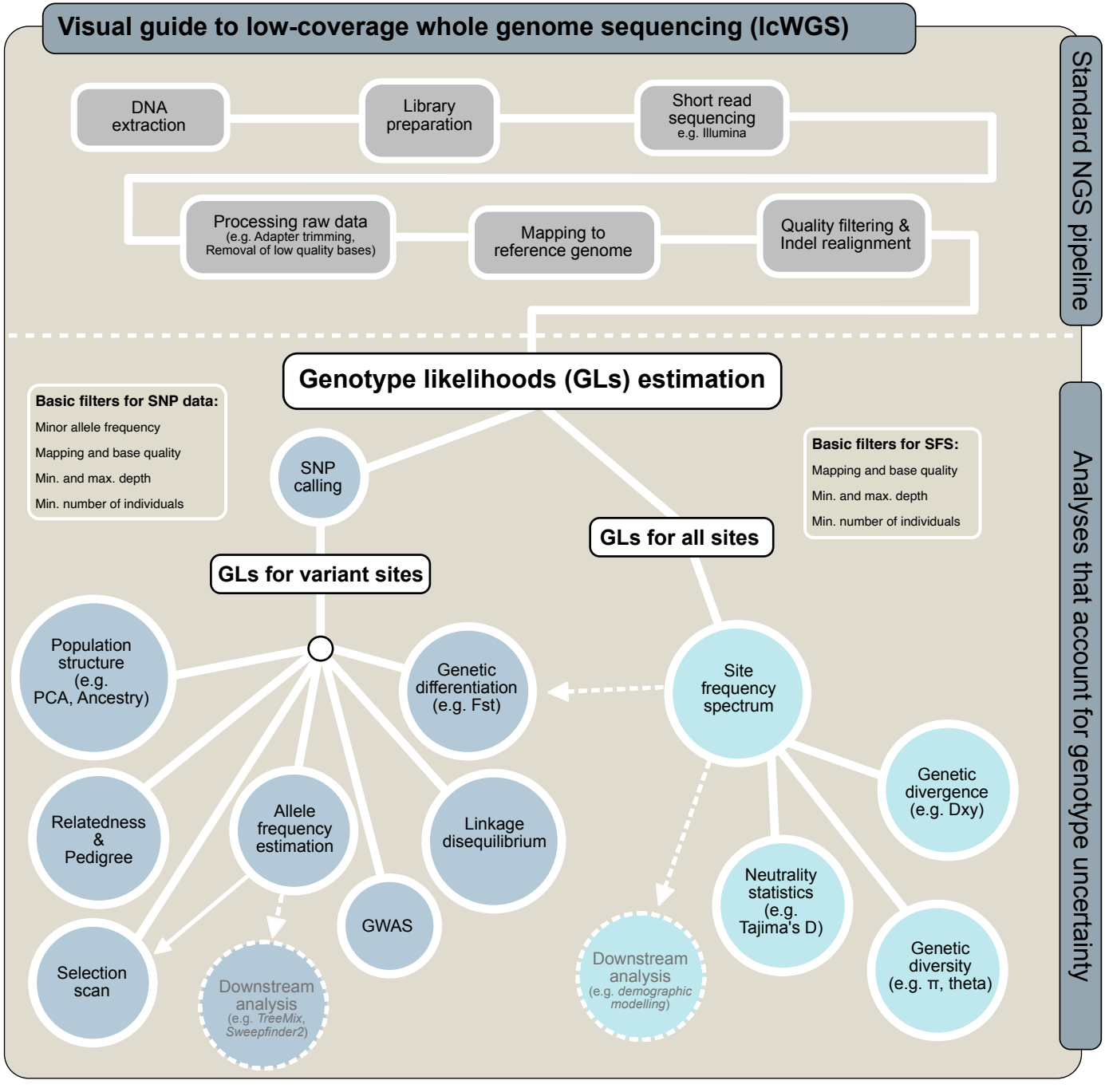
Visual guide to low-coverage whole genome sequencing (lcWGS)
Standard NGS pipeline
DNA extraction
Library preparation
Short read sequencing
e.g. Illumina
Processing raw data
(e.g. Adapter trimming, Removal of low quality bases)
Mapping to reference genome
Quality filtering & Indel realignment
Genotype likelihoods (GLs) estimation
Basic filters for SNP data:
Minor allele frequency
Mapping and base quality
Min. and max. depth
Min. number of individuals
SNP calling
GLs for variant sites
GLs for all sites
Basic filters for SFS:
Mapping and base quality
Min. and max. depth
Min. number of individuals
Population structure (e.g. PCA, Ancestry)
Genetic differentiation (e.g. Fst)
Relatedness & Pedigree
Allele frequency estimation
Linkage disequilibrium
Selection scan
GWAS
Downstream analysis
(e.g. TreeMix, Sweepfinder2)
Site frequency spectrum
Genetic divergence (e.g. Dxy)
Neutrality statistics (e.g. Tajima's D)
Genetic diversity (e.g. π, theta)
Downstream analysis
(e.g. demographic modelling)
Analyses that account for genotype uncertainty