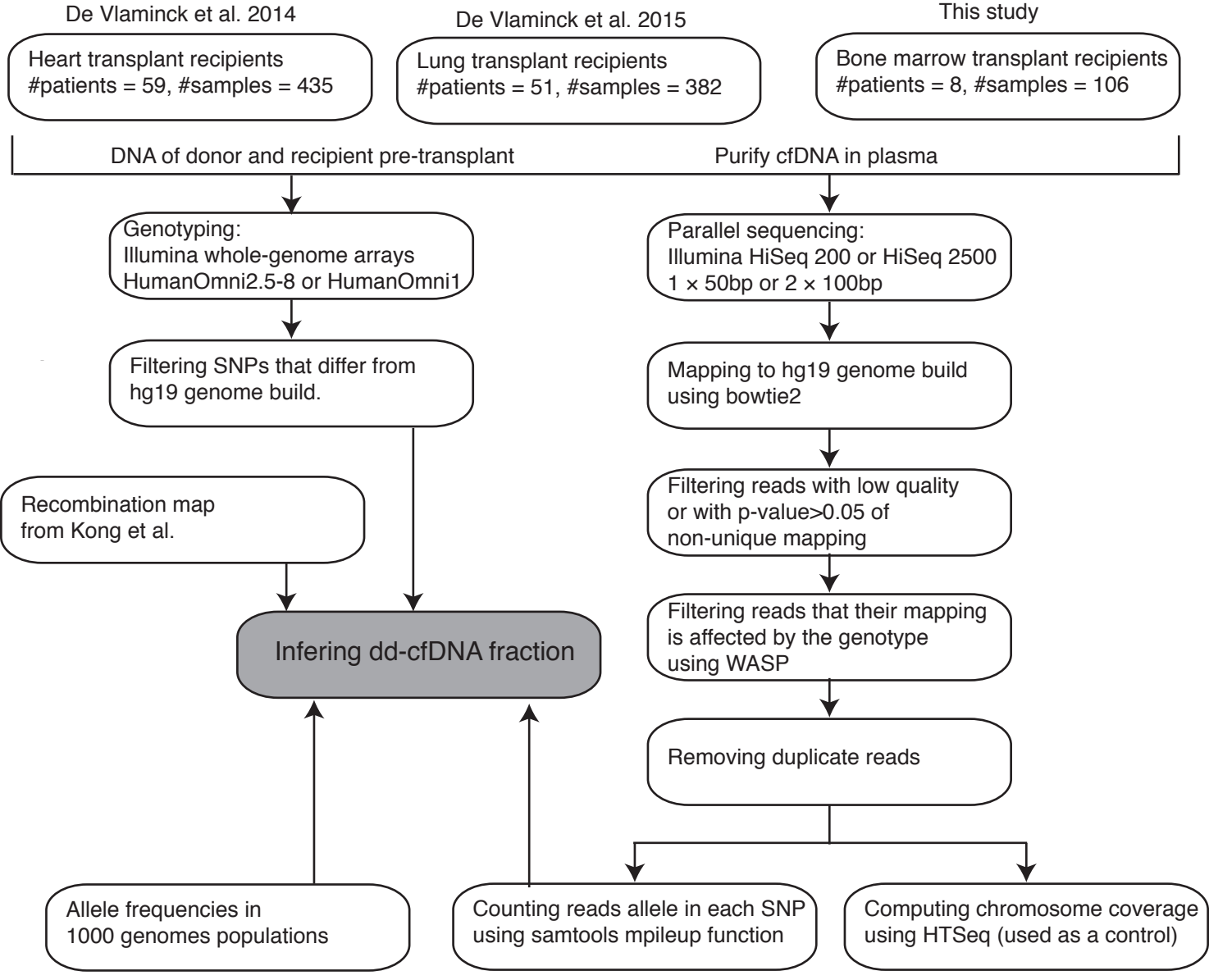
De Vlaminck et al. 2014
Heart transplant recipients
#patients = 59, #samples = 435
De Vlaminck et al. 2015
Lung transplant recipients
#patients = 51, #samples = 382
This study
Bone marrow transplant recipients
#patients = 8, #samples = 106
DNA of donor and recipient pre-transplant
Purify cfDNA in plasma
Genotyping:
Illumina whole-genome arrays
HumanOmni2.5-8 or HumanOmni1
Filtering SNPs that differ from
hg19 genome build.
Recombination map
from Kong et al.
Parallel sequencing:
Illumina HiSeq 200 or HiSeq 2500
1 × 50bp or 2 × 100bp
Mapping to hg19 genome build
using bowtie2
Filtering reads with low quality
or with p-value>0.05 of
non-unique mapping
Filtering reads that their mapping
is affected by the genotype
using WASP
Removing duplicate reads
Infering dd-cfDNA fraction
Allele frequencies in
1000 genomes populations
Counting reads allele in each SNP
using samtools mpileup function
Computing chromosome coverage
using HTSeq (used as a control)