



Figure 1-figure supplement 9: Local PCA analysis and identification of candidate genes using diversity parameters. (a) Relationship between genomic windows visualized using multidimensional scaling. (b) Two MSD coordinates of each window along the quinoa genome, candidate genomic regions are marked in different colors, which correspond with the colors on figure a. candidate regions are identified as the closest 1% window with the most extreme MDS coordinates. (c, d, e, f, and g) Principal component analysis using SNPs located within the candidate genomic regions identified by different analyses. (h and i) Venn diagrams represent the comparison of candidate genes identified by different analyses.