

CATS
(Cancer Genomic Test Standardized)
Format

Synopsis

**By Section of Genomic Data Management,
C-CAT**

v1.3.3

2025/07/16

I. Synopsis

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Example1. Only shortVariants

```
{
  "metaData": {
    "schemaVersion": "1.3.3",
    Note: Describe the version of CATS Format used.
    "referenceGenome": {
      "grcRelease": "GRCh37.p13"
    }
  },
  "testInfo": {
    "testId": "12345678901231900001",
    "testType": "tumor and matched-normal",
    "panelName": "Multi-gene Panel A",
    "panelVersion": "v1.3.1"
  },
  "sequencingSamples": [
    {
      "itemId": "sample01-tumor-dna",
      "tumorOrNormal": "tumor",
      "nucleicAcid": "DNA"
    }
  ],
  "variants": {
    "shortVariants": [
      {
        "itemId": "shortVariant-1",
        "chromosome": "2",
        "position": 29445258,
        "referenceAllele": "C",
        "alternateAllele": "T",
        Note: Describe "position" and "referenceAllele", "alternateAllele" according to the rules of VCF v4.3.
        "alternateAlleleFrequency": 0.54,
```

```
"transcripts": [  
  {  
    "transcriptId": "ENST00000389048.4",  
    "transcriptDatabaseName": "Ensembl",  
    "geneSymbol": "ALK",  
    "cdsChange": "c.3467G>A",  
    "aminoAcidsChange": "p.C1156Y"  
  }  
],  
"sampleItemId": "sample01-tumor-dna",  
Note: Describe the "itemId" of a relevant sequencingSamples instance.  
"variantOrigin": "somatic",  
"reported": true  
}  
]  
}  
}
```

Example2. Only copyNumberAlterations

```
{
  "metaData": {
    "schemaVersion": "1.3.3",
    "referenceGenome": {
      "grcRelease": "GRCh37.p13"
    }
  },
  "testInfo": {
    "testId": "12345678901231900001",
    "testType": "tumor and matched-normal",
    "panelName": "Multi-gene Panel A",
    "panelVersion": "v1.3.1"
  },
  "sequencingSamples": [
    {
      "itemId": "sample01-tumor-dna",
      "tumorOrNormal": "tumor",
      "nucleicAcid": "DNA"
    }
  ],
  "variants": {
    "copyNumberAlterations": [
      {
        "itemId": "copyNumberAlteration-1",
        "chromosome": "8",
        "startPosition": 128706589,
        "endPosition": 128801451,
        "copyNumberMetrics": [
          {
            "value": 11,
            "unit": "copy number"
          }
        ],
        "copyNumberAlterationType": "amplification",
        "transcripts": [
          {
            "geneSymbol": "MYC"
          }
        ]
      }
    ]
  }
}
```

```
    ],  
    "sampleItemId": "sample01-tumor-dna",  
    "variantOrigin": "somatic",  
    "reported": true  
  }  
]  
}  
}
```

Example3. Only rearrangements

```
{
  "metaData": {
    "schemaVersion": "1.3.3",
    "referenceGenome": {
      "grcRelease": "GRCh37.p13"
    }
  },
  "testInfo": {
    "testId": "12345678901231900001",
    "testType": "tumor and matched-normal",
    "panelName": "Multi-gene Panel A",
    "panelVersion": "v1.3.1"
  },
  "sequencingSamples": [
    {
      "itemId": "sample01-tumor-dna",
      "tumorOrNormal": "tumor",
      "nucleicAcid": "DNA"
    }
  ],
  "variants": {
    "rearrangements": [
      {
        "itemId": "rearrangement-1",
        "breakends": [
          Note: "breakends" has information on two breakpoints.
          {
            "chromosome": "2",
            "startPosition": 42510050,
            "endPosition": 42510050,
            "transcripts": [
              {
                "geneSymbol": "EML4"
              }
            ]
          }
        ],
        {
          "chromosome": "2",
```

```
        "startPosition": 29445240,  
        "endPosition": 29445240,  
        "transcripts": [  
            {  
                "geneSymbol": "ALK"  
            }  
        ]  
    },  
    ],  
    "orderedGenePairs": [  
        [  
            "EML4",  
            "ALK"  
        ]  
    ],  
    "rearrangementType": "gene fusion",  
    "sampleItemId": "sample01-tumor-dna",  
    "variantOrigin": "somatic",  
    "reported": true  
}  
]  
}  
}
```

Example4. shortVariants/copyNumberAlterations/rearrangements/otherBiomarkers

```
{
  "metaData": {
    "schemaVersion": "1.3.3",
    "referenceGenome": {
      "grcRelease": "GRCh37.p13"
    }
  },
  "testInfo": {
    "testId": "12345678901231900001",
    "testType": "tumor and matched-normal",
    "panelName": "Multi-gene Panel A",
    "panelVersion": "v1.3.1"
  },
  "sequencingSamples": [
    {
      "itemId": "sample01-tumor-dna",
      "tumorOrNormal": "tumor",
      "nucleicAcid": "DNA"
    }
  ],
  "variants": {
    "shortVariants": [
      {
        "itemId": "shortVariant-1",
        "chromosome": "2",
        "position": 29445258,
        "referenceAllele": "C",
        "alternateAllele": "T",
        "alternateAlleleFrequency": 0.54,
        "transcripts": [
          {
            "transcriptId": "ENST00000389048.4",
            "transcriptDatabaseName": "Ensembl",
            "geneSymbol": "ALK",
            "cdsChange": "c.3467G>A",
            "aminoAcidsChange": "p.C1156Y"
          }
        ]
      }
    ],
  },
}
```



```

        "sampleItemId": "sample01-tumor-dna",
        "variantOrigin": "somatic",
        "reported": true
    }
],
"copyNumberAlterations": [
    {
        "itemId": "copyNumberAlteration-1",
        "chromosome": "8",
        "startPosition": 128706589,
        "endPosition": 128801451,
        "copyNumberMetrics": [
            {
                "value": 11,
                "unit": "copy number"
            }
        ],
        "copyNumberAlterationType": "amplification",
        "transcripts": [
            {
                "geneSymbol": "MYC"
            }
        ],
        "sampleItemId": "sample01-tumor-dna",
        "variantOrigin": "somatic",
        "reported": true
    }
],
"rearrangements": [
    {
        "itemId": "rearrangement-1",
        "breakends": [
            {
                "chromosome": "2",
                "startPosition": 42510050,
                "endPosition": 42510050,
                "transcripts": [
                    {
                        "geneSymbol": "EML4"
                    }
                ]
            }
        ]
    }
]

```

```

        }
    ]
},
{
    "chromosome": "2",
    "startPosition": 29445240,
    "endPosition": 29445240,
    "transcripts": [
        {
            "geneSymbol": "ALK"
        }
    ]
}
],
"orderedGenePairs": [
    [
        "EML4",
        "ALK"
    ]
],
"rearrangementType": "gene fusion",
"sampleItemId": "sample01-tumor-dna",
"variantOrigin": "somatic",
"reported": true
}
]
},
"otherBiomarkers": [
    {
        "itemId": "biomarker-1",
        "biomarkerType": "MSI",
        "biomarkerMetrics": [
            {
                "value": 5.15,
                "unit": "%",
                "type": "percentage of MSI sites"
            }
        ]
    },
    "state": "stable",

```

```
    "sampleItemId": "sequence-1-tumor-dna",
    "reported": true
  },
  {
    "itemId": "biomarker-2",
    "biomarkerType": "TMB",
    "biomarkerMetrics": [
      {
        "value": 34.5680122,
        "unit": "Muts/Mb",
        "type": "Mutations per megabase"
      }
    ],
    "state": "high",
    "sampleItemId": "sequence-1-tumor-dna",
    "reported": true
  }
]
```