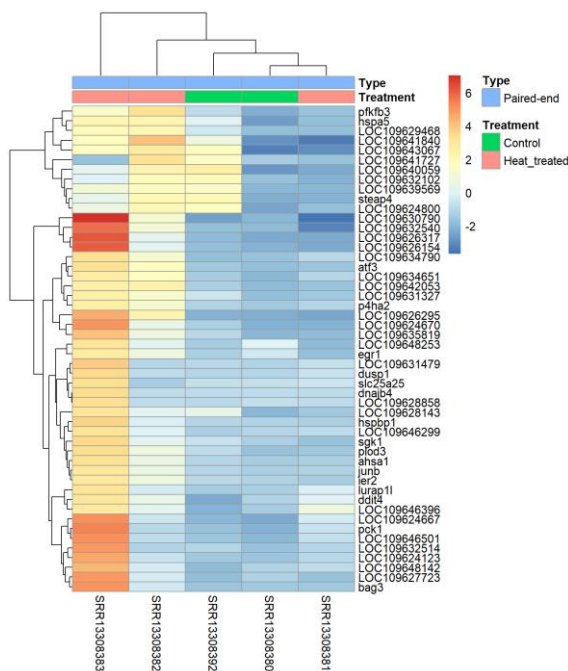


Arpan’s Supplementary files

Table AS1. Differential Transcript Expression Analysis Results from Ballgown for Heat Shock Protein gene family in Olive Flounder liver cells.

geneNames	geneIDs	feature	id	fc	pval	qval	logFC	abs_logFC
hspb8	MSTRG.7662	transcript	23941	6.272928	0.316777	0.900541	2.649139	2.649139
hspa5	MSTRG.2490	transcript	7582	3.98537	0.426874	0.900541	1.994714	1.994714
hsbbp1	MSTRG.9738	transcript	30266	3.472374	0.475943	0.900541	1.795922	1.795922
hspb1	MSTRG.3655	transcript	11179	2.388426	0.469895	0.900541	1.25606	1.25606
hspa13	MSTRG.6386	transcript	19889	1.614406	0.34975	0.900541	0.691003	0.691003
hsp90b1	MSTRG.1527	transcript	4569	1.613458	0.671804	0.930007	0.690156	0.690156
hspa9	MSTRG.411	transcript	1140	1.551572	0.478397	0.900541	0.633731	0.633731
hspe1	MSTRG.9700	transcript	30154	1.44582	0.693539	0.933978	0.531888	0.531888
hspb8	MSTRG.7662	transcript	23940	1.36581	0.385553	0.900541	0.449757	0.449757
hspa4	MSTRG.267	transcript	763	1.300703	0.7165	0.937507	0.379292	0.379292
hspd1	MSTRG.9701	transcript	30155	1.230241	0.651682	0.924556	0.298941	0.298941
hsp90ab1	MSTRG.7092	transcript	22259	0.83932	0.032699	0.900541	-0.25271	0.252706

A



B

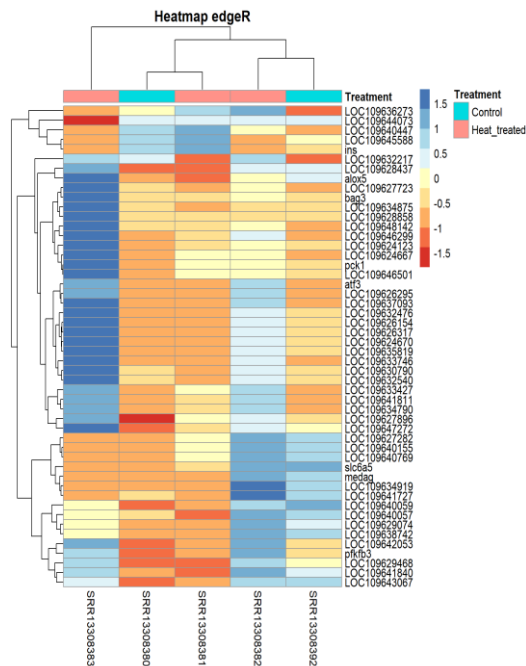


Figure AS1. Heatmap visualization of differentially expressed genes (DEGs) identified using DESeq2 (A) and edgeR (B) with standard filtering (minimum 20 reads, FDR < 0.1). Rows

represent individual DEGs, and columns represent samples. Expression levels are color-coded. Hierarchical clustering reveals groups of genes and samples with similar expression patterns.