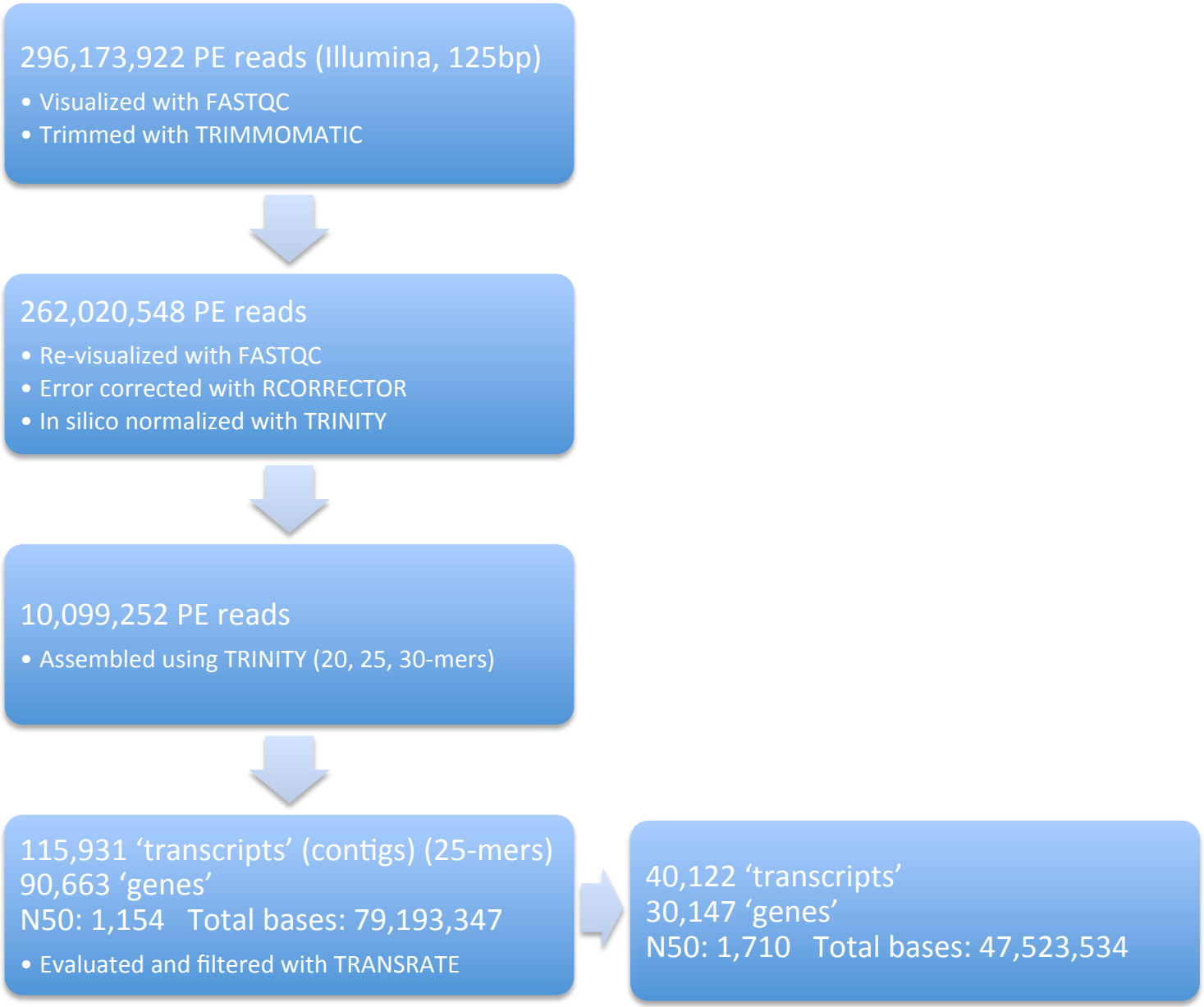
Idotea Assembly Summary



Raw Assembly

115,931 ‘transcripts’
90,663 ‘genes’
N50: 1,154 Total bases: 79,193,347

Completeness determined with BUSCO
* 68% found (many duplicates)

Coding sequences identified with TRANSDECODER
* 33,731 ‘peptides’ identified

Annotated with PANNZER (UniProtKB)
* 14,288 annotations (many duplicates)
* 1,330,727 GO terms assigned

Filtered Assembly

40,122 ‘transcripts’
30,147 ‘genes’
N50: 1,710 Total bases: 47,523,534

Completeness determined with BUSCO
* 61% found (many duplicates)

Coding sequences identified with TRANSDECODER
* 21,439 ‘peptides’ identified

Are the apparent duplicate genes paralogs or are they alleles?

Next...

- cd-hit will be run on all 3 assemblies to maximize finding potential transcripts
  - This will collapse potential paralogs, but with Idotea's high level of polymorphism many may actually be alleles
  - Duplicate BUSCOs and annotations should be reduced