906,300 reads (cv. Asha)

- 35,204 contigs

790,424 reads (cv. UPAS-120)

- 30,147 contigs

- Assembly using 454 “Newbler” assembler

- Assembly using Lasergene SeqMan Pro™ v 8.0.12

- SSR discovery using BatchPrimer3

- SSR primers designed using BatchPrimer3

- Primers synthesized for longer SSR (n ≥ 18 bp)

- PCR amplification validated in cv. Asha

- Polymorphism tested on 8 varieties

- 550 expected size

- 51 larger than expected size

- 18 multiple bands

- 153 did not amplify

- 71 polymorphic

- 479 monomorphic