

**Figures S17-18. Effect of PCR methodology and annealing temperature on template profiles in amplification reactions utilizing varying primer pools.** One-way clustered heatmaps of untransformed template utilization profiling during amplification of an uneven pooling of synthetic DNA templates and varying primer pools (Figure S17 = C1, C2 and C3 experiments with all ten templates present, and template ST1 at 1/10th the concentration of the other nine templates; Figure S18 = D1, D2, E1 and E2 experiments with four templates). For experiments C1, D1 and E1, only a single primer variant was used (806F\_v1), while in experiments C2, D2 and E2, 10 primers were used. In experiment C3, 9 primers were used (806F\_v1 was removed). Primer and template details are shown in Table 1. Samples (columns) are color-coded by amplification method (TAS or DePCR), amplification annealing temperature (45°C or 55°C), and average Ideal score. Each column represents the average of 7-8 technical replicates per condition and rarefaction to 7,000 sequences/replicate. Templates (rows) represent all 10 templates (ordered from top to bottom; ST1, ST4, ST6, ST7, ST8, ST11, ST15, ST23, ST39, and ST55). Ideal score comparisons between TAS and DePCR (across both annealing temperatures), within TAS (45°C or 55°C), and within DePCR (45°C or 55°C) are shown in tables. Asterisks indicate significant differences in measured values by annealing temperature (ANOVA,  $P < 0.01$ ). Intensity scales vary between experiments.

Fig. S17

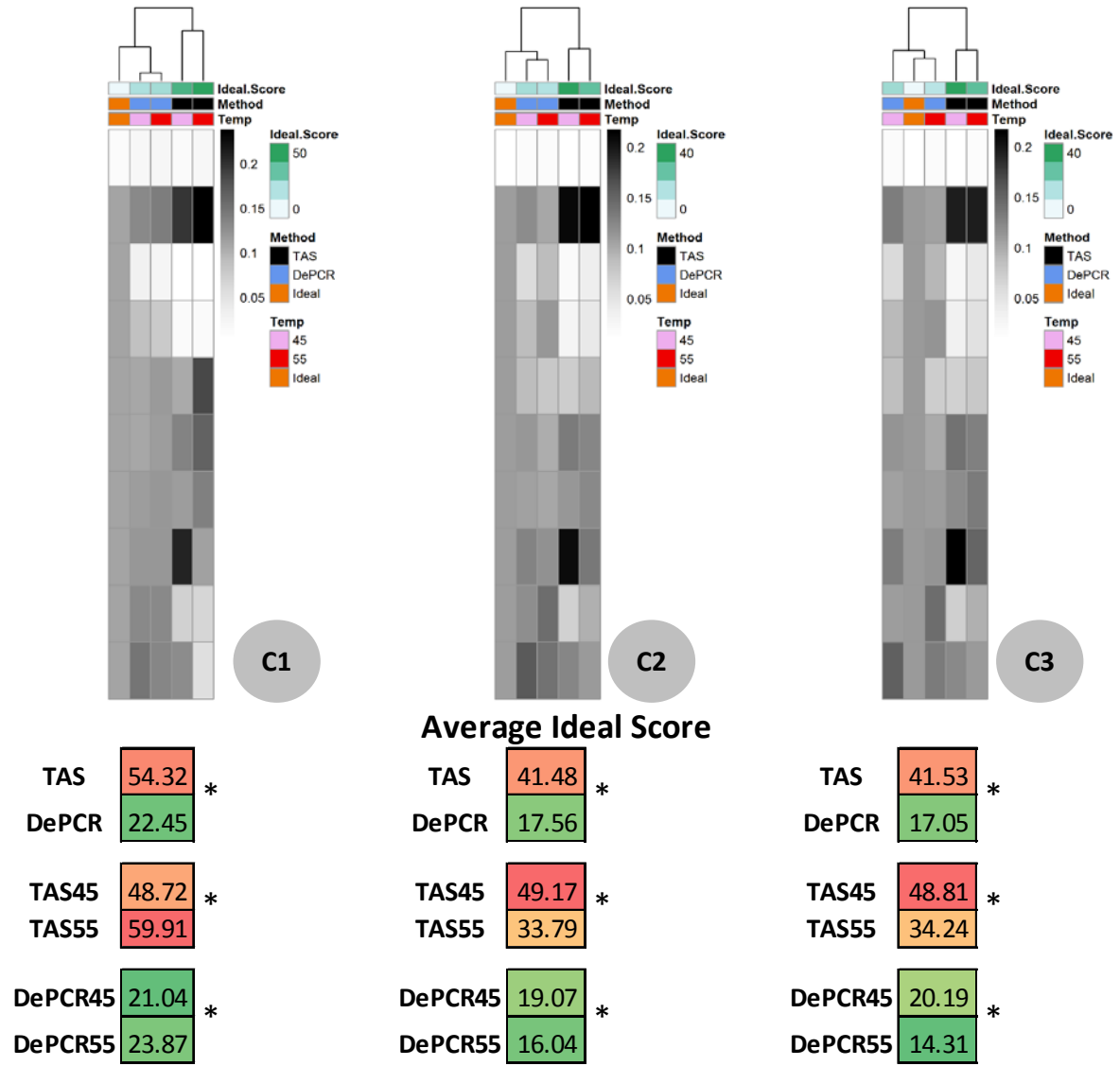
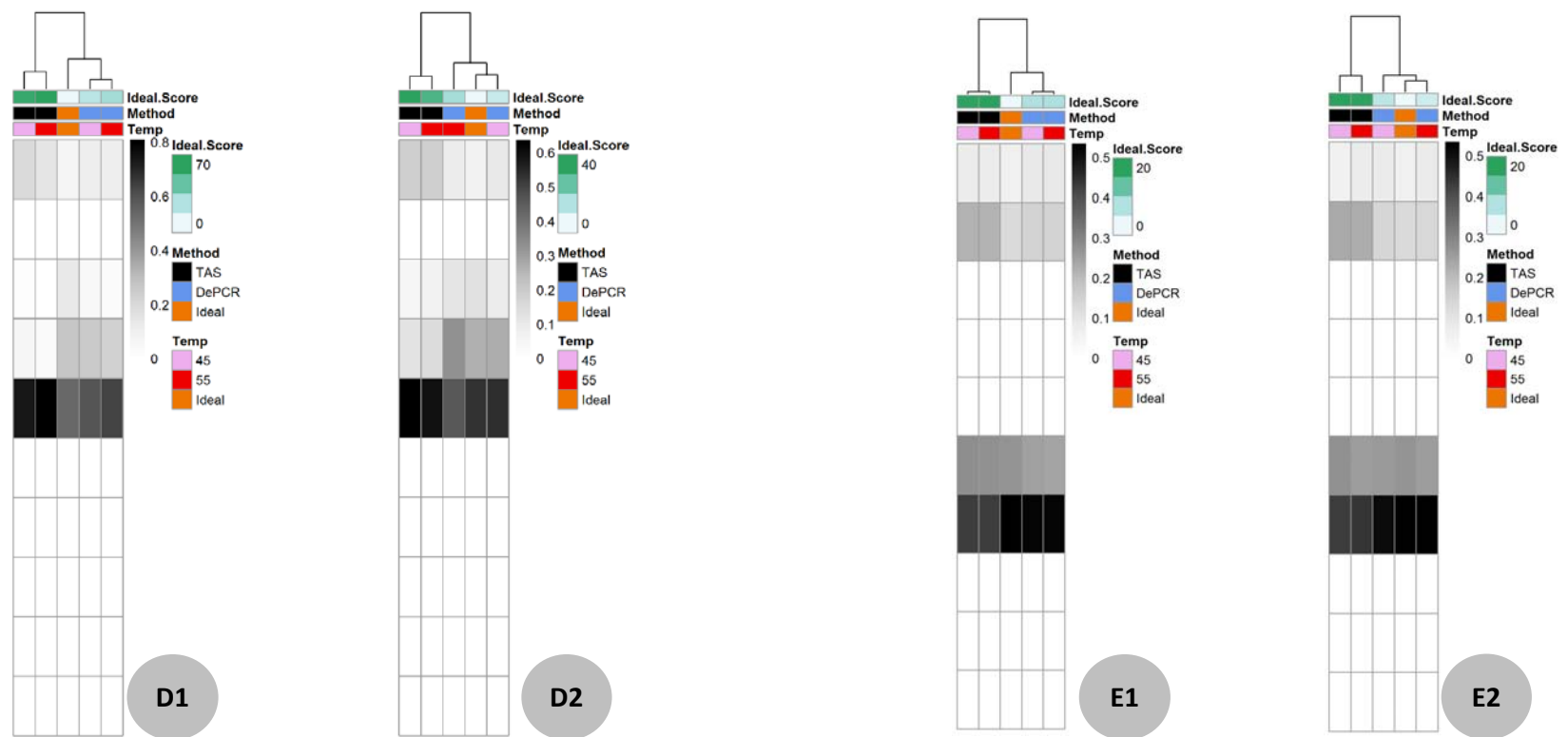


Fig. S18



**Average Ideal Score**

TAS	68.46 *	TAS	41.16 *
DePCR	24.27	DePCR	13.23
TAS45	65.95 *	TAS45	45.17 *
TAS55	70.96	TAS55	36.58
DePCR45	20.15 *	DePCR45	9.53 *
DePCR55	27.87	DePCR55	17.45

**Average Ideal Score**

TAS	20.53 *	TAS	21.50 *
DePCR	7.30	DePCR	4.91
TAS45	20.28	TAS45	21.66
TAS55	20.78	TAS55	21.35
DePCR45	7.11	DePCR45	5.95 *
DePCR55	7.47	DePCR55	3.87