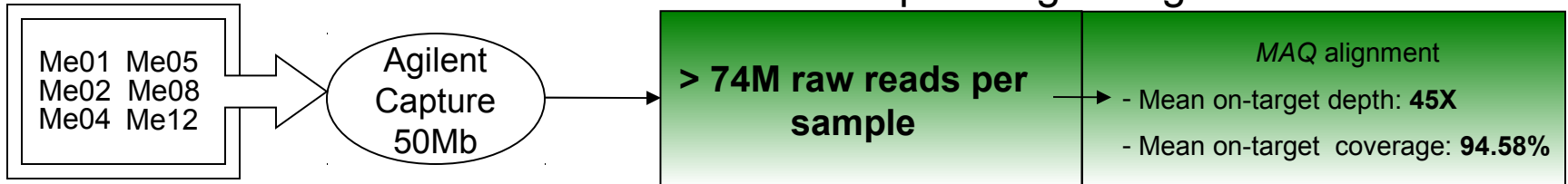


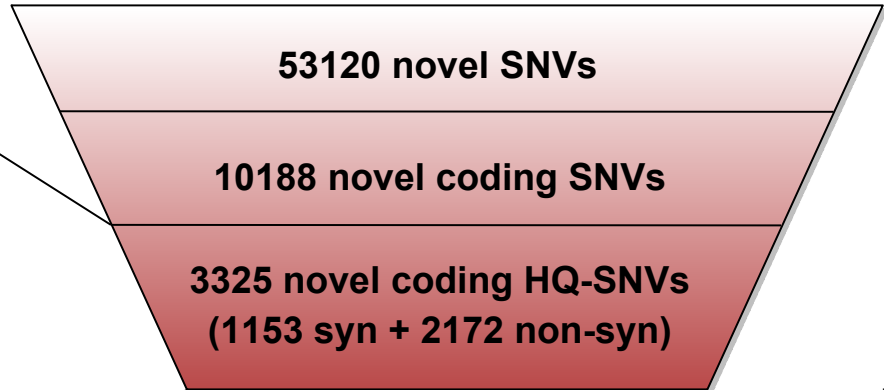
Sequencing & Alignment



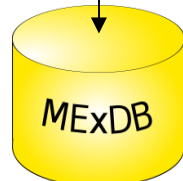
High-Quality Filtering Criteria

- Depth \geq 15
- QUAL \geq 150
- AF \geq 20%
- Coding Novel SNV
- Clinical rs (dbSNP132)
- Filtered out HLA genes
- Filtered out homologous genes
- Internal exome DB filtering

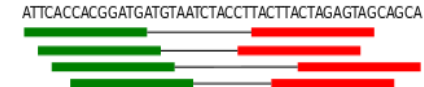
QUAL= SNV Call PHRED quality;
AF= Variation Allele Frequency



SIFT prediction tool



gBrowse



1770 genes with at least 1 non-syn HQ-SNV