PGDx

# CancerSELECT™ 125

# A pan-cancer assay to accurately identify tumor-specific alterations

## CancerSELECT 125 TEST

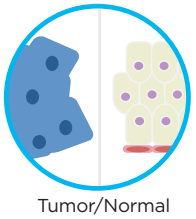
- Provides clinically actionable information to inform treatment decisions
- Reports microsatellite instability status (MSI) to assess potential response to checkpoint inhibitor therapies[1,2,3]


**Microsatellite Instability Status**

- Provides highly accurate information to increase confidence in treatment decisions
- Matched Normal sequencing accurately filters out germline variants[4] to increase assurance that identified alterations are somatic
- Comprehensive clinical annotation of all reported alterations, including FDA-approved therapies, clinical trials, and published literature
- Gene selection based on:
  - Clinical actionability
  - Known and likely regions for acquired resistance
  - Biological and functional relevance

## IN ADDITION TO TUMOR-ONLY SEQUENCING, CancerSELECT 125 OFFERS THE INCREASED CONFIDENCE OF A TUMOR/NORMAL OPTION

Tumor Only



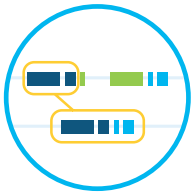
Tumor/Normal

## CancerSELECT 125 IDENTIFIES TUMOR-SPECIFIC (SOMATIC) MUTATIONS, AMPLIFICATIONS, AND REARRANGEMENTS WITH HIGH ACCURACY

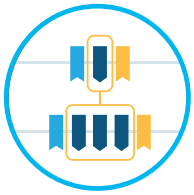
**Sequence Mutations**


Single Base Substitutions


Insertions and Deletions



**Genomic Rearrangements**



**Amplifications**

| CancerSELECT 125 ASSAY PERFORMANCE | | | | |
|---|---|---|---|---|
| Performance Specification | Sequence Mutations (≥5% MAF) | Amplification (≥4-fold or 8 copies) | Rearrangements (≥20% tumor content) | MSI-H |
| Sensitivity | >99% | >99% | >99% | >99% |
| Specificity | >99.9999%* | >99% | >99% | >99% |

*Per-base specificity provided for sequence mutation analyses (979,072 total bases evaluated in the 125-targeted-gene panel)

LEARN MORE ABOUT CancerSELECT 125 AT PERSONALGENOME.COM

FOR MORE DETAILS OR NOTIFICATION OF PRODUCT AVAILABILITY FOR ORDER, CONTACT INFO@PERSONALGENOME.COM

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## GENES EVALUATED IN CancerSELECT 125

*Full coding analysis in 117 well-characterized cancer genes, as well as †amplification analysis for 41 genes.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ABL1 | CDK6† | ERG | GNA11 | KRAS† | MYD88 | PMS2 | SMAD4 |
| AKT1† | CDKN2A | ESR1 | GNAQ | MAP2K1 | NBN | POLD1 | SMARCB1 |
| ALK† | CHEK2 | EZH2 | GNAS | MAP2K2 | NF1 | POLE | SMO |
| AR† | CREBBP | FANCA | HDAC2 | MEN1 | NOTCH1 | PTCH1 | SRC |
| ATM | CSF1R† | FANCD2 | HNF1A | MET† | NPM1 | PTEN | STK11 |
| ATRX | CTNNB1 | FANCG | HRAS | MLH1 | NRAS | PTPN11 | TERT |
| AXL† | DDR2 | FBXW7 | IDH1 | MLH3 | NTRK1† | RAD51 | TET2 |
| BCL2† | DNMT3A | FGFR1† | IDH2 | MPL | NTRK2† | RAF1 | TP53 |
| BRAF† | EGFR† | FGFR2† | JAK1 | MRE11A | NTRK3† | RARA | TSC1 |
| BRCA1† | EP300 | FGFR3† | JAK2† | MSH2 | PALB2 | RB1 | TSC2 |
| BRCA2 | EPHA2 | FGFR4† | JAK3 | MSH6 | PDGFRA† | RET† | VEGFA† |
| CCND1† | ERBB2† | FLT1† | KDR† | MST1R† | PDGFRB† | RNF43 | VHL |
| CCND2† | ERBB3† | FLT3† | KEAP1 | MTOR | PIK3CA† | ROS1† | |
| CCND3† | ERBB4 | FLT4† | KIT† | MYC† | PIK3CB† | RUNX1† | |
| CDK4† | ERCC3 | FOXL2 | KMT2A | MYCN† | PIK3R1 | SDHB | |

Rearrangements analyses for selected regions of 29 well-characterized cancer genes.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ALK | BRAF | EGFR | ETV5 | FGFR2 | NTRK2 | RAF1 | TMPRSS2 |
| AXL | BRCA1 | ERG | ETV6 | FGFR3 | NTRK3 | RARA | |
| BCR | BRCA2 | ETV1 | EWSR1 | MYC | PDGFRA | RET | |
| BCL2 | CBFB | ETV4 | FGFR1 | NTRK1 | PDGFRB | ROS1 | |

Microsatellite analysis for 5 well-characterized mononucleotide sequences

| | | | | |
|---|---|---|---|---|
| BAT-25 | BAT-26 | NR-21 | NR24 | MONO-27 |

## CancerSELECT 125 SEQUENCING KEY METRICS

| | |
|---|---|
| Regions Analyzed | Coding regions of 125 genes |
| Sequencing Method | Illumina next-generation sequencing |
| Bioinformatics | Patented PARE, Digital Karyotyping and VariantDx |
| Average Total Sequencing Coverage | 1,250X |
| Turnaround Time | 2-3 weeks |
| Sample Requirements | Tumor only or Tumor/Matched Normal* |
| Sample Types | Frozen tumor, FFPE, blood and saliva (cell lines and xenograft accepted for RUO) |
| DNA Input Required | 1ug (minimum 50 ng) |

*Matched Normal sample required for optimal results

## CancerSELECT 125 SEQUENCING DELIVERABLES & ANALYSES

| | |
|---|---|
| Regions Analyzed | 125 genes |
| Sample Prep and NGS Sequencing | ✓ |
| Sequence Mutation Analysis | ✓ |
| Rearrangement Analysis | ✓ |
| Amplification Analysis | ✓ |
| Microsatellite Instability Status | ✓ |
| Clinical Annotation | ✓ |

**References**
1. Le et al., 2015. N. Engl. J. Med. 2. Rizvi et al., 2015. Science 3. Snyder et al., 2014. N. Engl. J. Med. 4. Jones et al., 2015. Sci. Transl. Med.

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