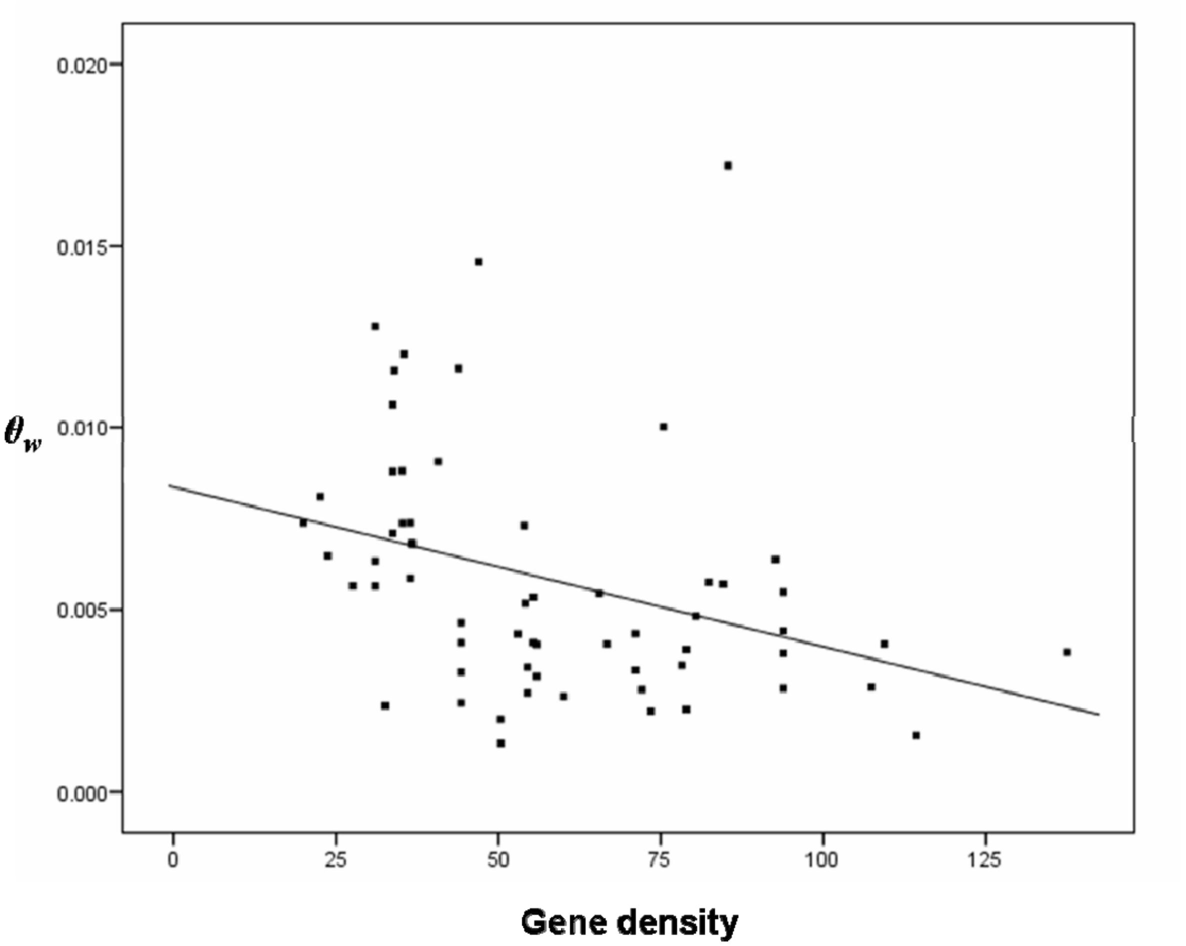
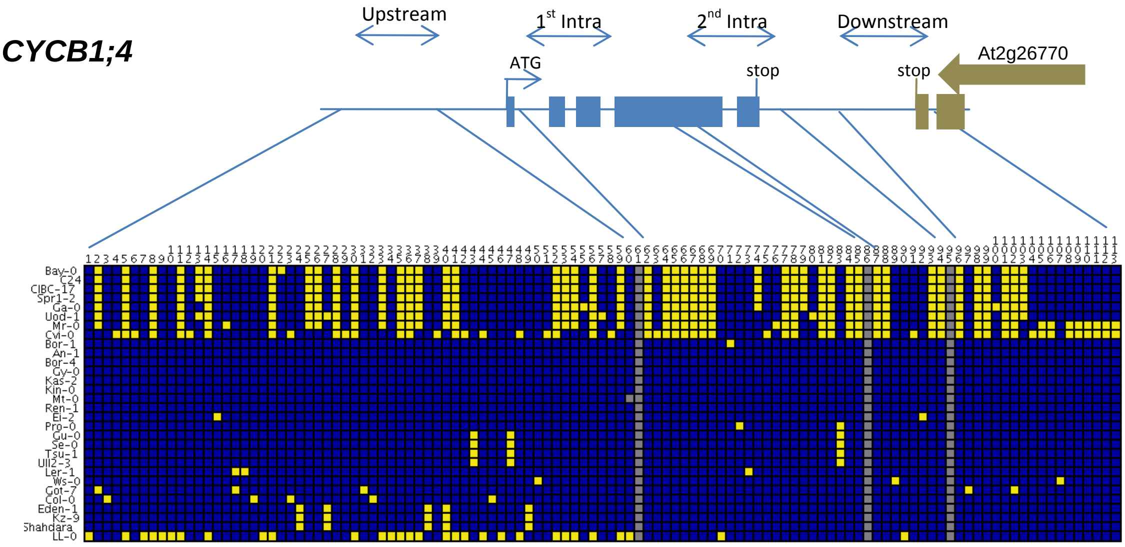
Supplemental Data, Sterken et al., (2009) A population genomics study of the Arabidopsis core cell cycle genes shows the signature of natural selection.

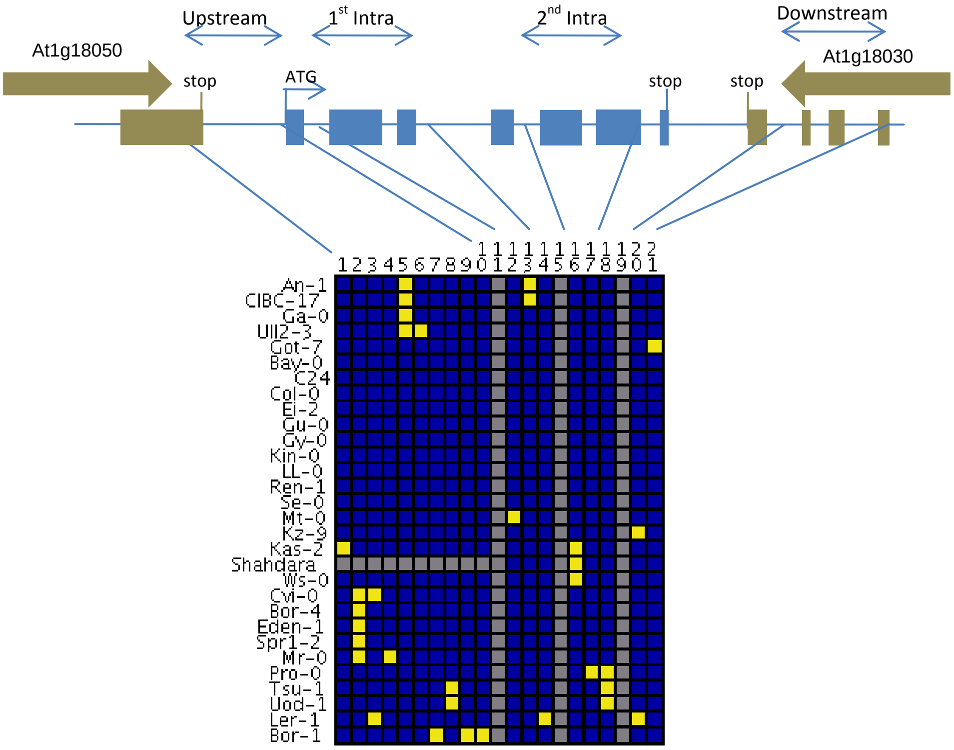


Supplemental Figure 1. Scatter between SNP diversity θ_w per CCC gene region and local gene density (measured in ORF per centiMorgan). $R^2 = 0.118$, Pearson correlation.

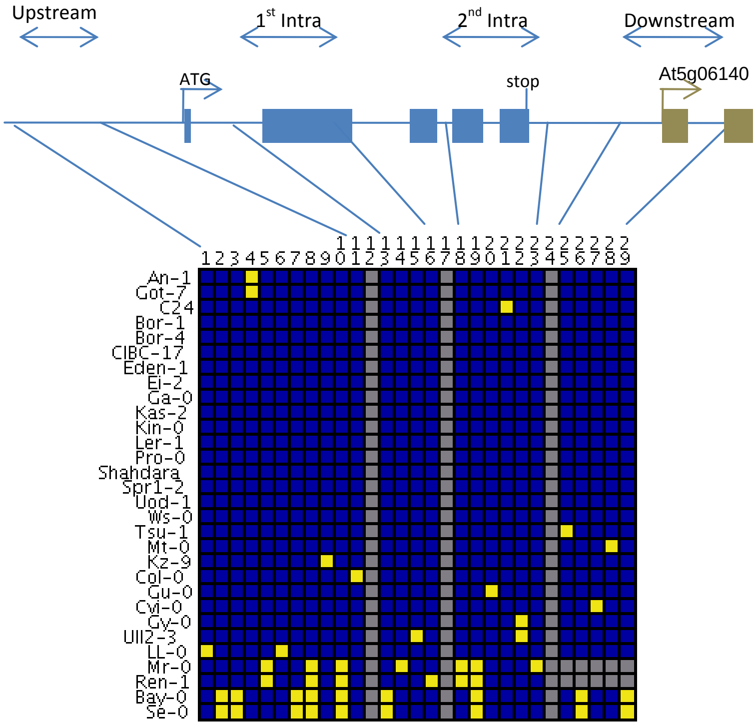
CYCB1;4



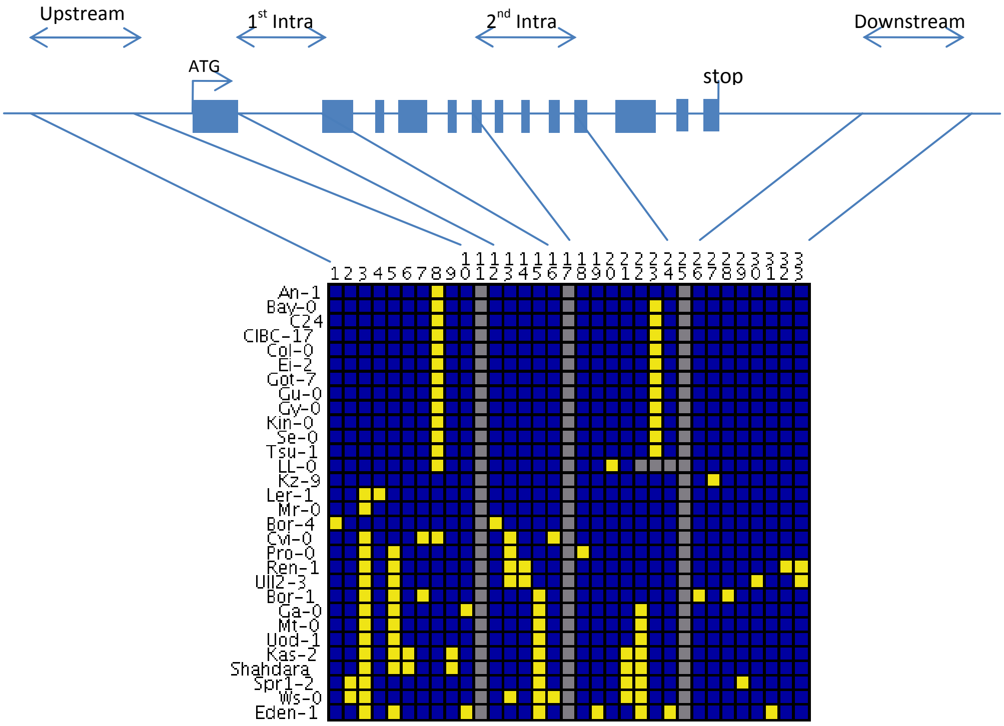
CDKD;3



CYCB1;2



E2Fa



Supplemental Figure 2. Visual representation of haplotypes of the *CYCB1;4*, *CDKD;3*, *CYCB1;2* and *E2Fa* loci.

Supplemental Table 1. List of accessions used

Seeds are available from the Nottingham *Arabidopsis* Stock Center (NASC) under the stock numbers indicated, or as part from the “2010” collection of Nordborg *et al*. (2005) under stock number N22660

Accession	Stock number
An-1	N22626
Bay-0	N22633
Bor-1	N22590
Bor-4	N22591
C24	N22620
CIBC-17	N22603
Col-0	N22625
Cvi-0	N22614
Eden-1	N22572
Ei-2	N22616
Ga-0	N22634
Got-7	N22608
Gu-0	N22617
Gy-0	N22631
Kas-2	N22638
Kin-0	N22654
Kz-9	N22607
L*er*-1	N22618
LL-0	N22650
Mr-0	N22640
Mt-0	N22642
Pro-0	N22649

Ren-1	N22610
Se-0	N22646
Shahdara	N22652
Spr1-2	N22582
Tsu-1	N22641
Ull2-3	N22587
Uod-1	N22612
Ws-0	N22623

Supplemental Table 2. Summary of nucleotide diversity

CCC	#genes	Average length (bp)	Average θ_w
Intron Sites	60	489	0.00662
Exon Sites	61	665	0.00338
Synonymous Sites	61	145	0.00745
Nonsynonymous Sites	61	520	0.00227
Total Intragenic Sites	61	1145	0.00474
Upstream Sites	58	535	0.00892
Downstream Sites	49	480	0.00697
Nordborg data set			
Intron Sites[a]	525	274	0.00761
Exon Sites[b]	759	430	0.00438
Synonymous Sites[b]	759	96	0.00985
Nonsynonymous Sites[b]	759	334	0.00249
Total Intragenic Sites	1029	507	0.00523
Upstream Sites	127	367	0.00670
Downstream Sites	120	309	0.00766

[a] Only fragments with at least 100 bp intron sites are analyzed.

[b] Only fragments with at least 80 codons are analyzed

Supplemental Table 3. Data for the CCC frameshifts

Gene name	Amino acids	Accessions	Frameshift position	Stop codon position
CDKB1;2	310	Kas-2	112	123
		An-1,CIBC-17 Ei-2,Gy-0 L*er*-1,LL-0,Pro-0	127	127
		Bay-0,Ga-0,Ull2-3	146	153
		Gu-0	301	undetermined
CYCD7;1	341	Mr-0	No	288
CYCA3;3	327	Uod-1	No	296

Supplemental Table 4. Summary statistics for coding sequence

Gene	*Ka*/*Ks*	*dN*[a]	*dS*[b]	*pN*[c]	*pS*[d]	MK-*p*[e]	MK-*p*[f]	γ[g]	γ 95% CI[h]	*k*[i]
CDKA;1	0.020	0	9	0	1	1	1	Na	Na	1
CDKB1;1	0.089	5	16	0	2	1	1	0.096	-1.093/1.448	1
CDKB1;2	na	na	na	na	na	na	na	na	na	na
CDKB2;1	0.028	2	15	2	1	0.088	1	-0.633	-1.887/0.704	1
CDKB2;2	0.019	1	14	1	6	1	1	-0.497	-1.865/0.943	1
CDKC;1	0.094	4	6	1	0	0.455	1	-0.192	-1.399/1.137	1
CDKC;2	0.114	6	13	1	1	1	1	-0.061	-1.193/1.236	1
CDKD;1	0.094	7	22	7	11	0.336	1	-1.027	-1.951/-0.030	1
CDKD;2	0.055	5	40	3	3	0.042	1	-0.546	-1.648/0.707	1
CDKD;3	0.096	5	19	2	2	0.253	1	-0.351	-1.477/0.947	1
CDKE;1	0.104	13	44	0	9	0.186	1	0.429	-0.667/1.766	1
CDKF;1	0.161	8	33	0	2	1	1	0.233	-0.920/1.580	2
CKS1	0.045	1	11	0	0	na	na	-0.211	-1.606/1.290	1
CKS2	0	0	7	0	4	1	1	na	na	1
CYCA1;1	0.077	6	19	6	10	0.485	1	-0.972	-1.947/0.108	1
CYCA1;2	0.293	22	15	11	5	0.758	1	-0.647	-1.349/0.173	4
CYCA2;1	0.315	29	27	5	1	0.209	1	0.209	-0.650/1.281	4
CYCA2;2	0.210	8	10	2	3	1	1	-0.137	-1.202/1.125	3
CYCA2;3	0.226	12	15	8	4	0.301	1	-0.805	-1.627/0.121	3
CYCA2;4	0.405	12	10	4	4	1	1	-0.267	-1.224/0.874	5
CYCA3;1	0.155	14	24	18	23	0.647	1	-1.470	-2.108/-0.809	2
CYCA3;2	0.186	16	37	8	20	1	1	-0.609	-1.411/0.308	2
CYCA3;3	0.453	25	22	26	2	0.000	0.017	-1.384	-1.902/-0.847	5
CYCA3;4	0.135	10	19	6	5	0.295	1	-0.678	-1.608/0.376	2
CYCB1;1	0.148	14	25	4	2	0.199	1	-0.170	-1.117/0.955	2
CYCB1;2	0.096	8	16	2	0	0.138	1	-0.148	-1.202/1.093	1
CYCB1;3	0.262	26	45	8	0	0.001	0.041	-0.217	-0.992/0.732	4
CYCB1;4	0.171	19	32	6	5	0.326	1	-0.227	-1.071/0.782	2
CYCB2;1	0.213	10	15	22	22	0.461	1	-1.875	-2.549/-1.232	3
CYCB2;2	0.304	13	13	6	0	0.059	1	-0.508	-1.382/0.532	4
CYCB2;3	0.284	11	14	3	6	0.704	1	-0.163	-1.136/1.011	4
CYCB2;4	0.150	9	17	3	0	0.060	1	-0.265	-1.285/0.929	2
CYCB3;1	0.213	14	21	4	2	0.377	1	-0.165	-1.112/0.964	3
CYCD1;1	0.127	6	16	5	13	1	1	-0.815	-1.804/0.301	2
CYCD2;1	0.233	10	13	3	2	0.639	1	-0.201	-1.211/1.009	3
CYCD3;1	0.262	14	13	6	3	0.700	1	-0.452	-1.325/0.597	4
CYCD3;2	0.168	16	28	6	3	0.140	1	-0.367	-1.211/0.656	2
CYCD3;3	0.257	10	13	0	2	0.5	1	0.341	-0.768/1.703	4
CYCD4;1	0.387	13	8	4	1	0.628	1	-0.221	-1.169/0.911	5
CYCD4;2	0.317	10	14	6	2	0.220	1	-0.682	-1.562/0.317	4
CYCD5;1	0.288	24	24	3	6	0.476	1	0.331	-0.593/1.494	4
CYCD6;1	0.247	16	18	7	7	1	1	-0.485	-1.295/0.487	3
CYCD7;1	0.319	25	25	28	20	0.426	1	-1.455	-1.966/-0.928	4

CYCH;1	0.326	8	9	4	3	1	1	-0.497	-1.512/0.666	4
DEL1	0.123	12	23	1	3	1	1	0.229	-0.840/1.506	2
DEL2	0.643	14	10	5	4	1	1	-0.317	-1.214/0.764	6
DEL3	0.268	14	18	3	2	0.644	1	-0.018	-0.966/1.156	4
DPa	0.048	2	18	1	4	0.504	1	-0.380	-1.675/0.998	1
DPb	0.280	5	13	2	3	0.621	1	-0.349	-1.475/0.960	4
E2Fa	0.170	3	5	1	0	0.444	1	-0.286	-1.507/1.052	2
E2Fb	0.221	5	10	1	2	1	1	-0.117	-1.283/1.264	3
E2Fc	0.244	8	9	0	1	1	1	0.238	-0.856/1.591	3
KRP1	0.552	19	6	8	6	0.287	1	-0.468	-1.265/0.477	6
KRP2	0.180	15	25	2	1	0.552	1	0.179	-0.808/1.369	2
KRP3	0.202	12	19	3	5	1	1	-0.119	-1.108/1.076	3
KRP4	0.277	16	19	5	2	0.410	1	-0.216	-1.091/0.894	4
KRP5	0.547	12	7	1	0	1	1	0.227	-0.838/1.522	6
KRP6	0.648	24	6	2	5	0.016	0.931	0.469	-0.489/1.684	6
KRP7	0.410	6	3	4	2	1	1	-0.656	-1.684/0.527	5
Rb	0.157	5	11	0	3	0.530	1	0.086	-1.116/1.487	2
Wee1	0.148	11	24	1	2	1	1	0.189	-0.874/1.481	2

[a] Total number of fixed non synonymous mutations
[b] Total number of fixed synonymous mutations
[c] Total number of polymorphic non synonymous mutations
[d] Total number of polymorphic non synonymous mutations
[e] *P*-value of the MK-test
[f] Bonferroni corrected *P*-value of the MK-test
[g] MKPRF selection parameter
[h] 95% Confidence Interval of the MKPRF selection parameter
[i] *Ka*/*Ks* cluster number based on partitioning around medoids algorithm