# SUPPLEMENTAL FIGURE LEGENDS

**Figure S1. Representative GC-MS chromatogram of oat FAMEs.** The identity of peaks that were quantified is shown in black. Minor peaks that were frequently below the limit of detection are shown in red. 18:1\* designates an unidentified isomer of 18:1.

**Figure S2. Principal component analysis (PCA) of genotype data matrix.** A. The 492 oat lines plotted along the first two principal components (PCs), colored with respect to line origin (AFRICore, Asoro, South America, North America, Europe, and Others). B. Analogous to A, except here the third and fourth PCs are plotted.

**Figure S3. Fatty acid phenotypes measured in two environments.** A. A heatmap of pairwise Spearman's rank correlations () between FAME measurements in each of the two environments, referred to as trait-environment combinations. Trait-environment combinations are ordered by hierarchical clustering, as pictured in B. Environments are differentiated by axis label color, with Env 1 in blue and Env 2 in gray. B. Hierarchical clustering of trait-environment combinations with environment indicated by label color as in A. C. A comparison of FAME distributions for measurements in the two environments. A heatmap (D) and dendrogram (E) of log-contrast transformed traits. F. A comparison of FAME proportions for measurements in the two environments.

**Figure S4. Correlations (*r*) and partial correlations (*pr*) between FAME BLUPs.** A. Overlaid histograms of the pairwise *r* and *pr* values between untransformed BLUPs, and heatmaps displaying pairwise *r* (B) and pairwise *pr* (C).

**Figure S5. Principal component analysis (PCA) of FAME BLUPs.** A. Oat lines plotted along the first and second (left) and third and fourth (center) principal components (PCs) from a PCA on the mean-centered and unit-variance scaled FAME best-linear unbiased predictors. Phenotypic variance explained plotted as a function of PC (right). Dots are shaded based on the total FAME BLUP of each line as indicated. B. Loadings of each FAME with respect to PC, with each FAME distinguished by a unique color (see legend). Note, saturated and unsaturated FAMEs are portrayed in warm and cool colors, respectively.

**Figure S6. Manhattan and quantile-quantile (QQ) plots for GWAS of the ten principal components (PCs).** Dotted lines denote the three significance thresholds considered, with a Bonferroni-corrected threshold of 5% in red, and 5 and 10% false-discovery rate (FDR) thresholds in light and dark gray, respectively. If a *p*-value passed the Bonferroni threshold, then the corresponding marker was portrayed in red.

**Figure S7. Manhattan and quantile-quantile (QQ) plots for GWAS of the ten FAME BLUPs.** Dotted lines denote the three significance thresholds considered, with a Bonferroni-corrected threshold of 5% in red, and 5 and 10% false-discovery rate (FDR) thresholds in light and dark gray, respectively. If a *p*-value passed the Bonferroni threshold, then the corresponding marker was portrayed in red.

**Figure S8. Manhattan and quantile-quantile (QQ) plots for GWAS of the ten quantile-transformed FAME BLUPs.** Dotted lines denote the three significance thresholds considered, with a Bonferroni-corrected threshold of 5% in red, and 5 and 10% false-discovery rate (FDR) thresholds in light and dark gray, respectively. If a *p*-value passed the Bonferroni threshold, then the corresponding marker was portrayed in red.

**Figure S9. Mean phenotypic differences between distinct homozygote classes at 152 significantly associated SNPs.** Genotype is plotted on the x-axis, with the mean number of phenotypic standard deviations away from the mean on the y-axis. Each centered and unit-variance scaled FAME BLUP (including total) is plotted, with warm colors for saturated and cool colors for unsaturated FAMEs. Total is indicated by a black line. The bold lines indicate that the pairwise t-test between genotype class means was significant at α=0.05 after correcting for multiple testing with a Bonferroni correction. To simplify the plots, only traits with significantly different means between genotypes are labeled. As lines with missing genotypes are excluded from these calculations, we present the genotype counts in the bottom right or left-hand corner of each plot.

# SUPPLEMENTAL TABLE LEGENDS

**Supplemental Table S1. Line-mean heritabilities (*hl*2) for untransformed BLUPs of 11 FAME traits.**

**Supplemental Table S2. Combined GWAS results for all significant SNPs detected at FDR of 10%.** For the traits, qn denotes quantile-normalized BLUPs, nt denotes non-transformed BLUPs. Linkage disequilibrium (LD) Subset, if 1, denotes SNPs that are in LD with at least 2 other significant SNPs across all analyses (see *Materials and Methods*). MAF = minor allele frequency. ∆*R*2*LR* is an approximation of the percent phenotypic variance explained (PVE) for each SNP expressed as the difference between the *R*2*LR* statistics (Sun *et al.* 2010) with or without the SNP included as a covariate in the GWAS model. See Supplemental Table 3 for *R*2*LR* statistics related to the multi-GWAS hits.

**Supplemental Table S3. Decomposition of variance explained by 148 SNPs detected using a ten trait multivariate GWAS model.** Linkage disequilibrium (LD) Subset, if 1, denotes SNPs that are in LD with at least two other significant SNPs across all analyses (see *Materials and Methods*). MAF = minor allele frequency. ∆*R*2*LR* is an approximation of the percent phenotypic variance explained (PVE) for each SNP expressed as the difference between the *R*2*LR* statistics (Sun *et al.* 2010) with or without the SNP included as a covariate in each trait's univariate model.