

Figure S1. Neighbor Joining tree of five cultivars from NCSU (Jackson Springs, NC) and NCGR (Corvallis, OR) based on SNP data (Ashrafi et al. Unpub.) and outgroup. *Vaccinium uliginosum* (L.) was used as an outgroup.

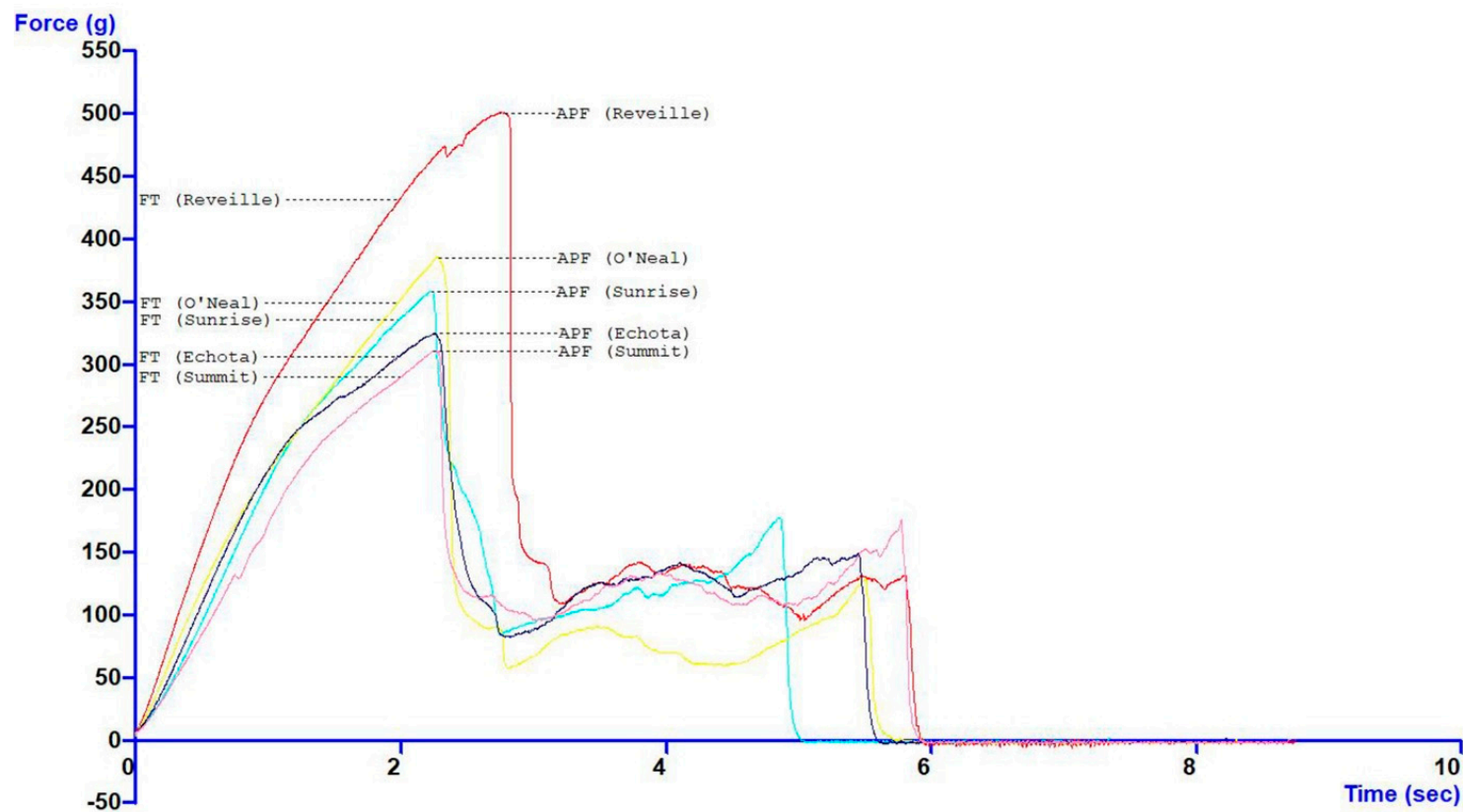


Figure S2. Texture analyzer graphical display of fruit puncture of genotypes 'Echota', 'O'Neal', 'Reveille', 'Summit', and 'Sunrise' and their respective force at target (FT) acquisition points, and absolute positive force (APF) puncture points for an individual fruit. Distance at positive force (DPF) (mm) is the distance the fruit depressed between FT and APF.

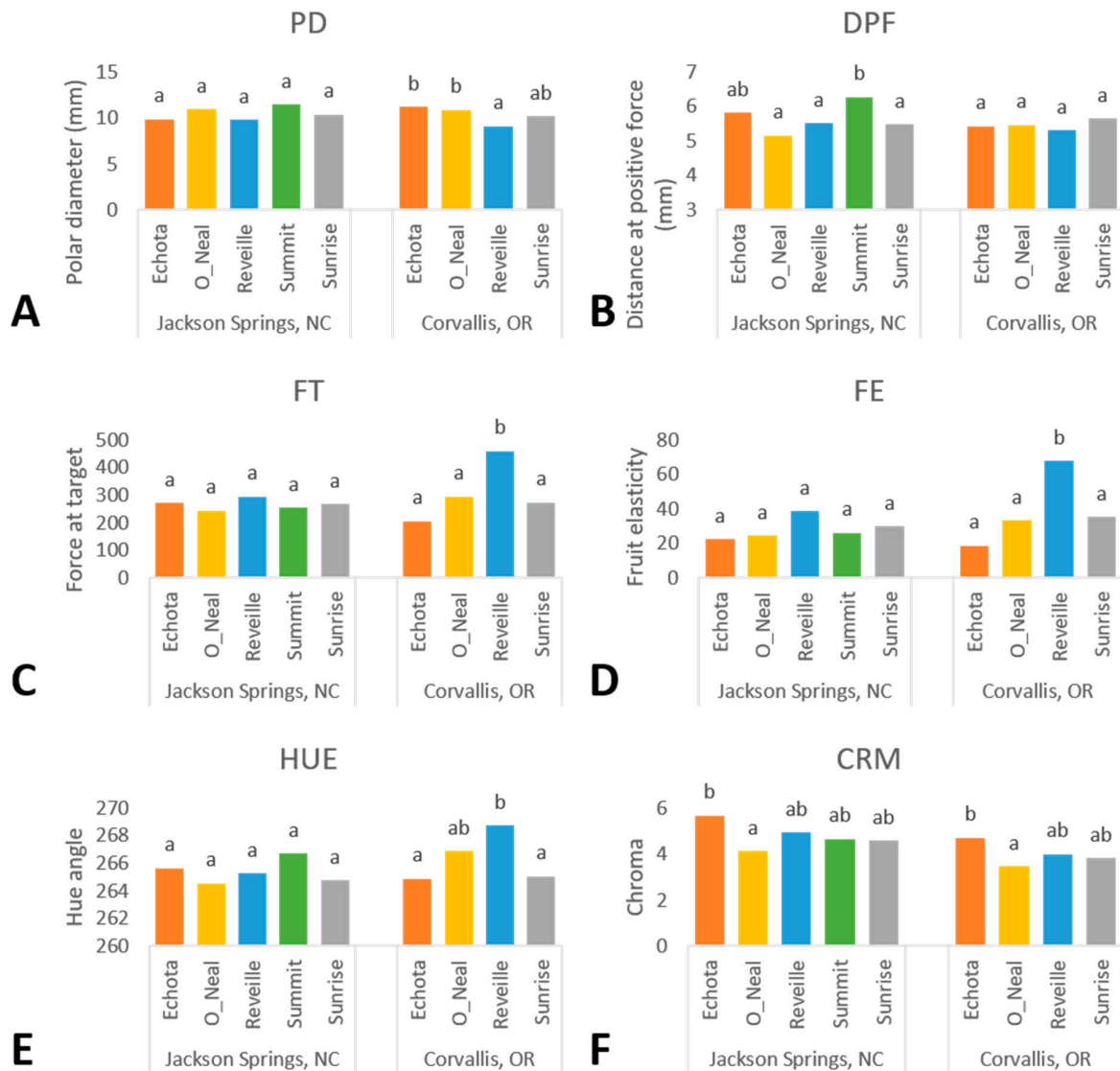


Figure S3. Genotypic means of phenotypic traits including polar diameter (PD) (A), distance at positive force (DPF) (B), force at target (FT) (C), fruit elasticity (FE) (D), hue angle (HUE) (E), and chroma (CRM) (F) evaluated within environments Corvallis and Jackson Springs using Models 1 and 2 in PROC GLIMMIX (SAS v9.4, Cary). Means between genotypes followed by the same letter within an environment are not significantly different using the least squares means (LSMEANS) Tukey HSD multiple comparisons procedure ($P < 0.05$). 'Summit' was excluded in Corvallis statistical analysis due to the unbalanced harvests in Year 2.

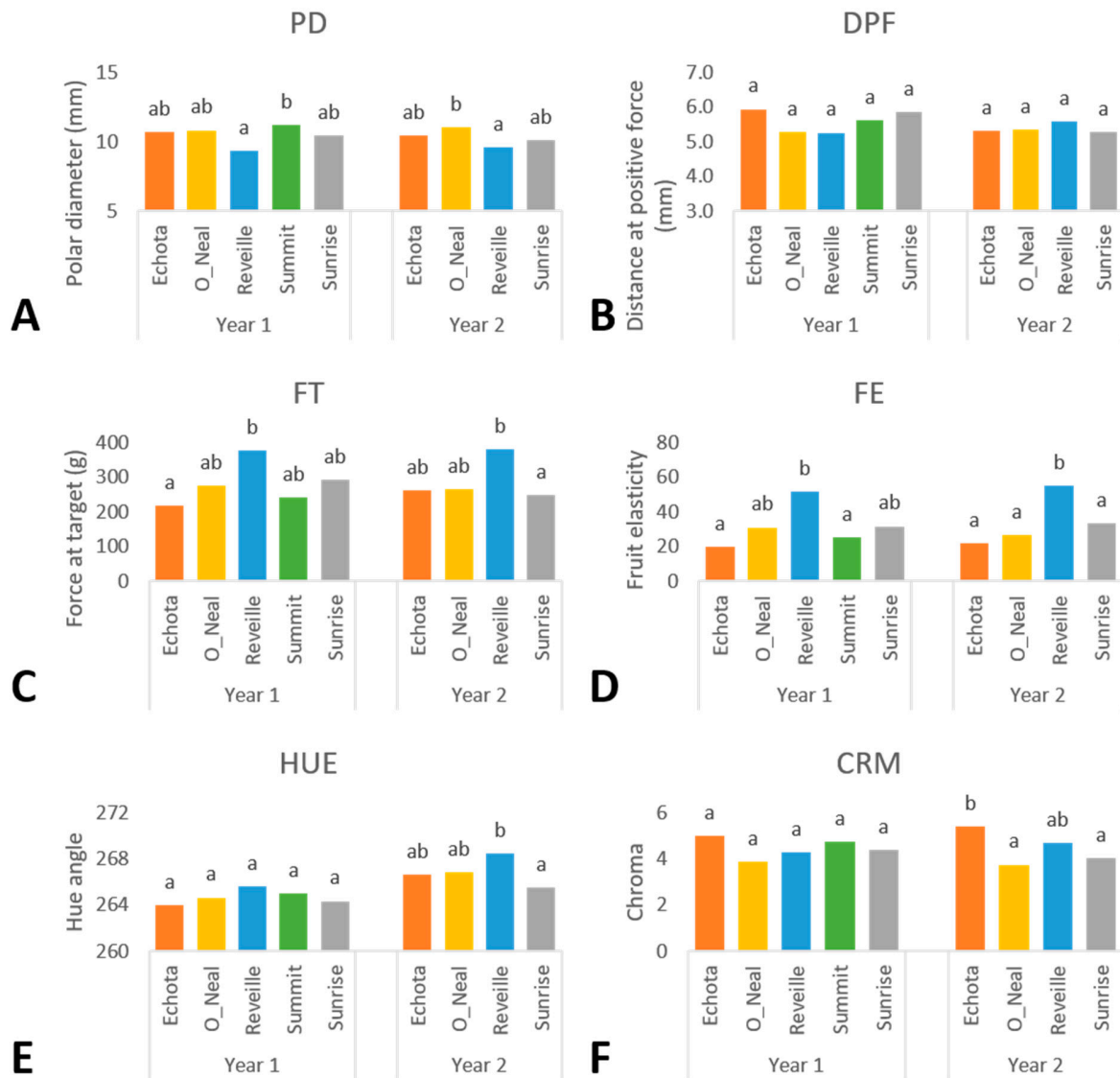


Figure S4. Genotypic means of phenotypic traits including polar diameter (PD) (A), distance at positive force (DPF) (B), force at target (FT) (C), fruit elasticity (FE) (D), hue angle (HUE) (E), and chroma (CRM) (F) evaluated within years 2019 and 2020 using Models 1 and 2 in PROC GLIMMIX (SAS v9.4, Cary). Means between genotypes followed by the same letter within a year are not significantly different using the least squares means (LSMEANS) Tukey HSD multiple comparisons procedure ($P < 0.05$). ‘Summit’ was excluded in Year 2 statistical analysis due to the unbalanced harvests in Corvallis.