Multiple methods exist to detect hard and soft selective sweeps, but most of these are limited to phased haplotype data, and cannot distinguish between hard and soft sweeps. Here, we apply the expected haplotype homozygosity measures H12 and H2/H1 of Garud *et al*. (2015) to multilocus genotype data, defining analogous statistics G12 and G123, paired with G2/G1. Methods applied to multilocus genotypes maintain comparable power and classification ability to the haplotype approach, and recover the same selection candidates in empirical data. Our approach will thus be invaluable in localizing and classifying adaptive targets in model- and non-model study systems.