

Figure S1. Experimental design used for generation of RNA-Seq data. (A) Temperature readings from a sensor that was with the plants throughout the experiment and shows the time of light / dark (gray shading indicates time without lights). (B) Three different experiments were conducted to assess the changes in gene expression in response to cold or heat stress in 14 day maize seedlings. In experiment 1 (time course - TC) one replicate for three inbreds was collected at each of the indicated time-points. In experiment 2 (inbred - hybrid - HY, second row) three biological replicates were sampled from three maize inbreds and their F1 hybrids at time 0 and two time points during the stress. In experiment 3 a single biological replicate was sampled for a panel of 25 genotypes under control and cold conditions at two time points.

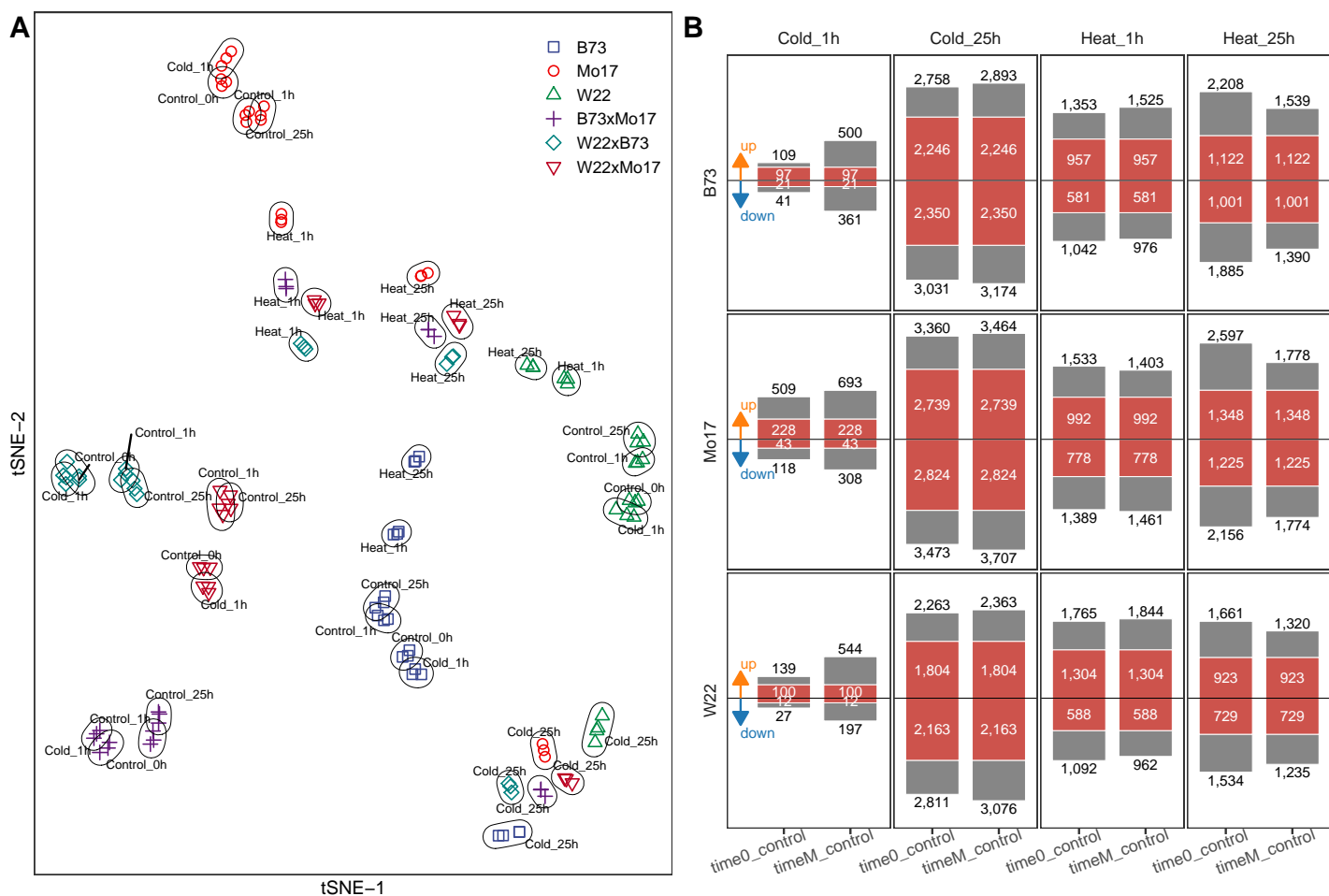


Figure 1. Identification of genes that are differentially expressed in response to heat or cold stress. (A) t-SNE clustering of samples from the HY experiment under control, cold and heat conditions. The genotypes are indicated by different symbols/colors and the conditions for each set of samples are indicated in the plot. (B) Number of differentially expressed genes (DEGs) under cold and heat conditions at 1 and 25 hour time points. For each time point the number of genes that showed differential expression (see Methods) relative to the control sampled at time 0 (the onset of the stress; time0_control) is shown as well as the number of genes that showed differential expression relative to the control sample collected at matching time point (i.e., 1h or 25h; timeM_control). Numbers inside red bar represent genes that are differentially expressed in both comparisons.

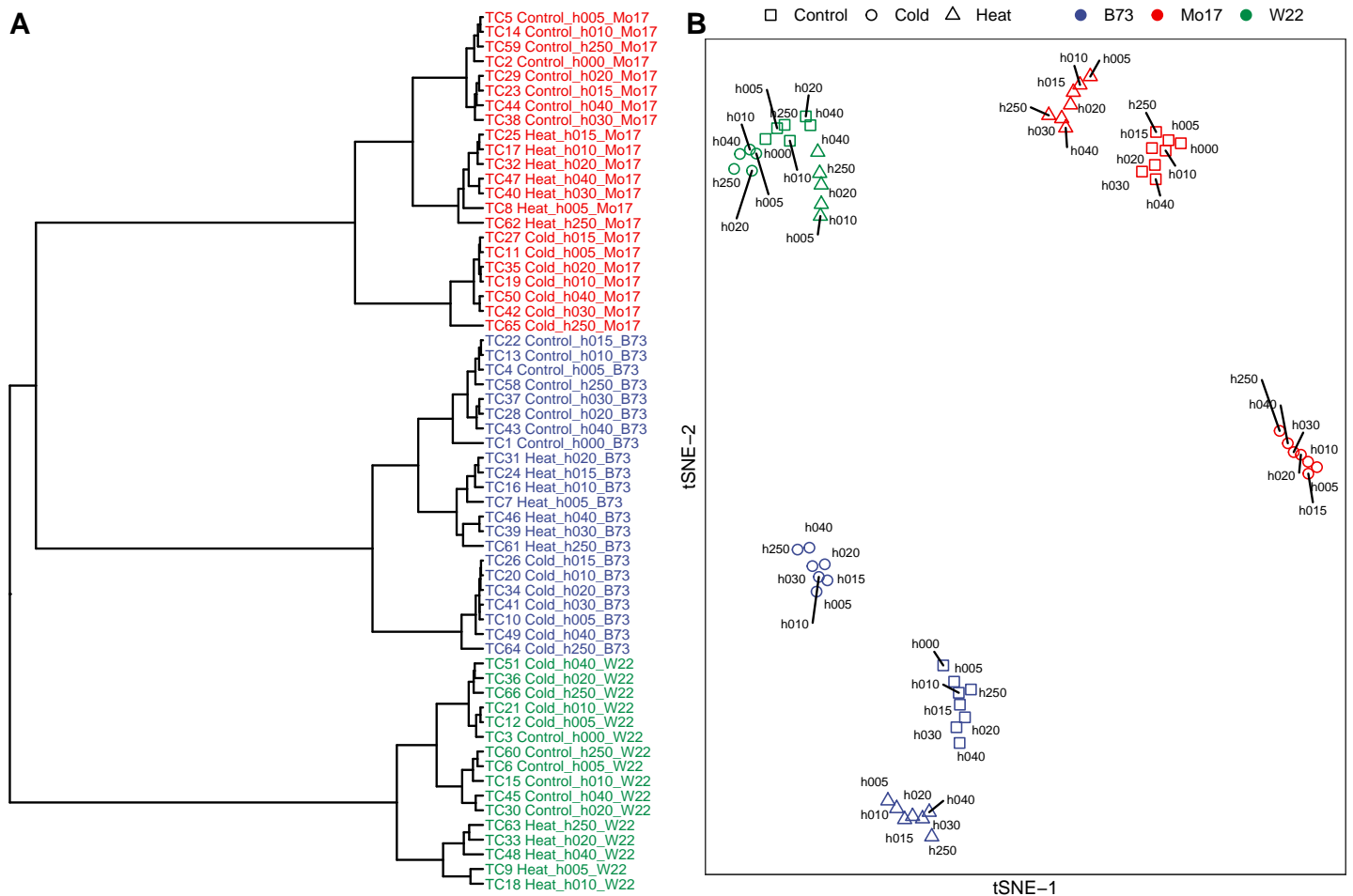


Figure S2. Hierarchical (A) and t-SNE (B) clustering of all samples from the time course (TC) experiment under control, cold and heat conditions. (A) The samples showed strong clustering by genotype (indicated by color of labels) and within each genotype the samples tend to cluster by treatment. (B) t-SNE plot shows similar clustering based on both genotype and treatment.

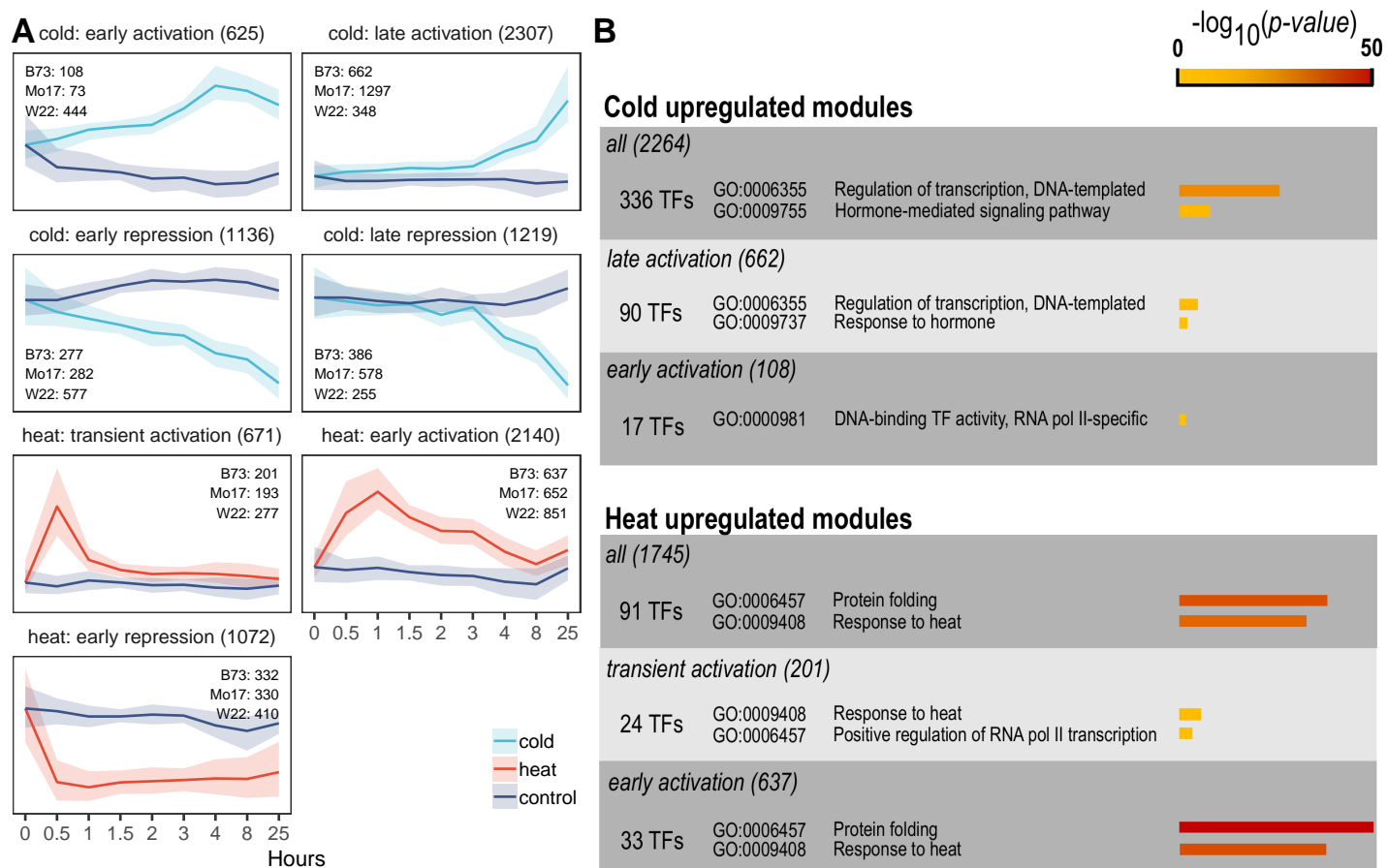


Figure 2. Expression profile and GO enrichment of cold- and heat-responsive gene clusters. B73, Mo17 and W22 genes that exhibit significant DE after 1 hour or 25 hours stress treatment were used to perform co-expression clustering based on their time-course expression pattern (see methods). (A) Expression pattern for the most abundant co-expression clusters that represent early, late or transient changes upon cold or heat treatment. The median expression level of control and stress conditions for the genes within each module is shown and the number of B73, Mo17 and W22 genes in each module is indicated. Ranges at each time point represent 25%-75% quantile expression levels. (B) For the set of all up-regulated genes under cold or heat conditions we determined the number of TFs and assessed GO enrichment. Two highly enriched GO terms (with significance $p < 0.01$) are shown for each module, and the significance level is indicated.

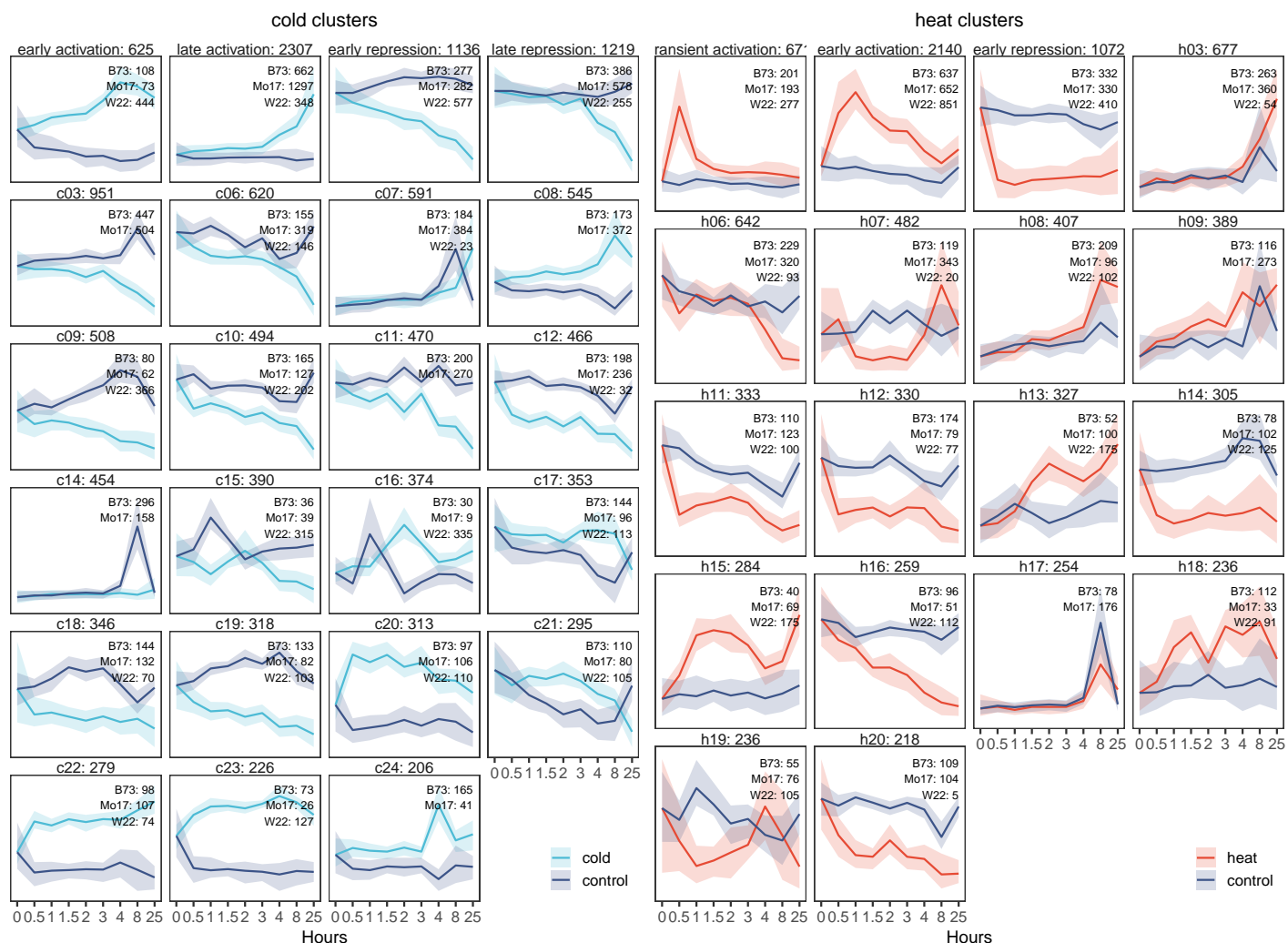


Figure S3. Expression profiles of cold- and heat-responsive gene clusters. B73, Mo17 and W22 genes that exhibit significant DE after 1 hour or 25 hours stress treatment were used to perform co-expression clustering based on their time-course expression pattern (see methods). The median expression level of control and stress conditions for the genes within each module is shown and the number of B73, Mo17 and W22 genes in each module is indicated. Ranges at each time point represent 25%-75% quantile expression levels.

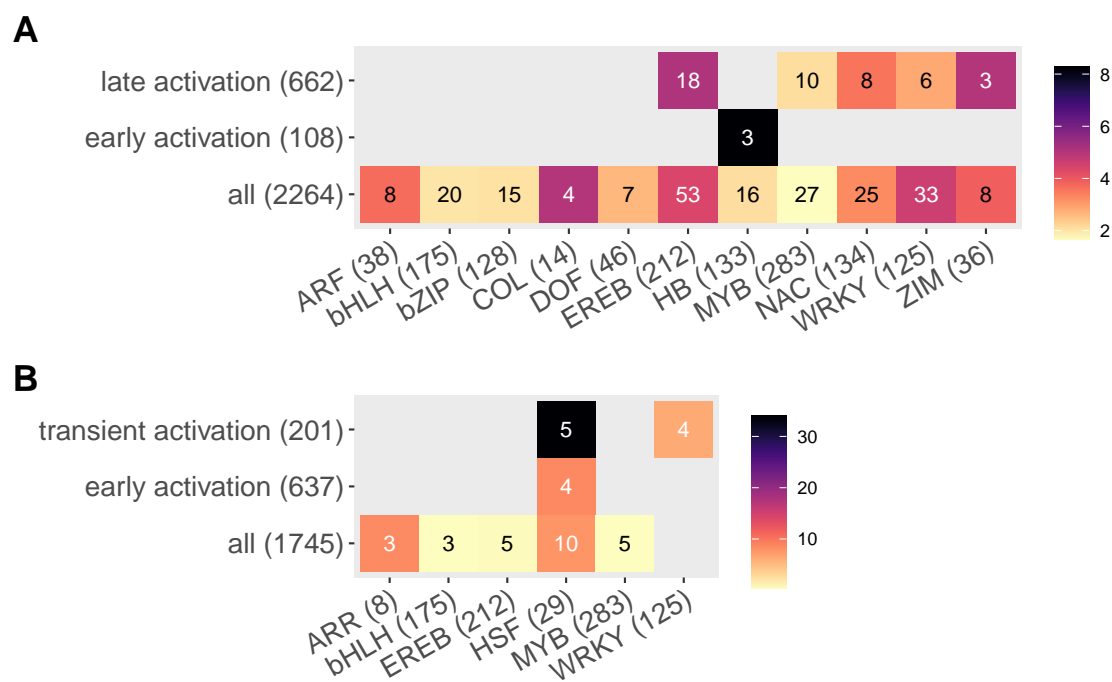


Fig S4. Transcription Factor Family Enrichment in Select DEG Modules. The TFs present in the overall set of up-regulated genes for cold (A) or heat (B) as well as TFs that are present in specific modules were assessed for potential enrichment of specific TF families. Numbers in parentheses indicate total group size, while numbers in tiles indicate how many DEGs of specific TF families were identified in each module. For modules including at least 3 TF members in a TF family, enrichment was assessed through hypergeometric test ($p < 0.05$). Transcription factor family assignments were pulled from Grassius TFDB (Yilmaz et al., 2009).

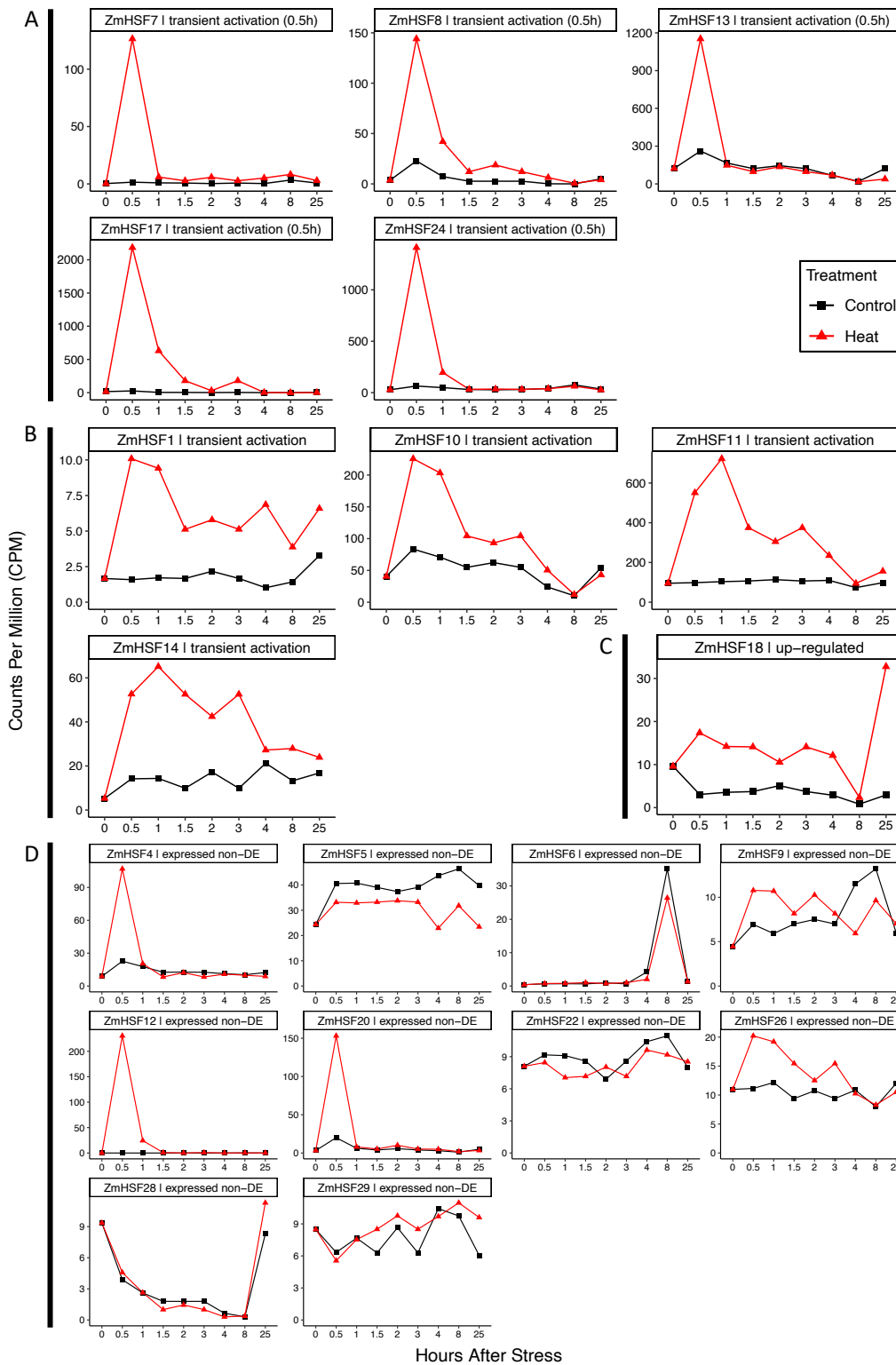


Figure S5. Characterization of maize Heat Shock Factors (HSF) response to heat stress. Time course expression pattern was shown for all 29 maize HSFs including: (A) 5 HSFs exhibit very strong activation at 0.5 hours of heat stress, but return to relatively normal levels by the 1 hour time point. (B) 4 HSFs classified as transient activation; (C) 1 HSF was significantly differentially expressed, but not assigned to a specific cold-upregulated module. (D) 10 HSFs are expressed but not assigned into a cold up-regulation module. Genes were considered expressed if expression was ≥ 5 cpm in least one treatment x time point.

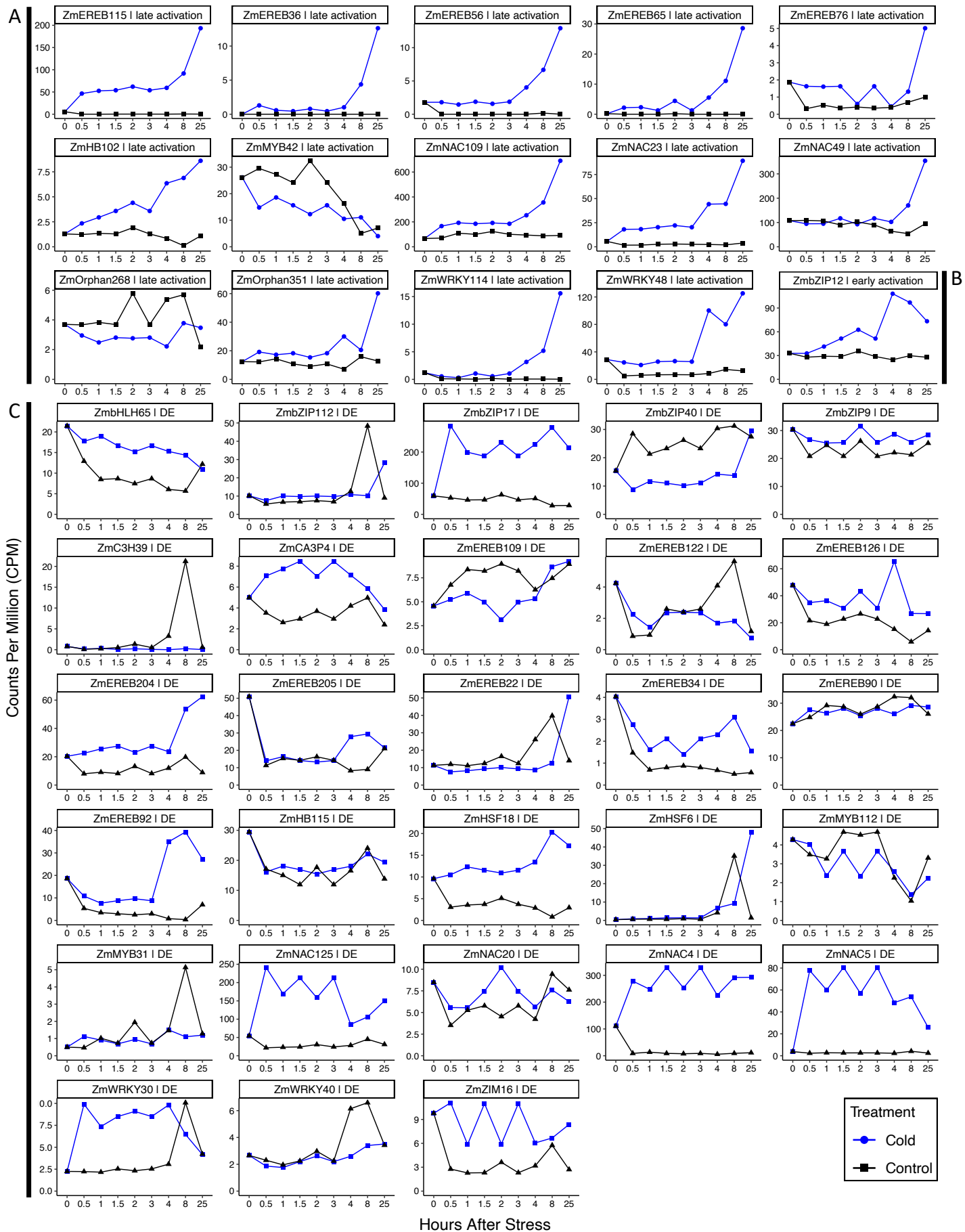


Figure S6. Characterization of TFs that have previously been reported to play a role in maize response to cold. Out of 235 previously reported cold stress-related TFs, 109 TFs were expressed with ≥ 5 CPM for at least one sample (treatment x time point), while 43 were differentially expressed in response to cold stress and assigned into cold up-regulated modules including: (A) late activation, (B) early activation, (C) differentially expressed (DE). DE cold up-regulated genes were identified in the hybrid experiment (3 replicates, 1h and 25h after stress) and TF gene response to cold stress in the time-series (1 replicate, 9 time points) may not depict cold up-regulation for each DE gene.

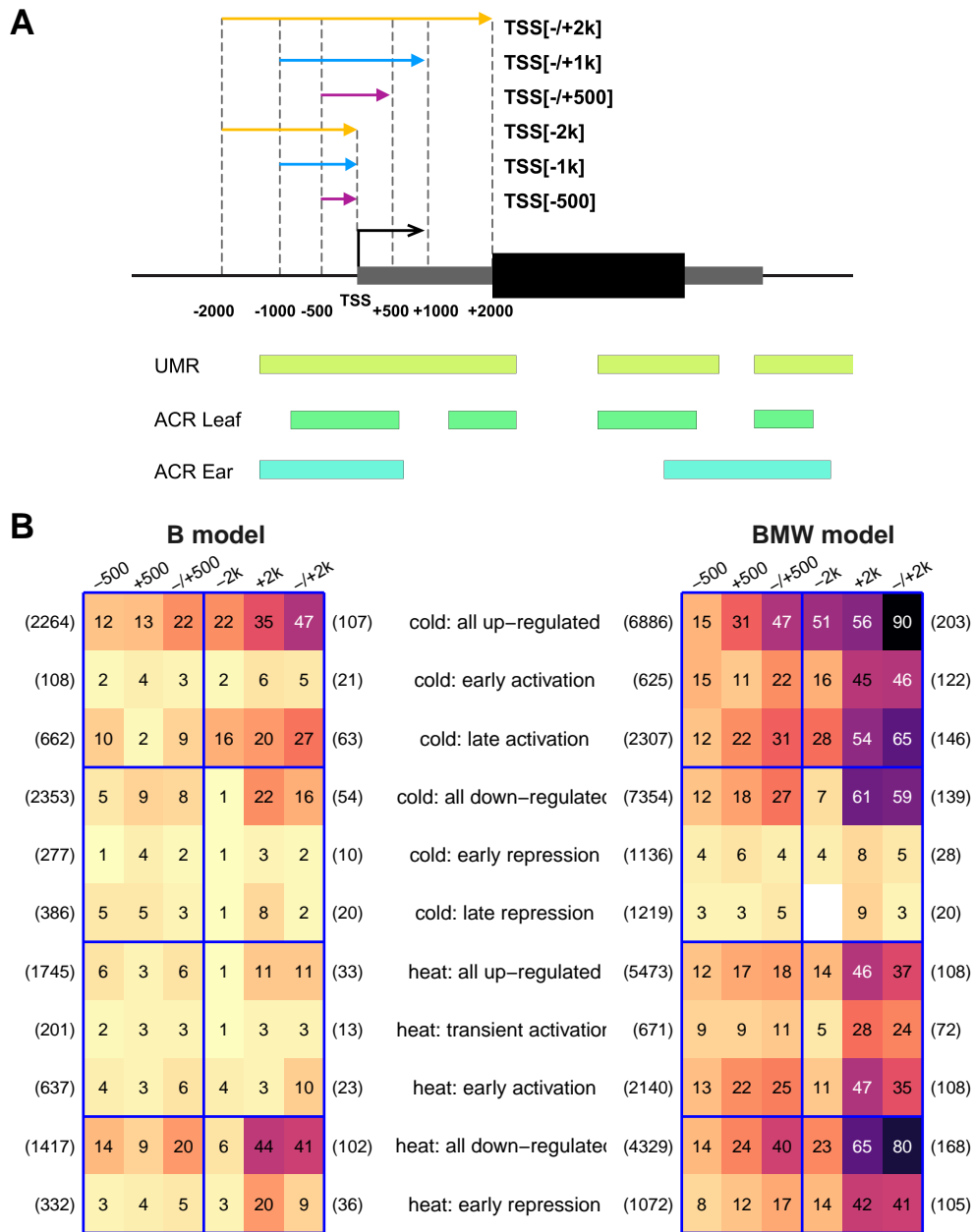


Figure 3. Identification of enriched motifs in cold- and heat-responsive genes. (A) Varying potential 'promoter' sequence spaces were utilized to search for motifs that are enriched in different sets of genes. The schematic indicates a representative gene with the transcription start site (TSS) indicated. The potential regions include different lengths of sequences upstream the promoter (-500, -1k, -2k) as well as sets of sequence that include both upstream and downstream sequence (i.e., +/-500). In addition, for each of these potential regions we also subset the sequence to only include regions that are unmethylated (UMR - unmethylated regions) or that are classified as accessible based on ATAC analysis (ACR - accessible chromatin region) in leaf or ear tissue (Ricci et al., 2019). (B) Co-expression modules as well as the entire set of cold-/heat- up-/down-regulated genes were used to search for enriched motifs (see Methods). The number of non-redundant motifs found using +/- 2k promoter sequence as well as different epigenetic filters (i.e., UMRs, ACRs) were shown. The numbers on the right side of the plot indicate the total number of non-redundant motifs found for each set of genes using +/-2k promoter space as well as the other promoter spaces of different sizes (shown in Figure S7).

		B model																																				
		-500				+500				-/+500				-1k				+1k				-/+1k				-2k				+2k				-/+2k				
		raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	
cold: all up-regulated (2264)		13	14	3	7	17	10	2	2	27	16	2	3	20	10	3	3	26	20	3	2	44	5	2	2	24	14	3	3	46	32	2	2	45	26	2	2	(228)
cold: early activation (108)		3	2			3	2			2	2	2	2	2	2	2	2	4	2			4	2	2	2	3	2	2	2	6	2			6	2	3	2	(60)
cold: late activation (662)		8	4	3	2	2	10	2	2	5	5	2	3	11	6	2	2	4	3	3	3	9	2	2	2	17	3	3	2	14	9	2	2	19	6	2	3	(98)
cold: all down-regulated (2353)		4	2	2	2	10	5	2	2	8	2	2	2	3	2	2	2	15	10	2	2	14	7	2	2	2	3	2	2	15	9	2	2	16	4	2	2	(129)
cold: early repression (277)		2	2	2	2	4	3			4	2	2	2	2	2	2	2	5	3			4	3	2	2	2	2	2	2	5	3		2	3	3	2	2	(60)
cold: late repression (386)		3	3	2	2	5	3		2	3	2	2	3	2	2	2	2	4	2		2	2	2	2	2	2	2	2	2	8	2		2	2	2	2	2	(64)
heat: all up-regulated (1745)		6	3	3	3	3	4	2	3	6	4	4	3	5	4	3	3	4	4	2	2	6	5	3	3	2	3	3	2	12	5	2	2	12	6	3	3	(84)
heat: transient activation (201)		3	2	2	3	2	2			3	3	2	3	2	3	2	2	3	2			2	2	2	2	3	2	2	2	4	3		2	2	2	3	3	(48)
heat: early activation (637)		5	3	2	3	3	5	2	3	7	7	4	3	4	3	2	3	4	8	2	3	3	11	2	3	3	2	2	2	3	3	2	3	12	4	3	3	(62)
heat: all down-regulated (1417)		14	5	2	2	14	14	2	2	17	11	2	2	9	3	2	3	27	22	2	2	23	13	2	2	7	6	2	3	39	27	2	2	31	18	2	4	(174)
heat: early repression (332)		2	2	2	2	4	3		2	4	3	2	2	2	2	2	2	5	5		2	13	3	2	2	2	2	2	2	21	4	2	2	9	4	2	2	(96)

		BMW model																																				
		-500				+500				-/+500				-1k				+1k				-/+1k				-2k				+2k				-/+2k				
		raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	raw	umr	acrE	acrL	
cold: all up-regulated (6886)		18	28	2	2	29	28	2	1	45	34	2	2	37	32	2	2	42	54	2	3	65	64	2	2	46	26	2	2	69	63	2	2	86	64	2	2	(370)
cold: early activation (625)		16	10			12	8			18	11	2	2	14	4	2	2	20	18			37	11	2	2	14	6	2	2	42	20			53	11	2	2	(197)
cold: late activation (2307)		17	17	2	3	23	12	2	2	29	14	3	3	25	6	2	3	32	15	2	2	54	32	2	3	27	18	2	3	65	38	2	2	58	26	2	3	(269)
cold: all down-regulated (7354)		14	4	2	2	15	16	2	2	33	16	2	3	8	8	2	2	44	34	2	2	25	16	2	2	6	5	2	2	55	32	2	2	54	24	2	2	(245)
cold: early repression (1136)		2	3	2	2	8	4			5	1	2	2	1	5	2	2	5	6			5	5	2	2	4	2	2	2	9	9		2	6	3	2	2	(83)
cold: late repression (1219)		3	2	2	2	2	4		2	5	2	2	2	3	2	2	2	7	3		2	5	4	3	2	2	2	2	2	7	4		2	5	6	2	2	(75)
heat: all up-regulated (5473)		14	10	3	2	19	23	2	3	21	17	2	3	11	10	2	4	27	17	2	2	29	28	3	3	13	4	2	2	50	27	2	2	35	14	2	4	(199)
heat: transient activation (671)		8	4	2	3	9	4			7	10	2	3	5	3	2	2	11	19			16	9	2	2	6	2	2	2	43	10		2	23	7	2	3	(146)
heat: early activation (2140)		12	9	2	2	17	9	2	2	27	19	3	3	12	10	2	2	8	16	2	3	24	15	2	3	10	10	2	2	45	29	2	3	23	14	3	3	(173)
heat: all down-regulated (4329)		20	17	2	2	39	33	2	2	43	34	2	2	27	14	2	3	41	45	2	2	54	37	2	3	21	15	2	2	67	68	2	2	80	47	2	2	(328)
heat: early repression (1072)		9	4	2	2	11	14		2	17	7	2	2	10	6	2	2	21	19		2	24	15	2	2	14	6	2	2	37	25	2	2	43	9	2	2	(178)

Figure S7. Number of enriched motifs found using B73 promoter spaces (“B model”) or B73/Mo17/W22 promoter spaces (“BMW model”) of different size and epigenetic filters. Co-expression modules as well as the entire set of cold-/heat-up-/down-regulated genes were searched for enriched motifs with varying lengths of promoter space and different filters based on methylation or chromatin accessibility. Identified motifs were compared with known TF binding motifs (cis-BP) and clustered based on sequence similarity. Numbers in each cell represent the number of non-redundant motifs found using the full set of sequences (raw), using only the unmethylated regions (umr) or using only accessible chromatin regions in leaf (acrL) or ear (acrE) inside different sized promoter spaces. Numbers in parentheses on the left side of plot indicate the number of genes in each co-expression module used for motif mining, while numbers on the right side of plot indicate the total number of non-redundant motifs found for each set of genes after sequence clustering.

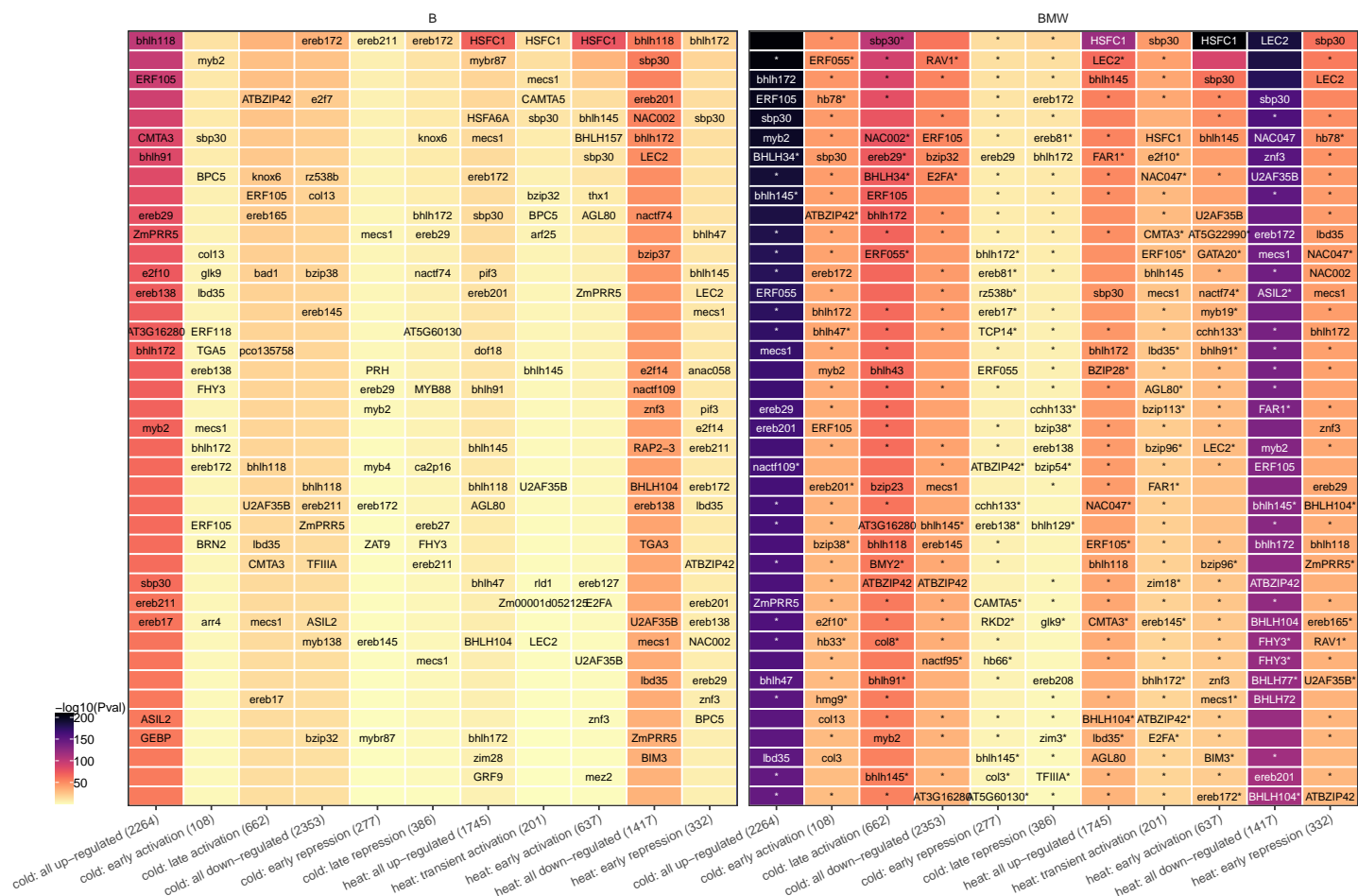


Figure S8. Enriched motifs include known transcription factor binding sites (TFBSs) as well as novel motifs. For each set of DEGs up to the top 40 most enriched motifs found using B73 promoter space (“B model”) or B73/Mo17/W22 promoter sequences (“BMW model”) are shown (p-value for enrichment is indicated by color). Some sets of DEGs have less than 40 motifs and only the significant ones are shown. If the enriched motif matched a previously characterized TFBS (Pearson correlation coefficient > 0.8) the name of the transcription factor is shown. In each cases there are a mixture of previously characterized motifs and novel motifs. TTS motifs with a “*” sign represent motifs not present in the top40 TSS motifs identified in the same list of genes.

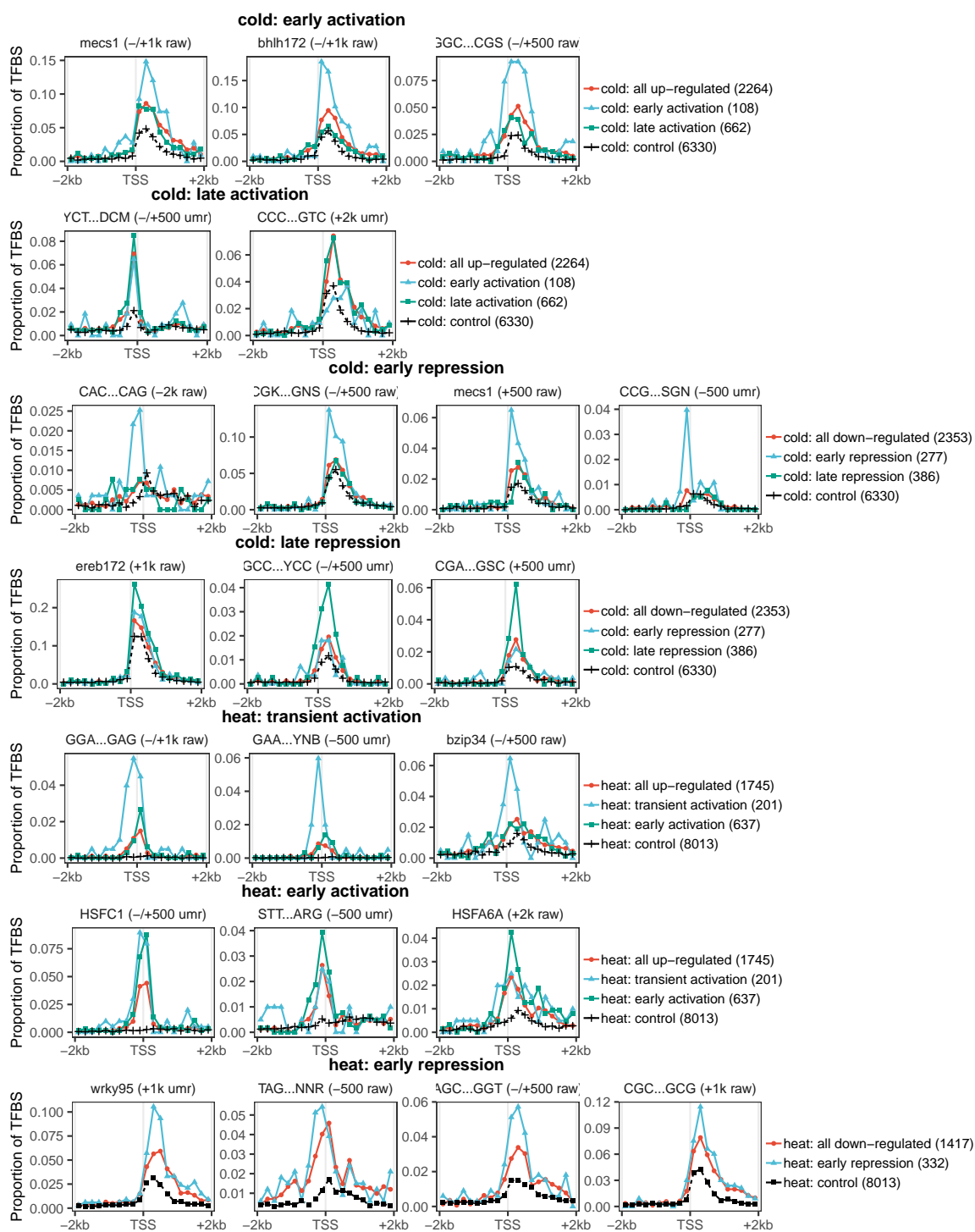


Figure S9. Meta plots of selected stress-responsive motifs in gene promoters. Two to four motifs from each of the seven co-expression clusters (cold early activation, cold late activation, etc.) with their relative locations in the TSS:-/+2k region cut into 40 bins. The occurrence of each motif in these bins were recorded and the proportion of genes contains the motif in each bin is plotted.

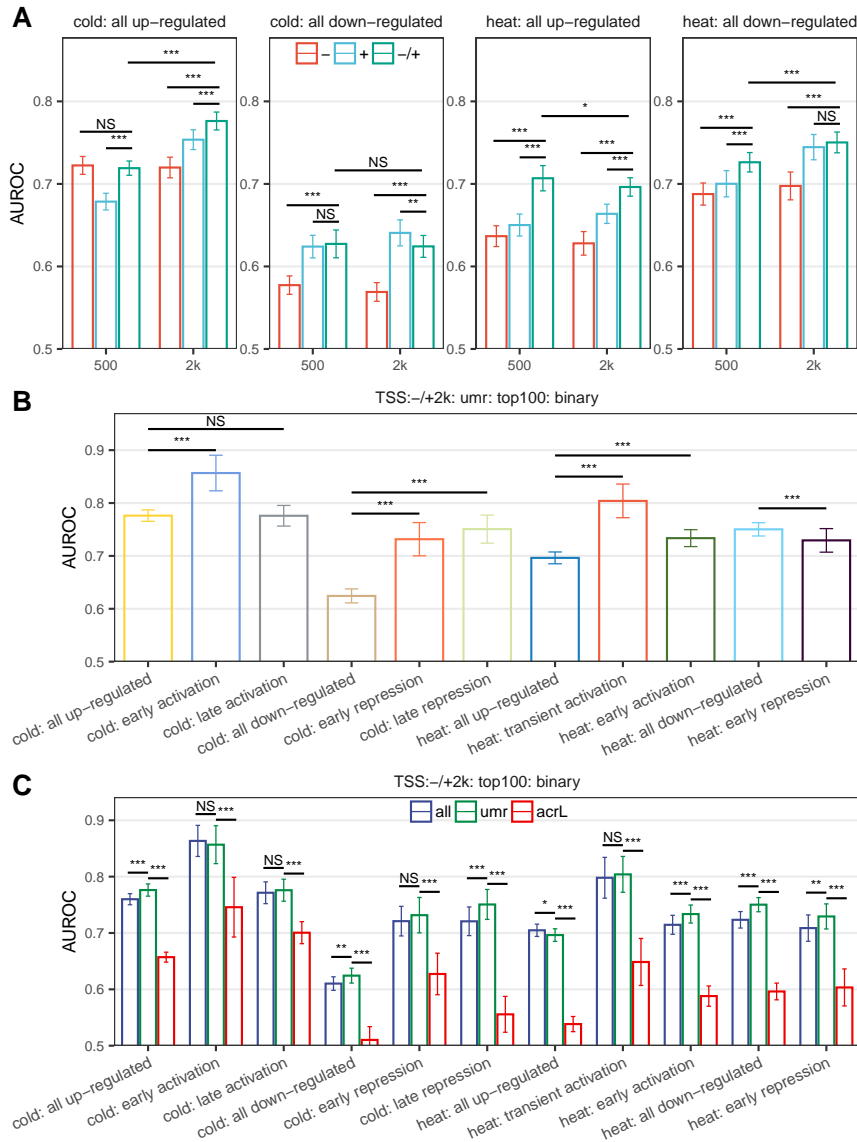


Figure 4. Performance (Area Under ROC Curve, AUROC) comparison of different machine learning models predicting cold and heat responsive expression. (A) performance comparison of models trained using small promoter spaces (-500, +500, -/+500) against large promoter spaces (-2k, +2k, -/+2k). In each case same epigenetic filters (UMR) and number of features (top100) were used for training; (B) performance comparison of models trained using the full set of DEGs against models trained using specific co-expression clusters. In each case same sized promoter spaces (-/+2k), epigenetic filters (UMR) and number of features (top100) were used; (C) performance comparison of models using all genomic sequence ("all", blue), UMR regions only ("umr", green) or using leaf accessible regions only ("acrL", red) with the same sized promoter spaces (-/+2k) and number of features (top100). In each training average AUROC (N=100 model runs) is shown along with the standard deviation. Pairwise comparisons were made using t-test with significance levels indicated (*: 0.05; **: 0.01; ***: 0.001)

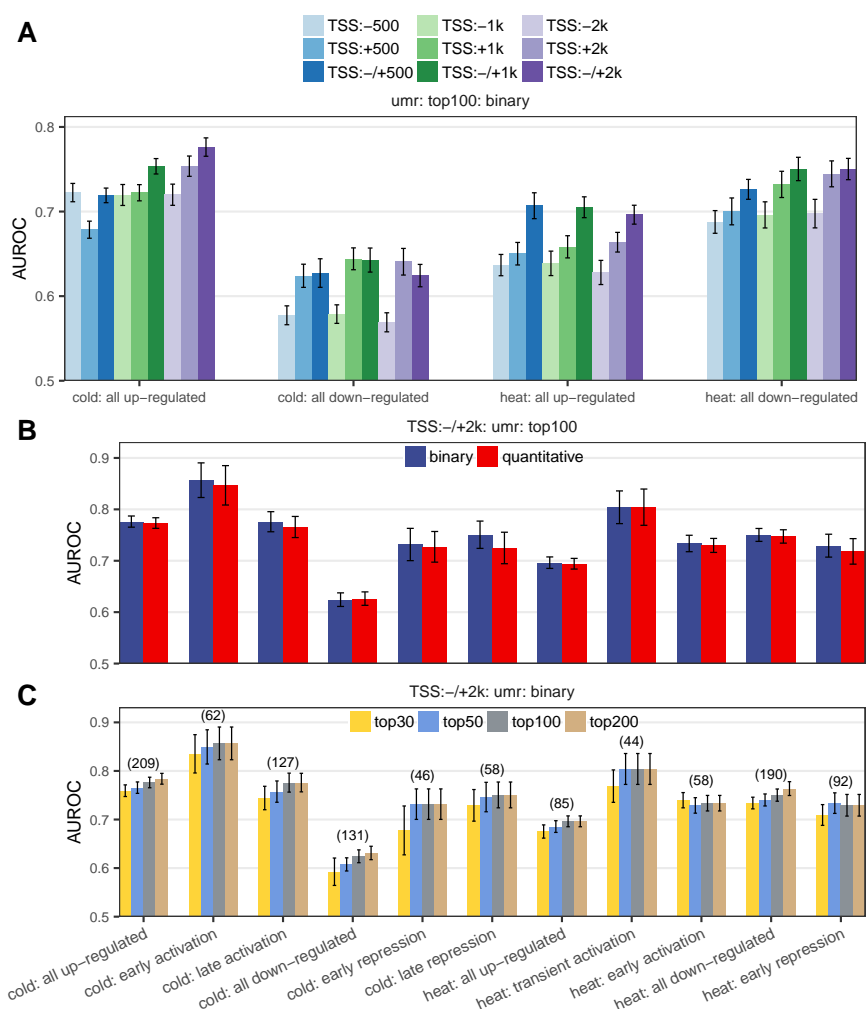


Figure S10. Performance (Area Under ROC Curve, AUROC) of machine learning models predicting cold and heat responsive expression. Models were trained to predict expression responses to heat or cold using: (A) different sizes of promoter sequences surrounding the TSS; (B) using “binary encoding” (0/1) or “quantitative encoding” (0/1/2/...) of motifs and and (C) using different numbers of mostly enriched motifs as input features. Number of non-redundant motifs used for model training are indicated on top of each set of bars in (C). In each training the average AUROC (N=100 model runs) is show along with the standard deviation.

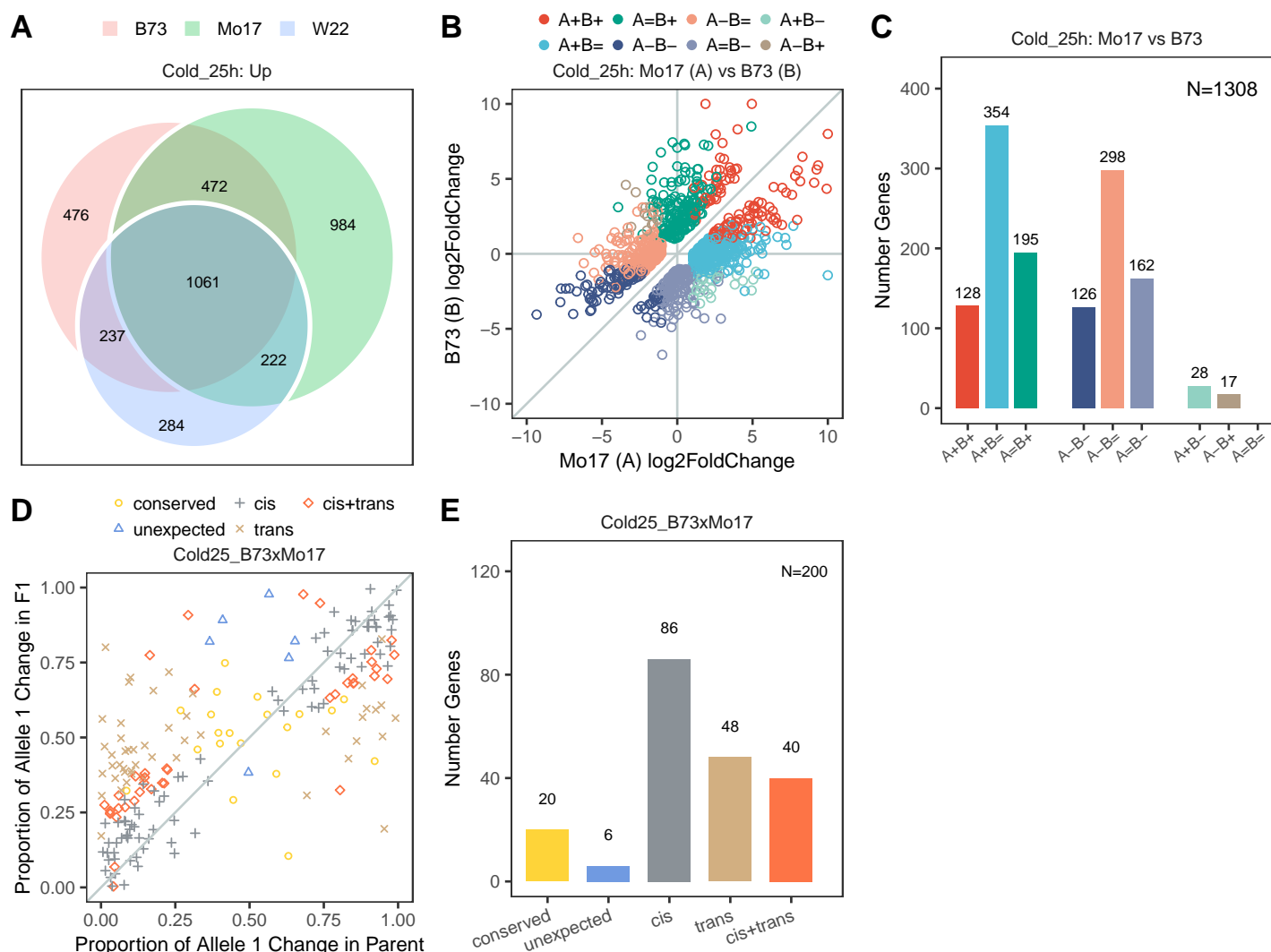


Figure 5. Characterization of genes with variable stress responsive patterns among inbreds. (A) A Venn diagram is used to assess genes that are up-regulated in response to 25h of cold stress for B73, Mo17 and W22. The overlap of DE genes at other time points is shown in Figure S11A. (B) For genes that show significantly stronger (or weaker) response to cold at 25h in B73 compared to Mo17 we show the log2 fold-change (cold 25h / control 25h) for both inbreds. The classification of differential responses for other genotype contrasts and timepoints is provided in Figure S12. Above the diagonal line are genes showing stronger cold response in Mo17 while those below the diagonal line represent genes showing stronger B73 response. Different colors indicate groups of genes with different DE status (e.g., red genes are ones up-regulated in both inbreds (but showing significantly different response), green are genes only up-regulated in Mo17). The number of genes in each category is shown in (C). For each class the response in the two genotypes (A and B) is indicated as up-regulated (“+”), down-regulated (“-”) or not DE (“=”). (D) For the subset of genes classified as having a response in only one of the two genotypes that also had SNPs we assessed allele-specific expression in the F1 hybrid. The proportion of allele 1 (B73) change in stress vs control of the F1 (x-axis) was compared to the proportion of the change in expression in the parental genotypes (y-axis). A maximum likelihood model was applied to classify cis- and trans- inheritance patterns and shown in different colors. The number of genes classified into each type of regulatory pattern for response to abiotic stress are shown in (E). Similar analyses for other genotypes, stress and time points are shown in Figure S13.

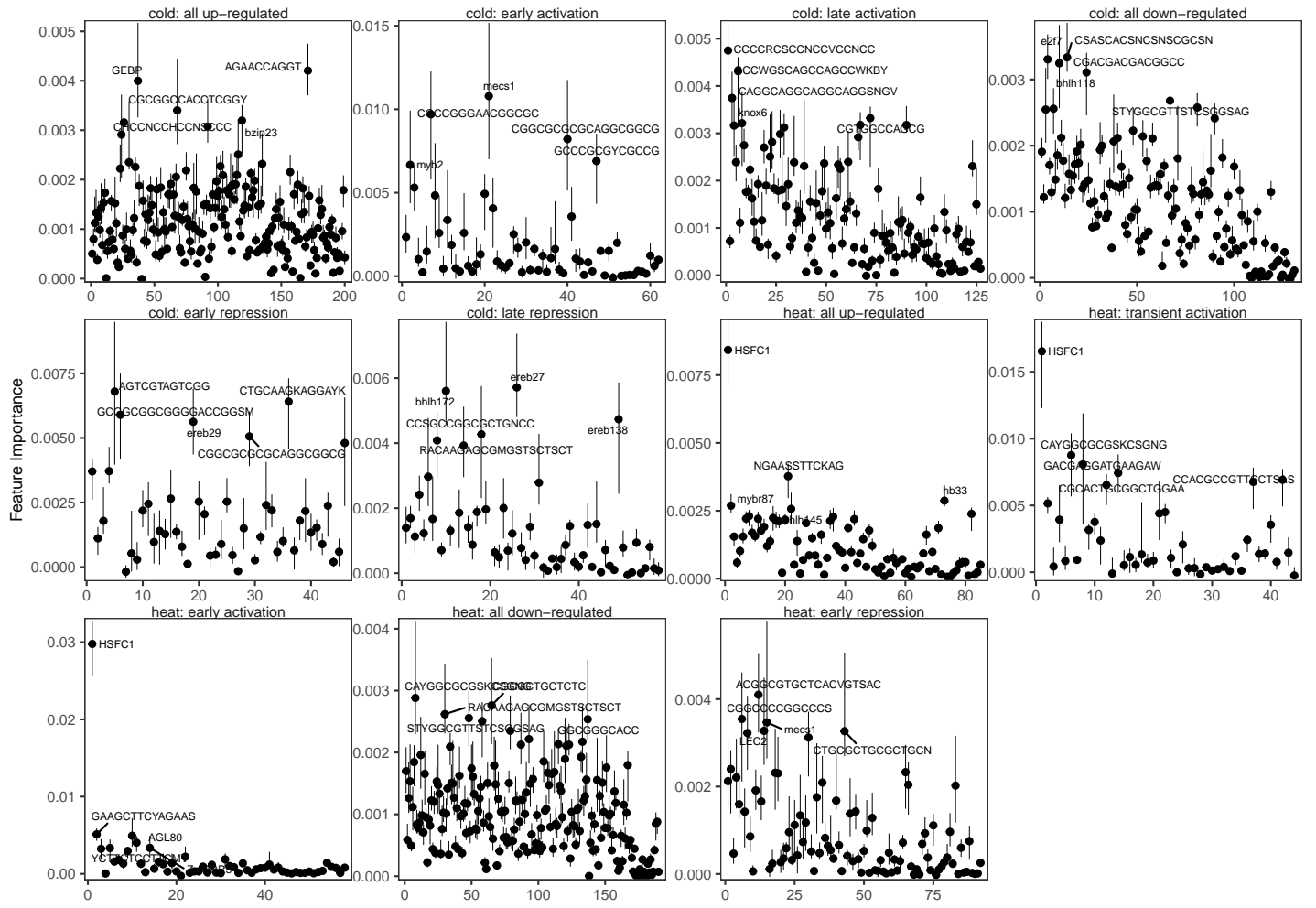


Figure S11. Relationship between motif enrichment level and feature importance score in different sets of stress-responsive genes. Motif enrichment levels are determined by hypergeometric test using motif occurrences in positive and negative gene sets and ranked from most significant to least significant in x-axis. Feature importance scores reported by 100 permutations of each random forest model training and showed in y-axis with error bar indicating 25-75% quantiles. Top 5 feature importance scores are labelled with motif names (known motif) or consensus sequences (novel motif). All feature importance score estimates are based on the models trained using “+/-2k”, “UMR”, “top200”, “binary” parameters.

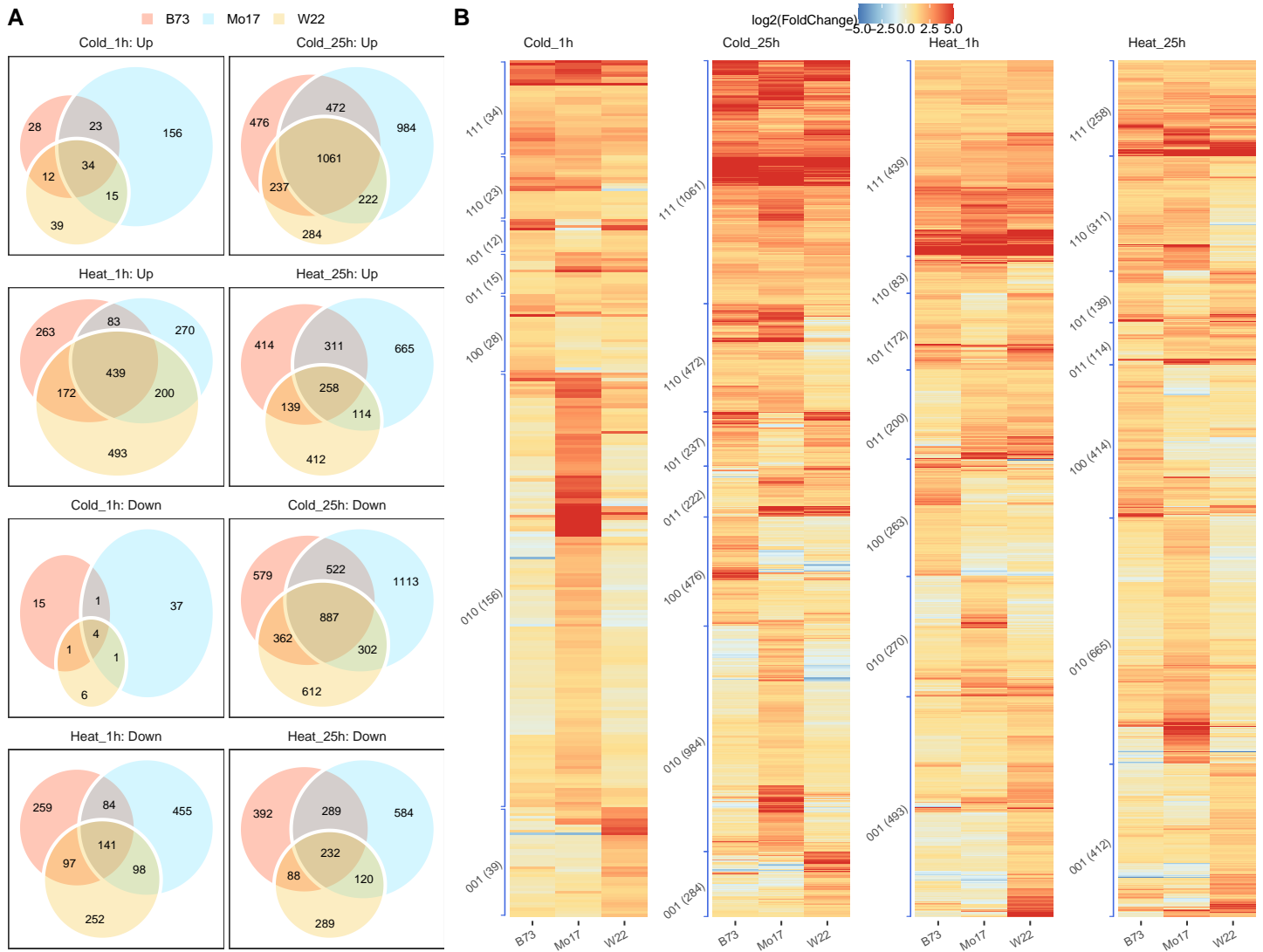


Figure S12. Comparison of heat- and cold-response gene expression in B73, Mo17 and W22. (A) At each time point for cold or heat stress we identified DEGs in all three genotypes and show the overlap of DEGs. The actual expression levels in all three genotypes for the non-redundant set of up-regulated genes is shown in (B). The genes are classified based on response in B73, Mo17 and W22 (0 indicates not DE and 1 indicates DE in the three genotypes such that '111' indicates DE in B73, Mo17 and W22 while '010' would indicate DE in Mo17 but not B73 or W22. Note that for some genes classified as having variable responses there are actually similar changes in all genotypes but there are other examples with clear response on some genotypes but not in others.

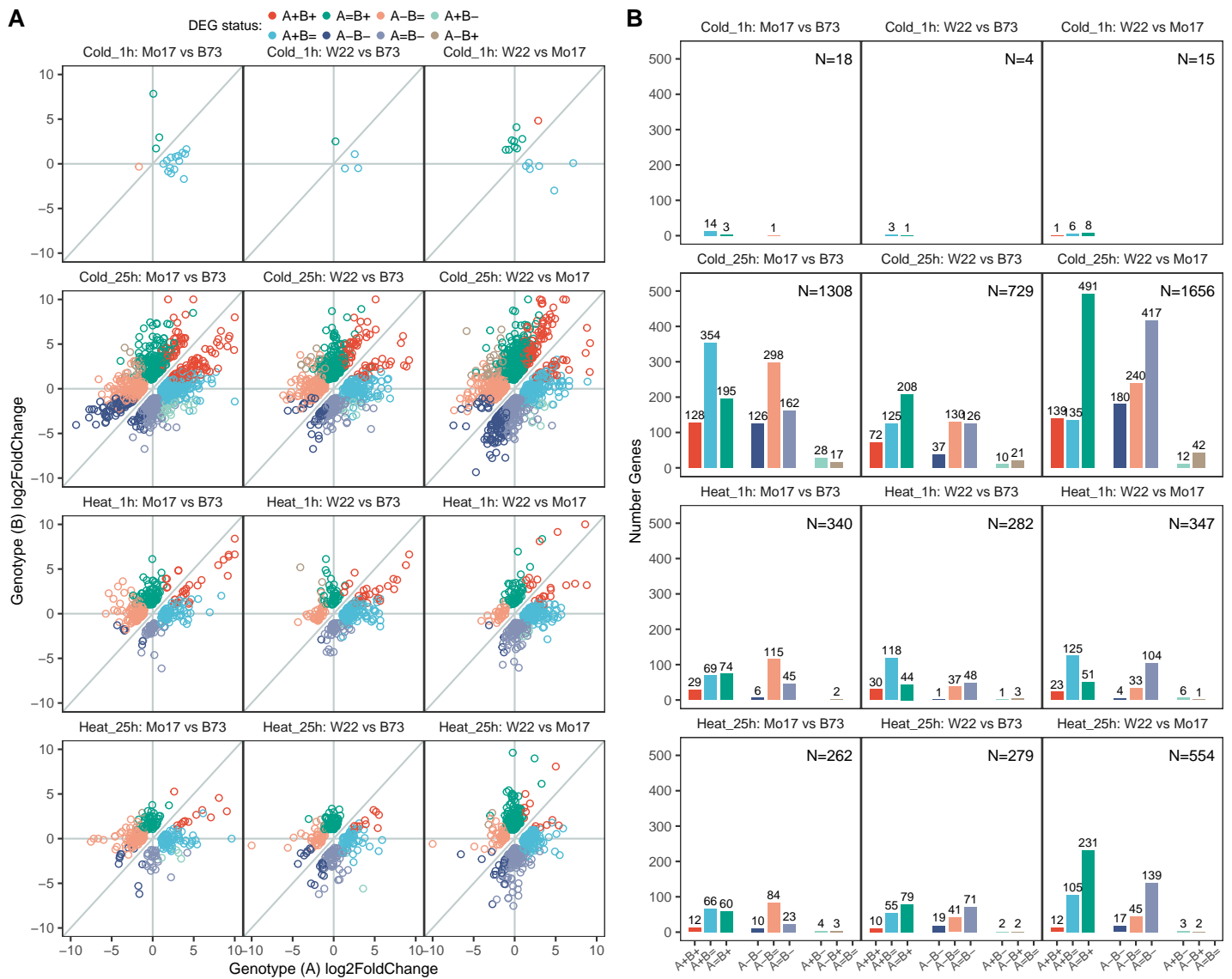


Figure S13. Characterization of genes with variable stress responsive patterns among inbreds. For each pair of genotypes we identified genes that show significantly stronger (or weaker) response to cold/heat at 1h or 25h time points using a generalized linear model (see methods). (A) Scatterplot showing the log2 fold-change (stress / control at a time point) for compared inbreds (A and B) in x- and y-axis. Above the diagonal line are genes showing stronger cold response in genotype A while those below the diagonal line represent genes showing stronger genotype B response. Different colors indicate groups of genes with different DE status (e.g., red genes are ones up-regulated in both inbreds (but showing significantly different response), green are genes only up-regulated in genotype B). (B) The number of genes in each category shown in (A). For each class the response in the two genotypes (A and B) is indicated as up-regulated (“+”), down-regulated (“-”) or not DE (=).

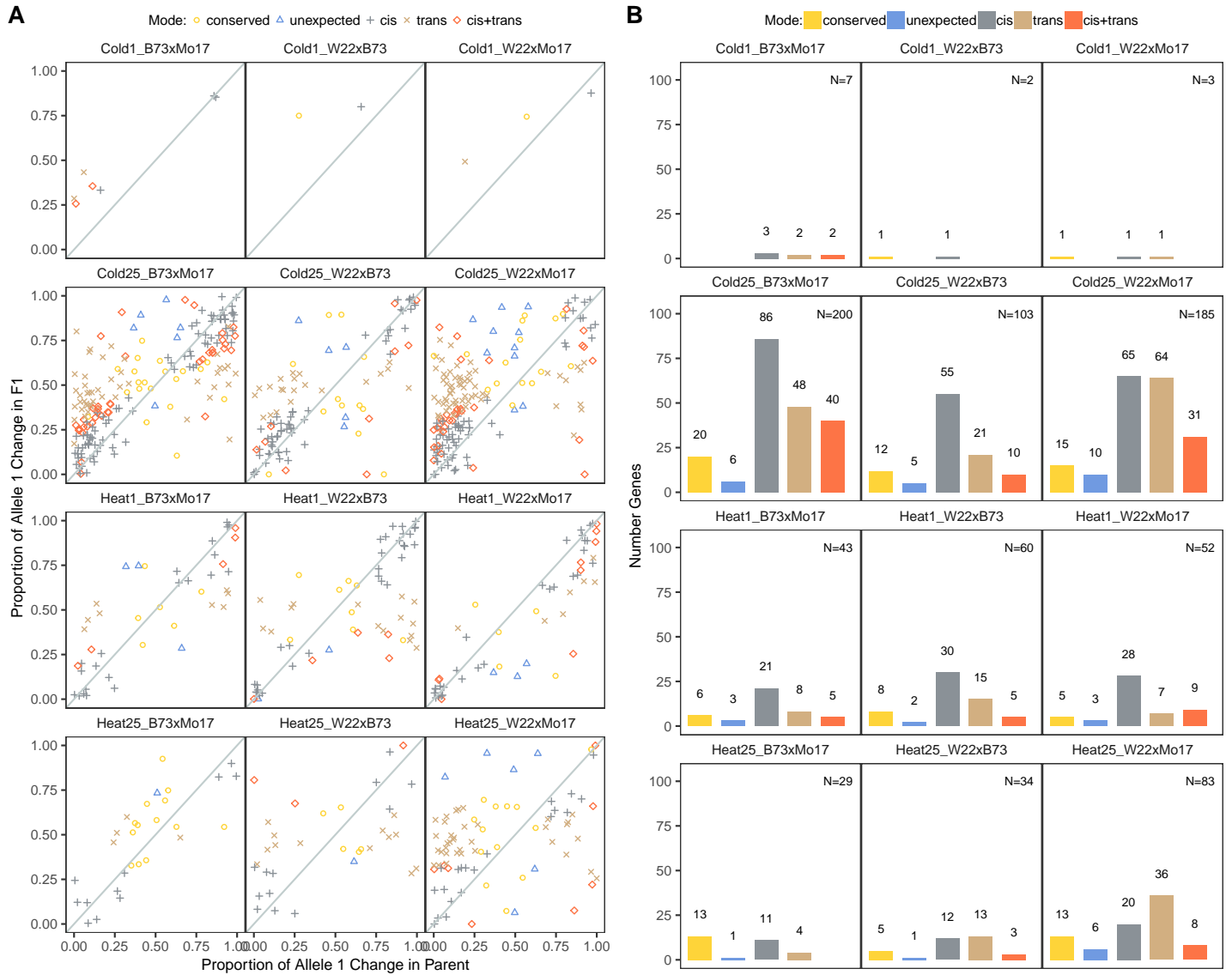


Figure S14. Cis/trans characterization of genes showing different stress response among inbreds. For the subset of genes classified as showing significantly different response among inbreds that also had SNPs we assessed allele-specific expression in the F1 hybrid. (A) For each pairwise genotype comparison the proportion of allele 1 change in stress vs control of the F1 (x-axis) was compared to the proportion of the change in expression in the parental genotypes (y-axis). A maximum likelihood model was applied to classify cis- and trans- inheritance patterns and shown in different colors. (B) The number of genes classified into each type of regulatory pattern in each pairwise comparison.

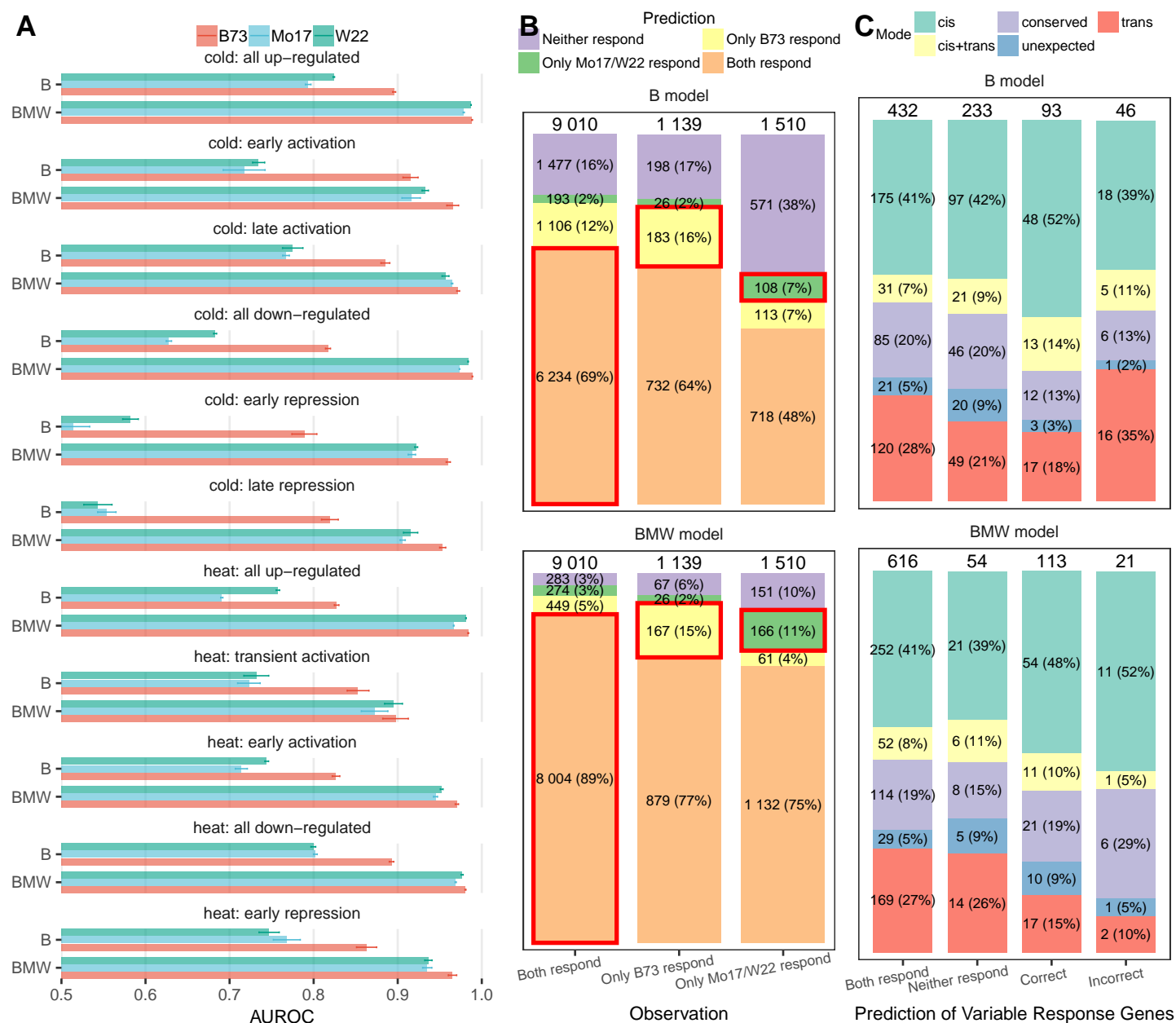


Figure 6. Cross-genotype performance of machine learning models predicting cold or heat responsive expression. Models were trained only using B73 sequence and labels ("B model") or data from all three genotypes ("BMW model"). (A) Area Under ROC curve (AUROC) for models predicting stress responsive expression in B73, Mo17 and W22. (B) Model prediction accuracy for genes showing consistent ("Both respond") or variable ("Only B73/Mo17/W22 respond") response patterns among genotypes. In each observed category the number and proportion of predictions were marked in the plot with the correct predictions highlighted with red boxes. (C) Dissection of regulatory patterns for genes showing variable response patterns among genotypes. Variable response genes were first grouped by whether model prediction agrees with observed status ("Correct" if the model correctly predicts one genotype responds but the other does not, "Incorrect" if the model predicts oppositely, "Both respond" and "Neither respond" if the model predicts both or neither genotypes respond - although in reality only one genotype responds). Then within each group the number of proportion of different regulatory patterns ("cis", "trans", etc) were marked.

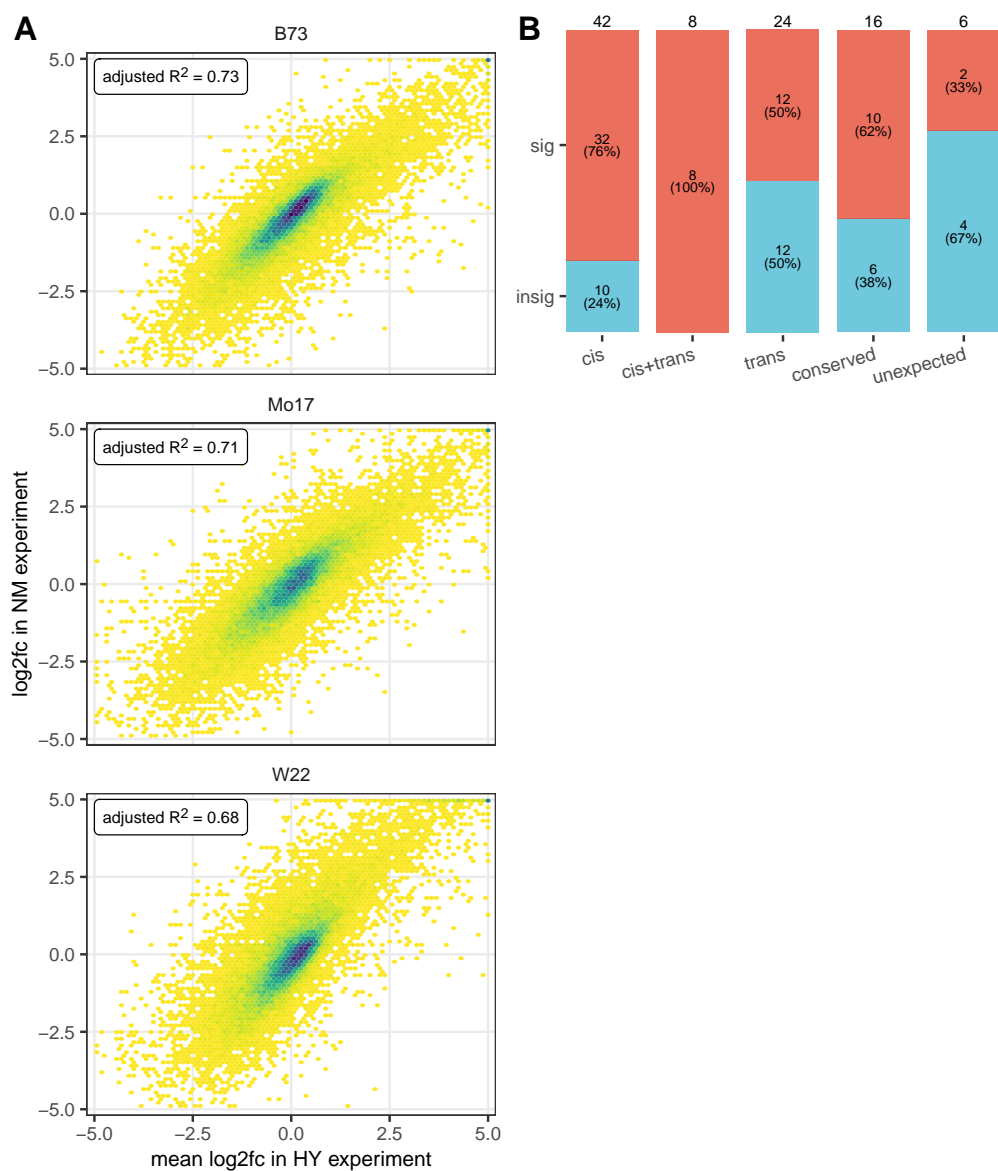


Figure S15. Identification of cis-regulatory variants associated with variable cold responsive pattern in a panel of 25 maize genotypes. (A) Consistency of log2 fold changes for each gene called between two experiments: the replicated HY experiment with 3 maize inbreds (x-axis) and the NM experiment with 25 maize genotypes (y-axis). Point density is shown to avoid over plotting. Linear regression is performed and the adjusted R^2 values are marked. (B) Cis-regulated variable response genes are enriched in having significantly associated local variants. Shown are proportions of genes with detected local associations for variable response genes under different regulatory patterns.

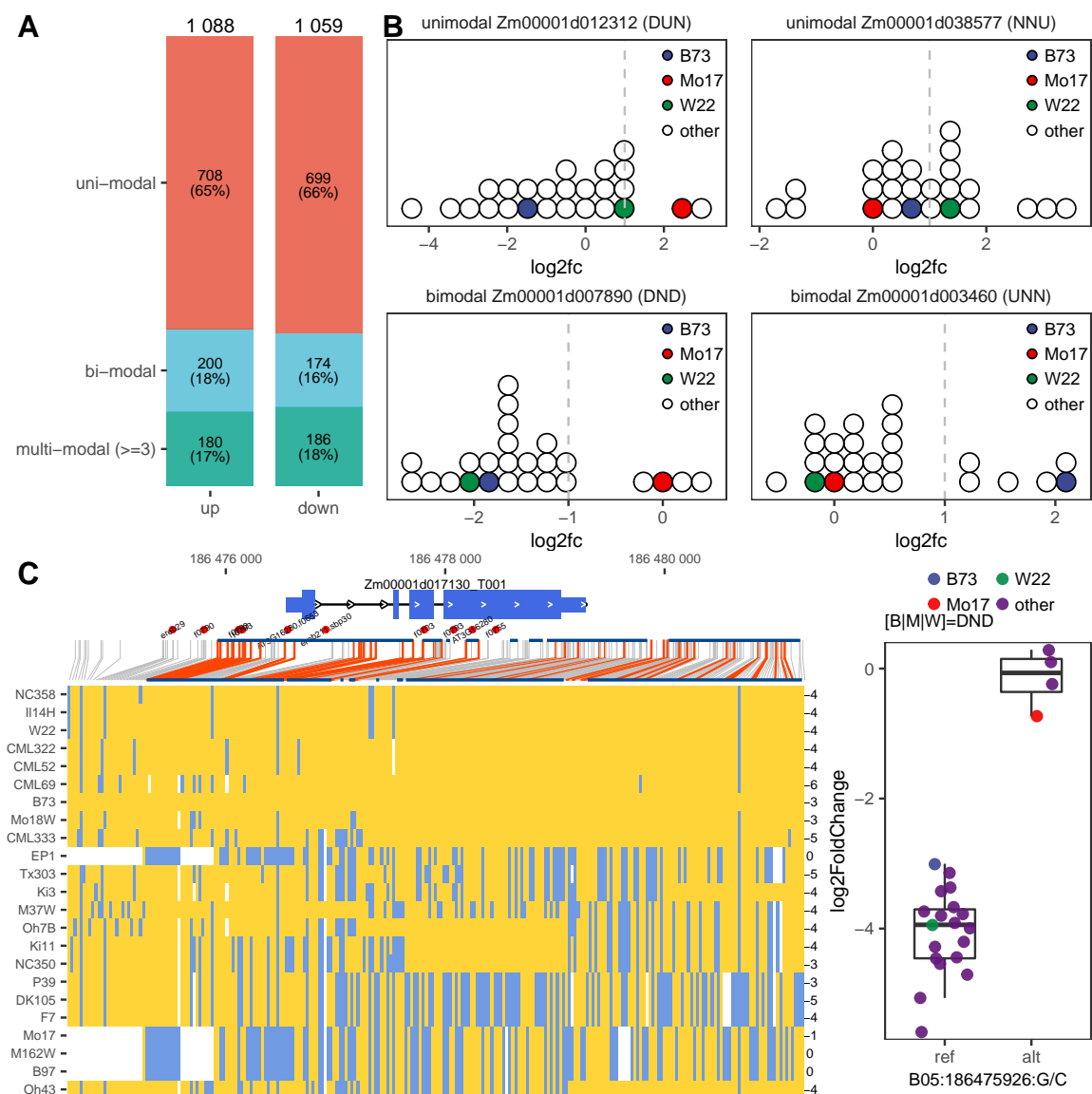


Figure 7. Identification of cis-regulatory variants associated with variable cold responsive pattern in a panel of 25 maize genotypes. (A) Proportion of ~2000 variable response genes showing uni-modal, bi-modal and multi-modal distributions of the log2 fold change ratios (cold/control); (B) Examples of two genes showing uni-modal log2fc ratios and two showing bi-modal ratio distributions; (C) Cis-regulatory variation associated with cold responsiveness in a maize mitochondrial transcription termination factor (mTERF17). Heatmap shows bi-allelic variants (SNP and short indels) within 2kb of the gene with yellow indicating reference (B73) allele and blue indicating alternate allele. Log2 fold change of each genotype is show on the right of the heatmap. Below the gene structure plot are locations of the most (top30) enriched cold-responsive motifs (red dots) with the motif name marked, as well as haplotype blocks (dark blue segments) identified using PLINK. Boxplot on the right shows the top associating variant and the log2fc distributions of genotypes carrying the two alleles.

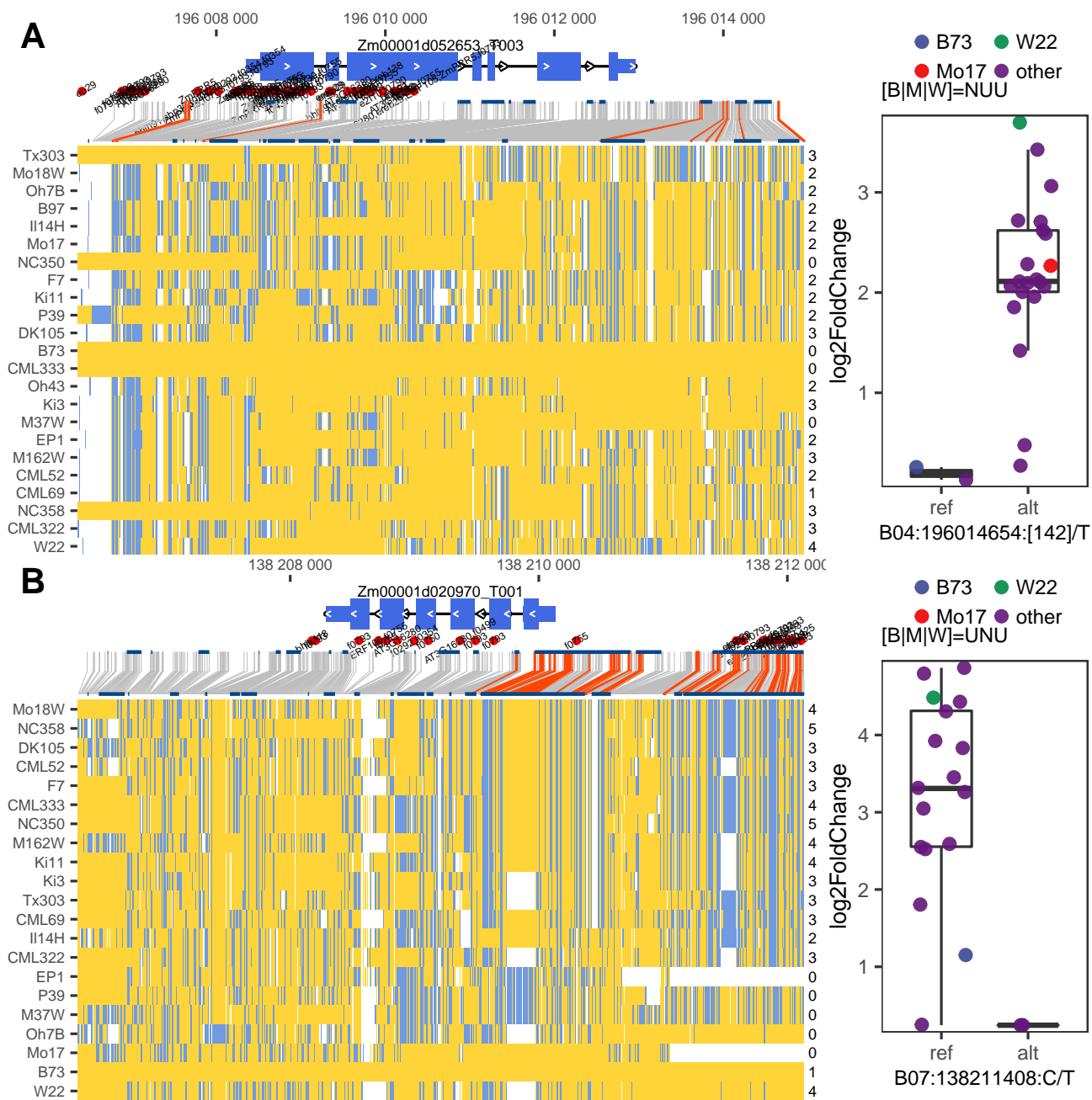


Figure S16. Cis-regulatory variation associated with cold responsive patterns in a respiratory burst oxidase (*rboh4*, panel A) and a dihydroflavonoid reductase (*df1*, panel B). Heatmap shows bi-allelic variants (SNP and short indels) within 2kb of the gene with yellow indicating reference (B73) allele and blue indicating alternate allele. Log2 fold change of each genotype is show on the right of the heatmap. Below the gene structure plot are locations of the most (top30) enriched cold-responsive motifs (red dots) with the motif name marked, as well as haplotype blocks (dark blue segments) identified using PLINK. Boxplot on the right shows the top associating variant and the log2fc distributions of genotypes carrying the two alleles.

Table S1. Sample statistics.

Experiment	Treatment	Timepoint	Genotype	Total Reads	Mapped Reads	Uniquely Mapped	Unique Mapping Rate
TC	Control	0	B73	28,181,337	27,062,086	25,289,509	93.4%
	Control	0	Mo17	30,180,390	27,971,462	26,613,733	95.1%
	Control	0	W22	30,502,250	28,553,107	27,142,187	95.1%
	Control	0.5	B73	30,686,634	29,933,075	28,298,002	94.5%
	Control	0.5	Mo17	32,980,583	30,596,046	29,070,157	95.0%
	Control	0.5	W22	27,174,028	25,256,472	23,967,595	94.9%
	Control	1	B73	27,176,416	26,369,629	24,803,906	94.1%
	Control	1	Mo17	22,604,309	20,991,963	19,925,551	94.9%
	Control	1	W22	31,464,296	29,329,929	27,861,358	95.0%
	Control	1.5	B73	35,016,090	33,682,265	31,786,402	94.4%
	Control	1.5	Mo17	30,629,531	28,435,634	27,042,081	95.1%
	Control	2	B73	29,695,948	28,818,773	27,135,381	94.2%
	Control	2	Mo17	33,305,507	30,759,949	28,890,539	93.9%
	Control	2	W22	28,075,515	25,979,440	24,594,355	94.7%
	Control	3	B73	30,839,593	29,737,064	28,039,778	94.3%
	Control	3	Mo17	32,388,859	29,645,313	28,014,990	94.5%
	Control	4	B73	39,204,669	37,874,734	35,579,022	93.9%
	Control	4	Mo17	35,677,206	32,606,367	30,715,333	94.2%
	Control	4	W22	28,265,345	25,970,415	24,605,416	94.7%
	Control	8	B73	31,385,793	30,364,334	28,437,307	93.7%
	Control	8	Mo17	29,586,166	27,353,374	25,704,730	94.0%
	Control	25	B73	34,357,136	33,131,990	31,280,321	94.4%
	Control	25	Mo17	28,924,942	26,522,801	25,056,084	94.5%
	Control	25	W22	43,387,049	39,856,001	37,807,910	94.9%
	Cold	0.5	B73	30,661,603	29,674,008	28,118,058	94.8%
	Cold	0.5	Mo17	28,040,124	25,941,754	24,663,330	95.1%
	Cold	0.5	W22	26,143,752	24,088,749	22,912,193	95.1%
	Cold	1	B73	29,377,633	26,919,308	25,199,171	93.6%
	Cold	1	Mo17	33,638,799	32,187,326	30,523,968	94.8%
	Cold	1	W22	28,064,946	26,175,090	24,872,859	95.0%
	Cold	1.5	B73	25,956,112	25,097,569	23,689,320	94.4%
	Cold	1.5	Mo17	34,440,636	31,934,149	30,214,394	94.6%
	Cold	2	B73	32,965,091	31,809,529	30,017,089	94.4%
	Cold	2	Mo17	26,992,337	24,906,737	23,587,035	94.7%
	Cold	2	W22	32,928,804	30,187,799	28,576,079	94.7%
	Cold	3	B73	35,540,441	34,397,671	32,451,500	94.3%
	Cold	3	Mo17	27,846,993	25,613,067	24,236,061	94.6%
	Cold	4	B73	27,800,603	26,835,252	24,259,469	90.4%
	Cold	4	Mo17	30,272,220	28,031,313	26,516,821	94.6%
	Cold	4	W22	31,073,004	28,836,404	27,184,796	94.3%
	Cold	8	B73	27,177,494	26,255,339	24,542,685	93.5%
	Cold	8	Mo17	25,225,488	23,330,956	22,005,443	94.3%
	Cold	25	B73	31,340,293	30,004,170	28,235,627	94.1%
	Cold	25	Mo17	35,742,025	32,898,655	30,681,879	93.3%
	Cold	25	W22	32,872,336	30,128,168	27,991,054	92.9%
	Heat	0.5	B73	29,474,456	28,751,072	27,198,497	94.6%
	Heat	0.5	Mo17	27,213,177	24,882,147	23,690,343	95.2%
	Heat	0.5	W22	31,303,744	29,013,265	27,637,979	95.3%
	Heat	1	B73	25,369,946	24,711,979	23,515,242	95.2%
	Heat	1	Mo17	29,803,039	27,471,542	26,034,513	94.8%
	Heat	1	W22	27,915,290	25,787,860	24,584,027	95.3%
	Heat	1.5	B73	32,801,983	31,354,074	28,439,301	90.7%
	Heat	1.5	Mo17	28,589,071	26,303,072	24,818,263	94.4%
	Heat	2	B73	35,917,788	34,841,234	32,927,254	94.5%
	Heat	2	Mo17	31,516,863	28,834,701	27,292,799	94.7%
	Heat	2	W22	30,004,365	27,434,377	25,992,352	94.7%
	Heat	3	B73	33,835,732	33,031,684	31,257,683	94.6%
	Heat	3	Mo17	27,661,355	25,406,512	24,046,854	94.6%
	Heat	4	B73	29,050,357	27,870,275	26,393,677	94.7%
	Heat	4	Mo17	35,475,222	32,243,952	30,536,681	94.7%

	Heat	4	W22	28,401,503	25,946,702	24,529,140	94.5%
	Heat	8	B73	36,249,480	35,093,467	33,087,126	94.3%
	Heat	8	Mo17	33,837,150	30,964,038	28,356,667	91.6%
	Heat	25	B73	27,040,245	26,352,673	24,901,506	94.5%
	Heat	25	Mo17	27,649,900	25,388,679	23,518,792	92.6%
	Heat	25	W22	34,860,380	32,225,356	30,645,798	95.1%
HY	Control	0	B73	29,511,949	28,569,878	26,879,316	94.1%
	Control	0	B73	36,540,087	35,296,228	33,326,113	94.4%
	Control	0	B73	29,662,186	28,568,305	26,887,353	94.1%
	Control	0	Mo17	32,825,829	30,260,314	27,831,524	92.0%
	Control	0	Mo17	38,223,106	35,359,417	33,423,525	94.5%
	Control	0	Mo17	29,690,126	27,550,696	26,095,890	94.7%
	Control	0	W22	29,745,197	27,598,340	26,147,775	94.7%
	Control	0	W22	31,139,608	28,932,803	27,290,764	94.3%
	Control	0	W22	35,019,412	32,500,957	30,797,921	94.8%
	Control	0	NA	28,534,582	26,956,354	25,483,954	94.5%
	Control	0	NA	28,451,191	27,024,008	25,533,034	94.5%
	Control	0	NA	37,751,383	34,977,927	33,197,816	94.9%
	Control	0	NA	27,858,036	26,163,535	24,756,783	94.6%
	Control	0	NA	29,187,255	27,427,173	25,809,314	94.1%
	Control	0	NA	30,847,559	28,767,544	27,266,624	94.8%
	Control	0	NA	28,310,859	26,784,940	25,301,491	94.5%
	Control	0	NA	33,543,162	31,632,269	29,824,496	94.3%
	Control	0	NA	27,097,032	25,110,587	23,747,374	94.6%
	Control	1	B73	32,111,622	30,769,605	29,028,594	94.3%
	Control	1	B73	35,136,788	34,392,143	32,739,847	95.2%
	Control	1	B73	34,765,920	33,742,430	32,089,728	95.1%
	Control	1	Mo17	27,952,101	25,533,634	24,152,399	94.6%
	Control	1	Mo17	32,089,405	29,994,056	28,612,403	95.4%
	Control	1	Mo17	30,884,254	28,792,960	27,477,375	95.4%
	Control	1	W22	27,463,291	25,406,343	23,963,627	94.3%
	Control	1	W22	30,052,500	28,368,670	26,992,364	95.1%
	Control	1	W22	39,053,409	36,446,031	34,667,396	95.1%
	Control	1	NA	30,115,000	28,539,429	26,881,527	94.2%
	Control	1	NA	32,824,999	31,055,642	29,202,438	94.0%
	Control	1	NA	32,023,922	29,271,524	27,568,135	94.2%
	Control	1	NA	29,992,309	28,673,906	27,211,810	94.9%
	Control	1	NA	30,526,599	29,414,775	27,910,557	94.9%
	Control	1	NA	31,546,065	29,565,854	28,123,261	95.1%
	Control	1	NA	27,154,351	25,667,959	24,320,788	94.8%
	Control	1	NA	32,054,314	30,912,784	29,389,907	95.1%
	Control	1	NA	29,524,250	27,648,850	26,337,496	95.3%
	Control	25	B73	34,096,262	33,228,963	31,724,716	95.5%
	Control	25	B73	28,309,908	27,777,761	26,508,640	95.4%
	Control	25	B73	29,460,358	28,771,921	27,429,261	95.3%
	Control	25	Mo17	31,052,392	29,051,969	27,800,908	95.7%
	Control	25	Mo17	35,953,863	33,395,095	31,856,395	95.4%
	Control	25	Mo17	32,277,892	30,158,579	28,863,987	95.7%
	Control	25	W22	31,912,767	30,031,569	28,624,051	95.3%
	Control	25	W22	31,339,039	29,317,286	27,969,111	95.4%
	Control	25	W22	28,910,940	27,224,017	25,978,391	95.4%
	Control	25	NA	39,796,204	38,134,598	36,417,156	95.5%
	Control	25	NA	29,612,376	28,436,470	27,074,904	95.2%
	Control	25	NA	29,378,257	27,444,335	26,216,616	95.5%
	Control	25	NA	33,233,186	31,834,138	30,384,247	95.4%
	Control	25	NA	26,095,853	24,737,604	23,585,574	95.3%
	Control	25	NA	30,022,451	27,867,308	26,601,314	95.5%
	Control	25	NA	30,812,945	29,472,860	28,144,916	95.5%
	Control	25	NA	29,852,753	28,567,400	27,254,420	95.4%
	Control	25	NA	30,686,374	28,821,136	27,554,429	95.6%
	Cold	1	B73	34,903,833	34,266,646	32,677,726	95.4%
	Cold	1	B73	31,063,862	30,347,478	28,868,606	95.1%
	Cold	1	B73	33,453,588	32,641,217	31,107,556	95.3%

Cold	1	Mo17	28,983,533	26,900,484	25,757,348	95.8%
Cold	1	Mo17	38,176,665	35,368,285	33,816,898	95.6%
Cold	1	Mo17	32,997,713	30,828,294	29,469,642	95.6%
Cold	1	W22	33,007,705	31,096,417	29,608,075	95.2%
Cold	1	W22	27,941,560	26,207,429	25,017,602	95.5%
Cold	1	W22	33,018,793	31,185,281	29,666,123	95.1%
Cold	1	NA	31,390,894	30,034,489	28,649,501	95.4%
Cold	1	NA	31,962,809	30,692,382	29,205,675	95.2%
Cold	1	NA	31,659,129	29,515,332	28,137,477	95.3%
Cold	1	NA	35,011,218	33,637,642	32,060,041	95.3%
Cold	1	NA	28,093,197	27,010,739	25,691,546	95.1%
Cold	1	NA	30,943,068	29,028,421	27,700,379	95.4%
Cold	1	NA	34,802,417	33,131,456	31,560,586	95.3%
Cold	1	NA	30,672,408	29,444,145	28,026,592	95.2%
Cold	1	NA	33,589,992	31,386,354	30,026,949	95.7%
Cold	25	B73	34,767,734	33,989,273	32,132,778	94.5%
Cold	25	B73	36,402,661	35,449,959	33,147,221	93.5%
Cold	25	B73	32,272,179	31,404,409	29,770,539	94.8%
Cold	25	Mo17	35,650,212	32,786,049	31,119,705	94.9%
Cold	25	Mo17	34,936,919	32,274,361	30,682,862	95.1%
Cold	25	Mo17	35,912,227	33,118,388	31,480,653	95.1%
Cold	25	W22	31,209,935	29,087,259	27,357,207	94.1%
Cold	25	W22	31,122,221	29,034,487	27,399,366	94.4%
Cold	25	W22	35,536,197	33,020,460	31,222,597	94.6%
Cold	25	NA	35,230,263	33,633,764	31,796,693	94.5%
Cold	25	NA	35,492,577	33,843,119	31,901,539	94.3%
Cold	25	NA	30,261,580	28,203,060	26,654,460	94.5%
Cold	25	NA	34,736,215	33,048,196	31,135,656	94.2%
Cold	25	NA	33,238,322	31,752,034	29,919,012	94.2%
Cold	25	NA	31,509,485	29,148,793	27,492,926	94.3%
Cold	25	NA	32,291,322	30,922,620	29,302,742	94.8%
Cold	25	NA	31,245,039	30,106,041	28,426,664	94.4%
Cold	25	NA	31,778,880	29,265,710	27,274,633	93.2%
Heat	1	B73	31,953,493	31,314,622	29,887,302	95.4%
Heat	1	B73	32,505,044	31,886,111	30,458,533	95.5%
Heat	1	B73	31,848,724	31,333,706	29,972,742	95.7%
Heat	1	Mo17	30,568,364	28,253,457	27,045,072	95.7%
Heat	1	Mo17	36,614,273	34,169,603	32,692,393	95.7%
Heat	1	Mo17	32,325,680	30,034,551	28,715,760	95.6%
Heat	1	W22	39,993,149	36,975,749	35,417,812	95.8%
Heat	1	W22	32,571,264	30,525,259	29,152,276	95.5%
Heat	1	W22	28,640,448	26,734,208	25,540,609	95.5%
Heat	1	NA	26,526,984	25,355,210	24,213,844	95.5%
Heat	1	NA	33,520,599	32,171,642	30,691,556	95.4%
Heat	1	NA	27,932,315	25,878,686	24,745,621	95.6%
Heat	1	NA	28,745,556	27,622,092	26,356,747	95.4%
Heat	1	NA	26,826,398	25,771,225	24,611,231	95.5%
Heat	1	NA	36,981,194	34,542,012	32,977,927	95.5%
Heat	1	NA	27,942,397	26,757,087	25,611,212	95.7%
Heat	1	NA	31,155,736	29,907,013	28,538,745	95.4%
Heat	1	NA	29,216,048	27,068,666	25,841,550	95.5%
Heat	25	B73	31,468,141	30,843,526	29,398,739	95.3%
Heat	25	B73	30,125,698	29,539,688	28,215,458	95.5%
Heat	25	B73	34,133,740	32,442,845	30,865,428	95.1%
Heat	25	Mo17	28,767,197	26,950,872	25,782,769	95.7%
Heat	25	Mo17	32,625,323	30,489,764	29,179,358	95.7%
Heat	25	Mo17	31,127,541	28,677,605	26,881,171	93.7%
Heat	25	W22	27,479,603	25,706,452	24,627,127	95.8%
Heat	25	W22	29,402,332	27,578,750	26,434,067	95.8%
Heat	25	W22	29,217,915	26,610,535	25,431,916	95.6%
Heat	25	NA	48,017,278	45,782,225	43,732,155	95.5%
Heat	25	NA	33,801,378	32,122,031	30,732,036	95.7%
Heat	25	NA	24,668,242	22,886,374	21,889,514	95.6%

NM	Heat	25	NA	31,755,624	30,344,797	29,040,871	95.7%
	Heat	25	NA	26,130,744	24,250,559	23,136,641	95.4%
	Heat	25	NA	31,023,212	27,915,677	26,651,646	95.5%
	Heat	25	NA	27,661,044	25,712,192	24,544,672	95.5%
	Heat	25	NA	31,289,047	28,932,326	27,601,370	95.4%
	Heat	25	NA	30,432,732	27,299,228	26,108,137	95.6%
	Control	1	B73	26,587,179	24,291,374	23,163,632	95.4%
	Control	1	Mo17	30,883,474	27,713,998	26,450,837	95.4%
	Control	1	W22	32,031,276	29,246,565	27,871,182	95.3%
	Control	1	B97	29,286,596	26,117,774	24,861,062	95.2%
	Control	1	CML322	30,385,620	26,789,101	24,931,434	93.1%
	Control	1	CML333	34,743,990	31,300,663	29,744,474	95.0%
	Control	1	CML52	29,439,900	26,204,229	24,968,074	95.3%
	Control	1	CML69	36,989,512	33,756,555	32,035,780	94.9%
	Control	1	DK105	33,687,408	30,069,395	28,656,541	95.3%
	Control	1	EP1	29,679,806	26,718,857	25,389,169	95.0%
	Control	1	F7	35,702,277	31,858,935	30,407,897	95.4%
	Control	1	II14H	28,848,039	26,170,503	24,917,465	95.2%
	Control	1	Ki11	30,976,771	28,575,481	27,223,463	95.3%
	Control	1	Ki3	33,357,672	30,593,678	29,218,161	95.5%
	Control	1	M162W	31,313,883	27,677,512	26,380,547	95.3%
	Control	1	M37W	30,324,473	27,201,334	25,915,010	95.3%
	Control	1	Mo18W	33,637,601	30,619,685	29,107,930	95.1%
	Control	1	MS71	27,940,573	25,139,487	23,946,469	95.3%
	Control	1	NC350	39,871,197	36,654,721	34,909,049	95.2%
	Control	1	NC358	34,778,132	30,598,312	29,146,392	95.3%
	Control	1	Oh43	27,476,161	24,339,679	23,168,500	95.2%
	Control	1	Oh7B	28,659,111	25,905,568	24,634,376	95.1%
	Control	1	P39	34,733,395	30,923,380	29,442,582	95.2%
	Control	1	PH207	24,432,326	22,078,393	20,967,368	95.0%
	Control	1	Tx303	32,623,536	30,196,169	28,737,339	95.2%
	Control	25	B73	28,919,942	27,283,307	25,983,641	95.2%
	Control	25	Mo17	31,641,626	28,306,210	27,065,225	95.6%
	Control	25	W22	26,352,171	23,680,939	22,372,288	94.5%
	Control	25	B97	30,355,464	26,917,795	25,620,216	95.2%
	Control	25	CML322	28,806,810	25,689,081	24,234,950	94.3%
	Control	25	CML333	33,292,485	29,988,706	28,557,348	95.2%
	Control	25	CML52	36,651,756	32,804,552	31,255,006	95.3%
	Control	25	CML69	28,921,330	26,138,562	24,866,164	95.1%
	Control	25	DK105	25,538,054	22,432,072	21,410,679	95.4%
	Control	25	EP1	32,453,291	28,636,003	27,265,754	95.2%
	Control	25	F7	30,203,141	27,026,780	25,739,590	95.2%
	Control	25	II14H	27,602,587	24,885,461	23,754,363	95.5%
	Control	25	Ki11	31,359,964	28,842,176	27,461,748	95.2%
	Control	25	Ki3	30,730,106	27,332,638	26,149,295	95.7%
	Control	25	M162W	33,915,504	30,664,105	29,211,208	95.3%
	Control	25	M37W	28,046,122	24,808,227	23,681,285	95.5%
	Control	25	Mo18W	30,332,802	27,232,153	25,986,610	95.4%
	Control	25	MS71	33,799,489	30,905,677	29,431,494	95.2%
	Control	25	NC350	35,141,311	31,289,888	29,809,905	95.3%
	Control	25	NC358	31,276,352	28,222,006	26,923,603	95.4%
	Control	25	Oh43	28,880,457	25,845,516	24,677,353	95.5%
	Control	25	Oh7B	31,481,467	28,312,980	26,957,755	95.2%
	Control	25	P39	28,140,676	25,612,098	24,376,224	95.2%
	Control	25	PH207	28,833,364	26,647,463	25,437,136	95.5%
	Control	25	Tx303	36,803,703	33,224,404	31,680,580	95.4%
	Cold	1	B73	31,394,134	30,381,151	28,960,764	95.3%
	Cold	1	Mo17	27,687,544	24,567,845	23,488,666	95.6%
	Cold	1	W22	31,781,847	29,436,289	28,134,266	95.6%
	Cold	1	B97	34,247,855	30,846,766	29,416,478	95.4%
	Cold	1	CML322	29,056,473	26,110,004	24,879,064	95.3%
	Cold	1	CML333	32,987,864	29,564,687	28,168,877	95.3%
	Cold	1	CML52	33,707,912	30,162,403	28,724,822	95.2%

Cold	1	CML69	30,078,181	27,539,126	26,256,156	95.3%
Cold	1	DK105	31,965,595	28,881,344	27,553,620	95.4%
Cold	1	EP1	30,818,780	27,200,881	16,578,956	61.0%
Cold	1	F7	33,757,160	30,683,239	27,140,290	88.5%
Cold	1	II14H	35,577,345	33,218,521	31,764,517	95.6%
Cold	1	Ki3	33,854,926	31,056,944	29,736,205	95.7%
Cold	1	M162W	35,281,842	32,134,483	30,716,843	95.6%
Cold	1	M37W	21,936,946	19,089,081	18,217,192	95.4%
Cold	1	Mo18W	25,114,922	21,379,379	20,416,661	95.5%
Cold	1	MS71	27,879,805	24,395,235	23,250,529	95.3%
Cold	1	NC350	28,956,265	24,920,246	23,798,344	95.5%
Cold	1	NC358	29,992,804	26,503,215	25,308,638	95.5%
Cold	1	Oh43	34,959,414	30,428,238	28,747,714	94.5%
Cold	1	Oh7B	26,855,483	24,477,954	23,259,772	95.0%
Cold	1	P39	37,211,725	34,443,517	32,890,736	95.5%
Cold	1	PH207	31,788,663	29,122,650	27,838,250	95.6%
Cold	1	Tx303	33,266,162	30,805,643	29,327,412	95.2%
Cold	25	B73	26,987,741	25,247,699	23,814,213	94.3%
Cold	25	Mo17	29,420,485	27,121,174	25,447,230	93.8%
Cold	25	W22	26,817,648	24,723,824	23,187,508	93.8%
Cold	25	B97	29,698,839	26,391,291	24,891,326	94.3%
Cold	25	CML322	27,056,819	24,198,342	22,781,989	94.1%
Cold	25	CML333	31,237,836	28,205,419	26,543,969	94.1%
Cold	25	CML52	28,500,747	25,453,381	24,103,800	94.7%
Cold	25	CML69	28,777,804	25,426,171	23,989,842	94.4%
Cold	25	DK105	28,503,681	25,190,842	23,907,449	94.9%
Cold	25	EP1	27,312,480	24,151,548	22,804,568	94.4%
Cold	25	F7	35,391,701	31,521,535	29,891,900	94.8%
Cold	25	II14H	37,332,174	34,063,666	32,395,041	95.1%
Cold	25	Ki11	29,728,973	26,193,399	24,790,781	94.6%
Cold	25	Ki3	27,145,513	24,501,843	23,099,566	94.3%
Cold	25	M162W	46,221,495	42,175,192	39,122,050	92.8%
Cold	25	M37W	44,048,114	40,489,504	37,739,557	93.2%
Cold	25	Mo18W	33,487,644	30,771,541	28,644,323	93.1%
Cold	25	MS71	45,258,905	41,452,542	38,713,232	93.4%
Cold	25	NC350	35,151,797	32,036,933	28,973,590	90.4%
Cold	25	NC358	38,910,670	35,076,497	32,750,461	93.4%
Cold	25	Oh43	40,194,534	36,954,298	34,656,461	93.8%
Cold	25	Oh7B	38,336,110	35,286,304	33,308,001	94.4%
Cold	25	P39	31,619,652	28,691,231	27,000,979	94.1%
Cold	25	PH207	37,978,300	34,487,850	31,669,391	91.8%
Cold	25	Tx303	32,977,718	30,477,101	28,123,723	92.3%