1. Whole genome shotgun sequencing
   - Selection of 2 highly recombinant progeny lines
   - WGS using 454/Roche GS-FLX technology

2. Reference genome mapping
   a) Map parental genomes
   - Uniquely mapped
   - 90% identity
   b) Map progeny genomes
   - NCBI Trace Archive
   - PlasmoDB (v5.4) [27]

3. SNP filtering and allele calling
   Filtering criteria:
   - Read depth
   - Base quality score
   - Single SNP per position
   - Identify SNPs between parental genomes
   - Poor parental base call
     1. Base call absent in one or both parents
     2. Quality Score <30
     3. Read Count <2
     4. Multiple SNPs per position
   - Good parental base call
     1. Base calls present for both parents
     2. Quality Score ≥30
     3. Read Count ≥2
   - Identify SNPs between progeny genomes
   - Poor progeny base call
     1. Quality score <30
     2. Read count <10
     3. Multiple SNPs per position
   - Good progeny base call
     1. Quality score ≥30
     2. Read count ≥10
   - Identify allele, based on parental SNP

Parents
- HB3, Dd2

Genetic cross
- Wellems et al. 1990 [24]

Progeny recombinants
- SC05
- 7C126

Shotgun libraries
- GS-FLX technology
- 454/Roche

Reference genome
- (3D7)

PlasmoDB (v5.4) [27]