TCGA Clinical Data Analysis

Prepearing clinical data to analysis following Hadley Wickham's Tidyverse manifesto.

1. Importing data

```
kirc_clin_raw <- read_delim("data/kirc_tcga_clinical_data.tsv", "\t",
                            escape_double = FALSE,
                            trim_ws = TRUE)
```

```
## Parsed with column specification:
## cols(
##   .default = col_character(),
##   `Diagnosis Age` = col_double(),
##   `Neoplasm American Joint Committee on Cancer Clinical Group Stage` = col_logical(),
##   `Neoplasm American Joint Committee on Cancer Clinical Regional Lymph Node N Stage` = col_logical()
##   `Neoplasm American Joint Committee on Cancer Clinical Primary Tumor T Stage` = col_logical(),
##   `Days to Sample Collection.` = col_double(),
##   `Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value` = col_double(),
##   `Days to Sample Procurement` = col_logical(),
##   `Disease Free (Months)` = col_double(),
##   `Performance Status` = col_double(),
##   `Lymphomatous Extranodal Site Involvement Indicator` = col_logical(),
##   `Fraction Genome Altered` = col_double(),
##   `Year Cancer Initial Diagnosis` = col_double(),
##   `Karnofsky Performance Score` = col_double(),
##   `Longest Dimension` = col_double(),
##   `Lymph nodes examined positive` = col_double(),
##   `Lymph Node(s) Examined Number` = col_double(),
##   `First Pathologic Diagnosis Biospecimen Acquisition Method Type` = col_logical(),
##   `Mutation Count` = col_double(),
##   `Oct embedded` = col_logical(),
##   `Overall Survival (Months)` = col_double()
##   # ... with 15 more columns
## )
```

```
## See spec(...) for full column specifications.
```

```
class(kirc_clin_raw)
```

```
## [1] "spec_tbl_df" "tbl_df"      "tbl"         "data.frame"
```

```
dim(kirc_clin_raw)
```

```
## [1] 538  89
```

```
names(kirc_clin_raw)
```

```
##  [1] "Study ID"
##  [2] "Patient ID"
##  [3] "Sample ID"
##  [4] "Diagnosis Age"
##  [5] "Neoplasm American Joint Committee on Cancer Clinical Distant Metastasis M Stage"
##  [6] "American Joint Committee on Cancer Metastasis Stage Code"
##  [7] "Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code"
##  [8] "Neoplasm Disease Stage American Joint Committee on Cancer Code"
##  [9] "American Joint Committee on Cancer Publication Version Type"
## [10] "American Joint Committee on Cancer Tumor Stage Code"
## [11] "Cancer Type"
## [12] "Cancer Type Detailed"
## [13] "Neoplasm American Joint Committee on Cancer Clinical Group Stage"
## [14] "Neoplasm American Joint Committee on Cancer Clinical Regional Lymph Node N Stage"
## [15] "Neoplasm American Joint Committee on Cancer Clinical Primary Tumor T Stage"
## [16] "Days to Sample Collection."
## [17] "Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value"
## [18] "Days to Sample Procurement"
## [19] "Disease Free (Months)"
## [20] "Disease Free Status"
## [21] "Disease code"
## [22] "Performance Status"
## [23] "Erythrocyte sedimentation rate"
## [24] "Ethnicity Category"
## [25] "Lymphomatous Extranodal Site Involvement Indicator"
## [26] "Form completion date"
## [27] "Fraction Genome Altered"
## [28] "Neoplasm Histologic Grade"
## [29] "Hemoglobin level"
## [30] "Neoplasm Histologic Type Name"
## [31] "Neoadjuvant Therapy Type Administered Prior To Resection Text"
## [32] "Prior Cancer Diagnosis Occurence"
## [33] "ICD-10 Classification"
## [34] "International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code"
## [35] "International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code"
## [36] "Idh level"
## [37] "Informed consent verified"
## [38] "Year Cancer Initial Diagnosis"
## [39] "Is FFPE"
## [40] "Karnofsky Performance Score"
## [41] "Primary Tumor Laterality"
## [42] "Longest Dimension"
## [43] "Primary Lymph Node Presentation Assessment Ind-3"
## [44] "Lymph nodes examined positive"
## [45] "Lymph Node(s) Examined Number"
## [46] "First Pathologic Diagnosis Biospecimen Acquisition Method Type"
## [47] "Mutation Count"
## [48] "New Neoplasm Event Post Initial Therapy Indicator"
## [49] "Oct embedded"
## [50] "Oncotree Code"
## [51] "Overall Survival (Months)"
## [52] "Overall Survival Status"
## [53] "Specimen Collection Method"
## [54] "Other Patient ID"
## [55] "Other Sample ID"
## [56] "Pathology Report File Name"
## [57] "Pathology report uuid"
## [58] "Performance Status Assessment Timepoint Category"
## [59] "Platelet count"
## [60] "Project code"
## [61] "Tissue Prospective Collection Indicator"
## [62] "Race Category"
## [63] "Did patient start adjuvant postoperative radiotherapy?"
## [64] "Tissue Retrospective Collection Indicator"
## [65] "Number of Samples Per Patient"
## [66] "Sample Initial Weight"
## [67] "Sample Type"
## [68] "Sample type id"
## [69] "Serum calcium level"
## [70] "Sex"
## [71] "Shortest Dimension"
## [72] "Tumor Tissue Site"
## [73] "Person Cigarette Smoking History Pack Year Value"
## [74] "Started Smoking Year"
## [75] "Stopped Smoking Year"
## [76] "Specimen Current Weight"
## [77] "Specimen Freezing Means"
## [78] "Specimen Second Longest Dimension"
## [79] "Stage Other"
## [80] "Adjuvant Postoperative Targeted Therapy Administered Indicator"
## [81] "Time between clamping and freezing"
## [82] "Time between excision and freezing"
## [83] "Tissue Source Site"
## [84] "Patient Smoking History Category"
## [85] "Primary Therapy Outcome Success Type"
## [86] "Person Neoplasm Status"
## [87] "Vial number"
## [88] "Patient's Vital Status"
## [89] "WBC"
```

```
glimpse(kirc_clin_raw)
```

```
## Rows: 538
## Columns: 89
## $ `Study ID`                                                                                    <chr>
## $ `Patient ID`                                                                                  <chr>
## $ `Sample ID`                                                                                   <chr>
## $ `Diagnosis Age`                                                                               <dbl>
## $ `Neoplasm American Joint Committee on Cancer Clinical Distant Metastasis M Stage`             <chr>
## $ `American Joint Committee on Cancer Metastasis Stage Code`                                    <chr>
## $ `Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code`                   <chr>
## $ `Neoplasm Disease Stage American Joint Committee on Cancer Code`                              <chr>
## $ `American Joint Committee on Cancer Publication Version Type`                                 <chr>
## $ `American Joint Committee on Cancer Tumor Stage Code`                                         <chr>
## $ `Cancer Type`                                                                                 <chr>
## $ `Cancer Type Detailed`                                                                        <chr>
## $ `Neoplasm American Joint Committee on Cancer Clinical Group Stage`                            <lgl>
## $ `Neoplasm American Joint Committee on Cancer Clinical Regional Lymph Node N Stage`            <lgl>
## $ `Neoplasm American Joint Committee on Cancer Clinical Primary Tumor T Stage`                  <lgl>
## $ `Days to Sample Collection.`                                                                  <dbl>
## $ `Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value`                      <dbl>
## $ `Days to Sample Procurement`                                                                  <lgl
## $ `Disease Free (Months)`                                                                       <dbl
## $ `Disease Free Status`                                                                         <chr
## $ `Disease code`                                                                                <chr
## $ `Performance Status`                                                                          <dbl
## $ `Erythrocyte sedimentation rate`                                                              <chr
## $ `Ethnicity Category`                                                                          <chr
## $ `Lymphomatous Extranodal Site Involvement Indicator`                                          <lgl
## $ `Form completion date`                                                                        <chr
## $ `Fraction Genome Altered`                                                                     <dbl
## $ `Neoplasm Histologic Grade`                                                                   <chr
## $ `Hemoglobin level`                                                                            <chr
## $ `Neoplasm Histologic Type Name`                                                               <chr
## $ `Neoadjuvant Therapy Type Administered Prior To Resection Text`                               <chr
## $ `Prior Cancer Diagnosis Occurence`                                                            <chr
## $ `ICD-10 Classification`                                                                       <chr
## $ `International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code` <chr
## $ `International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code`      <chr
## $ `Idh level`                                                                                   <chr
## $ `Informed consent verified`                                                                   <chr
## $ `Year Cancer Initial Diagnosis`                                                               <dbl
## $ `Is FFPE`                                                                                     <chr
## $ `Karnofsky Performance Score`                                                                 <dbl
## $ `Primary Tumor Laterality`                                                                    <chr
## $ `Longest Dimension`                                                                           <dbl
## $ `Primary Lymph Node Presentation Assessment Ind-3`                                            <chr
## $ `Lymph nodes examined positive`                                                               <dbl
## $ `Lymph Node(s) Examined Number`                                                               <dbl
## $ `First Pathologic Diagnosis Biospecimen Acquisition Method Type`                              <lgl
## $ `Mutation Count`                                                                              <dbl
## $ `New Neoplasm Event Post Initial Therapy Indicator`                                           <chr
## $ `Oct embedded`                                                                                <lgl
## $ `Oncotree Code`                                                                               <chr
## $ `Overall Survival (Months)`                                                                   <dbl
## $ `Overall Survival Status`                                                                     <chr
## $ `Specimen Collection Method`                                                                  <lgl
## $ `Other Patient ID`                                                                            <chr
## $ `Other Sample ID`                                                                             <chr
## $ `Pathology Report File Name`                                                                  <chr
## $ `Pathology report uuid`                                                                       <chr
## $ `Performance Status Assessment Timepoint Category`                                            <chr
## $ `Platelet count`                                                                              <chr
## $ `Project code`                                                                                <chr
## $ `Tissue Prospective Collection Indicator`                                                     <chr
## $ `Race Category`                                                                               <chr
## $ `Did patient start adjuvant postoperative radiotherapy?`                                      <chr
## $ `Tissue Retrospective Collection Indicator`                                                   <chr
## $ `Number of Samples Per Patient`                                                               <dbl
## $ `Sample Initial Weight`                                                                       <dbl
## $ `Sample Type`                                                                                 <chr
## $ `Sample type id`                                                                              <dbl
## $ `Serum calcium level`                                                                         <chr
## $ Sex                                                                                           <chr
## $ `Shortest Dimension`                                                                          <dbl
## $ `Tumor Tissue Site`                                                                 <chr
## $ `Person Cigarette Smoking History Pack Year Value`                                  <dbl
## $ `Started Smoking Year`                                                              <dbl
## $ `Stopped Smoking Year`                                                              <dbl
## $ `Specimen Current Weight`                                                           <lgl
## $ `Specimen Freezing Means`                                                           <lgl
## $ `Specimen Second Longest Dimension`                                                 <dbl
## $ `Stage Other`                                                                       <lgl
## $ `Adjuvant Postoperative Targeted Therapy Administered Indicator`                    <chr
## $ `Time between clamping and freezing`                                                <lgl
## $ `Time between excision and freezing`                                                <lgl
## $ `Tissue Source Site`                                                                <chr
## $ `Patient Smoking History Category`                                                  <dbl
## $ `Primary Therapy Outcome Success Type`                                              <chr
## $ `Person Neoplasm Status`                                                            <chr
## $ `Vial number`                                                                       <chr
## $ `Patient's Vital Status`                                                            <chr
## $ WBC                                                                                 <chr
```

```
skim(kirc_clin_raw)
```

Table 1: Data summary

Name	kirc_clin_raw
Number of rows	538
Number of columns	89
Column type frequency:	
character	54
logical	13
numeric	22
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Study ID	0	1.00
Patient ID	0	1.00
Sample ID	0	1.00
Neoplasm American Joint Committee on Cancer Clinical Distant Metastasis M Stage	504	0.06
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Publication Version Type	367	0.32
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Cancer Type	0	1.00
Cancer Type Detailed	0	1.00
Disease Free Status	99	0.82
Disease code	534	0.01
Erythrocyte sedimentation rate	527	0.02
Ethnicity Category	152	0.72
Form completion date	0	1.00

skim_variable	n_missing	complete_rate
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoplasm Histologic Type Name	0	1.00
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
ICD-10 Classification	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00
Idh level	451	0.16
Informed consent verified	0	1.00
Is FFPE	1	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
New Neoplasm Event Post Initial Therapy Indicator	503	0.07
Oncotree Code	0	1.00
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	1	1.00
Pathology Report File Name	1	1.00
Pathology report uuid	1	1.00
Performance Status Assessment Timepoint Category	428	0.20
Platelet count	93	0.83
Project code	534	0.01
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Did patient start adjuvant postoperative radiotherapy?	506	0.06
Tissue Retrospective Collection Indicator	18	0.97
Sample Type	0	1.00
Serum calcium level	172	0.68
Sex	0	1.00
Tumor Tissue Site	0	1.00
Adjuvant Postoperative Targeted Therapy Administered Indicator	506	0.06
Tissue Source Site	0	1.00
Primary Therapy Outcome Success Type	507	0.06
Person Neoplasm Status	35	0.93
Vial number	1	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: logical

skim_variable	n_missing	complete_rate	m
Neoplasm American Joint Committee on Cancer Clinical Group Stage	538	0.00	N
Neoplasm American Joint Committee on Cancer Clinical Regional Lymph Node N Stage	538	0.00	N
Neoplasm American Joint Committee on Cancer Clinical Primary Tumor T Stage	538	0.00	N
Days to Sample Procurement	538	0.00	N
Lymphomatous Extranodal Site Involvement Indicator	538	0.00	N
First Pathologic Diagnosis Biospecimen Acquisition Method Type	538	0.00	N
Oct embedded	503	0.07	0
Specimen Collection Method	538	0.00	N
Specimen Current Weight	538	0.00	N

skim_variable	n_missing	complete_rate	m
Specimen Freezing Means	538	0.00	N
Stage Other	538	0.00	N
Time between clamping and freezing	538	0.00	N
Time between excision and freezing	538	0.00	N

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd
Diagnosis Age	0	1.00	60.58	12.14
Days to Sample Collection.	503	0.07	545.26	566.08
Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value	0	1.00	0.00	0.00
Disease Free (Months)	99	0.82	40.30	31.64
Performance Status	399	0.26	0.24	0.48
Fraction Genome Altered	9	0.98	0.17	0.17
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76
Karnofsky Performance Score	490	0.09	88.33	20.56
Longest Dimension	36	0.93	1.66	0.66
Lymph nodes examined positive	407	0.24	0.34	1.44
Lymph Node(s) Examined Number	404	0.25	6.30	5.97
Mutation Count	87	0.84	73.85	127.76
Overall Survival (Months)	0	1.00	44.33	32.26
Number of Samples Per Patient	0	1.00	1.00	0.06
Sample Initial Weight	503	0.07	296.29	366.21
Sample type id	0	1.00	1.01	0.17
Shortest Dimension	36	0.93	0.38	0.21
Person Cigarette Smoking History Pack Year Value	516	0.04	28.55	15.77
Started Smoking Year	525	0.02	1978.38	17.35
Stopped Smoking Year	525	0.02	1994.77	15.12
Specimen Second Longest Dimension	36	0.93	0.94	0.31
Patient Smoking History Category	450	0.16	1.91	1.19

```
#View(kirc_clin_raw)
```

2. Cleaning data

Select variables based on NA count (> 50% complete is a good choice!).

@TODO PATRICK: simplify code NA_sum?

kirc_clean <- kirc_clin_raw %>%

summarise_all(~ sum(is.na(.)))

```
NA_fifty <- dim(kirc_clin_raw)[1]/2
```

```
NA_sum <- colSums(is.na(kirc_clin_raw))
NA_sum <- as.data.frame(NA_sum)
NA_sum <- tibble::rownames_to_column(NA_sum, "variables")
NA_sum <- NA_sum %>%
     filter(NA_sum < NA_fifty)

kirc_clean <- kirc_clin_raw %>%
     select(one_of(NA_sum$variables))
```

Remove duplicate observations:

```
kirc_clean0 <- kirc_clean %>%
     distinct_at('Patient ID', .keep_all = TRUE)
```

Remove nuneric variables with unique observations:

```
skim(kirc_clean0)
```

Table 5: Data summary

Name	kirc_clean0
Number of rows	537
Number of columns	55
Column type frequency:	
character	43
numeric	12
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Study ID	0	1.00
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Cancer Type	0	1.00
Cancer Type Detailed	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoplasm Histologic Type Name	0	1.00
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
ICD-10 Classification	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00
Informed consent verified	0	1.00

skim_variable	n_missing	complete_rate
Is FFPE	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Oncotree Code	0	1.00
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Tissue Retrospective Collection Indicator	18	0.97
Sample Type	0	1.00
Serum calcium level	172	0.68
Sex	0	1.00
Tumor Tissue Site	0	1.00
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd
Diagnosis Age	0	1.00	60.59	12.15
Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value	0	1.00	0.00	0.00
Disease Free (Months)	99	0.82	40.24	31.66
Fraction Genome Altered	9	0.98	0.17	0.17
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76
Longest Dimension	35	0.93	1.66	0.66
Mutation Count	86	0.84	73.85	127.76
Overall Survival (Months)	0	1.00	44.26	32.25
Number of Samples Per Patient	0	1.00	1.00	0.04
Sample type id	0	1.00	1.00	0.00
Shortest Dimension	35	0.93	0.38	0.21
Specimen Second Longest Dimension	35	0.93	0.94	0.31

@TODO PATRICK: function to select variables with unique observations?

kirc_cleanX <- kirc_clean1 %>%

summarise_if(is.numeric, ~ n=unique(.))

```r
kirc_clean1 <-  kirc_clean0  %>%
     select(!c('Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value',
               'Number of Samples Per Patient',
               'Sample type id'))
```

Remove character variables with unique observations:

```r
skim(kirc_clean1)
```

Table 8: Data summary

Name	kirc_clean1
Number of rows	537
Number of columns	52
Column type frequency:	
character	43
numeric	9
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Study ID	0	1.00
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Cancer Type	0	1.00
Cancer Type Detailed	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoplasm Histologic Type Name	0	1.00
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
ICD-10 Classification	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00

skim_variable	n_missing	complete_rate
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00
Informed consent verified	0	1.00
Is FFPE	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Oncotree Code	0	1.00
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Tissue Retrospective Collection Indicator	18	0.97
Sample Type	0	1.00
Serum calcium level	172	0.68
Sex	0	1.00
Tumor Tissue Site	0	1.00
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	
Diagnosis Age	0	1.00	60.59	12.15	26.00	52.00	61.00	70
Disease Free (Months)	99	0.82	40.24	31.66	-11.79	13.43	36.20	60
Fraction Genome Altered	9	0.98	0.17	0.17	0.00	0.06	0.12	0
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00	2007
Longest Dimension	35	0.93	1.66	0.66	0.40	1.20	1.50	2
Mutation Count	86	0.84	73.85	127.76	1.00	34.00	48.00	65
Overall Survival (Months)	0	1.00	44.26	32.25	0.00	18.10	38.96	63
Shortest Dimension	35	0.93	0.38	0.21	0.10	0.20	0.30	0
Specimen Second Longest Dimension	35	0.93	0.94	0.31	0.30	0.70	0.90	1

```r
kirc_clean2 <- kirc_clean1  %>%
     select(!c('Study ID', 'Cancer Type', 'Cancer Type Detailed',
               'Neoplasm Histologic Type Name', 'ICD-10 Classification',
               'International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code'
               'Informed consent verified', 'Is FFPE', 'Oncotree Code', 'Sample Type', 'Tumor Tissue Si
```

Remove character variables with similar information - check each one!

```r
skim(kirc_clean2)
```

Table 11: Data summary

Name	kirc_clean2

Table 11: Data summary

Number of rows	537
Number of columns	41
Column type frequency:	
character	32
numeric	9
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Tissue Retrospective Collection Indicator	18	0.97
Serum calcium level	172	0.68
Sex	0	1.00
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	
Diagnosis Age	0	1.00	60.59	12.15	26.00	52.00	61.00	70

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50
Disease Free (Months)	99	0.82	40.24	31.66	-11.79	13.43	36.20
Fraction Genome Altered	9	0.98	0.17	0.17	0.00	0.06	0.12
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00
Longest Dimension	35	0.93	1.66	0.66	0.40	1.20	1.50
Mutation Count	86	0.84	73.85	127.76	1.00	34.00	48.00
Overall Survival (Months)	0	1.00	44.26	32.25	0.00	18.10	38.96
Shortest Dimension	35	0.93	0.38	0.21	0.10	0.20	0.30
Specimen Second Longest Dimension	35	0.93	0.94	0.31	0.30	0.70	0.90

```r
table(kirc_clean2$`Overall Survival Status`, exclude = NULL)
```

```
##
## DECEASED   LIVING
##      177      360
```

```r
table(kirc_clean2$`Patient's Vital Status`, exclude = NULL)
```

```
##
## Alive  Dead  <NA>
##   360   174     3
```

```r
kirc_clean3 <- kirc_clean2  %>%
     select(!c('Sample ID', 'Overall Survival Status', 'Other Patient ID', 'Other Sample ID',
               'Pathology Report File Name', 'Pathology report uuid'))

# removing other variables not directly related to patient - check each one!
kirc_clean4 <- kirc_clean3  %>%
     select(!c('Form completion date','International Classification of Diseases for Oncology, Third Edi
```

3. Changing variables names

Using snake_style

```r
kirc_clean4 <- kirc_clean4 %>%
     rename(patient_id = 'Patient ID',
            age = 'Diagnosis Age',
            metastasis_stg = 'American Joint Committee on Cancer Metastasis Stage Code',
            neoplasm_ln_stg = 'Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code
            neoplasm_stg = 'Neoplasm Disease Stage American Joint Committee on Cancer Code',
            tumor_stg = 'American Joint Committee on Cancer Tumor Stage Code',
            disease_free_mth = 'Disease Free (Months)',
            disease_free_stt = 'Disease Free Status',
            ethnicity = 'Ethnicity Category',
            frac_genome_alter = 'Fraction Genome Altered',
            histology_grd = 'Neoplasm Histologic Grade',
            hemoglobin = 'Hemoglobin level',
            neoadj_therapy = 'Neoadjuvant Therapy Type Administered Prior To Resection Text',
            prior_cancer = 'Prior Cancer Diagnosis Occurence',
            year_diagnose = 'Year Cancer Initial Diagnosis',
            tumor_lateral = 'Primary Tumor Laterality',
            long_dim = 'Longest Dimension',
            primer_ln_ind3 = 'Primary Lymph Node Presentation Assessment Ind-3',
            mutation_cnt = 'Mutation Count',
            over_surv_mth = 'Overall Survival (Months)',
            platelet = 'Platelet count',
            tissue_prospect = 'Tissue Prospective Collection Indicator',
            race = 'Race Category',
            tissue_retrospect = 'Tissue Retrospective Collection Indicator',
            serum_ca = 'Serum calcium level',
            sex = 'Sex',
            short_dim = 'Shortest Dimension',
            second_long_dim = 'Specimen Second Longest Dimension',
            tissue_site = 'Tissue Source Site',
            person_neoplasm_stt = 'Person Neoplasm Status',
            vital_stt = "Patient's Vital Status",
            wbc = 'WBC')
```

4. Taming data

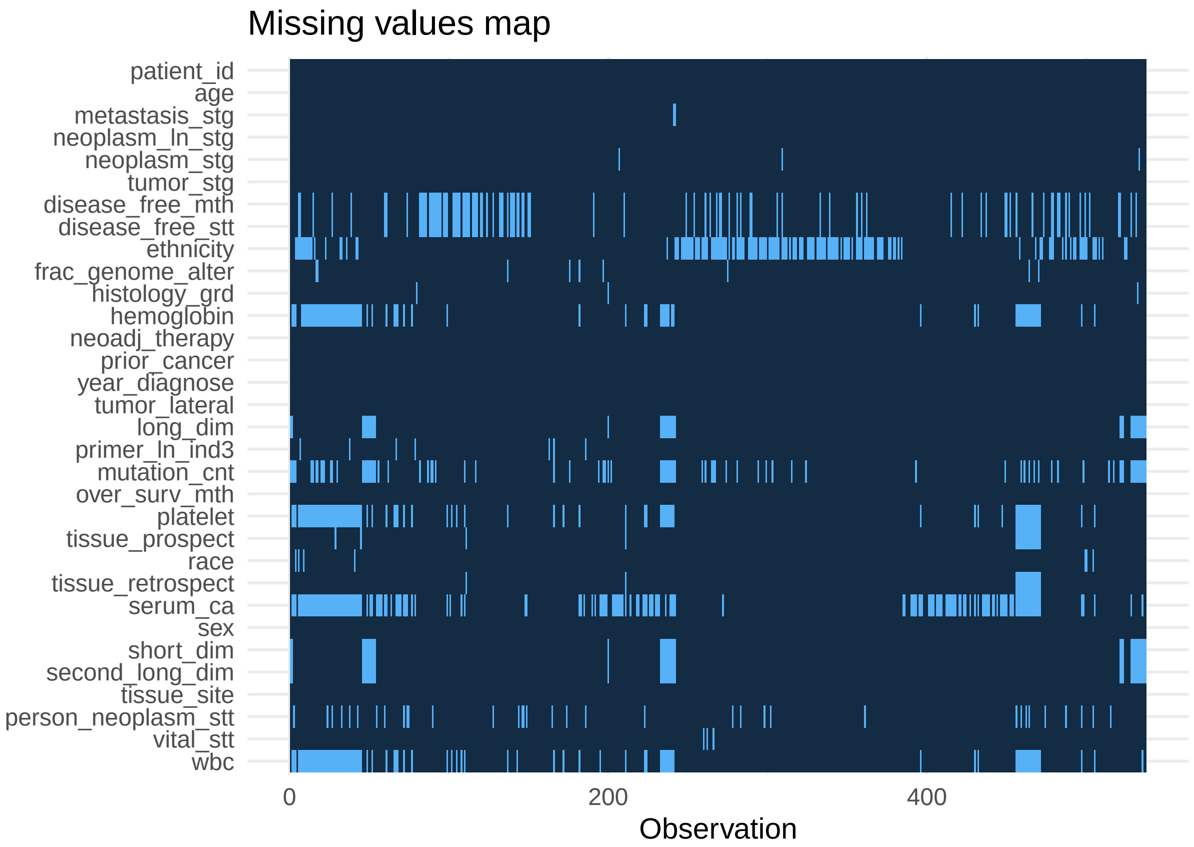
Use lubridate for dates

```
kirc_clean4 <- kirc_clean4 %>%
     mutate_if(is.character, as.factor) %>%
     mutate(patient_id = as.character(patient_id))
```

5. Checking NA patterns

Check distincts types of NAs: MCAR, MAR, MNAR

```
kirc_clean4  %>%
     missing_plot()
```



```
missing_glimpse(kirc_clean4)
```

```
##                                   label var_type   n missing_n missing_percent
## patient_id                   patient_id    <chr> 537         0             0.0
## age                                 age    <dbl> 537         0             0.0
## metastasis_stg           metastasis_stg    <fct> 535         2             0.4
## neoplasm_ln_stg         neoplasm_ln_stg    <fct> 537         0             0.0
## neoplasm_stg               neoplasm_stg    <fct> 534         3             0.6
## tumor_stg                     tumor_stg    <fct> 537         0             0.0
## disease_free_mth       disease_free_mth    <dbl> 438        99            18.4
## disease_free_stt       disease_free_stt    <fct> 438        99            18.4
## ethnicity                     ethnicity    <fct> 385       152            28.3
## frac_genome_alter     frac_genome_alter    <dbl> 528         9             1.7
## histology_grd             histology_grd    <fct> 534         3             0.6
## hemoglobin                   hemoglobin    <fct> 454        83            15.5
## neoadj_therapy           neoadj_therapy    <fct> 537         0             0.0
## prior_cancer               prior_cancer    <fct> 537         0             0.0
## year_diagnose             year_diagnose    <dbl> 537         0             0.0
## tumor_lateral             tumor_lateral    <fct> 537         0             0.0
## long_dim                       long_dim    <dbl> 502        35             6.5
## primer_ln_ind3           primer_ln_ind3    <fct> 530         7             1.3
## mutation_cnt               mutation_cnt    <dbl> 451        86            16.0
## over_surv_mth             over_surv_mth    <dbl> 537         0             0.0
## platelet                       platelet    <fct> 444        93            17.3
## tissue_prospect         tissue_prospect    <fct> 517        20             3.7
## race                               race    <fct> 530         7             1.3
## tissue_retrospect     tissue_retrospect    <fct> 519        18             3.4
## serum_ca                      serum_ca    <fct> 365       172             32.0
## sex                                sex    <fct> 537         0              0.0
## short_dim                    short_dim    <dbl> 502        35              6.5
## second_long_dim        second_long_dim    <dbl> 502        35              6.5
## tissue_site                tissue_site    <fct> 537         0              0.0
## person_neoplasm_stt person_neoplasm_stt    <fct> 502        35              6.5
## vital_stt                    vital_stt    <fct> 534         3              0.6
## wbc                                wbc    <fct> 441        96             17.9
```

6. Checking numeric variables

Check data distribution, plausible ranges, outliers;

Thinking about deleting outliers from dataset? Need to evaluate carefully each one!

@TODO PATRICK: codigo para analizar todas as variaveis numericas?

kirc_clean6 <- kirc_clean4 %>%

select_if(is.numeric) %>%

ggplot(aes(funs(.)) +

ge

@TODO PATRICK: codigo para analizar todas as variaveis numericas?

kirc_clean6 <- kirc_clean4 %>%

select_if(is.numeric) %>%

ggplot(aes(funs(.)) +

geom_boxplot(width = .5) +

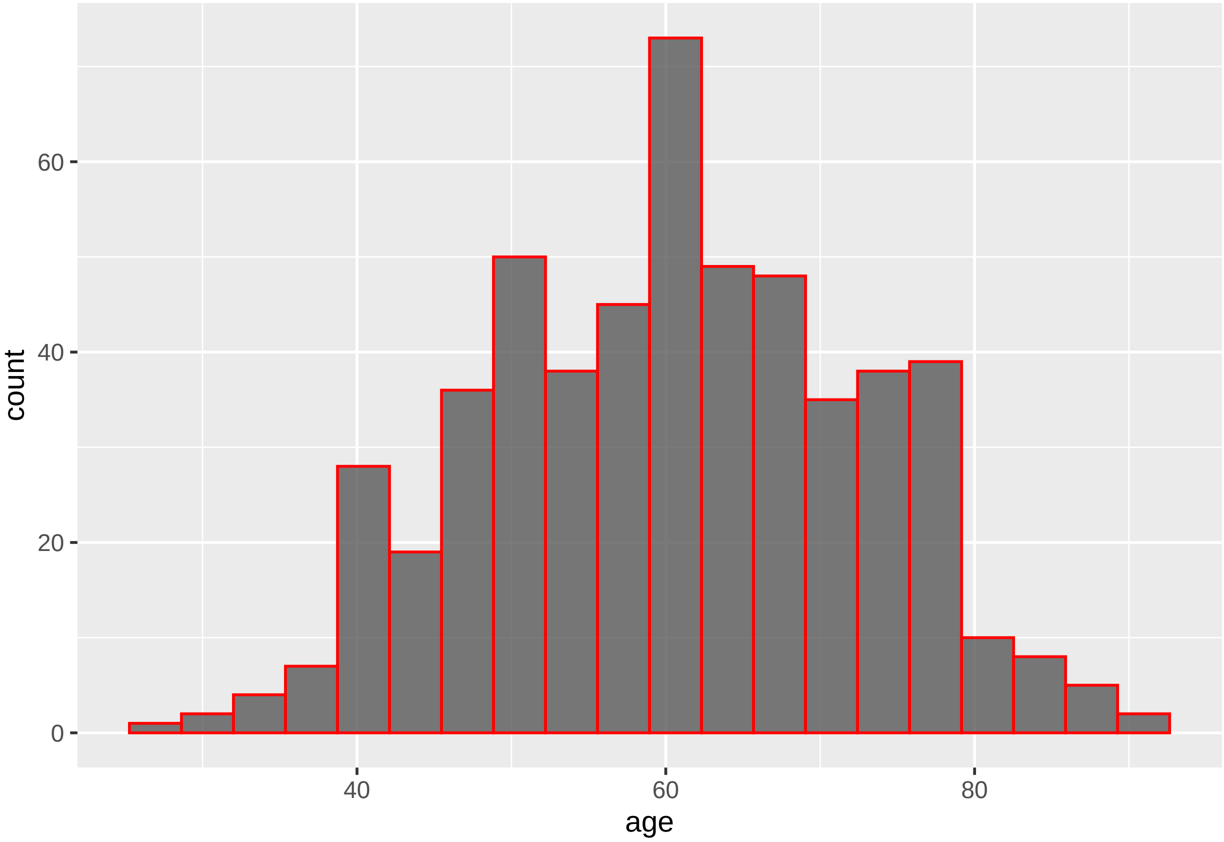
geom_jitter(width = 0.05, alpha = 0.2, color = “orange”)om_boxplot(width = .5) +

geom_jitter(width = 0.05, alpha = 0.2, color = “orange”)

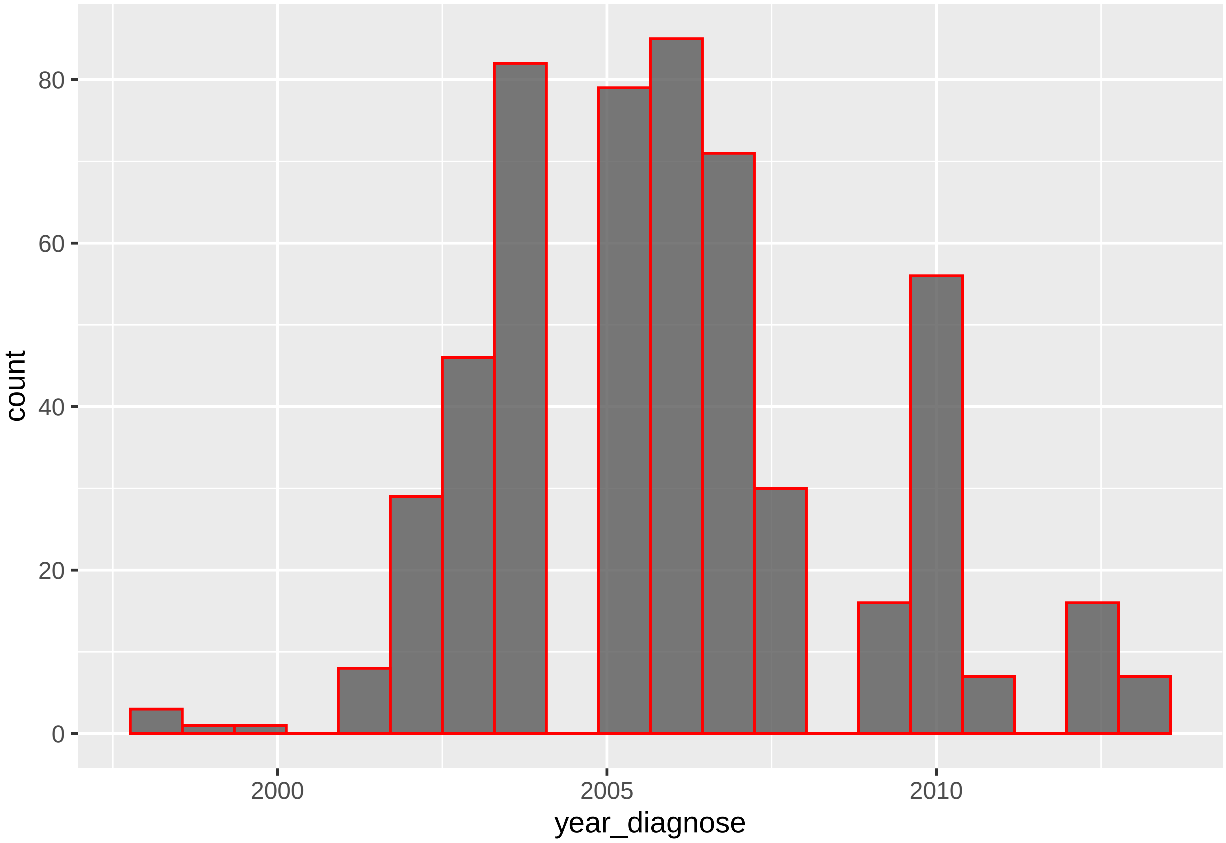
```
kirc_clean4 %>%
     select_if(is.numeric) %>%
     summary()
```

```
##       age        disease_free_mth frac_genome_alter year_diagnose
##  Min.   :26.00   Min.   :-11.79   Min.   :0.00000   Min.   :1998
##  1st Qu.:52.00   1st Qu.: 13.43   1st Qu.:0.06295   1st Qu.:2004
##  Median :61.00   Median : 36.20   Median :0.12065   Median :2006
##  Mean   :60.59   Mean   : 40.24   Mean   :0.17016   Mean   :2006
##  3rd Qu.:70.00   3rd Qu.: 60.51   3rd Qu.:0.20885   3rd Qu.:2007
##  Max.   :90.00   Max.   :133.84   Max.   :0.94770   Max.   :2013
##                  NA's   :99       NA's   :9
##     long_dim      mutation_cnt      over_surv_mth      short_dim
##  Min.   :0.400   Min.   :   1.00   Min.   :  0.00   Min.   :0.1000
##  1st Qu.:1.200   1st Qu.:  34.00   1st Qu.: 18.10   1st Qu.:0.2000
##  Median :1.500   Median :  48.00   Median : 38.96   Median :0.3000
##  Mean   :1.662   Mean   :  73.85   Mean   : 44.26   Mean   :0.3759
##  3rd Qu.:2.000   3rd Qu.:  65.50   3rd Qu.: 63.21   3rd Qu.:0.5000
##  Max.   :4.000   Max.   :1392.00   Max.   :149.05   Max.   :1.0000
##  NA's   :35      NA's   :86                         NA's   :35
##  second_long_dim
##  Min.   :0.3000
##  1st Qu.:0.7000
##  Median :0.9000
##  Mean   :0.9368
##  3rd Qu.:1.1000
##  Max.   :2.0000
##  NA's   :35
```

```
ggplot(kirc_clean4, aes(age)) +
     geom_histogram(bins = 20, alpha = 0.8, color = "red")
```



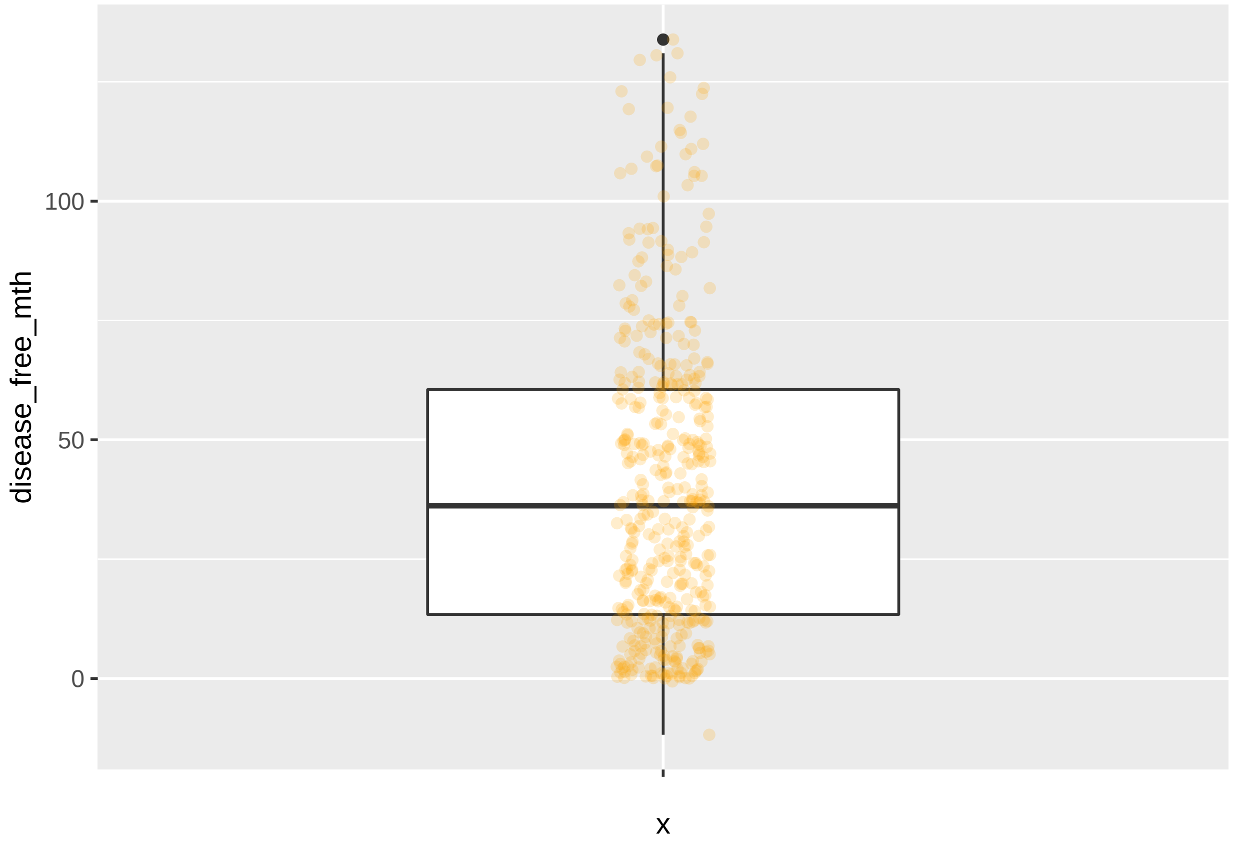
```
ggplot(kirc_clean4, aes(year_diagnose)) +
     geom_histogram(bins = 20, alpha = 0.8, color = "red")
```



```
ggplot(kirc_clean4, aes(x ='', y=disease_free_mth)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 99 rows containing non-finite values (stat_boxplot).

## Warning: Removed 99 rows containing missing values (geom_point).
```



```
boxplot.stats(kirc_clean4$disease_free_mth)
```

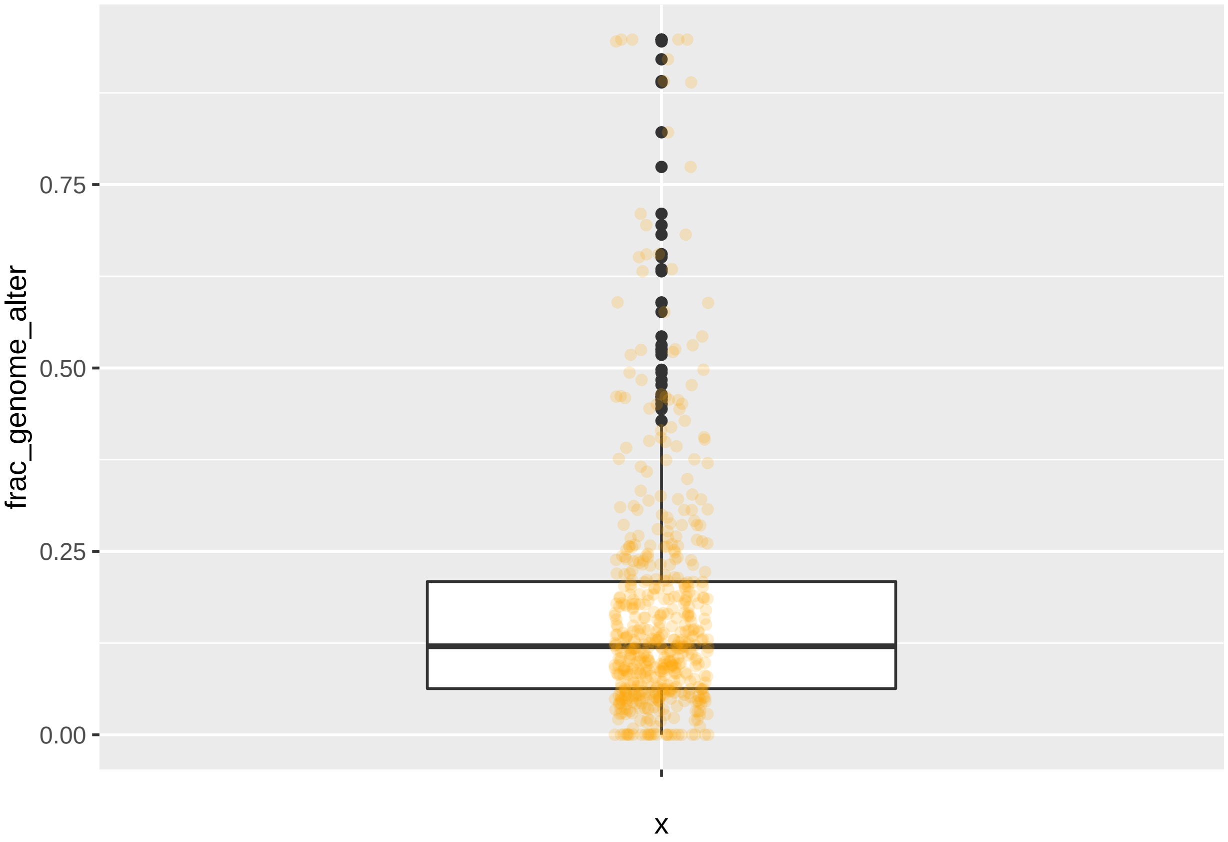
```
## $stats
## [1] -11.79  13.40  36.20  60.55 130.98
##
## $n
## [1] 438
##
## $conf
## [1] 32.6404 39.7596
##
## $out
## [1] 133.84
```

```
# filter(disease_free_mth >= 0)
```

```
ggplot(kirc_clean4, aes(x ='', y=frac_genome_alter)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 9 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 9 rows containing missing values (geom_point).
```



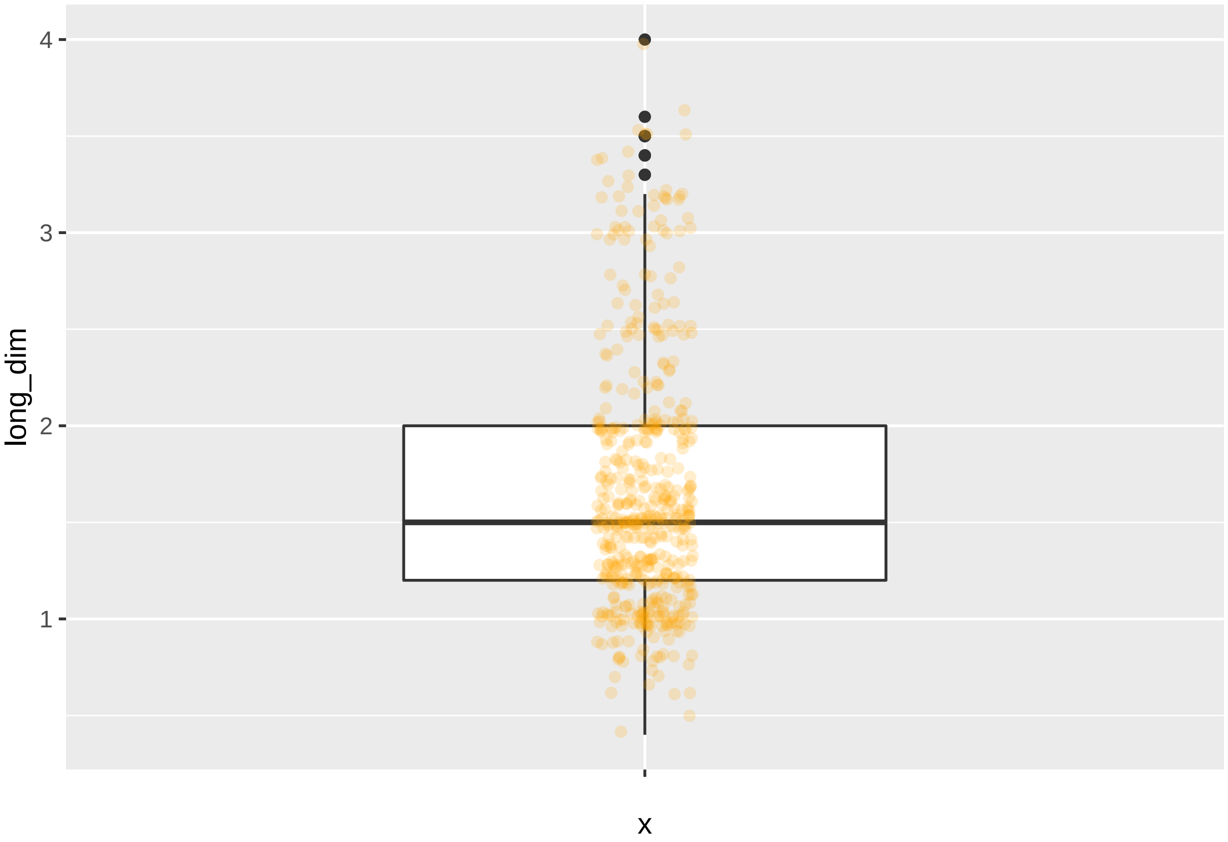
```
boxplot.stats(kirc_clean4$frac_genome_alter)
```

```
## $stats
## [1] 0.00000 0.06290 0.12065 0.20920 0.42800
##
## $n
## [1] 528
##
## $conf
## [1] 0.1105903 0.1307097
##
## $out
##  [1] 0.8213 0.6552 0.4608 0.9477 0.5888 0.9208 0.7741 0.4837 0.9477 0.4610
## [11] 0.6549 0.6511 0.5180 0.8910 0.8893 0.9477 0.5246 0.4568 0.4937 0.9477
## [21] 0.4438 0.6947 0.5218 0.4768 0.4593 0.4447 0.9452 0.6347 0.5311 0.4562
## [31] 0.4617 0.5256 0.6318 0.5430 0.4506 0.5764 0.7102 0.4641 0.5894 0.4976
## [41] 0.4513 0.6818
```

```
ggplot(kirc_clean4, aes(x ='', y=long_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```



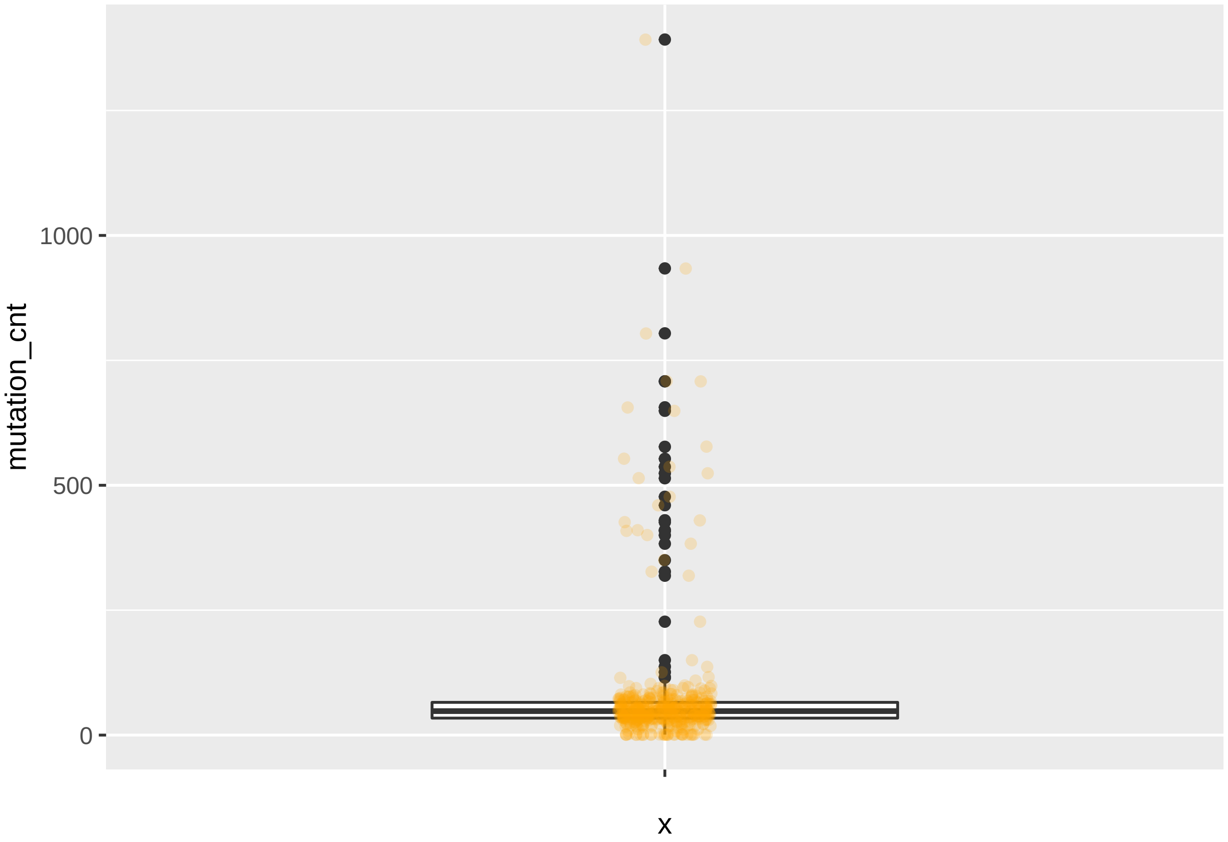
```
boxplot.stats(kirc_clean4$long_dim)
```

```
## $stats
## [1] 0.4 1.2 1.5 2.0 3.2
##
## $n
## [1] 502
##
## $conf
## [1] 1.443585 1.556415
##
## $out
##  [1] 3.3 4.0 3.3 3.5 3.4 3.5 3.5 3.4 3.4 3.5 3.6
```

```
ggplot(kirc_clean4, aes(x ='', y=mutation_cnt)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 86 rows containing non-finite values (stat_boxplot).
```

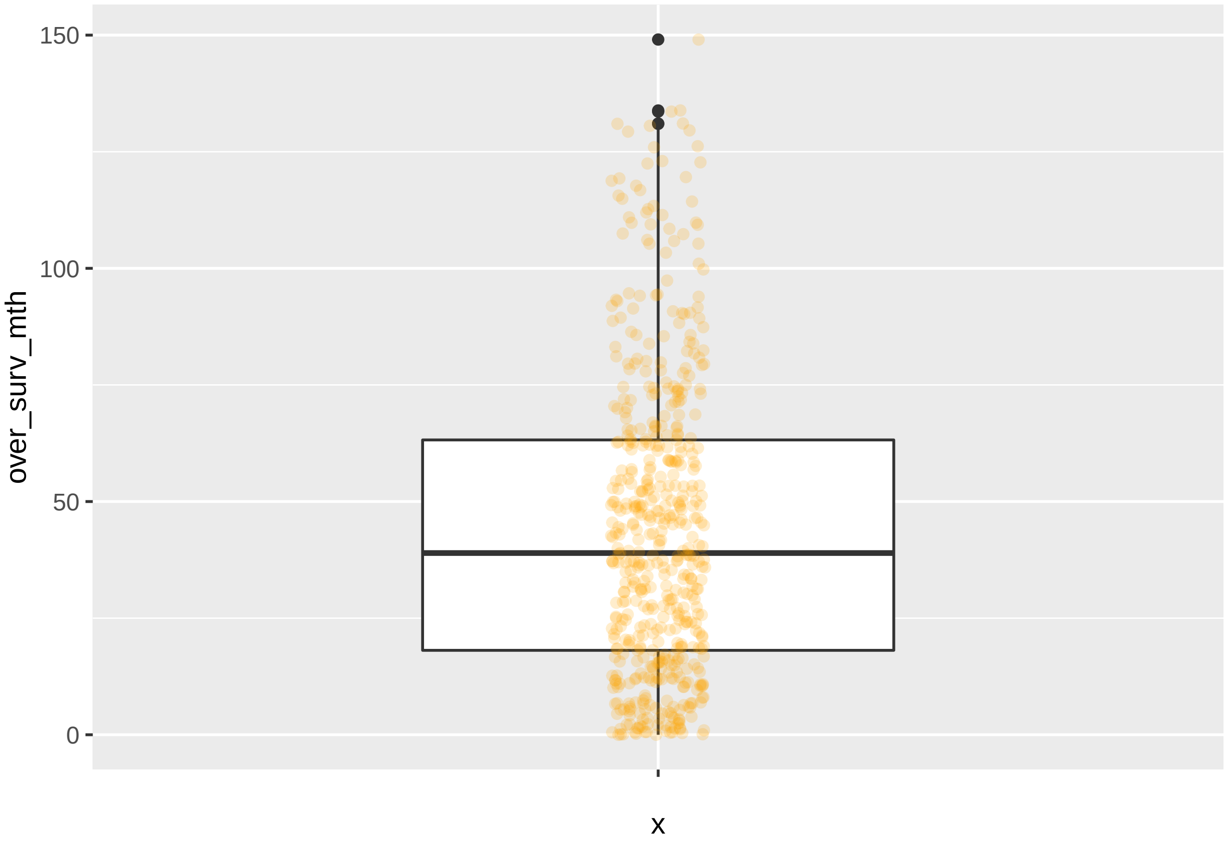
```
## Warning: Removed 86 rows containing missing values (geom_point).
```



```
boxplot.stats(kirc_clean4$mutation_cnt)
```

```
## $stats
## [1]   1.0  34.0  48.0  65.5 109.0
##
## $n
## [1] 451
##
## $conf
## [1] 45.65642 50.34358
##
## $out
##  [1]  514  656  577  537  477  150  137  708 1392  460  327  934  409  383  804
## [16]  319  524  426  227  553  400  350  410  430  708  649  126  116  115
```

```
ggplot(kirc_clean4, aes(x ='', y=over_surv_mth)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```



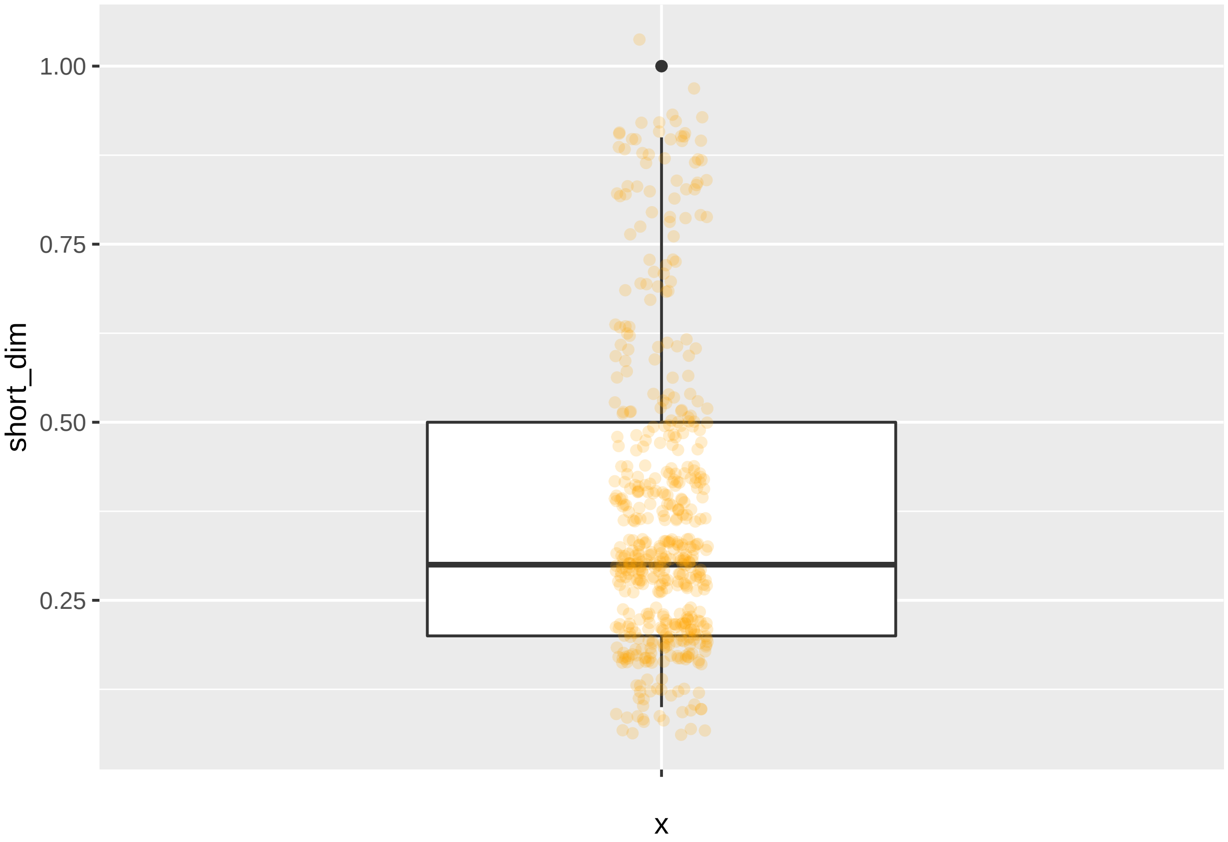
```
boxplot.stats(kirc_clean4$over_surv_mth)
```

```
## $stats
## [1]   0.00  18.10  38.96  63.21 130.55
##
## $n
## [1] 537
##
## $conf
## [1] 35.88431 42.03569
##
## $out
## [1] 133.84 149.05 131.04 130.98 133.61
```

```
ggplot(kirc_clean4, aes(x ='', y=short_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```



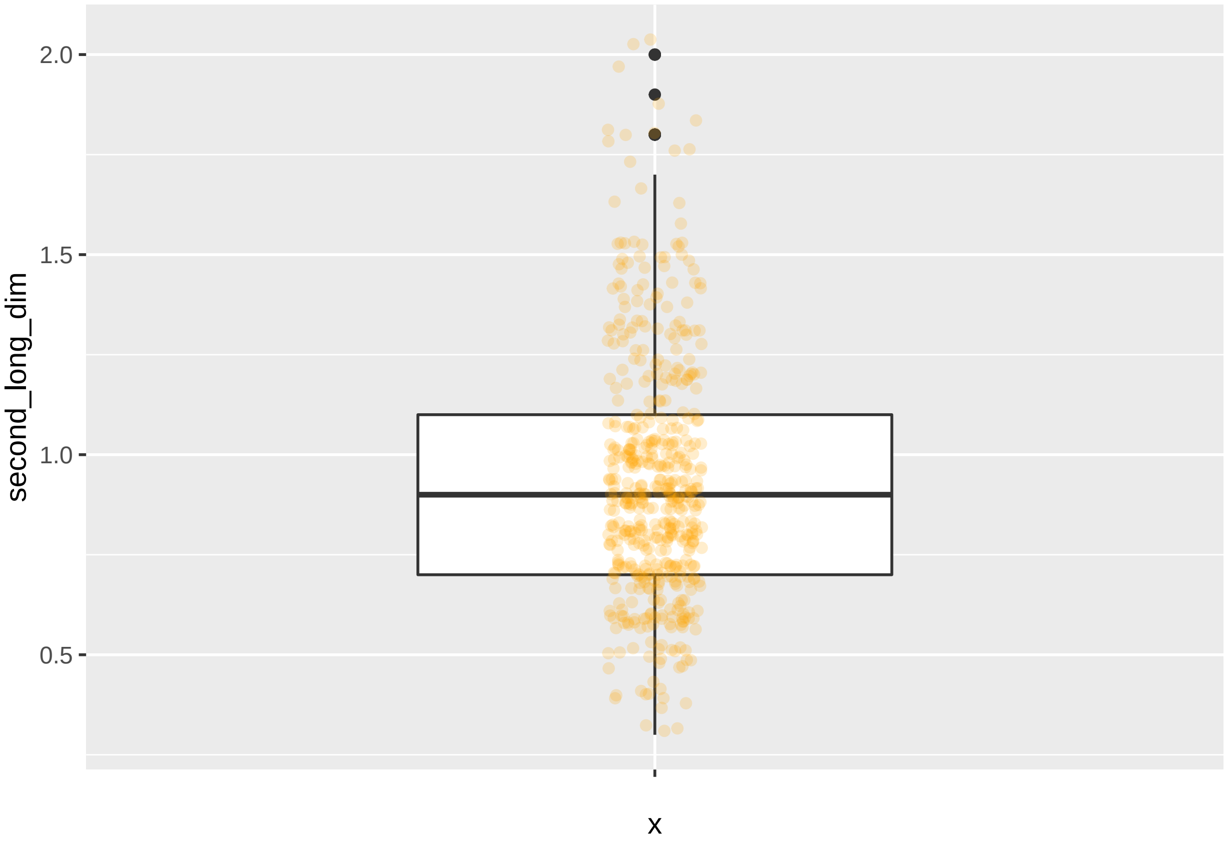
```
boxplot.stats(kirc_clean4$short_dim)
```

```
## $stats
## [1] 0.1 0.2 0.3 0.5 0.9
##
## $n
## [1] 502
##
## $conf
## [1] 0.2788443 0.3211557
##
## $out
## [1] 1 1
```

```
ggplot(kirc_clean4, aes(x ='', y=second_long_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```



```
boxplot.stats(kirc_clean4$second_long_dim)
```

```
## $stats
## [1] 0.3 0.7 0.9 1.1 1.7
##
## $n
## [1] 502
##
## $conf
## [1] 0.8717925 0.9282075
##
## $out
##  [1] 1.8 2.0 1.8 1.9 1.8 2.0 2.0 1.8 1.8 1.8 1.8
```

7. Checking categorical variables

Check frequency, lables and levels

```
kirc_clean4 %>%
     select_if(is.factor) %>%
     summary()
```

```
##  metastasis_stg neoplasm_ln_stg    neoplasm_stg   tumor_stg
##  M0   :426       N0:240          Stage I   :269   T1a    :142
##  M1   : 79       N1: 17          Stage II  : 57   T3a    :122
##  MX   : 30       NX:280          Stage III:125   T1b    :111
##  NA's:  2                        Stage IV  : 83   T2     : 55
##                                  NA's     :  3   T3b    : 53  
##                                                 T1     : 22  
##                                                 (Other): 32  
##             disease_free_stt                  ethnicity   histology_grd
##  DiseaseFree        :311     HISPANIC OR LATINO    : 26   G1  : 14     
##  Recurred/Progressed:127     NOT HISPANIC OR LATINO:359   G2  :230     
##  NA's               : 99     NA's                  :152   G3  :207     
##                                                           G4  : 78     
##                                                           GX  :  5     
##                                                           NA's:  3     
##                                                                        
##     hemoglobin  neoadj_therapy
##  Elevated:  5   No :519       
##  Low     :263   Yes: 18       
##  Normal  :186                 
##  NA's    : 83                 
##                               
##                               
##                               
##                                            prior_cancer   tumor_lateral
##  No                                              :459   Bilateral:  1  
##  Yes                                             : 72   Left     :253  
##  Yes, History of Prior Malignancy                :  2   Right    :283  
##  Yes, History of Synchronous/Bilateral Malignancy:  4                  
##                                                                        
##                                                                        
##                                                                        
##  primer_ln_ind3     platelet   tissue_prospect                        race    
##  NO  :395       Elevated: 38   NO  :465        ASIAN                    :  8  
##  YES :135       Low     : 46   YES : 52        BLACK OR AFRICAN AMERICAN: 56  
##  NA's:  7       Normal  :360   NA's: 20        WHITE                    :466  
##                 NA's    : 93                   NA's                     :  7  
##                                                                               
##                                                                               
##                                                                               
##  tissue_retrospect     serum_ca       sex       tissue_site 
##  NO  : 53          Elevated: 10   Female:191   BP     :142  
##  YES :466          Low     :204   Male  :345   BO     :107  
##  NA's: 18          Normal  :151   MALE  :  1   CJ     : 71  
##                    NA's    :172                A3     : 52  
##                                                CZ     : 40  
##                                                B8     : 33  
##                                                (Other): 92  
##  person_neoplasm_stt vital_stt         wbc     
##  TUMOR FREE:361      Alive:360   Elevated:164  
##  WITH TUMOR:141      Dead :174   Low     :  9  
##  NA's      : 35      NA's :  3   Normal  :268  
##                                  NA's    : 96  
##                                                
##                                                
##                                                
```

```
# agregating levels
kirc_clean5 <- kirc_clean4 %>%
     mutate(tumor_stg = fct_collapse(tumor_stg,
                             T1 = c('T1', 'T1a', 'T1b'),
                             T2 = c('T2', 'T2a', 'T2b'),
                             T3 = c('T3', 'T3a', 'T3b', 'T3c')))
kirc_clean5 <- kirc_clean4 %>%
     mutate(prior_cancer = fct_collapse(prior_cancer,
               Yes = c('Yes', 'Yes, History of Prior Malignancy', 'Yes, History of Synchronous/Bilateral

kirc_clean5 <- kirc_clean4 %>%
     mutate(sex = fct_collapse(sex, Male = c('MALE', 'Male')))

kirc_clean5 <- kirc_clean4 %>%
     mutate(tissue_site = fct_collapse(tissue_site,
                         A = c('A3', 'AK', 'AS'),
                         B = c('B0', 'B2', 'B4', 'B8', 'BP'),
                         C = c('CJ', 'CW', 'CZ'),
                         G = c('G6', 'GK'),
                         M = c('MM', 'MW')))

# droping levels
kirc_clean5 <- kirc_clean4 %>%
     mutate(race = fct_recode(race, NULL = 'ASIAN'))

# kirc_clean5 <- kirc_clean4 %>%
#     mutate(race = fct_drop(race, only = 'ASIAN'))

# recoding levels
# OBS: It can be donne latter, for regression analysis
# kirc_clean4 %>%
#      select_if(is.factor) %>%
#      summary()
#
# kirc_clean5 <- kirc_clean4 %>%
#      mutate(sex = fct_recode(sex, '1'='Male', '2'='Female'))
#
# kirc_clean5 <- kirc_clean4 %>%
#      mutate(sex = if_else(sex %in% c('Male', 'Female'), 1, 0))
```

8. Saving dataset

```
write_csv(kirc_clean5, path = "data/kirc_clinical_clean.csv")

rm(kirc_clean4, kirc_clean3, kirc_clean2, kirc_clean1, kirc_clean0, kirc_clean)
```

```
# table(kirc_clean4$metastasis_stg, exclude = NULL)
# table(kirc_clean4$neoplasm_ln_stg, exclude = NULL)
# table(kirc_clean4$neoplasm_stg, exclude = NULL)
# table(kirc_clean4$tumor_stg, exclude = NULL)
# table(kirc_clean4$disease_free_stt, exclude = NULL)
# table(kirc_clean4$ethnicity, exclude = NULL)
# table(kirc_clean4$histology_grd, exclude = NULL)
# table(kirc_clean4$hemoglobin, exclude = NULL)
# table(kirc_clean4$neoadj_therapy, exclude = NULL)
# table(kirc_clean4$prior_cancer, exclude = NULL)
# table(kirc_clean4$tumor_lateral, exclude = NULL)
# table(kirc_clean4$primer_ln_ind3, exclude = NULL)
# table(kirc_clean4$platelet, exclude = NULL)
# table(kirc_clean4$tissue_prospect, exclude = NULL)
# table(kirc_clean4$race, exclude = NULL)
# table(kirc_clean4$tissue_retrospect, exclude = NULL)
# table(kirc_clean4$serum_ca, exclude = NULL)
# table(kirc_clean4$sex, exclude = NULL)
# table(kirc_clean4$tissue_site, exclude = NULL)
# table(kirc_clean4$person_neoplasm_stt, exclude = NULL)
# table(kirc_clean4$wbc, exclude = NULL)
```