Single individuals Longshanks mice Legends Program/utilities --key-parameters Custom code* --key-parameters Linked-read Linked-read DATASETS BCL bc12fastq bc12fastq 150+13+12+150 150+13+12+150 --create-fastq-for-index-reads --create-fastq-for-index-reads Basecalling / -use-bases-mask=Y150,I13,I12,Y150 --use-bases-mask=Y150,I13,I12,Y150 external demultiplexing reference Standard Standard data FASTQ FASTQ ı bcl2fastqı □ bcl2fastq short-read short-read FASTQ FASTQ demult_fastq demult_fastq (Paired-end) (Paired-end) cutadapt cutadapt genome genome reference reference Read placement bwa bwa GRCh38 or mm10 mm10 READ ONE BARCODE TAG=BX READ TWO BARCODE TAG=BX Picard/markDup Picard/markDup READ ONE BARCODE TAG=BX READ TWO BARCODE TAG=BX awk/split BAM BAM method=diploid, nGen = 20, K = 4, SNP / molecule niterations = 60, readAware = TRUE, reference splitReadIterations = c(20, 40), ... calling haplotype panels HAPCUT2 Or BX_parse.pl STITCH STITCH -10X subsampling With LR short-read HAPCUT2 HAPCUT2 information phased Phasing molecules blocks phased phased molecules vcf molecules vcf blocks blocks **Population genetics** analyses **Benchmarking**

Heliconius butterflies

pick ROI.pl

deletions

