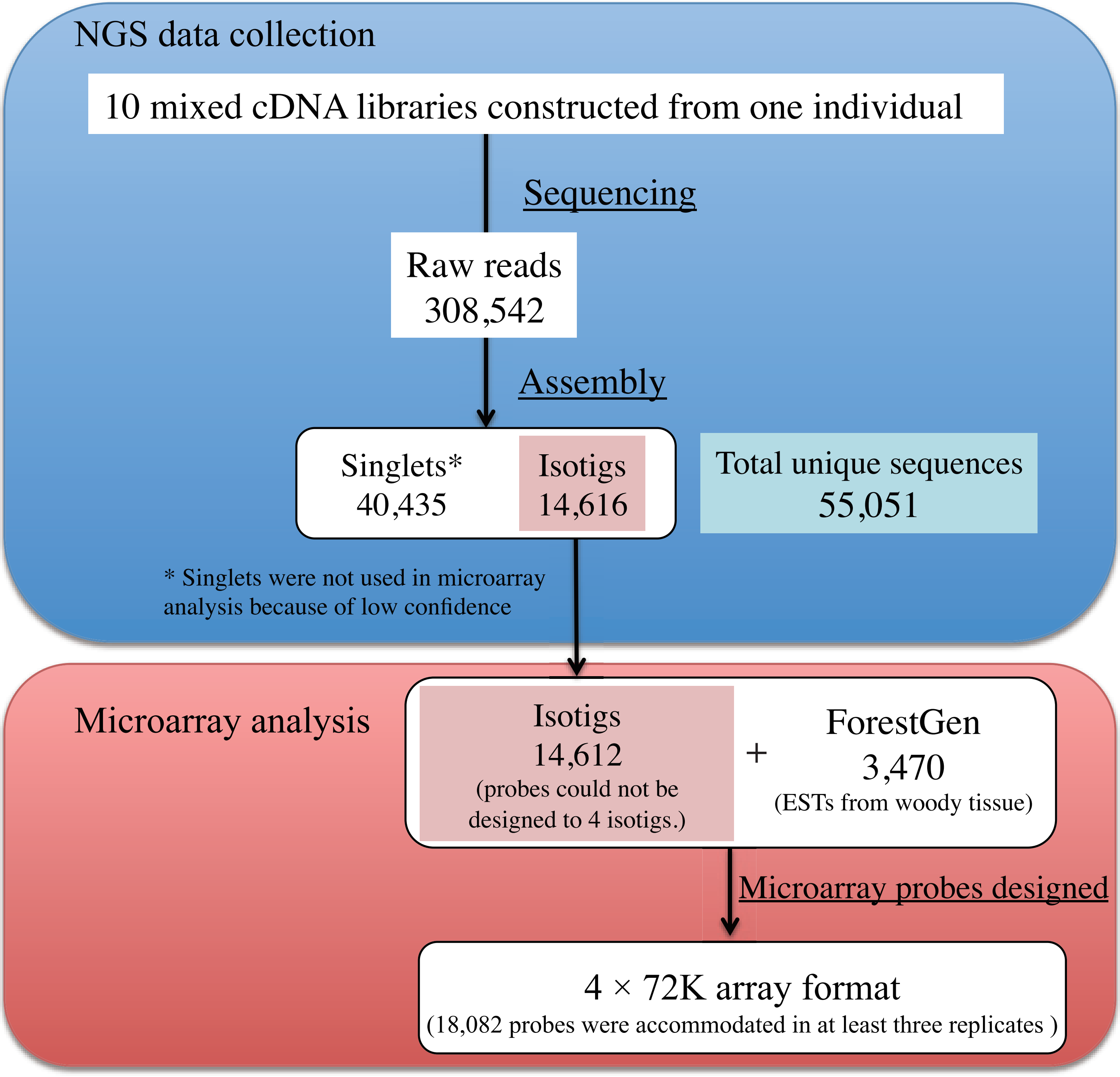
NGS data collection
10 mixed cDNA libraries constructed from one individual
Sequencing
Raw reads
308,542
Assembly
Singlets*
40,435
Isotigs
14,616
Total unique sequences
55,051
* Singlets were not used in microarray analysis because of low confidence
Microarray analysis
Isotigs
14,612
(probes could not be designed to 4 isotigs.)
+
ForestGen
3,470
(ESTs from woody tissue)
Microarray probes designed
4 × 72K array format
(18,082 probes were accommodated in at least three replicates)