**Supplemental Table S2: Consensus-derived Pre-defined Data Elements Captured in Full-Text Manuscript Review.**

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| --- | --- |
| **Category** | **Specific Data Element** |
| General Information | PMID (PubMed ID) |
| General Information | Institution(s) where validation took place |
| General Information | Year published |
| Test Information | Name of the NGS test panel(s) that was validated |
| Test Information | Number of genes for each panel that was validated |
| Test Information | Extraction method(s) used |
| Test Information | Library prep method(s) used |
| Test Information | Instrument platform(s) being validated |
| Bioinformatics Pipeline | Name of pipeline |
| Bioinformatics Pipeline | Variant types tested |
| Bioinformatics Pipeline | Number of samples used to validate this pipeline |
| Bioinformatics Pipeline | Minimum depth of coverage required to call a variant positive |
| Bioinformatics Pipeline | Minimum variant allele percentage required to call a variant positive |
| Bioinformatics Pipeline | Average depth of coverage for all nucleotides examined |
| Bioinformatics Pipeline | Was this pipeline included in more than one NGS test panel in the manuscript? If yes, please describe |
| Bioinformatics Pipeline | Were there unexpected regions of no coverage? If yes, describe the methods that were used to cover those regions (if any) |
| Bioinformatics Pipeline | Other depth of coverage comments |
| Bioinformatics Pipeline | Please indicate each expected function performed by this pipeline |
| Bioinformatics Pipeline | Variant types pipeline was expected to detect |
| Bioinformatics Pipeline | Sample types that were used in the validation |
| Bioinformatics Pipeline | Tumor specimens included in the validation |
| Tumor Analysis | Minimum tumor percentage of samples that underwent validation |
| Tumor Analysis | Average tumor percentage of samples that underwent validation |
| Tumor Analysis | Number of samples which had matched normal tissue samples also analyzed |
| Tumor Analysis | Tumor types included in the validation. For metastatic tumors of known primary, please check the primary tumor type |
| Orthogonal Method(s) | Please indicate the orthogonal method(s) being studied in the manuscript used to validate (eg, "gold standard” methods compared against the NGS pipeline) |
| Orthogonal Method(s) | Was the orthogonal method performed as a clinically validated test in a CLIA-certified laboratory? |
| Quality Control | QC metrics used for this pipeline and their results |
| Quality Control | Base quality score (Phred-like score, Q score) |
| Quality Control | Average (mean) read length |
| Quality Control | Median read length |
| Quality Control | Percentage of total reads that mapped to the reference genome |
| Quality Control | Percentage of reads at the region of interest (ROI) |
| Quality Control | Average uniformity of coverage across ROI |
| Quality Control | Percentage of duplicate reads |
| Quality Control | Variant quality score (Phred-like score calculated off the p value generated by the variant caller for a given variant) |
| Quality Control | Strand bias (also known as Forward/Reverse bias or F/R bias) |
| Quality Control | Mapping quality score (Phred-like score based off on the p value generated by the alignment software for each read) |
| Analytic Sensitivity of Pipeline | Single nucleotide variants |
| Analytic Sensitivity of Pipeline | Small deletions ≤21bp |
| Analytic Sensitivity of Pipeline | Larger deletions >21bp |
| Analytic Sensitivity of Pipeline | Small insertions ≤21bp |
| Analytic Sensitivity of Pipeline | Larger insertions >21bp |
| Analytic Sensitivity of Pipeline | Copy number variants- duplication of one or more genes |
| Analytic Sensitivity of Pipeline | Copy number variants - deletion of one or more genes |
| Analytic Sensitivity of Pipeline | Translocations (includes gene fusions and inversions) |
| Analytic Sensitivity of Pipeline | Small complex rearrangements ≤21 bp |
| Analytic Sensitivity of Pipeline | Large complex rearrangements > 21 bp |
| Analytic Sensitivity of Pipeline | Epigenetic variants |
| Analytic Sensitivity of Pipeline | OVERALL analytic sensitivity |
| Analytic Specificity of Pipeline | Single nucleotide variants |
| Analytic Specificity of Pipeline | Small deletions ≤21bp |
| Analytic Specificity of Pipeline | Larger deletions >21bp |
| Analytic Specificity of Pipeline | Small insertions ≤21bp |
| Analytic Specificity of Pipeline | Larger insertions >21bp |
| Analytic Specificity of Pipeline | Copy number variants- duplication of one or more genes |
| Analytic Specificity of Pipeline | Copy number variants - deletion of one or more genes |
| Analytic Specificity of Pipeline | Translocations (includes gene fusions and inversions) |
| Analytic Specificity of Pipeline | Small complex rearrangements ≤21 bp |
| Analytic Specificity of Pipeline | Large complex rearrangements > 21 bp |
| Analytic Specificity of Pipeline | Epigenetic variants |
| Analytic Specificity of Pipeline | OVERALL analytic sensitivity |
| Other specificity metrics | Other specificity metrics reported for this paper if provided |
| Confidence intervals (CI) | Positive decimal number for the CI if provided |
| General comments | Did the manuscript state that known FALSE positive variants were filtered out prior to analyzing the data? |
| General comments | Did study results vary by sample type, sample source (ie, specific organ or tissue), or any other specimen specific parameter even though they were tested on the same platform? If yes, please describe |
| General comments | Please enter any comments on indel-specific performance characteristics. If these are limited to a specific pipeline, please include that information |
| Limitations | Limitations of the study |

Data elements were captured for each pipeline described in manuscripts meeting criteria for full-text systematic review.