# Mapping table

## Clinical metadata (patient)

Insights types:

```typescript
interface FHIRPatient {
  id: string;
  gender?: string;
  vitalStatus?: boolean;
  hospital?: string;
  event?: string;
  age?: number;
  ageCategory?: AgeCategory | string;
  study?: string;
  cohort?: string;
  biosamples: FHIRBiosample[];
  zero2Category?: string;
  zero2Subcategory1?: string;
  zero2Subcategory2?: string;
  zero2FinalDiagnosis?: string;
  sequencingDate?: string;
  enrolmentDate?: string;
  enrolmentQuarter?: string;
  curationFinalisedAt?: string;
}
```

```typescript
type AgeCategory =
  | 'Infant (0-2)'
  | 'Child, Preschool (3-5)'
  | 'Child (6-12)'
  | 'Adolescent (13-19)'
  | 'Young Adult (20-25)'
  | 'Adult (26+)';
```

```typescript
interface FHIRBiosample {
  biosampleId: string;
  experimentalStrategy: string;
  sampleType: string;
}
```

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| `id` | Database: `zcczerodashhg38` <br> Table: `zcc_patient` <br> Field: `public_subject_id` | Resource: `Patient` <br> Field: `id` | |
| `gender` | Database: `zcczerodashhg38` <br> Table: `zcc_patient` <br> Field: `sex` | Resource: `Patient` <br> Field: `gender` | Gender value will always be lower case |

| | | | |
|---|---|---|---|
| vitalStatus | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `vital_status` | Resource: `Patient`<br>Field: `deceasedBoolean` | boolean type:<br>if vital_status == Dead then True else False |
| | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `enrolling_hospital` | Resource: `Patient`<br>Field: `managingOrganization.reference` | Refer to Organization/id |
| hospital | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `enrolling_hospital` | Resource: `Organization`<br>Fields:<br>`id`<br>`name` | convert `enrolling_hospital` to ID for id<br>`replace(" ", "-")` |
| | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `public_subject_id` | Resource: `Encounter`<br>Field: `id` | Prefix `enc-` public_subject_id |
| | HARDCODED | Resource: `Encounter`<br>Field: `status` | "in-progress" |
| | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `public_subject_id` | Resource: `Encounter`<br>Field: `subject.reference` | Refer to Patient/id |
| | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `enrolling_hospital` | Resource: `Encounter`<br>Field: `serviceProvider.reference` | Refer to Organization/id |

| | | | |
|---|---|---|---|
| `enrolmentDate` `enrolmentQuarter` | Database: `zcczerodashhg38` Table: `zcc_patient` Field: `enrolment_date` | Resource: `Encounter` Field: `period.start` | Format as ("%Y-%m-%d) |

```
1  {
2    "period": {
3      "start": <DATE>
4    }
5  }
```

`enrolmentQuarter` is additionally parsed via the `getEnrolmentQuarter` util to produce the `enrolmentQuarter` field (format `YYYY QQ` eg: `2018 Q3`)

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_analysis_set` Field: `analysis_set_id` | Resource: `Condition` Field: `id` | Prefix con- `analysis_set_id` |

| | | | |
|---|---|---|---|
| Diagnosis hierarchy `zero2Category` `zero2Subcategory1` `zero2Subcategory2` `zero2FinalDiagnosis` | Database: `zcczerodashhg38` Table: `zcc_analysis_set` Field: `zero2_category` `zero2_subcategory1` `zero2_subcategory2` `zero2_final_diagnosis` | Resource: `Condition` Fields: `category.coding.code` `code.text` | Final diagnosis is stored under the top-level `code`. The remaining hierarchy values are stored within `category` |

If Final diagnosis is missing we set code and display as **"Null"**

**If any value is missing for category we exclude that part.**

```
1  {
2    "code": {
3      "coding": [
4        {
5          "code": "NCIT:XXXX",
6          "display":
   <ZERO2_FINAL_DIAGNOSIS>
7        }
8      ]
9    },
10   "category": [
11     {
12       "coding": [
13         {
14           "code": <ZERO2_CATEGORY>,
15           "display": "zero2category"
16         }
17       ]
18     },
19     {
20       "coding": [
21         {
22           "code":
   <ZERO2_SUBCATEGORY1>,
```

```
23          "display":
    "zero2subcategory1"
24          }
25        ]
26      },
27      {
28        "coding": [
29          {
30            "code":
    <ZERO2_SUBCATEGORY2>,
31            "display":
    "zero2subcategory2"
32          }
33        ]
34      },
35    ]
36  }
```

| `event` | Database: `zcczerodashhg38` <br> Table: `zcc_analysis_set` <br> Field: `sequenced_event` | Resource: `Condition` <br> Field: `clinicalStatus` | In a coding list, under `display` <br><br> ```{ "clinicalStatus": { "coding": [ { "code": "NCIT:XXXX" "display": <EVENT> } ] } }``` <br><br> `display` is parsed via the `getStatus` util |

```
1  {
2    "clinicalStatus": {
3      "coding": [
4        {
5          "code": "NCIT:XXXX"
6          "display": <EVENT>
7        }
8      ]
9    }
10 }
```

| `age` <br> `ageCategory` | Database: `zcczerodashhg38` <br> Table: `zcc_analysis_set` <br> Field: `age_at_diagnosis` | Resource: `Condition` <br> Field: `onsetAge` | Under `value` . <VALUE> is a Floating value |

```
1  {
2    "onsetAge": {
3      "value": <VALUE>,
4      "unit": "years"
5    }
6  }
```

`onsetAge` is additionally parsed via the `getAgeCategory` util to produce the `ageCategory` field

> Note: If dont have age at diagnosis set it -1.0

| `curationFinalisedAt` | Database: `zcczerodashhg38` <br> Table: `zcc_analysis_set` <br> Field: | Resource: `Condition` <br> Field: `recordedDate` | Convert to ISOFormat + "Z" |

| | | | |
|---|---|---|---|
| | curation_finalised_at | | |
| | Database: zcczerodashhg38<br>Table: zcc_patient<br>Field: public_subject_id | Resource: Condition<br>Field: subject.reference | Refer to Patient/id |
| | Database: zcczerodashhg38<br>Table: zcc_analysis_set<br>Field: analysis_set_id | Resource: Condition<br>Field: stage.assessment.reference | Refer to DiagnosticReport/id |
| | HARDCODED | Resource: ResearchSubject<br>Field: id | PREFIX res- generate based on index+1 |
| | HARDCODE | Resource: ResearchSubject<br>Field: status | "active" |
| study | Database: zcczerodashhg38<br>Table: zcc_analysis_set<br>Field: study | Resource: ResearchSubject<br>Field: study | The studies themselves are stored in the ResearchStudy resource, under id / title . The parser currently infers the value directly from the reference field for convenience. |
| cohort | Database: zcczerodashhg38<br>Table: zcc_analysis_set<br>Field: cohort | Resource: ResearchSubject<br>Field: assignedArm | |
| | Database: zcczerodashhg38<br>Table: zcc_patient<br>Field: | Resource: ResearchSubject<br>Field: | Refer to Patient/id |

| | | | |
|---|---|---|---|
| | `public_subject_id` | `individual.reference` | |
| | Database: `zcczerodashhg38` Table: `zcc_analysis_set` Field: `study` | Resource: `ResearchStudy` Field: `id` `title` | convert `study` to ID for id `replace(" ", "-")` |
| | HARDCODED | Resource: `ResearchStudy` Field: `status` | "active" |
| `biosamples` | Database: `zcczerodashhg38` Table: `zcc_biosample` Field: `biosample_id` `sample_type` `sequencing_date` | Resource: `Specimen` Fields: `id` `type` `processing.procedure` `processing.timeDateTime` | `biosamples` is a list, with each element being an object with `biosampleId`, `experimentalStrategy` and `biosampleType`. Hence, multiple database fields are mapped to several fields within a single `Specimen` resource |

```
 1  {
 2    "id": <BIOSAMPLE_ID>,
 3    "type":{
 4      "coding":[
 5        {
 6          "system":
    "http://snomed.info/sct",
 7          "code": "119376003",
 8          "display": "Tissue specimen"
 9        }
10      ]
11    },
12    "processing": [
13        {
14        "description": <SAMPLE_TYPE>,
15        "procedure": {
16          "coding": [
17            {
18            "system":
    "http://purl.obolibrary.org/obo",
19            "code": "OMIT_xxxx",
20            "display":
    <SAMPLE_TYPE>
21            }
22          ]
23        },
24        "timeDateTime":
    <sequencing_date>
25        }
26      ]
27  }
```

| | | | convert sequencing_date to ISOFormat |
|---|---|---|---|
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_patient`<br>Field:<br>`public_subject_id` | Resource: `Specimen`<br>Field:<br>`Subject.reference` | Refer to Patient/id |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_biosample`<br>Field:<br>`biosample_uuid` | Resource:<br>`Observation`<br>Fields: `id` | PREFIX obs+ `biosample_uuid` |
| | HARDCODED | Resource:<br>`Observation`<br>Fields: `code` | ```
1     "code": {
2         "coding": [
3             {
4                 "system":
   "http://loinc.org",
5                 "code": "66746-9",
6                 "display": "Specimen
   type"
7             }
8         ]
9         }
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_biosample`<br>Field:<br>`biosample_type` | Resource:<br>`Observation`<br>Field: `component`<br>`[`<br>`code`<br>`valueCodeableConcept`<br>`]` | ```
1  "component": [
2    {
3      "code": {
4        "text": "Biosample Type"
5        },
6      "valueCodeableConcept": {
7        "coding": [
8          {
9            "system":
   "http://snomed.info/sct",
10           "code": "SNOMED_CODE",
11           "display": <BIOSAMPLE_TYPE>
12          }
13        ],
14        "text": <BIOSAMPLE_TYPE>
15      }
16    }
17 ]
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_biosample`<br>Field:<br>`biosample_status` | Resource:<br>`Observation`<br>Field: `component`<br>`[`<br>`code`<br>`valueCodeableConcept`<br> | ```
1  "component": [
2    {
3      "code": {
4        "text": "Biosample Status"
5        },
6      "valueCodeableConcept": {
7        "coding": [
8          {
9            "system":
   "http://www.ebi.ac.uk/efo",
10           "code": "EFO_xxxx",
11           "display":
   <BIOSAMPLE_STATUS>
12          }
13        ],
``` |

| | | | |
|---|---|---|---|
| | | | ```
14        "text": <BIOSAMPLE_STATUS>
15      }
16    }
17  ]
``` |
| | Database: `zcczerodashhg38`<br>Table: `zcc_biosample`<br>Field: `age_at_sample` | Resource: `Observation`<br>Field: `component` `[` `code` `valueQuantity` `]` | ```
1  "component": [
2    {
3      "code": {
4        "coding": [
5          {
6            "system":
   "http://loinc.org",
7            "code": "35659-2",
8            "display": "Age at
   specimen collection"
9          }
10        ]
11      },
12      "valueQuantity": {
13        "value": <AGE_AT_SAMPLE>,
14        "unit": "years",
15        "system": "https://ucum.org",
16        "code": "a"
17      }
18    }
19  ]
```<br><br>AGE_AT_SAMPLE should be stored as a floating value. |
| | Database: `zcczerodashhg38`<br>Table: `zcc_patient`<br>Field: `public_subject_id` | Resource: `Observation`<br>Field: `subject.reference` | Refer to Patient/id |
| | Database: `zcczerodashhg38`<br>Table: `zcc_biosample`<br>Field: `biosample_uuid` | Resource: `Observation`<br>Field: `specimen.reference` | Refer to Specimen/id |

## PDX data (PDX-Biobank)

| Insights field | Labmatrix API | FHIR resource | ZERO | NON-ZERO |
|---|---|---|---|---|
| | API: `api/qiagram/queryResults`<br>Field: `Public PDX ID` | Resource: `Specimen`<br>Field: `id` | Convert the public PDX ID to biosample uuid using the function available, suffix "-PDX"<br><br>Also Include **Disease abbreviation** | suffix "-PDX" |

| | | | | |
|---|---|---|---|---|
| | HARDCODED | Resource: `Specimen` <br> Field: `type` | ```json<br>{<br>  "code": {<br>    "coding": [<br>      {<br>        "system": "http://snomed.info/sct",<br>        "code": "67650000",<br>        "display": "Xenograft",<br>      }<br>    ]<br>  }<br>``` | ```json<br>{<br>  "code": {<br>    "coding": [<br>      {<br>        "system": "http://snomed.info/sct",<br>        "code": "67650000",<br>        "display": "Xenograft",<br>      }<br>    ]<br>  }<br>``` |
| | API: `api/qiagram/queryResults` <br> Field: `Subject Code` | Resource: `Specimen` <br> Field: `subject.reference` | Refer to Patient/Subject Code | Refer to Patient/Subject Code |
| | API: `api/qiagram/queryResults` <br> Field: `Public PDX ID` | Resource: `Observation` <br> Field: `id` | Convert the public PDX ID to biosample uuid using the function available, prefix "obs-" and suffix "-PDX" | prefix "obs-" and suffix "-PDX" |
| | HARDCODED | Resource: `Observation` <br> Field: `code` | ```json<br>{<br>  "code": {<br>    "coding": [<br>      {<br>        "system": "http://loinc.org",<br>        "code": "66746-9",<br>        "display": "Specimen type",<br>      }<br>    ]<br>  }<br>``` | ```json<br>{<br>  "code": {<br>    "coding": [<br>      {<br>        "system": "http://loinc.org",<br>        "code": "66746-9",<br>        "display": "Specimen type",<br>      }<br>    ]<br>  }<br>``` |
| | API: `api/qiagram/queryResults` <br> Field: `Subject Code` | Resource: `Observation` <br> Field: `subject.reference` | Refer to Patient/Subject Code | Refer to Patient/Subject Code |
| | API: `api/qiagram/queryResults` <br> Field: `Public PDX ID` | Resource: `Observation` <br> Field: `specimen.reference` | Refer to Specimen/BiosampleUUID("Public PDX ID) | Refer to Specimen/Public PDX ID |

| | API: `api/qiagram/queryResults` Field: `available` | Resource: `Observation` Field: `component` `[` `code` `valueString` `]` | ```
1  "component": [
2    {
3      "code": {
4        "system":
         "http://snomed.inf
         o/sct",
5        "code":
         "103328004",
6        "display":
         "Available"
7      },
8      "valueString":
         <available>
9    }
10 ]
``` | ```
1  "component": [
2    {
3      "code": {
4        "system":
         "http://snomed.info/
         sct",
5        "code":
         "103328004",
6        "display":
         "Available"
7      },
8      "valueString":
         <available>
9    }
10 ]
``` |
|---|---|---|---|---|
| | API: `api/qiagram/queryResults` Field: `passage` | Resource: `Observation` Field: `component` `[` `code` `valueQuantity` `]` | ```
1  {
2    "code": {"text":
       "Passage number"},
3    "valueQuantity":
       {"value":
       <passage>}
4  }
``` Passage should be stored as a floating value  If Passage is null then passage = 0.0 | ```
1  {
2    "code": {"text":
       "Passage number"},
3    "valueQuantity":
       {"value": <passage>}
4  }
``` Passage should be stored as a floating value  If Passage is null then passage = 0.0 |
| | API: `api/qiagram/queryResults` Field: `Subtype` | Resource: `Observation` Field: `component` `[` `code` `valueString` `]` | ```
1  {
2    "code": {"text":
       "Subtype"},
3    "valueString":
       <subtype>}
4  }
``` If subtype exist then we put this value else ignore | ```
1  {
2    "code": {"text":
       "Subtype"},
3    "valueString":
       <subtype>}
4  }
``` If subtype exist then we put this value else ignore |
| | API: `api/qiagram/queryResults` Field: `mouse_strain` | Resource: `Observation` Field: `component` `[` `code` `valueString` `]` | ```
1  {
2    "code": {"text":
       "Mouse Strain"},
3    "valueString":
       <mouse_strain>}
4  }
``` If subtype exist then we put this value else ignore | ```
1  {
2    "code": {"text":
       "Mouse Strain"},
3    "valueString":
       <mouse_strain>}
4  }
``` If subtype exist then we put this value else ignore |
| | API: `api/qiagram/q` | Resource: `Observation` Field: `component` | ```
1  {
2    "code": {"text":
       "Staging"},
3    "valueString":
       <staging>}
4  }
``` | ```
1  {
2    "code": {"text":
       "Staging"},
3    "valueString":
       <staging>}
4  }
``` |

| | | | | |
|---|---|---|---|---|
| | `ueryResults`<br>Field: `staging` | `[`<br>`code`<br>`valueString`<br>`]` | If subtype exist then we put this value else ignore | If subtype exist then we put this value else ignore |
| | API:<br>`api/qiagram/q`<br>`ueryResults`<br>Field: `grade` | Resource:<br>`Observation`<br>Field: `component`<br>`[`<br>`code`<br>`valueQuantity`<br>`]` | ```
1  {
2    "code": {"text":
   "Staging"},
3    "valueString":
   <staging>}
4  }
```<br><br>If subtype exist then we put this value else ignore | ```
1  {
2    "code": {"text":
   "Staging"},
3    "valueString":
   <staging>}
4  }
```<br><br>If subtype exist then we put this value else ignore |
| | API:<br>`api/qiagram/q`<br>`ueryResults`<br>Field: `validated`<br>`validation_ty`<br>`pe` | Resource:<br>`Observation`<br>Field: `component`<br>`[`<br>`code`<br>`valueString` ,<br>`code`<br>`valueString`<br>`]` | ```
1  {
2    "code": {"text":
   "Validated"},
3    "valueString":
   <validated>}
4  },
5  {
6    "code": {"text":
   "Validation
   method"},
7    "valueString":
   <validation_type>}
8  }
```<br><br>Only include when validated is "Yes" else ignore this entry | ```
1  {
2    "code": {"text":
   "Validated"},
3    "valueString":
   <validated>}
4  },
5  {
6    "code": {"text":
   "Validation
   method"},
7    "valueString":
   <validation_type>}
8  }
```<br><br>Only include when validated is "Yes" else ignore this entry |
| | API:<br>`api/qiagram/q`<br>`ueryResults`<br>Field: `Public PDX`<br>`ID` | Resource:<br>`Condition`<br>Field: `id` | Already handled in clinical section | Prefix "con-" Public PDX ID |
| Diagnosis hierarchy<br>`zero2Cate`<br>`gory`<br>`zero2Subc`<br>`ategory1`<br>`zero2Subc`<br>`ategory2`<br>`zero2Fina` | Database:<br>`zcczerodashhg`<br>`38`<br>Table:<br>`zcc_analysis_`<br>`set`<br>Field:<br>`zero2_categor`<br>`y` | Resource:<br>`Condition`<br>Fields:<br>`category.coding`<br>`.code`<br>`code.text` | Already handled in clinical section | Final diagnosis is stored under the top-level `code` . The remaining hierarchy values are stored within `category`<br><br>**If any value is missing we exclude that part.**<br><br>```
1  {
``` |

| lDiagnosis | zero2_subcategory1 zero2_subcategory2 zero2_final_diagnosis | | | ```json
 2    "code": {
 3      "coding": [
 4        {
 5          "code":
   "NCIT:XXXX",
 6          "display":
   <ZERO2_FINAL_DIAGNOS
   IS>
 7        }
 8      ]
 9    },
10    "category": [
11      {
12        "coding": [
13          {
14            "code":
   <ZERO2_CATEGORY>,
15
   "display":
   "zero2category"
16          }
17        ]
18      },
19      {
20        "coding": [
21          {
22            "code":
   <ZERO2_SUBCATEGORY1
   >,
23
   "display":
   "zero2subcategory1"
24          }
25        ]
26      },
27      {
28        "coding": [
29          {
30            "code":
   <ZERO2_SUBCATEGORY2
   >,
31
   "display":
   "zero2subcategory2"
32          }
33        ]
34      },
35    ]
36 }
``` |
| event | Database: `zcczerodashhg38` Table: `zcc_analysis_set` Field: `sequenced_event` | Resource: `Condition` Field: `clinicalStatus` | Already handled in clinical section | In a coding list, under `display` ```json
 1 {
 2    "clinicalStatus":
   {
 3      "coding": [
 4        {
 5          "code":
   "NCIT:XXXX"
 6          "display":
   <EVENT>
 7        }
 8      ]
 9    }
10 }
``` `display` is parsed via the `getStatus` |

| | | | | util |
|---|---|---|---|---|
| `age` `ageCategory` | Database: `zcczerodashhg38` Table: `zcc_analysis_set` Field: `age_at_diagnosis` | Resource: `Condition` Field: `onsetAge` | Already handled in clinical section | Under `value` . <VALUE> is a Floating value

```
1  {
2    "onsetAge": {
3      "value":
   <VALUE>,
4      "unit": "years"
5    }
6  }
```

`onsetAge` is additionally parsed via the `getAgeCategory` util to produce the `ageCategory` field

> Note: If dont have age at diagnosis set it `-1.0` |

## Molecular data (variant)

Insights type:

```
1  interface FHIRVariant {
2    // TODO
3  }
```

## Molecular data (SNV)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `gene` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | ```
1   "component": [
2     {
3       "code": {
4         "coding": [
5           {
6             "system":
   "https://loinc.org/",
7             "code": "48018-
   6"
8           }
9         ]
10      },
11      "valueString": "NRAS"
12    }
13  ]
``` |

| | | | |
|---|---|---|---|
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field:<br>`adjustedcopynumbe`<br>`r` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`quantity` | ```json
"component": [
  {
    "code": {
      "coding": [
        {
          "system": "ZD",
          "code": "adjusted-copy-number"
        }
      ]
    },
    "valueQuantity": {
      "value": 1.03,
      "unit": "count",
      "system": "https://ucum.org/",
      "code": "{#}"
    }
  }
]
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `adjustedvaf` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `altad` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `biallelic` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`boolean` | ```json
"component": [
  {
    "code": {
      "coding": [
        {
          "system": "ZD",
          "code": "biallelic"
        }
      ]
    },
    "valueBoolean": false
  }
]
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_snv`<br>Field: `chr` | Resource:<br>`observation`<br>Profile:<br>`genomicFindin`<br>`g` | |

| | | | |
|---|---|---|---|
| | | Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `classification` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_snv` Field: `consequence` | Resource: `observation` Profile: `molecularConsequence` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `copynumber` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | <div>```json<br>1  "component": [<br>2    {<br>3      "code": {<br>4        "coding": [<br>5          {<br>6            "system": "https://loinc.org/",<br>7            "code": "82155-3"<br>8          }<br>9        ]<br>10     },<br>11     "valueQuantity": {<br>12       "value": 1.99,<br>13       "unit": "count",<br>14       "system": "https://ucum.org/",<br>15       "code": "{#}"<br>16     }<br>17   }<br>18 ]<br>```</div> |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `depth` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` | Resource: `observation` | |

| | | | |
|---|---|---|---|
| | Table:<br>`zcc_curated_snv`<br>Field: `exon` | Profile: `variant`<br>Data Type:<br>`component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `genotype` | Resource:<br>`observation`<br>Profile: `genotype`<br>Data Type:<br>`component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_snv`<br>Field: `hgvs` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`codeableConcept` | protein version of hgvs<br>```<br>1  "component": [<br>2    {<br>3      "code": {<br>4        "coding": [<br>5          {<br>6            "system":<br>   "http://loinc.org/",<br>7            "code": "48005-3"<br>8          }<br>9        ]<br>10      },<br>11      "valueCodeableConcept":<br>   {<br>12        "coding": [<br>13          {<br>14            "system":<br>   "http://varnomen.hgvs.org/",<br>15            "code":<br>   "NM_001017524.2:p.<br>   (Gly5AlafsTer126)"<br>16          }<br>17        ]<br>18      }<br>19    }<br>20  ]<br>``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_snv`<br>Field: `hgvs` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`codeableConcept` | coding version of hgvs<br>```<br>1  "component": [<br>2    {<br>3      "code": {<br>4        "coding": [<br>5          {<br>6            "system":<br>   "http://loinc.org/",<br>7            "code": "48004-6"<br>8          }<br>9        ]<br>10      },<br>11      "valueCodeableConcept":<br>   {<br>12        "coding": [<br>13          {<br>14            "system":<br>   "http://varnomen.hgvs.org/",<br>15            "code":<br>   "NM_001017524.2:c.12del"<br>16          }<br>17        ]<br>18      }<br>``` |

```
19    }
20  ]
```

| | Database: `zcczerodashhg38`  Table: `zcc_curated_snv`  Field: `hotspot` | Resource: `observation`  Profile: `variant`  Data Type: `component`  Data Field: `value` | |
| --- | --- | --- | --- |
| | Database: `zcczerodashhg38`  Table: `zcc_consequence`  Field: `impact` | Resource: `observation`  Profile: `molecularConsequence`  Data Type: `component`  Data Field: `value` | |
| | Database: `zcczerodashhg38`  Table: `zcc_curated_sample_somatic_snv`  Field: `LOH` | Resource: `observation`  Profile: `variant`  Data Type: `component`  Data Field: `value` | |
| | Database: `zcczerodashhg38`  Table: `zcc_curated_sample_somatic_snv`  Field: `outlier` | Resource: `observation`  Profile: `variant`  Data Type: `component`  Data Field: `boolean` | |
| | Database: `zcczerodashhg38`  Table: `zcc_curated_sample_somatic_snv`  Field: `pathclass` | Resource: `observation`  Profile: `molecularConsequence`  Data Type: `component`  Data Field: `value` | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sampl e_somatic_snv` Field: `pathscore` | Resource: `observation` Profile: `molecularConse quence` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_snv` Field: `pecan` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `boolean` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sampl e_somatic_snv` Field: `platforms` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_snv` Field: `pos` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `hardcode` | `"component": [`<br>`  {`<br>`    "code": {`<br>`      "coding": [`<br>`        {`<br>`          "system":`<br>`"http://loinc.org/",`<br>`          "code": "81254-5"`<br>`        }`<br>`      ]`<br>`    },`<br>`    "valueRange": {`<br>`      "low": {`<br>`        "value": 15942195.0`<br>`      },`<br>`      "high": {`<br>`        "value": 15942196.0`<br>`      }`<br>`    }`<br>`  }`<br>`]` |
| | Database: `zcczerodashhg38` Table: | Resource: `observation` Profile: `variant` Data Type: | |

| | | | |
|---|---|---|---|
| | zcc_curated_snv<br>Field: ref | component<br>Data Field: value | |
| | Database:<br>zcczerodashhg38<br>Table:<br>zcc_curated_sampl e_somatic_snv<br>Field: reportable | Resource:<br>observation<br>Profile: variant<br>Data Type:<br>component<br>Data Field:<br>boolean | |
| | Database:<br>zcczerodashhg38<br>Table:<br>zcc_curated_sampl e_somatic_snv<br>Field:<br>research_candidat e | Resource:<br>observation<br>Profile: variant<br>Data Type:<br>component<br>Data Field:<br>boolean | |
| | Database:<br>zcczerodashhg38<br>Table:<br>zcc_curated_sampl e_somatic_snv<br>Field: rna_altad | Resource:<br>observation<br>Profile: variant<br>Data Type:<br>component<br>Data Field:<br>quantity | |
| | Database:<br>zcczerodashhg38<br>Table:<br>zcc_curated_sampl e_somatic_snv<br>Field: rna_depth | Resource:<br>observation<br>Profile: variant<br>Data Type:<br>component<br>Data Field:<br>quantity | |
| | Database:<br>zcczerodashhg38<br>Table:<br>zcc_curated_sampl e_somatic_snv<br>Field: rna_tpm | Resource:<br>observation<br>Profile: variant<br>Data Type:<br>component<br>Data Field:<br>quantity | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `rna_vaf` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `rna_vaf_no` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `subclonalLikelihood` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_snv` Field: `targetable` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `boolean` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_snv` Field: `transcript` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `codeableConcept` | ```
1  "component": [
2    {
3      "code": {
4        "coding": [
5          {
6            "system":
   "https://loinc.org/",
7            "code": "51958-7"
8          }
9        ]
10     },
11     "valueCodeableConcept":
   {
12       "coding": [
13         {
14           "system":
   "http://www.ncbi.nlm.nih.gov
   /refseq",
``` |

| | | | |
|---|---|---|---|
| | | | ```
15          "code":
    "NM_005378.6"
16          }
17        ]
18      }
19    }
20  ]
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `variant_id` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`identifier`<br>Data Field:<br>`identifier` | ZD internal variant_id<br>```
1        "identifier": [
2          {
3            "system": "ZD-
  snv-variant-id",
4            "value":
  "d3cfa1bd-0e05-ecff-284a-
  99fce30f4e89"
5          }
6        ]
``` |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field:<br>`vcf_filter_pass` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field:<br>`boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sampl`<br>`e_somatic_snv`<br>Field: `zygosity` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `alias` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`identifier`<br>Data Field:<br>`identifier` | |
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_genes`<br>Field:<br>`chromosomeBand_hg`<br>`38` | Resource:<br>`observation`<br>Profile: `variant`<br>Data Type:<br>`component`<br>Data Field: `value` | |

| | | | |
|---|---|---|---|
| | Database: zcczerodashhg38 <br> Table: zcc_genes <br> Field: end_hg38 | Resource: observation <br> Profile: variant <br> Data Type: component <br> Data Field: value | |
| | Database: zcczerodashhg38 <br> Table: zcc_genes <br> Field: entrezUID | Resource: observation <br> Profile: variant <br> Data Type: identifier <br> Data Field: identifier | |
| | Database: zcczerodashhg38 <br> Table: zcc_genes <br> Field: fullname | Resource: observation <br> Profile: variant <br> Data Type: identifier <br> Data Field: identifier | |
| | Database: zcczerodashhg38 <br> Table: zcc_genes <br> Field: start_hg38 | Resource: observation <br> Profile: variant <br> Data Type: component <br> Data Field: value | |
| | Database: zcczerodashhg38 <br> Table: zcc_genes <br> Field: strand_hg38 | Resource: observation <br> Profile: variant <br> Data Type: component <br> Data Field: value | |
| | Database: zcczerodashhg38 <br> Table: zcc_curated_snv <br> Field: alt | Resource: observation <br> Profile: variant <br> Data Type: component <br> Data Field: value | |

## Molecular data (CNV)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `rna_tpm` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `bkpt1` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `range` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `bkpt2` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `range` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `chr` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `classification` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `cn_type` | Resource: `observation` Profile: `molecularConsequence` Data Type: `component` Data Field: `value` | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `fc` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `maxCN` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `minCN` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `minMinorAlleleCN` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `pathclass` | Resource: `observation`<br>Profile: `molecularConsequence`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `pathscore` | Resource: `observation`<br>Profile: `molecularConsequence`<br>Data Type: `component`<br>Data Field: `quantity` | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `platforms` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `rna_median_tpm` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `rna_tpm` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `rna_zscore` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cnv`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cnv` Field: `variant_id` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `alias` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `chromosomeBand_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `end_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `entrezUID` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `fullname` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `gene` | Resource: `observation` Profile: `genomicFinding` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `start_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `strand_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |

## Molecular data (ARMCNV)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `arm` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `avecopynumber` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `aveminminorallelecn` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `quantity` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `chr` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `classification` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_armcnv` Field: `cn_type` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somat | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | `ic_armcnv`<br>Field: `cytoband` | | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_armcnv`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_armcnv`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_armcnv`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_armcnv`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

## Molecular data (CYTOBANDCNV)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_cytobandcnv`<br>Field: `arm` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_cytobandcnv`<br>Field: `avecopynumber` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

| | | | |
|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `chr` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `classification` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `cn_type` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `custom_cn` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `cytoband` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_cytobandcnv`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_cytobandcnv` Field: `targetable` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `boolean` | |

## Molecular data (RNA)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `alias` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `chromosomeBand_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `end_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `entrezUID` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `fullname` | Resource: `observation` Profile: `variant` Data Type: `identifier` Data Field: `identifier` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `gene` | Resource: `observation` Profile: `genomicFinding` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` Table: `zcc_genes` Field: `start_hg38` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
| | Database: `zcczerodashhg38` | Resource: `observation` Profile: `variant` | |

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|---|---|---|---|
| | Table: `zcc_genes`<br>Field: `strand_hg38` | Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `classification` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `counts` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `fc` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `fdr` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `fpkm` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_rnaseq`<br>Field: `fpkm_mean` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somat | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

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|---|---|---|---|
| | `ic_rnaseq`<br>Field: `fpkm_median` | | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `gene_expression` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `logCPM` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `logFC` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `lr` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_rnaseq`<br>Field: `outlier` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

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|---|---|---|---|
| | ic_rnaseq`<br>Field: `pvalue` | | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `tpm` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `tpm_mean` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat ic_rnaseq`<br>Field: `tpm_median` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

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|---|---|---|---|
| | ic_rnaseq`<br>Field: `zscore_mean` | | |

## Molecular data (METHGENE)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `classification` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `lower` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `median` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `meth_status` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_methy lation_genes`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

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|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_methylation_genes`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_methylation_genes`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_methylation_genes`<br>Field: `upper` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `alias` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `chromosomeBand_hg38` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `end_hg38` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `entrezUID` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `fullname` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38` | Resource: `observation`<br>Profile: `genomicFinding` | |

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Table: `zcc_genes`<br>Field: `gene` | Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `start_hg38` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_genes`<br>Field: `strand_hg38` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |

## Molecular data (METHGROUP)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_methylation`<br>Field: `classification` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_classifier`<br>Field: `description` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `external_group_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_classifier`<br>Field: `external_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `group_name` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_methylation`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

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|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_methylation`<br>Field: `interpretation` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_methylation`<br>Field: `match_zcc` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_class` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_class_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somatic_methylation`<br>Field: `meth_class_score` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table:<br>`zcc_methylation_classifier`<br>Field: `version` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `meta`<br>Data Field: `version` | |
| | Database: `zcczerodashhg38`<br>Table:<br>`zcc_methylation_classifier`<br>Field: `meth_classifier_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `id`<br>Data Field: `id` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_evidence` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_family` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group` | Resource: `observation`<br>Profile: `variant` | |

| | Field: `meth_group_id` | Data Type: `id`<br>Data Field: `id` | |
|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_summary` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_group`<br>Field: `meth_superfamily` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_classifier`<br>Field: `name` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_methylation_predictions`<br>Field: `meth_class_score` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_methylation`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_methylation`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_methylation`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |

## Molecular data (SV)

| Insights field | Internal db | FHIR resource | Notes |
|---|---|---|---|
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |

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|---|---|---|---|
| | ic_sv`<br>Field: `chr_bkpt1` | | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `chr_bkpt2` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `classification` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `disrupted` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `end_af` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `end_fusion` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `end_gene_exons` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_curated_sv`<br>Field: `end_gene_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |

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|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `in_molecular_report` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `inframe` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `mark_disrupted` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `pathclass` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `pathscore` | Resource: `observation`<br>Profile: `molecularConsequence`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `platforms` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `ploidy` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

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|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `pos_bkpt1` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `range` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `pos_bkpt2` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `range` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `reportable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `research_candidate` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_chr_bkpt1` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_chr_bkpt2` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_end_fusion` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |

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|---|---|---|---|
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_end_gene_exons` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_pos_bkpt1` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_pos_bkpt2` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_start_fusion` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rna_start_gene_exons` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somatic_sv`<br>Field: `rnaconf` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database: `zcczerodashhg38`<br>Table: `zcc_curated_sample_somat | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |

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| | ic_sv`<br>Field: `somaticscore` | | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `start_af` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `start_fusion` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `start_gene_exons` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `quantity` | |
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_curated_sv`<br>Field: `start_gene_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `sv_type` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `value` | |
| | Database:<br>`zcczerodashhg38`<br>Table:<br>`zcc_curated_sample_somat<br>ic_sv`<br>Field: `targetable` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `component`<br>Data Field: `boolean` | |
| | Database:<br>`zcczerodashhg38`<br>Table: `zcc_curated_sv`<br>Field: `variant_id` | Resource: `observation`<br>Profile: `variant`<br>Data Type: `identifier`<br>Data Field: `identifier` | |

| | Database: `zcczerodashhg38` Table: `zcc_curated_sample_somatic_sv` Field: `wgsconf` | Resource: `observation` Profile: `variant` Data Type: `component` Data Field: `value` | |
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