Initially filtered SNVs

SNPiR-filtered SNVs

Filtered Variants

Detection of somatic mutations as an union set derived both from VarScan2 and MuTect

Filtered SNVs

Overlap SNVs for comparison of heterogeneity in expressed genotypes between H358 and PDXs

Overlap SNVs for identification of tumor-specific non-synonymous mutations

Filtering potential RNA-seq false positive variants found at 5’ read ends, in repetitive regions, within 4 bp of splice junctions, in homopolymers and in known RNA-editing sites using SNPiR package

Initially filtered SNVs

Uniquely mapped reads

De-duplication, Split ‘N’ Trim, MQ Reassignment, Indel-Realignment & Base Recalibration

Filtered & Recalibrated reads

Variant calling using GATK HaplotypeCaller and filtration

Overlap SNVs for comparison of heterogeneity in expressed genotypes between H358 and PDXs

Overlap fraction to WES Bulk cells

Overlap fraction to dbSNP137

- Initially filtered SNVs
- SNPiR-filtered SNVs
- SNVs overlapped with WES