Using archaeogenomic and computational approaches to unravel the history of local adaptation in crops

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Supplementary Figures

Figure S1. A. Probability landscape of population survival (*p*) for a given number of loci (*g*) under selection coefficient (*s*) for an inbreeding cereal such as barley. B. Linear regression of the maximum selection load (total amount of selection) carried across loci for different selection coefficients without any population extinction in simulations (from Allaby, Fuller & Kitchen 2014).

Figure S2. Genomic profiles of Gypsy-, Copia-, and LINE-type retrotransposons in modern and archaeobotanical cotton. (Palmer *et al.* 2012b).

Figure S3. Cluster analysis of archaeological *Gossyium barbadense* read variants mapped to *Arabidopsis thaliana* metabolic Pathways**.** Reads were mapped to the KEGG *A. thaliana* metabolic pathway. The number of major nodes between reads were used to create a distance metric between variants, which were then grouped by

K-median clustering using the “Pheatmap” package in R. Groupings have 7 nodes or fewer between all points.

Figure S4. Archaeological *Gossyium barbadense* read variants mapped to *Arabidopsis thaliana* metabolic Pathways. Variants are represented by stars, for colour key see Figure S3.

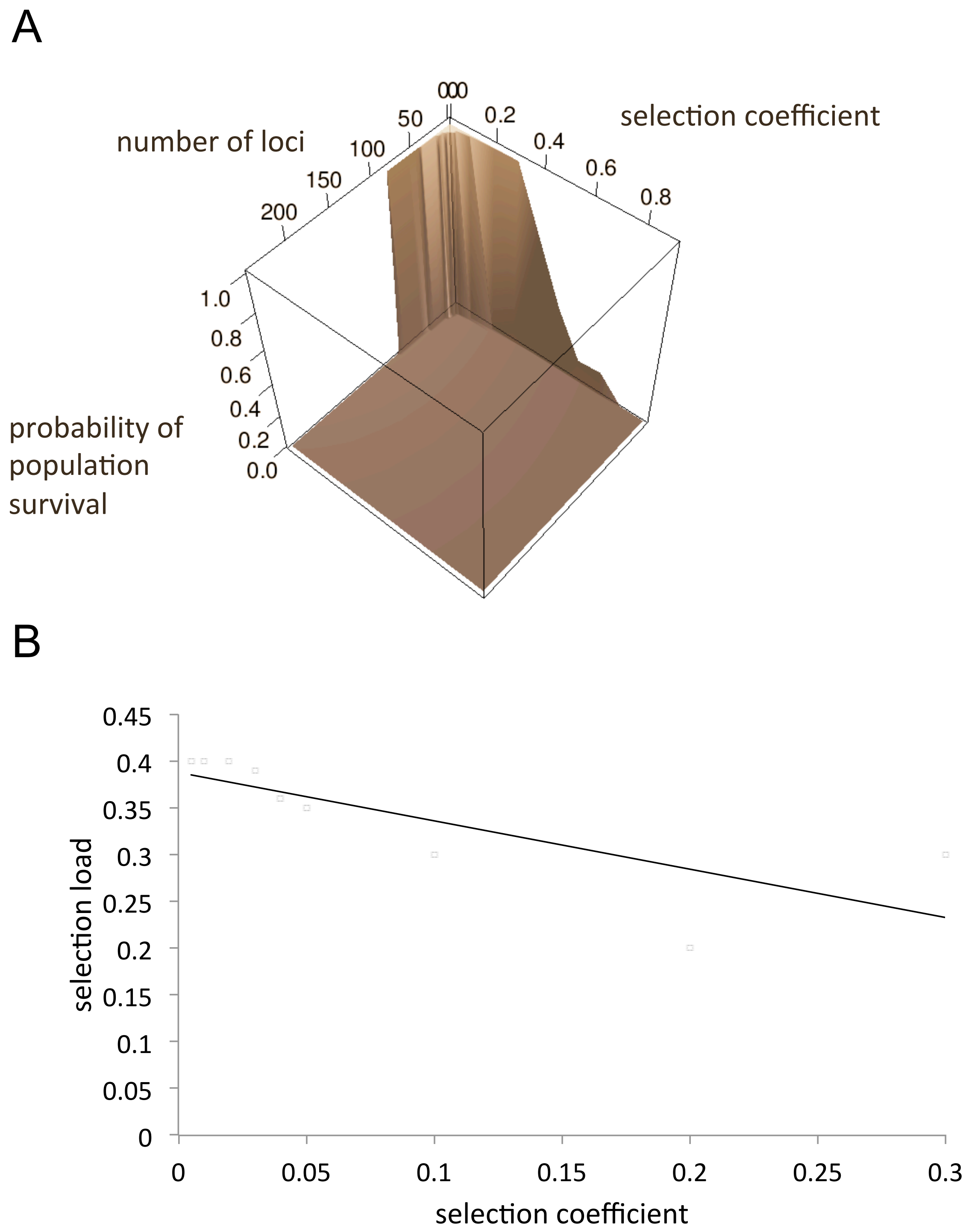
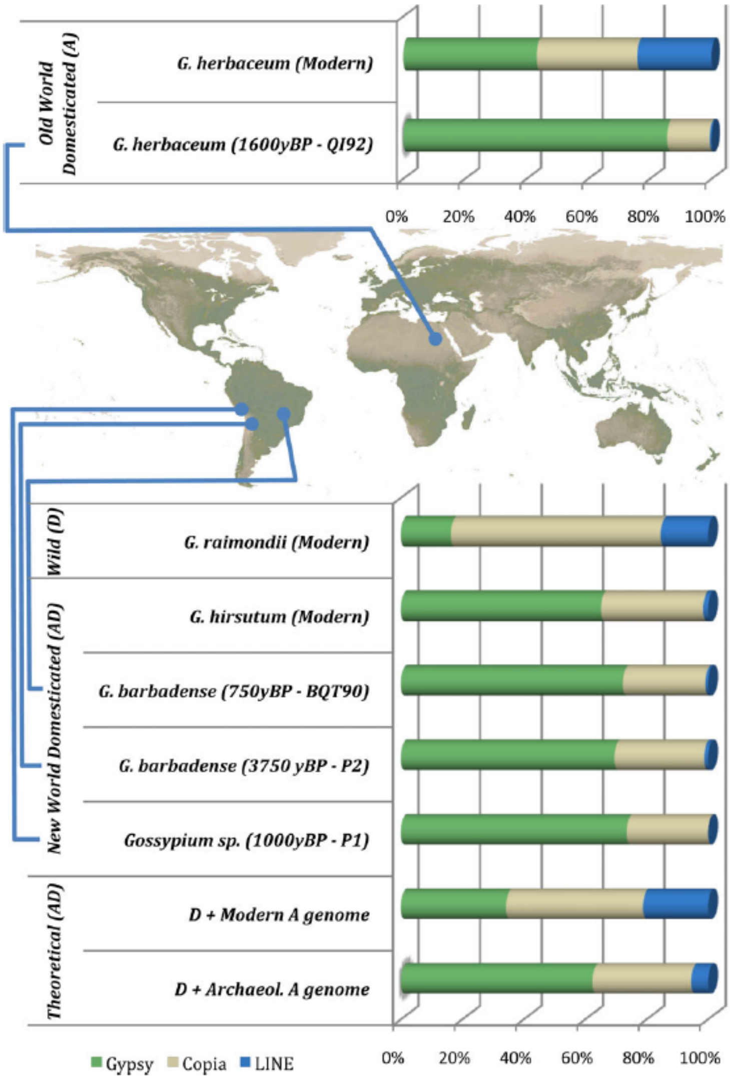
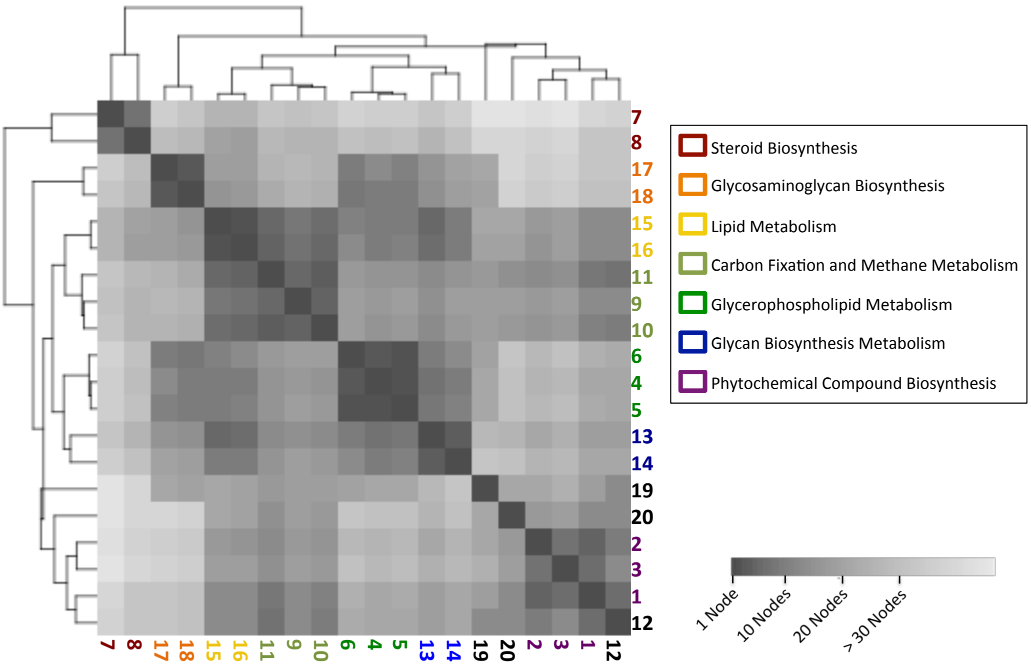

A
number of loci
000
50
100
150
200
0.2
0.4
0.6
0.8
selection coefficient
1.0
0.8
0.6
0.4
0.2
0.0
probability of population survival
B
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
selection load
0
0.05
0.1
0.15
0.2
0.25
0.3
selection coefficient

Figure S1.



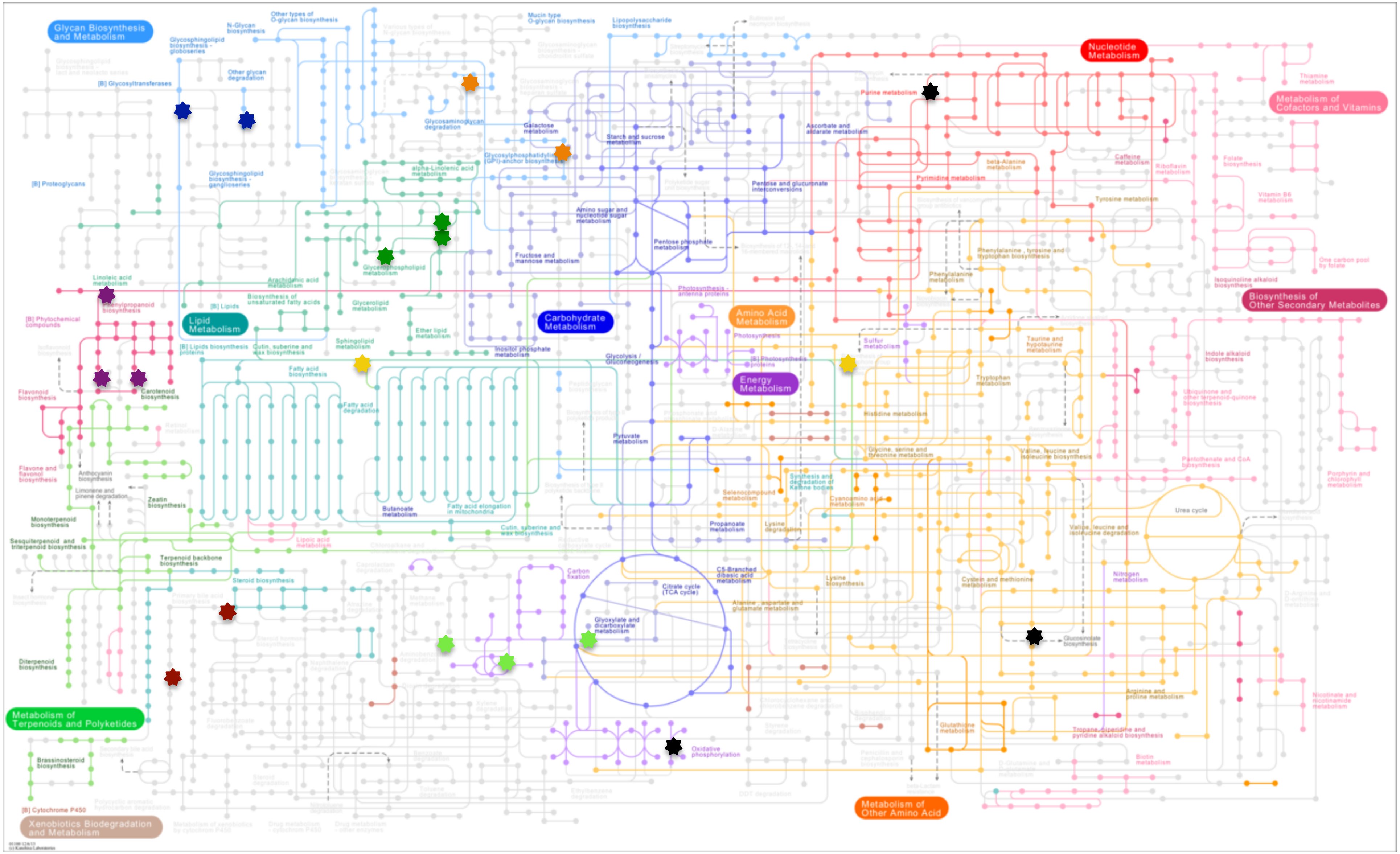
Old World Domesticated (A)
G. herbaceum (Modern)
G. herbaceum (1600yBP - QI92)
0%
20%
40%
60%
80%
100%
Wild (D)
G. raimondii (Modern)
New World Domesticated (AD)
G. hirsutum (Modern)
G. barbadense (750yBP - BQT90)
G. barbadense (3750 yBP - P2)
Gossypium sp. (1000yBP - P1)
Theoretical (AD)
D + Modern A genome
D + Archaeol. A genome
Gypsy
Copia
LINE

Figure S2.



7
8
17
18
15
16
11
9
10
6
4
5
13
14
19
20
2
3
1
12
Steroid Biosynthesis
Glycosaminoglycan Biosynthesis
Lipid Metabolism
Carbon Fixation and Methane Metabolism
Glycerophospholipid Metabolism
Glycan Biosynthesis Metabolism
Phytochemical Compound Biosynthesis
1 Node
10 Nodes
20 Nodes
> 30 Nodes

Figure S3


Glycan Biosynthesis and Metabolism
N-Glycan biosynthesis
Other types of O-glycan biosynthesis
Mucin type O-glycan biosynthesis
Lipopolysaccharide biosynthesis
Glycosphingolipid biosynthesis - globoseries
Other glycan degradation
[B] Glycosyltransferases
[B] Proteoglycans
Glycosphingolipid biosynthesis - gangliosereis
Glycosaminoglycan degradation
Galactose metabolism
Starch and sucrose metabolism
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
alpha-Linolenic acid metabolism
Amino sugar and nucleotide sugar metabolism
Pentose and glucuronate interconversions
Ascorbate and aldarate metabolism
Purine metabolism
Nucleotide Metabolism
Metabolism of Cofactors and Vitamins
Thiamine metabolism
Pyrimidine metabolism
beta-Alanine metabolism
Caffeine metabolism
Riboflavin metabolism
Folate biosynthesis
Vitamin B6 metabolism
Tyrosine metabolism
One carbon pool by folate
Isoquinoline alkaloid biosynthesis
Biosynthesis of Other Secondary Metabolites
Pentose phosphate metabolism
Fructose and mannose metabolism
Phenylalanine, tyrosine and tryptophan biosynthesis
Phenylalanine metabolism
Glycerophospholipid metabolism
Arachidonic acid metabolism
Linoleic acid metabolism
Phenylpropanoid biosynthesis
[B] Phytochemical compounds
Biosynthesis of unsaturated fatty acids
[B] Lipids
Lipid Metabolism
Glycerolipid metabolism
Carbohydrate Metabolism
Photosynthesis - antenna proteins
Amino Acid Metabolism
Photosynthesis
Ether lipid metabolism
Sphingolipid metabolism
Inositol phosphate metabolism
[B] Lipids biosynthesis proteins
Cutin, suberine and wax biosynthesis
Fatty acid biosynthesis
Glycolysis / Gluconeogenesis
[B] Photosynthesis proteins
Energy Metabolism
Sulfur metabolism
Taurine and hypotaurine metabolism
Indole alkaloid biosynthesis
Tryptophan metabolism
Ubiquinone and other terpenoid-quinone biosynthesis
Flavonoid biosynthesis
Carotenoid biosynthesis
Fatty acid degradation
Histidine metabolism
Pyruvate metabolism
Glycine, serine and threonine metabolism
Valine, leucine and isoleucine biosynthesis
Pantothenate and CoA biosynthesis
Porphyrin and chlorophyll metabolism
Flavone and flavonol biosynthesis
Anthocyanin biosynthesis
Limonene and pinene degradation
Zeatin biosynthesis
Synthesis and degradation of ketone bodies
Selenocompound metabolism
Cyanoamino acid metabolism
Butanoate metabolism
Fatty acid elongation in mitochondria
Monoterpenoid biosynthesis
Cutin, suberine and wax biosynthesis
Propanoate metabolism
Lysine degradation
Urea cycle
Valine, leucine and isoleucine degradation
Sesquiterpenoid and triterpenoid biosynthesis
Lipoic acid metabolism
Terpenoid backbone biosynthesis
Steroid biosynthesis
Carbon fixation
C5-Branched dibasic acid metabolism
Citrate cycle (TCA cycle)
Lysine biosynthesis
Cysteine and methionine metabolism
Nitrogen metabolism
Alanine, aspartate and glutamate metabolism
Glyoxylate and dicarboxylate metabolism
Glucosinolate biosynthesis
Diterpenoid biosynthesis
Arginine and proline metabolism
Nicotinate and nicotinamide metabolism
Metabolism of Terpenoids and Polyketides
Glutathione metabolism
Tropane, piperidine and pyridine alkaloid biosynthesis
Oxidative phosphorylation
Biotin metabolism
Brassinosteroid biosynthesis
[B] Cytochrome P450
Metabolism of Other Amino Acid
Xenobiotics Biodegradation and Metabolism
01100 12/6/13
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