Marker's QC stats Correlations: missing & heterozygosity = -0.21200 mean coverage 150 100 50 0 150 mean ref depth 100 50 0 60 mean alt depth 40 20 0 0.3 missing genotypes 0.2 0.1 0.0 150 Statistics MAC 100 50 0 observed heterozygosity 0.6 0.4 0.2 0.0 1.0 inbreeding coefficient (Fis) 0.5 0.0 -0.5 **-**60 SNP position on read 40 20 1.050 1.025 SNPs per locus 1.000 0.975 0.950 -