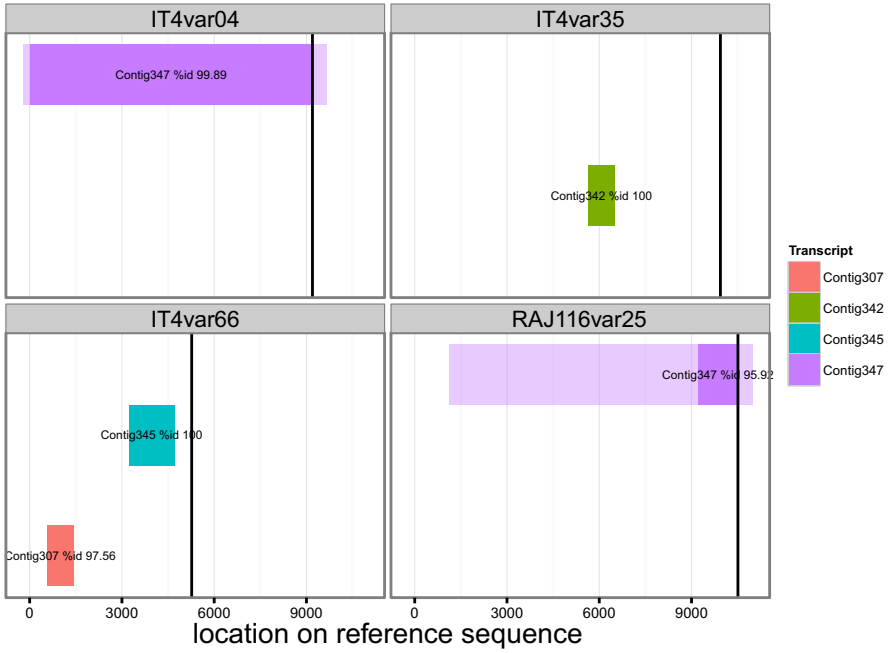
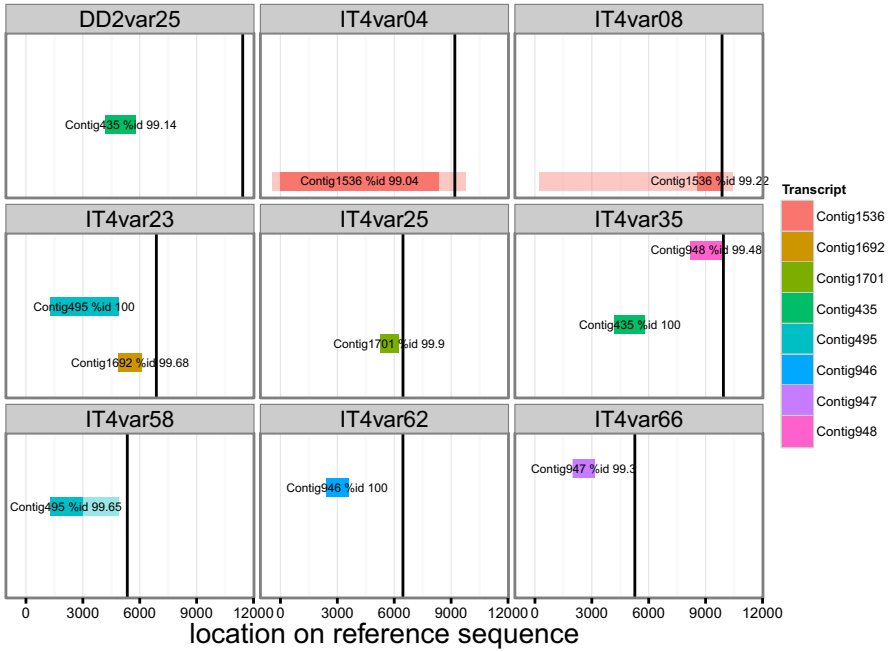
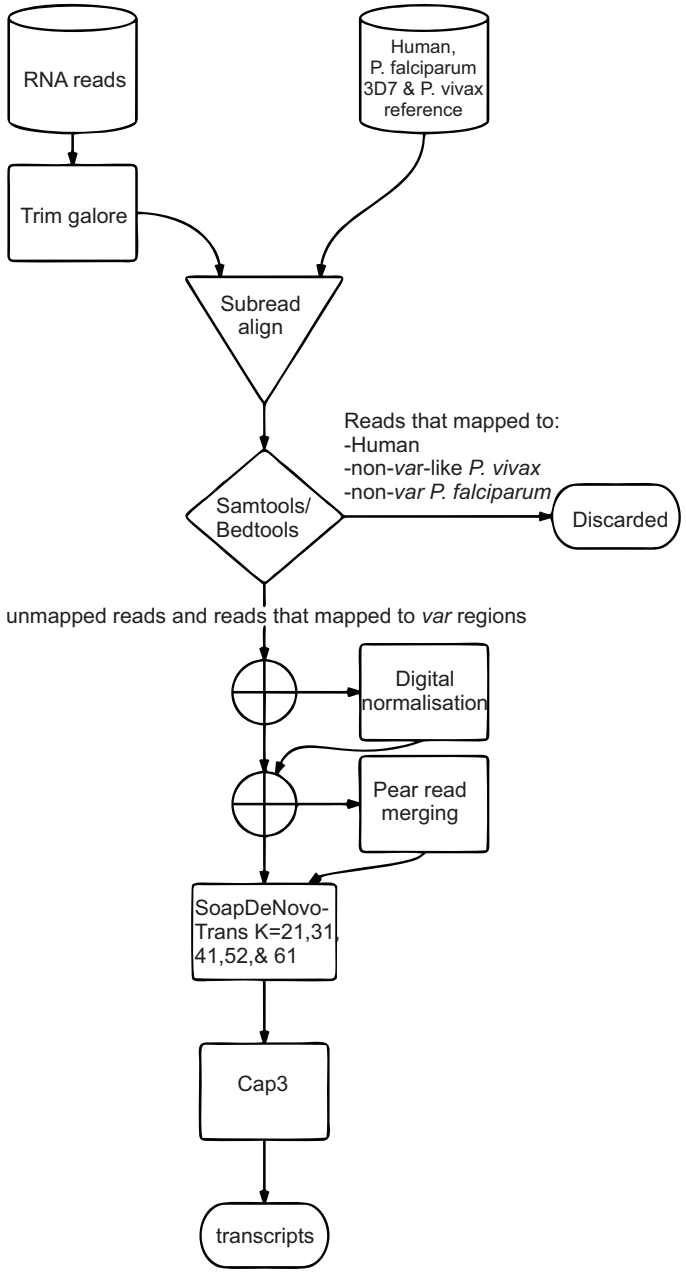
s2a)


IT4var04
IT4var35
IT4var66
RAJ116var25
Contig347 %id 99.89
Contig342 %id 100
Contig345 %id 100
Contig307 %id 97.56
Contig347 %id 95.92
Transcript
Contig307
Contig342
Contig345
Contig347
0
3000
6000
9000
location on reference sequence

s2b)


DD2var25
IT4var04
IT4var08
IT4var23
IT4var25
IT4var35
IT4var58
IT4var62
IT4var66
Contig435 %id 99.14
Contig1536 %id 99.04
Contig1536 %id 99.22
Contig495 %id 100
Contig1692 %id 99.68
Contig1701 %id 99.9
Contig948 %id 99.48
Contig435 %id 100
Contig495 %id 99.65
Contig946 %id 100
Contig947 %id 99.3
Transcript
Contig1536
Contig1692
Contig1701
Contig435
Contig495
Contig946
Contig947
Contig948
0
3000
6000
9000
12000
location on reference sequence

s2c)


RNA reads
Human, P. falciparum 3D7 & P. vivax reference
Trim galore
Subread align
Reads that mapped to:
-Human
-non-var-like P. vivax
-non-var P. falciparum
Samtools/ Bedtools
Discarded
unmapped reads and reads that mapped to var regions
Digital normalisation
Pear read merging
SoapDeNovo-Trans K=21,31, 41,52,& 61
Cap3
transcripts