1   Lin_SupMat_figure_Bobcat reference genome_R2_JHered.pdf

2   ## <u>**Supplementary Figure for**</u>

3   *Title:* A Reference Genome Assembly of the Bobcat, *Lynx rufus*

4   *Author names:* Meixi Lin[1,C]; Merly Escalona[2]; Ruta Sahasrabudhe[3]; Oanh Nguyen[3]; Eric

5   Beraut[4]; Michael R. Buchalski[5,*]; Robert K. Wayne[1,*]
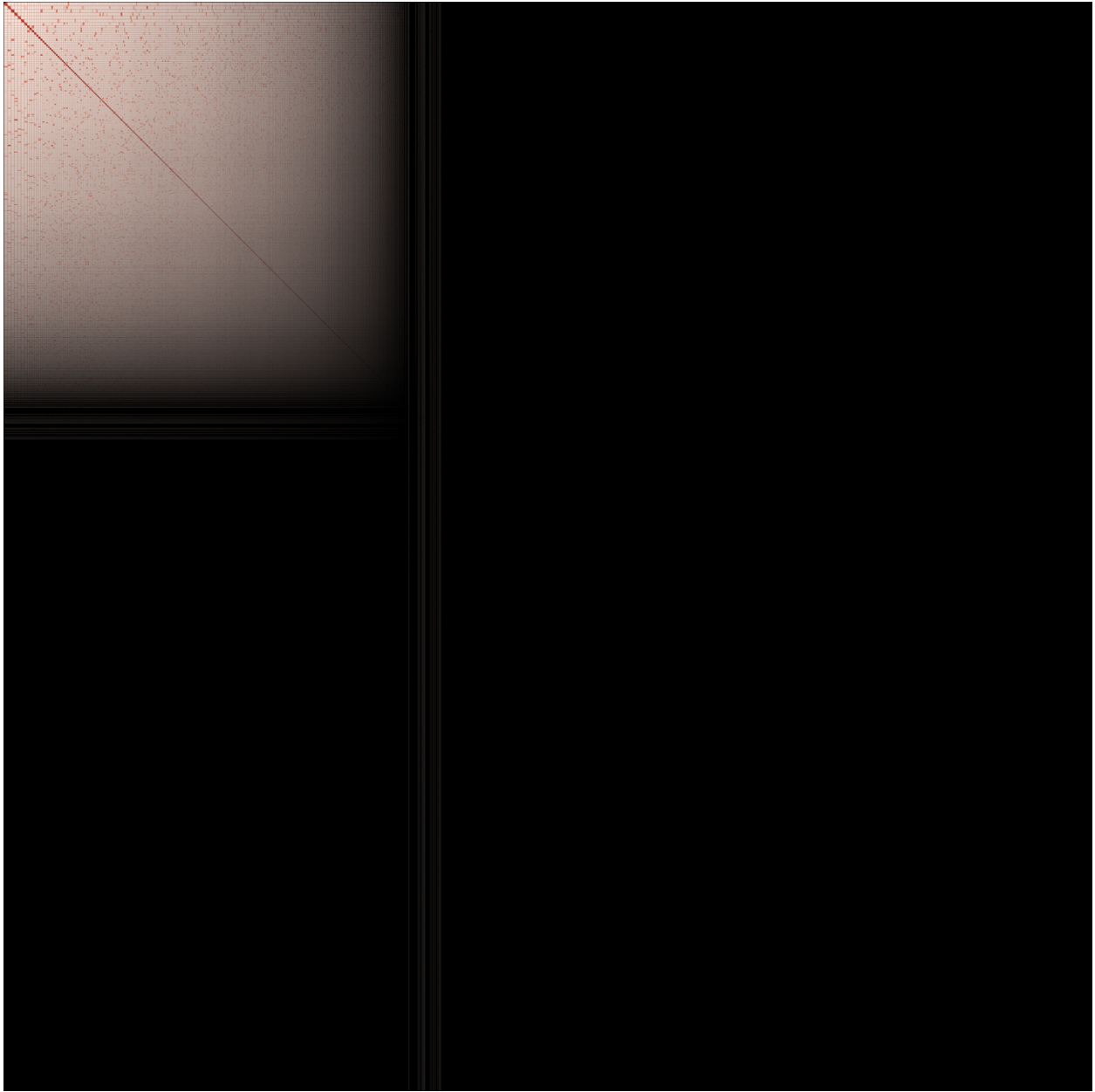
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7   *: Contributed equally

8   ***Table of Contents:***

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Supplementary Figure 1. The Omni-C contact map for the alternate genome assembly
(GCA_022079275.1) generated with PretextSnapshot. Omni-C contact maps translate proximity
of genomic regions in 3-D space to contiguous linear organization. Each cell in the contact map
corresponds to sequencing data supporting the linkage (or join) between two of such regions.
Scaffolds are separated by black lines and higher density corresponds to higher levels of
fragmentation. This alternate assembly consists of haplotigs (contigs of clones with the same
haplotype) in heterozygous regions and is not as complete and more fragmented than the primary
assembly (GCA_022079265.1; Figure 2C).

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