

# mCode Value Sets

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## Contents

OMOP Concept Distribution Plots . . . . .	2
Valueset Data . . . . .	27

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This vignette explores reconfiguring the mCode to OMOP Mappings.

```
library(mOMOP)
library(tidyverse)
```

Combining all the maps into a single map between all the value sets and mappings.

```
complete_map <- list(CANCER_STAGING, GENOMICS, ICD10CM, LOINC,
  SNOMED, SPECIMEN, UNITS_OF_MEASUREMENT) %>% map(mutate_all,
  as.character) %>% bind_rows()
complete_map
```

```
## # A tibble: 215,272 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537692
## 2 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537780
## 3 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537798
## 4 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537804
## 5 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537805
## 6 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537808
## 7 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537809
## 8 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537821
## 9 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537827
## 10 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537830
## # ... with 215,262 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
```

Names of value sets:

```
value_sets <- complete_map %>% rubix::split_by(col = value_set_name)
names(value_sets)
```

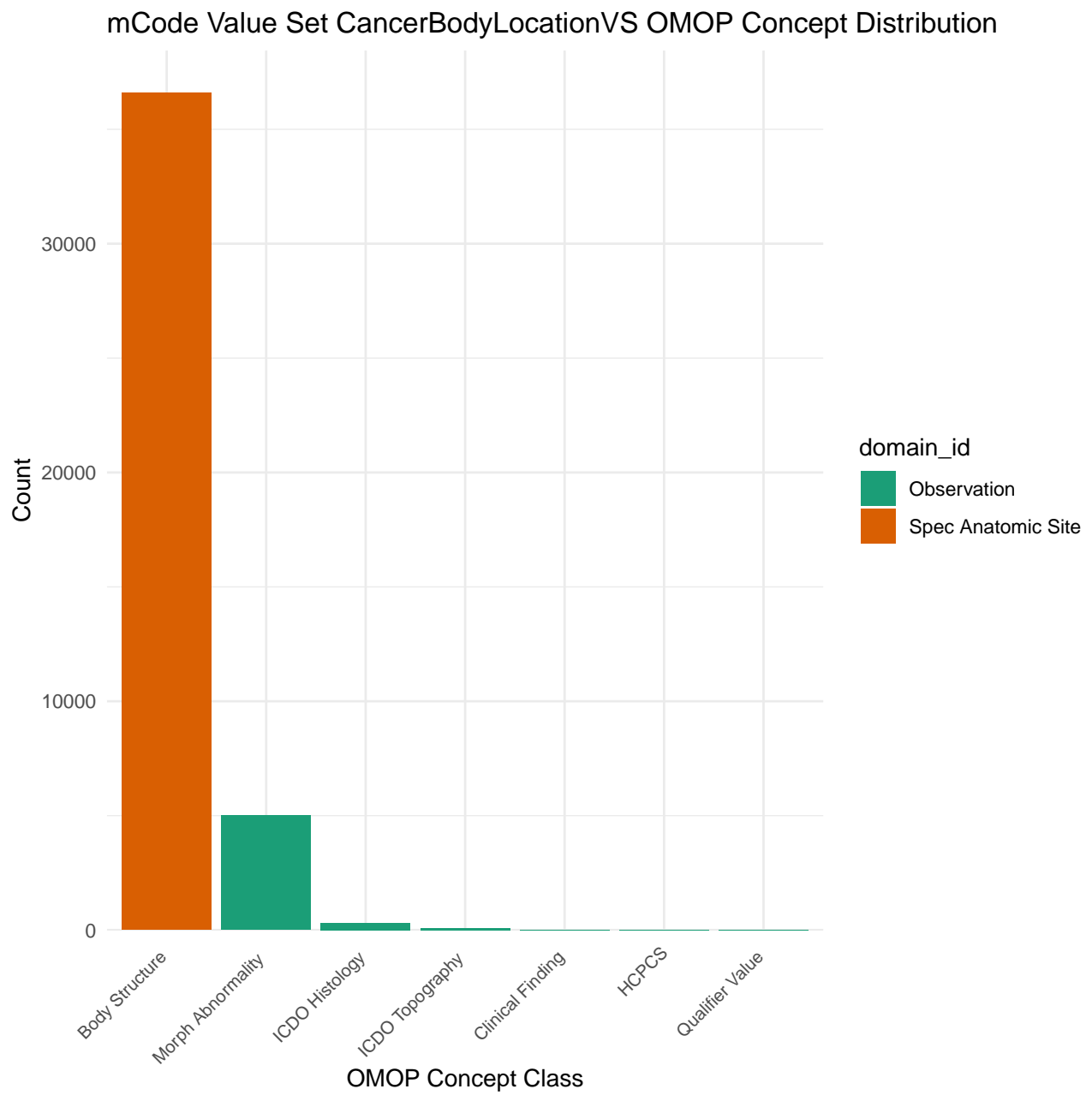
```
## [1] "CancerBodyLocationVS"
## [2] "CancerDiseaseStatusEvidenceTypeVS"
```

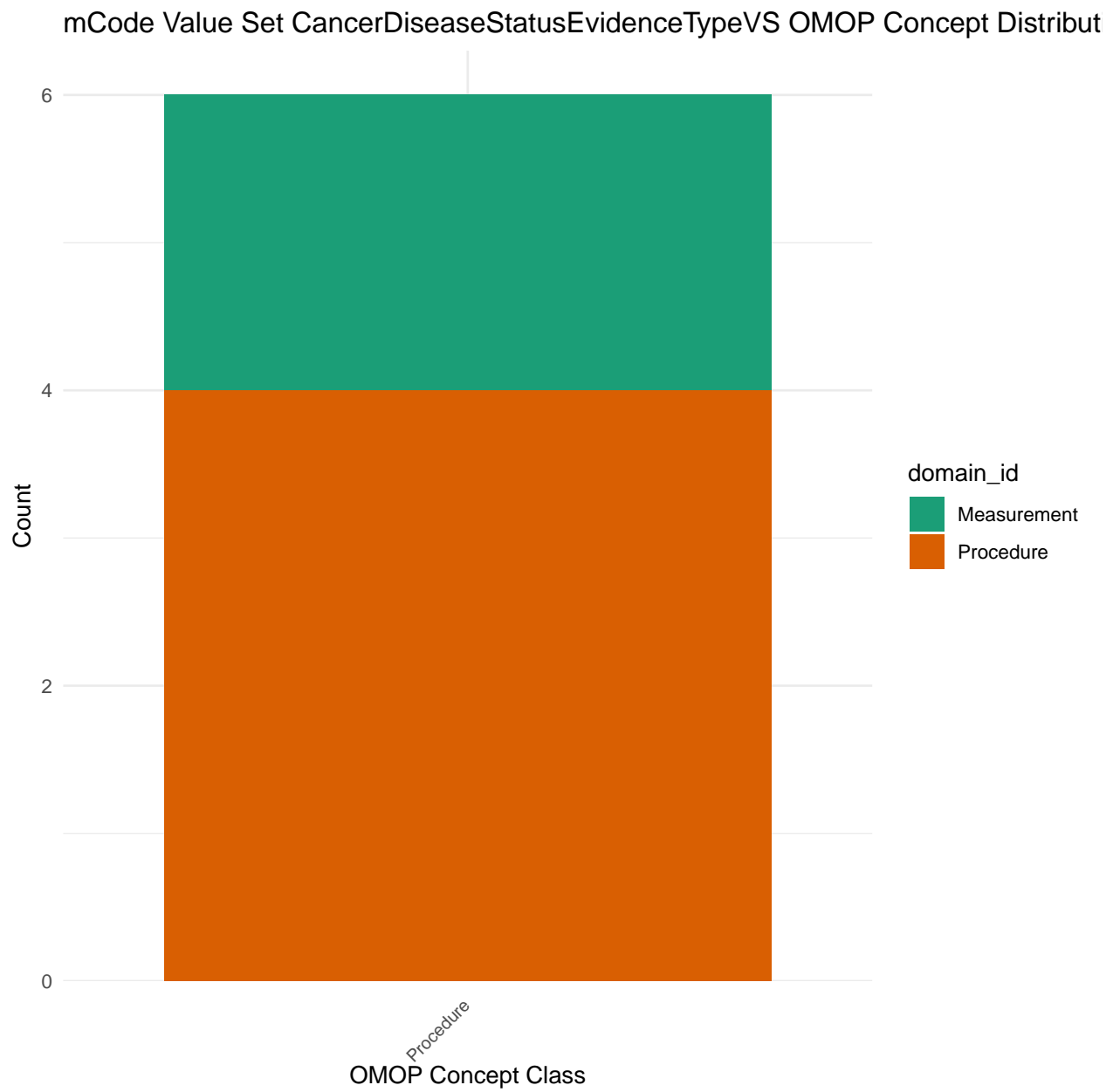
```
## [3] "CancerDisorderVS"
## [4] "CancerRelatedSurgicalProcedureVS"
## [5] "CancerStagingSystemVS"
## [6] "ClinVarVS"
## [7] "ComorbidConditionVS"
## [8] "ConditionStatusTrendVS"
## [9] "GeneticSpecimenTypeVS"
## [10] "HGNCVS"
## [11] "HistologyMorphologyBehaviorVS"
## [12] "LateralityVS"
## [13] "PrimaryOrUncertainBehaviorCancerDisorderVS"
## [14] "RadiationProcedureVS"
## [15] "RadiationTargetBodySiteVS"
## [16] "SecondaryCancerDisorderVS"
## [17] "TNMDistantMetastasesCategoryVS"
## [18] "TNMPrimaryTumorCategoryVS"
## [19] "TNMRegionalNodesCategoryVS"
## [20] "TNMStageGroupVS"
## [21] "TreatmentIntentVS"
## [22] "TreatmentTerminationReasonVS"
## [23] "TumorMarkerTestVS"
## [24] "UnitsOfLengthVS"
## [25] "YesNoUnknownVS"
```

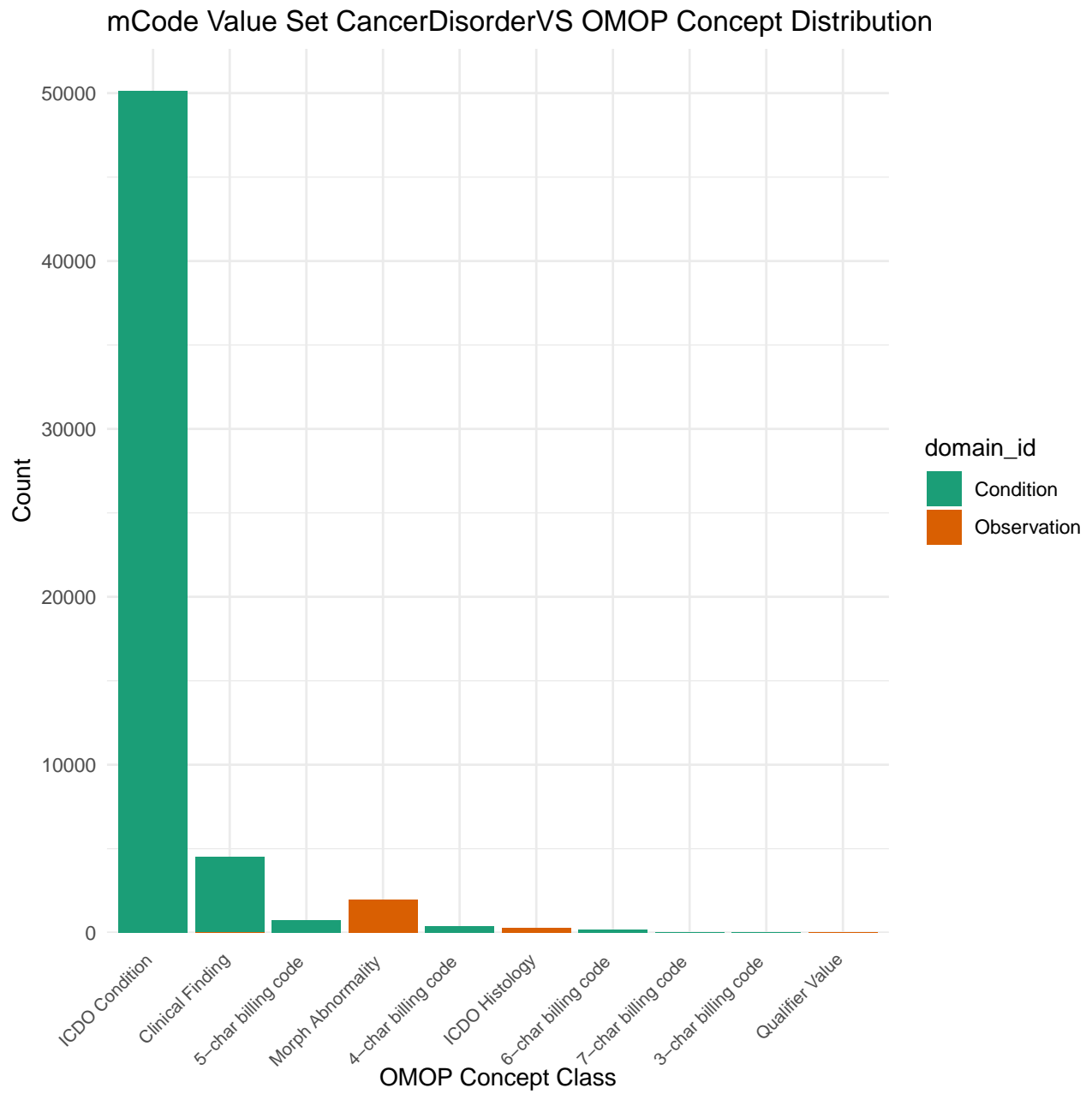
## OMOP Concept Distribution Plots

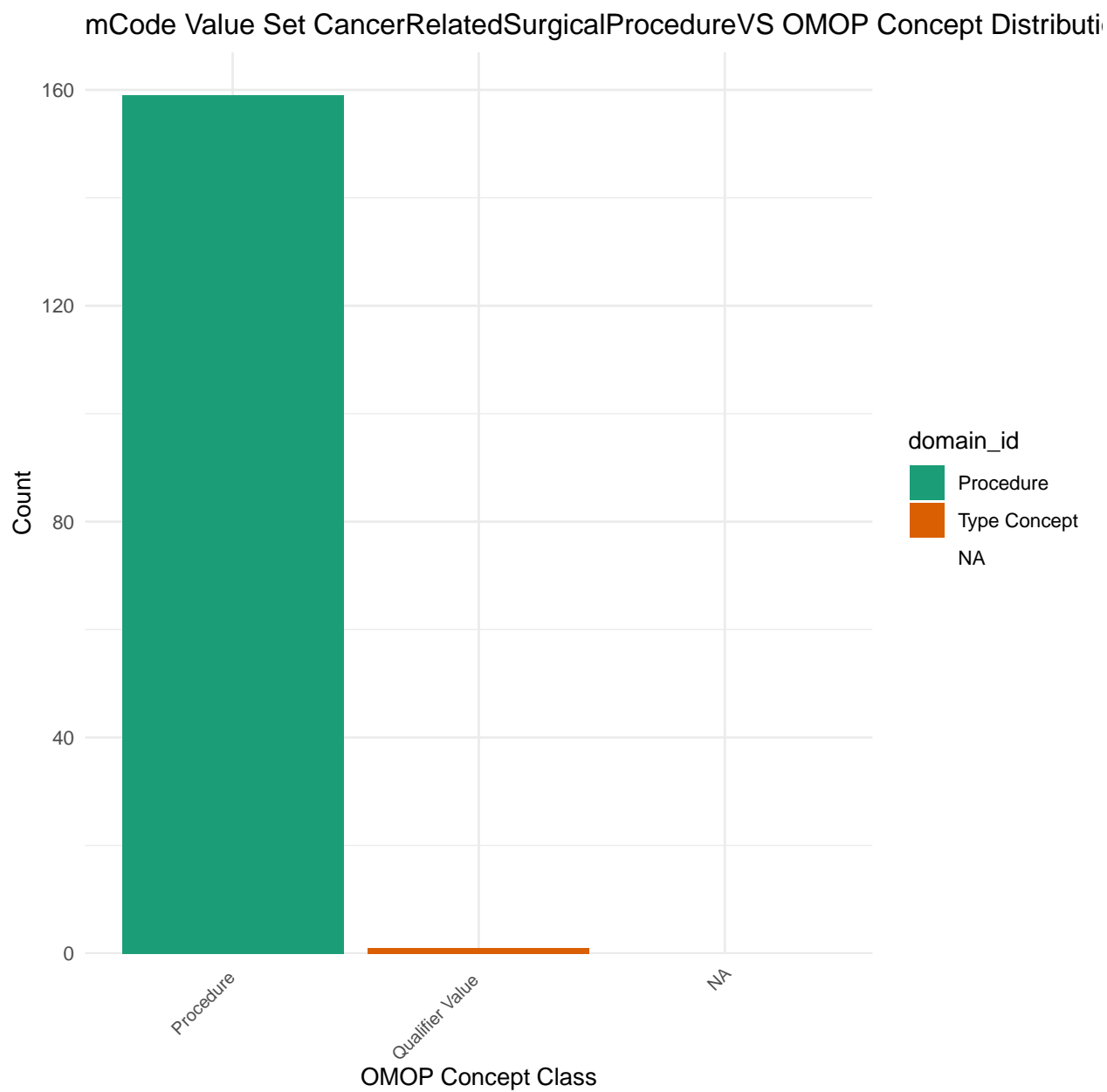
Each mCode value set's OMOP mapping distribution is plotted for visual comparison of the way the concepts are represented in OMOP.

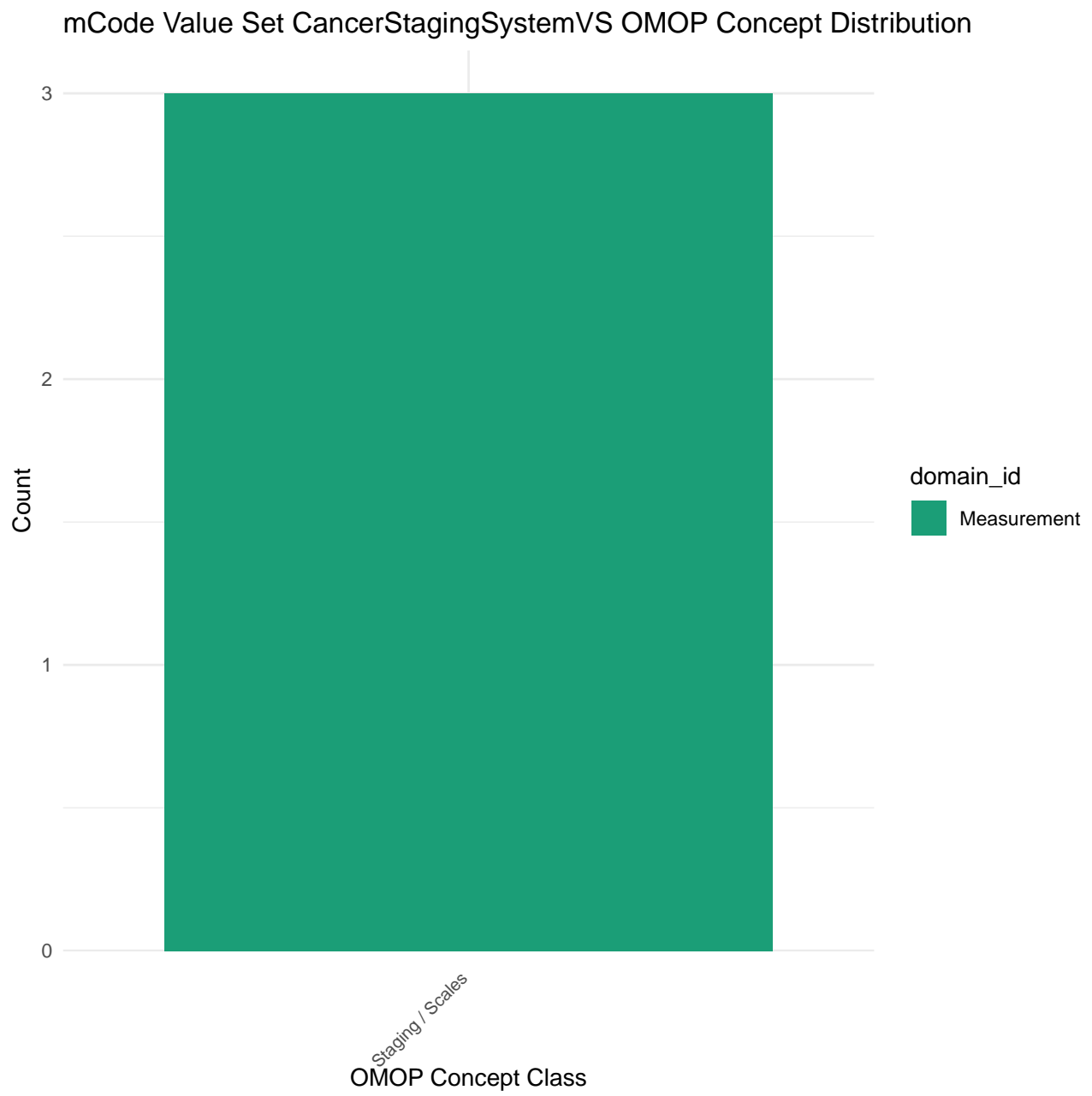
```
for (i in seq_along(value_sets)) {
  df <- value_sets[[i]] %>% count(domain_id, vocabulary_id,
    concept_class_id)
  p <- ggplot2::ggplot(data = df, aes(x = reorder(concept_class_id,
    -n), y = n, fill = domain_id)) + ggplot2::geom_bar(stat = "identity") +
    ggplot2::theme_minimal() + ggplot2::scale_y_continuous(expand = expansion(mult = c(0,
    0.05))) + ggplot2::labs(title = sprintf("mCode Value Set %s OMOP Concept Distribution",
    names(value_sets)[i]), x = "OMOP Concept Class", y = "Count") +
    ggplot2::scale_fill_brewer(palette = "Dark2") + ggplot2::theme(axis.text.x = element_text(angle
    hjust = 1.1, size = 8))
  print(p)
}
```

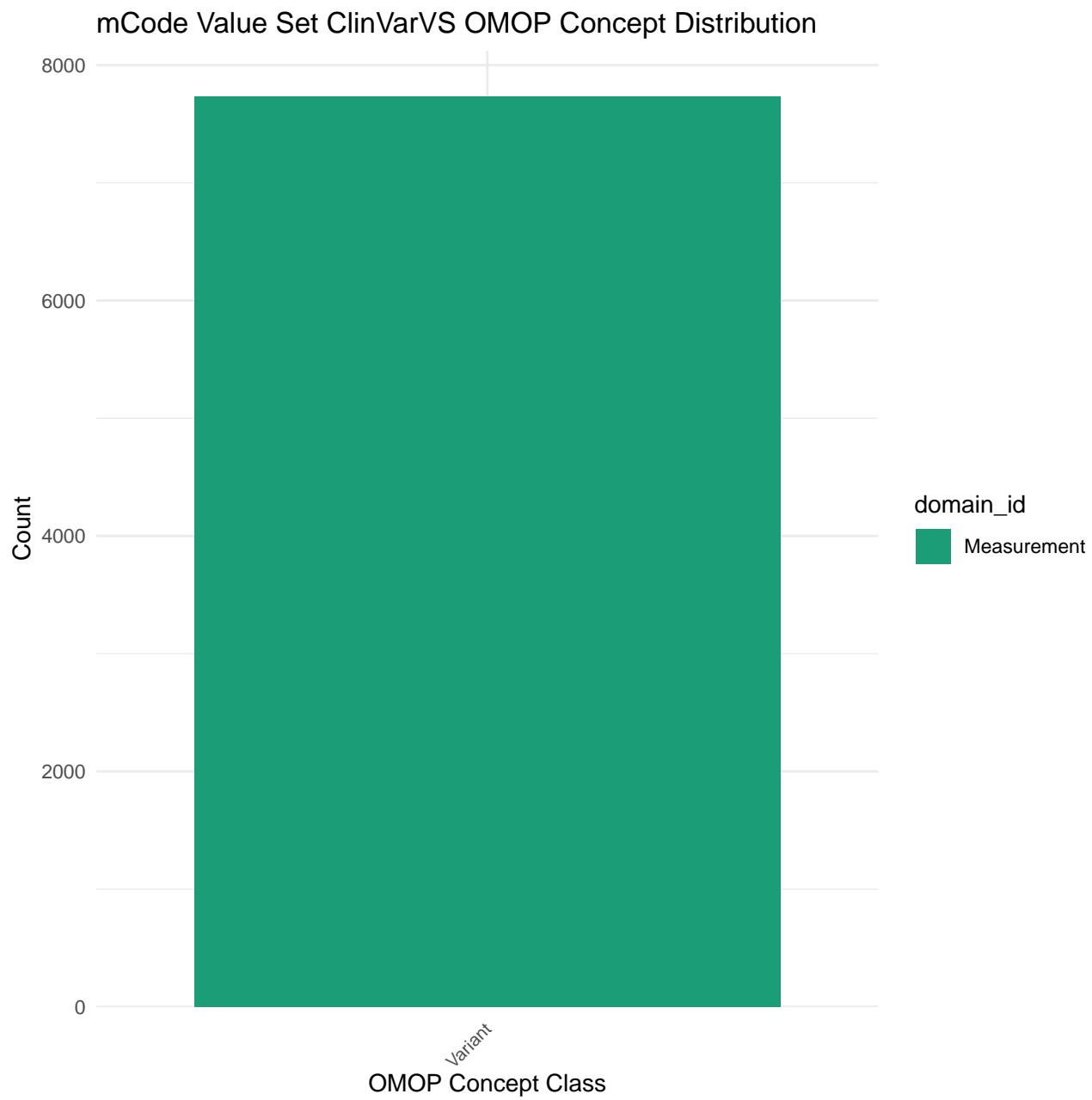






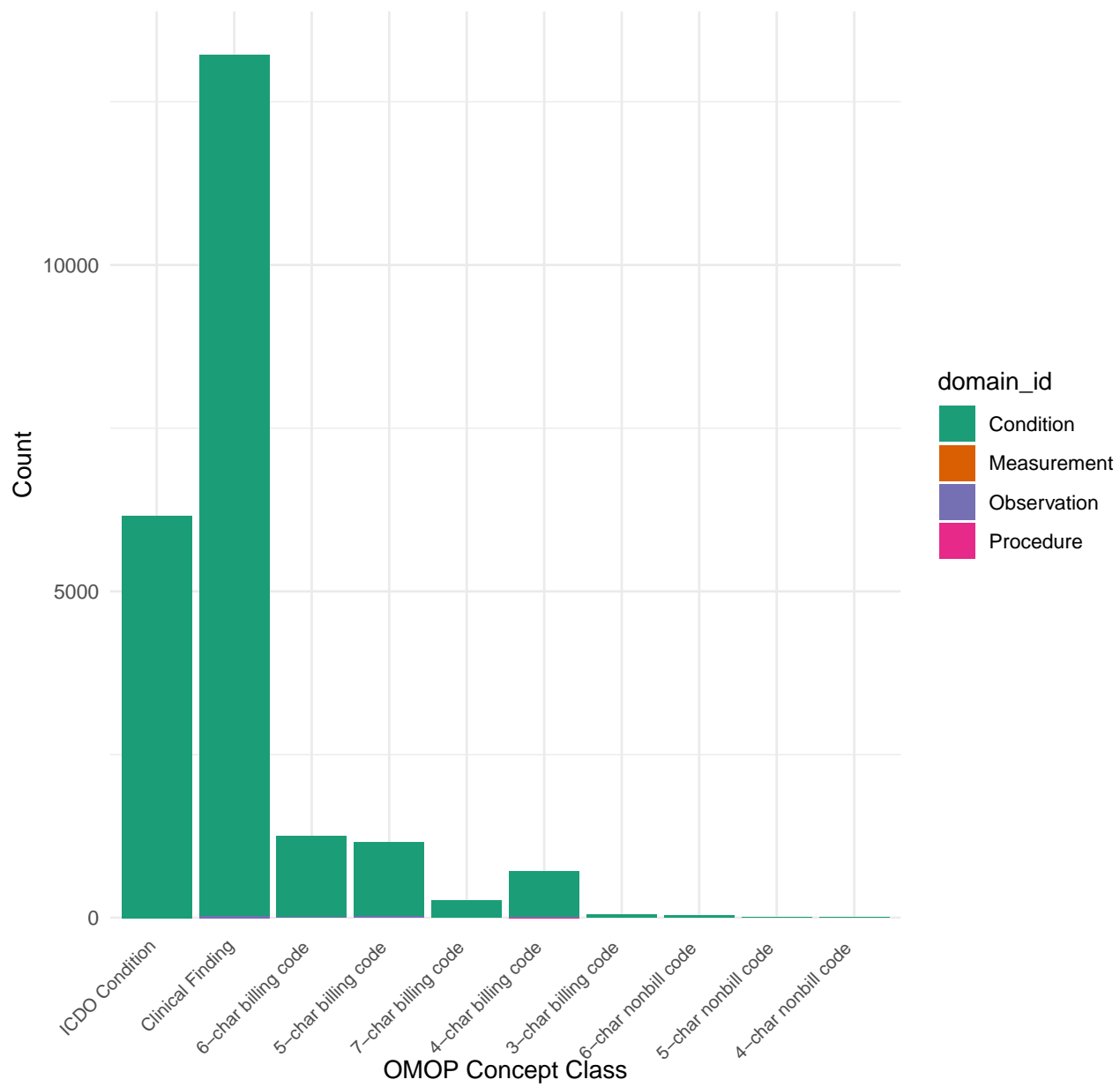


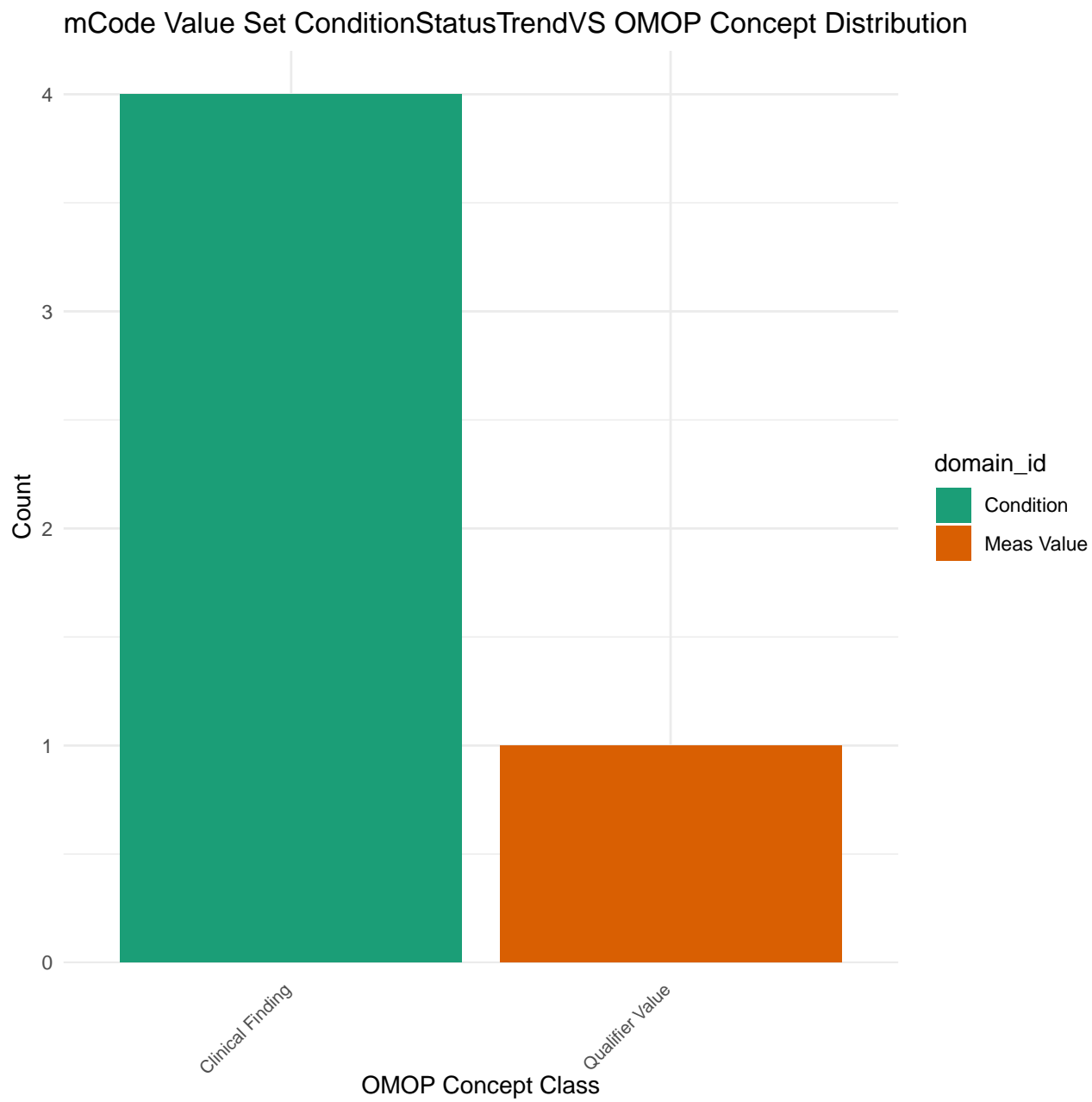


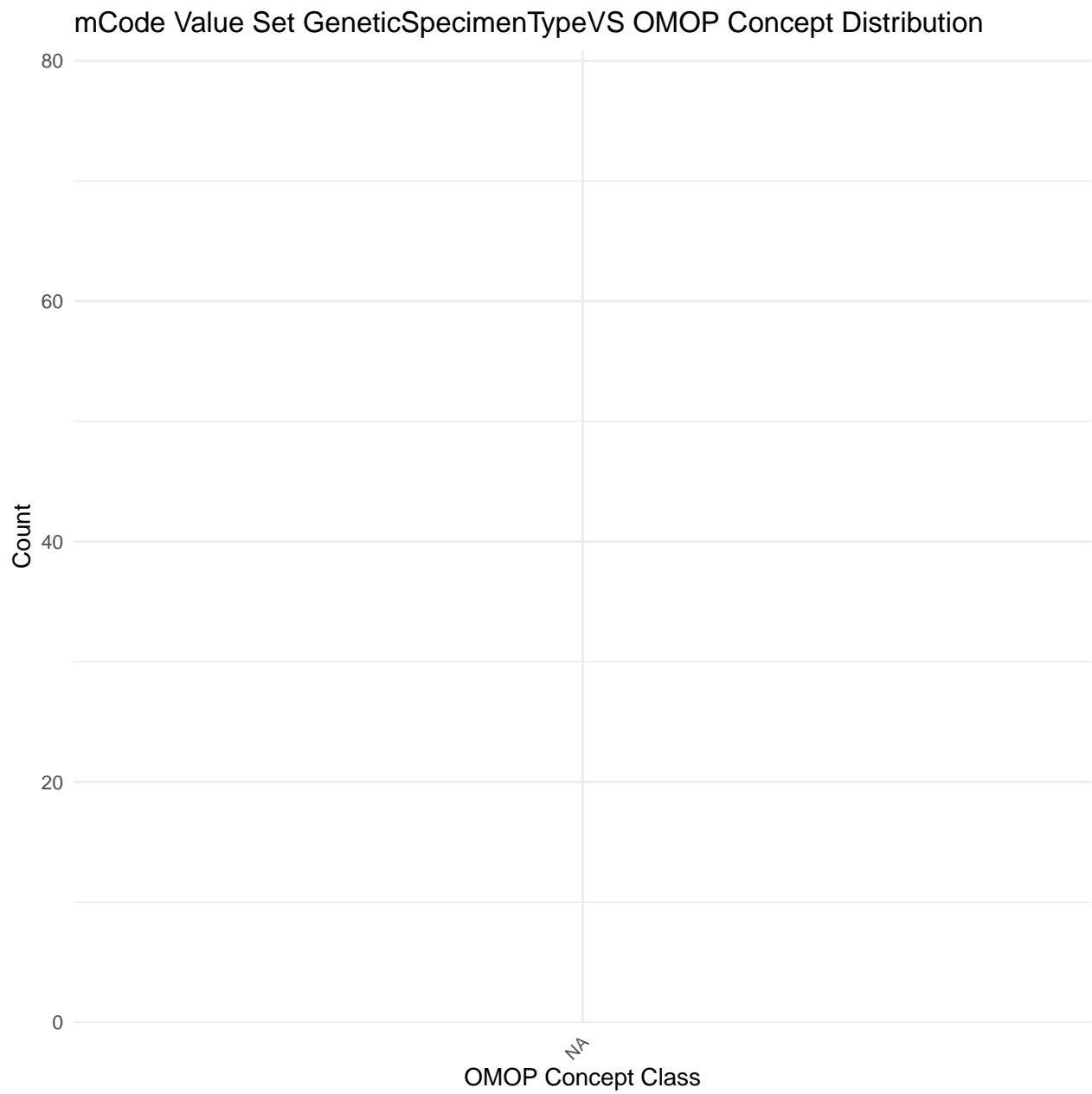


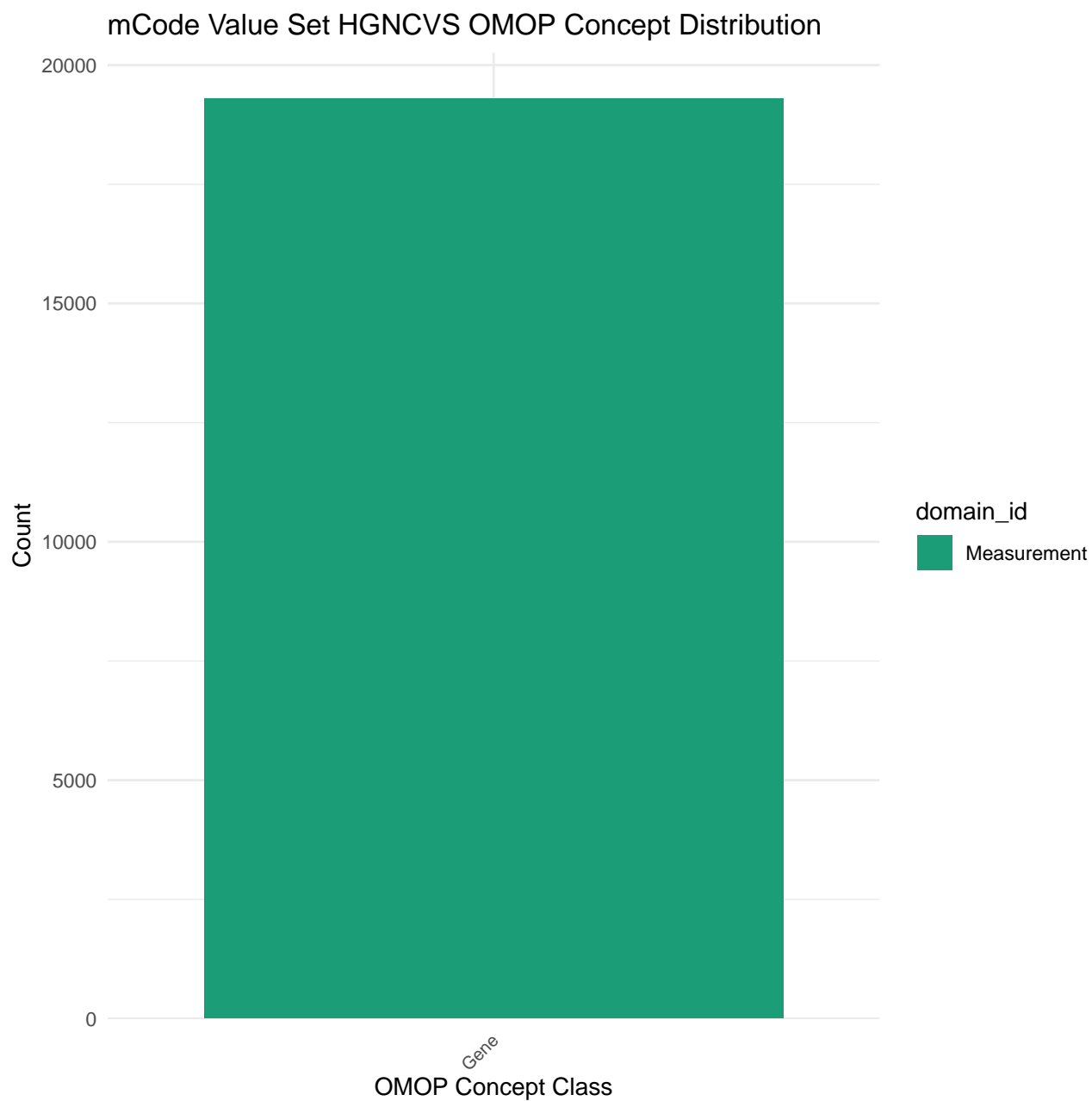


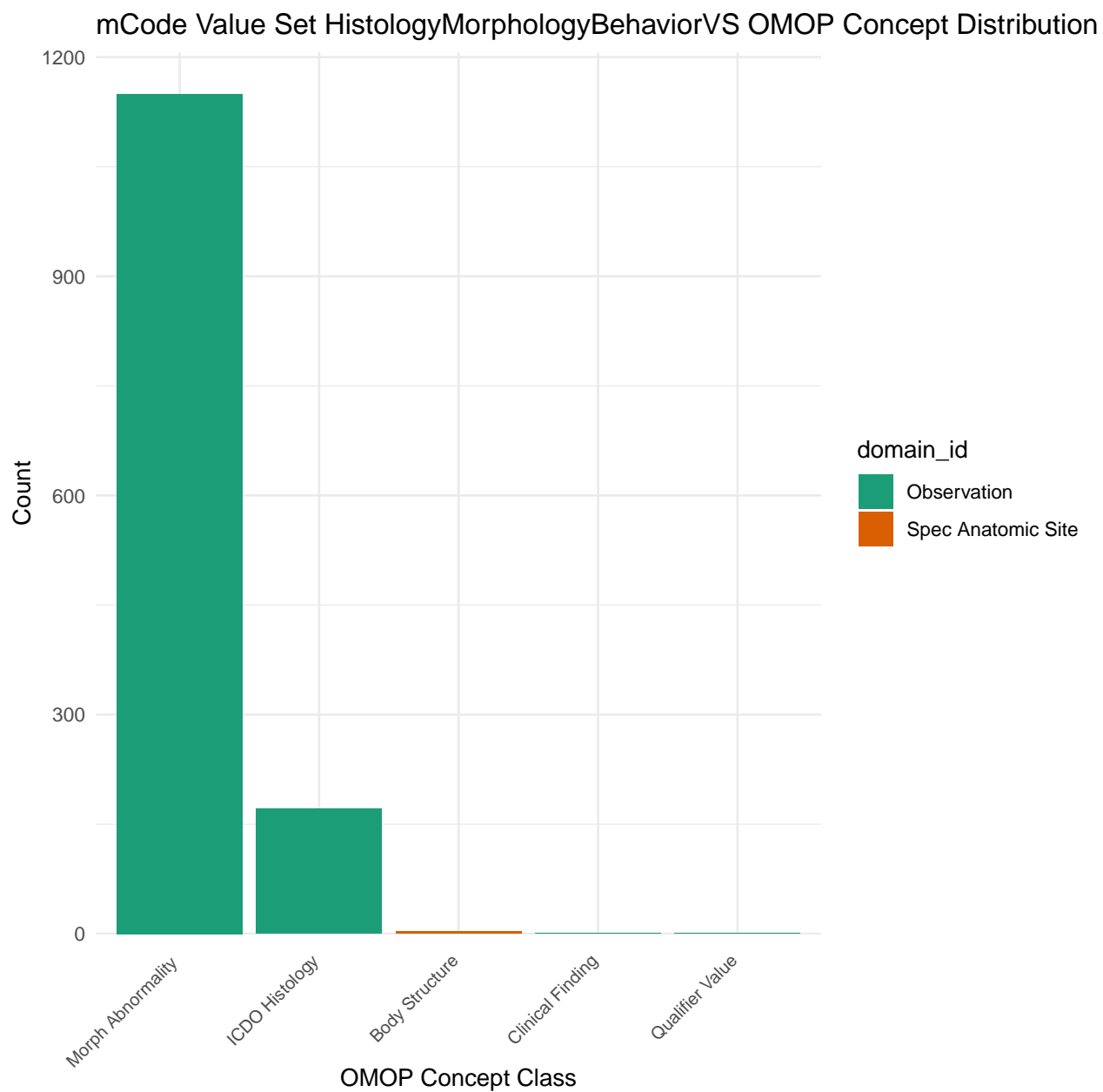
mCode Value Set ComorbidConditionVS OMOP Concept Distribution

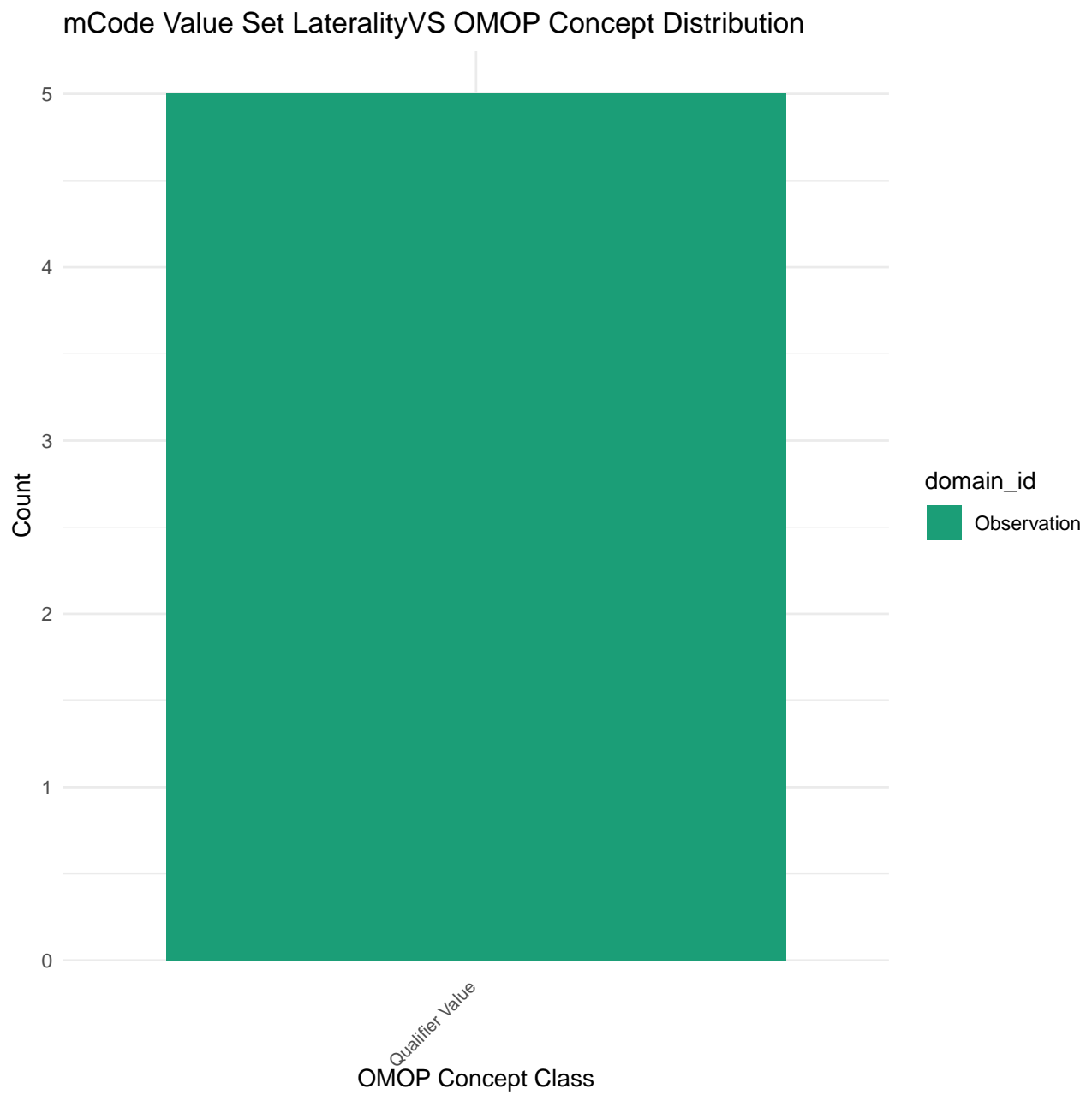


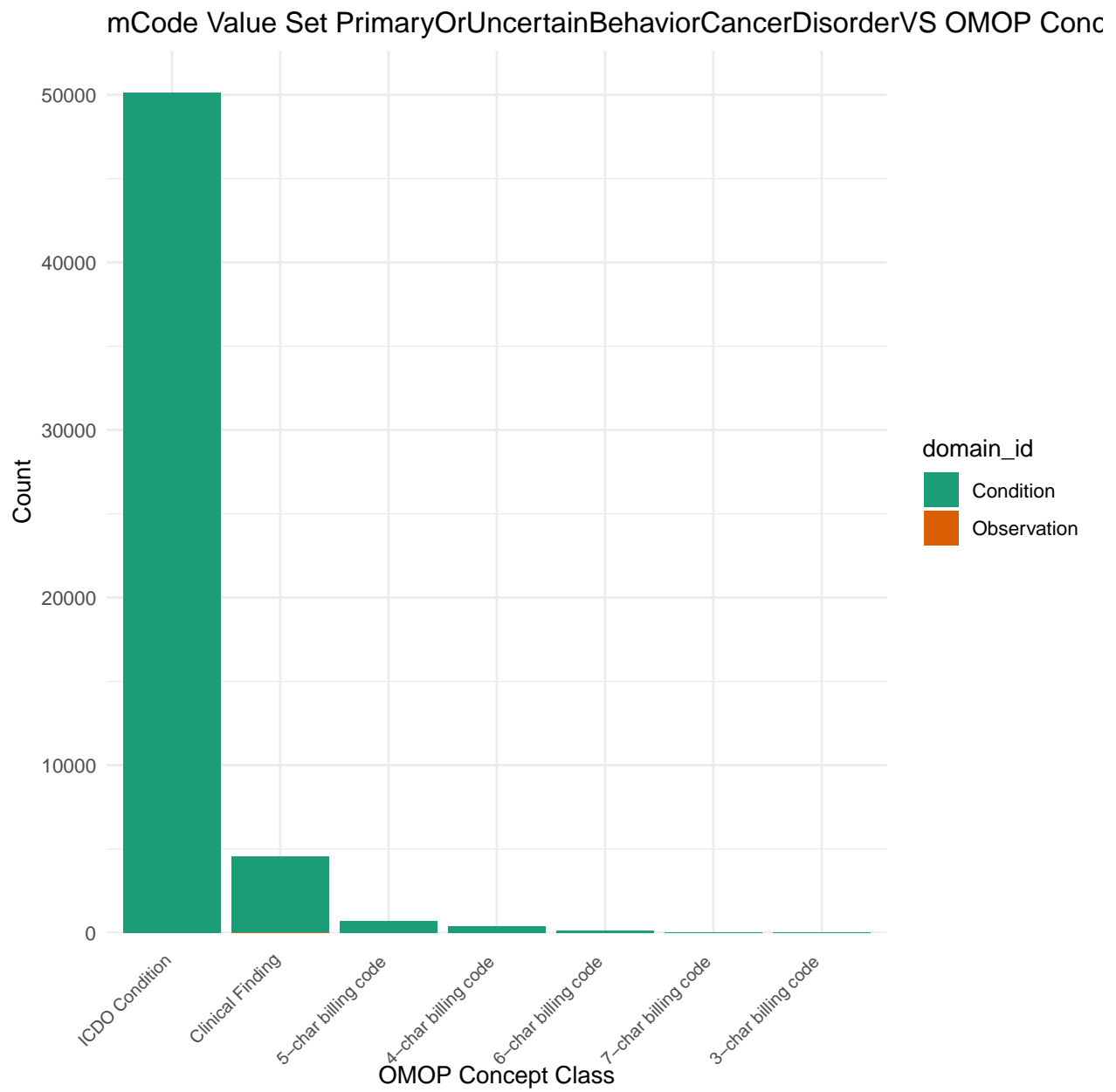


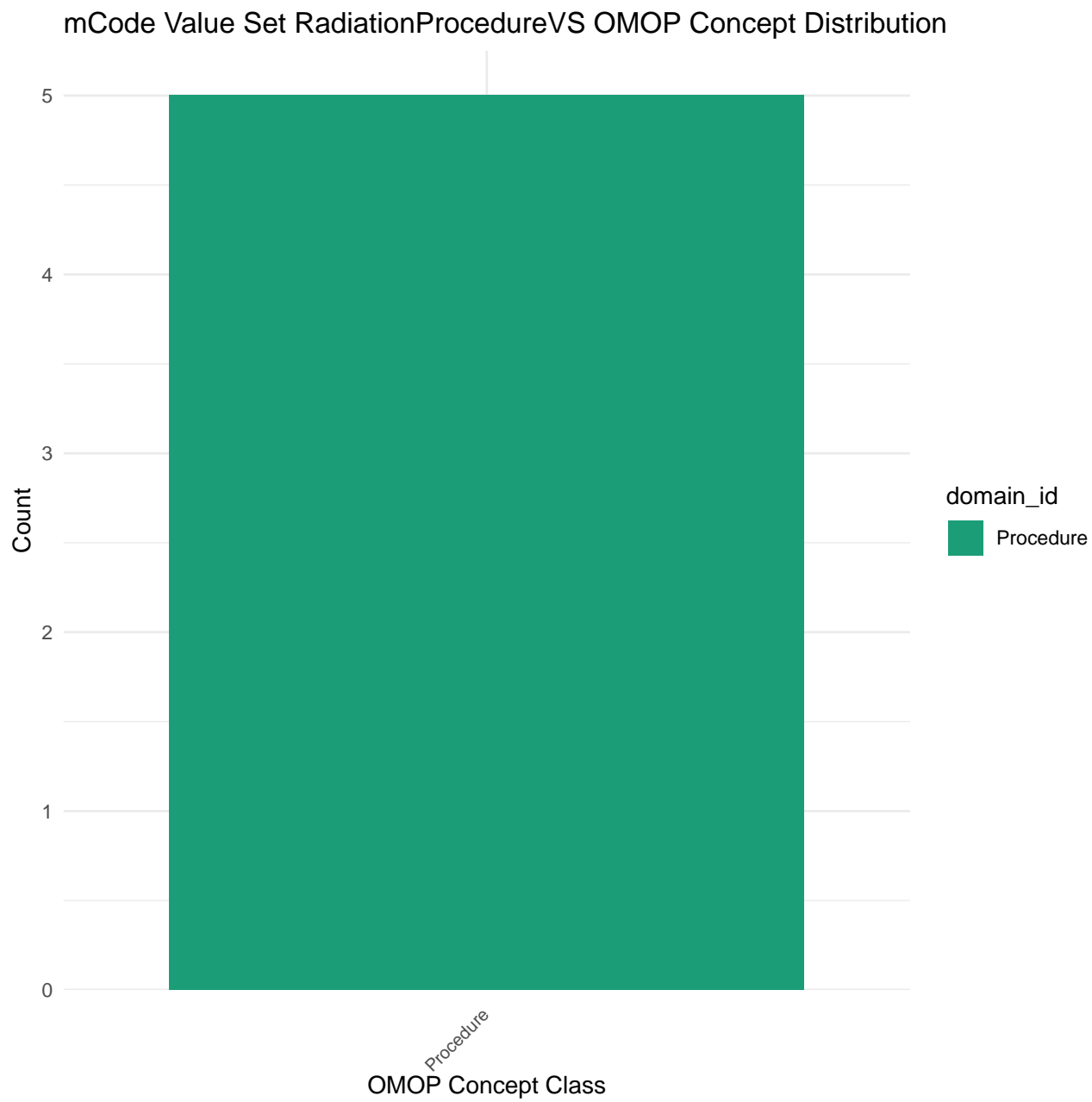




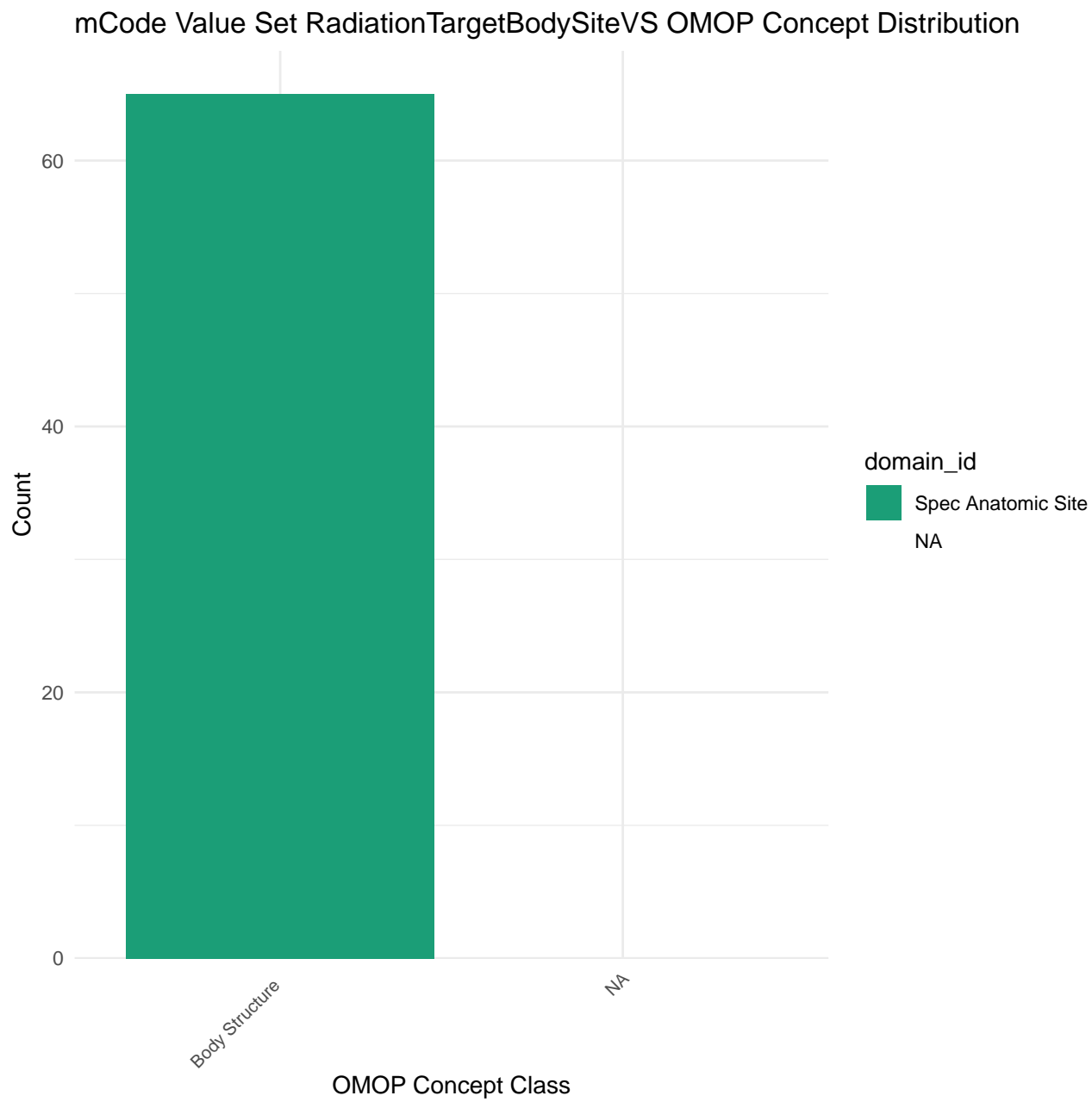


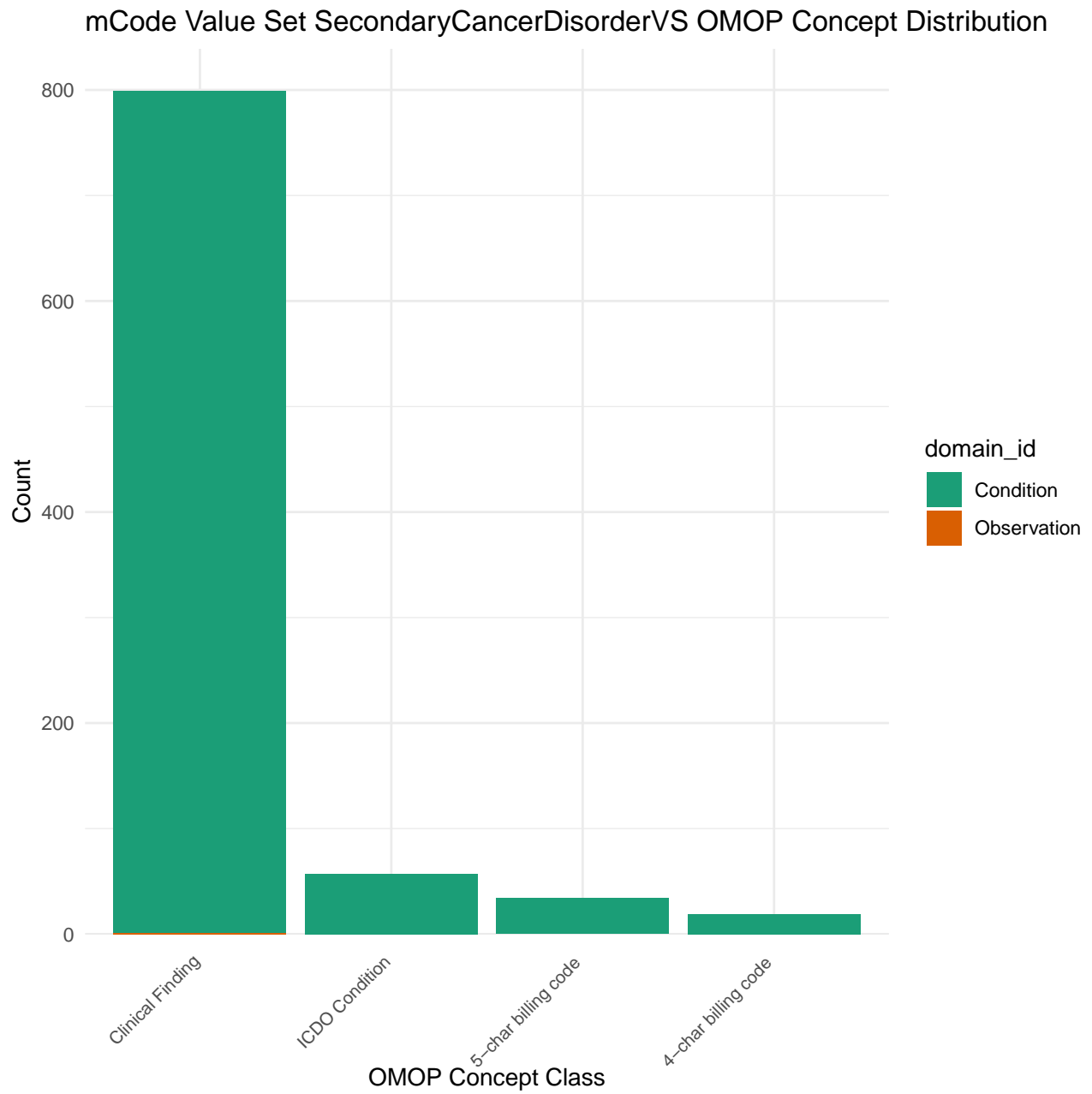


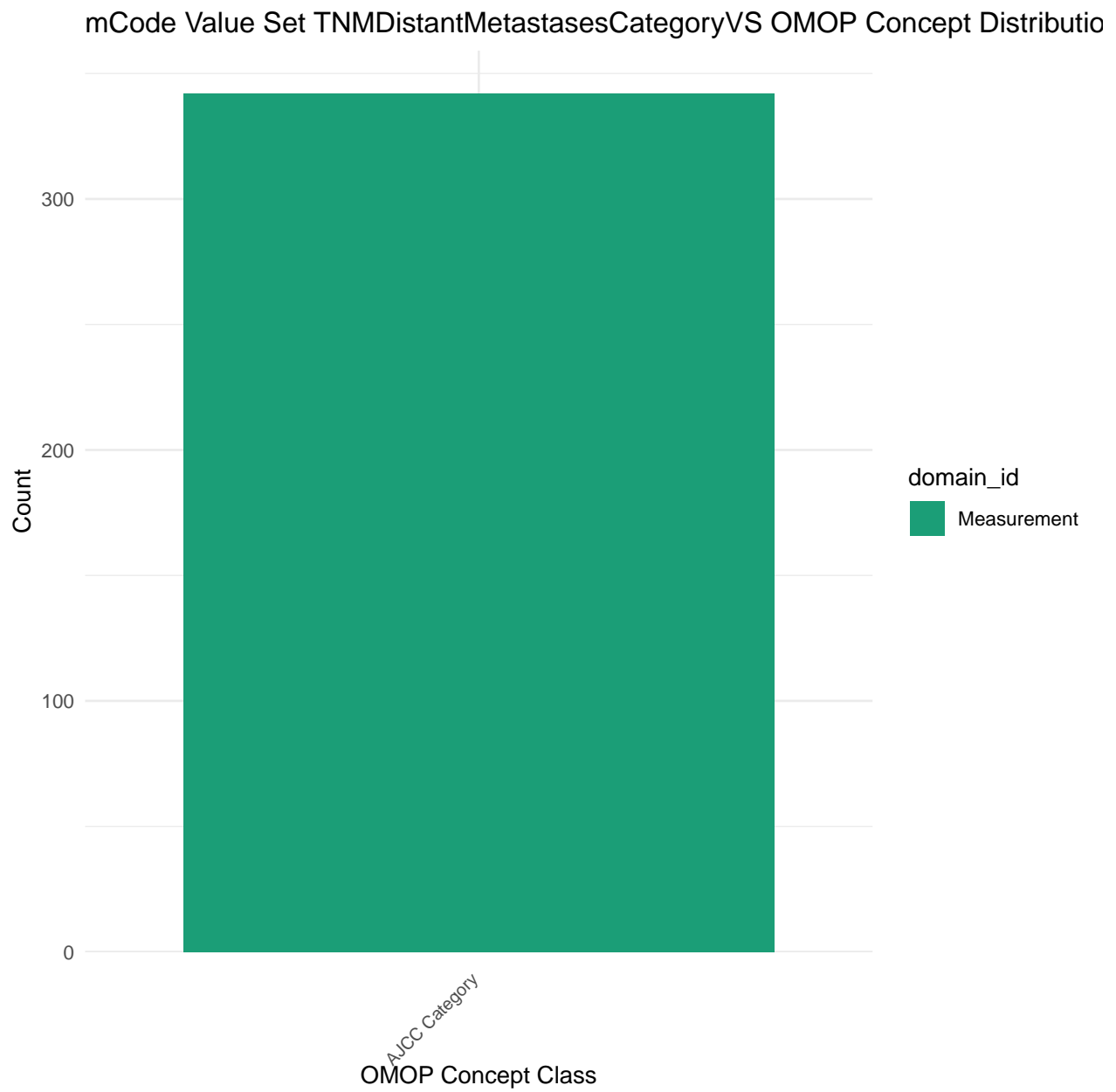


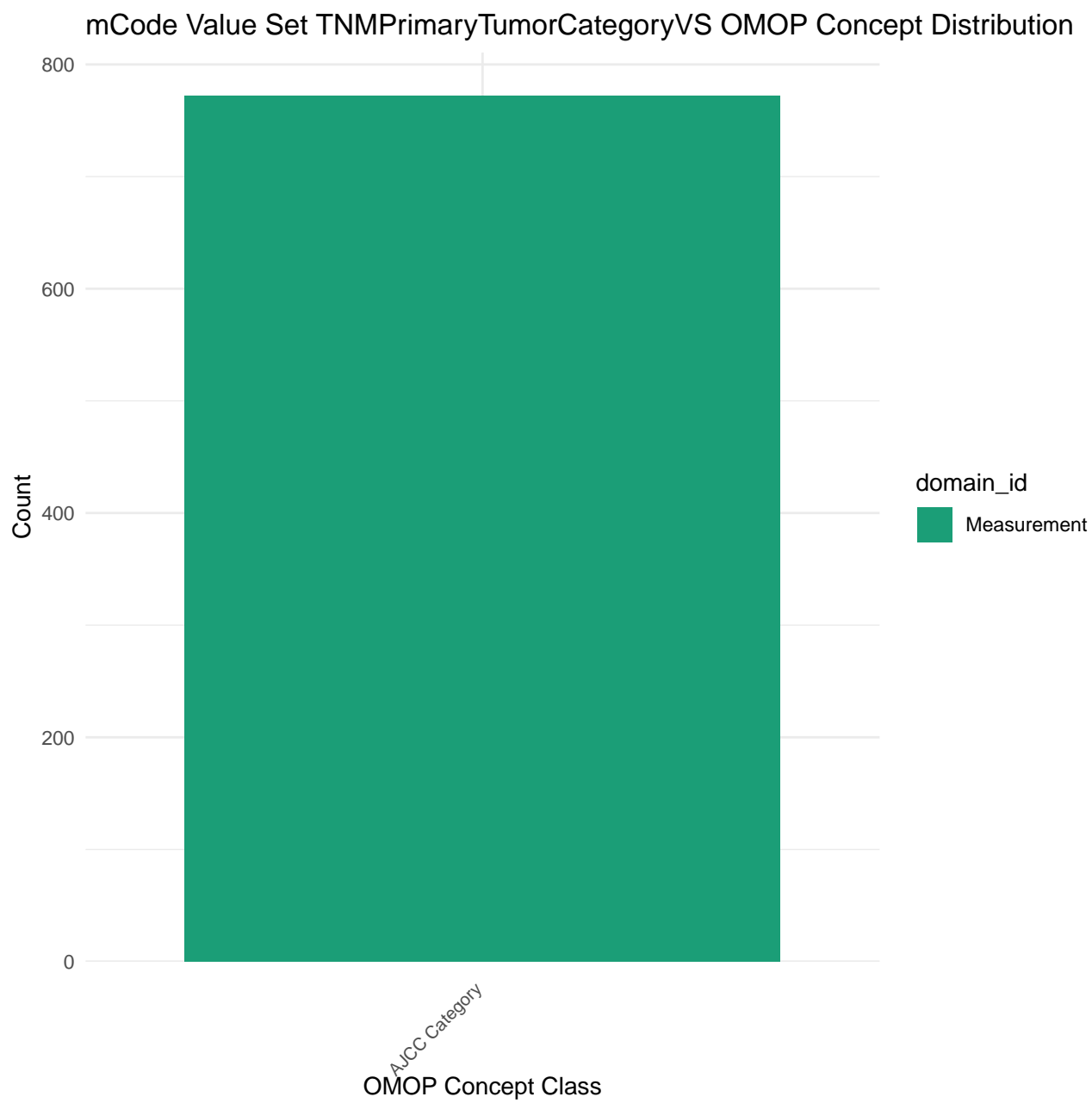


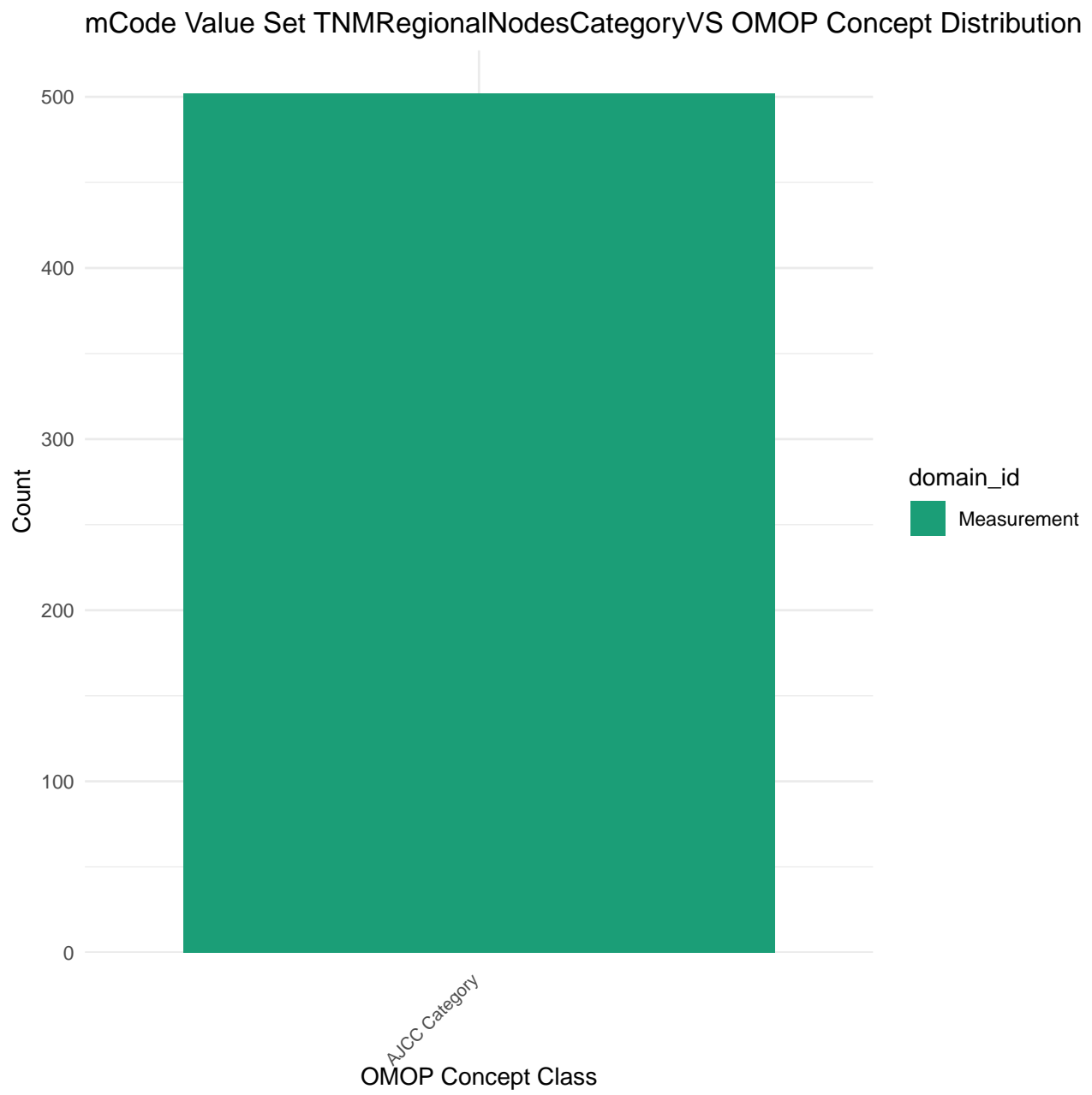


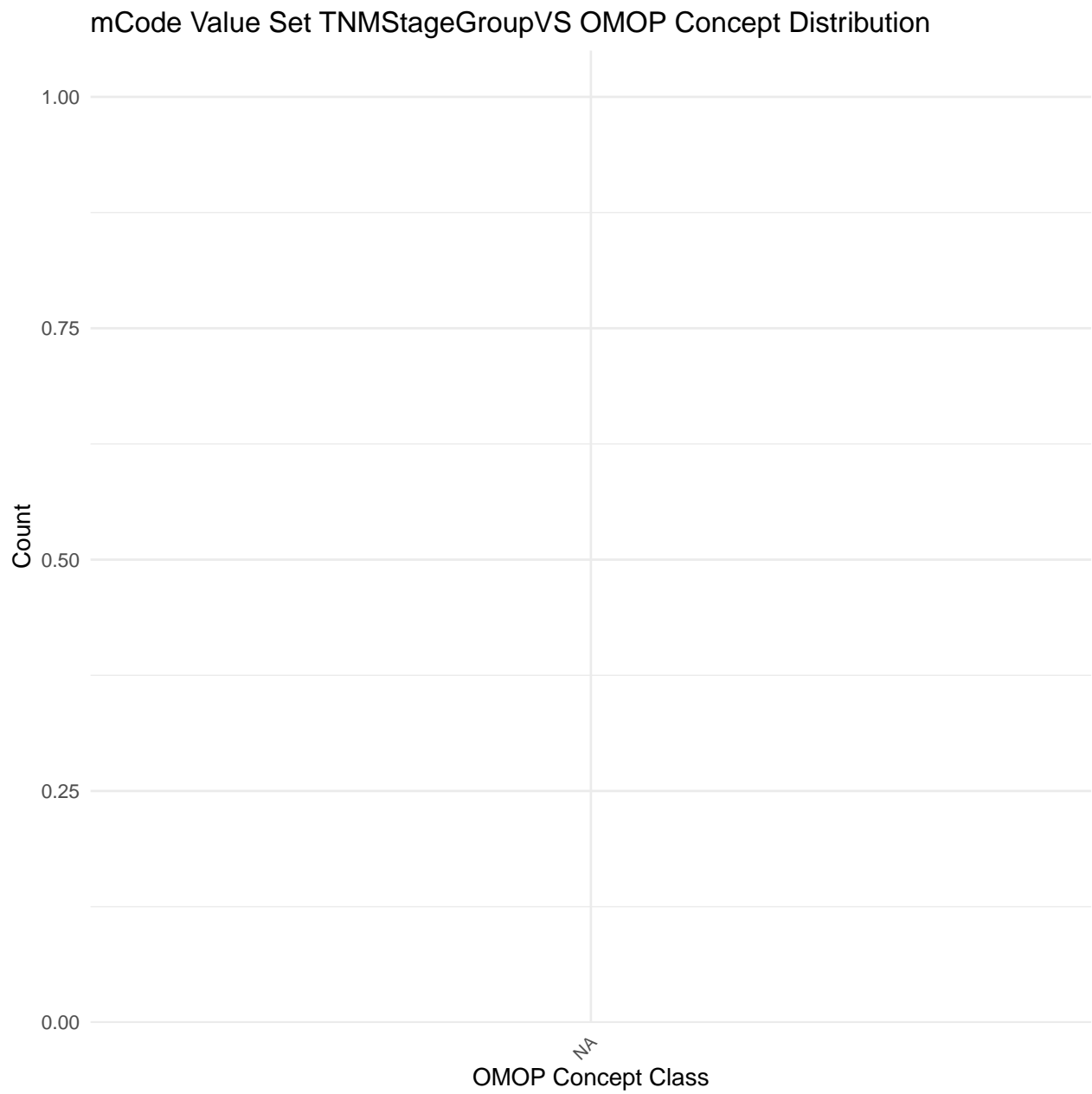


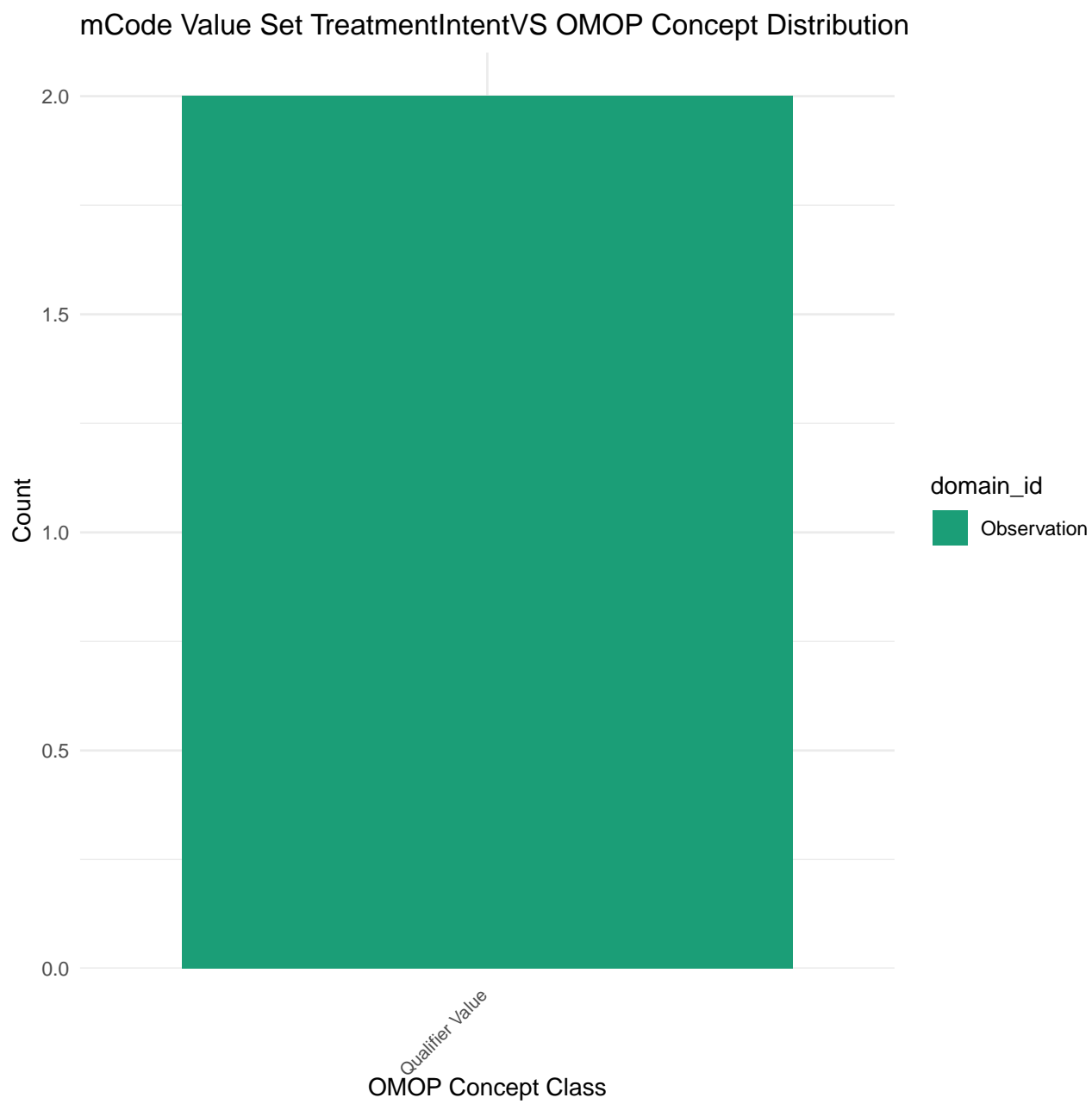


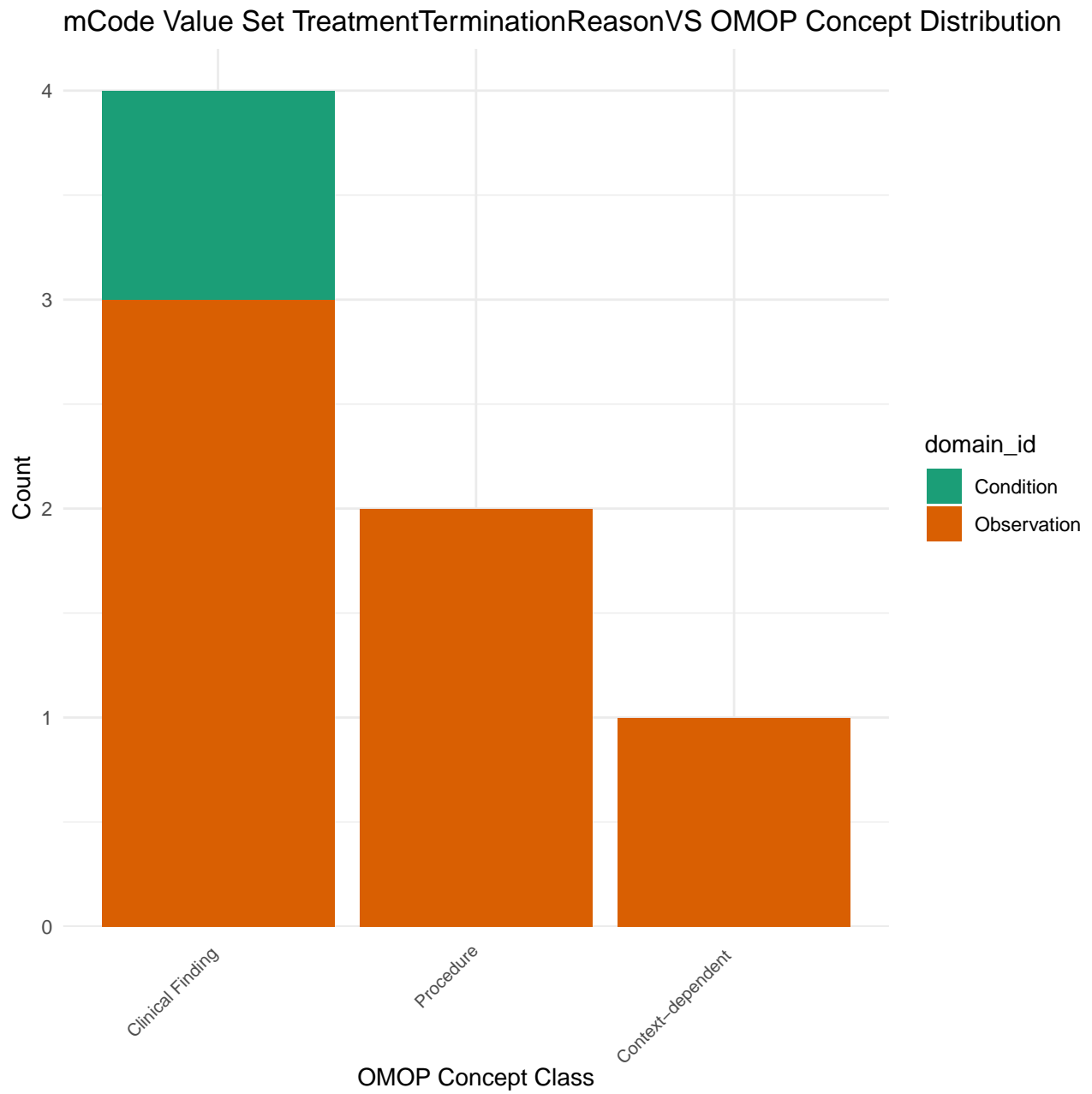




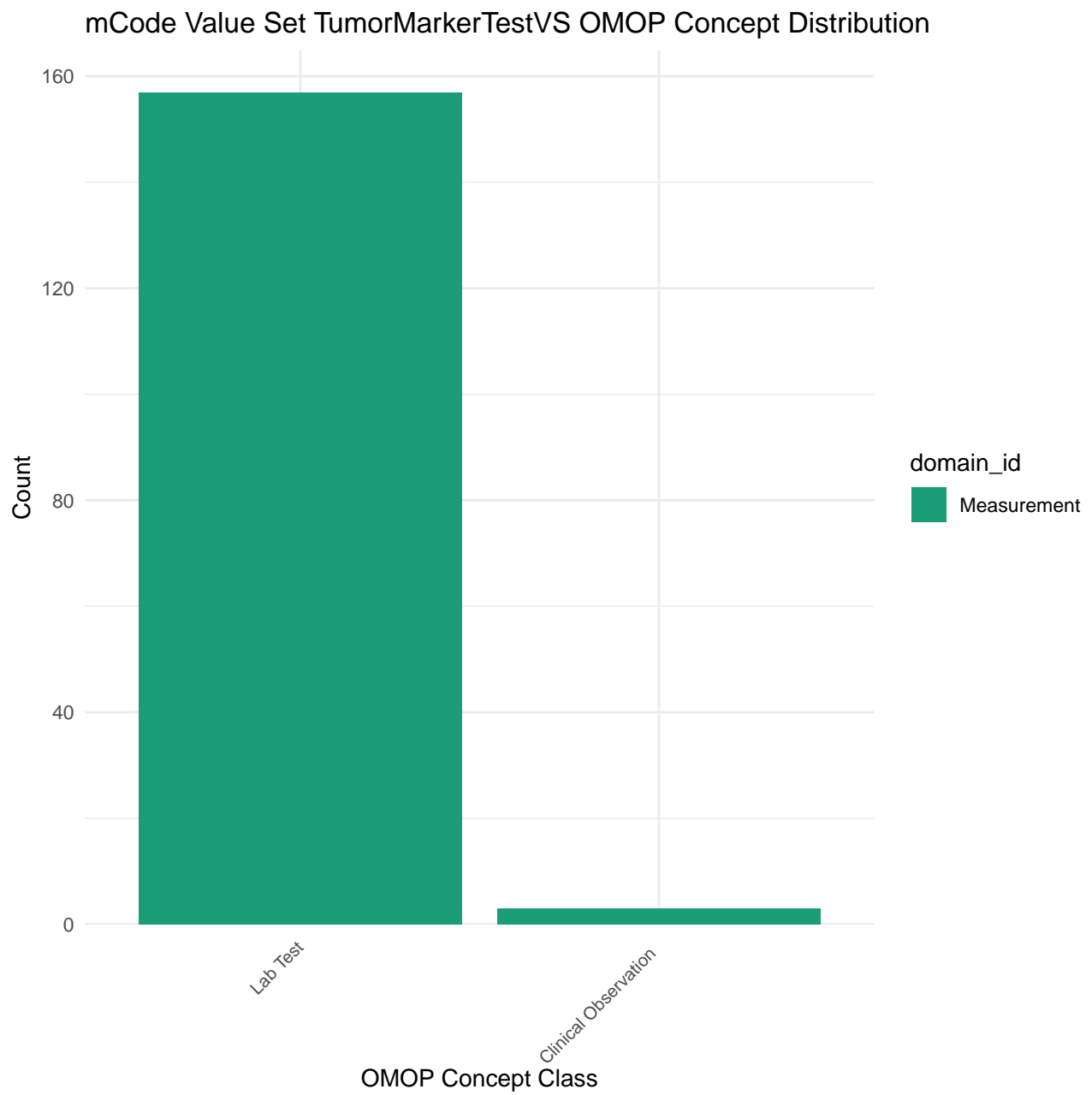




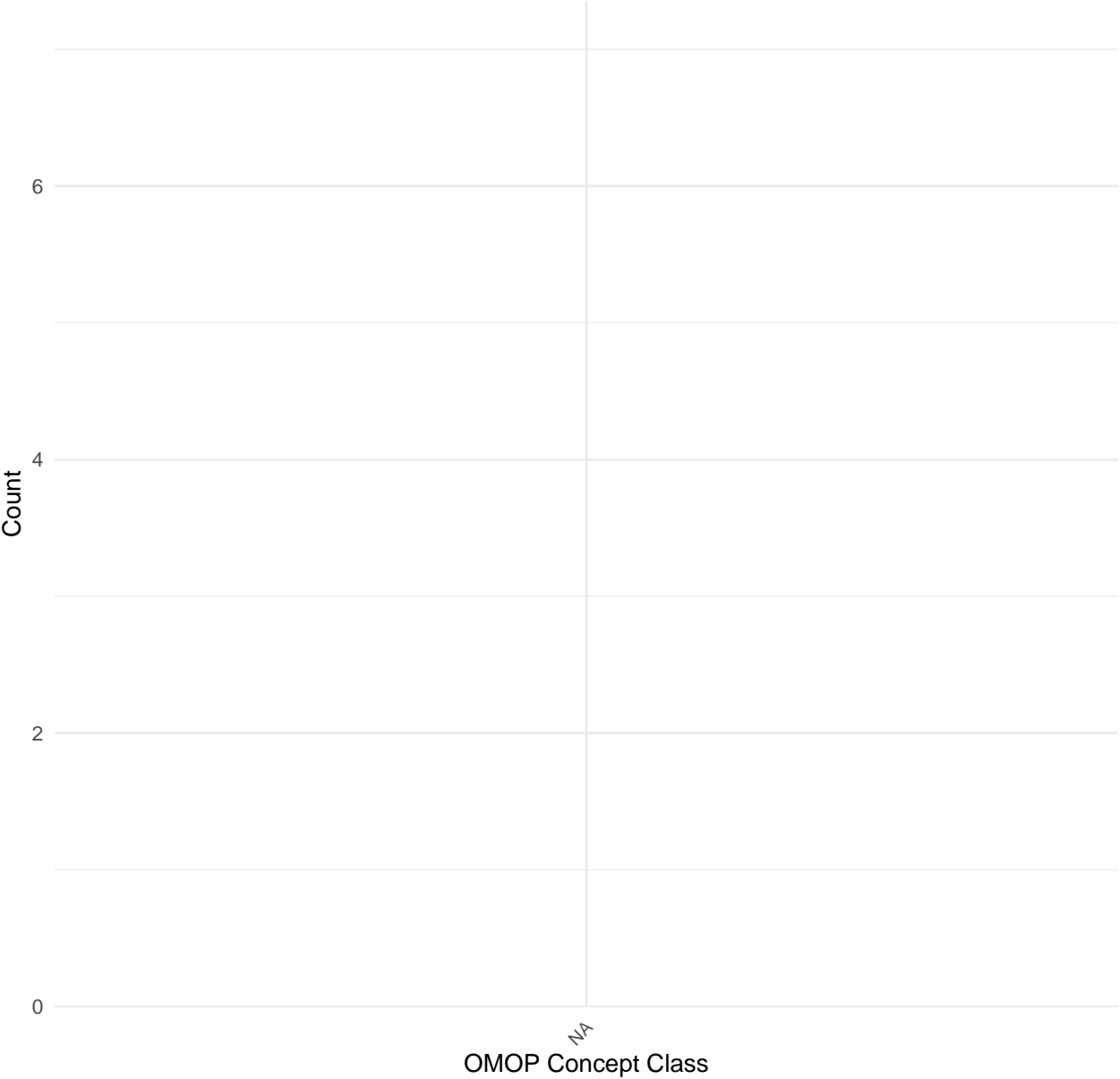


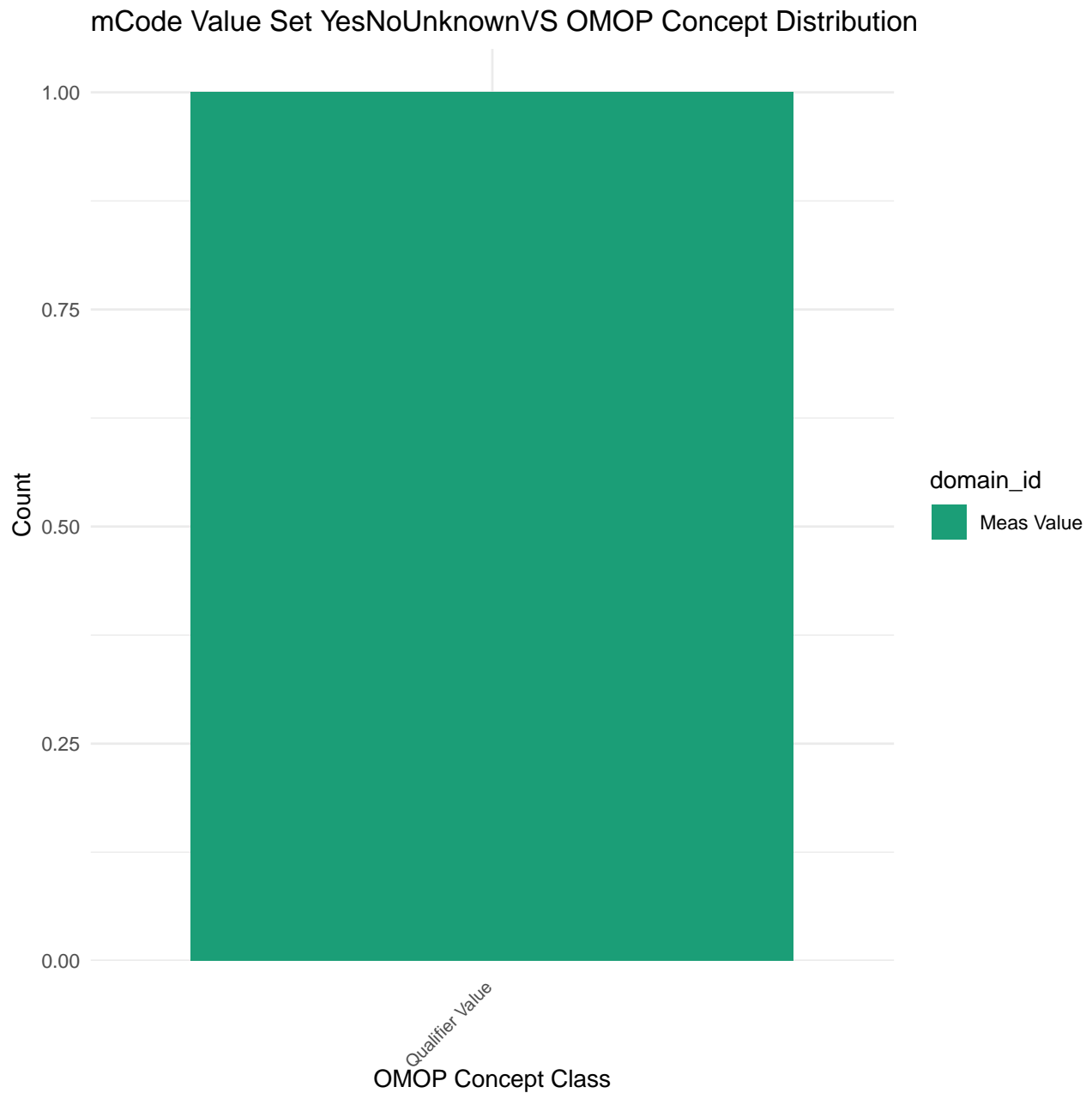






mCode Value Set UnitsOfLengthVS OMOP Concept Distribution





## Valueset Data

value\_sets

```
## $CancerBodyLocationVS
## # A tibble: 42,022 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA>          4048384
## 2 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA>          4002852
## 3 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA>          36717763
## 4 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA>          4230944
```

```

## 5 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 42605189
## 6 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 4097829
## 7 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 4265989
## 8 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 4143459
## 9 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 4093877
## 10 CancerBodyLoc~ SNOMED CT includes codes ~ <NA> <NA> 4300995
## # ... with 42,012 more rows, and 20 more variables: concept_name <chr>,
## # domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## # standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## # valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## # descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## # `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## # Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $CancerDiseaseStatusEvidenceTypeVS
## # A tibble: 6 x 26
## value_set_name code_system logical_definit~ code code_description concept_id
## <chr> <chr> <chr> <chr> <chr> <chr>
## 1 CancerDisease~ SNOMED CT <NA> <NA> <NA> 4180938
## 2 CancerDisease~ SNOMED CT <NA> <NA> <NA> 4098214
## 3 CancerDisease~ SNOMED CT <NA> <NA> <NA> 46272623
## 4 CancerDisease~ SNOMED CT <NA> <NA> <NA> 4240345
## 5 CancerDisease~ SNOMED CT <NA> <NA> <NA> 4353605
## 6 CancerDisease~ SNOMED CT <NA> <NA> <NA> 4303425
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## # vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## # concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## # invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## # all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## # Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## # Specimen <chr>, X14 <chr>
##
## $CancerDisorderVS
## # A tibble: 58,222 x 26
## value_set_name code_system logical_definit~ code code_description concept_id
## <chr> <chr> <chr> <chr> <chr> <chr>
## 1 CancerDisorde~ ICD-10-CM <NA> C00.0 Malignant neopl~ 35206047
## 2 CancerDisorde~ ICD-10-CM <NA> C00.1 Malignant neopl~ 35206048
## 3 CancerDisorde~ ICD-10-CM <NA> C00.2 Malignant neopl~ 35206049
## 4 CancerDisorde~ ICD-10-CM <NA> C00.3 Malignant neopl~ 35206050
## 5 CancerDisorde~ ICD-10-CM <NA> C00.4 Malignant neopl~ 35206051
## 6 CancerDisorde~ ICD-10-CM <NA> C00.5 Malignant neopl~ 35206052
## 7 CancerDisorde~ ICD-10-CM <NA> C00.6 Malignant neopl~ 35206053
## 8 CancerDisorde~ ICD-10-CM <NA> C00.8 Malignant neopl~ 35206054
## 9 CancerDisorde~ ICD-10-CM <NA> C00.9 Malignant neopl~ 35206055
## 10 CancerDisorde~ ICD-10-CM <NA> C01 Malignant neopl~ 35206056
## # ... with 58,212 more rows, and 20 more variables: concept_name <chr>,
## # domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## # standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## # valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## # descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## # `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## # Measurement <chr>, Specimen <chr>, X14 <chr>
##

```

```

## $CancerRelatedSurgicalProcedureVS
## # A tibble: 163 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4067441
## 2 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4171194
## 3 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4002559
## 4 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4087575
## 5 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4170198
## 6 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4029571
## 7 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4010266
## 8 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4270496
## 9 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4273866
## 10 CancerRelated~ SNOMED CT      <NA>          <NA> <NA>          4119922
## # ... with 153 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $CancerStagingSystemVS
## # A tibble: 3 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 CancerStaging~ SNOMED CT      <NA>          <NA> <NA>          40485522
## 2 CancerStaging~ SNOMED CT      <NA>          <NA> <NA>          40483646
## 3 CancerStaging~ SNOMED CT      <NA>          <NA> <NA>          4123019
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## #   all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## #   Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## #   Specimen <chr>, X14 <chr>
##
## $ClinVarVS
## # A tibble: 7,735 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968119
## 2 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968121
## 3 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968122
## 4 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968123
## 5 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968124
## 6 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968125
## 7 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968127
## 8 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968128
## 9 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968129
## 10 ClinVarVS      ClinVar      Includes codes ~ <NA> <NA>          35968130
## # ... with 7,725 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,

```

```

## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $ComorbidConditionVS
## # A tibble: 22,874 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 ComorbidCondi~ ICD-10-CM   <NA>          A52.~ Syphilitic endo~ 45537731
## 2 ComorbidCondi~ ICD-10-CM   <NA>          B18.0 Chronic viral h~ 35205769
## 3 ComorbidCondi~ ICD-10-CM   <NA>          B18.1 Chronic viral h~ 35205770
## 4 ComorbidCondi~ ICD-10-CM   <NA>          B18.2 Chronic viral h~ 35205771
## 5 ComorbidCondi~ ICD-10-CM   <NA>          B20   Human immunodef~ 35205776
## 6 ComorbidCondi~ ICD-10-CM   <NA>          C00.0 Malignant neopl~ 35206047
## 7 ComorbidCondi~ ICD-10-CM   <NA>          C00.1 Malignant neopl~ 35206048
## 8 ComorbidCondi~ ICD-10-CM   <NA>          C00.2 Malignant neopl~ 35206049
## 9 ComorbidCondi~ ICD-10-CM   <NA>          C00.3 Malignant neopl~ 35206050
## 10 ComorbidCondi~ ICD-10-CM   <NA>          C00.4 Malignant neopl~ 35206051
## # ... with 22,864 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $ConditionStatusTrendVS
## # A tibble: 5 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 ConditionStat~ SNOMED CT   <NA>          <NA> <NA>          9190
## 2 ConditionStat~ SNOMED CT   <NA>          <NA> <NA>          4149524
## 3 ConditionStat~ SNOMED CT   <NA>          <NA> <NA>          4234874
## 4 ConditionStat~ SNOMED CT   <NA>          <NA> <NA>          4150631
## 5 ConditionStat~ SNOMED CT   <NA>          <NA> <NA>          46271098
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## #   all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## #   Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## #   Specimen <chr>, X14 <chr>
##
## $GeneticSpecimenTypeVS
## # A tibble: 77 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 GeneticSpecim~ http://ter~ <NA>          SKN   Skin          1027716
## 2 GeneticSpecim~ http://ter~ <NA>          PLC   Placenta      1032268
## 3 GeneticSpecim~ http://ter~ <NA>          SAL   Saliva        1033195
## 4 GeneticSpecim~ http://ter~ <NA>          SPT   Sputum        1033465
## 5 GeneticSpecim~ http://ter~ <NA>          WND   Wound         1033739
## 6 GeneticSpecim~ http://ter~ <NA>          BON   Bone          1585831

```

```

## 7 GeneticSpecim~ http://ter~ <NA>          SKN   Skin          1585833
## 8 GeneticSpecim~ http://ter~ <NA>          MAR   Marrow        3310432
## 9 GeneticSpecim~ http://ter~ <NA>          WND   Wound          3311979
## 10 GeneticSpecim~ http://ter~ <NA>         BLD   Whole blood     3326584
## # ... with 67 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $HGNCVS
## # A tibble: 19,297 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>        <chr>        <chr> <chr>          <chr>
## 1 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944910
## 2 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944911
## 3 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944912
## 4 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944913
## 5 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944914
## 6 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944916
## 7 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944917
## 8 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944920
## 9 HGNCVS        http://www~ All codes in ht~ <NA> <NA>          35944921
## 10 HGNCVS       http://www~ All codes in ht~ <NA> <NA>          35944922
## # ... with 19,287 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $HistologyMorphologyBehaviorVS
## # A tibble: 1,325 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>        <chr>        <chr> <chr>          <chr>
## 1 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4264447
## 2 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4029663
## 3 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          37311513
## 4 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          36403182
## 5 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4030124
## 6 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4228267
## 7 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4029175
## 8 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4186244
## 9 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4267422
## 10 HistologyMorp~ SNOMED CT includes codes ~ <NA> <NA>          4028856
## # ... with 1,315 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,

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## # Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $LateralityVS
## # A tibble: 5 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 LateralityVS  SNOMED CT  <NA>          <NA> <NA>          4197258
## 2 LateralityVS  SNOMED CT  <NA>          <NA> <NA>          4161551
## 3 LateralityVS  SNOMED CT  <NA>          <NA> <NA>          4080761
## 4 LateralityVS  SNOMED CT  <NA>          <NA> <NA>          4300877
## 5 LateralityVS  SNOMED CT  <NA>          <NA> <NA>          4280221
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## #   all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## #   Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## #   Specimen <chr>, X14 <chr>
##
## $PrimaryOrUncertainBehaviorCancerDisorderVS
## # A tibble: 55,909 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.0 Malignant neopl~ 35206047
## 2 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.1 Malignant neopl~ 35206048
## 3 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.2 Malignant neopl~ 35206049
## 4 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.3 Malignant neopl~ 35206050
## 5 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.4 Malignant neopl~ 35206051
## 6 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.5 Malignant neopl~ 35206052
## 7 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.6 Malignant neopl~ 35206053
## 8 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.8 Malignant neopl~ 35206054
## 9 PrimaryOrUnce~ ICD-10-CM  <NA>          C00.9 Malignant neopl~ 35206055
## 10 PrimaryOrUnce~ ICD-10-CM  <NA>          C01 Malignant neopl~ 35206056
## # ... with 55,899 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $RadiationProcedureVS
## # A tibble: 5 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>      <chr>          <chr> <chr>          <chr>
## 1 RadiationProc~ SNOMED CT  <NA>          <NA> <NA>          40489482
## 2 RadiationProc~ SNOMED CT  <NA>          <NA> <NA>          4165039
## 3 RadiationProc~ SNOMED CT  <NA>          <NA> <NA>          4024005
## 4 RadiationProc~ SNOMED CT  <NA>          <NA> <NA>          4213601
## 5 RadiationProc~ SNOMED CT  <NA>          <NA> <NA>          40317890
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,

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## # all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## # Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## # Specimen <chr>, X14 <chr>
##
## $RadiationTargetBodySiteVS
## # A tibble: 66 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4215878
## 2 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4055510
## 3 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4074816
## 4 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4075241
## 5 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4075246
## 6 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4075247
## 7 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4081786
## 8 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4241958
## 9 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4353165
## 10 RadiationTarg~ SNOMED CT      <NA>          <NA> <NA>          4209428
## # ... with 56 more rows, and 20 more variables: concept_name <chr>,
## # domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## # standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## # valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## # descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## # `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## # Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $SecondaryCancerDisorderVS
## # A tibble: 909 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45532940
## 2 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45552289
## 3 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45542632
## 4 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45542633
## 5 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45532941
## 6 SecondaryCanc~ ICD-10-CM      <NA>          C7B.~ Secondary carci~ 45600534
## 7 SecondaryCanc~ ICD-10-CM      <NA>          C7B.1 Secondary Merke~ 45566619
## 8 SecondaryCanc~ ICD-10-CM      <NA>          C7B.8 Other secondary~ 45571543
## 9 SecondaryCanc~ ICD-10-CM      <NA>          C77.0 Secondary and u~ 35206319
## 10 SecondaryCanc~ ICD-10-CM      <NA>          C77.1 Secondary and u~ 35206320
## # ... with 899 more rows, and 20 more variables: concept_name <chr>,
## # domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## # standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## # valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## # descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## # `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## # Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $TNMDistantMetastasesCategoryVS
## # A tibble: 342 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537692
## 2 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA>          1537780

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## 3 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537798
## 4 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537804
## 5 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537805
## 6 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537808
## 7 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537809
## 8 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537821
## 9 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537827
## 10 TNMDistantMet~ http://can~ includes codes ~ <NA> <NA> 1537830
## # ... with 332 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $TNMPrimaryTumorCategoryVS
## # A tibble: 772 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>         <chr>      <chr> <chr>          <chr>
## 1 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537693
## 2 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537694
## 3 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537700
## 4 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537783
## 5 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537786
## 6 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537787
## 7 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537788
## 8 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537789
## 9 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537790
## 10 TNMPrimaryTum~ http://can~ includes codes ~ <NA> <NA> 1537791
## # ... with 762 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $TNMRegionalNodesCategoryVS
## # A tibble: 502 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>         <chr>      <chr> <chr>          <chr>
## 1 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537695
## 2 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537781
## 3 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537782
## 4 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537784
## 5 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537785
## 6 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537792
## 7 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537799
## 8 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537800
## 9 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537802
## 10 TNMRegionalNo~ http://can~ includes codes ~ <NA> <NA> 1537806
## # ... with 492 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,

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## # standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## # valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## # descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## # `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## # Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $TNMStageGroupVS
## # A tibble: 1 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 TNMStageGroup~ http://can~ includes codes ~ <NA> <NA>          <NA>
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## # vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## # concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## # invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## # all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## # Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## # Specimen <chr>, X14 <chr>
##
## $TreatmentIntentVS
## # A tibble: 2 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 TreatmentInte~ SNOMED CT <NA>          <NA> <NA>          4162591
## 2 TreatmentInte~ SNOMED CT <NA>          <NA> <NA>          4179711
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## # vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## # concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## # invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## # all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## # Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## # Specimen <chr>, X14 <chr>
##
## $TreatmentTerminationReasonVS
## # A tibble: 7 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4082735
## 2 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4243225
## 3 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4105886
## 4 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4052625
## 5 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4019958
## 6 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4030023
## 7 TreatmentTerm~ SNOMED CT <NA>          <NA> <NA>          4146955
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## # vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## # concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## # invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## # all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## # Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## # Specimen <chr>, X14 <chr>
##
## $TumorMarkerTestVS
## # A tibble: 160 x 26

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##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 TumorMarkerTe~ LOINC          <NA>          1695~ 5-Hydroxyindole~ 3005148
## 2 TumorMarkerTe~ LOINC          <NA>          3120~ 5-Hydroxyindole~ 3023028
## 3 TumorMarkerTe~ LOINC          <NA>          1692~ 5-Hydroxyindole~ 3014670
## 4 TumorMarkerTe~ LOINC          <NA>          1693~ 5-Hydroxyindole~ 3021106
## 5 TumorMarkerTe~ LOINC          <NA>          1694~ 5-Hydroxyindole~ 3021385
## 6 TumorMarkerTe~ LOINC          <NA>          7282~ 5-Hydroxyindole~ 43055680
## 7 TumorMarkerTe~ LOINC          <NA>          1457~ 5-Hydroxyindole~ 3009461
## 8 TumorMarkerTe~ LOINC          <NA>          2597~ 5-Hydroxyindole~ 3010801
## 9 TumorMarkerTe~ LOINC          <NA>          4754~ 5-Hydroxyindole~ 3051403
## 10 TumorMarkerTe~ LOINC          <NA>          7476~ 5-Hydroxyindole~ 44816667
## # ... with 150 more rows, and 20 more variables: concept_name <chr>,
## #   domain_id <chr>, vocabulary_id <chr>, concept_class_id <chr>,
## #   standard_concept <chr>, concept_code <chr>, valid_start_date <chr>,
## #   valid_end_date <chr>, invalid_reason <chr>, ancestors_of <chr>,
## #   descendants_of <chr>, all_codes <chr>, Observation <chr>, Condition <chr>,
## #   `Spec Anatomic Site` <chr>, Drug <chr>, `Meas Value` <chr>,
## #   Measurement <chr>, Specimen <chr>, X14 <chr>
##
## $UnitsOfLengthVS
## # A tibble: 7 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 UnitsOfLength~ http://uni~ <NA>          pm   Picometer      <NA>
## 2 UnitsOfLength~ http://uni~ <NA>          nm   Nanometer      <NA>
## 3 UnitsOfLength~ http://uni~ <NA>          mm   Millimeter     <NA>
## 4 UnitsOfLength~ http://uni~ <NA>          cm   Centimeter     <NA>
## 5 UnitsOfLength~ http://uni~ <NA>          m    Meter          <NA>
## 6 UnitsOfLength~ http://uni~ <NA>          ft-us Foot        <NA>
## 7 UnitsOfLength~ http://uni~ <NA>          in-us Prostate specif~ <NA>
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## #   all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## #   Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## #   Specimen <chr>, X14 <chr>
##
## $YesNoUnknownVS
## # A tibble: 1 x 26
##   value_set_name code_system logical_definit~ code code_description concept_id
##   <chr>          <chr>          <chr>          <chr> <chr>          <chr>
## 1 YesNoUnknownVS SNOMED CT   <NA>          <NA> <NA>          4188539
## # ... with 20 more variables: concept_name <chr>, domain_id <chr>,
## #   vocabulary_id <chr>, concept_class_id <chr>, standard_concept <chr>,
## #   concept_code <chr>, valid_start_date <chr>, valid_end_date <chr>,
## #   invalid_reason <chr>, ancestors_of <chr>, descendants_of <chr>,
## #   all_codes <chr>, Observation <chr>, Condition <chr>, `Spec Anatomic
## #   Site` <chr>, Drug <chr>, `Meas Value` <chr>, Measurement <chr>,
## #   Specimen <chr>, X14 <chr>

```