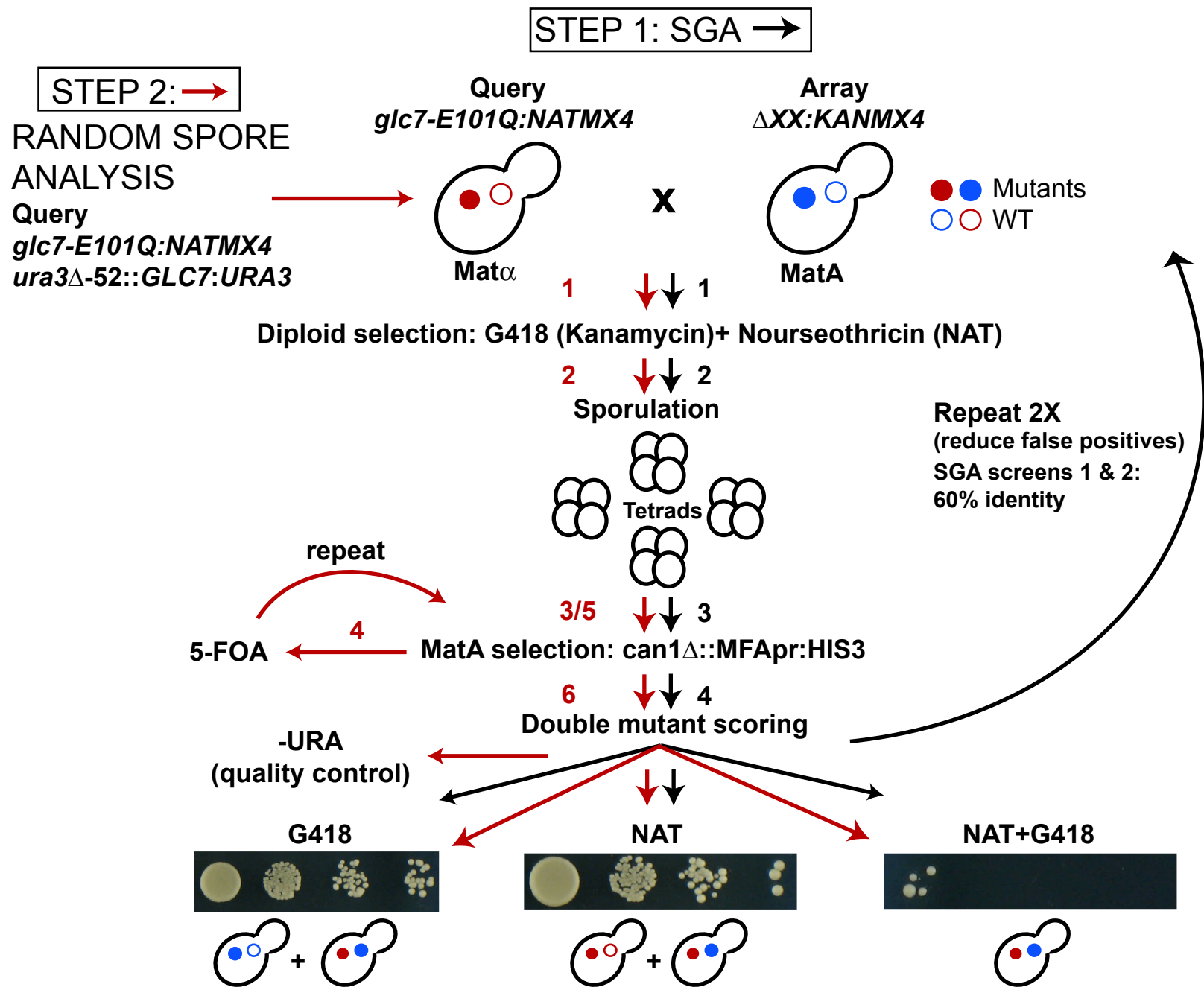




-URA
(quality control)

G418

NAT

NAT+G418

Additional File 3: SGA and random spore analysis methods. In the modified SGA confirmation scheme (red arrows) mutants found in the screen were mated with a *glc7-E101* strain bearing a wild type *GLC7* allele integrated at the *URA3* locus. After diploid selection (1), sporulation (2) and haploid *MATa* selection (3), 5-FOA resistant haploid *MATa* were selected (4,5). Finally, mutant scoring was made by spotting on G418 (both array and double mutant selection), Nourseothricin (NAT; both query and double mutant selection) and Nourseothricin + G418 (NAT+G418; double mutant selection).