performed in mutant strain *crr1-2*.

(**B**) For comparison, genomic data from the current study is included to demonstrate the pattern of SNVs in the two haplotypes at this locus. Haplotype 1 reads are from CC-1010 and haplotype 2 reads from CC-1009.

(**C**) Using this approach, the "2137" and *crr1-2* data were scored for haplotype in each block. The resulting haplotypes from the RNA-seq data are compared to the indicated DNA haplotypes.

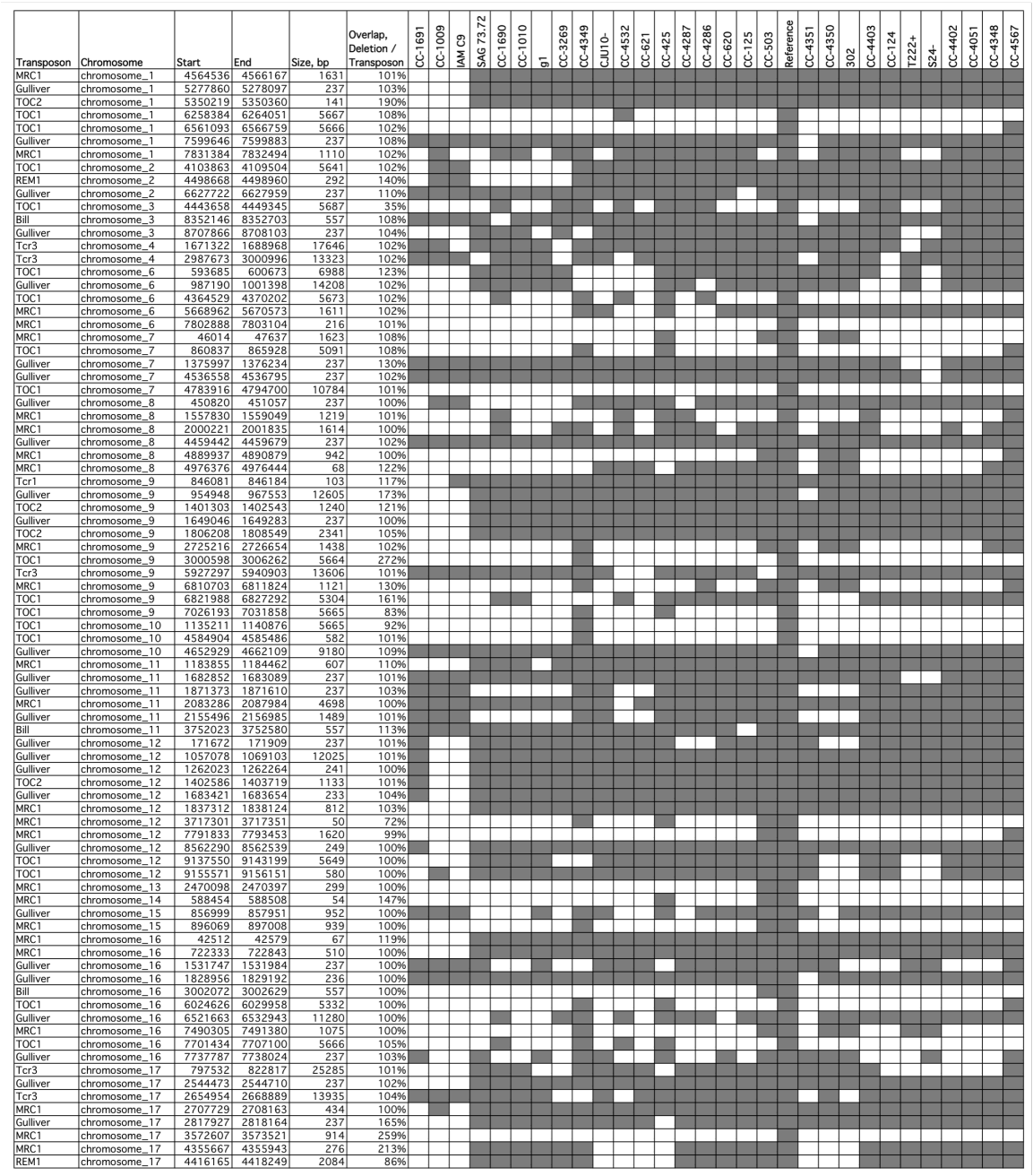
Transversions

A -> C	29,483
G -> T	29,715
A -> T	17,238
T -> A	17,468
C -> A	29,294
T -> G	29,098
C -> G	32,082
G -> C	31,725

Transitions

A -> G	77,280
C -> T	77,003
G -> A	76,862
T -> C	77,392

Supplemental Table 1. Transversions and Transitions for all SNVs
The 524,640 SNVs that were identified in this study were subdivided into each of the possible transversions and transitions.



Transposon	Chromosome	Start	End	Size, bp	Overlap, Deletion / Transposon	CC-1691	CC-1009	IAM C9	SAG 73.72	CC-1690	CC-1010	g1	CC-3269	CC-4349	CJU10-	CC-4532	CC-621	CC-425	CC-4287	CC-4286	CC-620	CC-125	CC-503	Reference	CC-4351	CC-4350	302	CC-4403	CC-124	T222+	S24-	CC-4402	CC-4051	CC-4348	CC-4567
MRC1	chromosome_1	4564536	4566167	1631	101%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_1	5277860	5278097	237	103%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
TOC2	chromosome_1	5350219	5350360	141	190%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
TOC1	chromosome_1	6258384	6264051	5667	108%											■								■												
TOC1	chromosome_1	6561093	6566759	5666	102%																			■												■
Gulliver	chromosome_1	7599646	7599883	237	108%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_1	7831384	7832494	1110	102%		■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC1	chromosome_2	4103863	4109504	5641	102%		■	■					■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
REM1	chromosome_2	4498668	4498960	292	140%		■	■					■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_2	6627722	6627959	237	110%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■		■	■	■	■	■	■	■	■	■	■
TOC1	chromosome_3	4443658	4449345	5687	35%					■				■			■		■	■	■		■	■		■	■		■	■		■	■	■	■
Bill	chromosome_3	8352146	8352703	557	108%		■	■	■		■	■	■	■		■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_3	8707866	8708103	237	104%		■	■	■	■	■	■		■		■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Tcr3	chromosome_4	1671322	1688968	17646	102%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Tcr3	chromosome_4	2987673	3000996	13323	102%	■	■	■		■	■	■	■	■	■		■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC1	chromosome_6	593685	600673	6988	123%				■	■	■	■	■				■	■	■	■	■	■	■	■		■	■	■		■		■	■	■	■
Gulliver	chromosome_6	987190	1001398	14208	102%				■	■	■	■	■				■	■	■	■	■	■	■	■		■	■	■		■		■	■	■	■
TOC1	chromosome_6	4364529	4370202	5673	102%					■				■		■		■		■															
MRC1	chromosome_6	5668962	5670573	1611	102%									■	■						■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_6	7802888	7803104	216	101%																			■											
MRC1	chromosome_7	46014	47637	1623	108%													■					■	■		■	■								
TOC1	chromosome_7	860837	865928	5091	108%									■				■						■											■
Gulliver	chromosome_7	1375997	1376234	237	130%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_7	4536558	4536795	237	102%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■
TOC1	chromosome_7	4783916	4794700	10784	101%																			■												
Gulliver	chromosome_8	450820	451057	237	100%		■	■					■	■	■	■	■	■		■	■	■	■	■		■	■	■	■			■	■	■	■
MRC1	chromosome_8	1557830	1559049	1219	101%					■						■		■	■					■		■	■	■							■
MRC1	chromosome_8	2000221	2001835	1614	100%								■	■		■		■	■	■		■	■	■		■	■	■				■		■	■
Gulliver	chromosome_8	4459442	4459679	237	102%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_8	4889937	4890879	942	100%																			■			■								
MRC1	chromosome_8	4976376	4976444	68	122%										■				■		■	■	■	■		■	■								■
Tcr1	chromosome_9	846081	846184	103	117%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_9	954948	967553	12605	173%					■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC2	chromosome_9	1401303	1402543	1240	121%					■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_9	1649046	1649283	237	100%					■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC2	chromosome_9	1806208	1808549	2341	105%					■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_9	2725216	2726654	1438	102%									■										■		■	■								■
TOC1	chromosome_9	3000598	3006262	5664	272%									■										■		■	■								■
Tcr3	chromosome_9	5927297	5940903	13606	101%	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_9	6810703	6811824	1121	130%									■										■		■	■								■
TOC1	chromosome_9	6821988	6827292	5304	161%					■	■			■			■		■	■	■	■	■	■		■	■		■	■	■	■	■	■	■
TOC1	chromosome_9	7026193	7031858	5665	83%									■					■																
TOC1	chromosome_10	1135211	1140876	5665	92%									■										■											
TOC1	chromosome_10	4584904	4585486	582	101%									■										■											
Gulliver	chromosome_10	4652929	4662109	9180	109%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_11	1183855	1184462	607	110%				■	■	■		■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_11	1682852	1683089	237	101%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■		■	■	■	■
Gulliver	chromosome_11	1871373	1871610	237	103%	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_11	2083286	2087984	4698	100%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_11	2155496	2156985	1489	101%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Bill	chromosome_11	3752023	3752580	557	113%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_12	171672	171909	237	101%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_12	1057078	1069103	12025	101%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_12	1262023	1262264	241	100%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC2	chromosome_12	1402586	1403719	1133	101%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_12	1683421	1683654	233	104%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_12	1837312	1838124	812	103%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_12	3717301	3717351	50	72%									■					■					■											
MRC1	chromosome_12	7791833	7793453	1620	99%																			■											■
Gulliver	chromosome_12	8562290	8562539	249	100%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
TOC1	chromosome_12	9137550	9143199	5649	100%				■	■	■	■			■	■	■	■	■	■	■	■	■	■		■		■	■		■	■	■	■	■
TOC1	chromosome_12	9155571	9156151	580	100%		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■		■	■		■	■	■	■	■
MRC1	chromosome_13	2470098	2470397	299	100%																			■											
MRC1	chromosome_14	588454	588508	54	147%													■						■											
Gulliver	chromosome_15	856999	857951	952	100%	■	■	■				■		■					■	■	■	■	■	■		■		■	■	■	■	■	■	■	■
MRC1	chromosome_15	896069	897008	939	100%																			■											
MRC1	chromosome_16	42512	42579	67	119%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_16	722333	722843	510	100%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_16	1531747	1531984	237	100%	■	■	■	■				■	■	■	■		■	■	■	■	■	■	■		■	■	■			■	■	■	■	■
Gulliver	chromosome_16	1828956	1829192	236	100%	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Bill	chromosome_16	3002072	3002629	557	100%																			■											
TOC1	chromosome_16	6024626	6029958	5332	100%									■				■						■											■
Gulliver	chromosome_16	6521663	6532943	11280	100%					■			■	■		■		■	■	■		■	■	■		■	■		■	■		■	■	■	■
MRC1	chromosome_16	7490305	7491380	1075	100%									■										■						■	■				
TOC1	chromosome_16	7701434	7707100	5666	105%					■				■		■		■						■											
Gulliver	chromosome_16	7737787	7738024	237	103%	■					■	■		■	■		■		■		■		■	■		■	■		■		■				■
Tcr3	chromosome_17	797532	822817	25285	101%				■	■	■		■	■	■	■	■		■	■	■	■	■	■		■	■		■	■	■	■	■	■	■
Gulliver	chromosome_17	2544473	2544710	237	102%				■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Tcr3	chromosome_17	2654954	2668889	13935	104%	■	■	■	■	■	■			■		■	■	■	■	■	■	■	■	■		■		■	■	■	■	■	■	■	■
MRC1	chromosome_17	2707729	2708163	434	100%		■		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
Gulliver	chromosome_17	2817927	2818164	237	165%				■	■	■	■	■	■	■	■	■	■		■	■	■	■	■		■	■	■	■	■	■	■	■	■	■
MRC1	chromosome_17	3572607	3573521	914	259%																			■											
MRC1	chromosome_17	4355667	4355943	276	213%				■	■	■	■	■	■					■	■	■	■	■	■		■	■		■	■	■	■	■	■	■
REM1	chromosome_17	4416165	4418249	2084	86%				■	■	■	■	■	■					■	■	■	■	■	■		■	■		■	■	■	■	■	■	■

Supplemental Table 2. Transposon Position Jumping at 84 Loci.
The coordinates of eight different *C. reinhardtii* transposons were identified in the reference genome sequence. Those that had substantial overlap with the coordinates of large deletions identified in one or more of the sequenced strains are presented. Gray boxes indicate that the transposon sequence is present in that strain, and white boxes indicate that the transposon sequence is absent.

Gene ID	Gene Name	Gene Description	Haplotype 2 Variant
Cre01.g009650	BUG25	Basal body protein and putative AP2 domain transcription factor	9112 bp deletion removes all of exon 1 and part of exon 2 in BUG25. 1 other gene is completely removed and 1 other gene is partially removed.
Cre01.g009800	FAP289	Flagellar Associated Protein, coiled-coil	79,864 bp deletion completely removes FAP289 and 6 other genes, and partially removes 2 other genes.
Cre01.g012100	ARS4	Arylsulfatase	77 bp deletion removes part of exon 6 in ARS4. Also, 1 frame shift InDel, 1 in-frame InDel, and 17 nonsynonymous codons.
Cre01.g012800	FAP230	Flagellar Associated Protein	15,260 bp deletion causes complete loss of FAP230 and partial loss of 2 other genes
Cre01.g013300	DEG10	DegP-type protease	1 in frame InDel, 11 non-synonymous codons
Cre01.g016500	DLD2	Dihydrolipoamide dehydrogenase	1 in frame InDel, 21 non-synonymous codons
Cre01.g044100	AMYB3	Beta-amylase	10 non-synonymous codons
Cre02.g113850	PBGD2 / HEM3	Porphobilinogen deaminase	2 frame shift InDels, 2 non-synonymous codons
Cre02.g118950	PRPS17	Plastid ribosomal protein S17	1 in frame InDel
Cre06.g252200	TOC34	Translocon at the outer envelope membrane of chloroplasts, 75 kD	14 non-synonymous codons
Cre06.g255450	MAT3	Retinoblastoma protein	6 non-synonymous codons
Cre06.g260450	LCI20	2-oxoglutarate/malate translocator	1 in frame InDel
Cre08.g360050	DUR1	Urea carboxylase/allophanate hydrolase	1 in frame InDel, 16 non-synonymous codons
Cre08.g360100	DUR2	Allophanate hydrolase	7 non-synonymous codons
Cre09.g386750	HSP90A	Heat shock protein 90A	1 frame shift
Cre09.g394200	FAP102	Flagellar Associated Protein	Insertion in 5th exon of FAP102.
Cre09.g395950	AOX1	Alternative oxidase	1 in frame InDel, 2 non-synonymous codons
Cre09.g396650	PAT2	Phosphate acetyltransferase	1626 bp deletion removes exon 17. A second 105 bp deletion removes part of exon 18.
Cre09.g396700	ACK1	Acetate kinase	9 non-synonymous codons
Cre09.g399400	FAP199 / TGL15	Triacylglycerol lipase	265 bp deletion removes most of exon 1.
Cre09.g403900	FAP294	Flagellar Associated Protein	12,661 bp deletion removes FAP294 and 2 other genes, and partially removes 2 more genes.
Cre10.g419050	ATP1B	Mitochondrial F1F0 ATP synthase, alpha subunit	3 in frame InDels, 3 non-synonymous codons
Cre10.g465550	CLPD1	ClpD chaperone, Hsp100 family	1 in frame InDel, 3 non-synonymous codons
Cre10.g465900	CDKA1	Cyclin dependent protein kinase	21,642 bp deletion removes CDKA1 and 5 other genes, and partially removes 1 other gene.
Cre12.g487850	CGL49 / ARL11	ARF/SAR superfamily small monomeric GTP binding protein	27,736 bp deletion removes all of CGL49 and 3 other genes, and partially removes 1 other gene.
Cre12.g488500	ARC6	unannotated in Phytozome10	12 non-synonymous codons
Cre12.g490700	MIN1	Mini-eyespot protein	1 in frame InDel, 3 non-synonymous codons
Cre12.g495100	PSR1	Phosphorus starvation response protein, Myb-like transcriptional regulator	1 in frame InDel, 4 non-synonymous codons
Cre12.g547100	CGL2 / SMM43	S-adenosyl-L-methionine-dependent methyltransferase	23,595 bp deletion removes all of CGL2 and 4 other genes, and part of 1 other gene.
Cre12.g554250	LPB1	Low Photochemical Bleaching protein	2 in frame InDels, 7 non-synonymous codons
Cre12.g554300	NSS6	Sodium:solute symporter	5 in frame InDels, 24 non-synonymous codons
Cre16.g652400	FAL18	Similar to Flagellar Associated Protein FAP183	A 579 bp inverion reverses the orientation of exon 22. A second 762 bp inversion reverses the orientation of exon 23.
Cre16.g654150	FAP63	Flagellar Associated Protein	17,916 bp deletion removes 5' UTR of FAP63 and completely removes 4 other genes.
Cre17.g698850	ISA2	Isoamylase-type starch debranching enzyme	19,265 bp inversion disrupts ISA2 and 1 other gene. 2 other genes in reverse orientation. Also, 1 in frame InDel, 9 non-synonymous codons.
Cre17.g699500	TTLL9 / FAP267 / TTL8	Tubulin tyrosine ligase	2412 bp inversion disrupts TTLL9.
Cre17.g713200	OMT2	Chloroplast oxoglutarate-malate translocator	17,076 bp deletion removes part of OMT2 and completely removes 2 other genes.
Cre17.g720400	HMA1	Heavy metal transporting ATPase	5 in frame InDels, 24 non-synonymous codons
Cre17.g728900	FSA1 / TAL3	Transaldolase	22,593 bp deletion completely removes FSA1 and 1 other gene, and partially removes 2 other genes.
Cre17.g730100	RSEP1 / RSE1	Intramembrane metalloprotease	2 frame shifts, 2 in frame InDels, 21 non-synonymous codons
Cre17.g739650	MFT1 / MAE1	MATE efflux family protein	4 in frame InDels, 28 non-synonymous codons

Supplemental Table 3. Examples of Genes with Predicted Haplotype 2-Specific Variants

Gene ID	Gene Name	GO Identifiers	GO Names
Cre01.g053450	CYA1	GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre02.g100500	CYG22	GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre02.g103200		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre04.g217450		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre05.g237800	CYG64	GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre06.g290200	CYG39	GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre07.g318551	CYA8	GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre07.g342350		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre08.g362100		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre08.g373200		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre09.g386900		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre10.g429750		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre11.g467651		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre13.g567800		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling
Cre13.g605100		GO:0007154, GO:0007165, GO:0023052, GO:0044700	cell communication, signal transduction, signaling, single organism signaling

Supplemental Table 4. Enrichment of Gene Ontology Terms in Laboratory-Originated Loss-of-Function Mutations

Original Strain	Sequence-Verified Clone
CC-124	CC-5074
CC-125	CC-5075
CC-425	CC-5076
CC-503	CC-5077
CC-620	CC-5078
CC-621	CC-5079
CC-1009	CC-5080
CC-1010	CC-5081
CC-1690	CC-5082
CC-1691	CC-5083
CC-2290	CC-5084
CC-3269	CC-5085
CC-4051	CC-5086
CC-4286	CC-5087
CC-4287	CC-5088
CC-4348	CC-5089
CC-4350	CC-5090
CC-4351	CC-5091
CC-4402	CC-5092
CC-4403	CC-5093
CC-4425	CC-5094
CC-4504	CC-5095
pcc1-1	CC-5096
CC-4603	CC-5097
IAM C-9	CC-5098
SAG 73.72	CC-5099
S24-	CC-5100
T222+	CC-5101
g1	CC-5102
CJU10-	CC-5103

Supplemental Table 5. Sequence-Verified Clones Available from the Chlamydomonas Resource Center