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PCR based target enrichment for variant confirmation, gene panels and multiplex PCR sample tracking in a whole exome sequencing workflow

Product portfolio

Our offering comprises best-in-class PCR assays for targeted resequencing of all human canonical exons of protein coding genes (both Sanger and massively parallel sequencing)

WGS/WES variant validation

1 million PCR assays, of which over 10,000 have been validated for variant confirmation

Sample ID panel

An optimized 50-SNP multiplex panel to identify your samples in a single PCR reaction

NGS gap filling

Extend your preferred enrichment method with our assays to fill low coverage regions

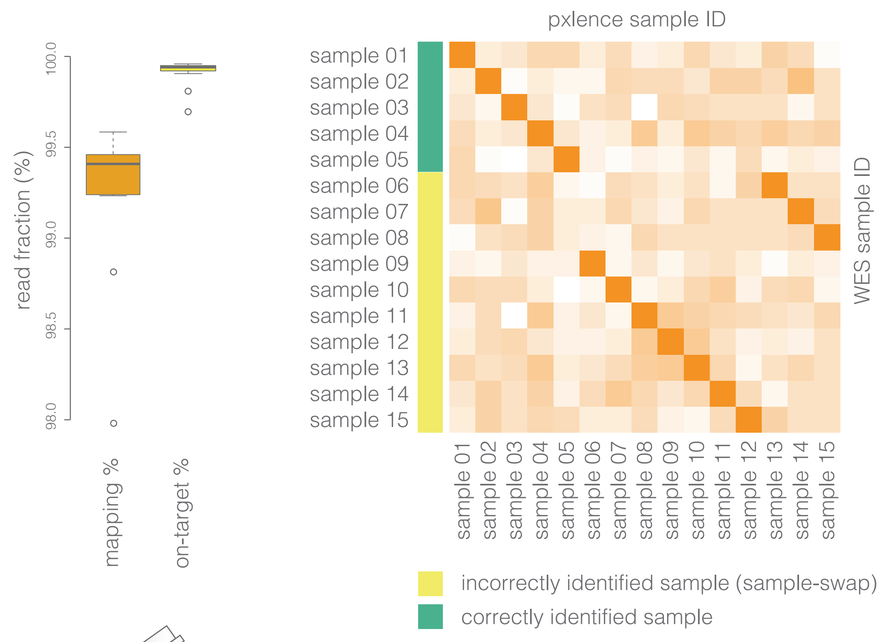
All our assays have been thoroughly validated *in silico*, resulting in an off-the-shelf PCR success rate of >97%. The optimized design parameters allow uniform PCR conditions while ensuring uniform sequencing coverage.

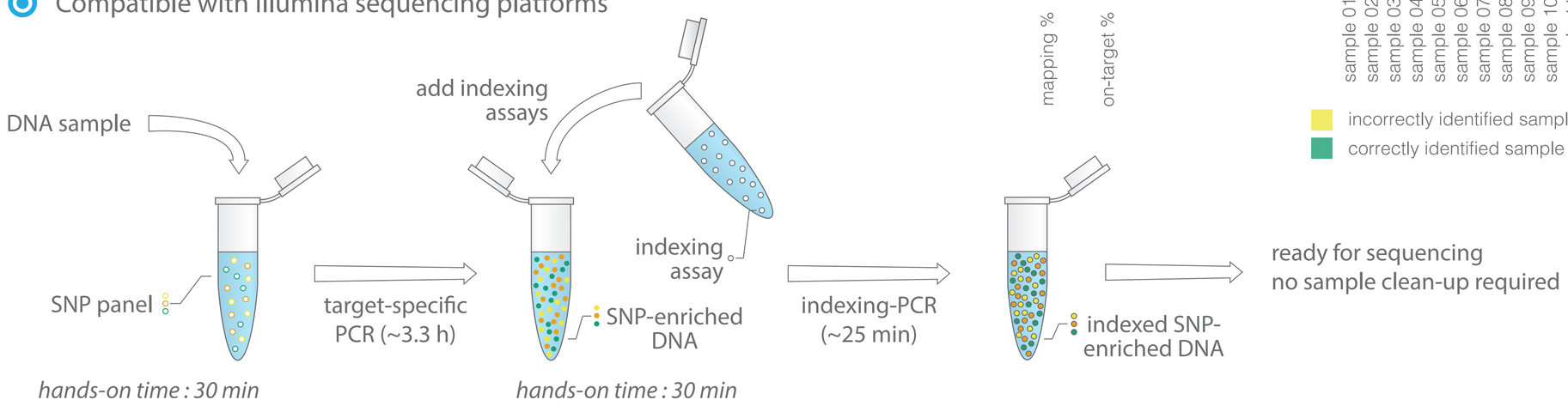
- ✓ Avoid SNPs in primer annealing sites
- ✓ Minimize secondary structures
- ✓ Maximize assay specificity
- ✓ Optimize GC content, annealing temperature and other parameters

Single-tube 2-step multiplex PCR sample ID sequencing panel

Characteristics

- Easy-to-use protocol (automatible)
- 1 h hands-on time, 5 h total time
- 50 polymorphic SNPs, including 5 gender markers
- No clean-up prior to sequencing
- Only 4 pipeting steps
- Works with high-quality, FFPE and liquid biopsy samples
- Compatible with Illumina sequencing platforms



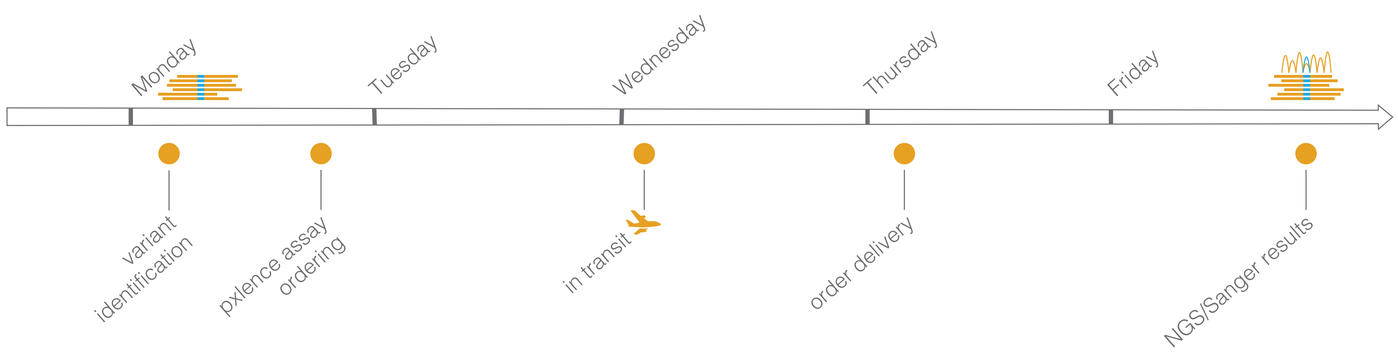


Best-in-class assays for WGS/WES variant validation

Almost 1 million PCR assays for targeted resequencing of all human canonical exons of protein coding genes

Our two available assay databases - a long (350-750 bp) and short (125-275 bp) assay-set - cover over 97.99% and 98.71% of the human canonical exome, respectively. In approximately 94.01% of these assays, no SNPs are present in the primer annealing sites. For the remaining assays, SNP(s) are located outside the critical 5 bp 3' region. Over 77% of the assays, no aspecific annealing sites harboring less than 3 mismatches can be identified, resulting in a minimal non-specific product generation.

Our short assay delivery times allows WGS/WES variant identification to validation in approximately one week.



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