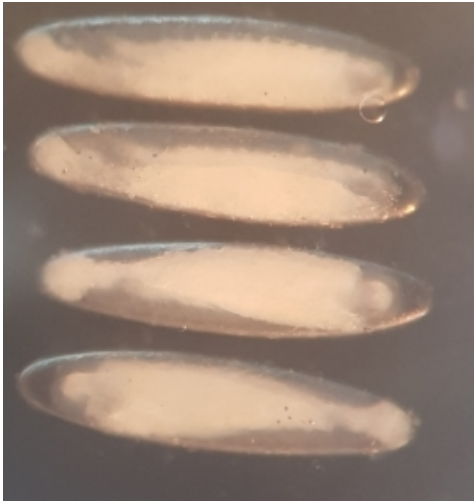


Genetic improvement of the black soldier fly

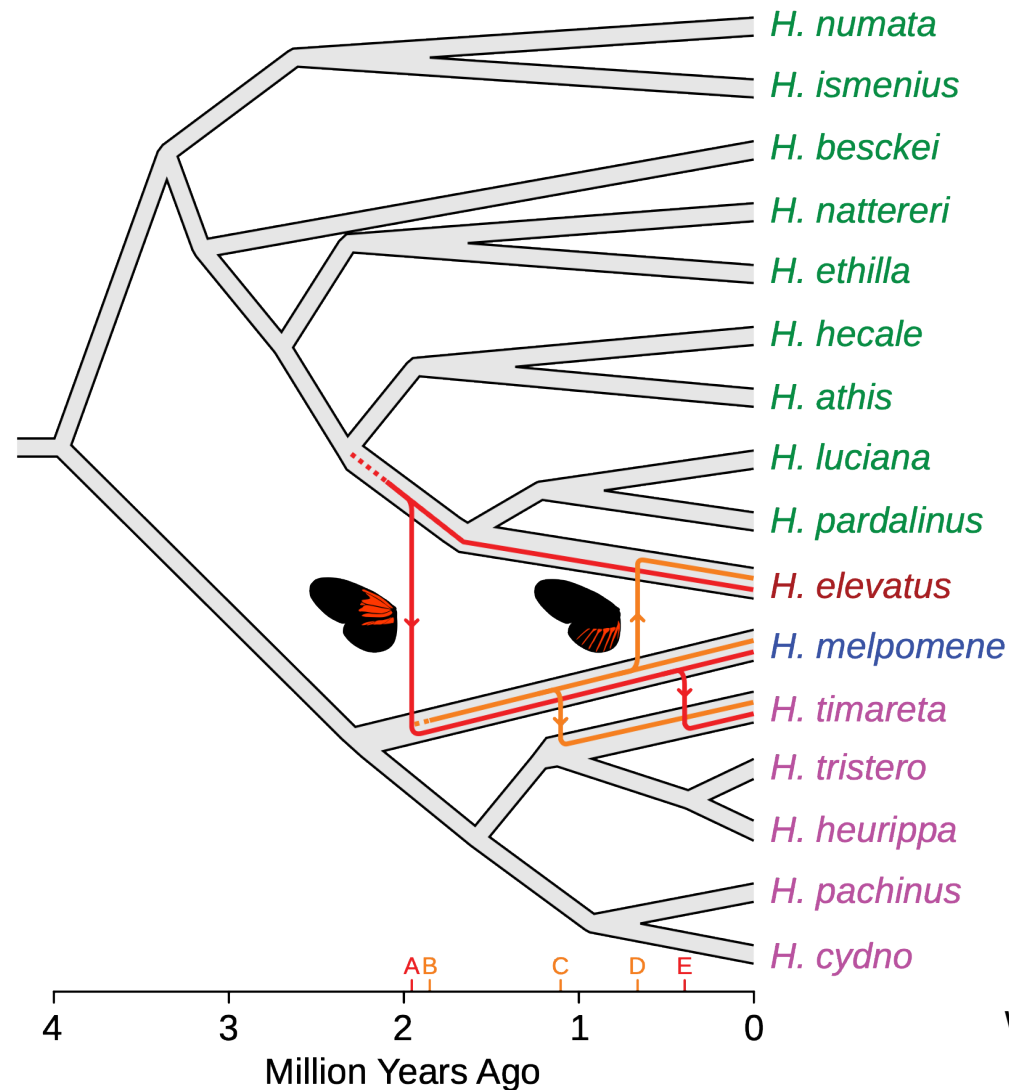


Chris Jiggins

Tom Generalovic, Richard Durbin, Shane McCarthy, Miha Pipan (Better Origins) and Christoph Sandrock



Ancient introgression events explain origins of novel wing patterns

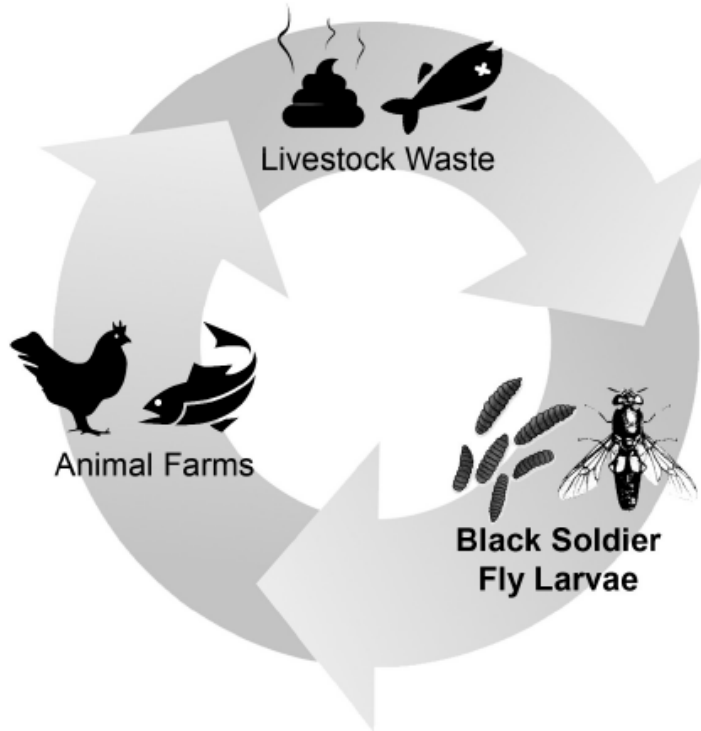


Black Soldier Fly is a bio-catalyst in the bioconversion of animal & brewing wastes into mass protein and lipid production.

Costs of Pre- and Post-Consumer Food Waste



Costs of Livestock Production



Benefits of BSF



Summary:

- Generate high quality reference genome
- Search for patterns of divergence and admixture across the global range of the Black Soldier Fly
- Use ‘evolve and resequence’ to identify genes underlying industry relevant traits

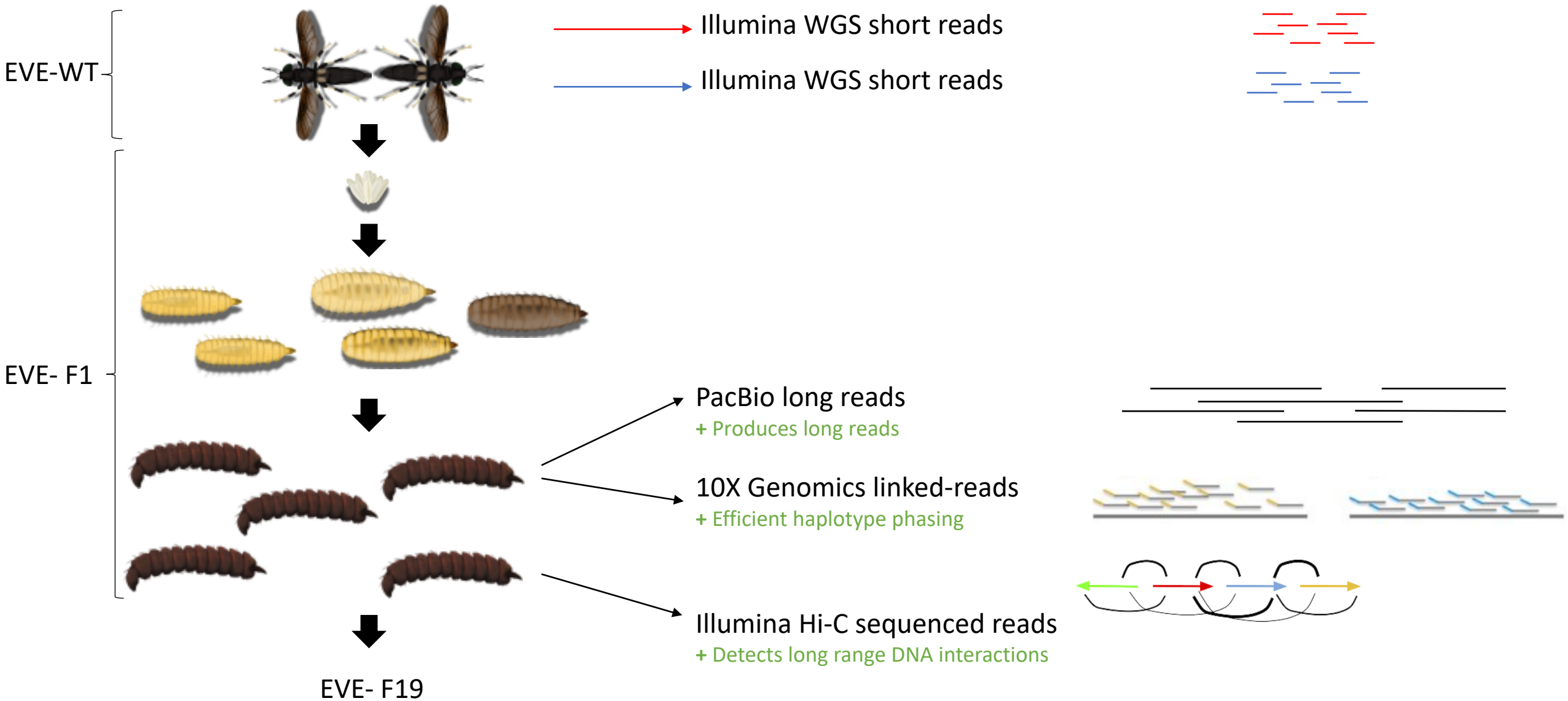
ARTICLE

Genomic landscape and genetic manipulation of the black soldier fly *Hermetia illucens*, a natural waste recycler

Shuai Zhan ^{1,2}, Gangqi Fang^{1,2}, Minmin Cai³, Zongqing Kou¹, Jun Xu¹, Yanghui Cao¹, Liang Bai¹, Yixiang Zhang^{1,2}, Yongmao Jiang^{1,2}, Xingyu Luo^{1,2}, Jian Xu^{1,2}, Xia Xu^{1,2}, Longyu Zheng³, Ziniu Yu³, Hong Yang⁴, Zhijian Zhang⁵, Sibao Wang ^{1,2}, Jeffery K. Tomberlin⁶, Jibin Zhang³ and Yongping Huang ^{1,2}



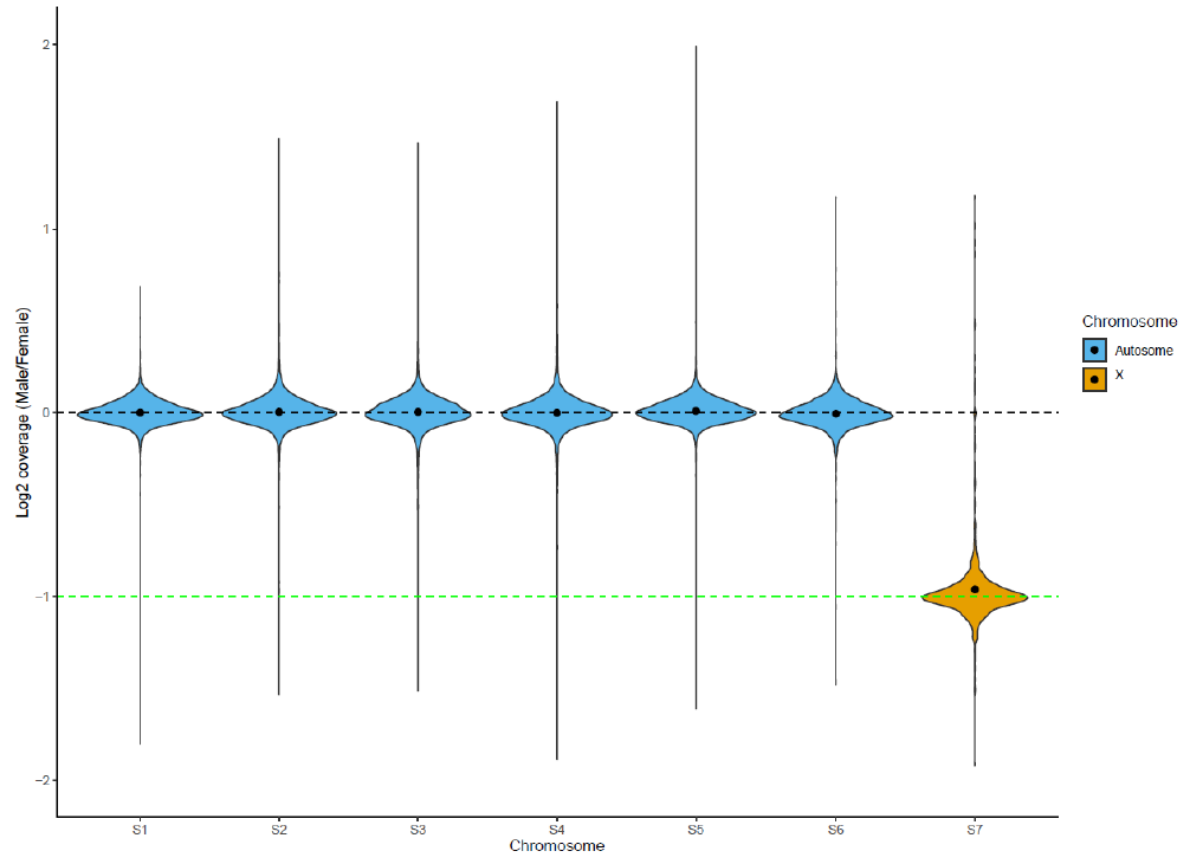
Genome assembly



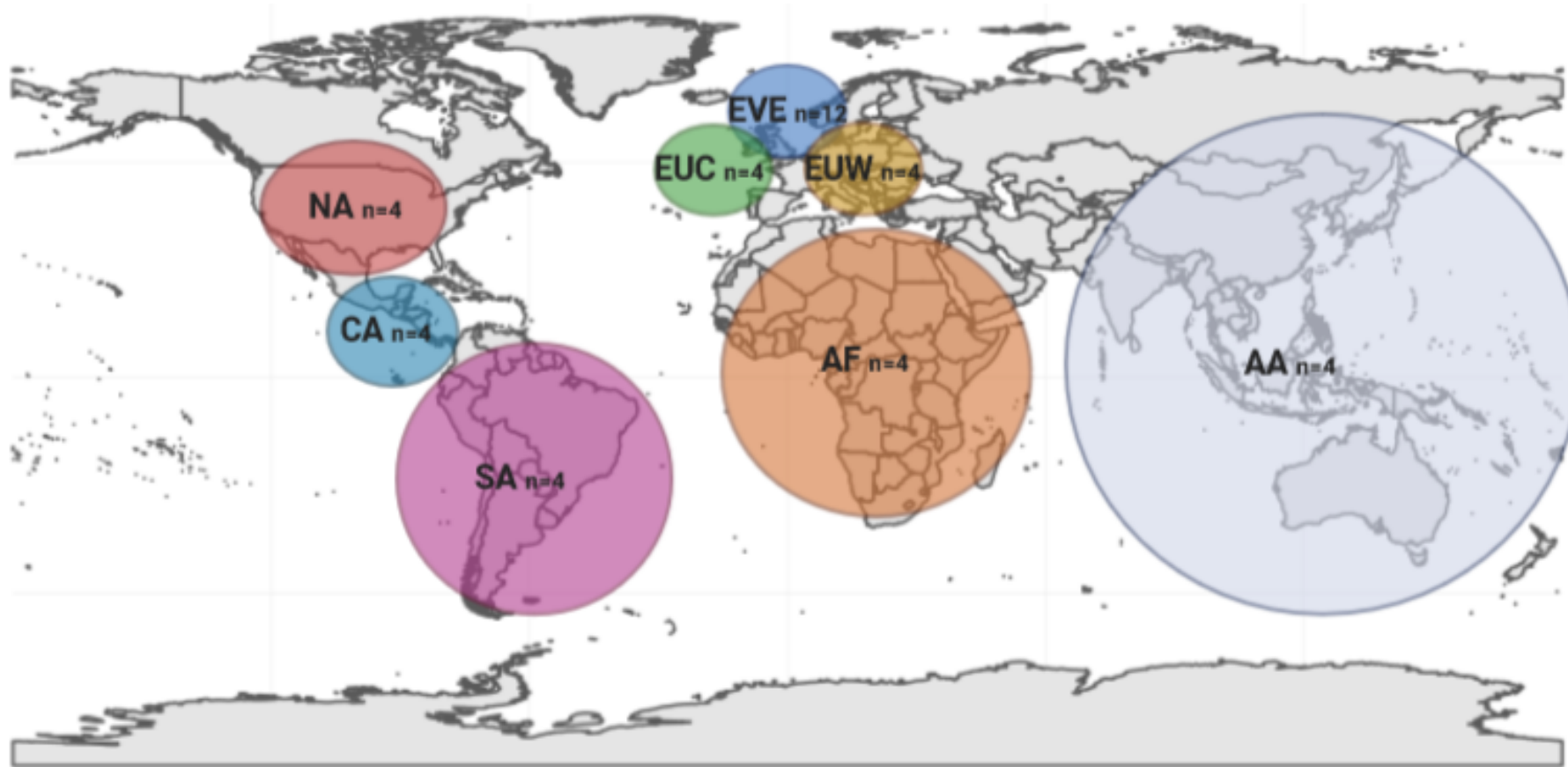
- **1.01 Gb** genome assembly
 - Repeat rich (**67%** of genome)
 - Curated **99.8%** of scaffolds into **7 chromosomes**
 - **16 Mb** contig and **181 Mb** scaffold N50's
-
- Annotate **17,664** protein-coding genes
 - Highly complete annotation **98.2%** BUSCOs



Identification of sex chromosome by read coverage of males and females

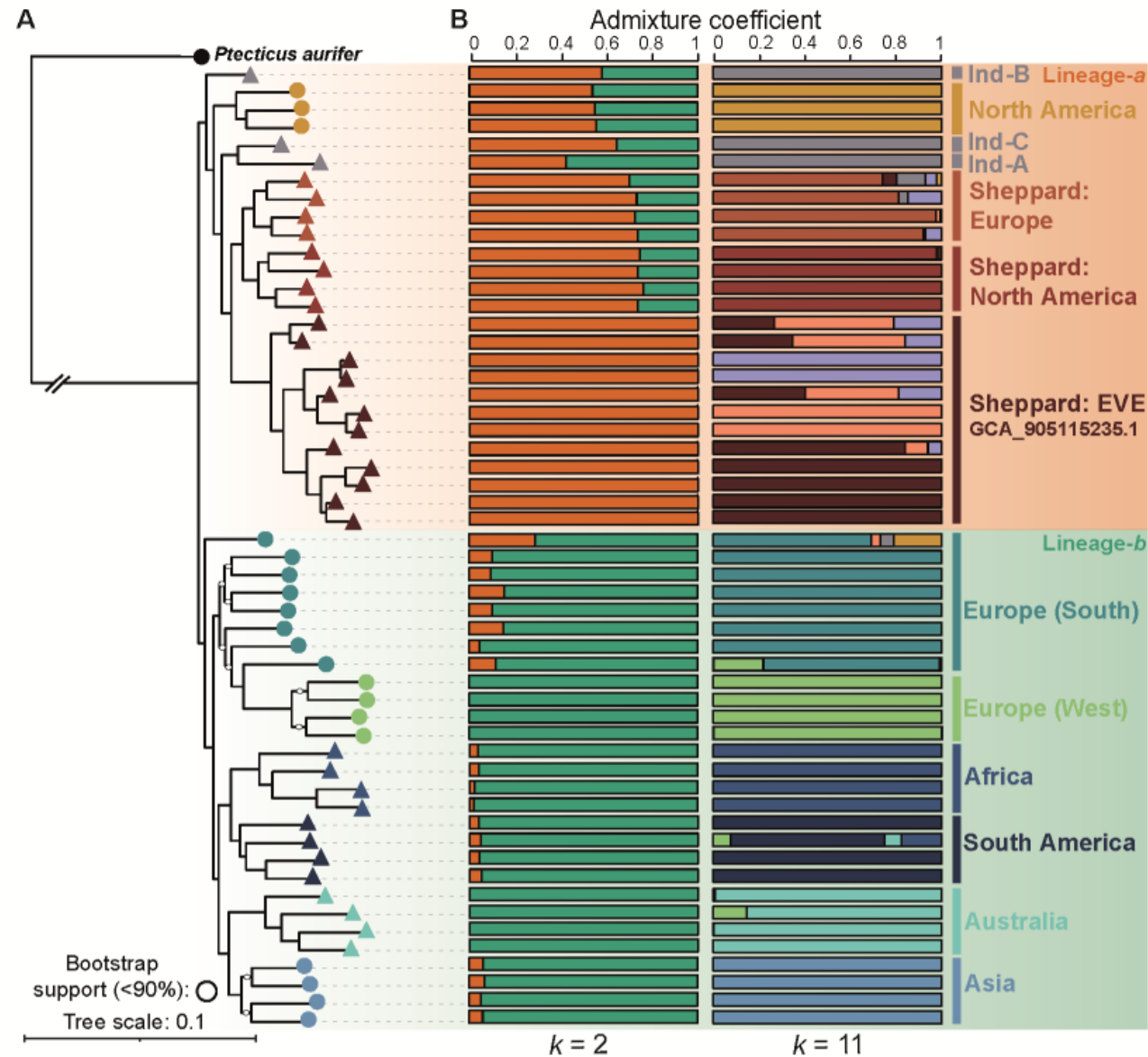


Part II: Survey global BSF genetic diversity

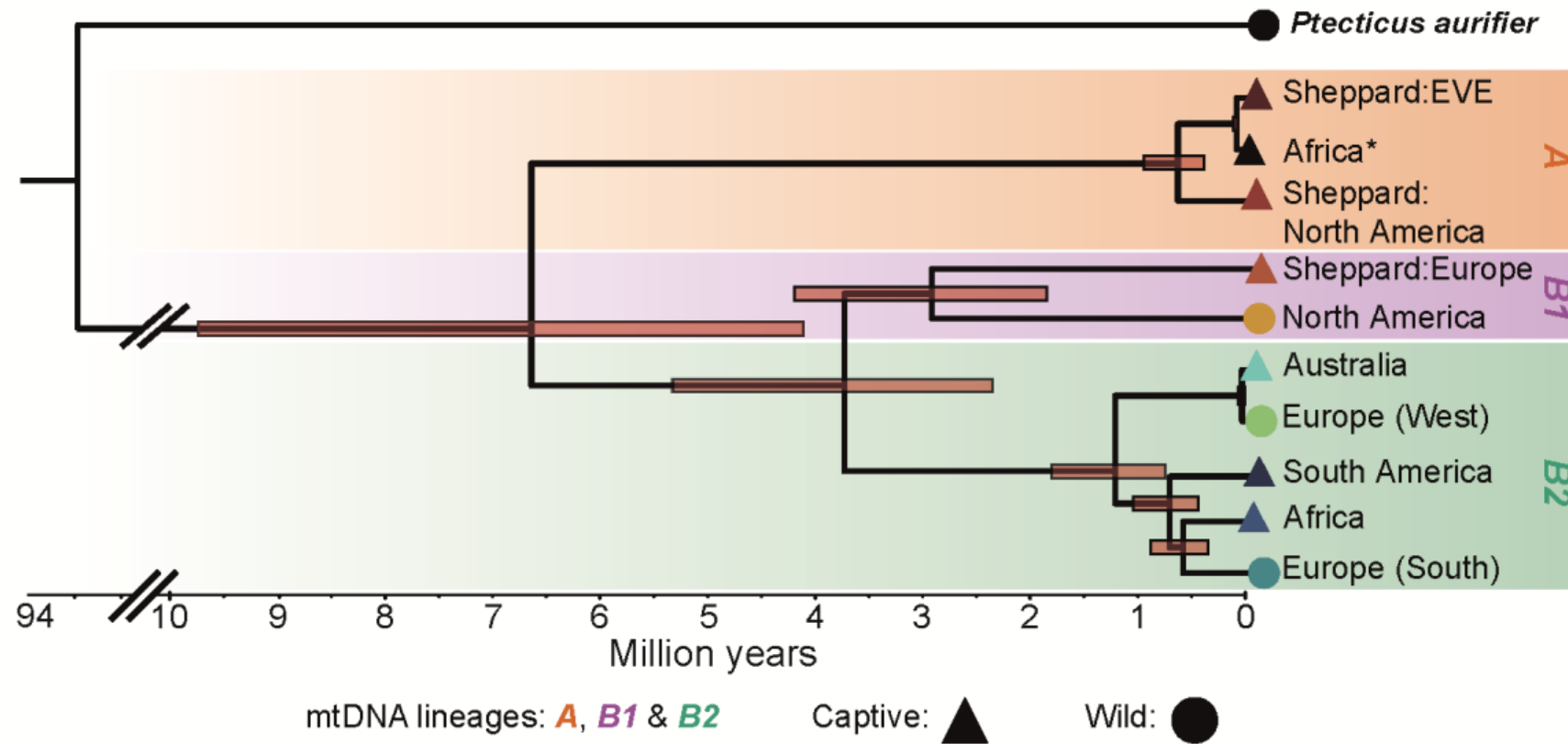


Thanks to Christoph Sandrock for access to samples, see also Kaya et al BMC Biology 2021

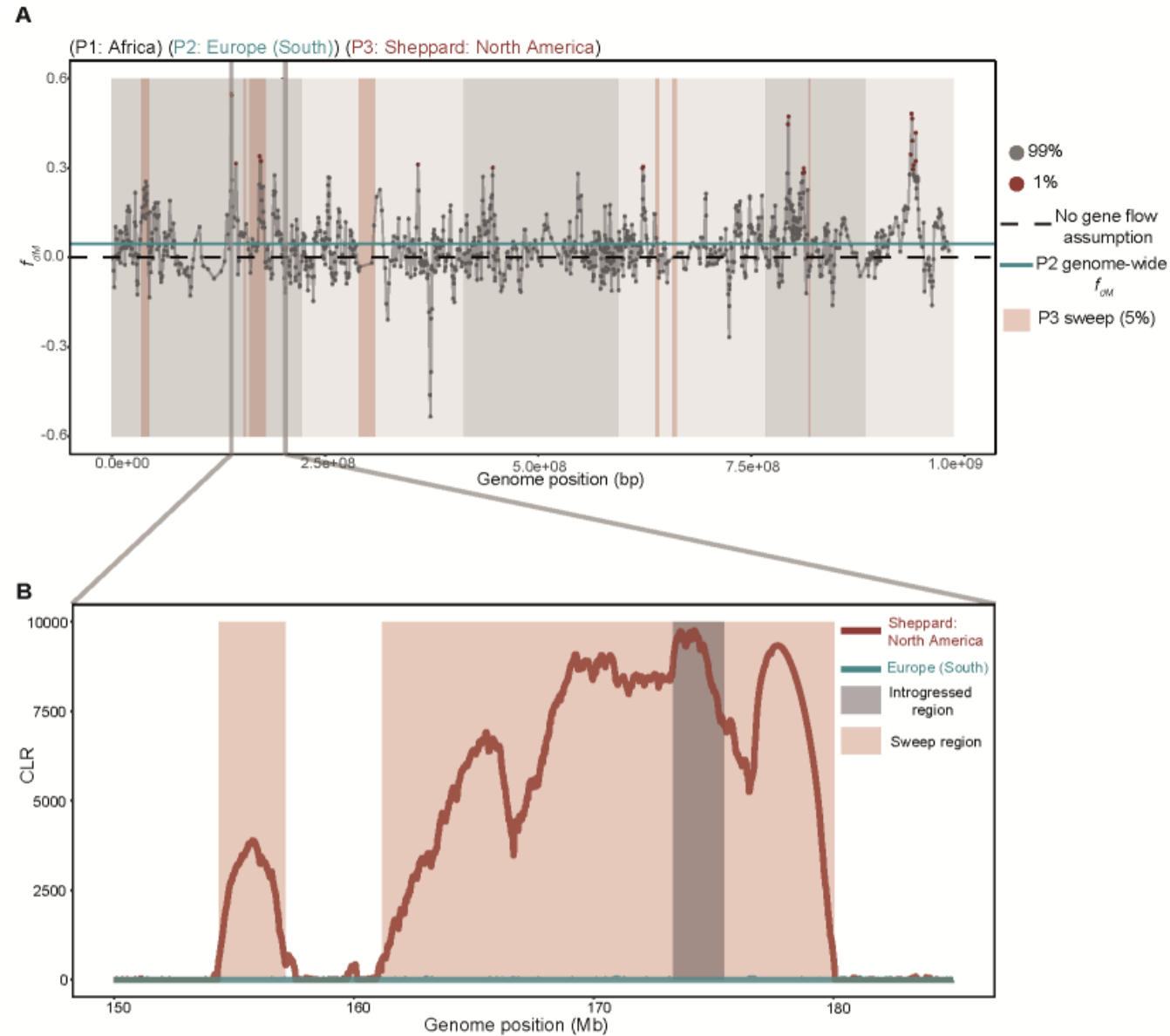
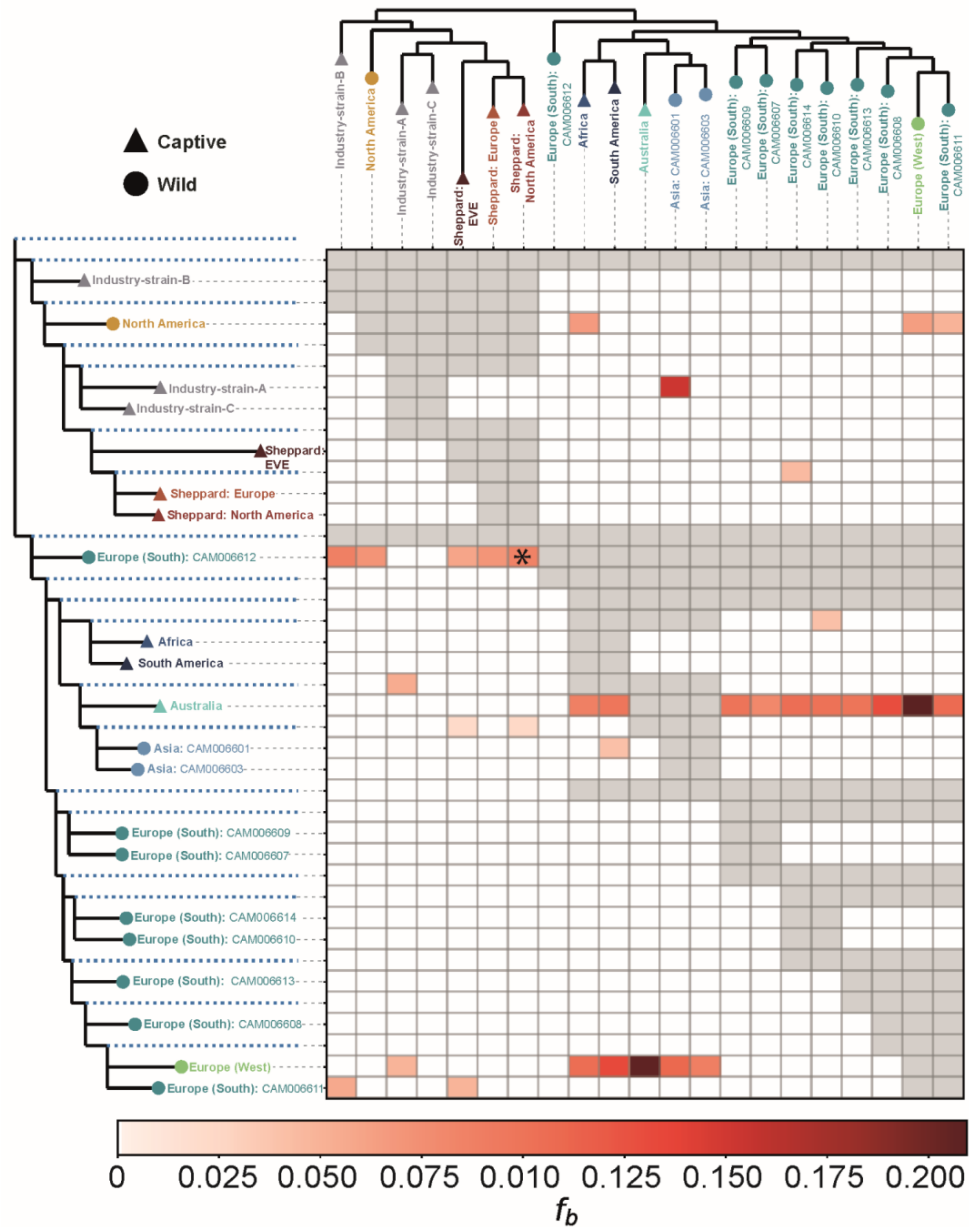
Deep divergence in global population structure



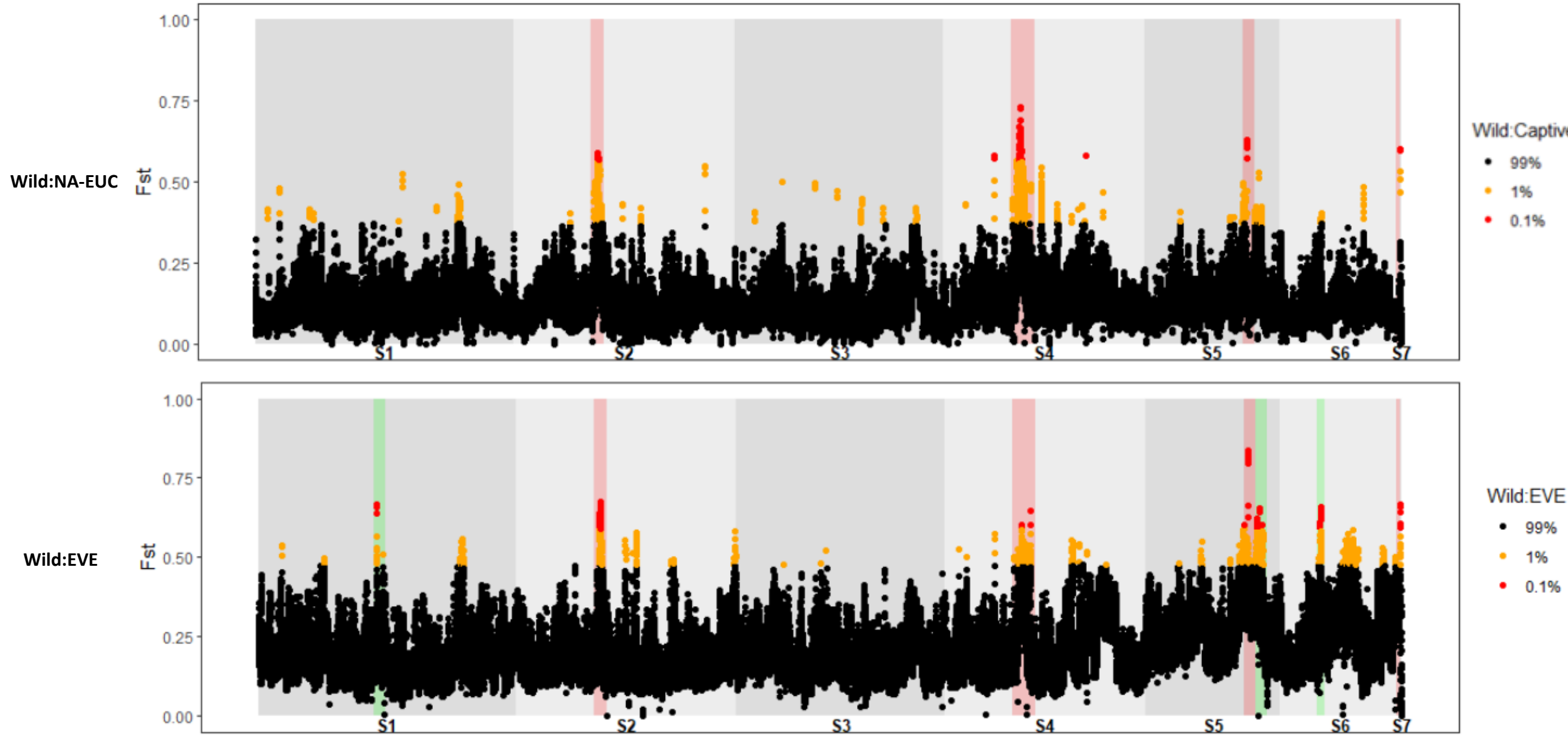
Deep divergence in global population structure



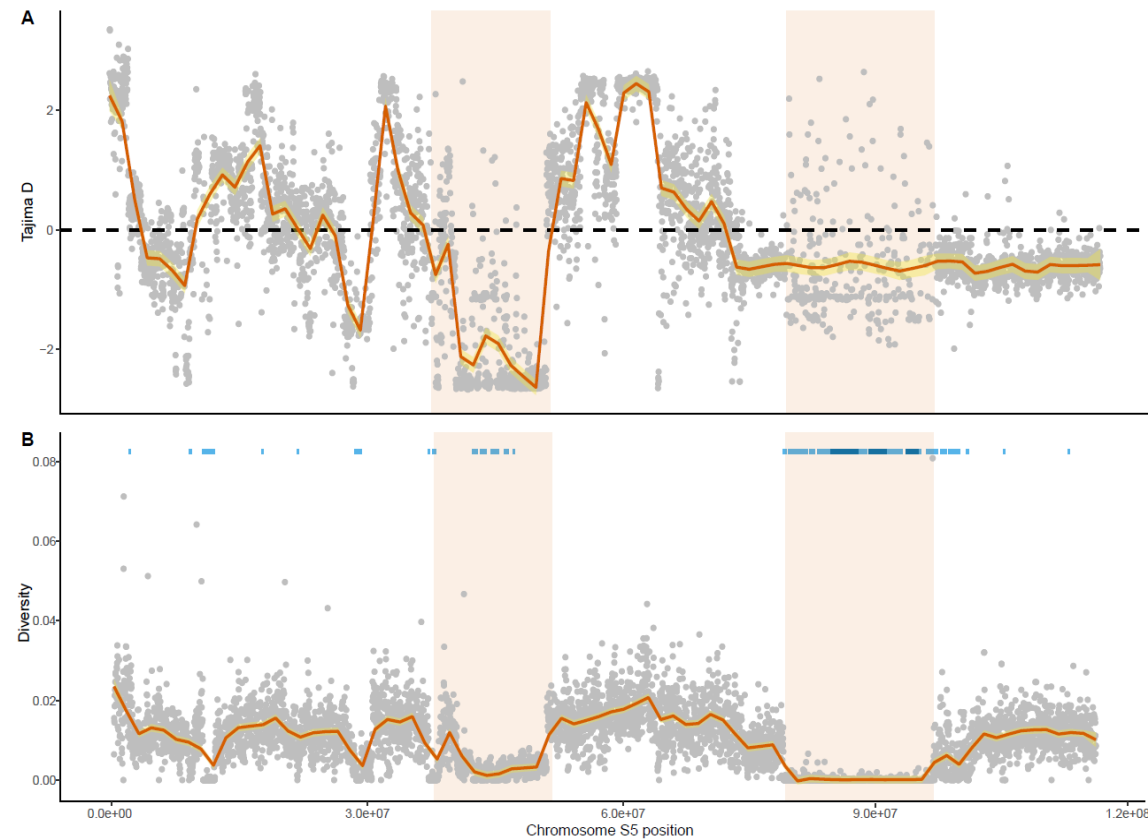
Signatures of introgression between lineages



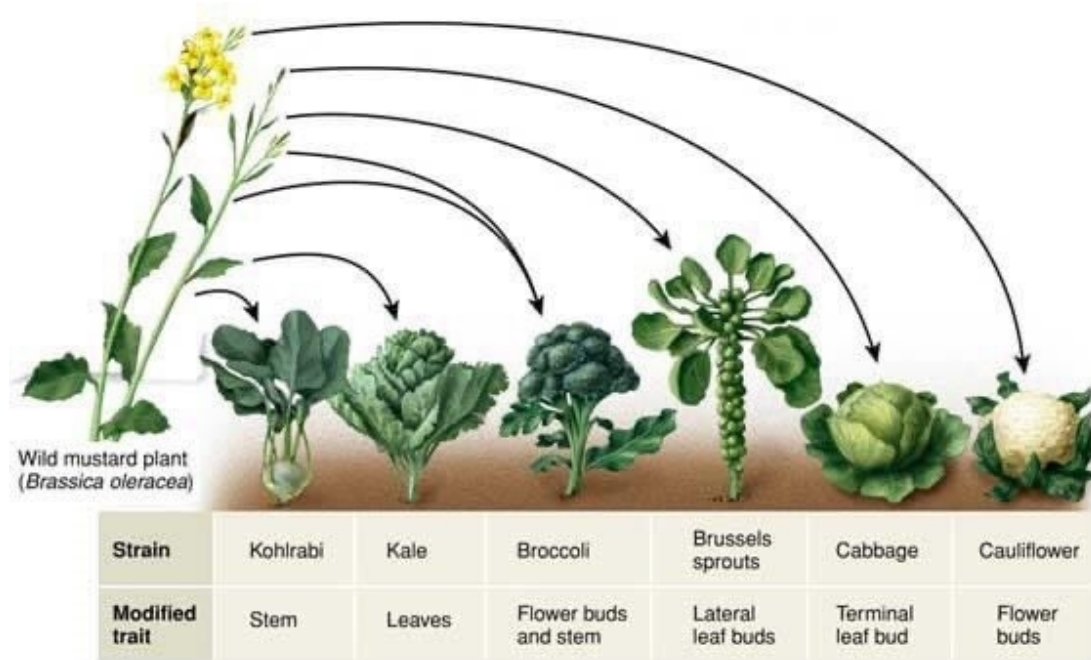
Parallel signatures of domestication



Chromosome 5 shows strong signatures of reduced diversity – selection or inbreeding?



Evolve and Resequence



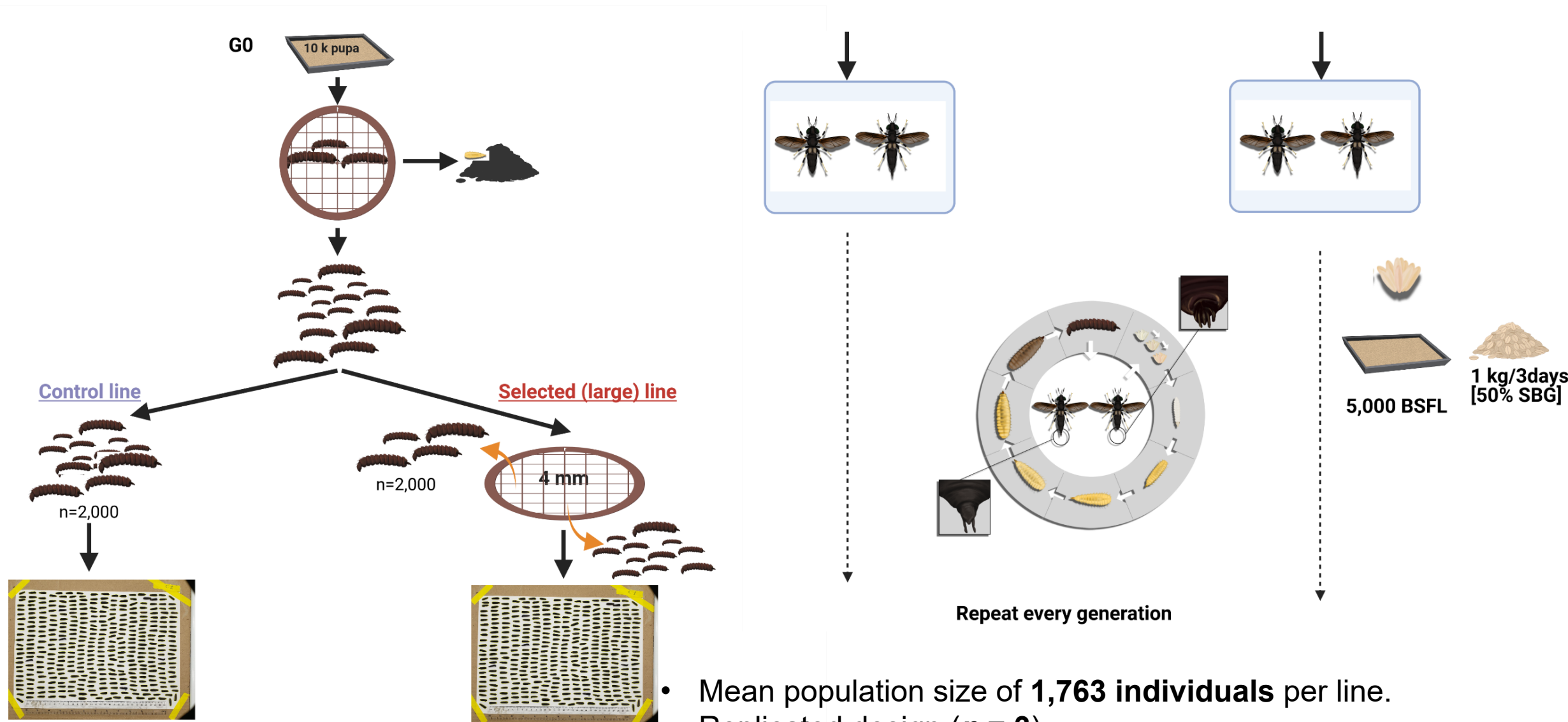
Body size

Growth rate (generations per year)

Nutritional properties

Fecundity

Methods:



- Mean population size of **1,763 individuals** per line.
- Replicated design ($n = 3$).
- **Internal controls** to capture stochastic variation per replicate.
- Selection threshold between the top **13 – 27%** “largest” pupa

Black Soldier Fly pupal size is a heritable trait

Estimate heritability of trait:

$$h_2 = R/S$$

$$S = 0.81 - 0.67$$

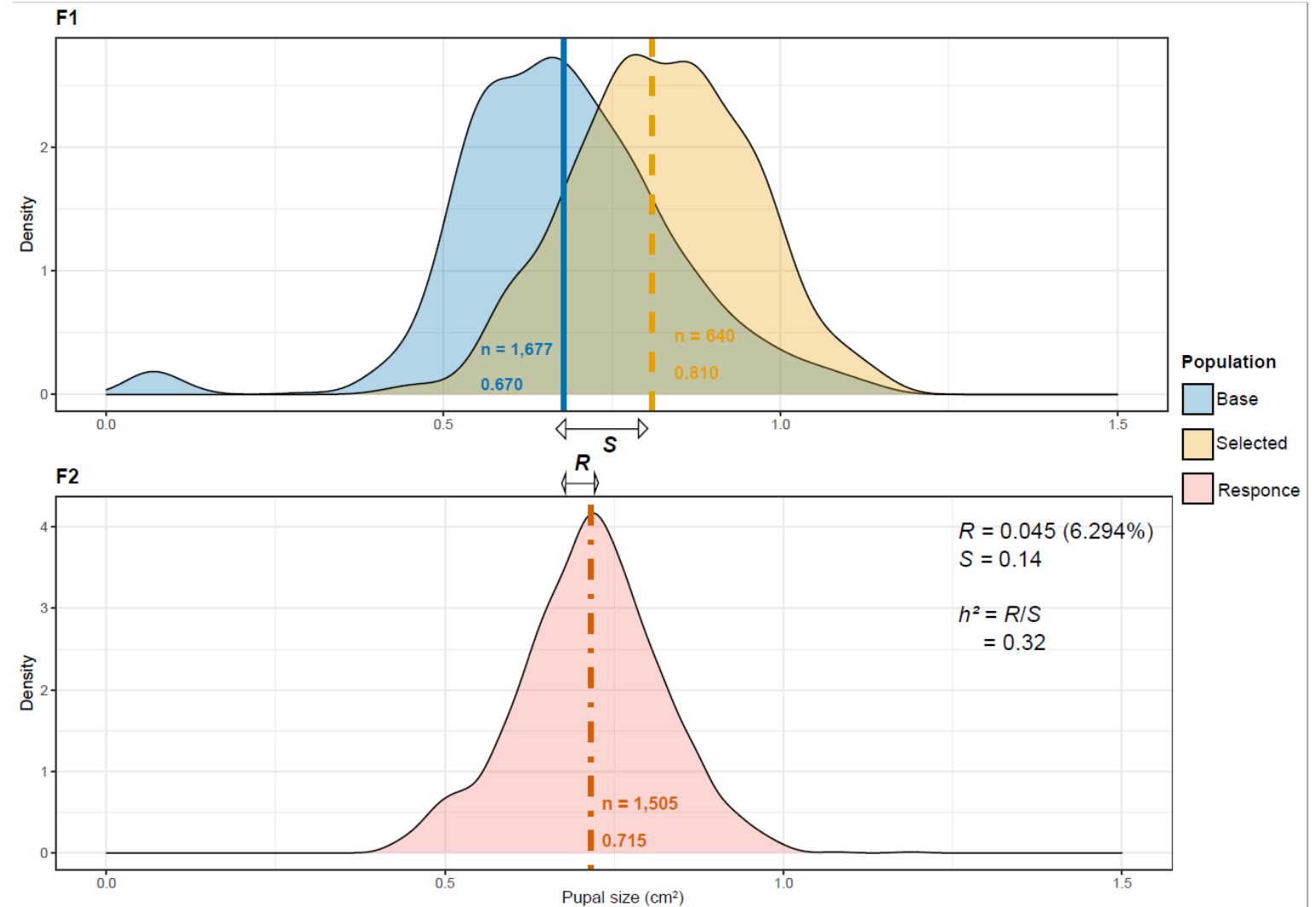
$$R = 0.715 - 0.67$$

$$h_2 = 0.045/0.14$$

$$h_2 = 0.32$$

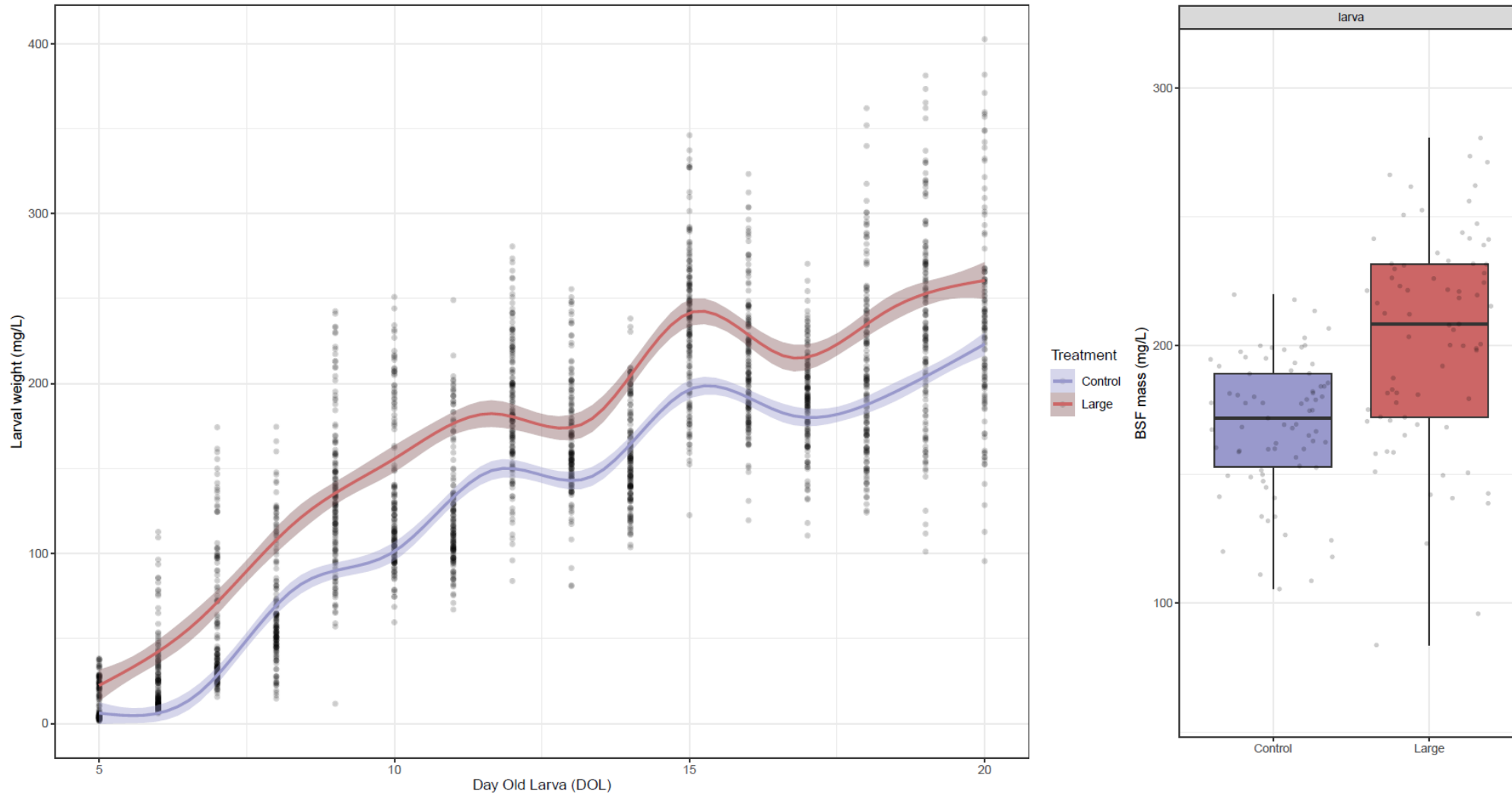
$$\text{Overall } h_2 = 0.32-0.45$$

$$\text{mean} = 0.39$$



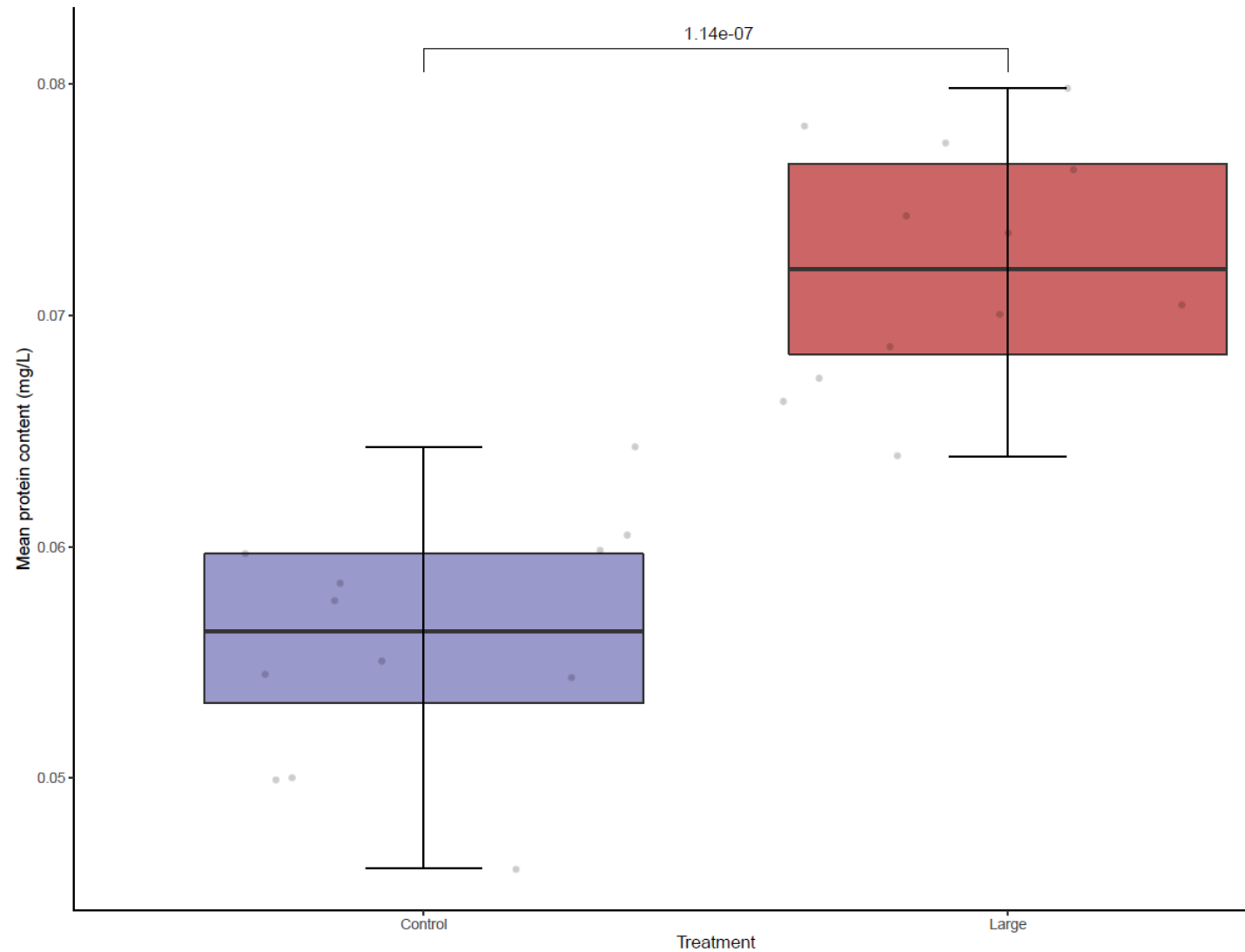
Pupal size increase of 17% over seven generations (approx. nine months) across replicates

Larval growth rates respond to selection for large size



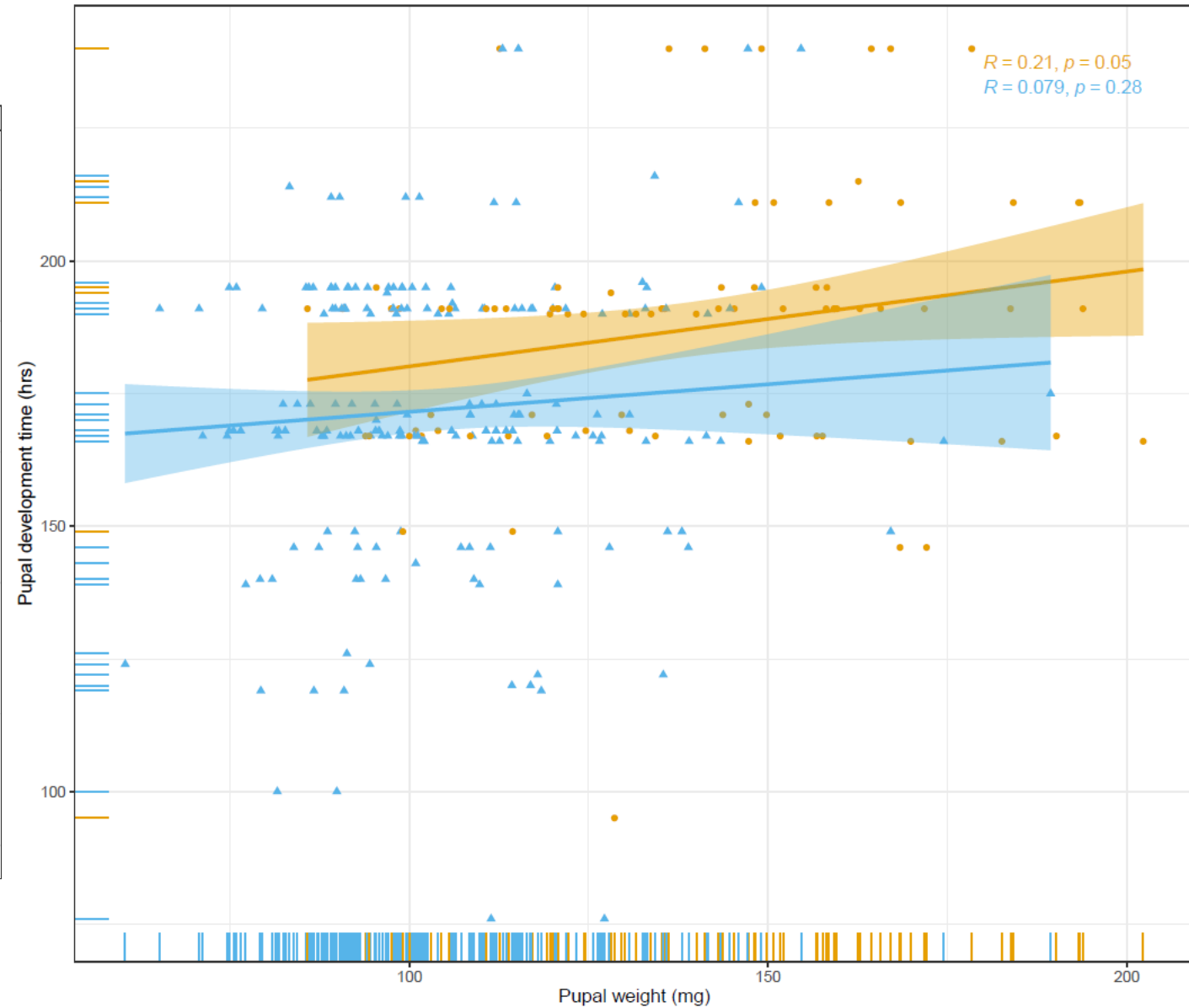
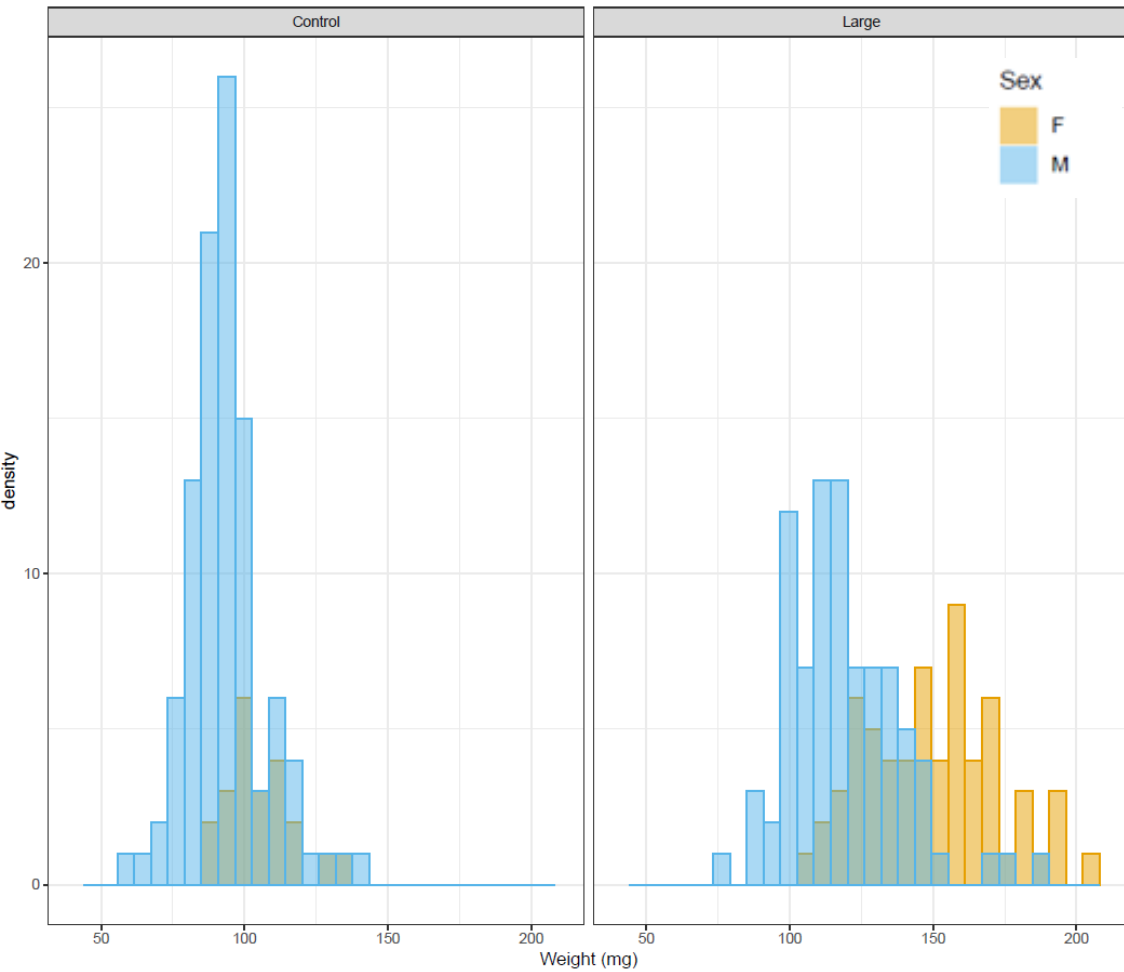
- 16.57% **biomass increase** at harvest day (Day 12).

Protein content also improves in large lines

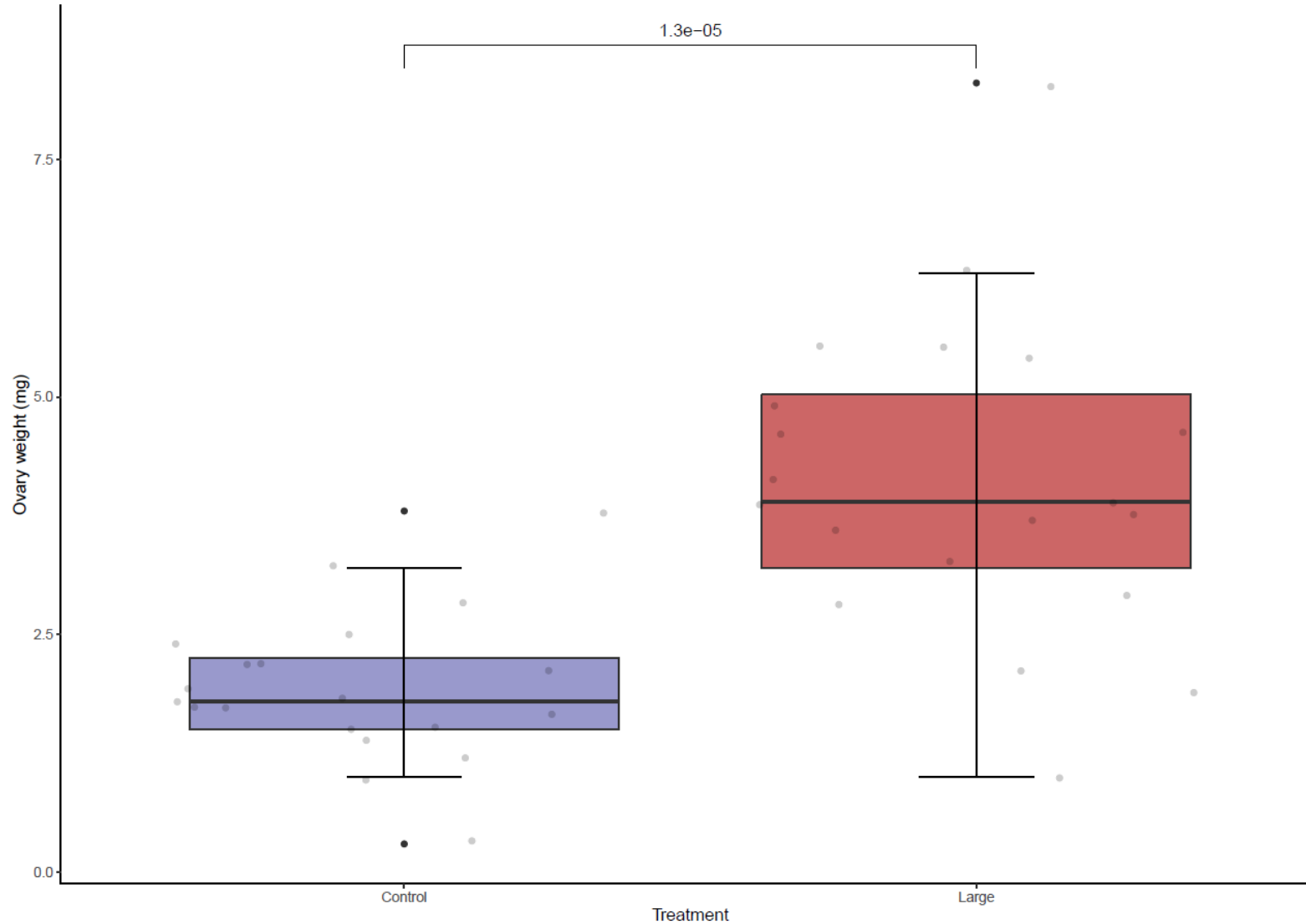


- Protein content shows 1.83% increase in selected population.

Female BSF invest into larger “size” at the trade-off of longer development



Increased ovary weights (possibly fecundity?)

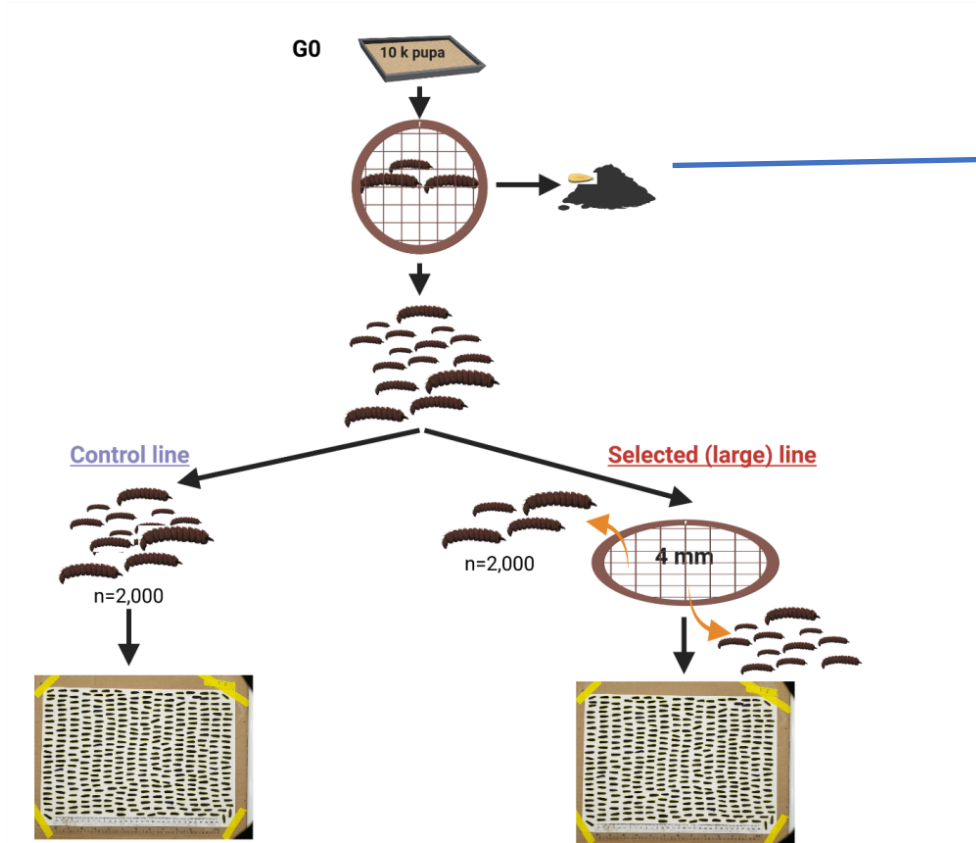


Treatment	n	Ovary weight (mg)
Control	20	1.935
Large	20	4.105



- A **double increase** in ovary weights (e.g. double the brood size) in selected line.

Resequencing of replicate lines to identify selected loci



32 individuals of base population

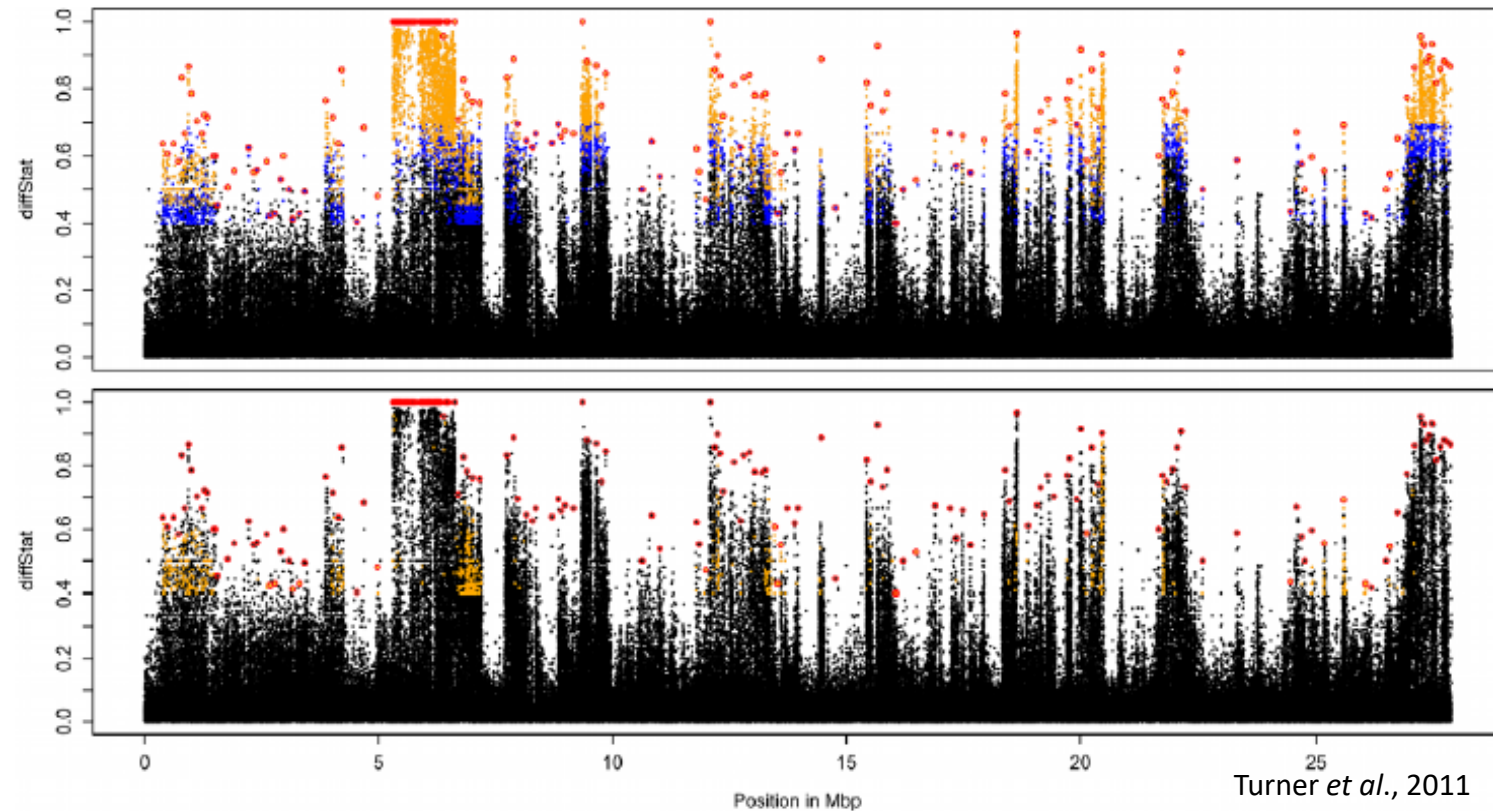
Repeated across three replicates

32 individuals of
control population

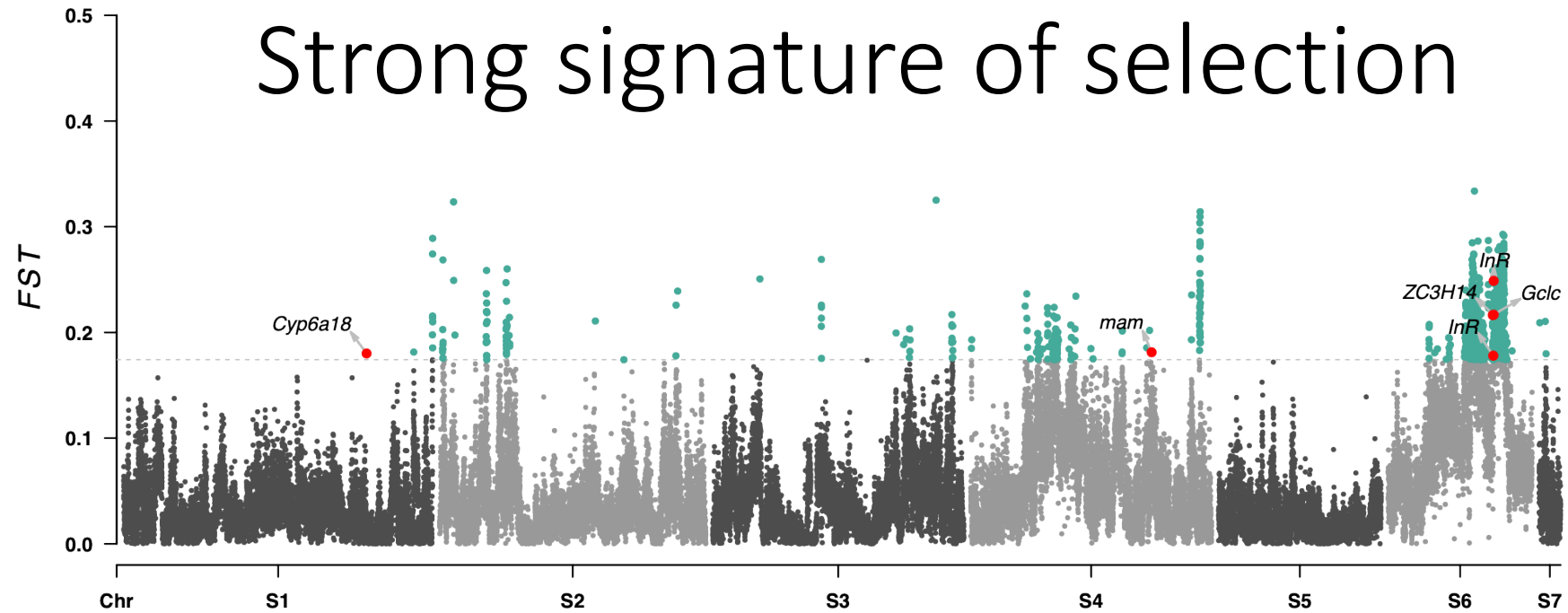
32 individuals of
large population

Seven generations of selection

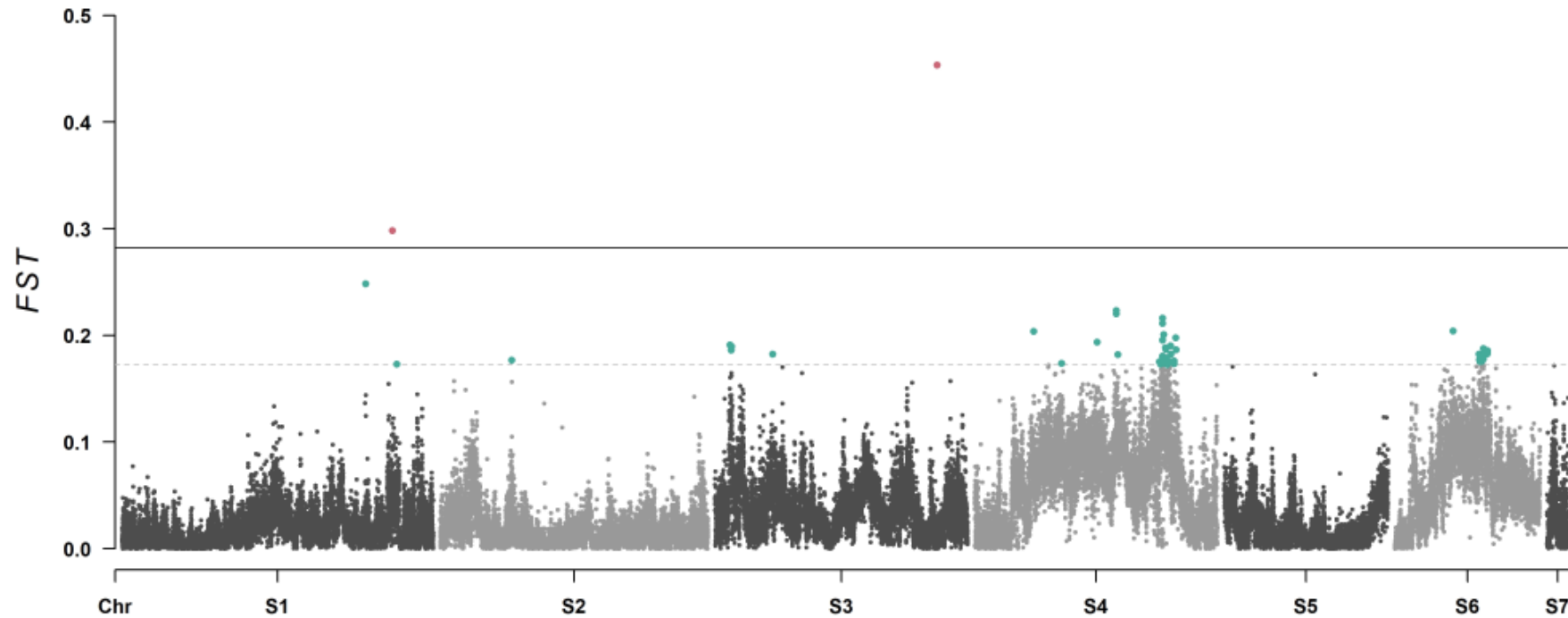
Size is typically a polygenic trait and difficult to identify specific genes



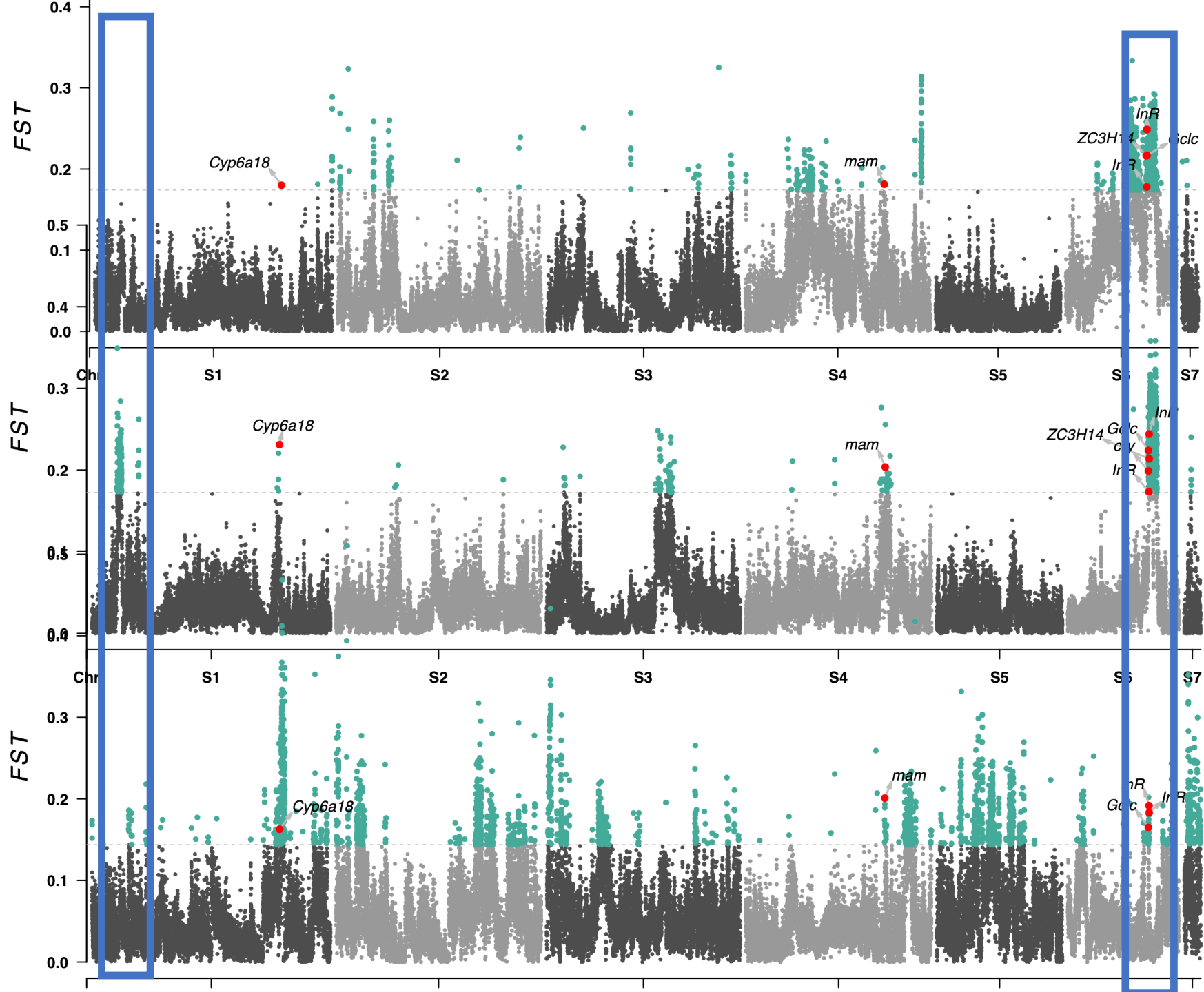
Strong signature of selection



Selected



Control



Conclusions

- Generated high quality reference genome which is now publicly available
- Considerable genetic diversity across the globe including deep divergence
- Putative signatures of selection/domestication
- Rapid response to selection is highly repeatable at phenotypic level, less so at the genetic level



Tom Generalovic –
PhD student



Miha Pipan – Better
Origins



Shane McCarthy –
Sanger Institute



Richard Durbin – U
of Cambridge



Christoph Sandrock
FiBL Switzerland

Wenjun Zhao - PhD student
Sam Leonard – MPhil student

