Comparing Putative Enhancer Usage Between Different Species in

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A current longstanding debate within the field of evolutionary biology seeks to determine the level of contribution for different drivers of phenotypic variation, either mutations to protein coding sequences or changes to the genome's gene regulation. Cis-regulatory elements known as enhancers have been shown to contribute to phenotypic diversity and lie upstream of the coding region of genes. Enhancers that reside within open chromatin confirmations (as opposed to closed conformation) may actively control the transcription of genes and are known as putative enhancers. Additionally, DNA's conformation has been shown to be heritable, indicating heritability of differing accessibility to enhancers, due to conformational regulation. With this in mind, our study aims to compare putative enhancer usage between different strains of (fruit fl 5 ٻ E

and thorough comparison of the putative enhancer usage between and within fly strains.

The main goal of this summer's project was to continue in-lab work in regenerating DNA libraries from two previously completed natural isolates, as well as generating additional DNA libraries for sequencing. Previously, this lab has generated three DNA libraries of unique natural isolates: Oregon-R (North America), BOG 2 (Bogota, Columbia), Canton-S (Zimbabwe). Two of these libraries (BOG 2 and Canton-S) were found to be of low quality when run through the pipeline, and thus required additional replacement samples to be sequenced to ensure the validity of our data and results. In addition to regenerating DNA libraries for BOG 2 and Canton-S, we also aimed to generate additional libraries from non- species, notably and . The final goal of this summer was to further our research and understanding about the domains of evolutionary biology and genetics, specifically through research of other studies and previous literature pertaining to ATAC-Seq and our current work. ent woituwtoo ł our nd ṅ s y l' yt Ʒ elisnd h Ă h ȿ ivyon ṅ s h Ʈ

lysis buffer then tagmented with the Tn5 transposase. The samples of fragmented DNA were amplified using PCR with uniquely labeled barcodes for each biological replicate and technical replicate (PCR

Figure 1: ATAC-seq library preparation. A) Hyperactive Tn5 transposase tagmentation of open chromatin. B) Depiction of the contents of each read before, during, and after PCR