

Figure S1: Known regulatory interactions within SOM clusters. Graph of interactions found in the GEA_CLR database from the UCSC Interaction Browser between two genes within a single cluster. Orange lines indicate an activating interaction, blue lines are repressing interaction and grey lines are unknown.

Distance between duplicated gene pairs when both genes are in the SOM

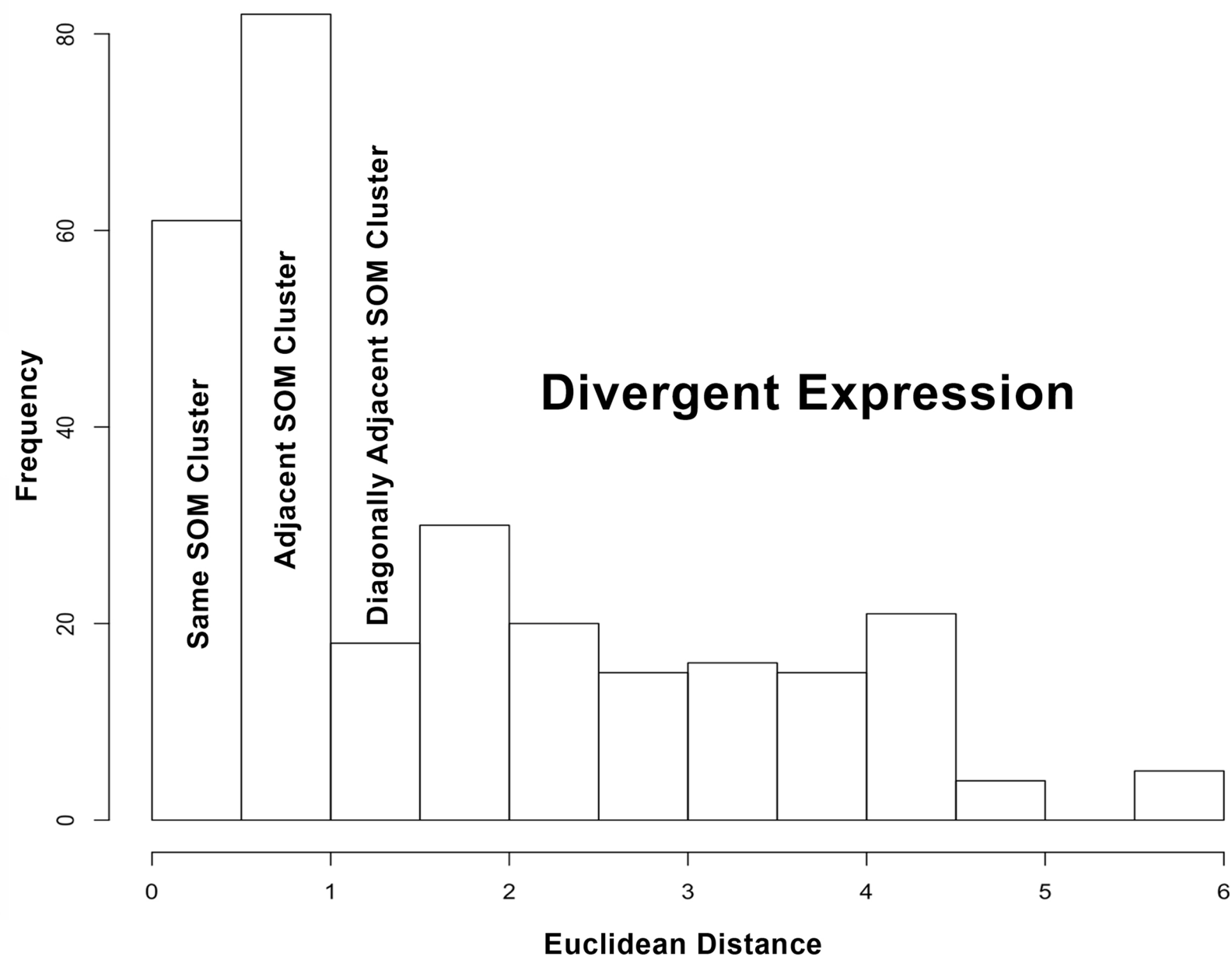


Figure S2: Distance between pairs of duplicated genes in the SOM. A histogram showing the distance between SOM clusters containing duplicate gene pairs arising from the teleost-specific genome duplication event. Distances were calculated using the Euclidean distance between clusters on the SOM grid. Therefore, a distance of 1 indicates that the two genes in the pair were in adjacent clusters, and a distance of 1.4 indicates that the two genes were in diagonally adjacent clusters. Any larger distances indicate that the genes were at least 2 clusters apart.

Table S1. RNAseq data and differential gene expression analysis

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Table S2. SOM clustering analysis

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Table S3. SOM cluster motif enrichment analysis

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Table S4. SOM assignment of Nkx2.5 differentially expressed genes

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Table S5. Hand-curated list of heart markers

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Table S6. SOM cluster assignment of duplicated zebrafish genes

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