

Congenica<sup>®</sup>  
Oncology

# Transforming cancer care





# It's time to change the way we treat cancer

With the advances in Precision Oncology, over a quarter of all individuals diagnosed with advanced cancer are now eligible for a treatment based on the genomic analysis of their tumour.

To help accelerate the diagnostic journey of patients and drive the integration of Precision Oncology into routine clinical care, Congenica has developed a fully automated diagnostic oncology platform that reduces reporting times from hours to minutes, and alleviates the pressures on expert staff.



  
Congenica®



Sample Prep



Sequencing



Secondary Analysis  
Alignment &  
Variant Calling



Tertiary Analysis  
Variant  
Interpretation



Report  
Actionable  
Outcomes



Treatment



# From data to report without manual intervention

Congenica's scalable end-to-end solution provides fully hands-off, evidence-based interpretation of next-generation sequencing (NGS) data coupled with automated, user-friendly reporting of actionable insights. To support rapid treatment decisions, therapy recommendations are powered by region-specific best practice guidelines with authorised therapeutic assertions from the FDA, EMA and MHRA.

Sample information

Free-text summary

Summary of actionable findings with tumour-type specific, regional therapy recommendations

Mutational Signatures

Summary of additional driver gene variants (without associated therapies)

Audit trail

| Congenica Ltd<br>Welcome Genome Campus<br>Cambridge CB10 1DR<br>+44(0)1223499945                                      |                                      |                                         |                                          |            |
|-----------------------------------------------------------------------------------------------------------------------|--------------------------------------|-----------------------------------------|------------------------------------------|------------|
| Sample ID                                                                                                             | 2023-112345                          | Neoplastic cellularity (pathology est.) | 40%                                      |            |
| Sex                                                                                                                   | Female                               | Assay                                   | TruSight Oncology 500                    |            |
| Tumor Type                                                                                                            | Colorectal Adenocarcinoma (COADREAD) |                                         |                                          |            |
| Request date                                                                                                          | 2022/12/15                           | Report date                             | 2022/12/21                               |            |
| <b>Summary</b>                                                                                                        |                                      |                                         |                                          |            |
| Actionable mutations detected.                                                                                        |                                      |                                         |                                          |            |
| Summary written by user@congenica.com 2022/12/21 at 15:35                                                             |                                      |                                         |                                          |            |
| <b>Potentially actionable findings (AMP/CAP/ASCO Tier 1A)</b>                                                         |                                      |                                         |                                          |            |
| Biomarker                                                                                                             | Alteration                           | Details                                 | Therapy**                                | Indication |
| BRAF                                                                                                                  | V600E                                | VAF 24.01% (554x)                       | celecoxib +/- encorafenib                | EMA, ESMO  |
| KRAS                                                                                                                  | G13D                                 | VAF 6.32% (680x)                        | cetuximab +/- irinotecan +/- oxaliplatin | EMA, ESMO  |
| **Predicted response to a therapy is based on an integrated interpretation of all biomarkers present in the analysis. |                                      |                                         |                                          |            |
| <b>Tumour Mutation Burden (TMB)</b>                                                                                   |                                      | <b>MSI</b>                              |                                          |            |
| 65.6 mut/Mb                                                                                                           |                                      | MSI-Unstable                            |                                          |            |
| <b>Additional Drivers</b>                                                                                             |                                      |                                         |                                          |            |
| Biomarker                                                                                                             | Alteration                           | Details                                 | AMP/CAP/ASCO Tier                        |            |
| MSH3                                                                                                                  | K383Rfs*32                           | VAF 44.26% (549x)                       | 2D                                       |            |
| QC review PASSED by user@congenica.com at 2022/12/21                                                                  |                                      |                                         |                                          |            |

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|---------------------------------------------------------------------------------------------------------------------------------------|----------------|----------|------------------|----------|----------------|
| <b>Assay Information</b>                                                                                                              |                |          |                  |          |                |
| Sample ID                                                                                                                             | 2023-112345    | Assay ID | Iso500_v1_TSO500 |          |                |
| For panel scope, product literature can be found here: <a href="#">TruSight Oncology 500 Assay 1 For pan-cancer biomarkers in DNA</a> |                |          |                  |          |                |
| <b>Analysis Methodology</b>                                                                                                           |                |          |                  |          |                |
| Analysis was run using Congenica's Oncology platform, version 3.4                                                                     |                |          |                  |          |                |
| Report template: version 2022-11-21                                                                                                   |                |          |                  |          |                |
| Collator: version 2022-03-24                                                                                                          |                |          |                  |          |                |
| Tertiary Pipeline Output: version 2022-05-10                                                                                          |                |          |                  |          |                |
| The transcripts used for this analysis are from Ensembl release 100, transcript IDs are listed below:                                 |                |          |                  |          |                |
| Gene                                                                                                                                  | Transcript     | Gene     | Transcript       | Gene     | Transcript     |
| ABL1                                                                                                                                  | NM_005157.4    | ABL2     | NM_007314.3      | ABRAXAS1 | NM_139076.3    |
| ACVR1                                                                                                                                 | NM_001105.4    | ACVR1B   | NM_020328.3      | ADGRA2   | NM_032777.9    |
| AKT1                                                                                                                                  | NM_001014432.1 | AKT2     | NM_001626.4      | AKT3     | NM_005465.4    |
| ALK                                                                                                                                   | NM_004304.4    | ALOX12B  | NM_001139.2      | APC      | NM_152424.3    |
| ANKRD11                                                                                                                               | NM_001256182.1 | ANKRD26  | NM_014915.2      | AMER1    | NM_000338.5    |
| AR                                                                                                                                    | NM_000044.3    | ARAF     | NM_001654.4      | APC      | NM_000338.5    |
| ARID1A                                                                                                                                | NM_006015.4    | ARID1B   | NM_020732.3      | ARFRP1   | NM_003224.4    |
| ARID5B                                                                                                                                | NM_032199.2    | ASXL1    | NM_015336.5      | ARID2    | NM_152641.2    |
| ATM                                                                                                                                   | NM_000051.3    | ATR      | NM_001184.3      | ATRX     | NM_018263.4    |
| URKA                                                                                                                                  | NM_198433.1    | AURKB    | NM_004217.3      | AXIN1    | NM_003002.3    |
| XIN2                                                                                                                                  | NM_004655.3    | AXL      | NM_021913.4      | B2M      | NM_004948.2    |
| AP1                                                                                                                                   | NM_004656.3    | BARD1    | NM_000465.2      | BBC3     | NM_001127240.2 |
| TL0                                                                                                                                   | NM_003921.4    | BCL2     | NM_000633.2      | BCL2L1   | NM_136578.1    |
| 2L11                                                                                                                                  | NM_001204108.1 | BCL2L2   | NM_001199836.1   | BCL6     | NM_001706.4    |
| OR                                                                                                                                    | NM_001123385.1 | BCORL1   | NM_021946.4      | BCR      | NM_004327.3    |
| IC3                                                                                                                                   | NM_001165.4    | BLM      | NM_000057.2      | BMPR1A   | NM_004320.2    |
| AF                                                                                                                                    | NM_004333.4    | BRCA1    | NM_007294.3      | BRCA2    | NM_000059.3    |
| 4                                                                                                                                     | NM_058243.2    | BRIP1    | NM_032043.2      | BTG1     | NM_001731.2    |
| K                                                                                                                                     | NM_000081.2    | CALR     | NM_004343.3      | CARD11   | NM_032415.4    |
| 8                                                                                                                                     | NM_001228.4    | CBFB     | NM_001755.2      | CBL      | NM_005188.3    |
| 3                                                                                                                                     | NM_003880.4    | CCND1    | NM_053056.2      | CCND2    | NM_001759.3    |
| 3                                                                                                                                     | NM_001760.3    | CCNE1    | NM_001238.2      | CD274    | NM_014143.3    |
| CD276                                                                                                                                 | NM_001024736.1 | CD74     | NM_001025159.2   | CD79A    | NM_001783.3    |
| CD79B                                                                                                                                 | NM_000626.2    | CDC73    | NM_024529.4      | CDH1     | NM_004360.3    |

Assay information

Analysis methodology

List of transcript IDs per gene




# Platform performance

Our platform uses proprietary algorithms and publicly available data sets with statistical power for evidence-based, automated driver analysis and classification for high analytical performance.

| HD832 Verification | Precision (%) | Sensitivity (%) | Specificity (%) | Accuracy (%) |
|--------------------|---------------|-----------------|-----------------|--------------|
| SNVs (>15% VAF)    | 100           | 100             | 99.99           | 100          |
| Indels (>15% VAF)  | 98.9          | 96              | 99.99           | 99.99        |



Get in touch  
to learn more

-  [www.congenica.com/contact-us](http://www.congenica.com/contact-us)
-  [hello@congenica.com](mailto:hello@congenica.com)
-  [@congenica](https://twitter.com/congenica)

## Features & benefits



Fully automated, cost-effective and scalable end-to-end solution for significantly reduced turnaround times and increased operational efficiency



Therapeutic matching based on regional best-practice guidelines with authorised therapeutic assertions from the FDA, EMA and MHRA to support prompt treatment decisions



Accurate reporting of single nucleotide variants (SNVs), insertions and deletions (indels), structural variants, microsatellite instability (MSI) and tumour mutation burden (TMB) for confident detection of causal variants



Easy-to-interpret and user-friendly report focused on actionable insights to enable rapid patient treatment



Automated, evidence-based provision of actionable insights for unbiased and accurate variant interpretation



CE/IVD approved software for highest confidence in diagnostic outcome