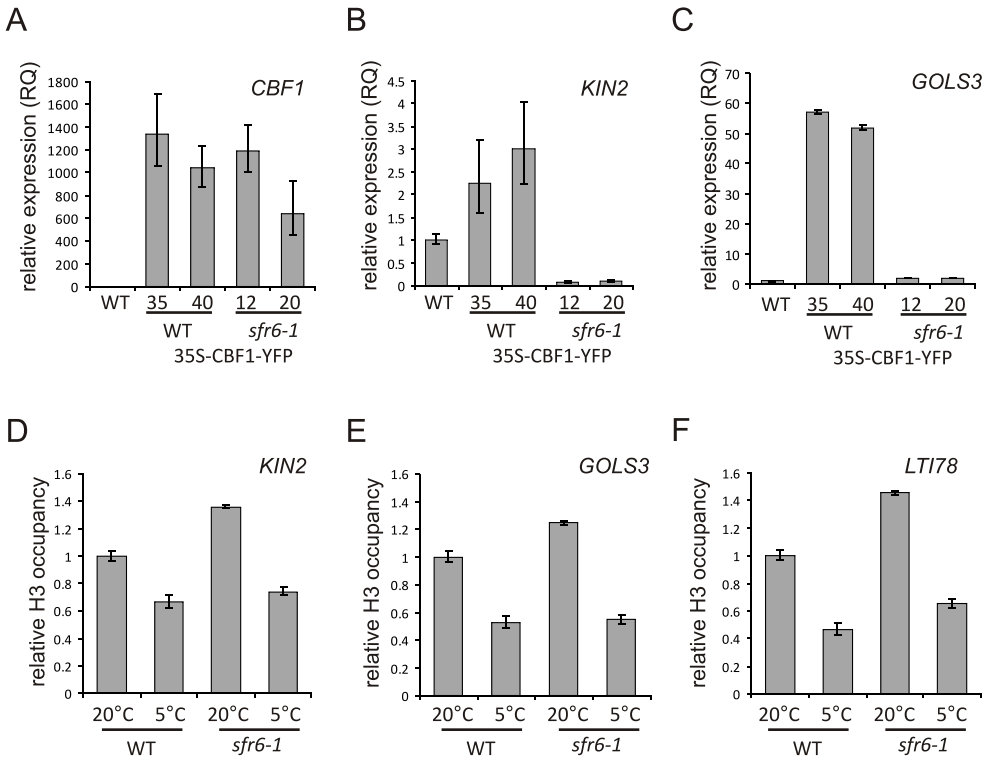
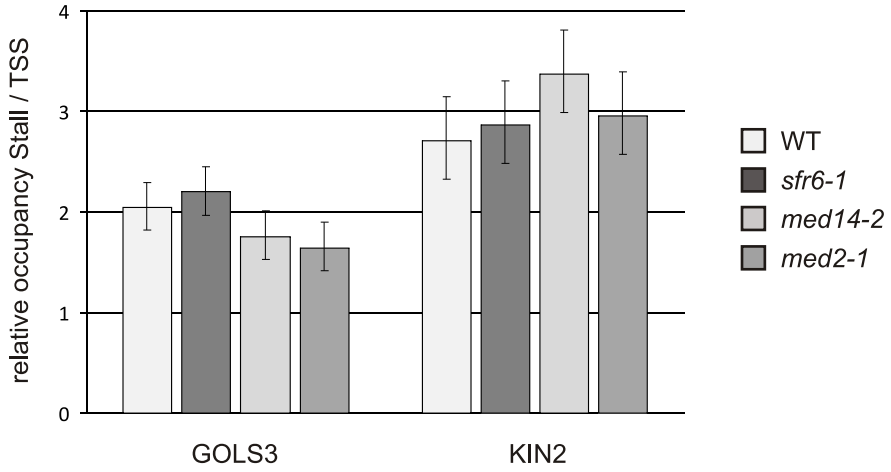


Supplemental Figure 1. Overexpression of CBF1-YFP elicits *COR* gene expression in WT but not *sfr6-1*. H3 occupancy at *COR* gene promoters alters in response to cold by equivalent amounts in WT and *sfr6-1*. (A) to (C) CBF1-YFP overexpression elicits expression of *COR* genes in wild type but not *sfr6-1* plants. qRT-PCR analysis of *CBF1* **(A)**, *KIN2* **(B)** and *GOLS3* **(C)** in 8-day-old transgenic *Arabidopsis* seedlings of Col-0 (WT Lines 35 and 40) and *sfr6-1* (lines 12 and 20) expressing 35S-CBF1-YFP compared with non-transgenic Col-0 plants (WT) at ambient temperature. Expression is shown after normalisation to *PEX4*. Each value represents the mean of three technical replicates for each sample normalised to the mean of three technical replicates for *PEX4*. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test. **(D) to (F)** ChIP qRT-PCR analysis of relative levels of histone H3 at *KIN2* **(D),** *GOLS3* **(E)** and *LTI78* **(F)** promoters in 3-week-old plants exposed to 5C or maintained at 20C for 4 h indicates that cold treatment reduces Histone H3 occupancy at *COR* gene promoters and acts independently of SFR6/MED16. Data represent proportion of histone H3 at a given promoter referenced against input and standardised against relative *PEX4* histone H3 occupancy. Each value represents the mean of three technical replicates. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's *t*-test. Data are representative of 2 biological replicates.



Supplemental Figure 2. The ratio of RNA polymerase II occupancy at stall sites to occupancy at TSS sites in WT Col-0 and *sfr6-1, med2-1 and med14-2 mutant* plants after 4h at 5C is similar. Data used to calculate ratios are the same as those shown in Figure 2 and Figure 6. Pol II abundance at the stall site is referenced to input and standardised to Pol II abundance at the TSS referenced to input. Each value represents the mean of three technical replicates for each sample. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test.

A

Transcription Factors (TF)

Check All | Check Enriched | Check None | Check Inverted | Refresh

#P = Number of promoters with TF sites; #S = Number of predicted TF sites

Enriched TF sites

P-value	Name	#P	#S	Select	P-value	Name	#P	#S	Select
< 10^{-3}	ABRE binding site motif	9	10		< 10^{-7}	ABRE-like binding site motif	30	40	
< 10^{-4}	CACGTGMOTIF	21	46		< 10^{-6}	CBF1 BS in cor15a	5	5	
< 10^{-10}	DRE core motif	48	70		< 10^{-9}	DREB1A/CBF3	31	42	
< 10^{-7}	EveningElement promoter moti	16	18		< 10^{-8}	LTRE promoter motif	15	17	
< 10^{-3}	TATA-box Motif	64	126						

Non-enriched TF sites

0.0018	ABFs binding site motif	7	8		0.0365	ABREATRD22	4	4	
0.0010	ACGTABREMOTIFA2OSEM	17	20		0.3719	ARF binding site motif	18	20	
0.2084	ATHB1 binding site motif	2	4		0.0801	ATHB2 binding site motif	8	9	
0.3442	ATHB2ATCONSENSUS	1	2		0.1336	ATHB5ATCORE	3	6	
0.4755	ATHB6 binding site motif	2	2		0.0205	AtMYB2 BS in RD22	10	11	
0.0109	AtMYC2 BS in RD22	23	28		0.5537	BoxII promoter motif	19	22	
0.1004	CARGCW8GAT	36	110		0.2110	CArG promoter motif	5	10	
0.0426	CCA1 binding site motif	18	20		0.4013	CDA1ATCAB2	2	2	
0.2440	E2F binding site motif	2	2		0.4100	E2FAT	1	1	
0.0297	GADOWNAT	9	10		0.8354	GAREAT	22	24	
0.0010	GBF1/2/3 BS in ADH1	5	10		0.0032	GBOXLERBCS	6	7	
0.3057	GCC-box promoter motif	4	4		0.5653	Gap-box Motif	4	5	
0.0777	HY5AT	1	1		0.9278	Hexamer promoter motif	2	2	
0.4391	Ibox promoter motif	18	22		0.1542	L1-box promoter motif	9	9	
0.3249	LEAFYATAG	5	5		0.5152	MYB binding site promoter	13	18	
0.8973	MYB1 binding site motif	1	1		0.0172	MYB1AT	56	96	
0.3641	MYB1LEPR	8	9		0.3883	MYB2AT	13	16	
0.5989	MYB3 binding site motif	2	2		0.2338	MYB4 binding site motif	42	64	
0.0109	MYCATERD1	23	28		0.4763	RAV1-B binding site motif	5	5	
0.1851	SV40 core promoter motif	10	10		0.6417	T-box promoter motif	24	30	
0.4658	TGA1 binding site motif	2	2		0.2750	UPRE2AT	1	1	
0.4658	UPRMOTIFIAT	2	2		0.0250	UPRMOTIFIIAT	5	5	
0.7305	W-box promoter motif	32	54		0.0206	Z-box promoter motif	4	4	

Depleted TF sites

No binding factors found

B

Transcription Factors (TF)

Check All | Check Enriched | Check None | Check Inverted | Refresh

#P = Number of promoters with TF sites; #S = Number of predicted TF sites

Enriched TF sites

No binding factors found

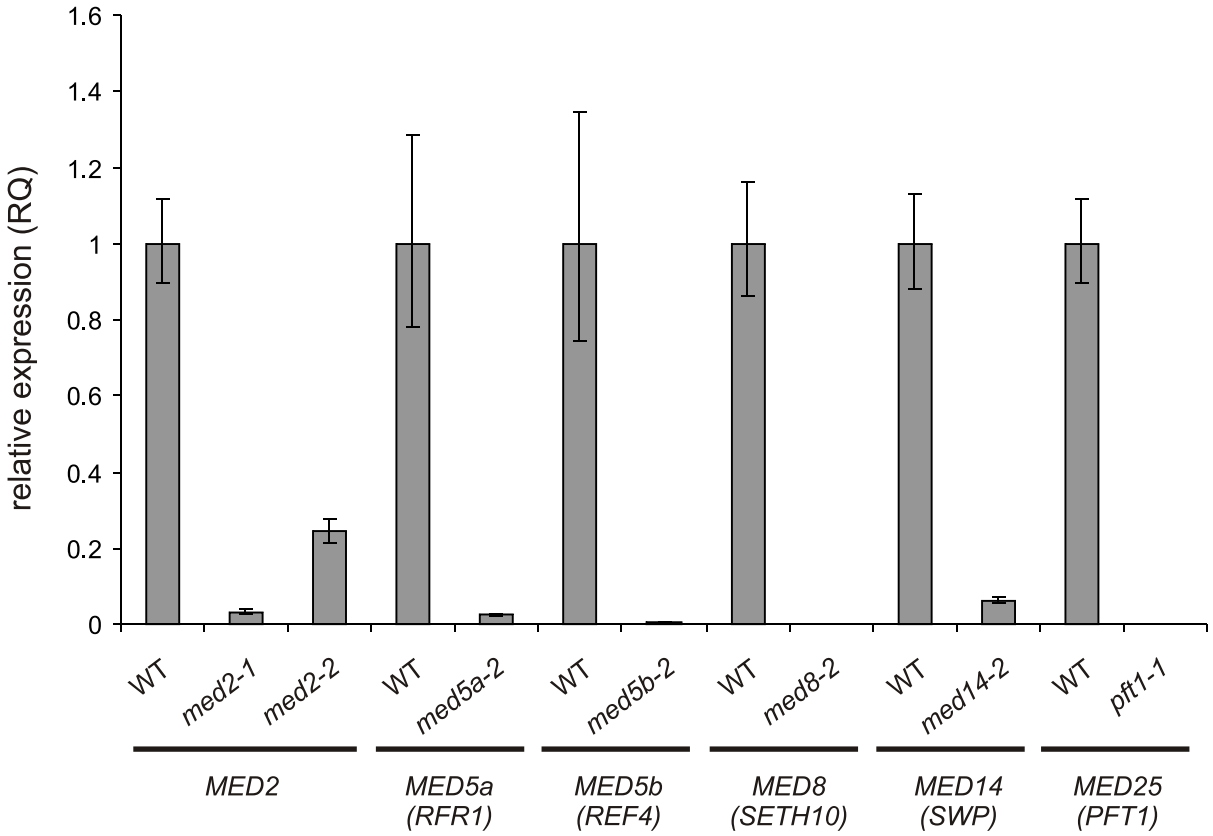
Non-enriched TF sites

0.2046	ABFs binding site motif	4	4		0.4399	ABRE binding site motif	4	4	
0.0547	ABRE-like binding site motif	21	30		0.5318	ABREATRD22	2	2	
0.0288	ACGTABREMOTIFA2OSEM	17	22		0.0617	AGCBOXNPGLB	4	4	
0.6035	AGL2ATCONSENSUS	1	1		0.0448	AP1 BS in AP3	2	2	
0.7154	ARF binding site motif	23	30		0.4523	ATHB1 binding site motif	2	6	
0.8297	ATHB2 binding site motif	6	9		0.1714	ATHB2ATCONSENSUS	2	4	
0.1908	ATHB5ATCORE	4	10		0.1494	ATHB6 binding site motif	5	5	
0.4189	AtMYB2 BS in RD22	9	10		0.6270	AtMYC2 BS in RD22	23	32	
0.7543	BoxII promoter motif	27	40		0.1221	CACGTGMOTIF	15	32	
0.6034	CARGCW8GAT	43	124		0.9625	CArG promoter motif	2	4	
0.7448	CCA1 binding site motif	17	20		0.1908	CDA1ATCAB2	4	4	
0.2281	DRE core motif	18	25		0.7082	DREB1A/CBF3	4	5	
0.4210	E2F binding site motif	2	2		0.2478	EveningElement promoter moti	7	7	
0.0087	GADOWNAT	13	14		0.8705	GAREAT	34	47	
0.6634	GBF1/2/3 BS in ADH1	1	2		0.2956	GBOXLERBCS	3	3	
0.1357	GCC-box promoter motif	7	8		0.0038	Gap-box Motif	15	15	
0.0974	HY5AT	1	1		0.2956	Hexamer promoter motif	8	9	
0.9244	Ibox promoter motif	21	24		0.5076	L1-box promoter motif	11	12	
0.9113	LEAFYATAG	4	4		0.1295	LTRE promoter motif	6	7	
0.0492	MYB binding site promoter	27	30		0.5460	MYB1 binding site motif	4	4	
0.9637	MYB1AT	53	129		0.5142	MYB1LEPR	12	14	
0.0995	MYB2 binding site motif	3	3		0.3514	MYB2AT	21	24	
0.9769	MYB3 binding site motif	1	1		0.3554	MYB4 binding site motif	54	105	
0.6270	MYCATERD1	23	32		0.0026	PRHA BS in PAL1	1	1	
0.7790	RAV1-B binding site motif	6	6		0.9023	RY-repeat promoter motif	1	2	
0.5971	SV40 core promoter motif	12	14		0.7972	T-box promoter motif	34	56	
0.8296	TATA-box Motif	58	179		0.0385	TELO-box promoter motif	12	15	
0.1827	TGA1 binding site motif	4	4		0.0671	UPRE2AT	2	2	
0.1827	UPRMOTIFIAT	4	4		0.9123	UPRMOTIFIIAT	1	1	
0.2162	W-box promoter motif	51	90		0.1087	Z-box promoter motif	4	4	

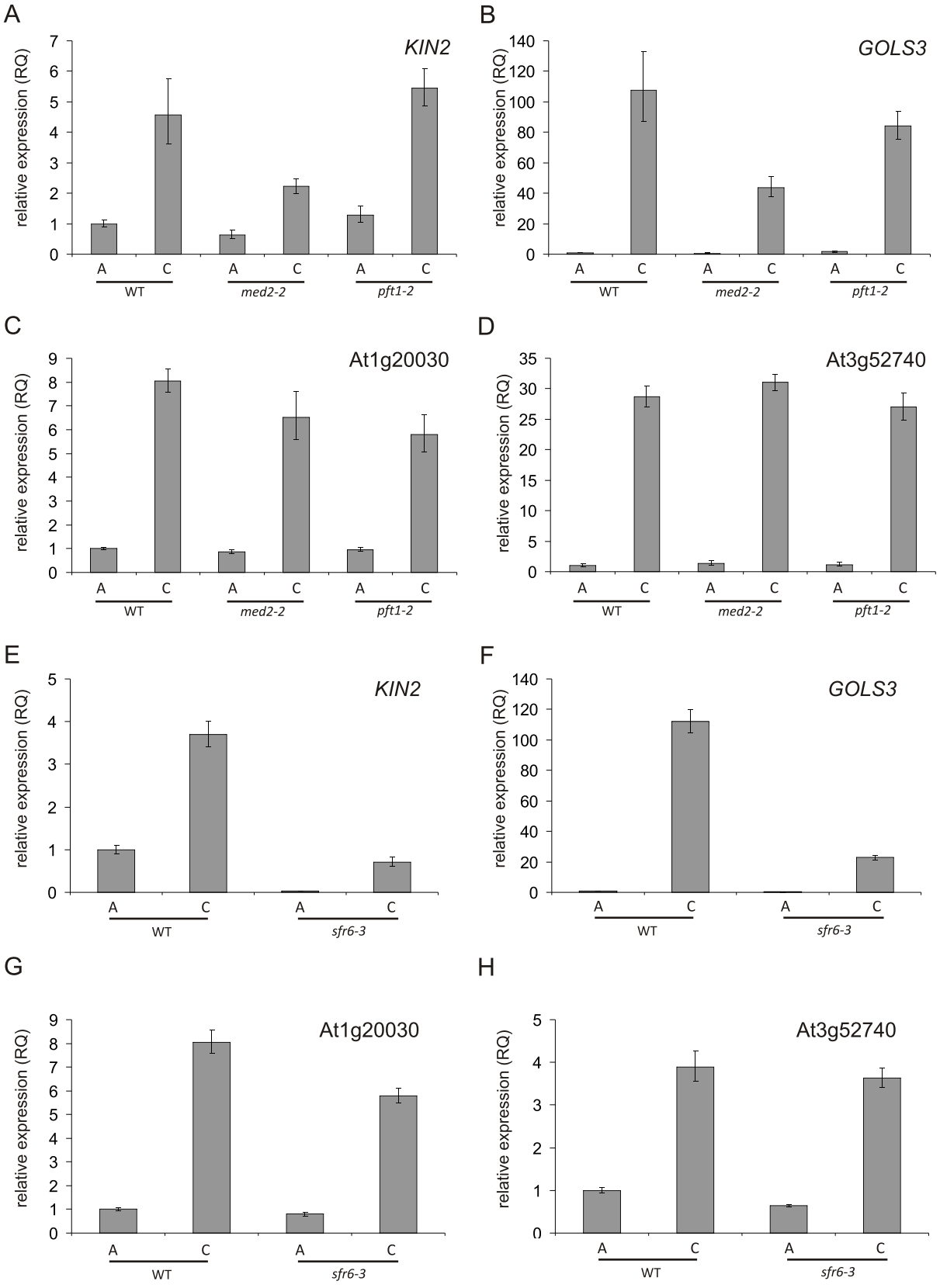
Depleted TF sites

No binding factors found

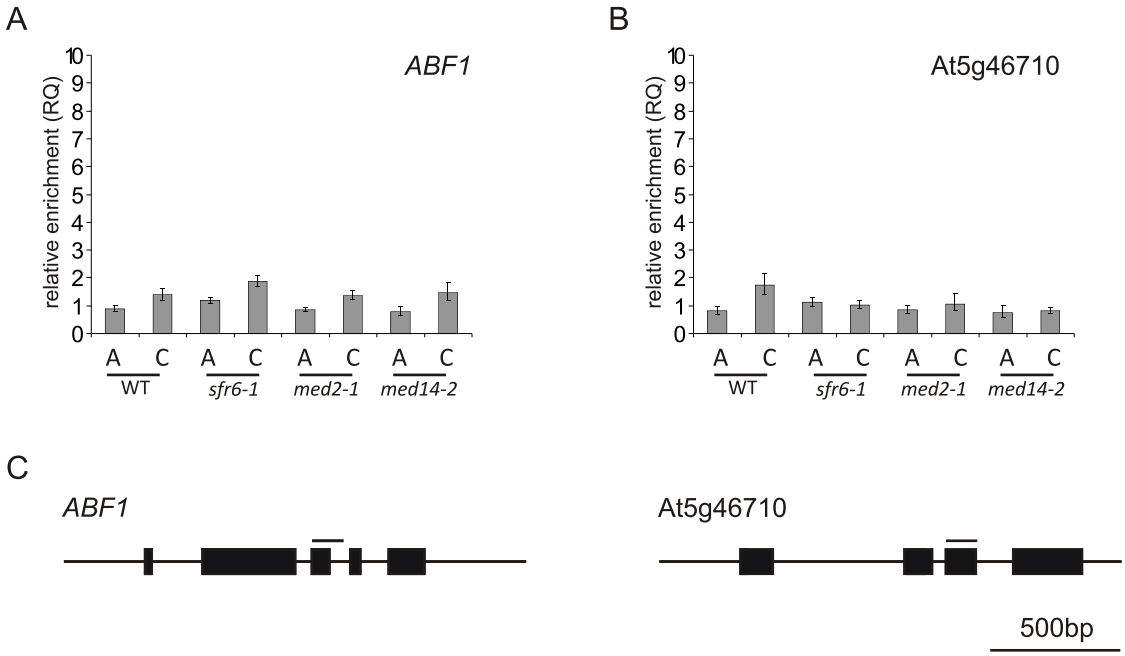
Supplemental Figure 3. CRT/DRE and EE are enriched in cold upregulated genes that are downregulated in *sfr6* mutants. The Athena program was used to detect the presence of known transcription factor binding sites in **(A)** the 81 cold upregulated genes that showed reduced expression in *sfr6* mutants (Supplemental Dataset 2) and in **(B)** the 81 cold upregulated genes that showed wild type levels of expression in *sfr6* mutants (Supplemental Dataset 3).



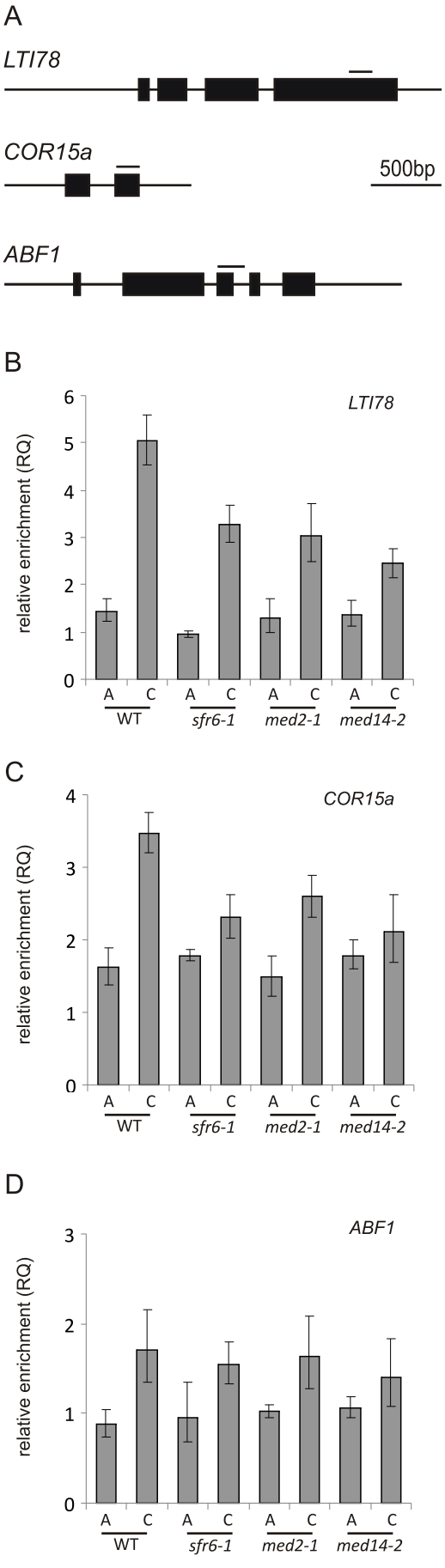
Supplemental Figure 4. Mediator subunit transcript levels in Mediator subunit mutants. Expression is shown after normalisation to *PEX4* using qRT-PCR. Relative quantitation of transcript was made from 8-day-old seedlings of WT Col-0 and mutant plants. Expression is shown after normalisation to *PEX4* using qRT-PCR. Each value represents the mean of three technical replicates for each sample normalised to the mean of three technical replicates for *PEX4*. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test. Results are representative of at least 2 biological replicates.



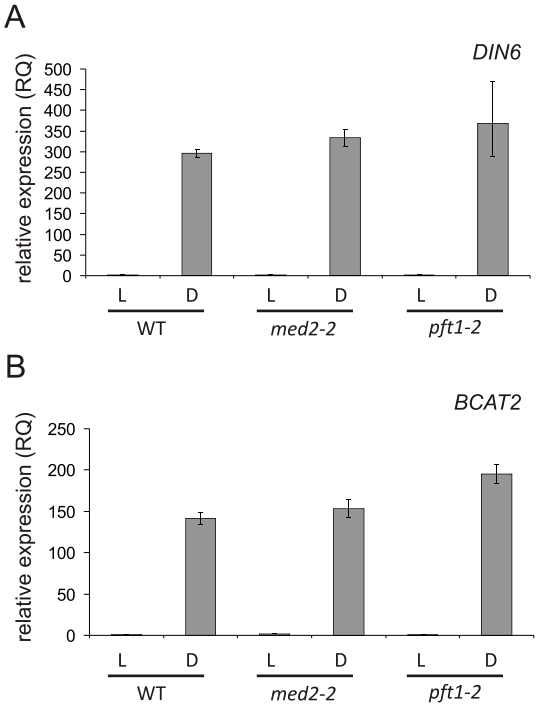
Supplemental Figure 5. Cold-responsive gene expression in *med2-2*, *pft1-2* and *sfr6-3* compared with wild type is similar to that seen in *med2-1*, *pft1-1* and *sfr6-1* respectively. (A) to (D) Expression of *KIN2* **(A)**, *GOLS3* **(B)**, At1g20030 **(C)** and At3g52740 **(D)** in Col-0 WT, *med2-2* and *pft1-2*. **(E) to (H)** Expression of *KIN2* **(E)**, *GOLS3* **(F)**, At1g20030 **(G)** and At3g52740 **(H)** in Col-0 WT and *sfr6-3*. Measurements were made on 8-day-old seedlings of WT Col-0 and Mediator subunit mutants exposed to cold (C) temperatures (5C) for 6 h or maintained at ambient (A) temperature (20C).



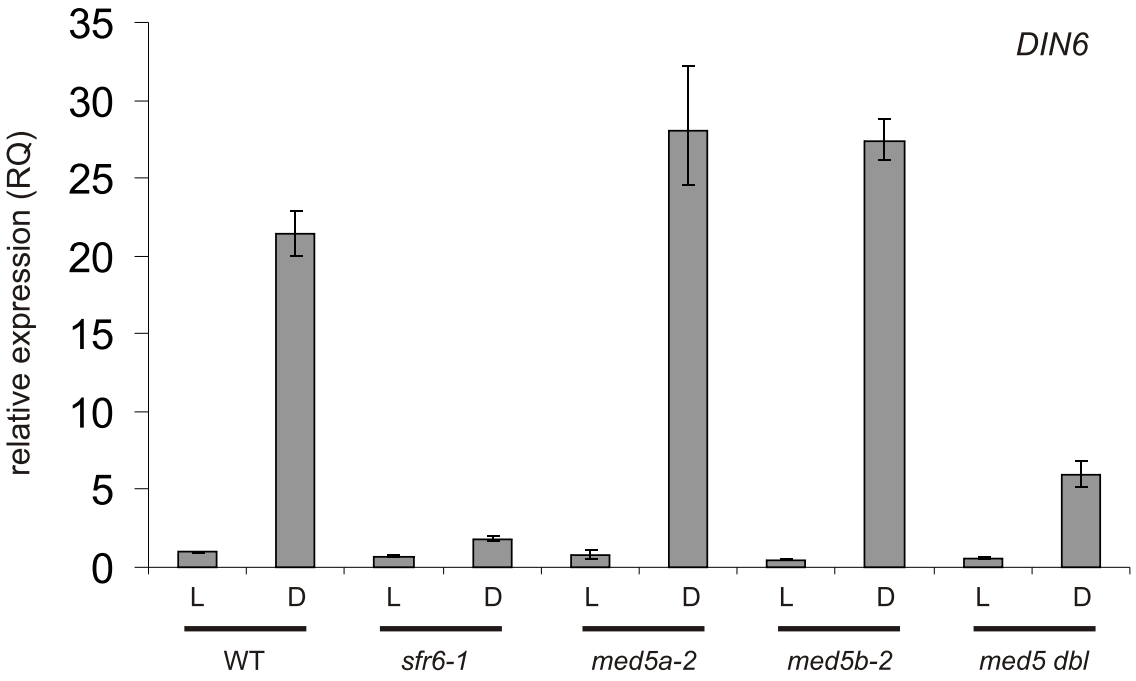
Supplemental Figure 6. RNA polymerase II recruitment and progression along cold-responsive genes in WT Col-0, *sfr6-1*, *med2-1* and *med14-2* mutants. (A) to (B) Pol II abundance was measured in 14-day-old seedlings of WT Col-0 and Mediator subunit mutants exposed to cold (C) temperatures (5C) or maintained at ambient (A) temperature (20C) for 6 h. in the middle of the transcribed region of *ABF1* **(A)** and At5g46710 **(B)** at the positions shown in **(C)**. Thick black bars indicate the exons of the gene and thin black lines above show the regions amplified by the primers in each ChIP reaction. ChIP enrichment at each location is referenced to input and enrichment at each location was standardised to Pol II abundance at *PEX4* in the same ChIP sample. Each value represents the mean of three technical replicates for each sample normalised to the mean of three technical replicates for *PEX4*. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test. Results are representative of 2 biological replicates.



Supplemental Figure 7. Mediator recruitment to further CRT- and EE-containing genes. ChIP qRT-PCR analysis of relative abundance of MED6 (a core Mediator subunit) at the transcribed region of genes in 14-day-old seedlings *of* Col-0 (WT), *sfr6-1*, *med2-1* and *med14-2* mutants. Mediator recruitment was monitored at the positions shown in **(A)**. Thick black bars indicate the exons of the gene and thin black lines above show the regions amplified by the primers in each ChIP reaction. **(B) to (C)** Mediator recruitment to two CBF-controlled CRT-containing genes, *LTI78* **(B)** and *COR15A* **(C)** increases in the cold and, as at *KIN2* and *GOLS3*, is impaired in *sfr6*, *med2* and *med14* mutants. **(D)** Mediator recruitment to one further EE-containing gene, *ABF1* increases slightly in response to cold but is unaffected in *sfr6*, *med2* and *med14* mutants. ChIP enrichment is referenced to input and standardised to MED6 abundance at *PEX4* in the same ChIP sample. Values were calculated using the $\Delta\Delta C_T$ method and the error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's *t*-test. Data is from one preliminary experiment only and serves as a comparison with other replicated experiments on different genes of the same class. Error bars indicate the level of variation between technical replicates within this experiment.



Supplemental Figure 8. Dark-responsive gene expression is not reduced in *med2-2* and *pft1-2,* similar to *med2-1* and *pft1-1* respectively. Expression of *DIN6* **(A)** and *BCAT2* **(B)** in *med2-2* and *pft1-2*. Measurements were made on 8-day-old seedlings of WT Col-0 and Mediator subunit mutants exposed to darkness (D) or maintained in the light (L) for 6 h. Expression is shown after normalisation to *PEX4*. Each value represents the mean of three technical replicates for each sample normalised to the mean of three technical replicates for *PEX4*. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test. Results are representative of 2 biological replicates.



Supplemental Figure 9. Expression of dark-induced *DIN6* is reduced in *med5amed5b* double mutants but not in *med5a* or *med5b* single mutants. Measurements were made on 8-day-old seedlings of WT Col-0 and Mediator subunit mutants exposed to darkness (D) or maintained in the light (L) for 6 h. Expression is shown after normalisation to *PEX4*. Each value represents the mean of three technical replicates for each sample normalised to the mean of three technical replicates for *PEX4*. The error bars represent RQ_{MIN} and RQ_{MAX} and constitute the acceptable error level for a 95% confidence level according to Student's t-test. Results are representative of 2 biological replicates.

Supplemental Table 1. Table showing frequencies of occurrence of heptamer sequences in the promoters of the 81 genes misregulated in *sfr6* mutants, and probabilities of occurrence relative to whole genome. Ten motifs used to produce consensus for CRT/DRE (Figure 3) are denoted by superscript ”a”, and single EE-like motif by superscript “b”.

Motif	Observed occurrence	Expected occurrence	Occurrence probability
gaccgac[a]	16	1.19	2.5×10^{-13}
atgtcgg[a]	19	2.18	2.7×10^{-12}
aaatatc[b]	60	23.68	2.9×10^{-10}
cttcttc	25	5.75	2.6×10^{-9}
agaagaa	42	14.63	4.1×10^{-9}
gccgaca[a]	12	1.22	7.1×10^{-9}
accgaca[a]	16	2.48	9.6×10^{-9}
cgacatc[a]	14	1.85	1.1×10^{-8}
gtcggta[a]	13	1.67	2.7×10^{-8}
gtcggca	10	1.03	1.5×10^{-7}
agccgac	10	1.11	3.0×10^{-7}
acacgtg	15	3.18	1.4×10^{-6}
aataatg	38	16.26	2.9×10^{-6}
gccgacc	7	0.62	4.1×10^{-6}
aagaaga	37	15.87	4.1×10^{-6}
accgact[a]	11	1.87	4.4×10^{-6}
cacgtgg	11	1.88	4.6×10^{-6}
aggtcgg[a]	8	0.95	7.1×10^{-6}
aactgat	17	4.61	7.1×10^{-6}
aagaaaa	82	48.74	8.5×10^{-6}
acgtggc	10	1.66	9.5×10^{-6}
agaggaa	18	5.26	1.1×10^{-5}
acgtcgg[a]	8	1.1	2.0×10^{-5}
cgtggca	9	1.45	2.1×10^{-5}
cacacac	15	4.22	3.6×10^{-5}
attatta[c]	49	26.11	4.1×10^{-5}

Supplemental Data. Hemsley et al. (2014). Plant Cell 10.1105/tpc.113.117796

Supplemental Table 2. Table showing frequencies of occurrence of heptamer sequences in the promoters of the 81 genes not misregulated in *sfr6* mutants, and probabilities of occurrence relative to whole genome.

Motif	Observed occurrences	Expected occurrences	Occurrence probability
aggccca	24	2.27	$6.4x10^{-17}$
ggcccaa	24	3.66	$1.6x10^{-12}$
aacccta	24	3.9	$5.7x10^{-12}$
aagccca	27	5.1	$8.8x10^{-12}$
cttcttc	26	5.9	$9.6x10^{-10}$
agcccat	20	3.56	$1.5x10^{-9}$
accctaa	19	3.72	$1.7x10^{-8}$
agaagaa	38	13.37	$2.8x10^{-8}$
atgggcc	15	2.5	$6.9x10^{-8}$
gggccta	12	1.53	$8.3x10^{-8}$
aaaccct	23	6.53	$4.2x10^{-7}$
aaacaaa	82	45.06	$4.9x10^{-7}$
attgggc	17	4.04	$1.3x10^{-6}$
ccctaaa	19	5.06	$1.6x10^{-6}$
acacgcg	9	1.06	$1.8x10^{-6}$
accctag	10	1.6	$7.1x10^{-6}$
aatgggc	15	3.81	$1.1x10^{-5}$
aaagccc	18	5.67	$2.8x10^{-5}$
agcccaa	17	5.23	$3.4x10^{-5}$
aagaaga	32	14.75	$6.7x10^{-5}$
taattaa	41	21.35	$1.0x10^{-4}$
gcccata	12	3.18	$1.2x10^{-4}$
aacaaaa	72	45.06	$1.3x10^{-4}$

Supplemental Data. Hemsley et al. (2014) Plant Cell 10.1105/tpc.113117796

Supplemental Table 3 Oligonucleotides used in this study.

Primers for cloning

Gene	forward primer	reverse primer
CBF1	CCTCTAGAGGTACCATGAACTCATTTTCAGCTTT	GGCTCGAGGTAACTCCAAAGCGACACGT

Primers for real time qRT-PCR detection of transcripts

Gene	AGI code	forward primer	reverse primer
PEX4	At5g25760	TCATAGCATTGATGGCTCATCCT	ACCCTCTCACATCACCAGATCTTAG
KIN2	At5g15970	CAACAGGCGGGAAAGAGTAT	CAACAACAAGTACGATGAGTACGA
GOLS3	At1g09350	CAAAGTTGTCCCTCCCACAC	GAGCATGGCCAAGACAAGAT
At3g52740	At3g52740	GAAGCATCGGAGAGAGATCG	AGCAGTACGTGCAGACGAGA
At1g20030	At1g20030	TTTCGCTCCCTGAAGAAGAA	CCTTGACATAACTCCGGAGAAG
At1g68500	At1g68500	AGCTCTGTGTGGTTGCCTTT	CGTCCCAAACAACATCATTG
At5g62360	At5g62360	AGCCATGCTCAAATTGGTTC	TGGGTACGTTGTGAAAGTGC
At5g46710	At5g46710	CCATGAAACTTGCATTGAGC	CGAGAACCCAAATCGAGAAA
ABF1	At1g49720	AATGAAAACCCATAATAGTGAGGTAA	ATTGTCTTTTGGCCAGCAAT
SZF2	At2g40140	TCAAAAACCCCAACCACTTC	TGCACCGCACATATCTCTTC
LTI78	At5g52310	GCACCCAGAAGAAGTTGAACA	TCATGCTCATTGCTTTGTCC
COR15A	At2g42540	CGTTGATCTACGCCGCTAAAG	CTCACCATCTGCTAATGCC
DIN6	At3g47340	GGCCAAGAGAGTTCGTGTTC	AGACGTTGATGGGCCAAGTA
BCAT2	At1g10070	CGCAAAACTCTGGTTCTACCTC	GATGCAGCTTGTGCGTTGTA
SFR6	At4g04920	CGCTGAGAGATTCTGGTGGA	TGAAACTATCCCATCCTCTGC
MED14	At3g04740	TAGCTTTGGTTCAGGCGTTT	GGCCATAGTTGGTCAGGAGA
PFT1	At1g25540	GGAACGGAATGAGAATGGTG	ATTGTTGGAAGCTGCTTTGG
MED2 (MED32)	At1g11760	GCGACTAGTCTCCCTCCCATT	CCATCGAACCGCTCTACTCATC
MED5a (MED33a; RFR1)	At3g23590	GCCTTGCATGCCCATTGTA	GGAAGTCAAACCAACGTTTCG
MED5b (MED33b; REF4)	At2g48110	GCCCTGCATGCCTATTGTG	TCGCTCCAGCGCTTCACT
MED8	At2g03070	AAAGTCAGATACCAGCACTTCAT	CTGTCCTTGAGACATGCTATGC

Primers for ChIP

Gene/position	AGI code	forward primer	reverse primer
GOLS3 pro	At1g09350	TCGGTACGTCTTTTTCTTTTCA	CTTGTAAGCCAAAATGCTCAA
KIN2 pro	At5g15970	AAACGACACGTGATGTCTTGA	TGCCACGTGTAATCTGAAACC
PEX4 pro	At5g25760	CTCGCCGGATCAATTCTTAG	TAAGGAAACGAAACCGGATG
TSI-A	silent	CTCGTGAGGGTTTGTGAGGT	AGTATAAGCGCCCACCCAGT
PEX4 Mid	At5g25760	CTTGGACGCTTCAGTCTGTG	GAACGCCCATGGTTACATTT
GOLS3 -500	At1g09350	TGCATATTTTTACCAAAACAAAAA	ATTTTCTTCTTTTGTCCTAACGTC
GOLS3 TSS	At1g09350	CCATAATCACGGCCTCAAAG	TCATCTCAGGTGCCATCTTG
GOLS3 Stall	At1g09350	GGAACCGGAGACTACGTGAA	GCCTTGGTCCAATAGCTGTC
GOLS3 Mid	At1g09350	TGGGGCAGCTACCACTATACA	GAGCATGGCCAAGACAAGAT
GOLS3 End	At1g09350	TTCACAGGAAACCGAAAACC	ACAAGAACCTCGCTCGTCAG
GOLS3 3IGR	At1g09350	TGCAATTGGTAAGTTCTTCATTTT	TTTTAGAAGAGATTGTGTGTTGCAT
KIN2 -500	At5g15970	ATGAAAATACGGGAGGTTCG	GTTGTTGCATATGCGTTTGG
KIN2 TSS	At5g15970	GATTACACGTGGCACCACAC	GGAAGGCATTCTTGTTGGTC
KIN2 Stall	At5g15970	GCTGGCAAAGCTGAGGTACT	CCATGGTCAACACAAAATCAA
KIN2 End	At5g15970	AGTATATCGGATGCGGCAGT	TCCCAAATTTTATTTGAAAATCC
KIN2 3IGR	At5g15970	CGAAATCGTTGTGGTCAATG	ACAATGACGCAGAGCAAACA
At3g52740 -500	At3g52740	AGTTGAGTTTGGTCACACAAAAA	AACCTAAAATTCTATCAAGTGATCAAG
At3g52740 TSS	At3g52740	CGTCGACGTGTAAGACAACC	TTGCAGGAAACAAAAAGATGAA
At3g52740 Stall	At3g52740	TGATGAACATCGACGATACGA	GCTTCGGTTTCTCTTCAAGC
At3g52740 End	At3g52740	TCGTCTGCACGTACTGCTCT	TTGAGGAACAAGAACCACATTT
At3g52740 3IGR	At3g52740	TGCAATGTGTCCGCTCTAAA	TAGGAAAACGGGCAAATGTC
At1g20030 TSS2	At1g20030	CATGAGAAAAAGAAAAAGAATCTCG	AAGAAAAGAGAGAATAAACATTAGCC
At1g20030 Mid	At1g20030	GAATAGCGTCGACGGGAAG	GTAGCTATAGGCGCGTGGAC
At1g20030 End	At1g20030	TGTGGTGGTTCTTCTGACCA	CAACGTTTGGTCATGTGGAGT
At1g20030 -250	At1g20030	AATGGTTTCTTAGGACACTTGAA	TTTTATGGCTTGGAGTTGGA
At1g20030 3IGR	At1g20030	ACATGGGCTATTCCTCAACG	TTAGGCGCTGGAGGAGTTC
At5g46710 MID	At5g46710	TGCCTGCATGGTCTGTTATC	CAAGGGAGGTAATGGATGCT
LTI78 MID	At5g52310	GACTCCGGTCAATGAGAAGG	CCGCCACATAATCTCTACCC
COR15a MID	At2g42540	CAGATGGTGAGAAAGCGAAAG	CTTGTTTGCGGCTTCTTTTC
ABF1 MID	At1g49720	CAGGCTTATACCTTGGAACTGG	TTCAGCCTGCAACATAGAGAGA