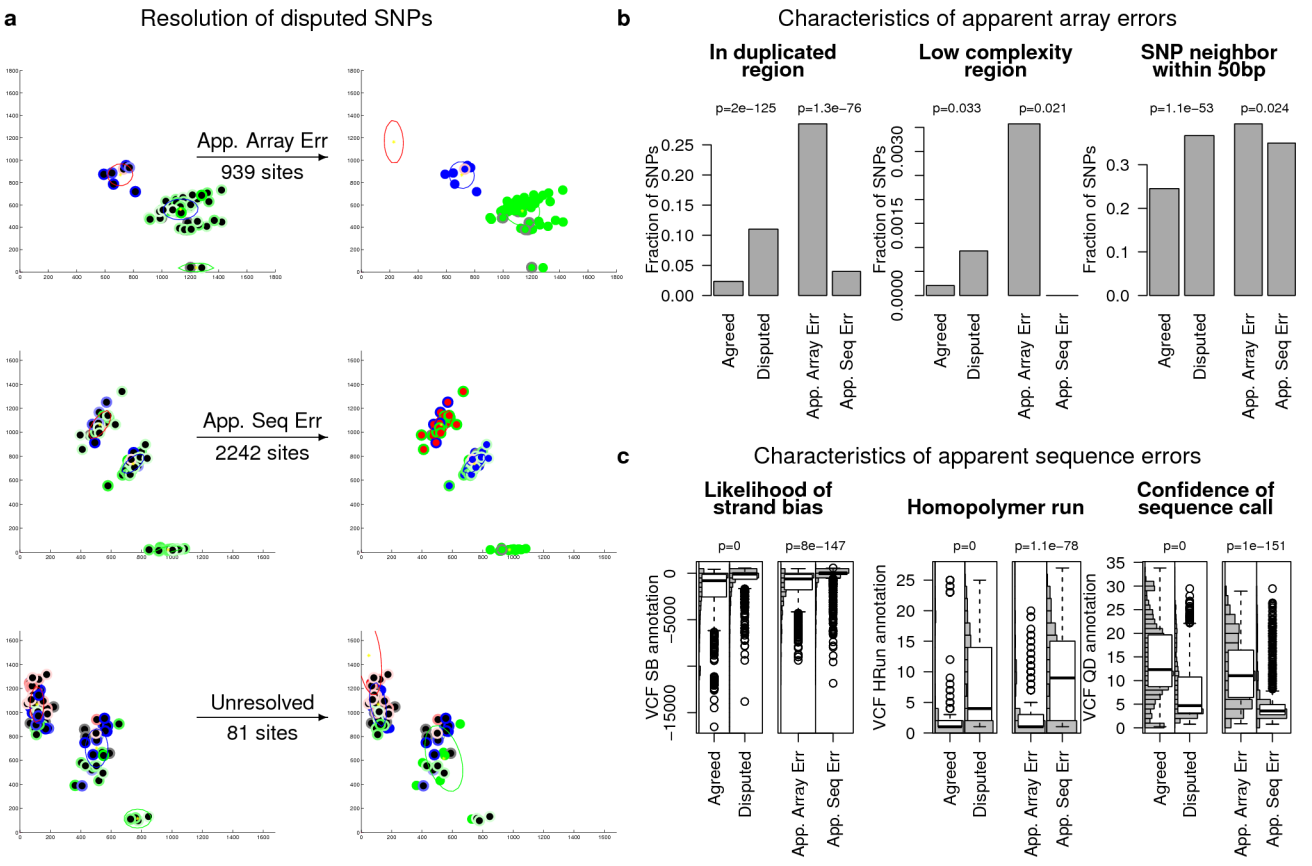
a
Resolution of disputed SNPs
App. Array Err
939 sites
App. Seq Err
2242 sites
Unresolved
81 sites
b
Characteristics of apparent array errors
In duplicated region
Low complexity region
SNP neighbor within 50bp
p=2e−125
p=1.3e−76
p=0.033
p=0.021
p=1.1e−53
p=0.024
Fraction of SNPs
Agreed
Disputed
App. Array Err
App. Seq Err
c
Characteristics of apparent sequence errors
Likelihood of strand bias
Homopolymer run
Confidence of sequence call
p=0
p=8e−147
p=0
p=1.1e−78
p=0
p=1e−151
VCF SB annotation
VCF HRun annotation
VCF QD annotation