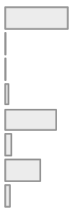
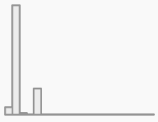
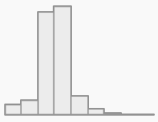
# Data Frame Summary

## csv_input

**Dimensions**: 158100 x 21
**Duplicates**: 0

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 1 | project_id<br>[factor] | 1. BEATAML1.0-COHORT<br>2. BEATAML1.0-CRENOLANIB<br>3. CGCI-BLGSP<br>4. CGCI-HTMCP-CC<br>5. CMI-ASC<br>6. CMI-MBC<br>7. CMI-MPC<br>8. CPTAC-2<br>9. CPTAC-3<br>10. CTSP-DLBCL1<br>[ 58 others ] | 1481 ( 0.9%)<br>119 ( 0.1%)<br>447 ( 0.3%)<br>861 ( 0.5%)<br>94 ( 0.1%)<br>645 ( 0.4%)<br>60 ( 0.0%)<br>1024 ( 0.6%)<br>4077 ( 2.6%)<br>175 ( 0.1%)<br>149117 (94.3%) | | 158100<br>(100.0%) | 0<br>(0.0%) |
| 2 | case_id<br>[factor] | 1. 00016c8f-a0be-4319-9c42-4<br>2. 00021f80-e72d-4c18-9e36-7<br>3. 00026454-8225-4395-b536-4<br>4. 0002f311-f263-4816-95f5-f<br>5. 00039740-17c1-4430-a112-5<br>6. 00041061-3fe2-417a-a333-2<br>7. 00048fa6-4318-42ef-9709-7<br>8. 0004bacb-64f9-4823-a962-6<br>9. 0004d251-3f70-4395-b175-c<br>10. 000520f2-c081-4757-8f5c-0<br>[ 84559 others ] | 1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>3 ( 0.0%)<br>1 ( 0.0%)<br>158088 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |
| 3 | case_submitter_id<br>[factor] | 1. 01BR001<br>2. 01BR008<br>3. 01BR009<br>4. 01BR010<br>5. 01BR015<br>6. 01BR017<br>7. 01BR018<br>8. 01BR020<br>9. 01BR023<br>10. 01BR025<br>[ 84481 others ] | 3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>3 ( 0.0%)<br>158070 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |
| 4 | sample_id<br>[factor] | 1. 000002fc-53a0-420e-b2aa-a<br>2. 00020a53-a03e-4806-8cf6-a<br>3. 000225dc-7d01-504a-967f-f<br>4. 0002a8e8-b820-47d7-a45f-3<br>5. 0003bde8-b7af-46d7-908f-2<br>6. 0003bfc0-c5aa-4087-8ebe-2<br>7. 0004971d-f77b-4116-a49a-e<br>8. 00069694-c259-4b10-8353-5<br>9. 0006a6a4-bdec-4942-960c-c<br>10. 00072b50-23e0-4437-89cc-3<br>[ 107651 others ] | 2 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>2 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>158088 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 5 | sample_submitter_id<br>[factor] | 1. 0065bfd9-e1b9-43a8-9379-9<br>2. 012baf0d-2c53-4409-91ec-2<br>3. 012ff650-0db2-41a2-a309-3<br>4. 01bf1906-9bdc-41c3-89a0-b<br>5. 01d1ffca-4235-4dfe-bf62-5<br>6. 01de44a7-81fa-4e25-aba5-9<br>7. 01f203fd-e664-4d78-bea0-7<br>8. 02345909-96ed-4f40-a623-7<br>9. 02ac4d5b-a5e7-4e2c-8ede-f<br>10. 02f6afea-1e5b-4151-bafd-c<br>[ 107604 others ] | 2 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>2 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>158088 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |
| 6 | portion_id<br>[factor] | 1. 00012d1d-f6ca-4133-9a82-b<br>2. 0001ab72-8fa0-4b52-9202-5<br>3. 00026551-91bc-49da-abbc-1<br>4. 0002b969-6506-46fb-9b6a-e<br>5. 0002c07e-726f-4b58-9d55-1<br>6. 0002f5a0-c16b-5810-b0d7-1<br>7. 00034baa-35a9-5d56-89e1-7<br>8. 0003c41c-27c6-53cb-bac0-d<br>9. 0004689e-43d0-4a55-95d3-4<br>10. 000490e7-cf60-40af-b463-2<br>[ 118442 others ] | 1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>158090 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |
| 7 | portion_submitter_id<br>[factor] | 1. BLGSP-71-06-00001-01A-11<br>2. BLGSP-71-06-00001-01B-01<br>3. BLGSP-71-06-00001-99A-01<br>4. BLGSP-71-06-00002-01C-01<br>5. BLGSP-71-06-00002-01D-01<br>6. BLGSP-71-06-00002-99A-01<br>7. BLGSP-71-06-00004-01A-11<br>8. BLGSP-71-06-00004-01B-01<br>9. BLGSP-71-06-00004-99A-01<br>10. BLGSP-71-06-00007-01A-11<br>[ 25489 others ] | 2 ( 0.0%)<br>2 ( 0.0%)<br>1 ( 0.0%)<br>2 ( 0.0%)<br>2 ( 0.0%)<br>1 ( 0.0%)<br>2 ( 0.0%)<br>2 ( 0.0%)<br>1 ( 0.0%)<br>2 ( 0.0%)<br>64631 (100.0%) | | 64648<br>(40.9%) | 93452<br>(59.1%) |
| 8 | analyte_id<br>[factor] | 1. 000109ad-4b03-5ddb-a308-e<br>2. 00011725-8ad4-509d-8fe7-9<br>3. 00014e23-c05c-4a2c-9c19-f<br>4. 0001c4de-9a36-44b8-9db9-f<br>5. 0001c7b1-381d-4143-92b9-f<br>6. 00025eb5-d192-4e33-8809-8<br>7. 000286ef-5d06-42f7-9abd-4<br>8. 0002e4c6-6d59-59d7-af2b-4<br>9. 00041799-fd3d-41b5-bd5f-7<br>10. 00041c1d-47fa-421e-8dde-6<br>[ 157591 others ] | 1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>158090 (100.0%) | | 158100<br>(100.0%) | 0<br>(0.0%) |

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 9 | analyte_submitter_id<br>[factor] | 1. ANALYTE1<br>2. ANALYTE10<br>3. ANALYTE100<br>4. ANALYTE101<br>5. ANALYTE102<br>6. ANALYTE103<br>7. ANALYTE104<br>8. ANALYTE105<br>9. ANALYTE106<br>10. ANALYTE107<br>[ 65010 others ] | 1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>1 ( 0.0%)<br>65010 (100.0%) | | 65020<br>(41.1%) | 93080<br>(58.9%) |
| 10 | a260_a280_ratio<br>[numeric] | Mean (sd) : 1.956 (12.109)<br>min < med < max:<br>0 < 1.88 < 1761<br>IQR (CV) : 0.1 (6.191) | 148 distinct values | | 21559<br>(13.6%) | 136541<br>(86.4%) |
| 11 | amount<br>[logical] | All NA's | | | 0<br>(0.0%) | 158100<br>(100.0%) |
| 12 | analyte_quantity<br>[logical] | All NA's | | | 0<br>(0.0%) | 158100<br>(100.0%) |
| 13 | analyte_type<br>[factor] | 1. DNA<br>2. FFPE DNA<br>3. FFPE RNA<br>4. GenomePlex (Rubicon) Ampl<br>5. Repli-G (Qiagen) DNA<br>6. Repli-G X (Qiagen) DNA<br>7. RNA<br>8. Total RNA | 25122 (38.6%)<br>38 ( 0.1%)<br>38 ( 0.1%)<br>1054 ( 1.6%)<br>20631 (31.7%)<br>2177 ( 3.3%)<br>13919 (21.4%)<br>2041 ( 3.1%) |  | 65020<br>(41.1%) | 93080<br>(58.9%) |
| 14 | analyte_type_id<br>[factor] | 1. D<br>2. E<br>3. G<br>4. H<br>5. R<br>6. S<br>7. T<br>8. W<br>9. X | 24407 (37.9%)<br>38 ( 0.1%)<br>1054 ( 1.6%)<br>1180 ( 1.8%)<br>12856 (20.0%)<br>38 ( 0.1%)<br>2041 ( 3.2%)<br>20631 (32.0%)<br>2177 ( 3.4%) | | 64422<br>(40.7%) | 93678<br>(59.3%) |
| 15 | analyte_volume<br>[logical] | All NA's | | | 0<br>(0.0%) | 158100<br>(100.0%) |
| 16 | concentration<br>[numeric] | Mean (sd) : 0.216 (0.137)<br>min < med < max:<br>0 < 0.16 < 2.1<br>IQR (CV) : 0.02 (0.631) | 637 distinct values |  | 49717<br>(31.4%) | 108383<br>(68.6%) |
| 17 | normal_tumor_genotype_snp_match<br>[factor] | 1. Yes | 3642 (100.0%) | | 3642<br>(2.3%) | 154458<br>(97.7%) |
| 18 | ribosomal_rna_28s_16s_ratio<br>[numeric] | Mean (sd) : 1.524 (0.518)<br>min < med < max:<br>0 < 1.53 < 4.42<br>IQR (CV) : 0.5 (0.34) | 166 distinct values |  | 768<br>(0.5%) | 157332<br>(99.5%) |

| No | Variable | Stats / Values | Freqs (% of Valid) | Graph | Valid | Missing |
|---|---|---|---|---|---|---|
| 19 | spectrophotometer_method [factor] | 1. PicoGreen<br>2. UV Spec | 17101 (35.0%)<br>31719 (65.0%) | | 48820 (30.9%) | 109280 (69.1%) |
| 20 | state [factor] | 1. released | 65020 (100.0%) | | 65020 (41.1%) | 93080 (58.9%) |
| 21 | well_number [logical] | All NA's | | | 0 (0.0%) | 158100 (100.0%) |

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