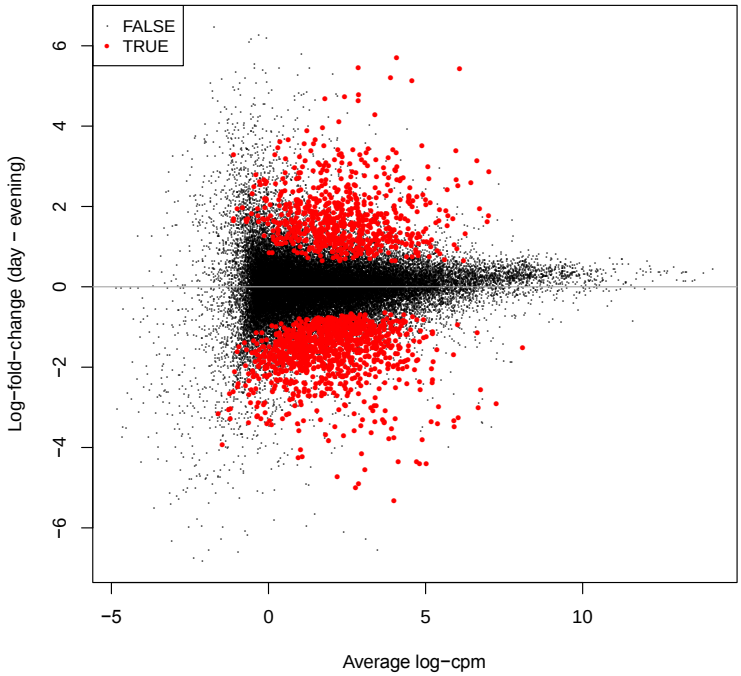

Fig S1. A fitted model MD-plot of the contrast between samples from 20:30 and 12:30 in the warm acclimated fish (N=3). Red dots indicate genes that were considered differentially expressed (FDR <0.05). Mean expression levels are indicated by $\log_2$ counts per million mapped reads (log-cpm).

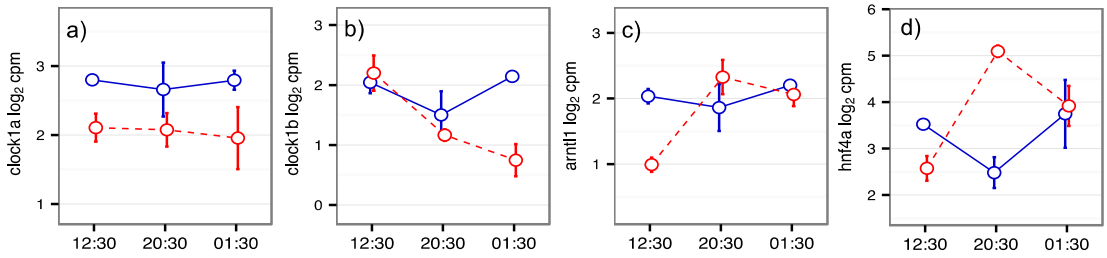

Fig S2. Line plots of selected time and/or temperature responsive genes in male Arctic char liver after one month acclimation at 15°C (red dashed line) or 8°C (blue solid line). Values are mean $\log_2$ counts per million mapped reads (cpm) ± SD. N=3 in each point. Expression levels were not standardized for gene length and therefore are not comparable between genes. Full gene names: a) *circadian locomotor output cycles kaput 1a*, b) *circadian locomotor output cycles kaput 1b*, c) *aryl hydrocarbon receptor nuclear translocator-like protein 1*, d) *hepatocyte nuclear factor 4 alpha*.

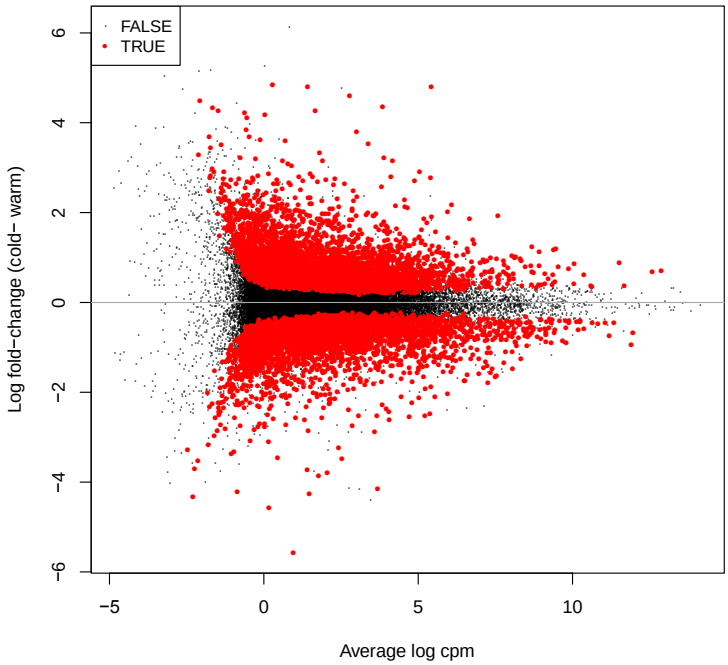

Fig S3. A fitted model MD-plot of the midpoint contrast between samples from the cold (8°C) and warm (15°C) temperatures (N=9). Red dots indicate genes that were considered differentially expressed (FDR <0.05). Expression levels are indicated by $\log_2$ counts per million mapped reads (log-cpm).

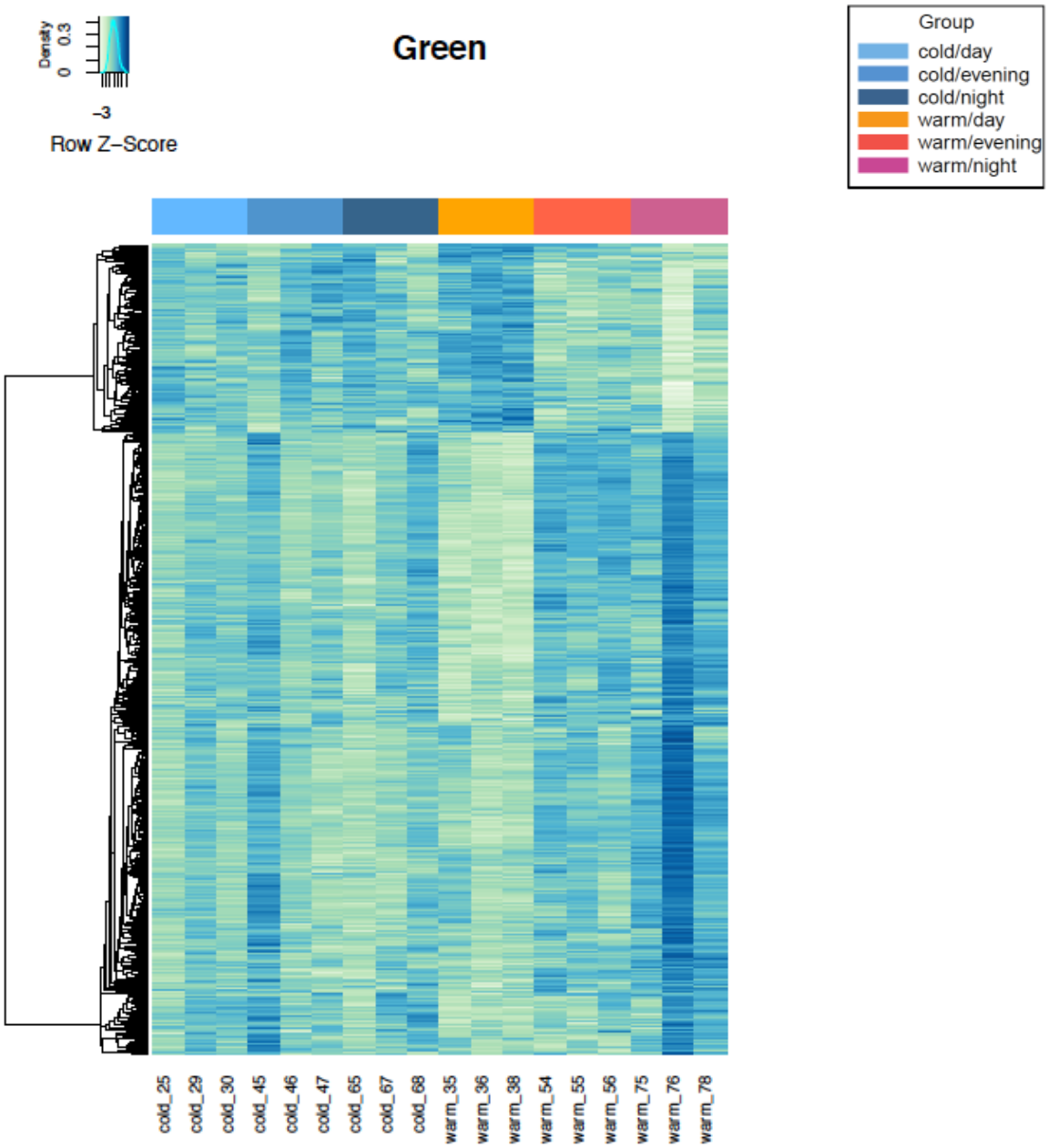

Fig S4. A heatmap showing the clustering of genes from Green module, which was significantly correlated with time in WGCNA. The list of genes belonging to the module is shown in Table S6.

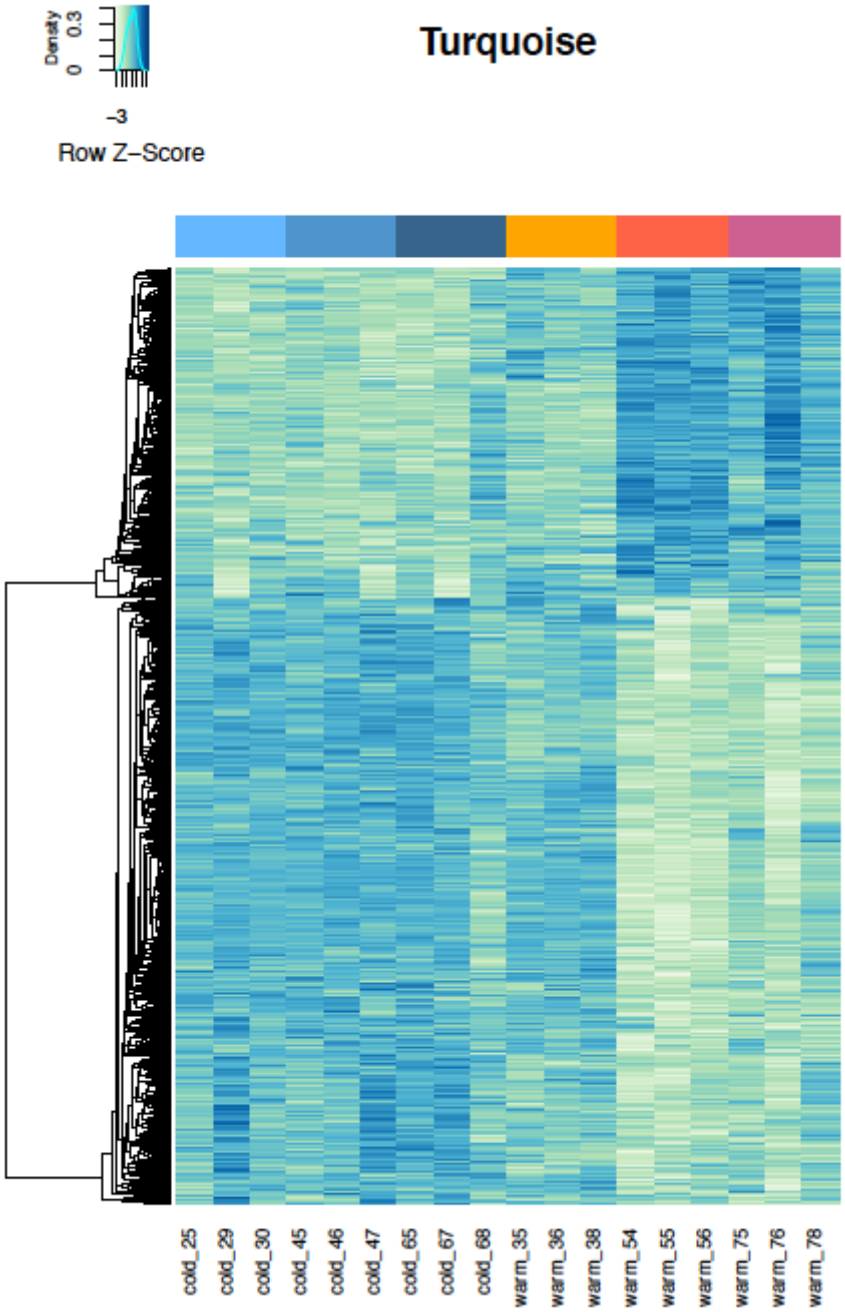

Fig S5. A heatmap showing the clustering of genes from Turquoise module, which was significantly correlated with temperature in WGCNA. Legend for color bar is shown in Fig S4. The list of genes belonging to the module is shown in Table S6.

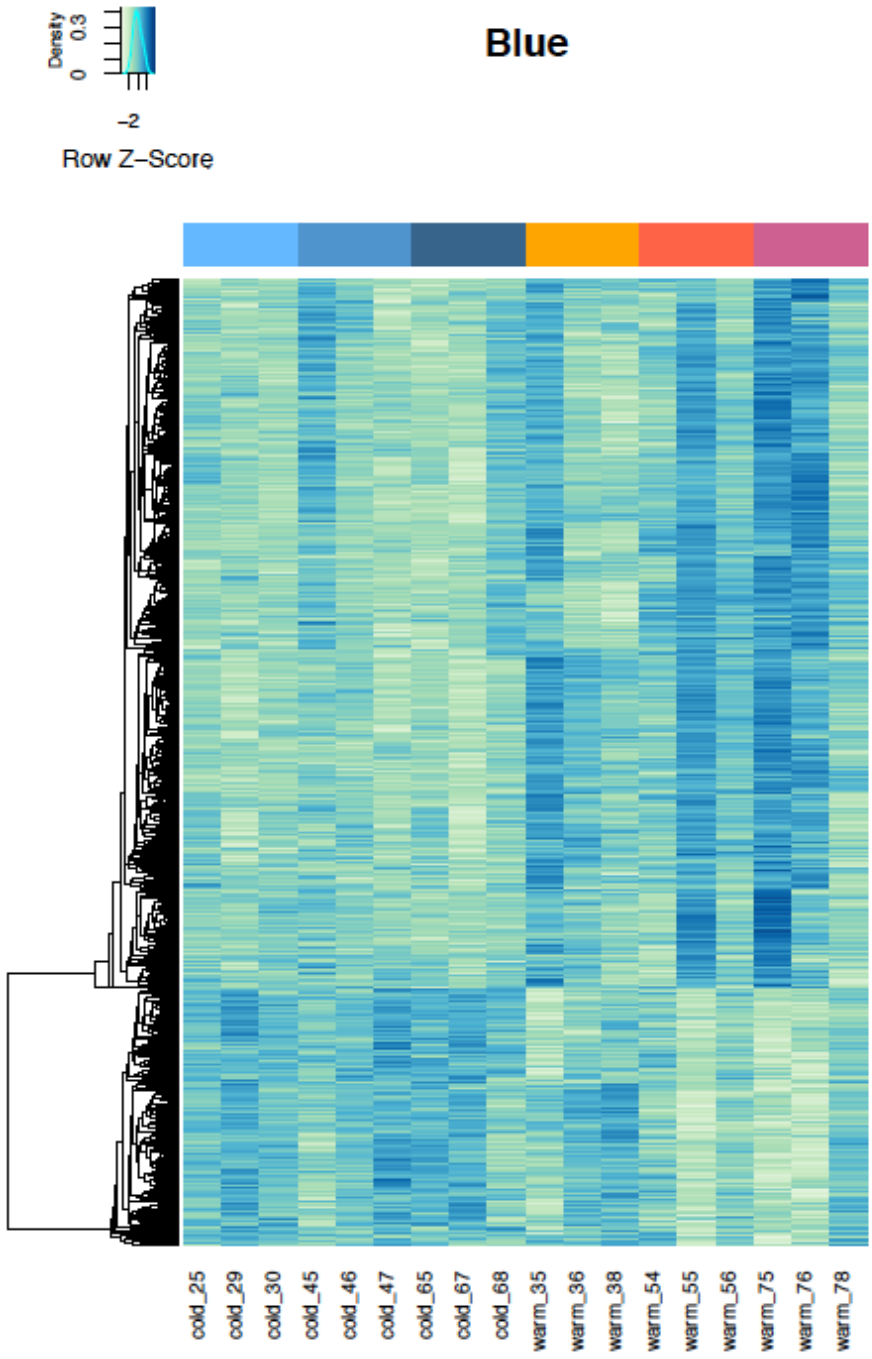

Fig S6. A heatmap showing the clustering of genes from Blue module, which was significantly correlated with temperature in WGCNA. Legend for color bar is shown in Fig S4. The list of genes belonging to the module is shown in Table S6.

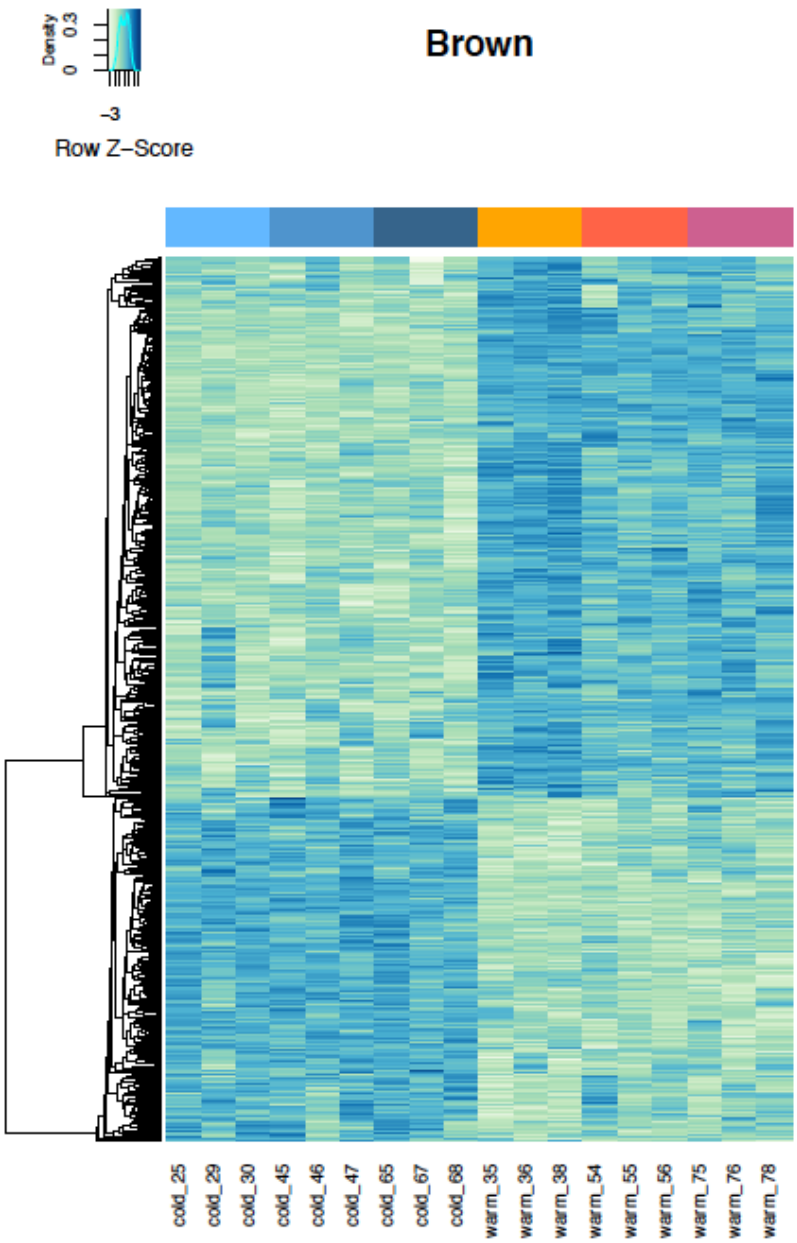

Fig S7. A heatmap showing genes belonging to the brown module, which was significantly correlated with temperature in WGCNA. Legend for the color bar is shown in Fig S4. The list of genes belonging to the module is shown in Table S6.

Table S1. Results of BLASTn comparing known conserved cDNA sequences of paralogous gene pairs in salmonids to the *de novo* Arctic char transcriptome assembly. Different cluster IDs indicates that the paralogs were matching to separate contigs in the transcriptome.

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Table S2. Linear model results and annotations for the genes (clusters) with significant pairwise changes between three time points (12:30 and 20:30 and 01:30) in Arctic char acclimated at 15°C for one month. Log_2 fold change (Log2FC) >0 indicates higher expression at the earlier time point. T-test values for each contrast are followed by unadjusted P-values (FDR <0.05 based on limma "global" option was used to filter results). Empty cells indicate the gene was not differentially expressed in a given contrast. Annotations for predicted open reading frame peptide sequences were prioritized with zebrafish protein sequences, predicted Atlantic salmon protein sequences and NCBI nr-database (genbank_id). Additionally, gene symbols were combined from human, zebrafish, salmon and NCBI orthologs when available.

Click here to Download Table S2

Table S3. Linear model results and annotations for the genes (clusters) with significant pairwise changes between three time points (12:30 and 20:30 and 01:30) in Arctic char acclimated at 8°C for one month. Log_2 fold change (Log2FC) >0 indicates higher expression at the earlier time point. T-test values for each contrast are followed by unadjusted P-values (FDR <0.05 based on limma "global" option was used to filter results). Empty cells indicate the gene was not differentially expressed in a given contrast. Annotations for predicted open reading frame peptide sequences were prioritized with zebrafish protein sequences, predicted Atlantic salmon protein sequences and NCBI nr-database (genbank_id). Additionally, gene symbols were combined from human, zebrafish, salmon and NCBI orthologs when available.

Click here to Download Table S3

Table S4. Linear model results and annotations for the genes (clusters) with a significant time-temperature interaction effect. P-values were adjusted for multiple comparisons using Benjamini-Hochberg method (FDR <0.05). Annotations for predicted open reading frame peptide sequences were prioritized with zebrafish protein sequences, predicted Atlantic salmon protein sequences and NCBI nr-database (genbank_id). The counts of transcripts within genes are identical because read counts were obtained at the gene level (annotations were retrieved for transcripts). Additionally, gene symbols were combined from human, zebrafish, salmon and NCBI orthologs when available.

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Table S5. Linear model results and annotations for the genes (clusters) with a significant temperature midpoint difference (across three time points at 8°C vs. 15°C). Log_2 fold change >0 indicates expression was higher at the low temperature. P-values were adjusted for multiple comparisons using Benjamini-Hochberg method (FDR <0.05). Annotations for predicted open reading frame peptide sequences were prioritized with zebrafish protein sequences, predicted Atlantic salmon protein sequences and NCBI nr-database (genbank_id). The counts of transcripts within genes are identical because read counts were obtained at the gene level (annotations were retrieved for transcripts). Additionally, gene symbols were combined from human, zebrafish, salmon and NCBI orthologs when available.

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Table S6. Modules of genes significantly correlated with sampling time or temperature in Arctic char liver. GS = gene significance, p.GS= P-value of gene significance. Gene symbol = annotation.

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Putative upstream regulators with target genes from Ingenuity Pathway Analysis for gene modules identified with WGCNA in Arctic char liver tissue. Each sheet contains the results for one module.

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Script 1

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