2020 Ab titer data: Median (at Day 0) based normalisation

Reading dataset from experimental datafile

```
setwd("/home/pramod/Documents/GitHub/2021-Ab-titer-data-normalisation")
data_2020_metadata <- read_csv("metadata_cmipb_2020.csv")
```

```
## Rows: 195 Columns: 1

## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): specimen_id subject_id  visit   Timepoint   infancy_vac

##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
json_subject <- fromJSON("subject.json")
json_specimen <- fromJSON("specimen.json")
subject_specimen  <- left_join(json_specimen, json_subject) %>%
  dplyr::select(specimen_id, subject_id, planned_day_relative_to_boost)
```

```
## Joining, by = "subject_id"
```

```
titers_2020 <- read_csv("2020LD_ab_titer.csv") %>%
  left_join(subject_specimen) %>%
  mutate(
    antigen = replace(antigen, antigen =='1% PFA PT', 'PT'),
    isotype_antigen = paste0(isotype,"_",antigen, "_", unit),
    ab_titer_original = ab_titer, ## Kepping ab)titer_original for final dataframe
  )
```

```
## Rows: 31520 Columns: 7

## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (3): isotype, antigen, unit
## dbl (3): specimen_id, ab_titer, lower_limit_of_detection
## lgl (1): is_antigen_specific

##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

## Joining, by = "specimen_id"
```

Count NA and below LOD samples per Isotype and Antigen pair

Remove features with more than 80% missing values

```
count_samples <- titers_2020 %>%
  group_by(isotype_antigen) %>%
  summarise(count_samples = n())

count_0 <- titers_2020 %>%
  group_by(isotype_antigen) %>%
  filter(is.na(ab_titer) == TRUE | ab_titer < lower_limit_of_detection) %>%
  summarise(count_0 = n(), percentage_0 = (count_0/394)* 100) %>%
  arrange(desc(percentage_0))

count_0
```

```
## # A tibble: 73 x 3
##    isotype_antigen    count_0 percentage_0
##    <chr>                <int>        <dbl>
##  1 IgE_OVA_IU/ML          394        100
##  2 IgG4_PD1_IU/ML         394        100
##  3 IgE_Measles_IU/ML      393         99.7
##  4 IgE_PD1_IU/ML          389         98.7
##  5 IgG4_Measles_IU/ML     389         98.7
##  6 IgE_ACT_IU/ML          387         98.2
##  7 IgE_BETV1_IU/ML        381         96.7
##  8 IgG2_BETV1_IU/ML       380         96.4
##  9 IgG3_BETV1_IU/ML       380         96.4
## 10 IgE_FHA_IU/ML          379         96.2
## # ... with 63 more rows
```

```
remove_features <- count_0[count_0$percentage_0 > 80,]$isotype_antigen
titers_2020_feature_removed <- titers_2020[!titers_2020$isotype_antigen %in% remove_features, ]
```

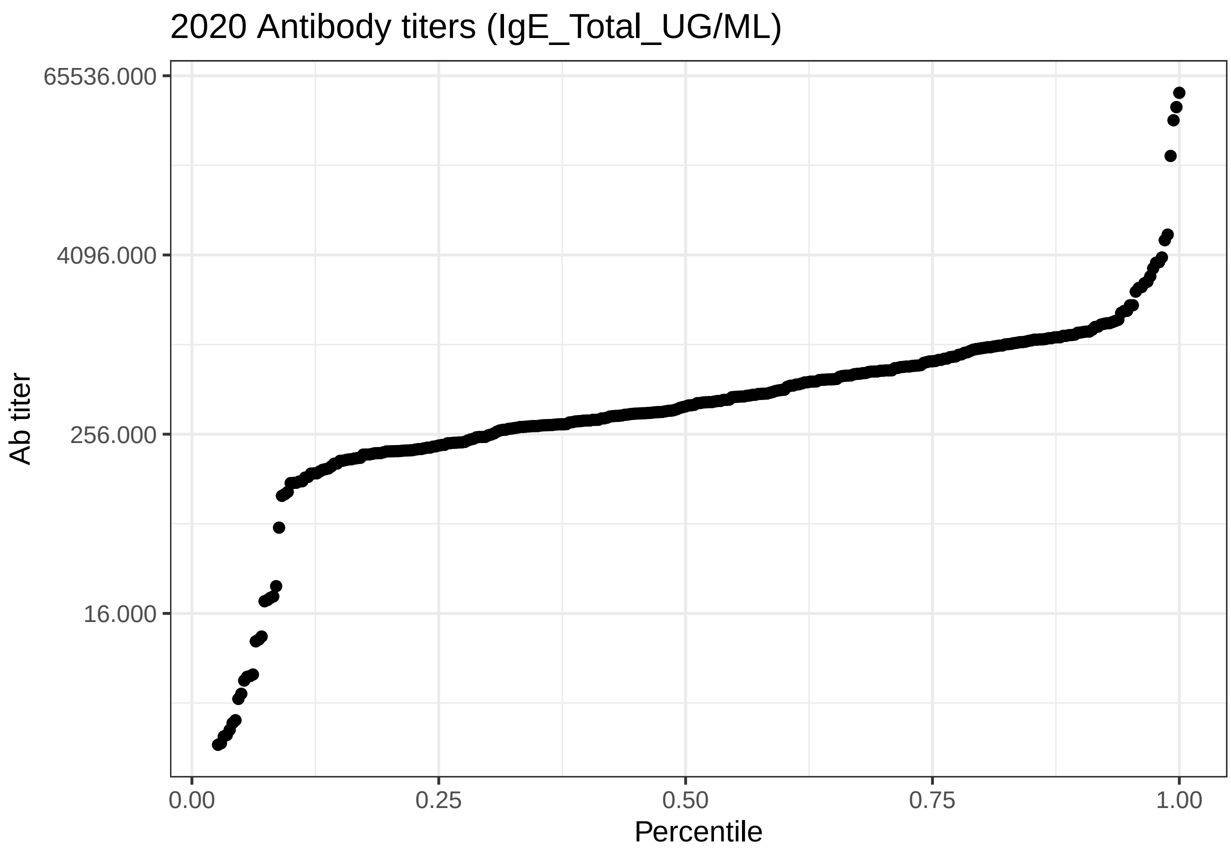
Replace not detechetd values with lower__limit__of__detection

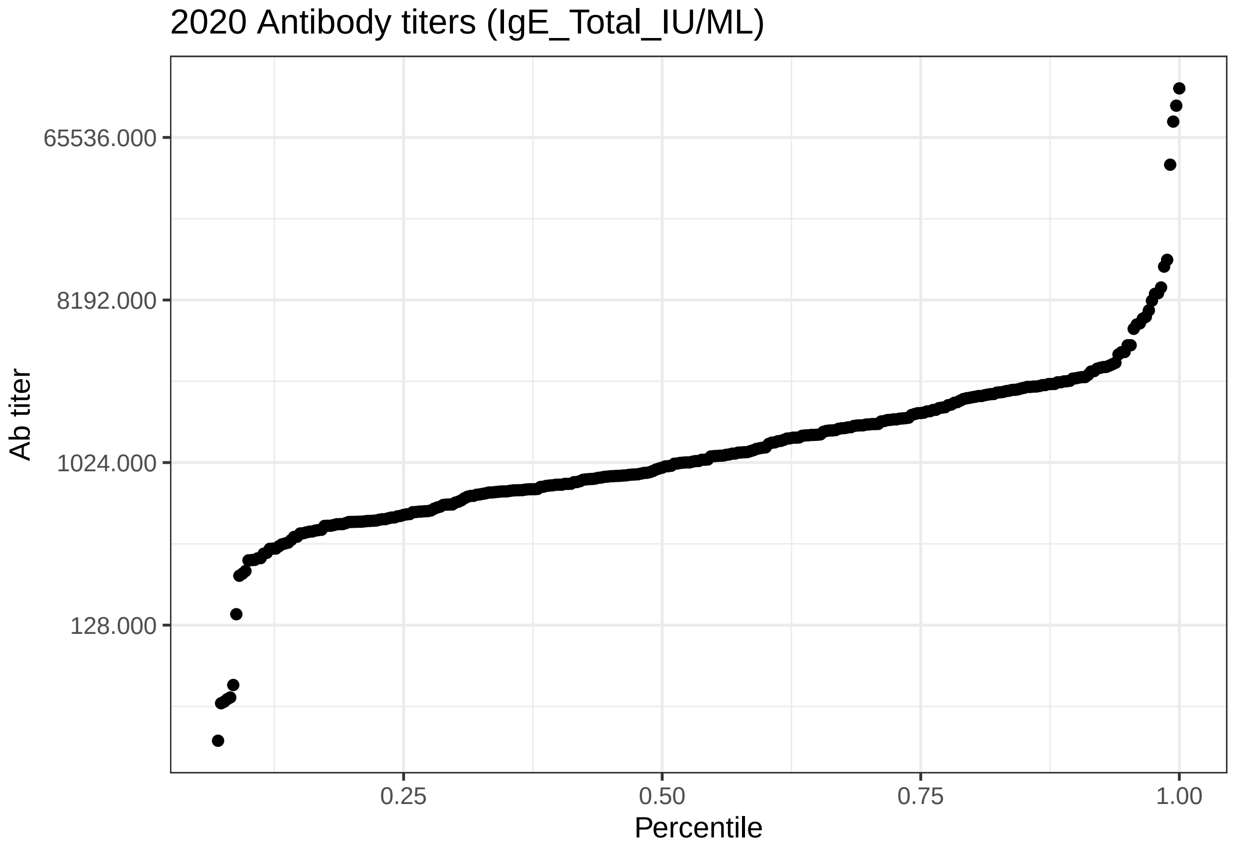
```
titers_2020_feature_removed_lod <- titers_2020_feature_removed %>%
  mutate(
    lower_limit_of_detection = if_else(isotype_antigen == "IgE_Total_UG/ML", 2.09613325980121, lower_lin
    ab_titer = if_else(ab_titer < lower_limit_of_detection, lower_limit_of_detection, ab_titer)
  )

## QC for LOD outliers
## No Outliers detected
lod_outlier <- titers_2020_feature_removed_lod %>%
  group_by(isotype_antigen) %>%
  #slice_min(MFI_normalized, n=2) %>%
  #arrange(desc(MFI_normalized)) %>%
  summarise(min = min(ab_titer), lod = lower_limit_of_detection, fc_min_max = lower_limit_of_detection/r
  filter(fc_min_max > 3)
```

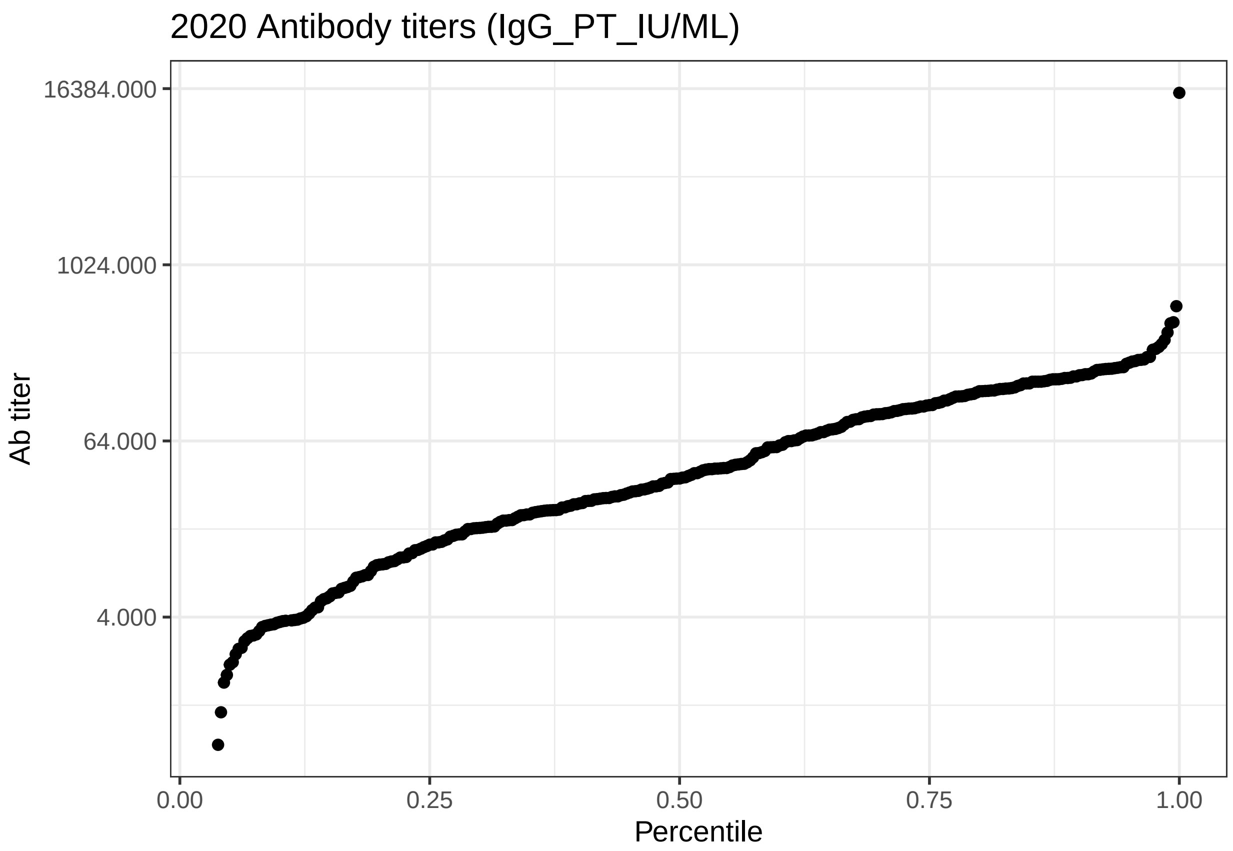
```
## `summarise()` has grouped output by 'isotype_antigen'. You can override using the `.groups` argument
```

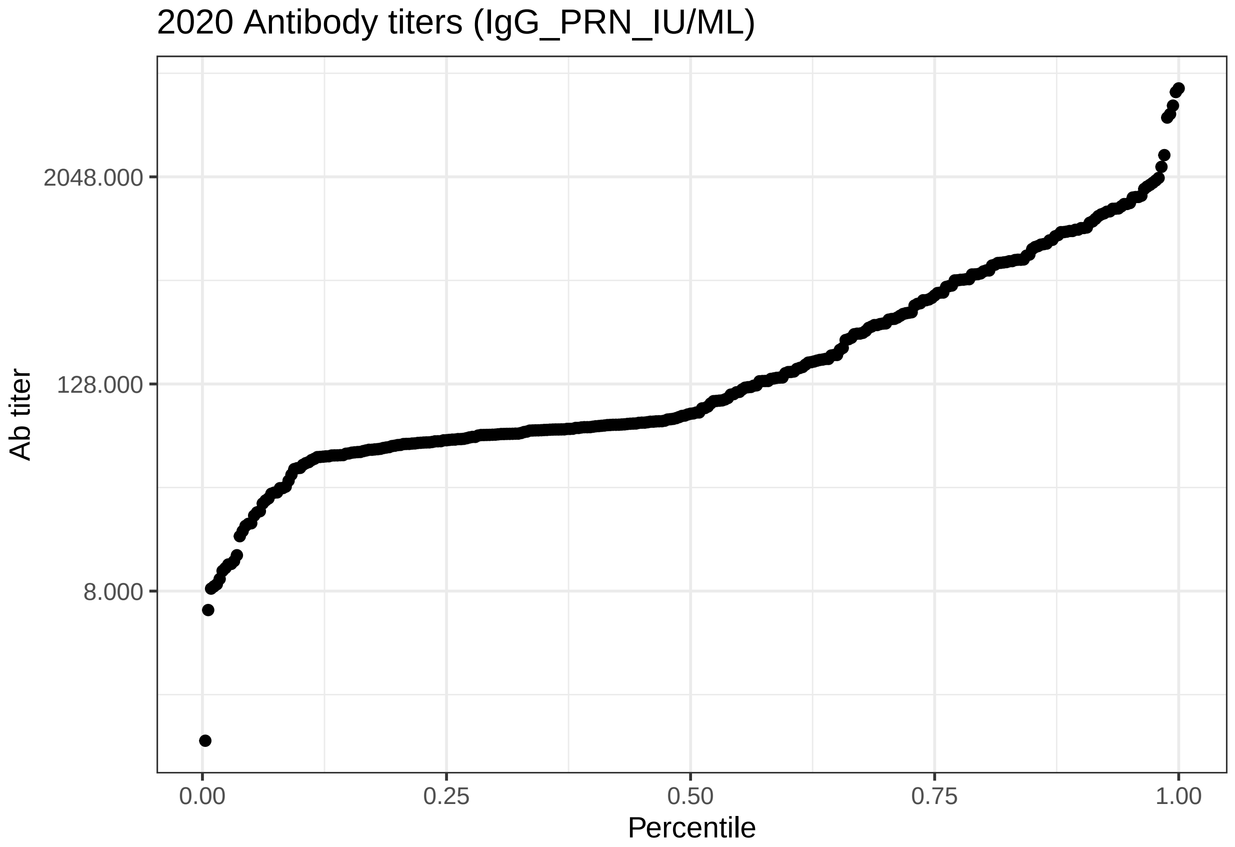
Identifying outlier ab titers.

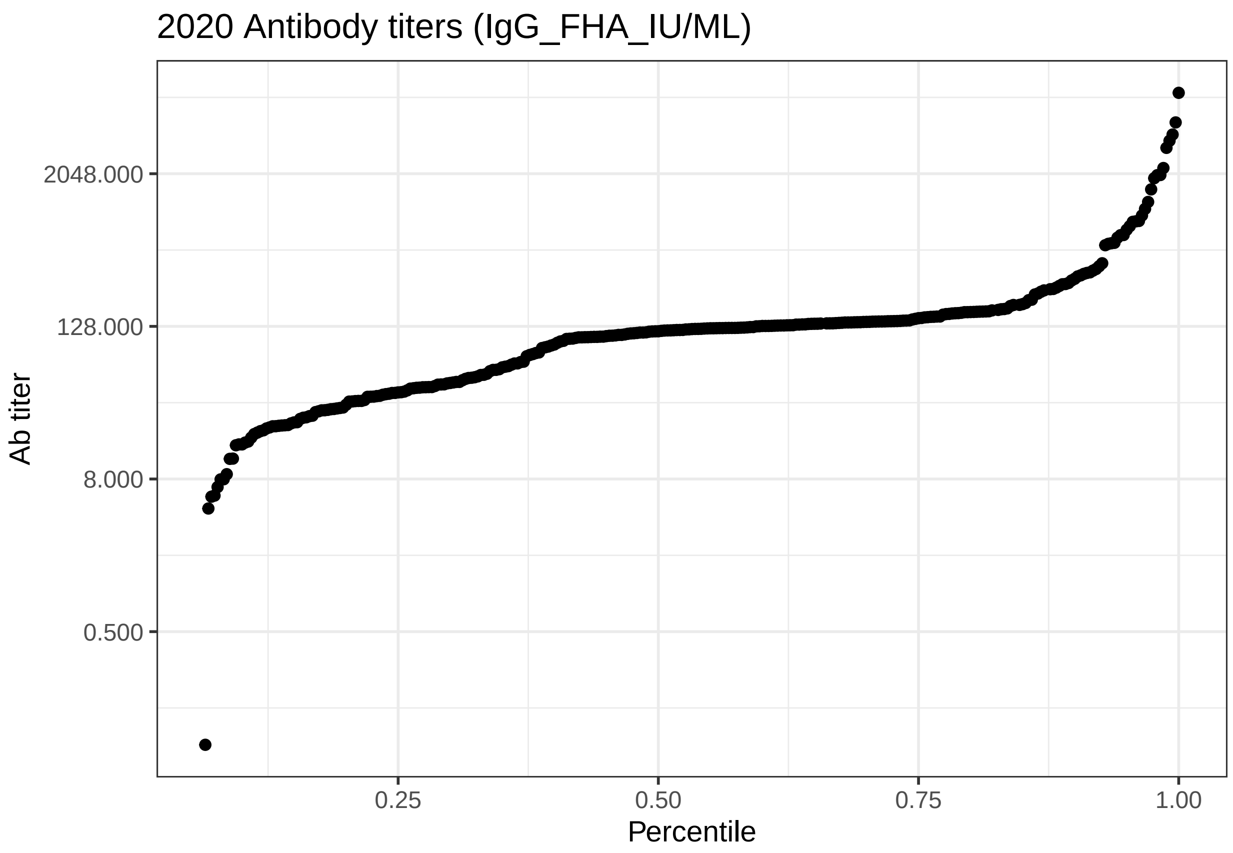
```
## If second_max_value/max_value > 3 then set max_value = LOD
top_outlier <- titers_2020_feature_removed_lod %>%
  group_by(isotype_antigen) %>%
  slice_max(ab_titer, n=2) %>%
  arrange(desc(ab_titer)) %>%
  summarise(fc_min_max = max(ab_titer)/min(ab_titer)) %>%
  filter(fc_min_max > 3)

## If first_value/LOD > 3 then set LOD as first_value
bottom_outlier <- titers_2020_feature_removed_lod %>%
  group_by(isotype_antigen) %>%
  slice_min(ab_titer, n=2) %>%
  arrange(desc(ab_titer)) %>%
  summarise(fc_min_max = max(ab_titer)/min(ab_titer)) %>%
  filter(fc_min_max > 2)

## Ploting cummulative distribution to identify outliers.
#Our transformation function
scaleFUN <- function(x) sprintf("%.3f", x)

#for(select_ia in c('IgE_Total'))
for(select_ia in unique(titers_2020_feature_removed_lod$isotype_antigen))
{
plot1 <- titers_2020_feature_removed_lod %>%
  mutate(subject_id = as.factor(subject_id)) %>%
  filter(isotype_antigen == select_ia, planned_day_relative_to_boost < 50) %>%
  arrange(desc(ab_titer)) %>%
  ggplot(aes(y=ab_titer)) +  stat_ecdf(geom = "point", pad = FALSE) +
  labs(y = "Ab titer", x = "Percentile")+ ggtitle(paste0("2020 Antibody titers (" , select_ia, ")")) + 
  scale_y_continuous(trans = 'log2', labels=scaleFUN)

plot(plot1)
}
```

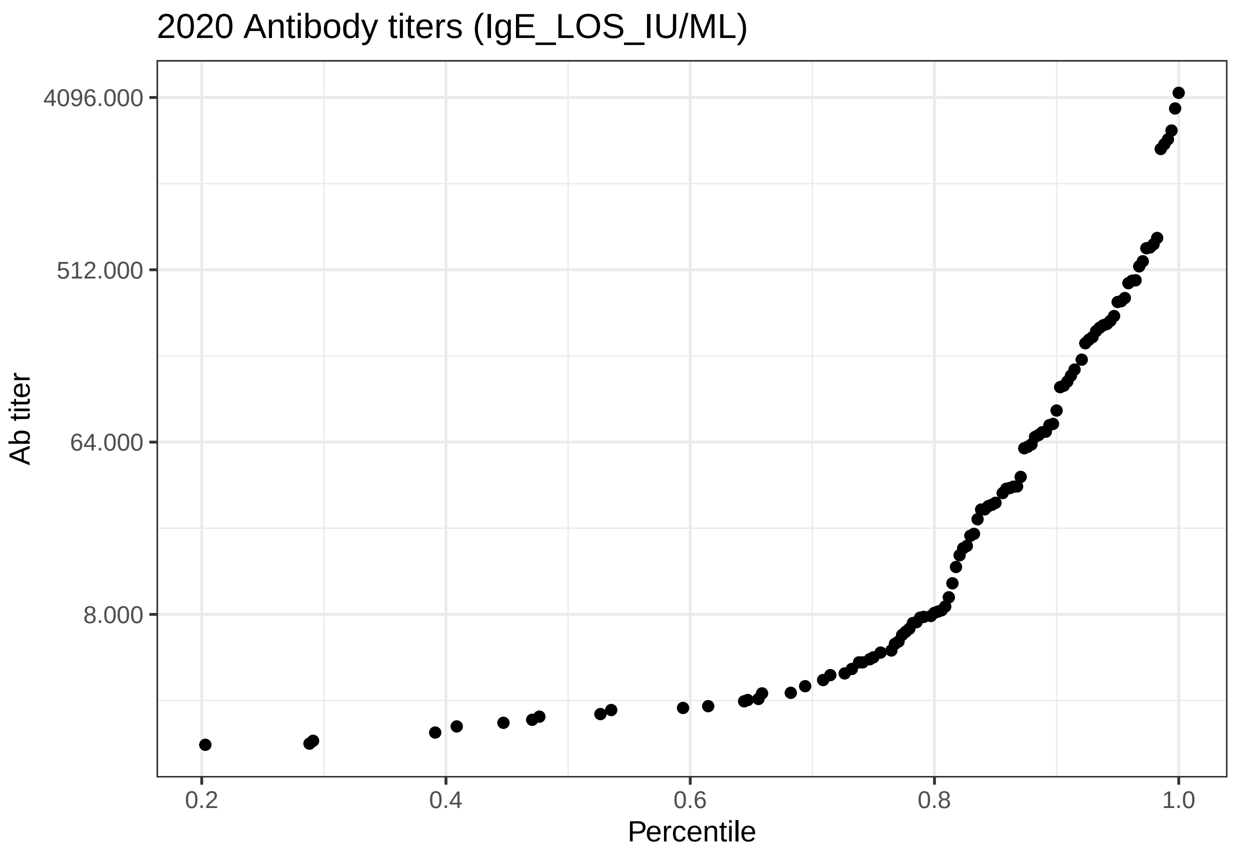

2020 Antibody titers (IgE_Total_UG/ML)
65536.000
4096.000
256.000
16.000
Ab titer
0.00
0.25
0.50
0.75
1.00
Percentile

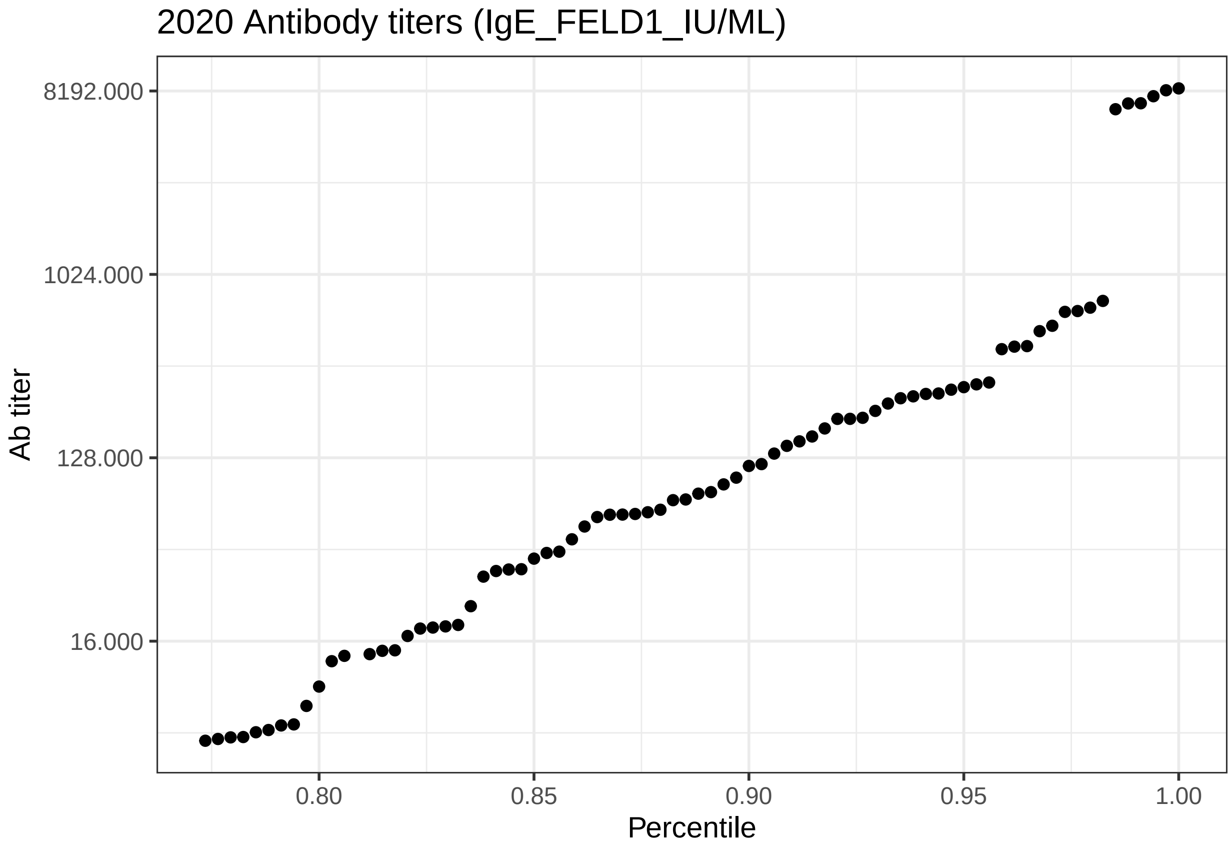

2020 Antibody titers (IgE_Total_IU/ML)
Ab titer
65536.000
8192.000
1024.000
128.000
0.25
0.50
0.75
1.00
Percentile

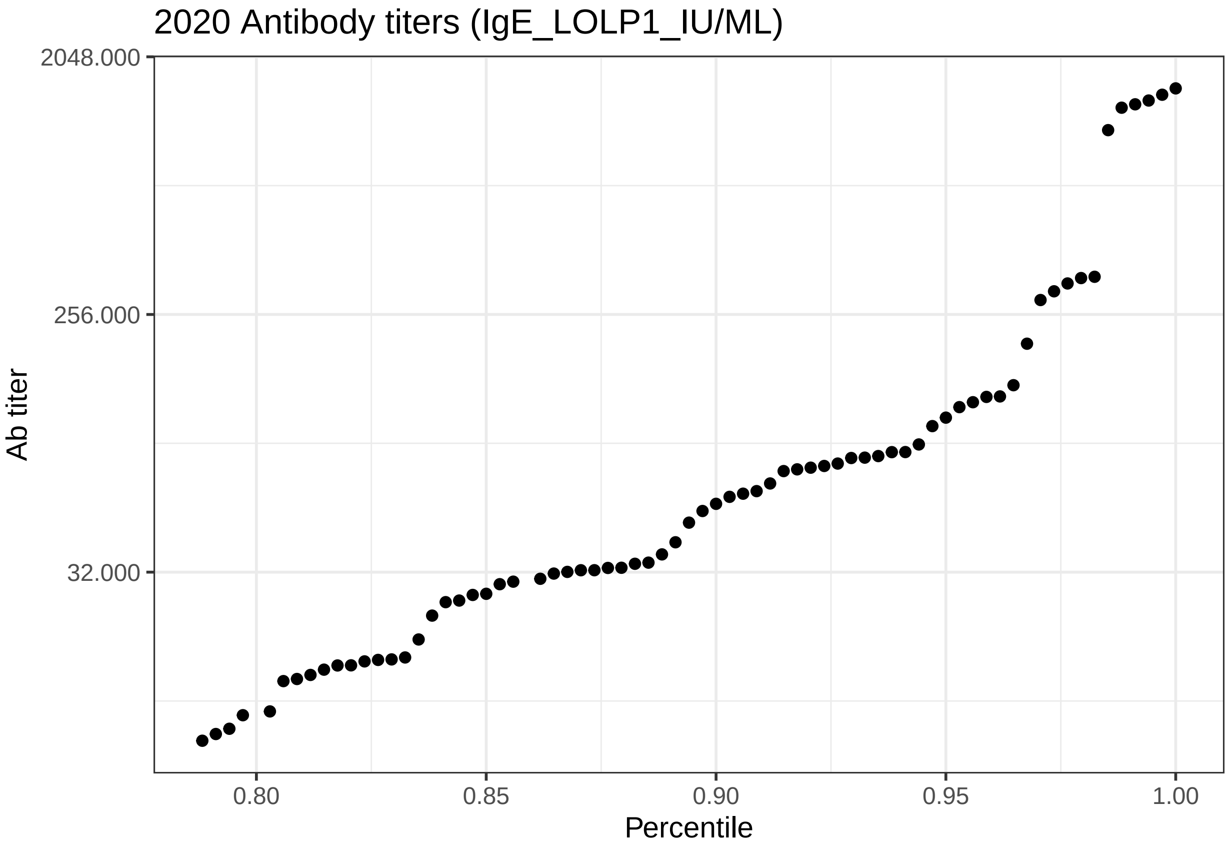

2020 Antibody titers (IgG_PT_IU/ML)
Ab titer
16384.000
1024.000
64.000
4.000
0.00
0.25
0.50
0.75
1.00
Percentile

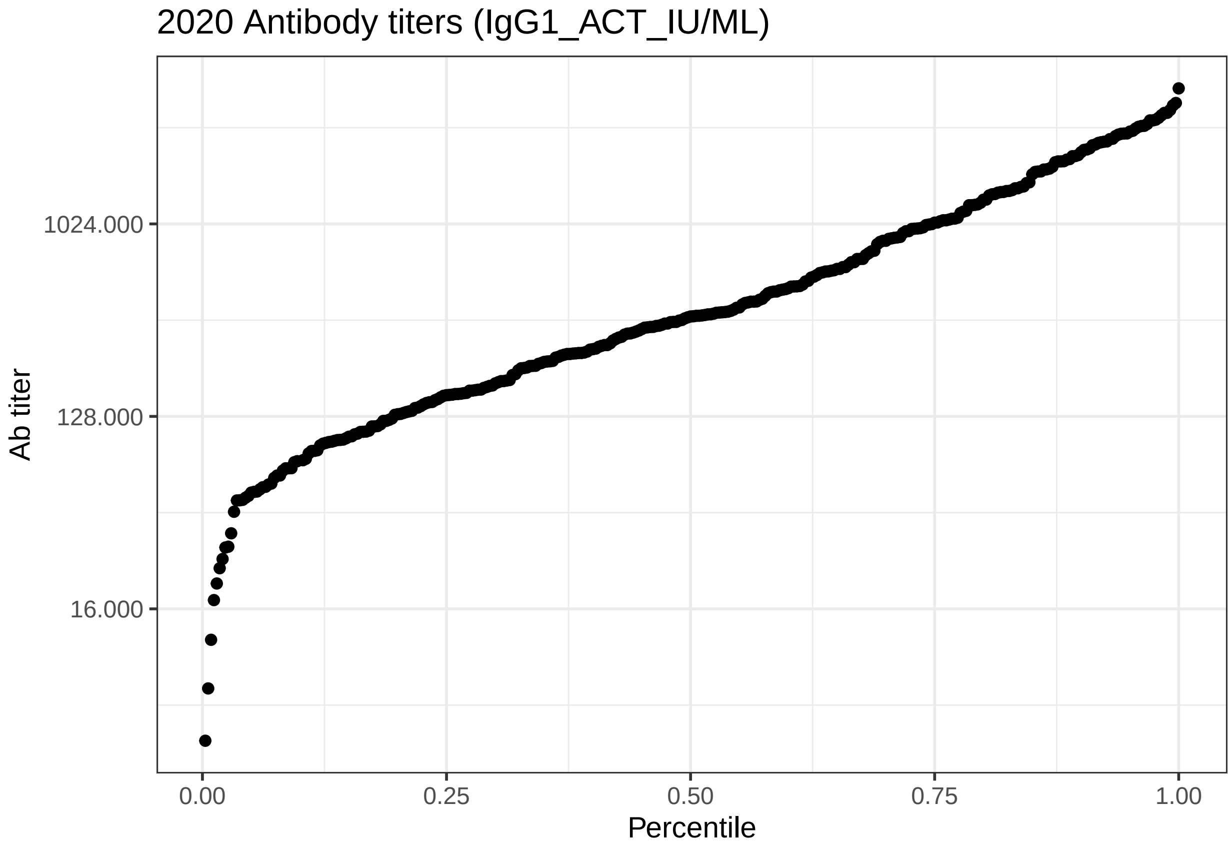

2020 Antibody titers (IgG_PRN_IU/ML)
Ab titer
2048.000
128.000
8.000
0.00
0.25
0.50
0.75
1.00
Percentile

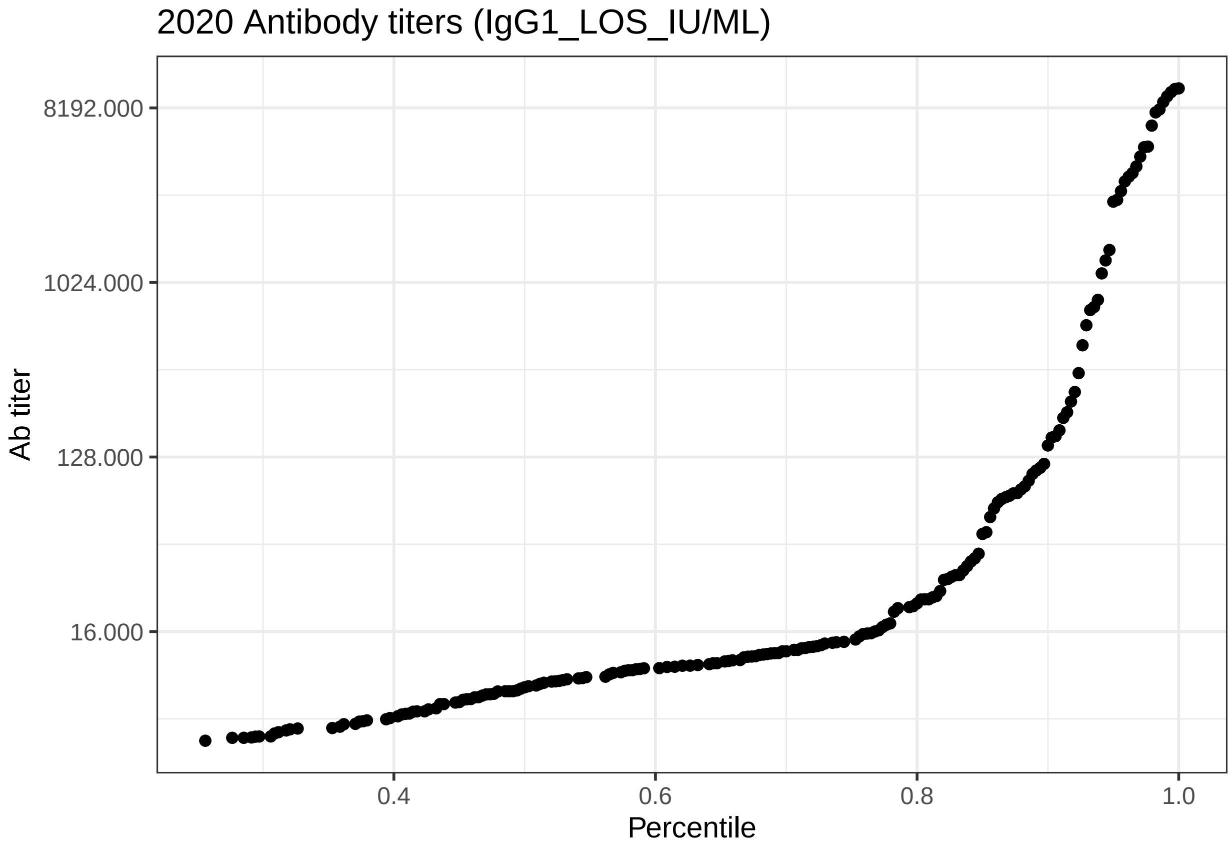

2020 Antibody titers (IgG_FHA_IU/ML)
Ab titer
2048.000
128.000
8.000
0.500
0.25
0.50
0.75
1.00
Percentile

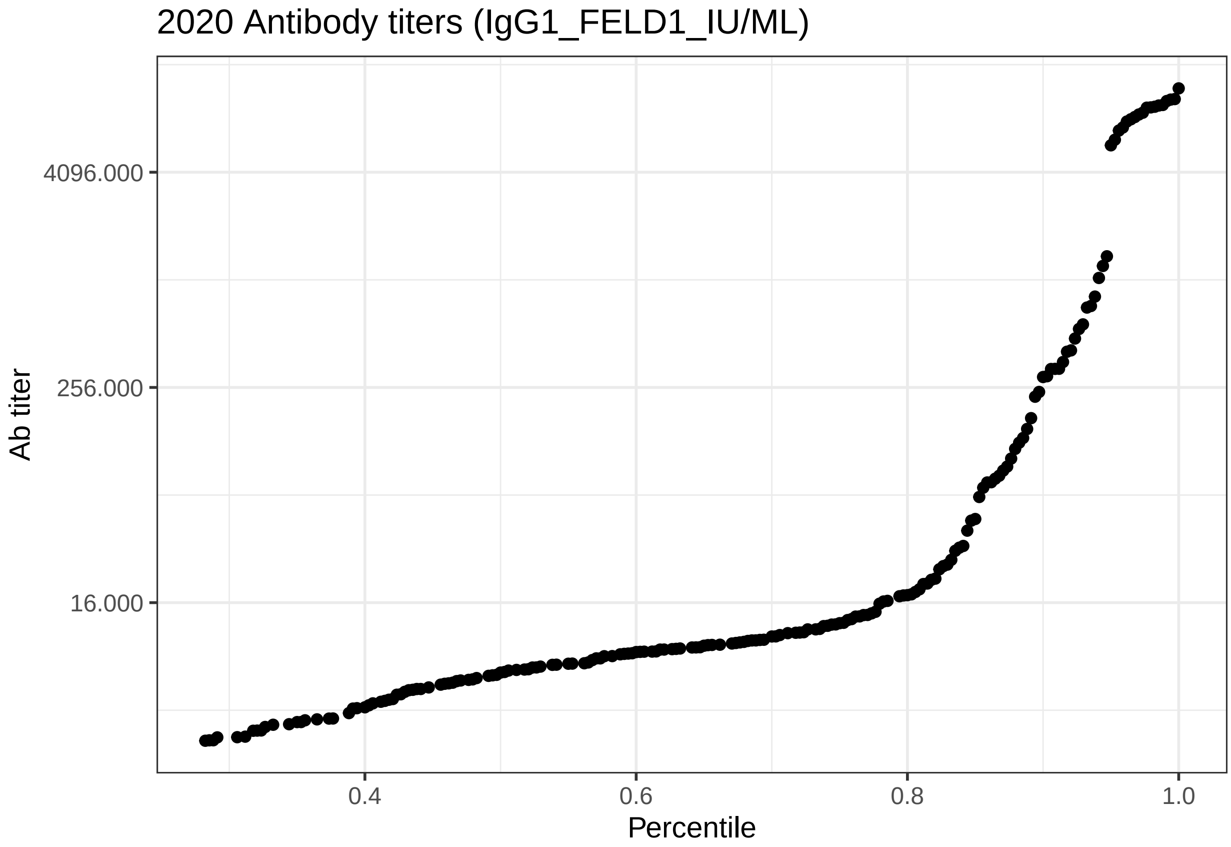

2020 Antibody titers (IgE_LOS_IU/ML)
4096.000
512.000
64.000
8.000
Ab titer
0.2
0.4
0.6
0.8
1.0
Percentile

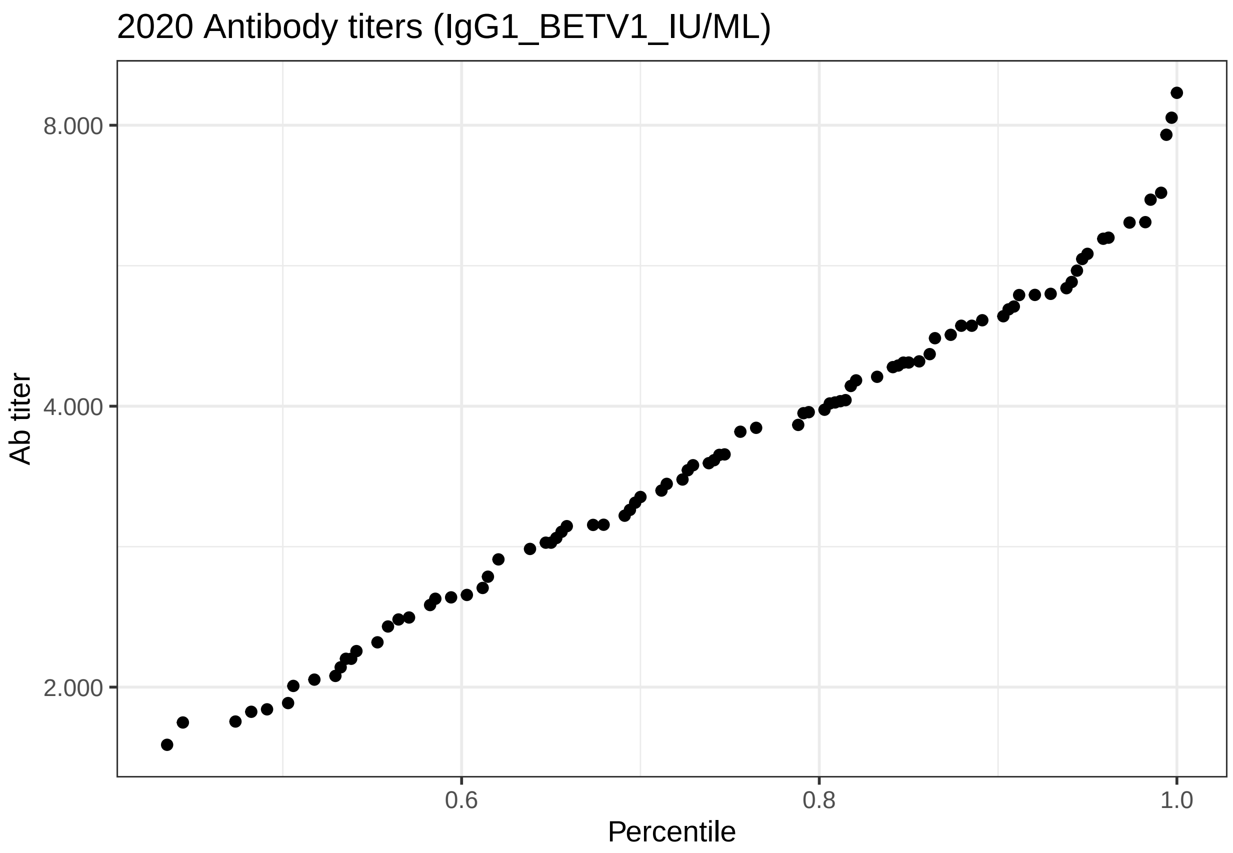

2020 Antibody titers (IgE_FELD1_IU/ML)
Ab titer
8192.000
1024.000
128.000
16.000
0.80
0.85
0.90
0.95
1.00
Percentile

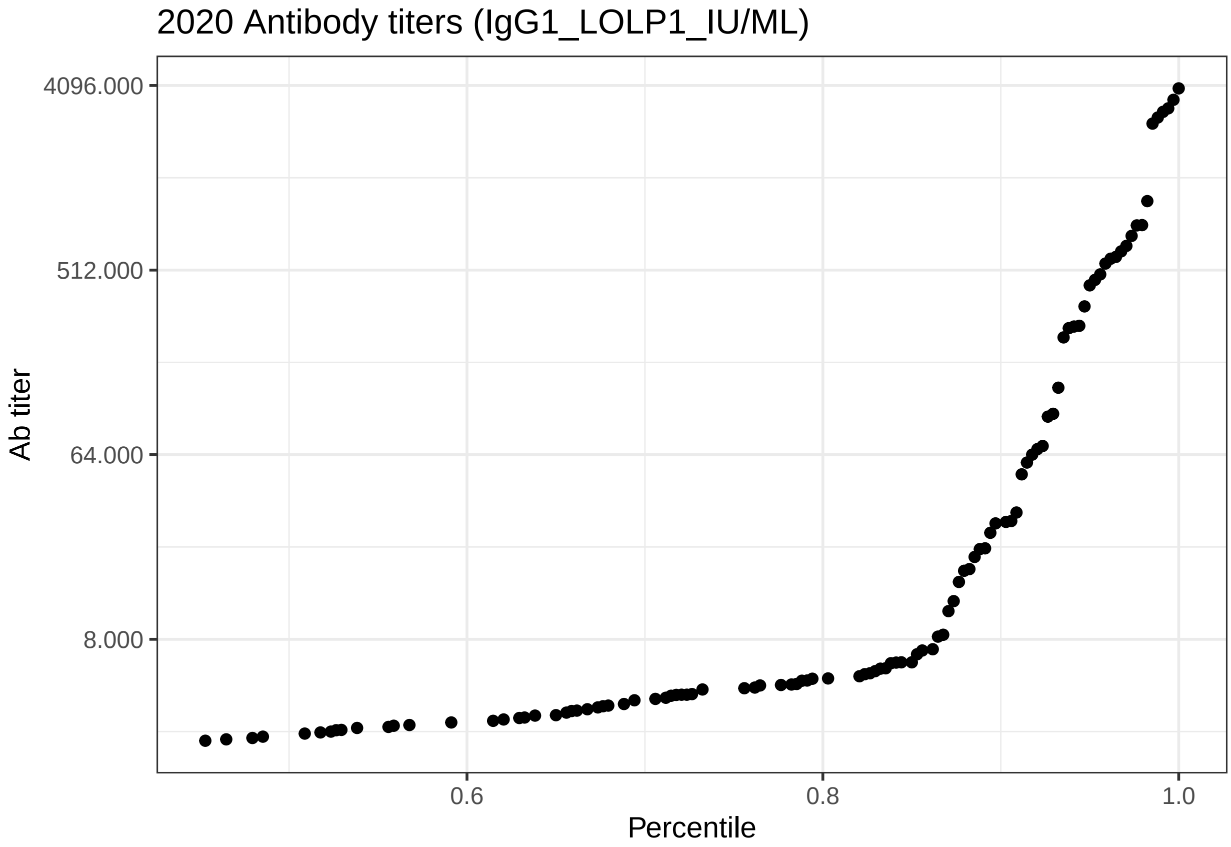

2020 Antibody titers (IgE_LOLP1_IU/ML)
Ab titer
2048.000
256.000
32.000
0.80
0.85
0.90
0.95
1.00
Percentile

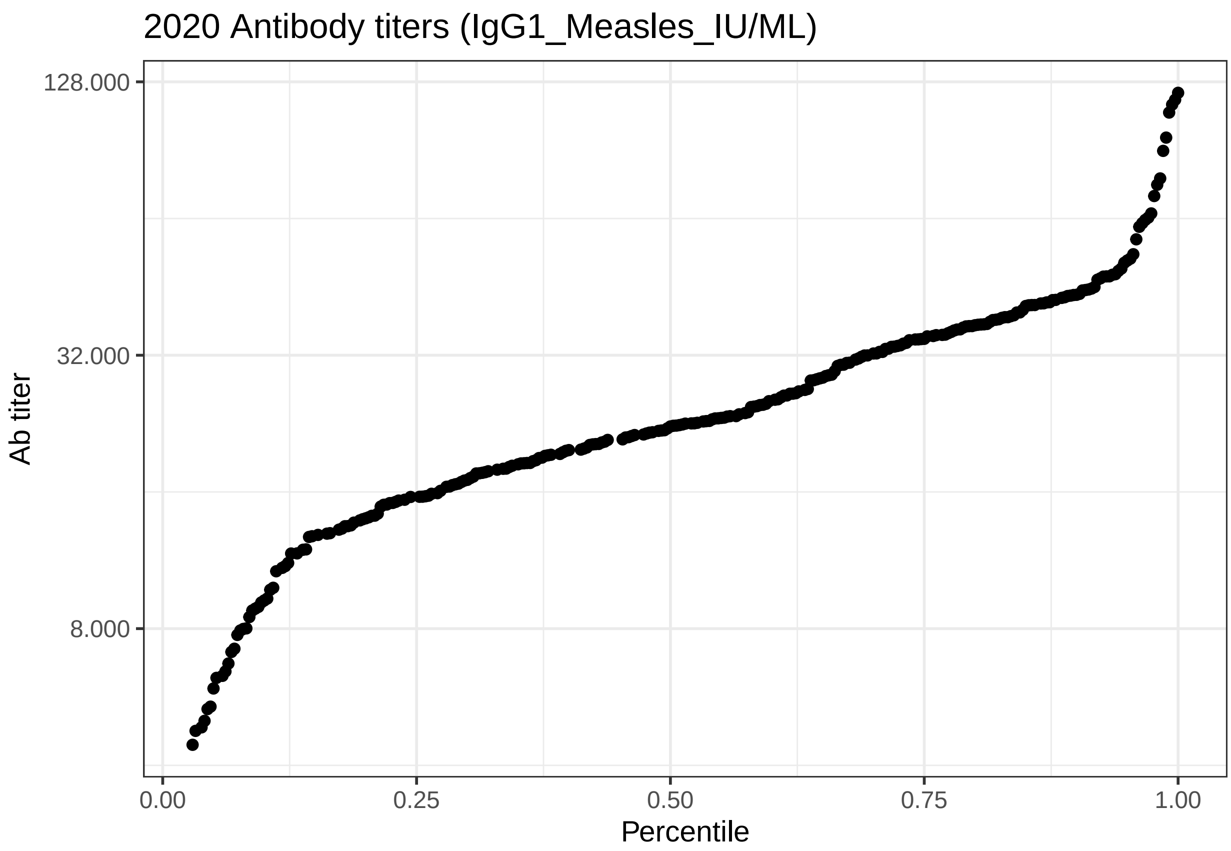

2020 Antibody titers (IgG1_ACT_IU/ML)
Ab titer
1024.000
128.000
16.000
0.00
0.25
0.50
0.75
1.00
Percentile

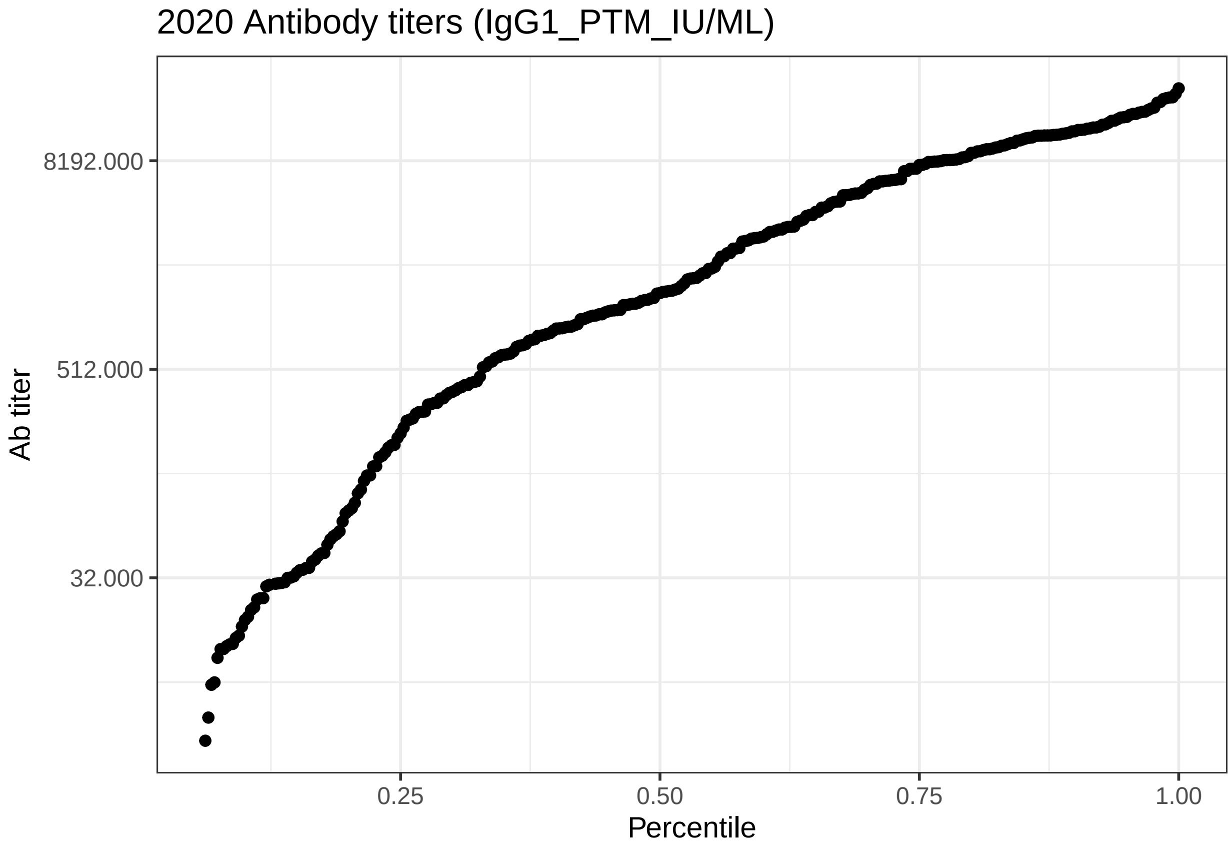

2020 Antibody titers (IgG1_LOS_IU/ML)
Ab titer
8192.000
1024.000
128.000
16.000
0.4
0.6
0.8
1.0
Percentile

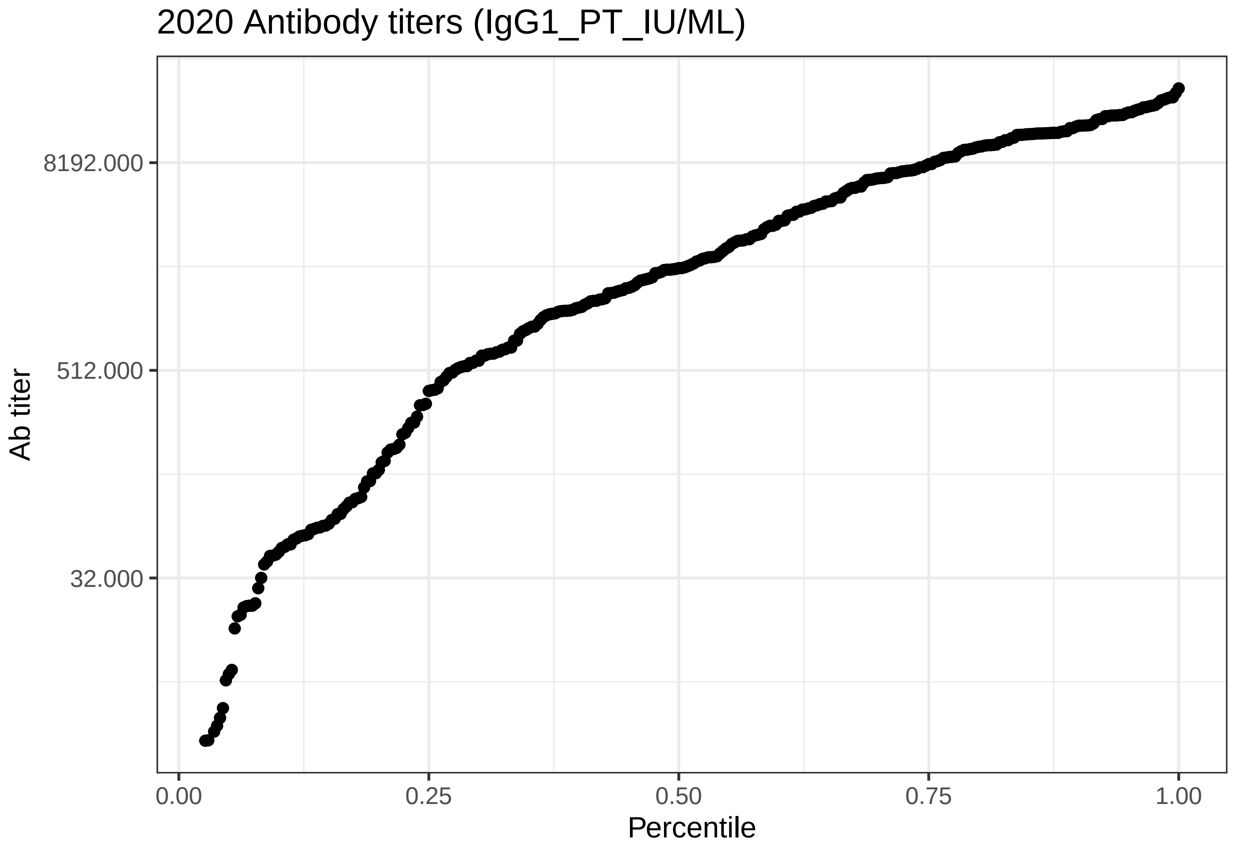

2020 Antibody titers (IgG1_FELD1_IU/ML)
Ab titer
4096.000
256.000
16.000
Percentile
0.4
0.6
0.8
1.0

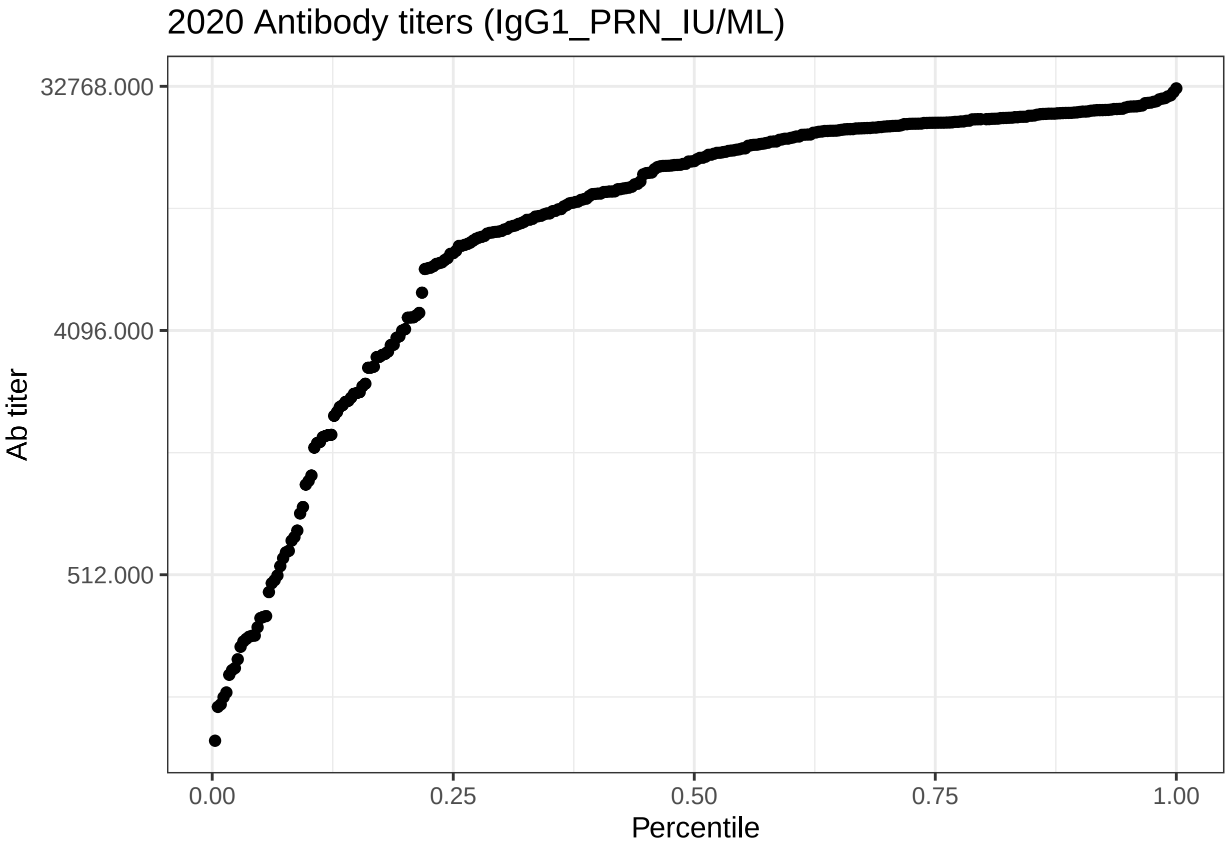

2020 Antibody titers (IgG1_BETV1_IU/ML)
Ab titer
8.000
4.000
2.000
0.6
0.8
1.0
Percentile

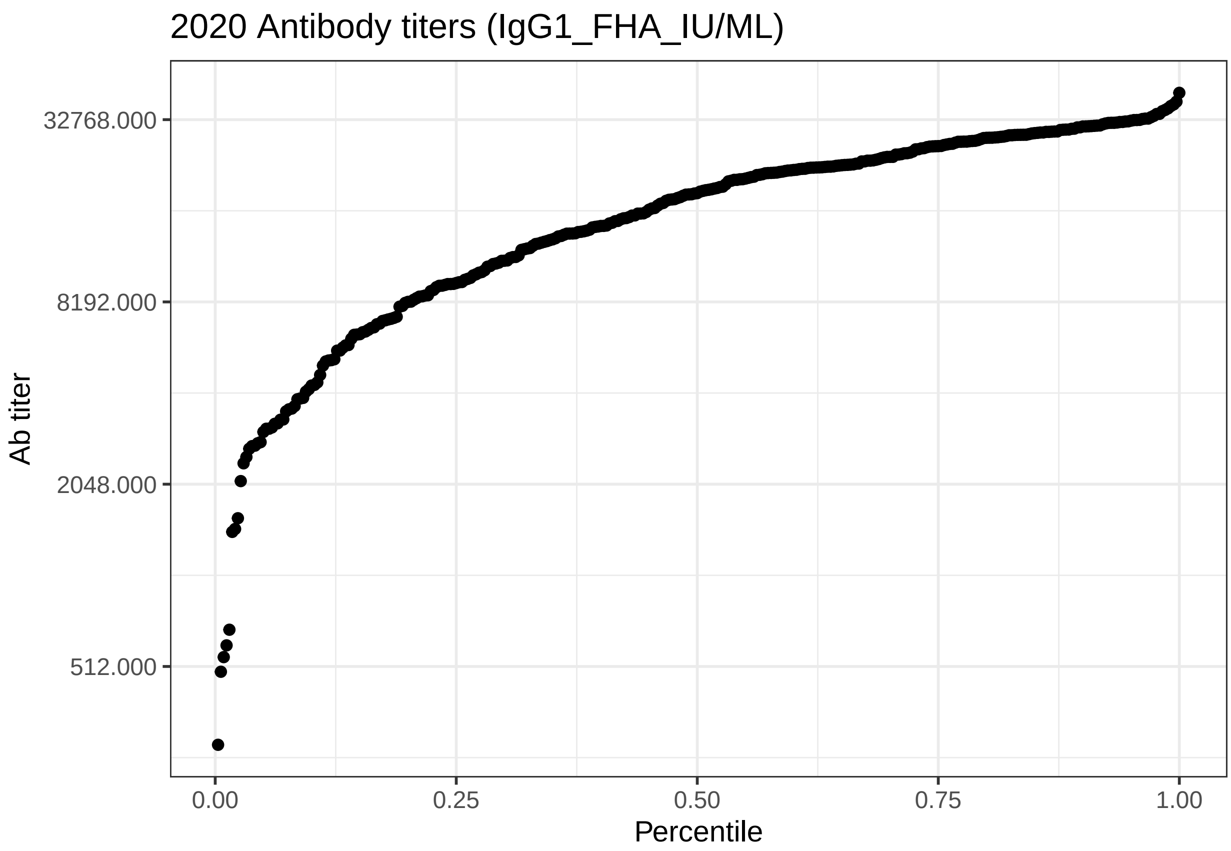

2020 Antibody titers (IgG1_LOLP1_IU/ML)
Ab titer
4096.000
512.000
64.000
8.000
0.6
0.8
1.0
Percentile

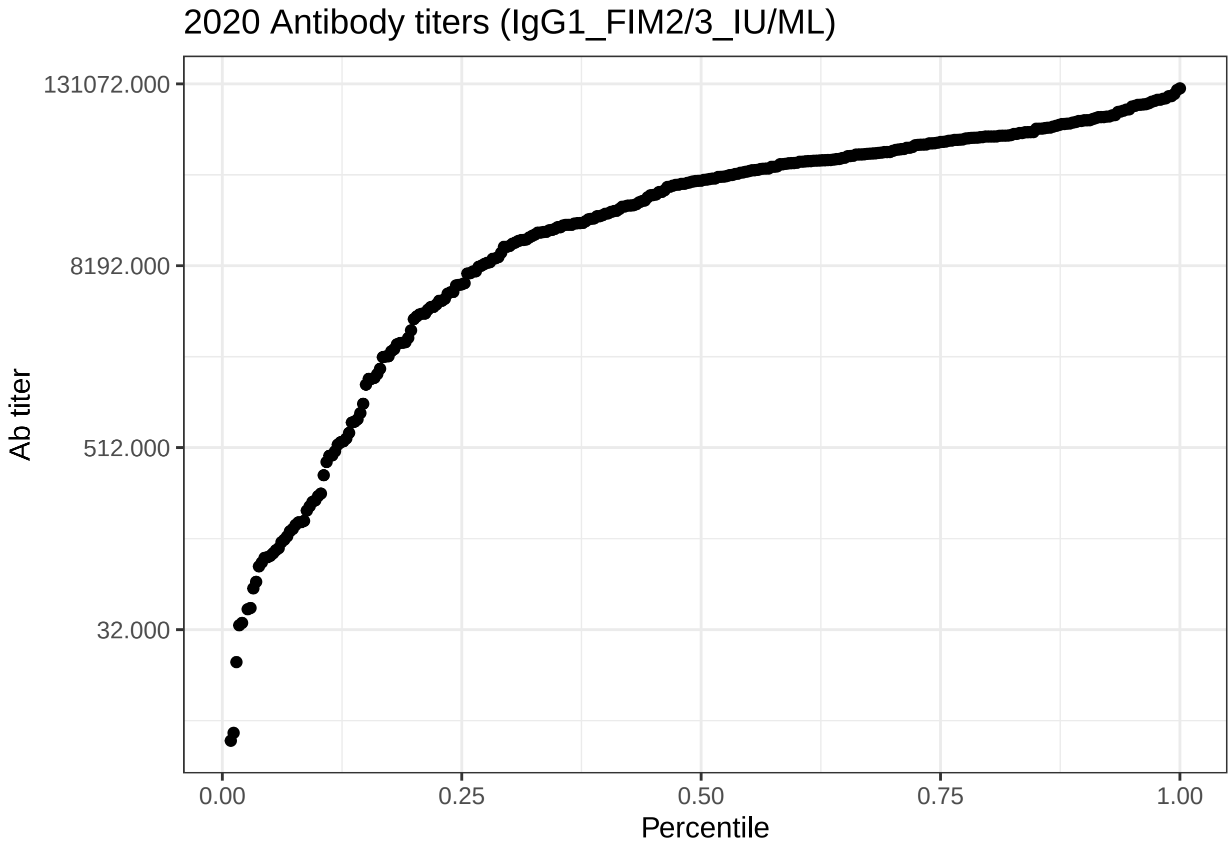

2020 Antibody titers (IgG1_Measles_IU/ML)
Ab titer
128.000
32.000
8.000
0.00
0.25
0.50
0.75
1.00
Percentile

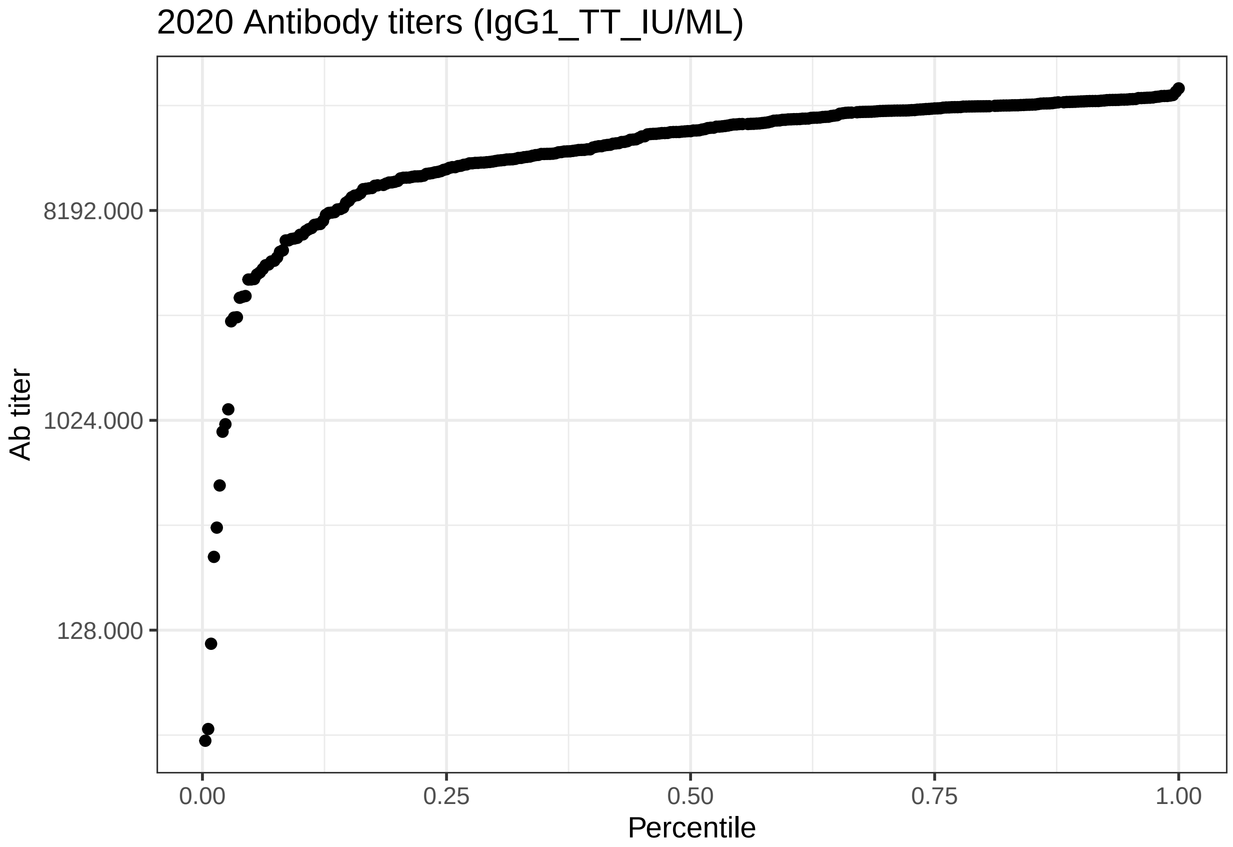

2020 Antibody titers (IgG1_PTM_IU/ML)
Ab titer
8192.000
512.000
32.000
0.25
0.50
0.75
1.00
Percentile

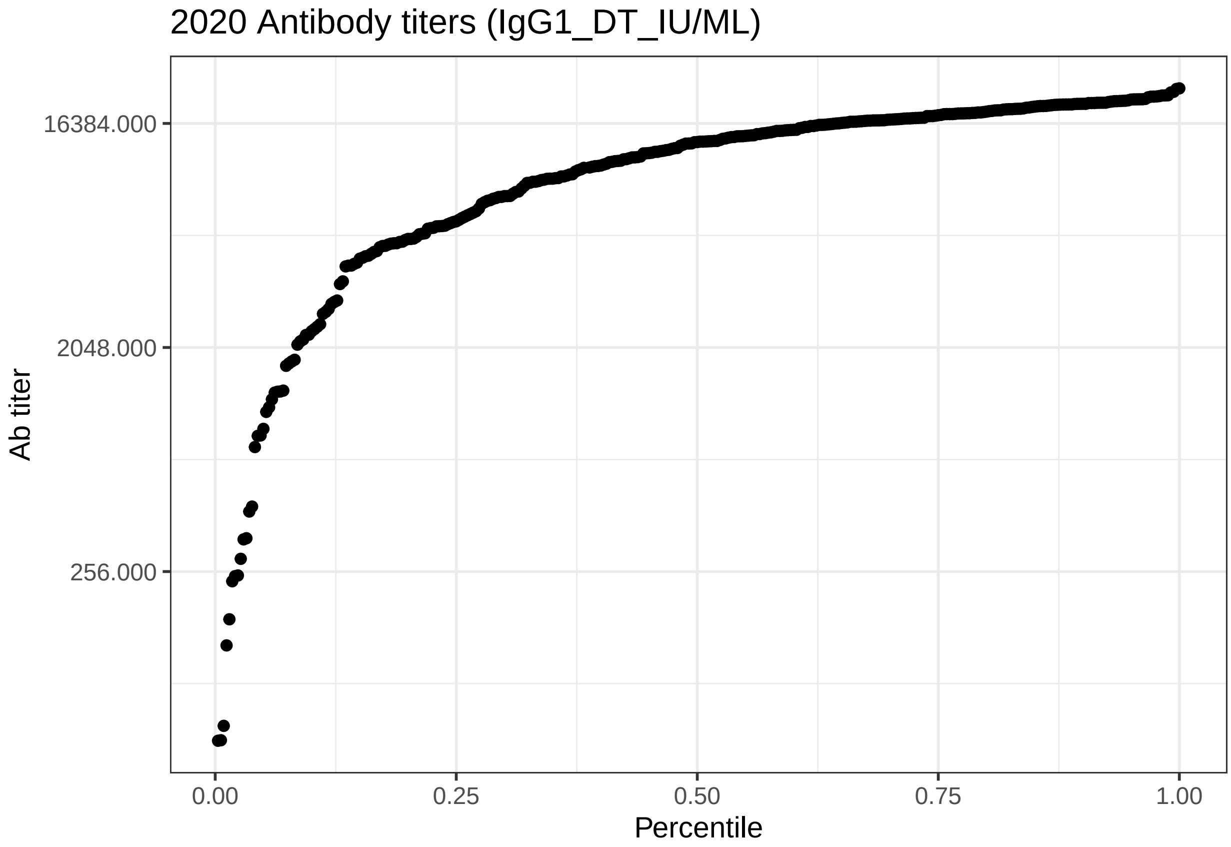

2020 Antibody titers (IgG1_PT_IU/ML)
Ab titer
8192.000
512.000
32.000
0.00
0.25
0.50
0.75
1.00
Percentile

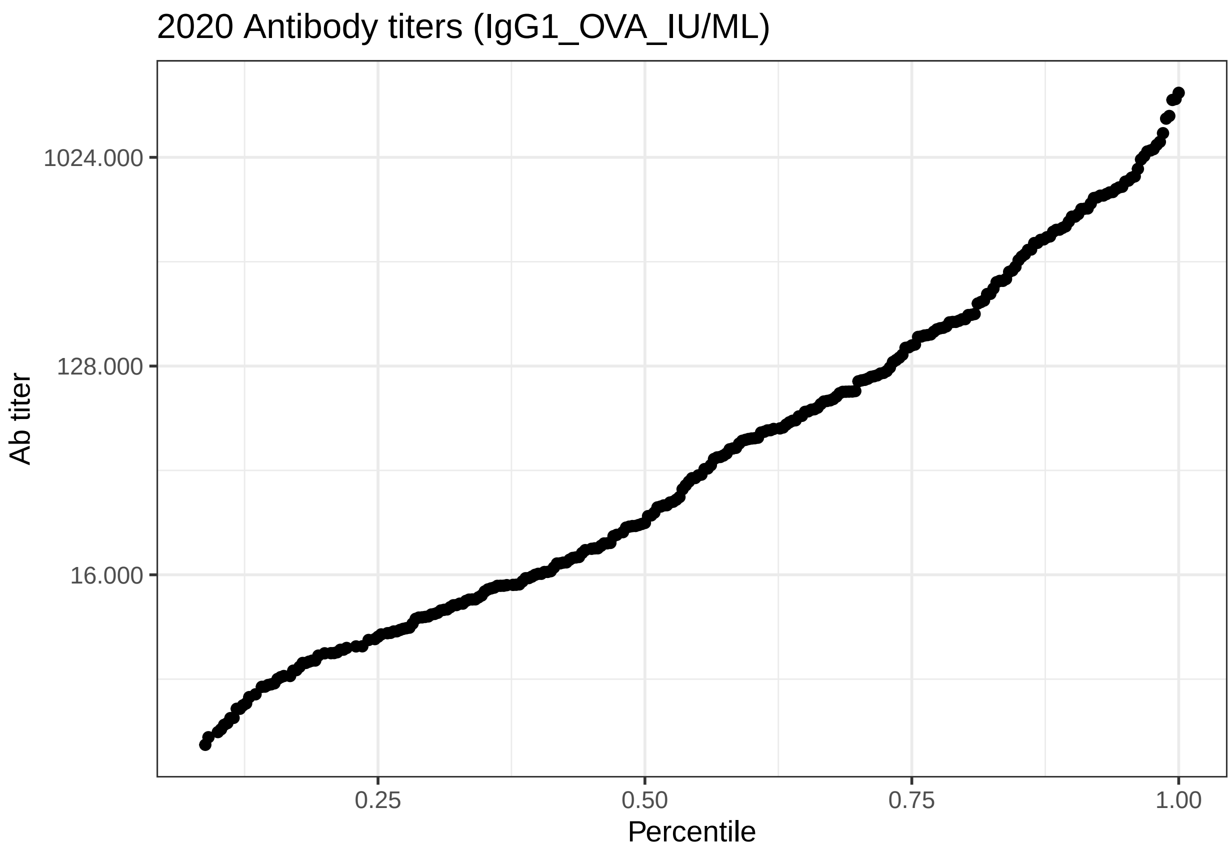

2020 Antibody titers (IgG1_PRN_IU/ML)
32768.000
4096.000
512.000
Ab titer
0.00
0.25
0.50
0.75
1.00
Percentile

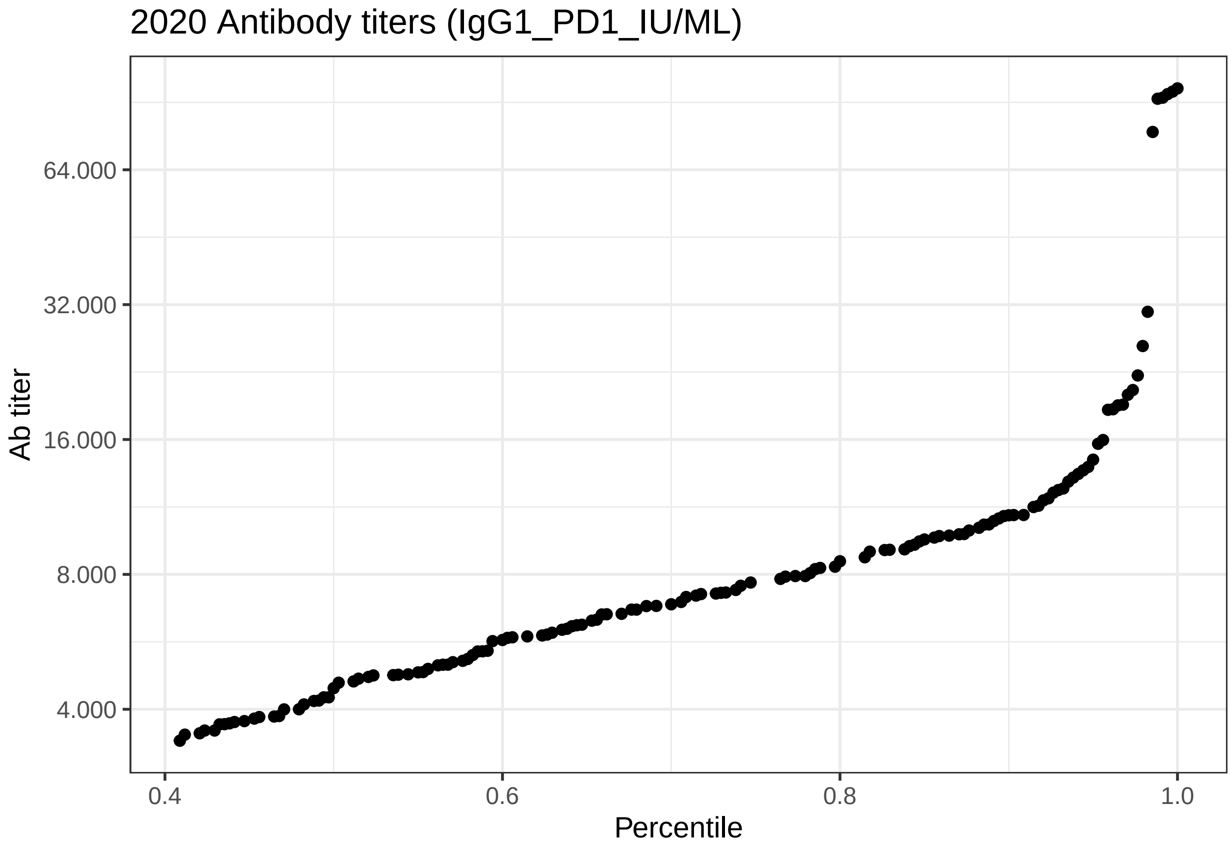

2020 Antibody titers (IgG1_FHA_IU/ML)
Ab titer
32768.000
8192.000
2048.000
512.000
0.00
0.25
0.50
0.75
1.00
Percentile

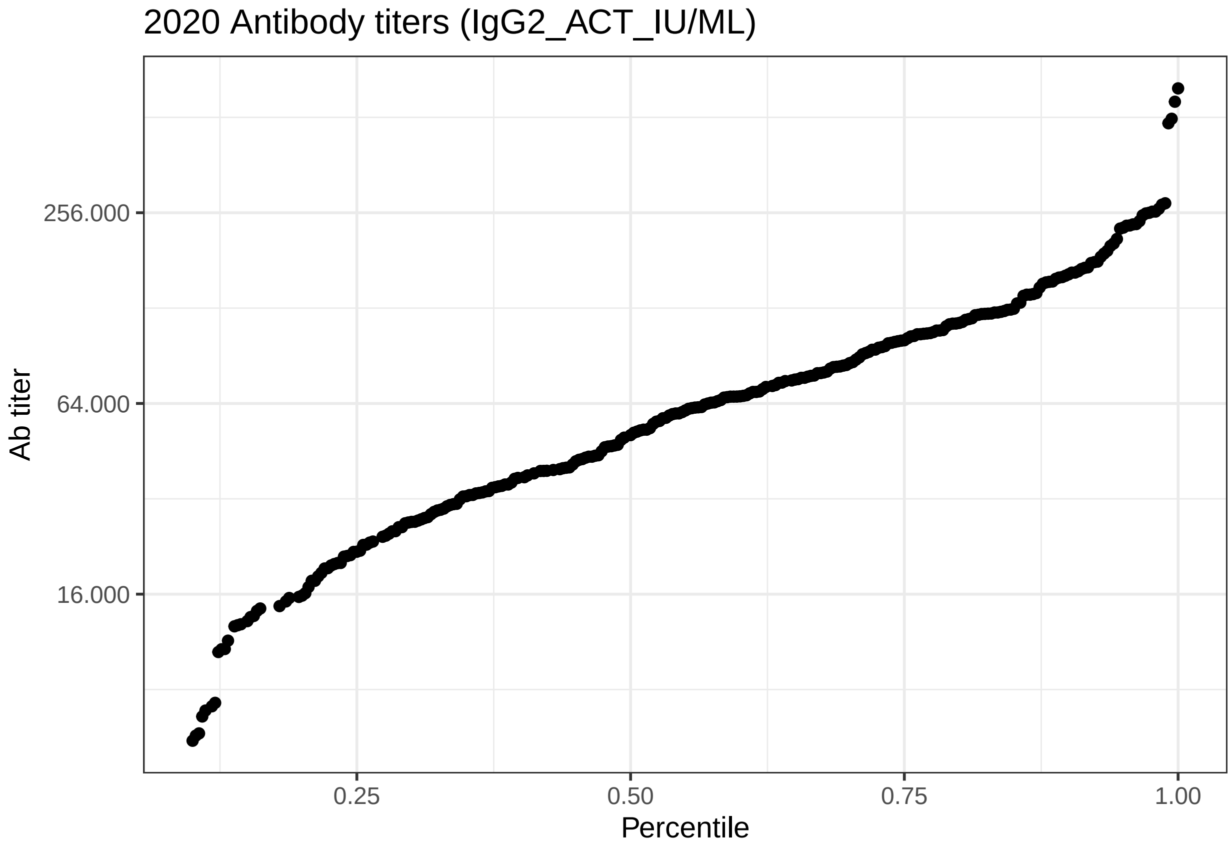

2020 Antibody titers (IgG1_FIM2/3_IU/ML)
Ab titer
131072.000
8192.000
512.000
32.000
0.00
0.25
0.50
0.75
1.00
Percentile

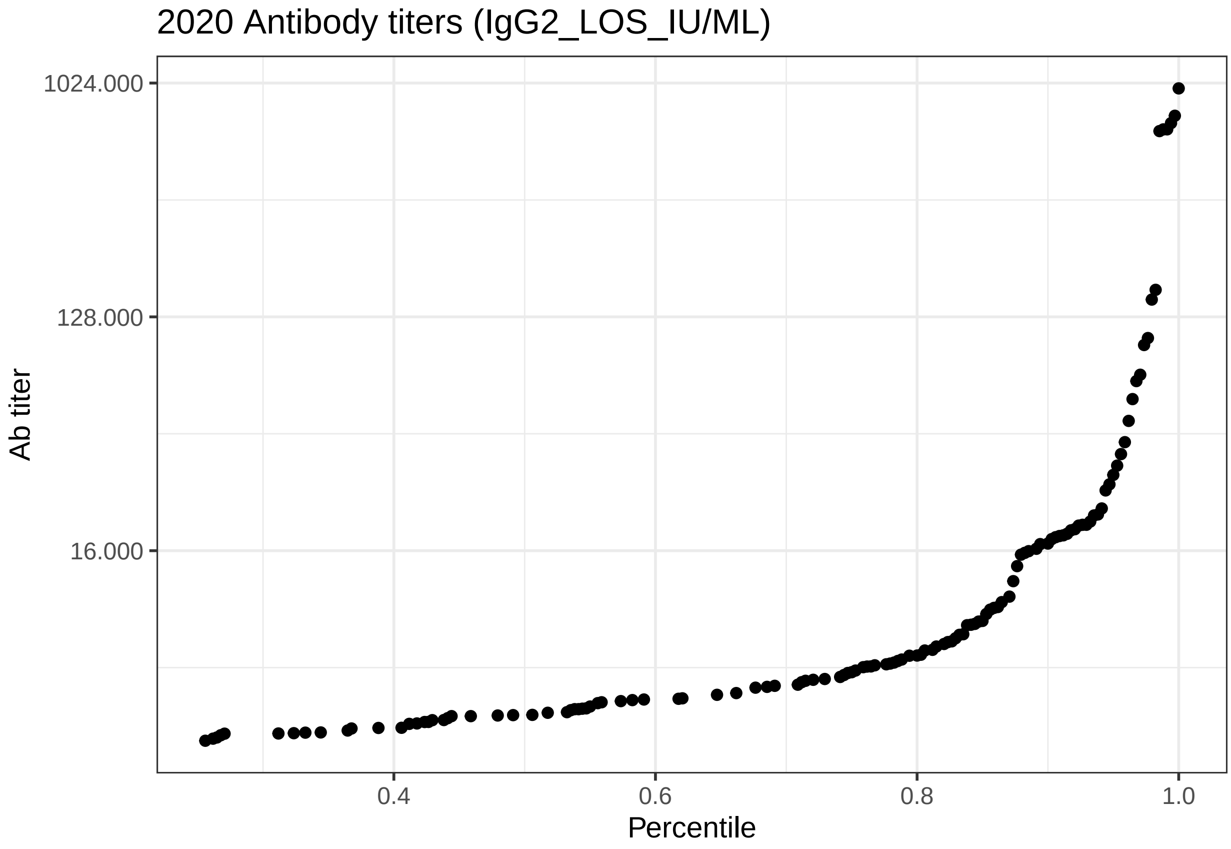

2020 Antibody titers (IgG1_TT_IU/ML)
Ab titer
8192.000
1024.000
128.000
0.00
0.25
0.50
0.75
1.00
Percentile

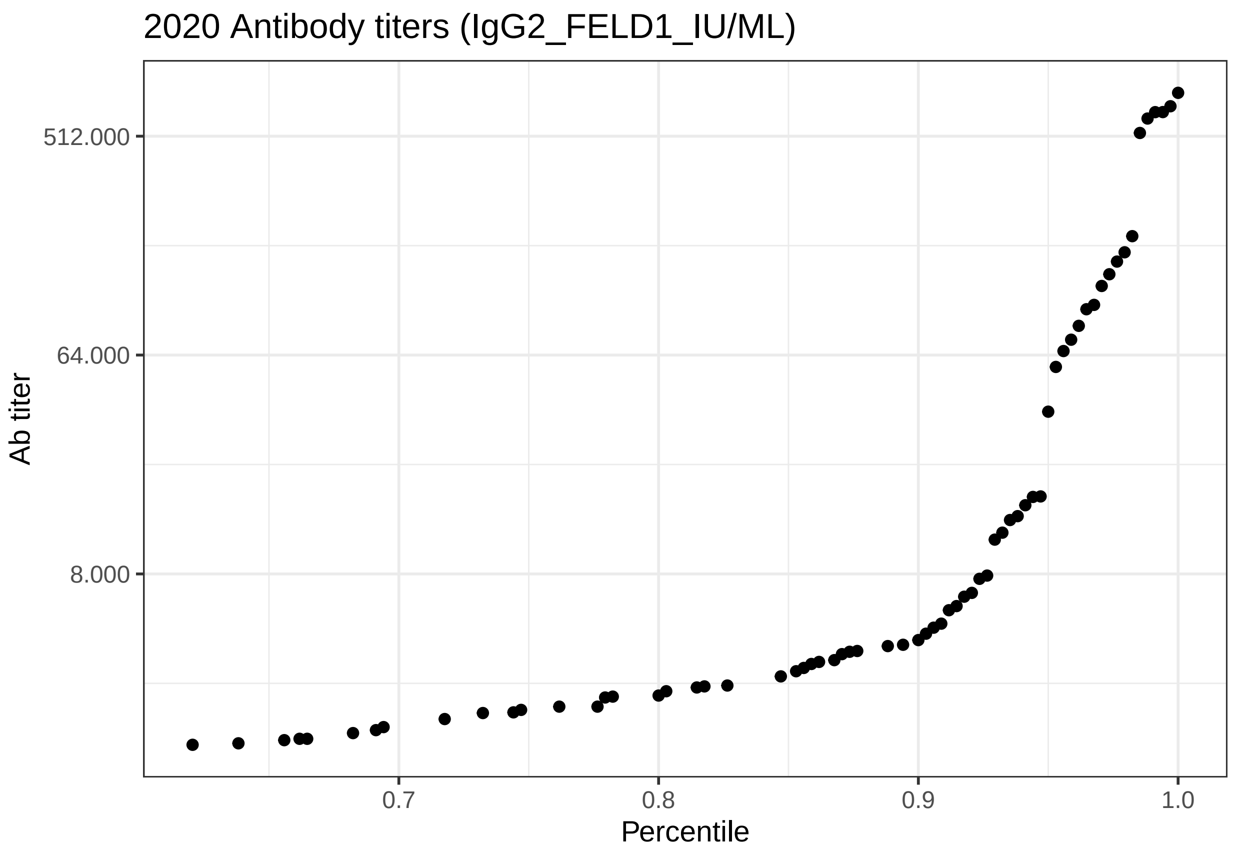

2020 Antibody titers (IgG1_DT_IU/ML)
Ab titer
16384.000
2048.000
256.000
0.00
0.25
0.50
0.75
1.00
Percentile

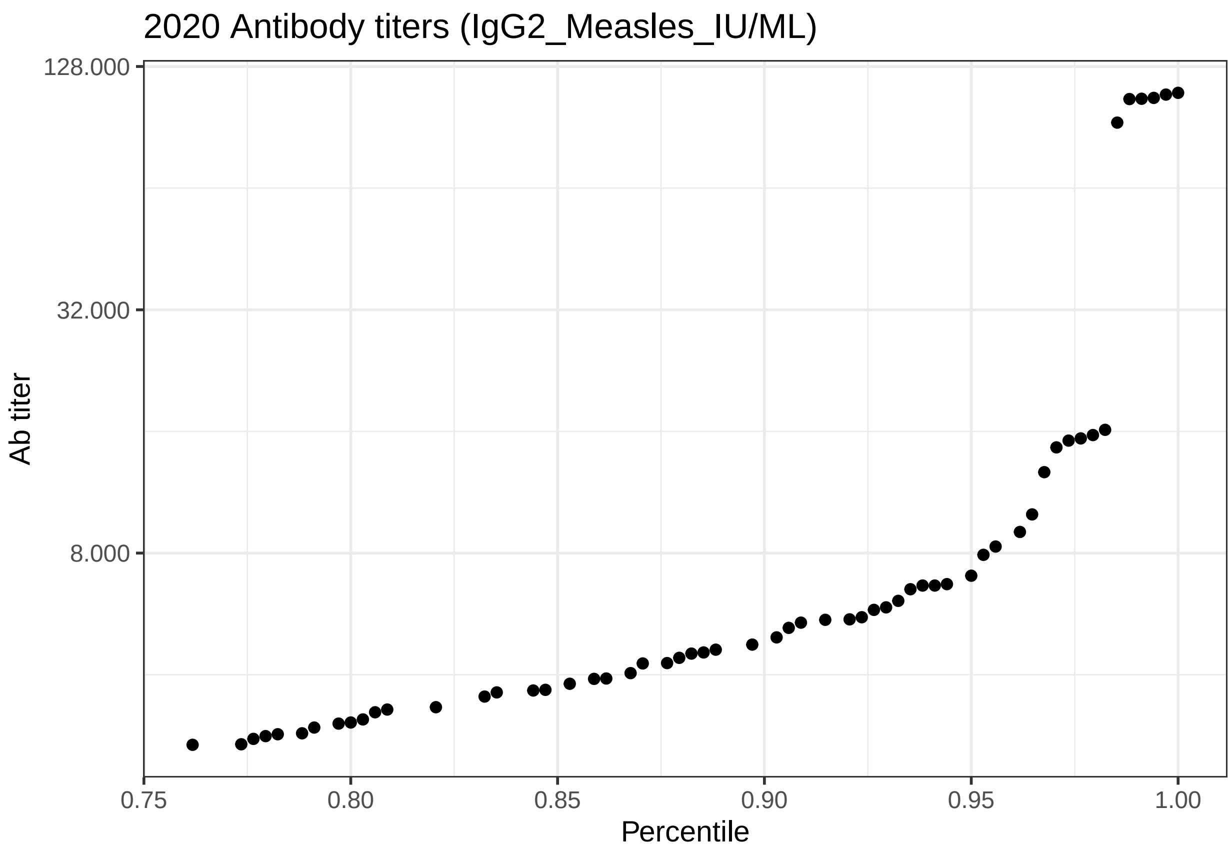

2020 Antibody titers (IgG1_OVA_IU/ML)
Ab titer
1024.000
128.000
16.000
0.25
0.50
0.75
1.00
Percentile

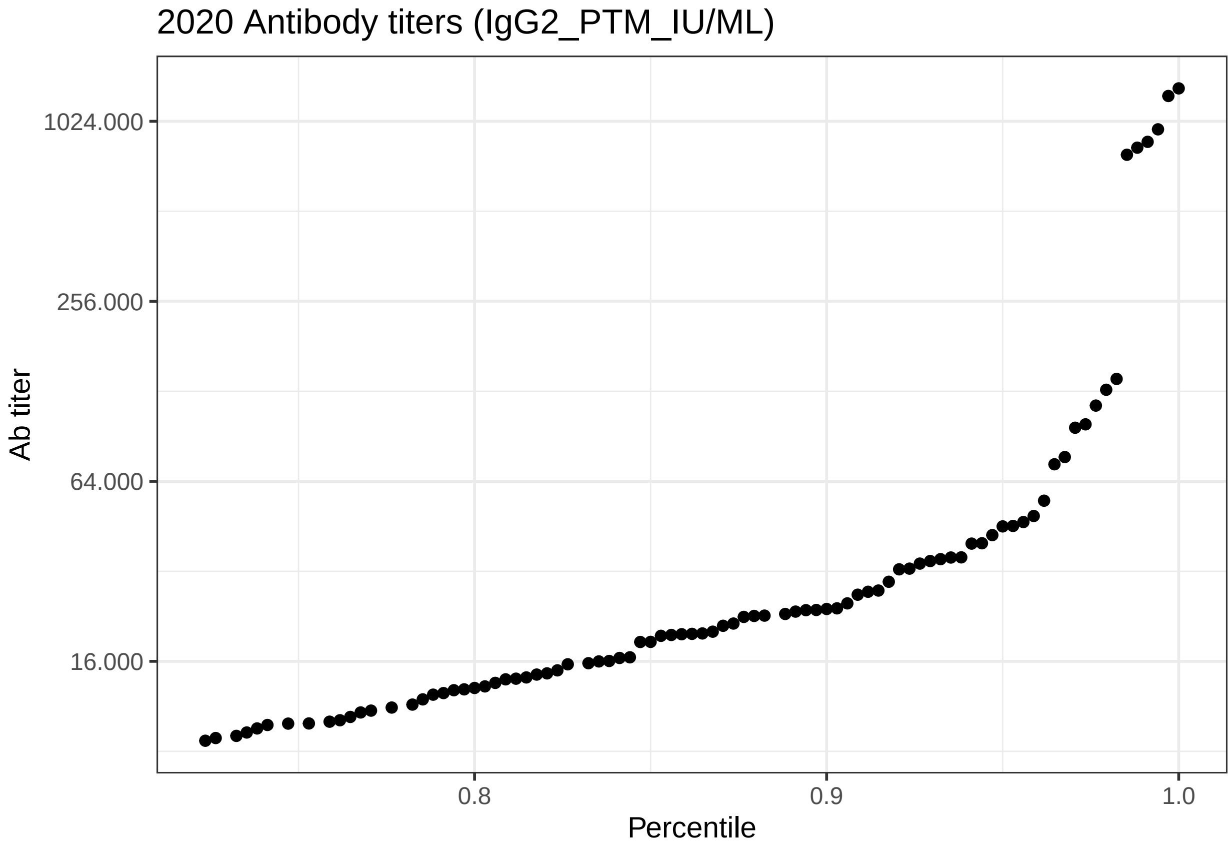

2020 Antibody titers (IgG1_PD1_IU/ML)
Ab titer
64.000
32.000
16.000
8.000
4.000
0.4
0.6
0.8
1.0
Percentile

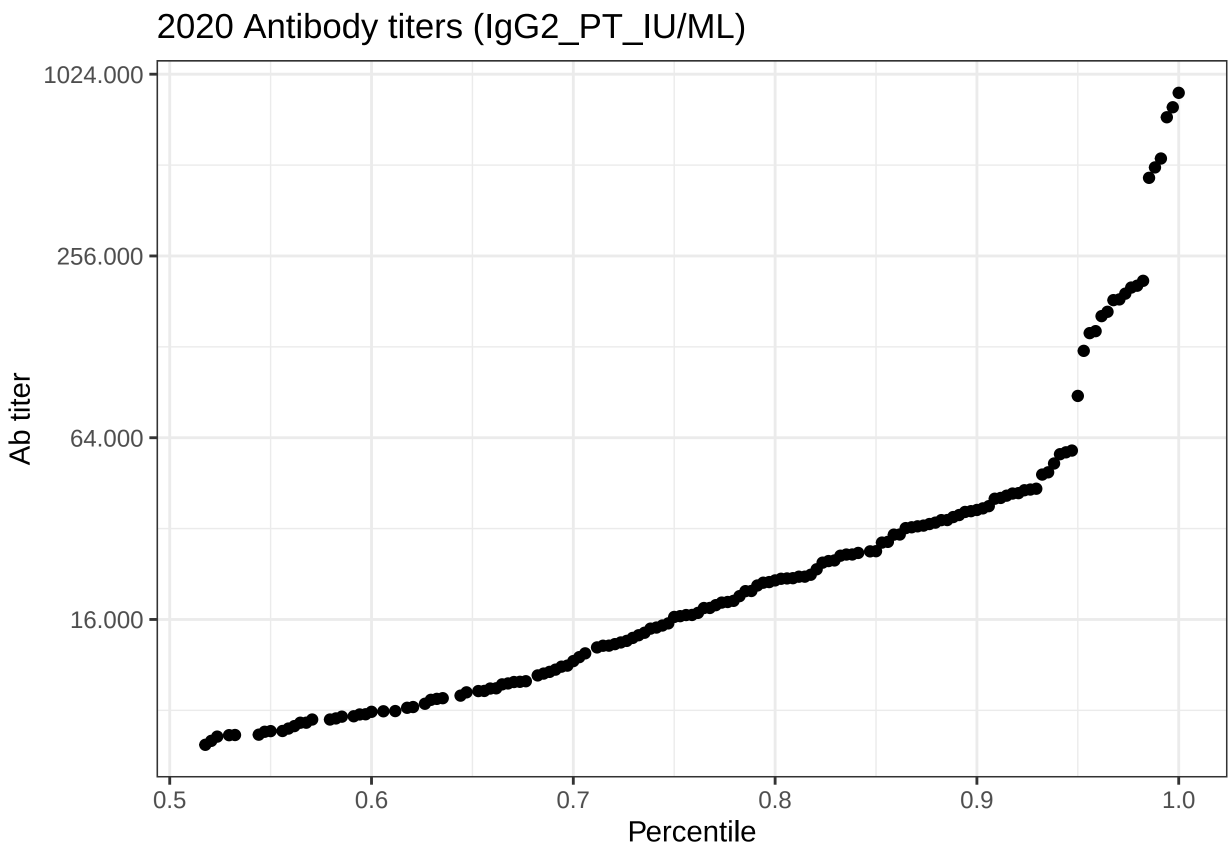

2020 Antibody titers (IgG2_ACT_IU/ML)
Ab titer
256.000
64.000
16.000
0.25
0.50
0.75
1.00
Percentile

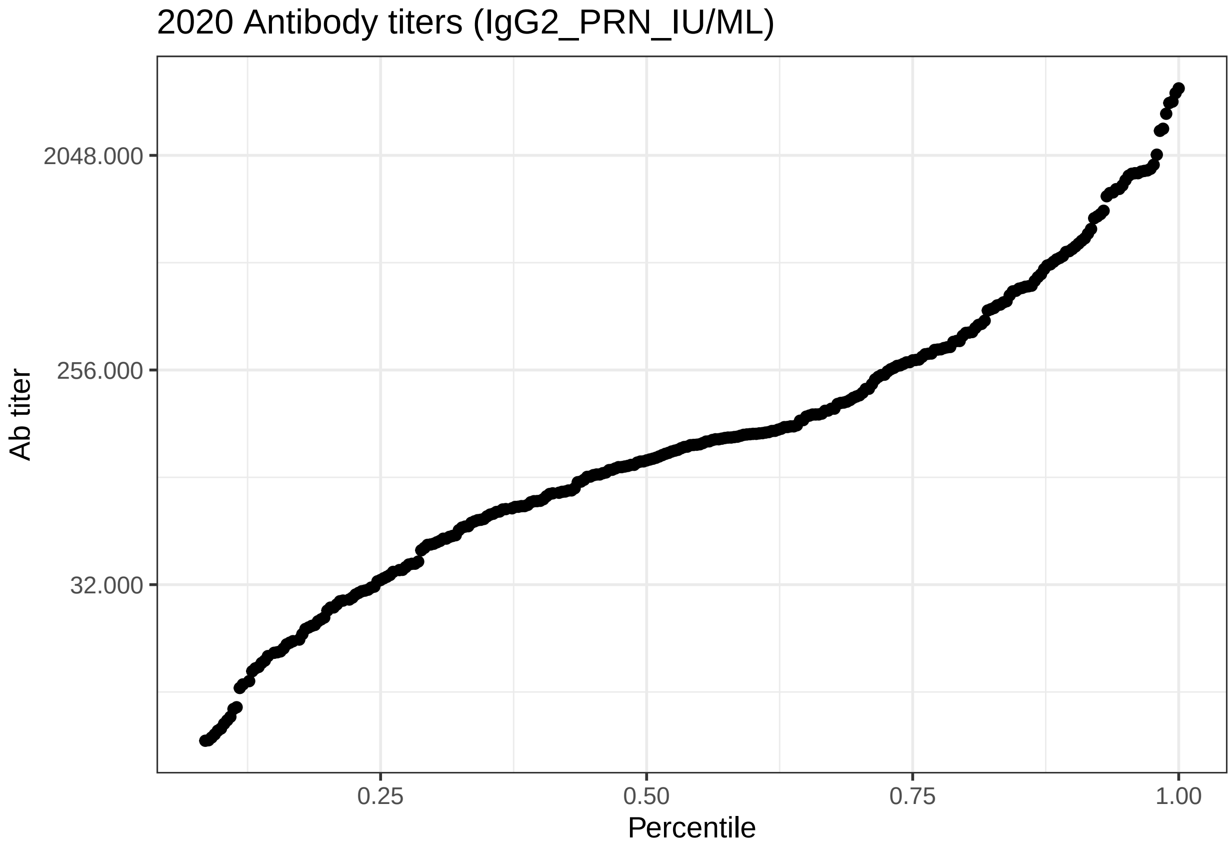

2020 Antibody titers (IgG2_LOS_IU/ML)
1024.000
128.000
16.000
Ab titer
0.4
0.6
0.8
1.0
Percentile

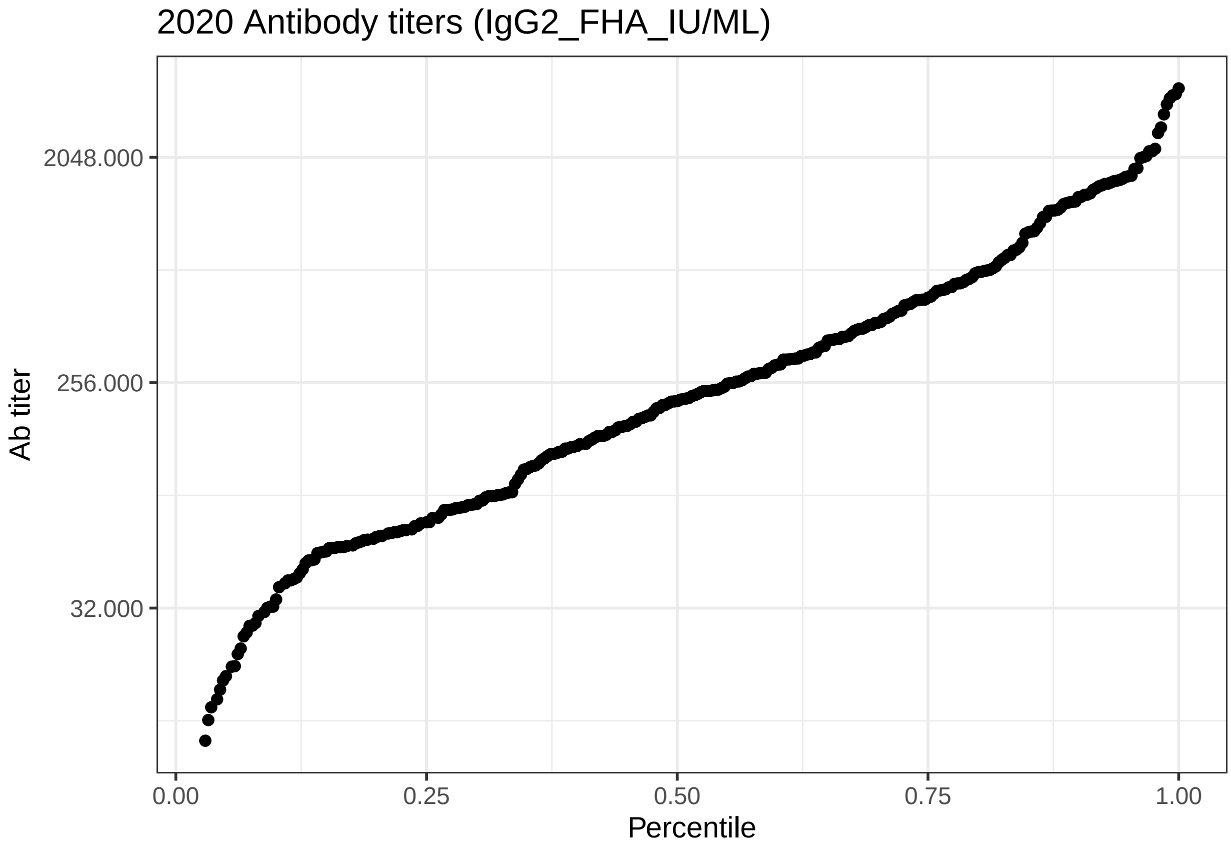

2020 Antibody titers (IgG2_FELD1_IU/ML)
Ab titer
512.000
64.000
8.000
0.7
0.8
0.9
1.0
Percentile

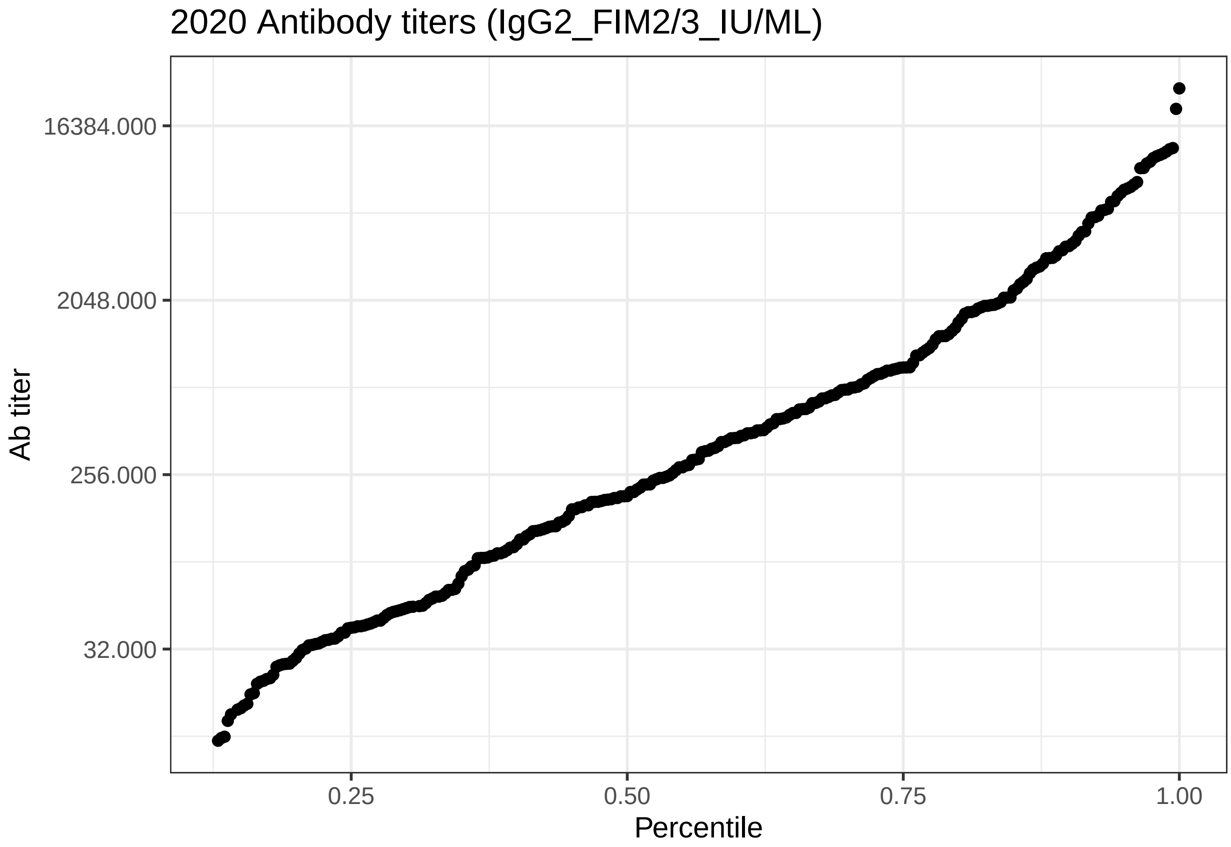

2020 Antibody titers (IgG2_Measles_IU/ML)
128.000
32.000
8.000
Ab titer
0.75
0.80
0.85
0.90
0.95
1.00
Percentile

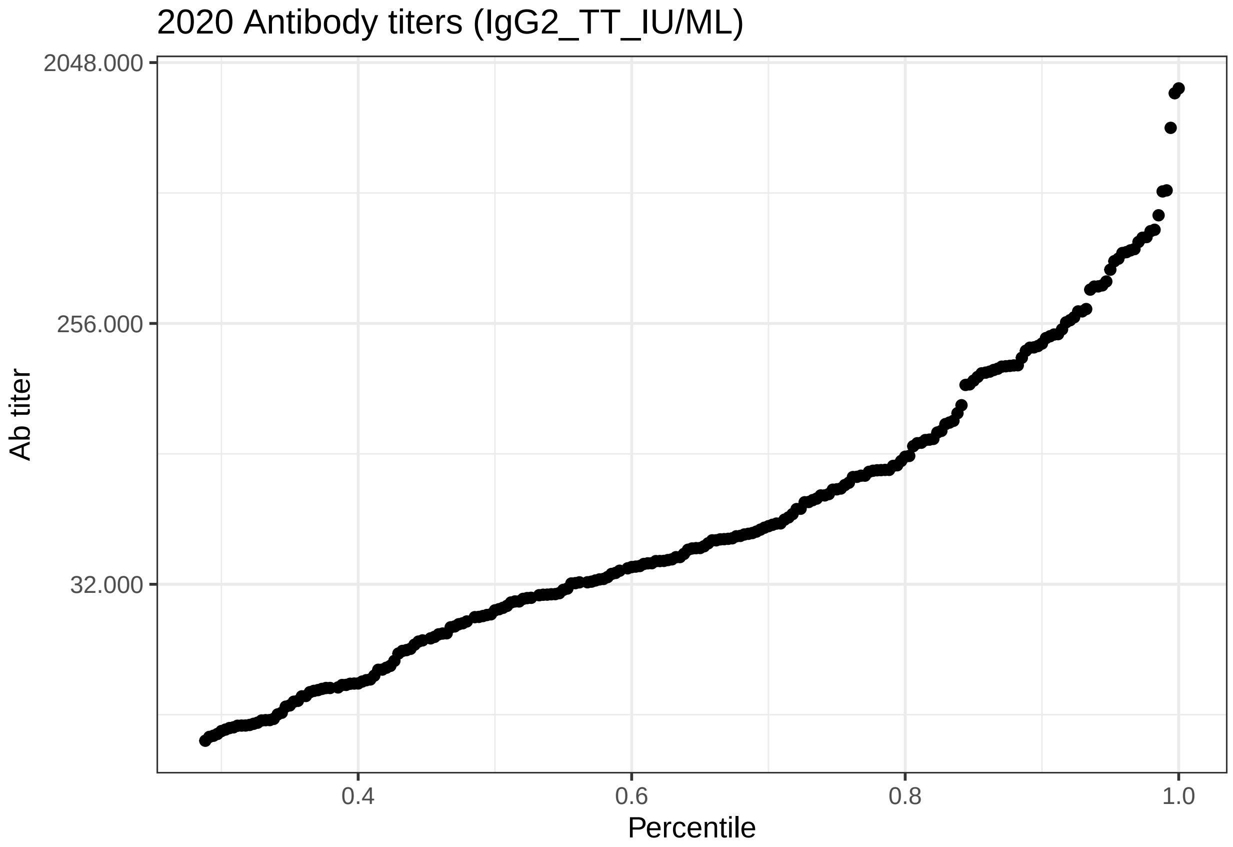

2020 Antibody titers (IgG2_PTM_IU/ML)
Ab titer
1024.000
256.000
64.000
16.000
0.8
0.9
1.0
Percentile

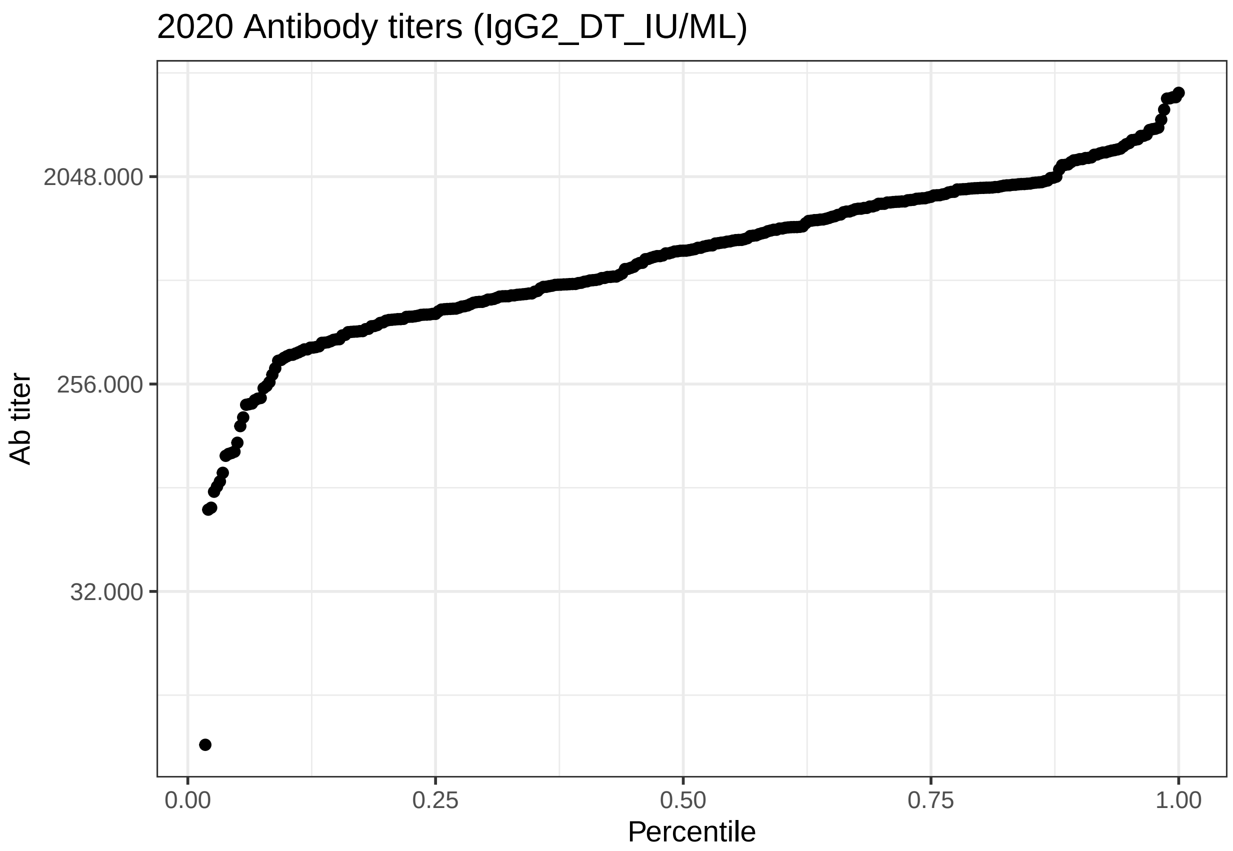

2020 Antibody titers (IgG2_PT_IU/ML)
Ab titer
1024.000
256.000
64.000
16.000
0.5
0.6
0.7
0.8
0.9
1.0
Percentile

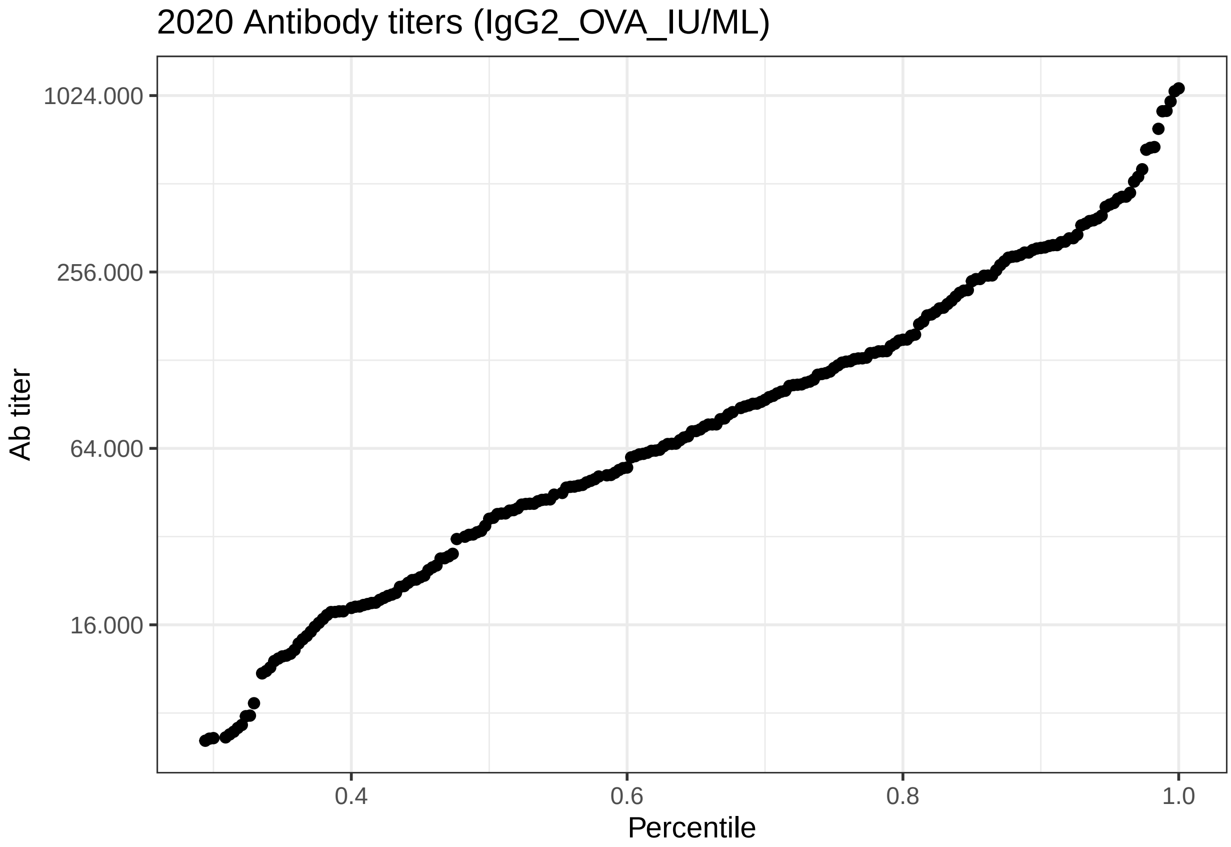

2020 Antibody titers (IgG2_PRN_IU/ML)
Ab titer
2048.000
256.000
32.000
Percentile
0.25
0.50
0.75
1.00

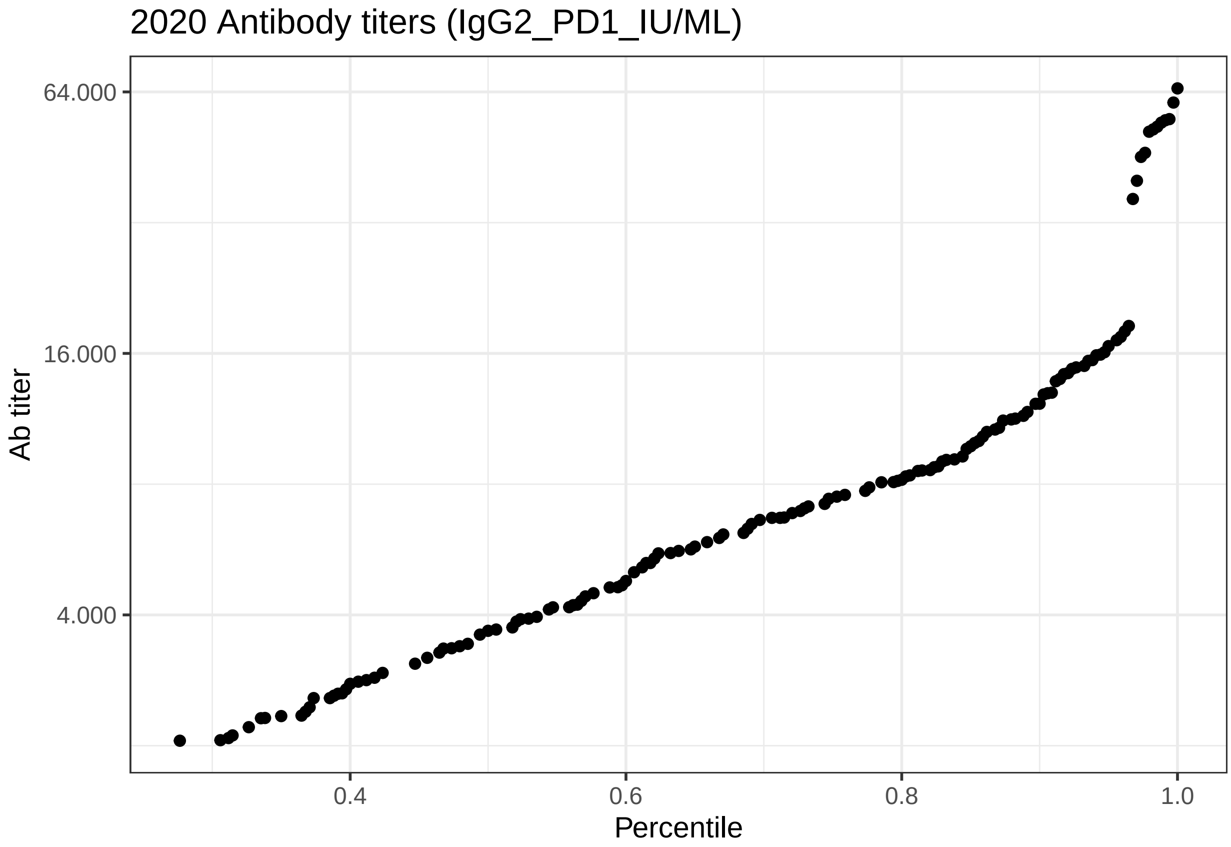

2020 Antibody titers (IgG2_FHA_IU/ML)
Ab titer
2048.000
256.000
32.000
0.00
0.25
0.50
0.75
1.00
Percentile


2020 Antibody titers (IgG2_FIM2/3_IU/ML)
Ab titer
16384.000
2048.000
256.000
32.000
0.25
0.50
0.75
1.00
Percentile

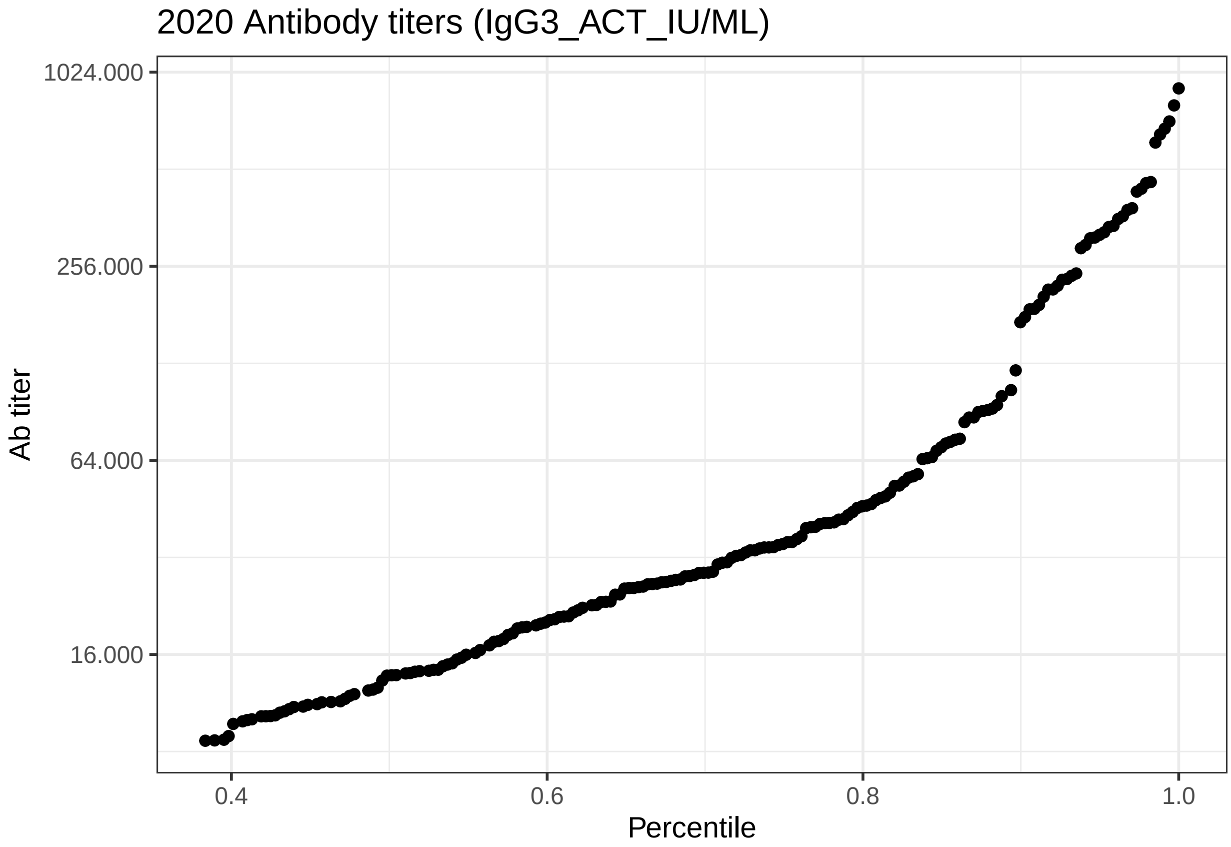

2020 Antibody titers (IgG2_TT_IU/ML)
Ab titer
2048.000
256.000
32.000
0.4
0.6
0.8
1.0
Percentile

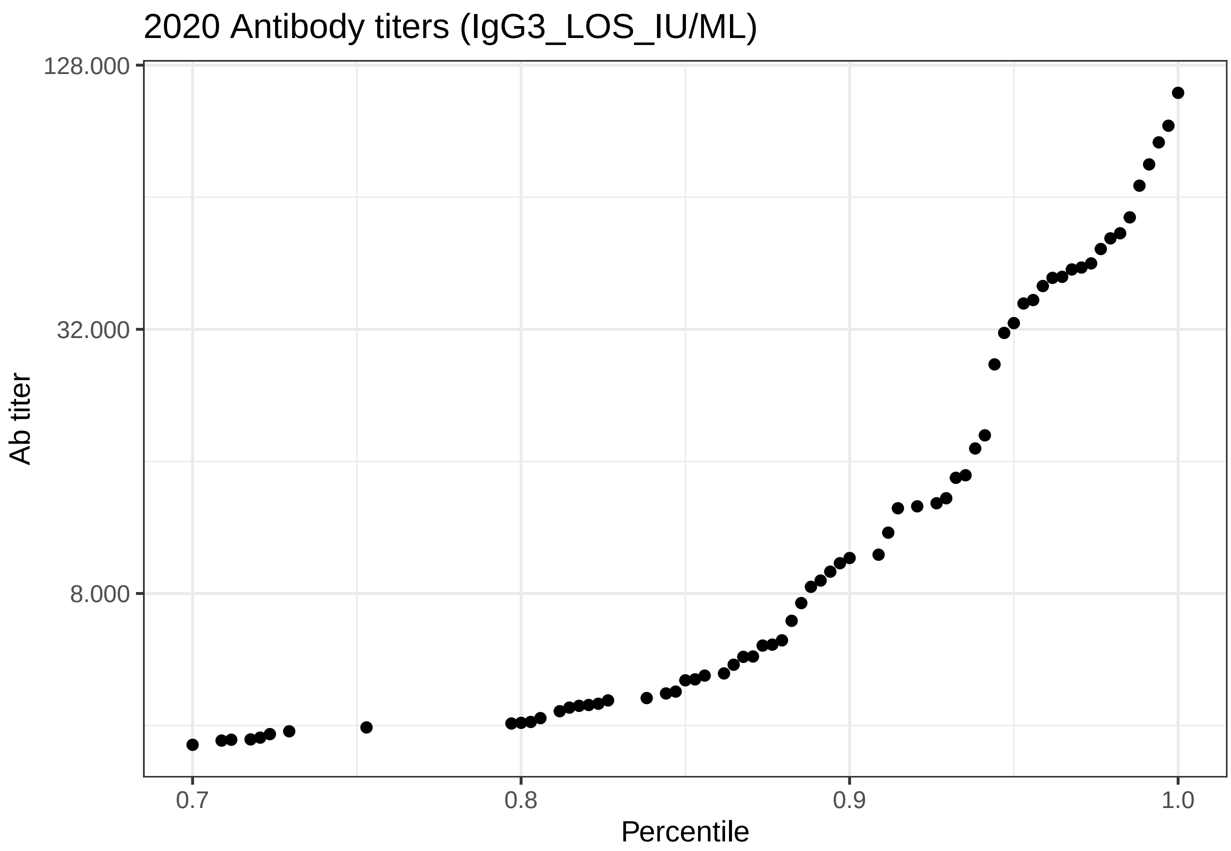

2020 Antibody titers (IgG2_DT_IU/ML)
Ab titer
2048.000
256.000
32.000
0.00
0.25
0.50
0.75
1.00
Percentile

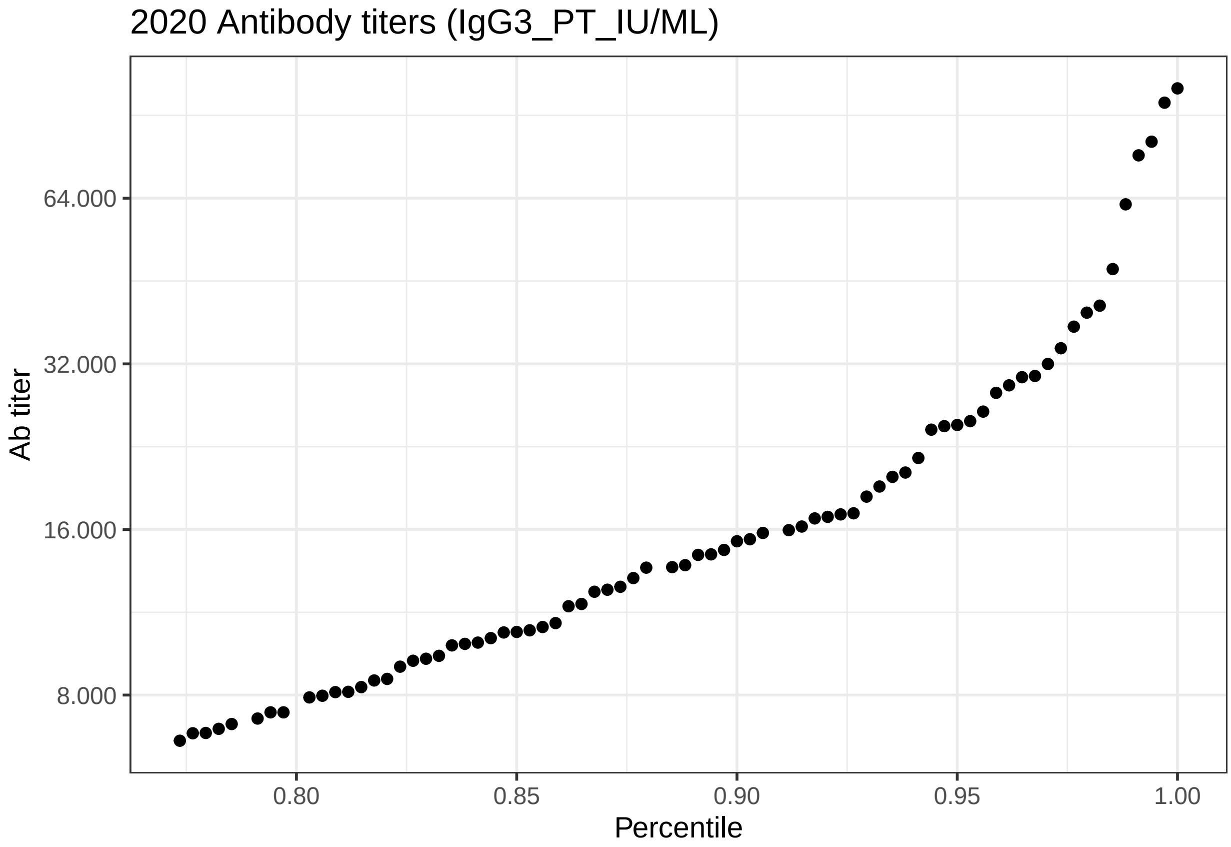

2020 Antibody titers (IgG2_OVA_IU/ML)
Ab titer
1024.000
256.000
64.000
16.000
0.4
0.6
0.8
1.0
Percentile

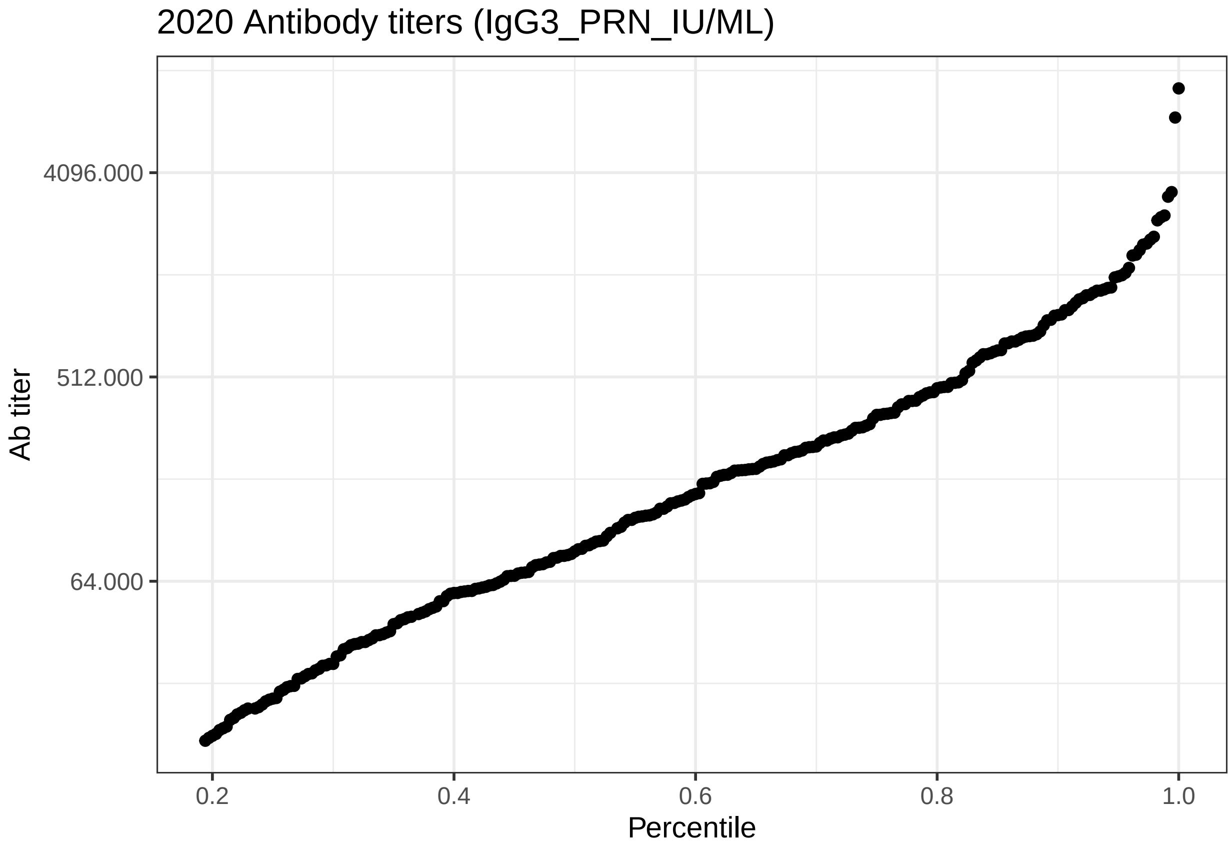


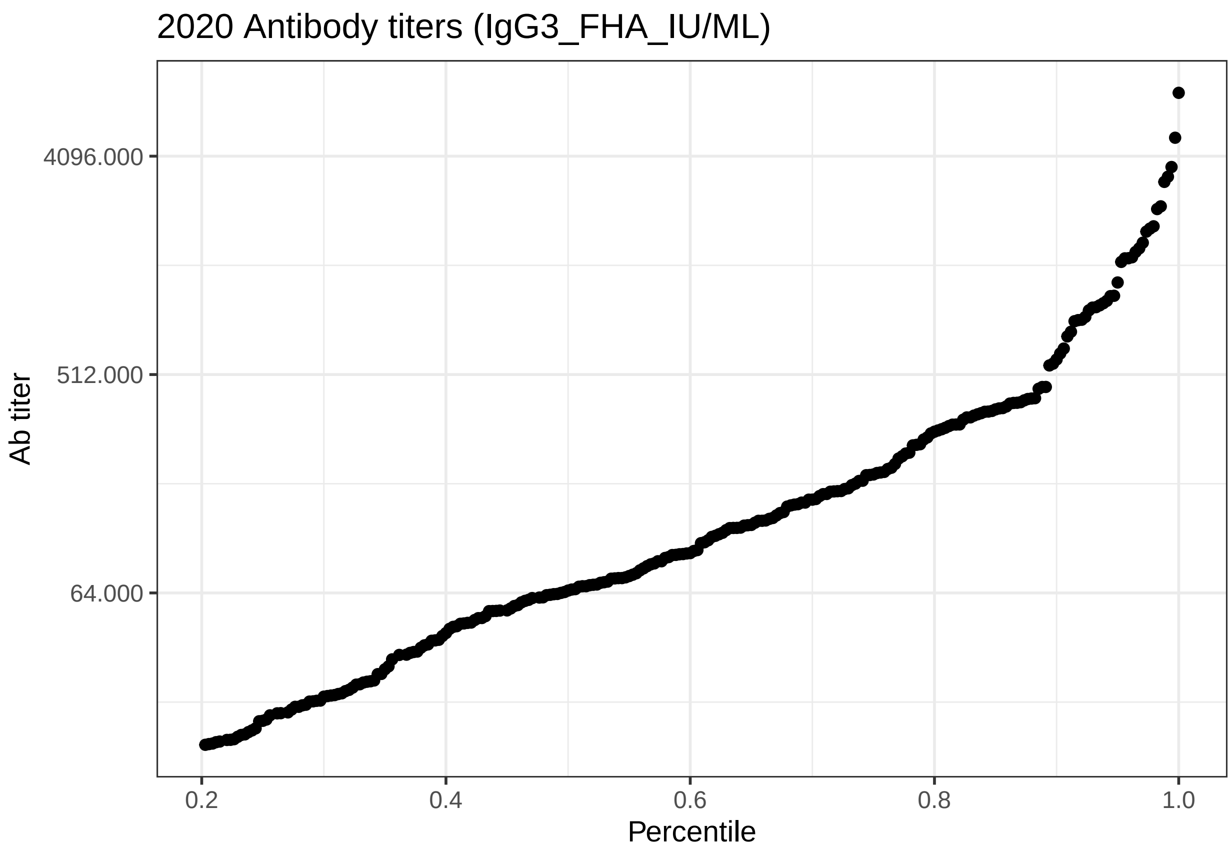
```
## Warning: Removed 1 rows containing non-finite values (stat_ecdf).
```

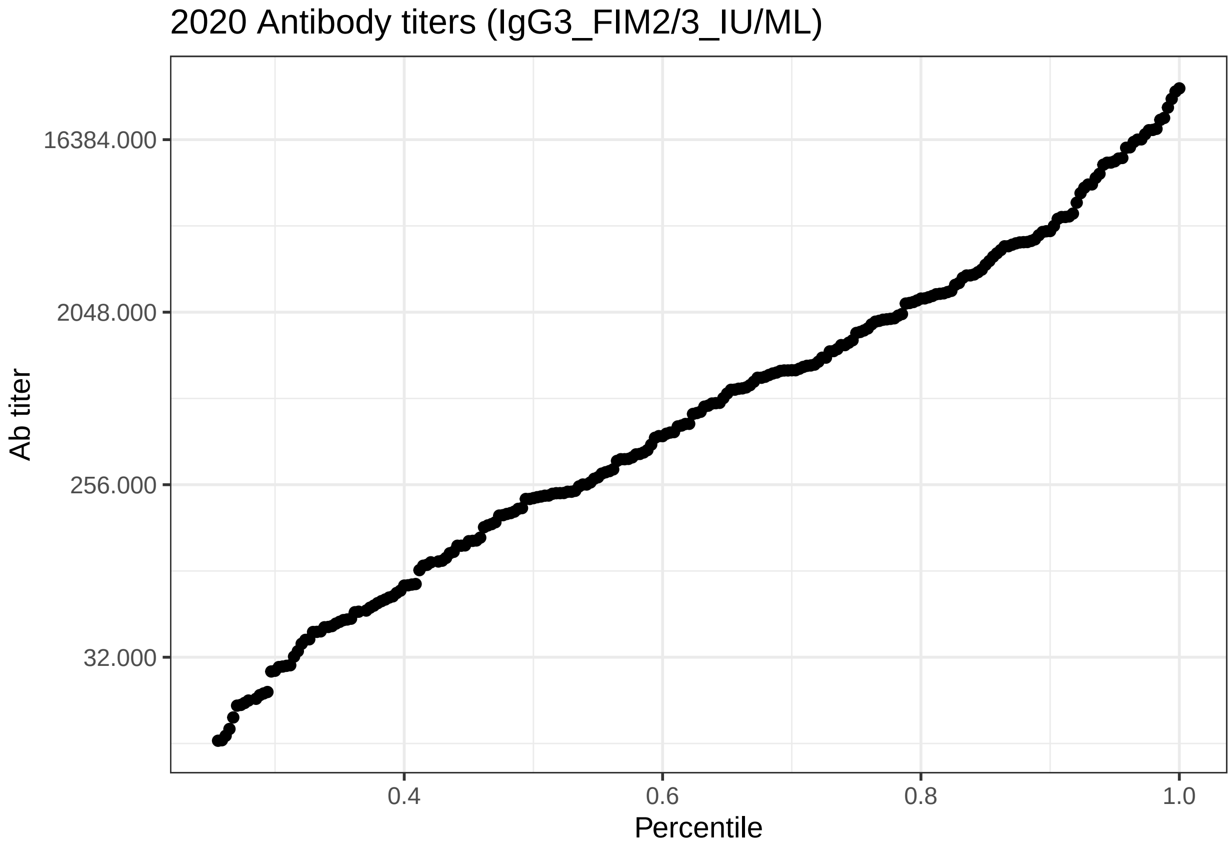

2020 Antibody titers (IgG3_ACT_IU/ML)
1024.000
256.000
64.000
16.000
Ab titer
0.4
0.6
0.8
1.0
Percentile

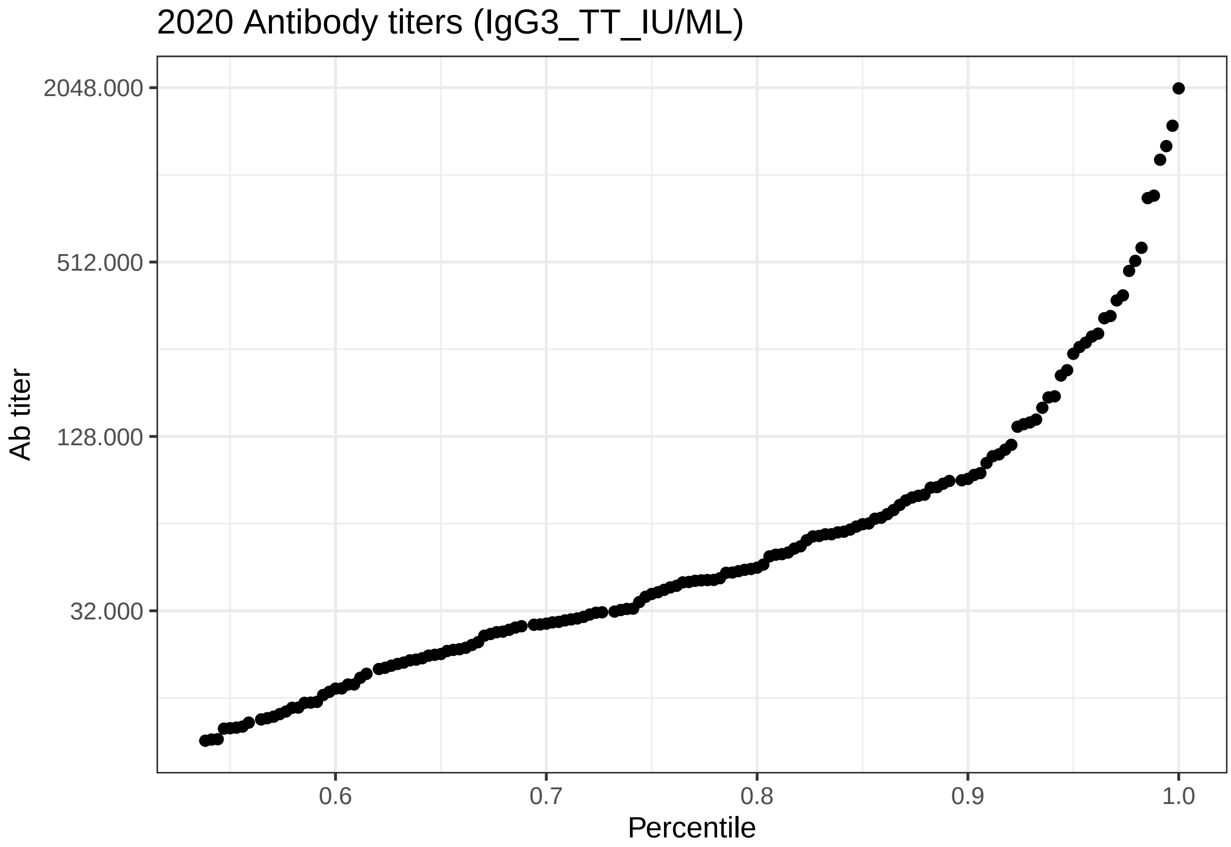

2020 Antibody titers (IgG3_LOS_IU/ML)
Ab titer
128.000
32.000
8.000
0.7
0.8
0.9
1.0
Percentile

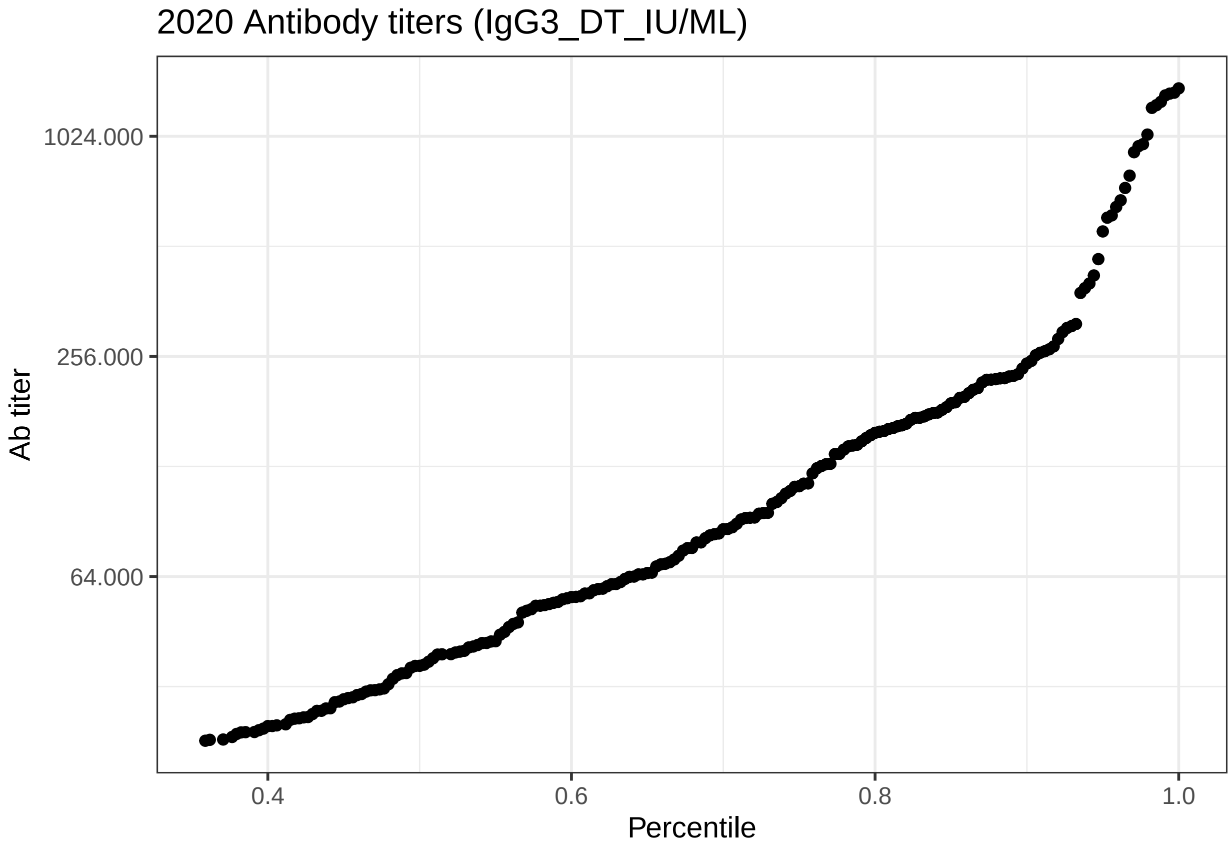

2020 Antibody titers (IgG3_PT_IU/ML)
Ab titer
64.000
32.000
16.000
8.000
0.80
0.85
0.90
0.95
1.00
Percentile

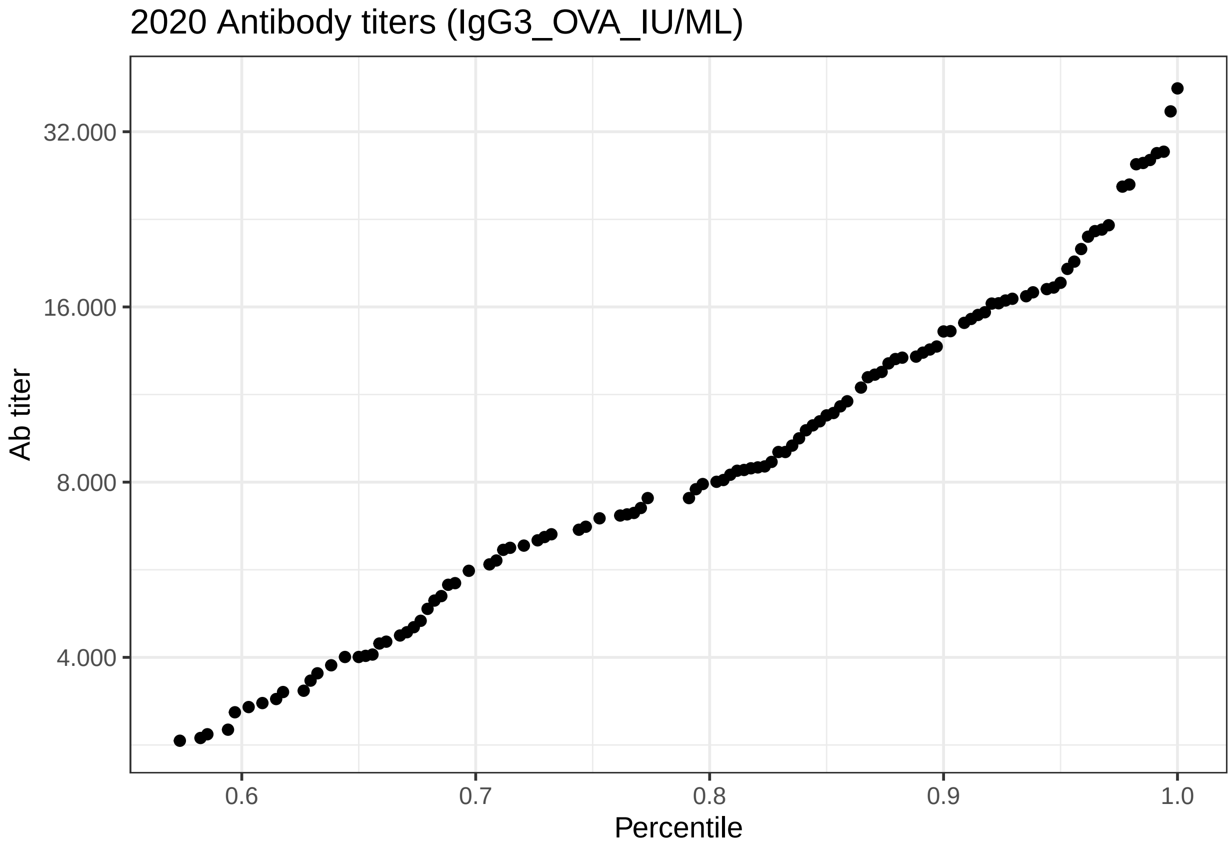

2020 Antibody titers (IgG3_PRN_IU/ML)
Ab titer
4096.000
512.000
64.000
0.2
0.4
0.6
0.8
1.0
Percentile

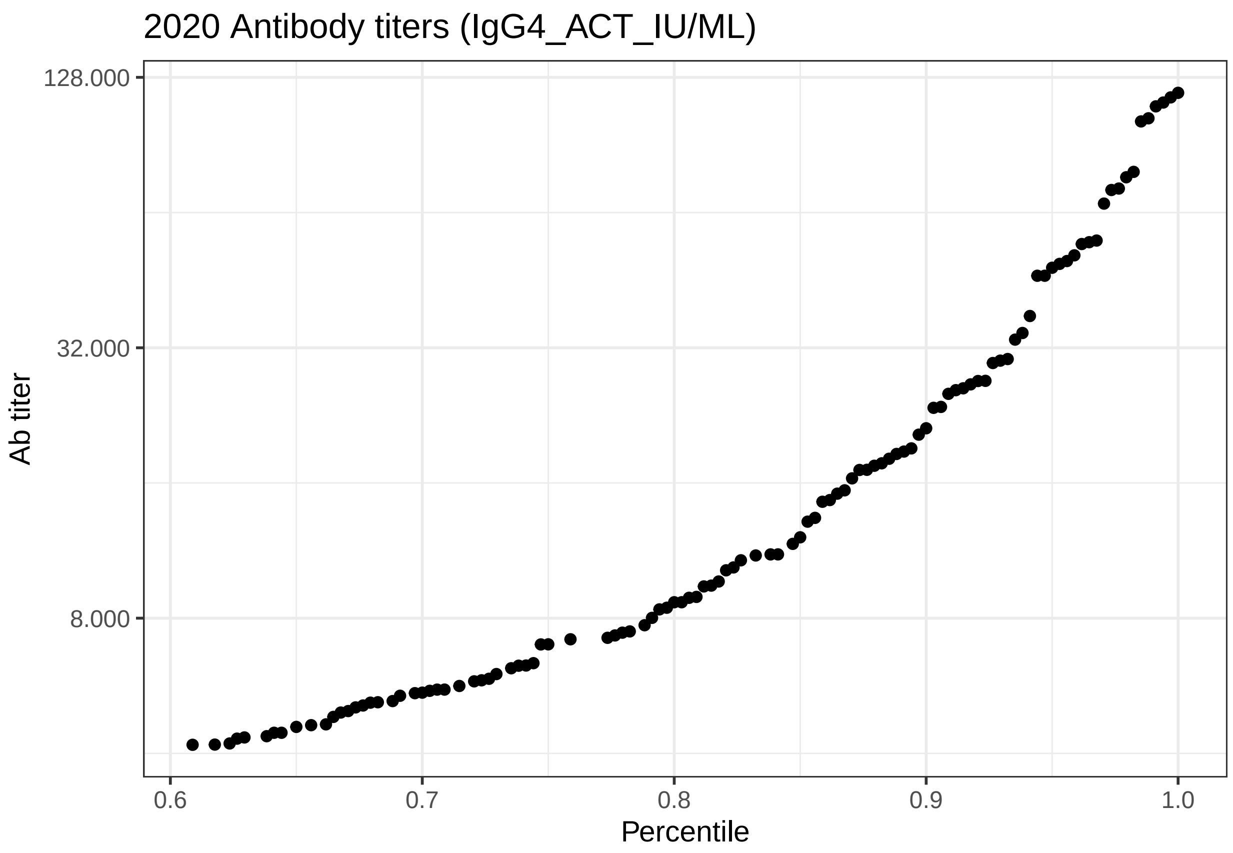

2020 Antibody titers (IgG3_FHA_IU/ML)
Ab titer
4096.000
512.000
64.000
0.2
0.4
0.6
0.8
1.0
Percentile

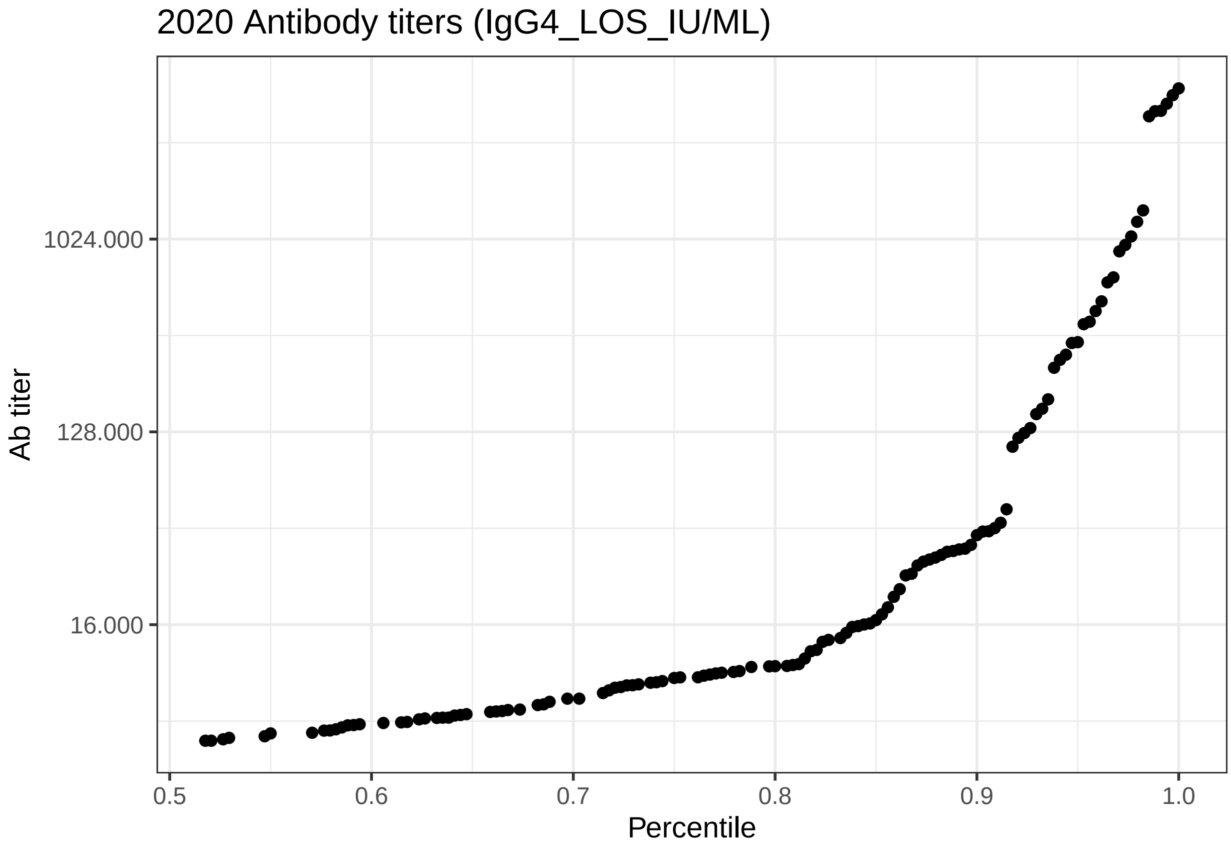

2020 Antibody titers (IgG3_FIM2/3_IU/ML)
Ab titer
16384.000
2048.000
256.000
32.000
0.4
0.6
0.8
1.0
Percentile

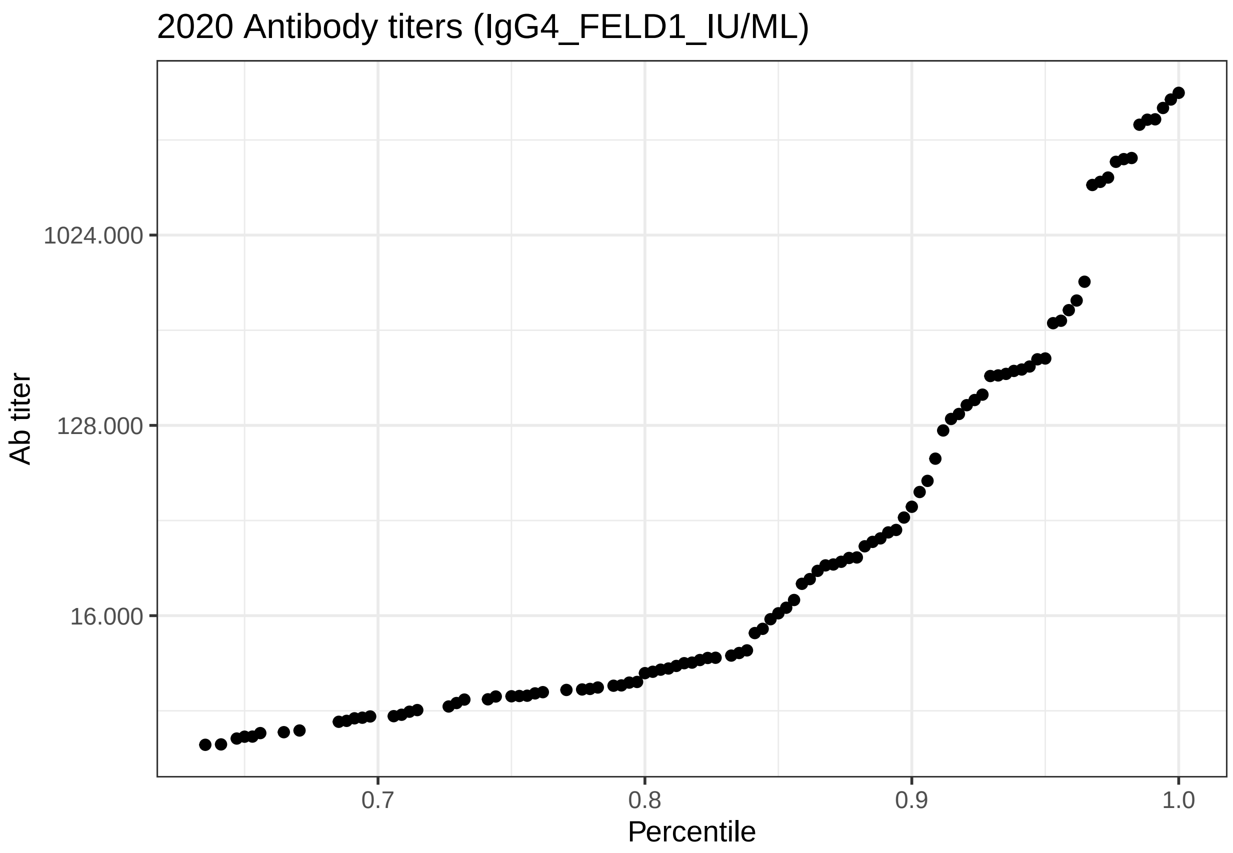

2020 Antibody titers (IgG3_TT_IU/ML)
2048.000
512.000
128.000
32.000
Ab titer
0.6
0.7
0.8
0.9
1.0
Percentile

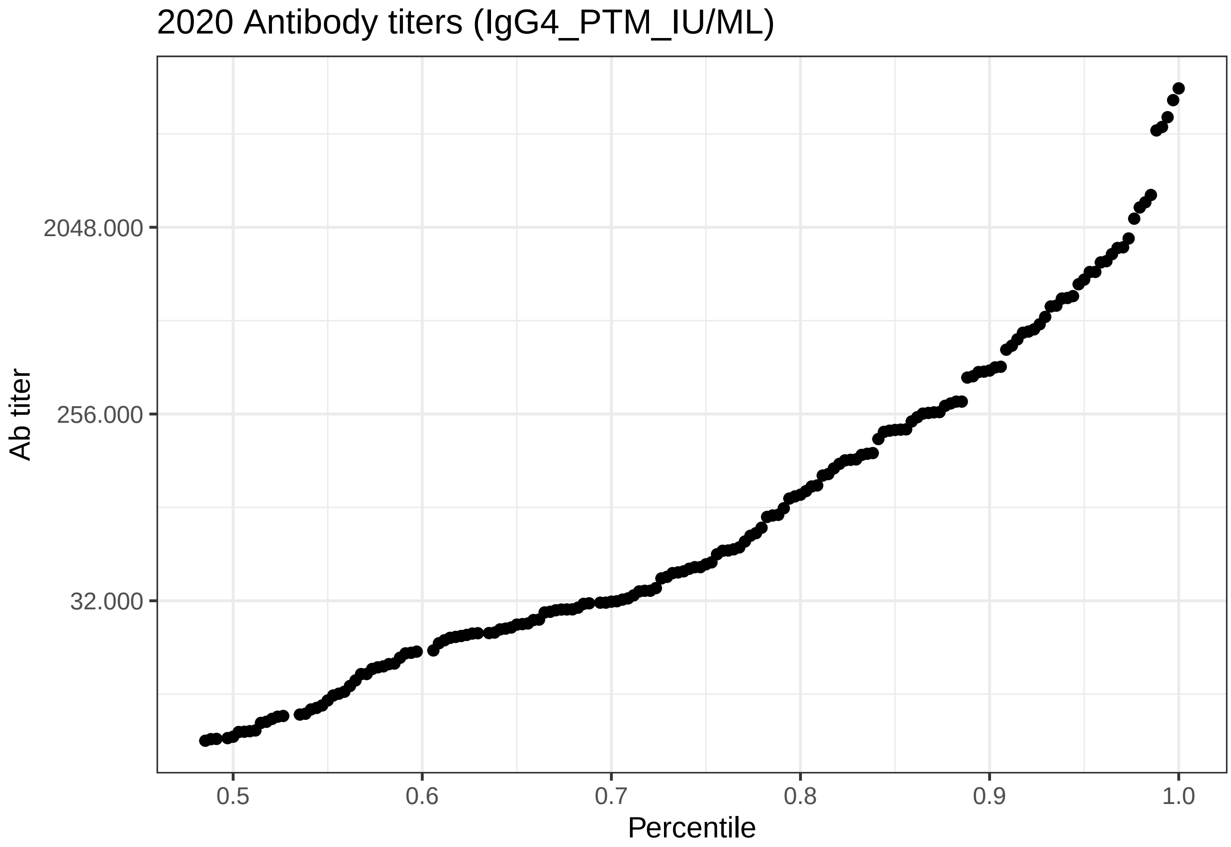

2020 Antibody titers (IgG3_DT_IU/ML)
Ab titer
1024.000
256.000
64.000
0.4
0.6
0.8
1.0
Percentile

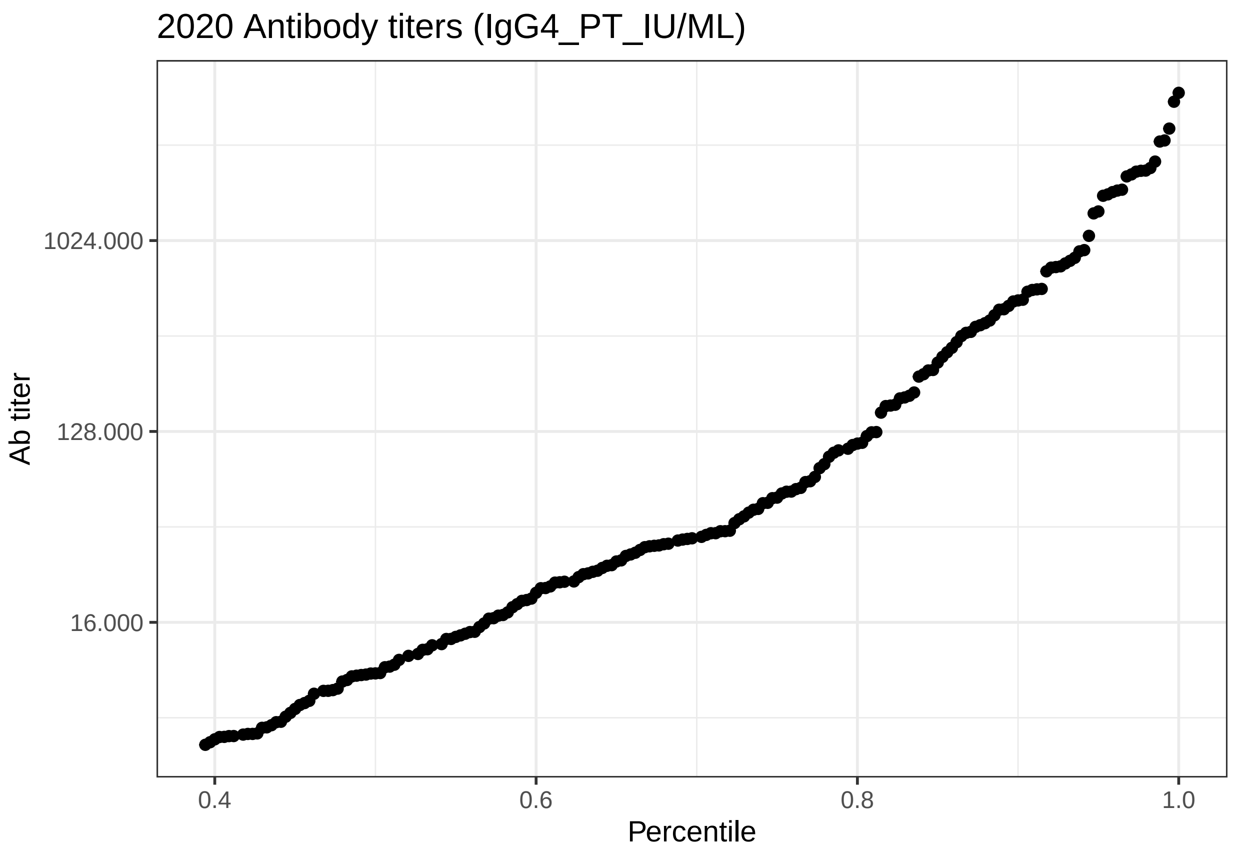

2020 Antibody titers (IgG3_OVA_IU/ML)
Ab titer
32.000
16.000
8.000
4.000
0.6
0.7
0.8
0.9
1.0
Percentile

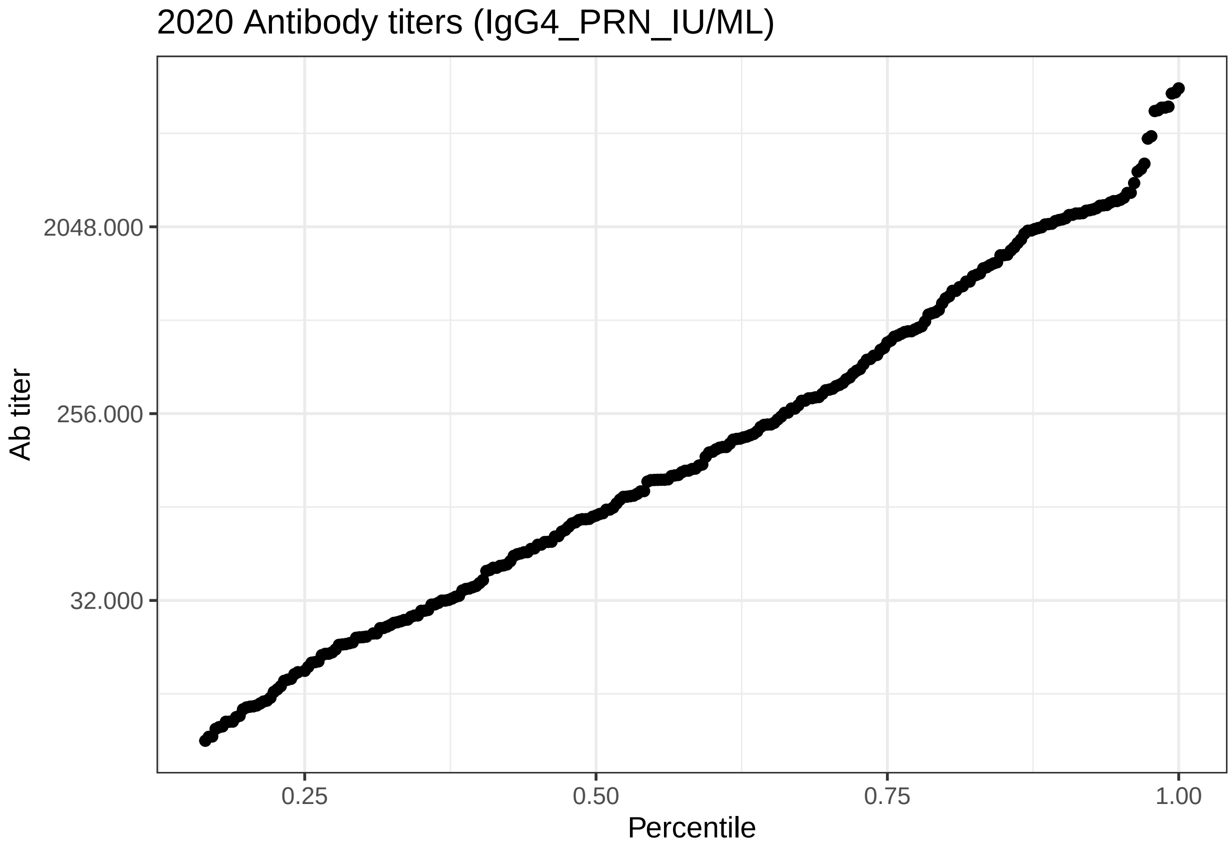

2020 Antibody titers (IgG4_ACT_IU/ML)
Ab titer
128.000
32.000
8.000
0.6
0.7
0.8
0.9
1.0
Percentile

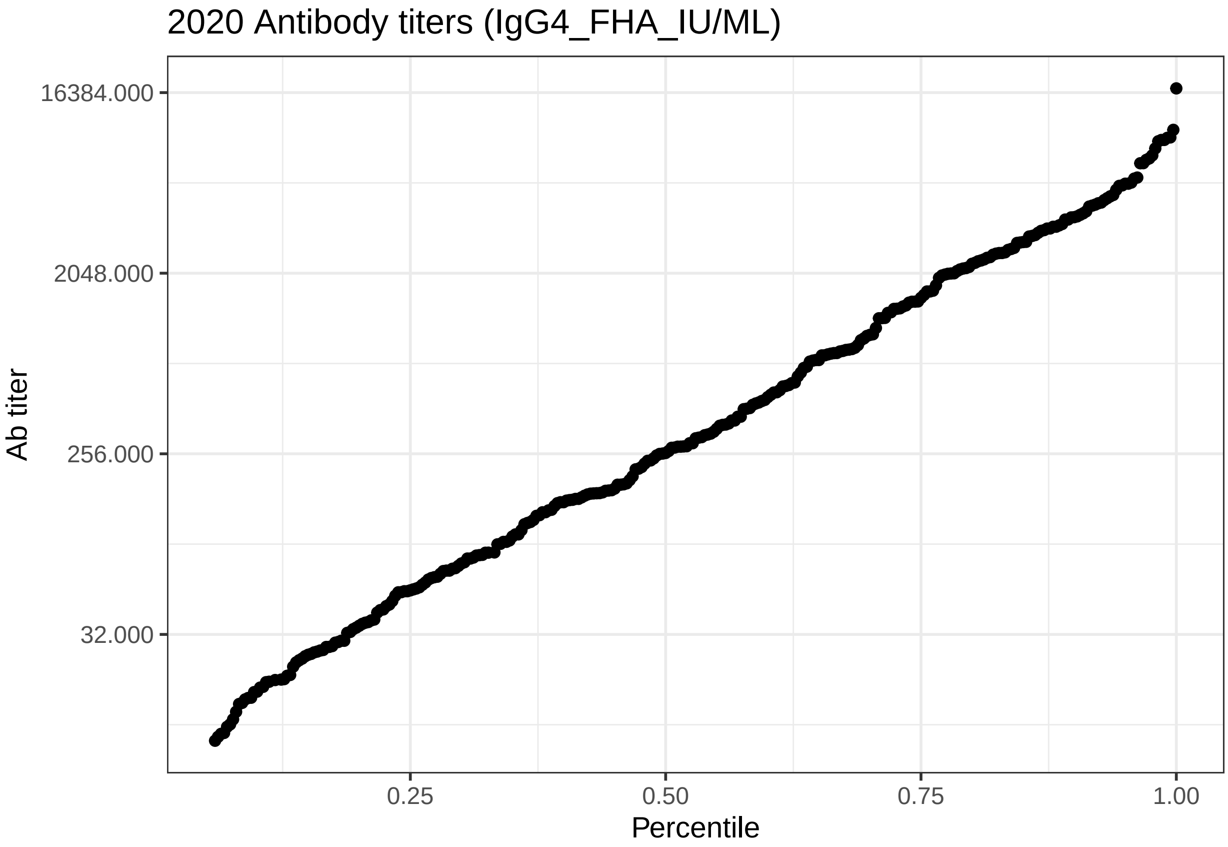

2020 Antibody titers (IgG4_LOS_IU/ML)
Ab titer
1024.000
128.000
16.000
0.5
0.6
0.7
0.8
0.9
1.0
Percentile

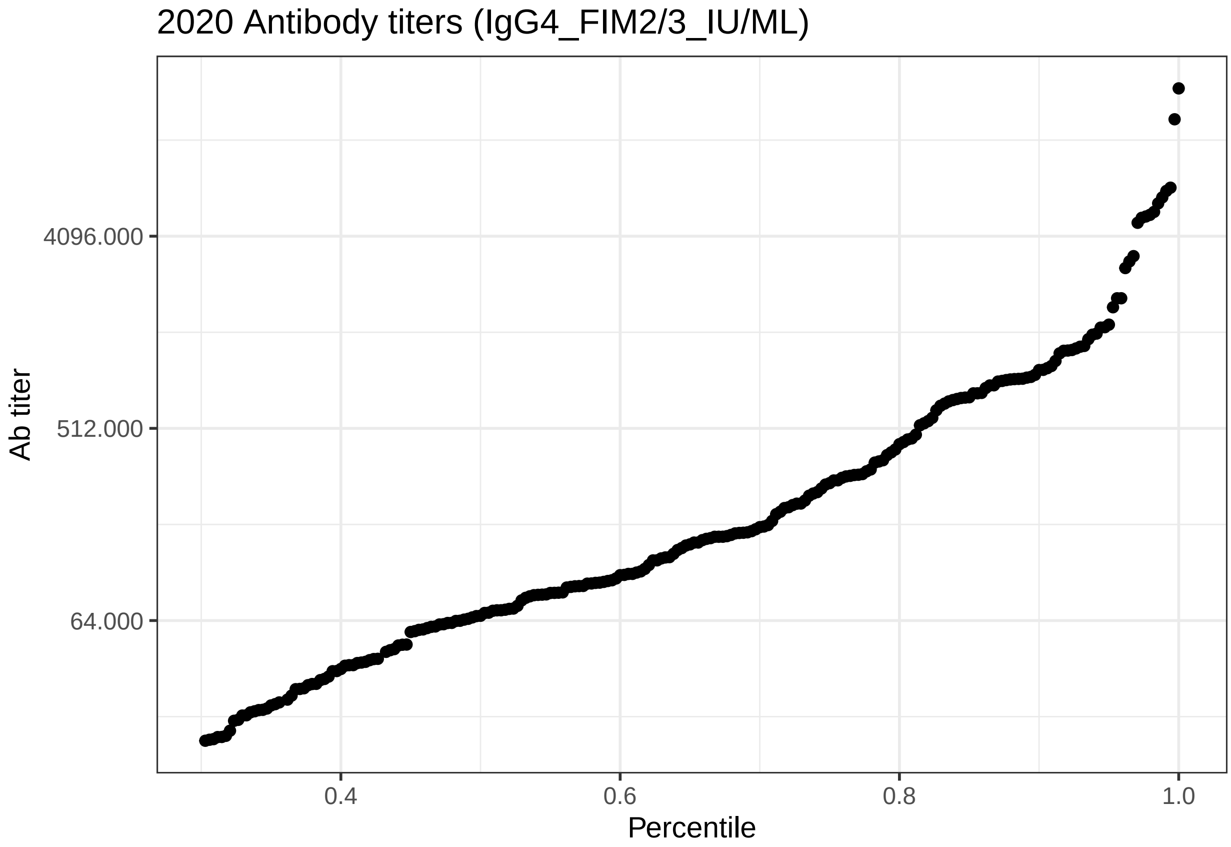

2020 Antibody titers (IgG4_FELD1_IU/ML)
Ab titer
1024.000
128.000
16.000
0.7
0.8
0.9
1.0
Percentile

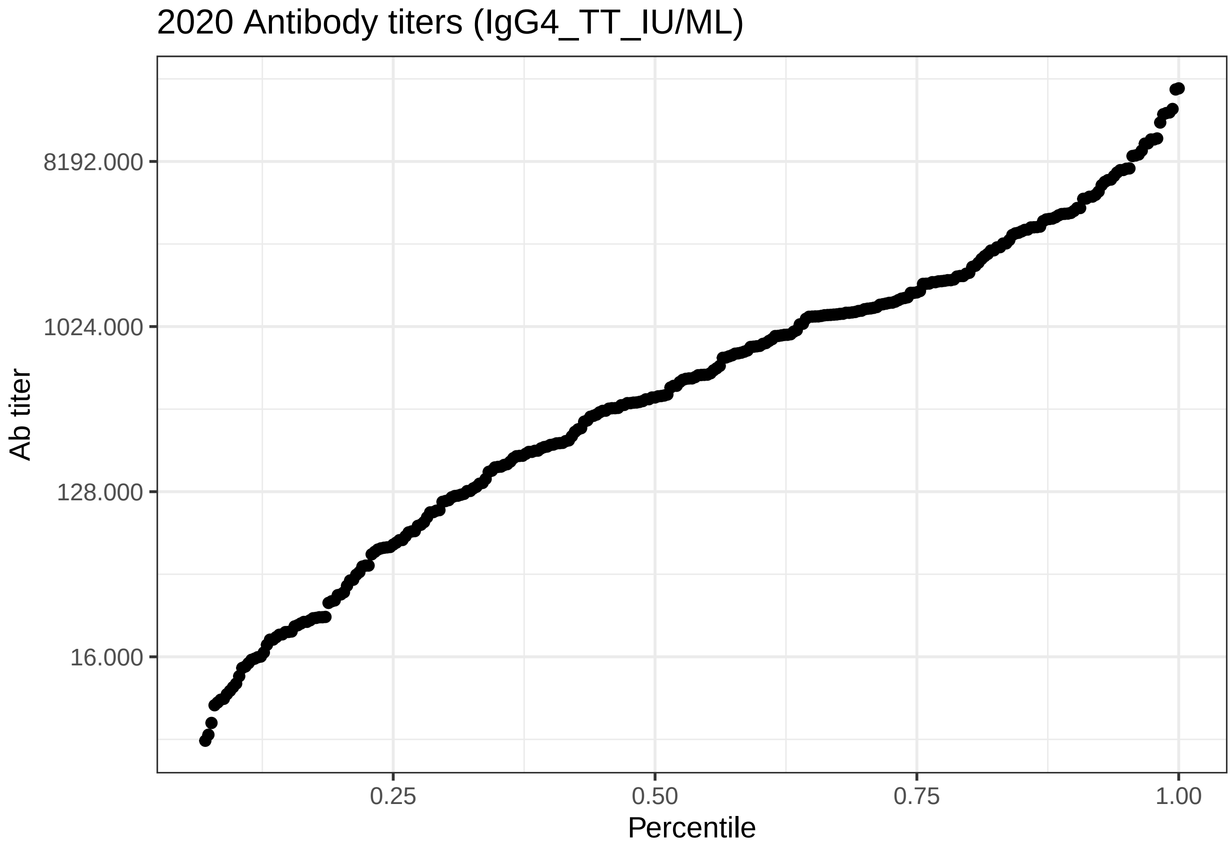

2020 Antibody titers (IgG4_PTM_IU/ML)
Ab titer
2048.000
256.000
32.000
0.5
0.6
0.7
0.8
0.9
1.0
Percentile

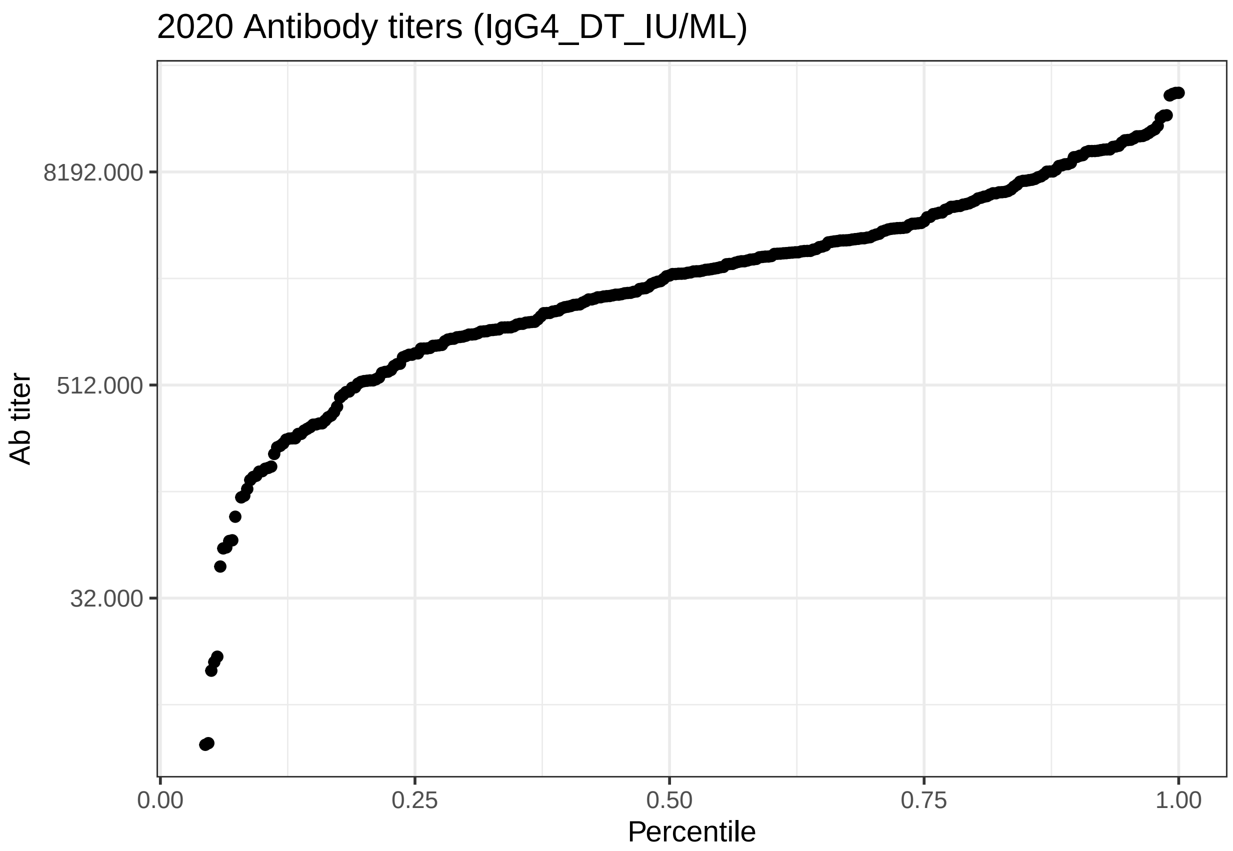

2020 Antibody titers (IgG4_PT_IU/ML)
Ab titer
1024.000
128.000
16.000
0.4
0.6
0.8
1.0
Percentile

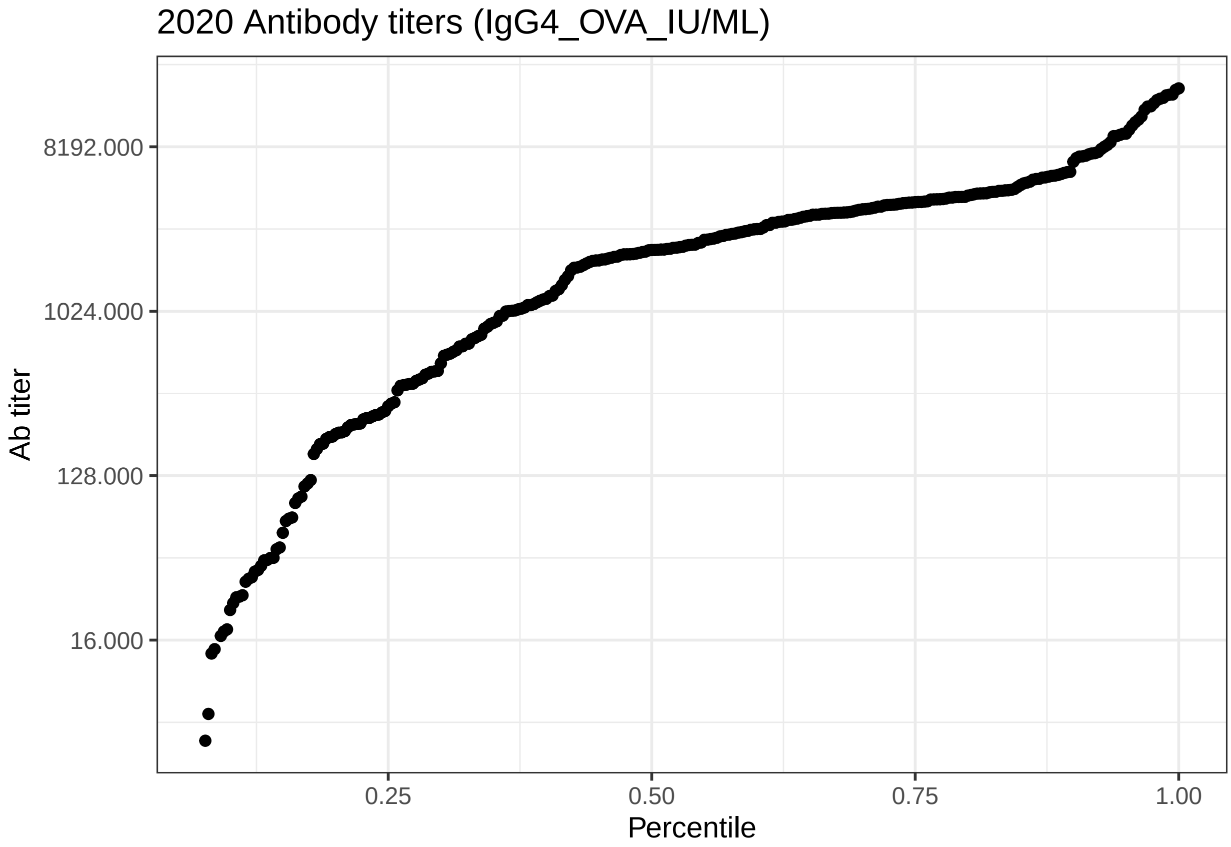

2020 Antibody titers (IgG4_PRN_IU/ML)
Ab titer
2048.000
256.000
32.000
0.25
0.50
0.75
1.00
Percentile


2020 Antibody titers (IgG4_FHA_IU/ML)
Ab titer
16384.000
2048.000
256.000
32.000
0.25
0.50
0.75
1.00
Percentile


2020 Antibody titers (IgG4_FIM2/3_IU/ML)
Ab titer
4096.000
512.000
64.000
0.4
0.6
0.8
1.0
Percentile


2020 Antibody titers (IgG4_TT_IU/ML)
Ab titer
8192.000
1024.000
128.000
16.000
0.25
0.50
0.75
1.00
Percentile

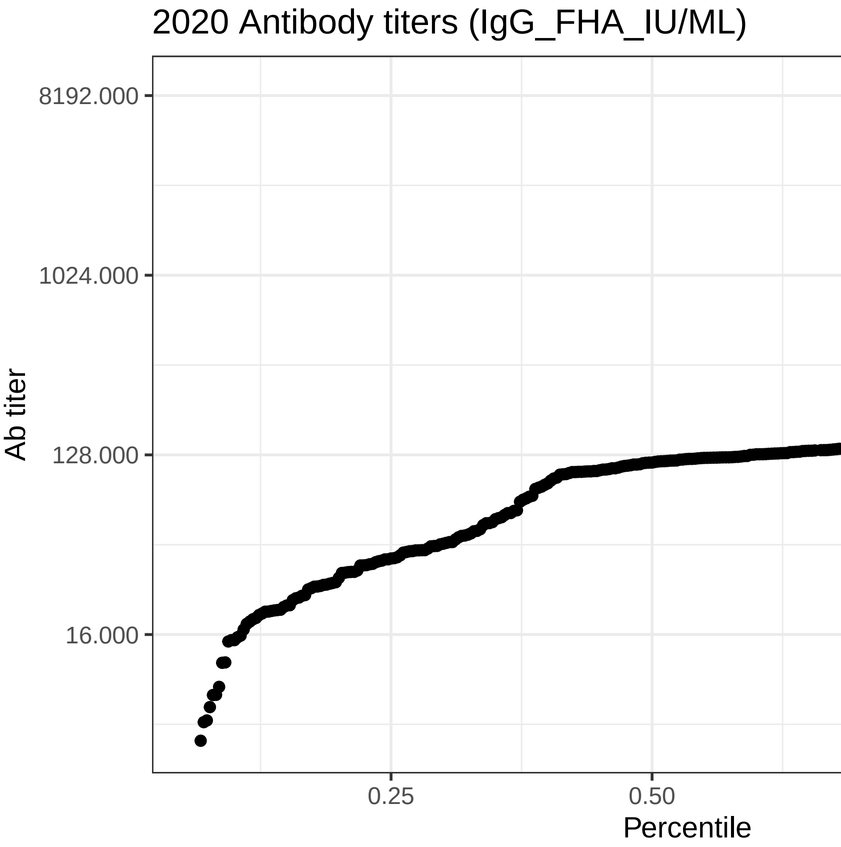

2020 Antibody titers (IgG4_DT_IU/ML)
Ab titer
8192.000
512.000
32.000
0.00
0.25
0.50
0.75
1.00
Percentile



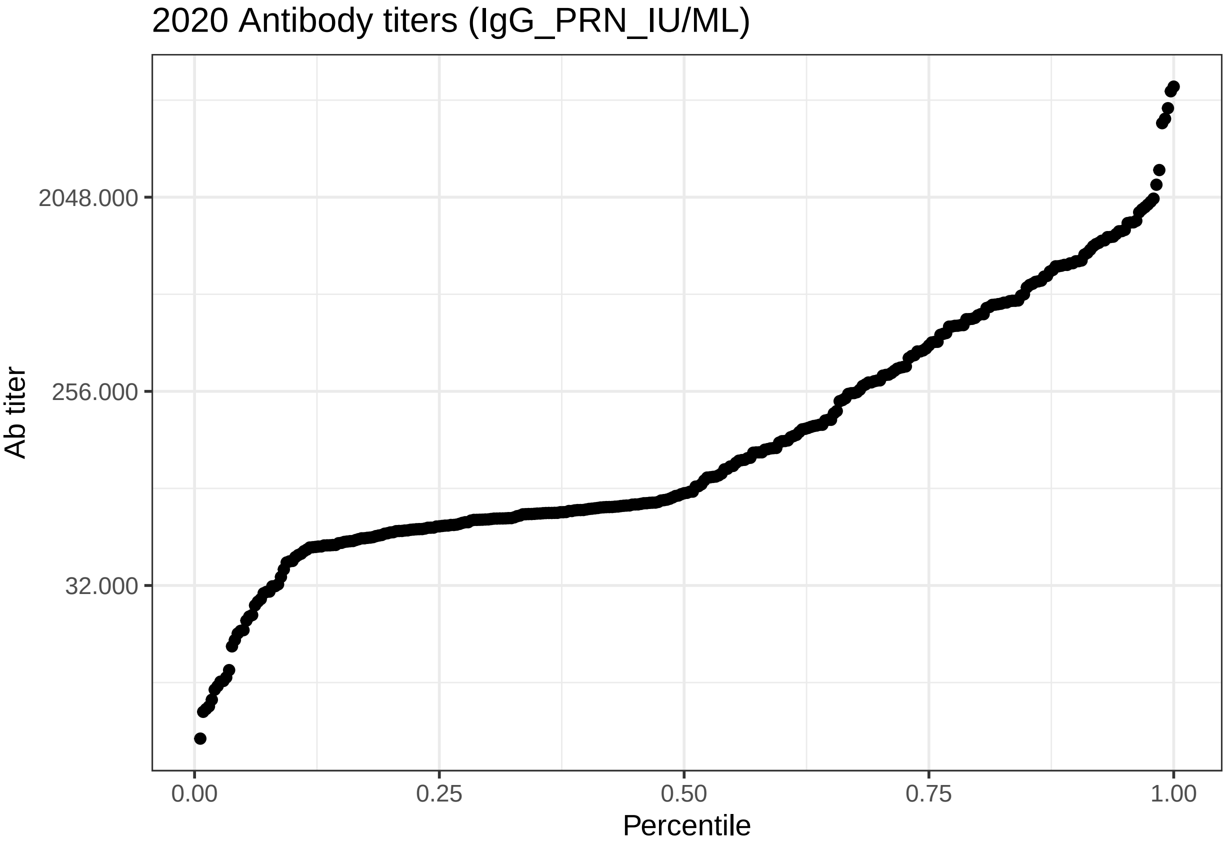
LOD Corrections

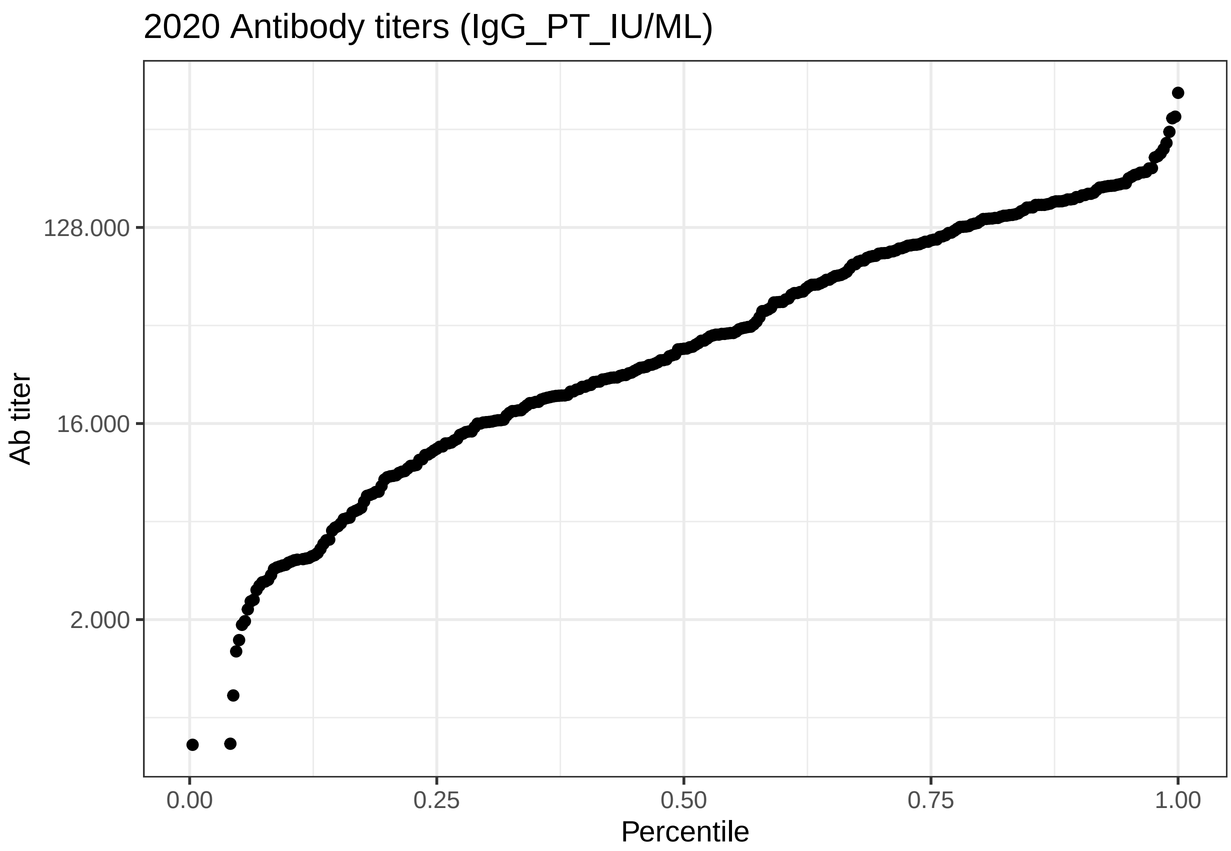
1. Top outliers: IgG_PT

```
titers_2020_feature_removed_lod_corrected <- titers_2020_feature_removed_lod %>%
  mutate(
    lower_limit_of_detection = if_else(isotype_antigen == "IgG_FHA_IU/ML", 4.67953450834645, lower_limi
    lower_limit_of_detection = if_else(isotype_antigen == "IgG_PRN_IU/ML", 6.20594906363301, lower_limi
    ab_titer = if_else(isotype_antigen == "IgG_PT_IU/ML" & ab_titer > 15000 , lower_limit_of_detection,
  ) %>%
  mutate(ab_titer = if_else(ab_titer < lower_limit_of_detection | is.na(ab_titer) == TRUE, lower_limit_

## Validation plots
for(select_ia in c("IgG_FHA_IU/ML", "IgG_PRN_IU/ML", "IgG_PT_IU/ML"))
{
plot1 <- titers_2020_feature_removed_lod_corrected %>%
  mutate(subject_id = as.factor(subject_id)) %>%
  filter(isotype_antigen == select_ia, planned_day_relative_to_boost < 50) %>%
  arrange(desc(ab_titer)) %>%
  ggplot(aes(y=ab_titer)) +  stat_ecdf(geom = "point", pad = FALSE) +
  labs(y = "Ab titer", x = "Percentile")+ ggtitle(paste0("2020 Antibody titers (" , select_ia, ")")) +
  scale_y_continuous(trans = 'log2', labels=scaleFUN)
plot(plot1)
}
```



2. **Bottom outliers: IgG__FHA, IgG__PRN**





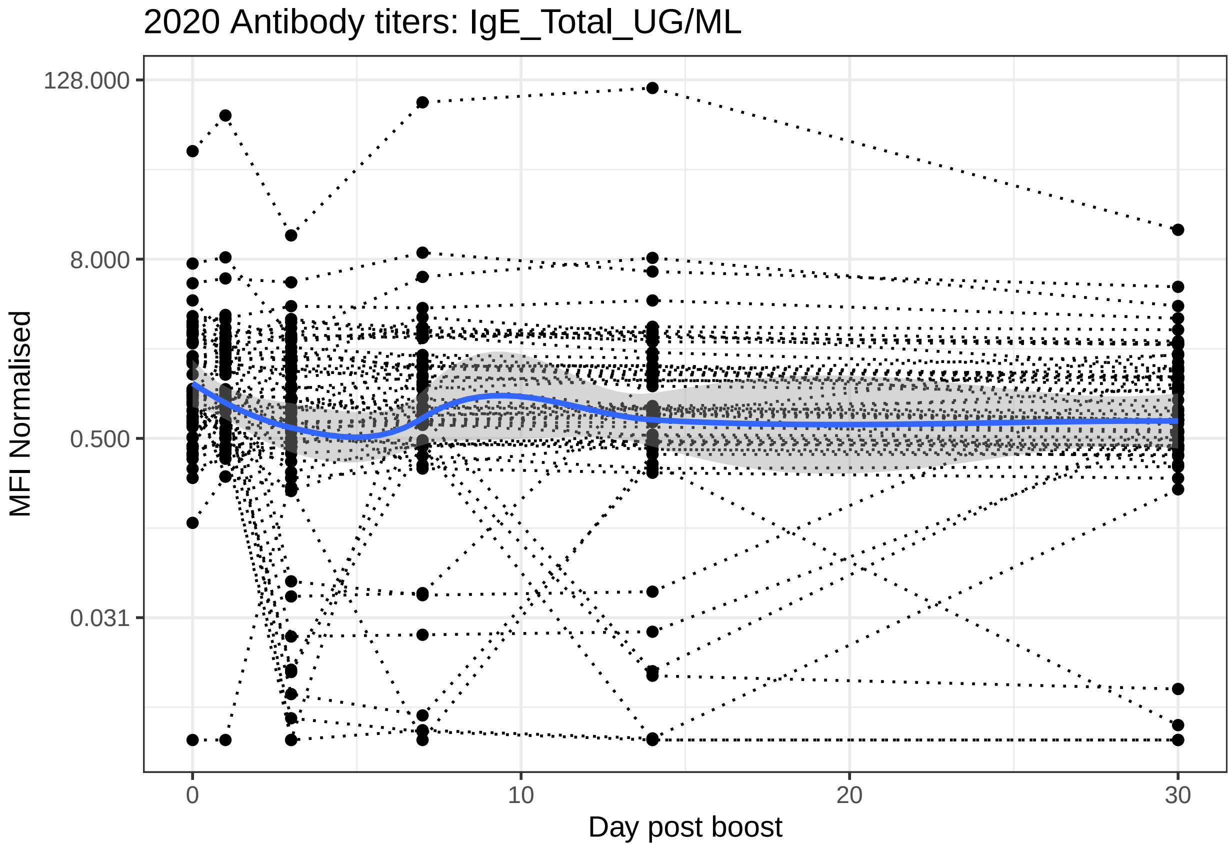
### Performing median based normalisation

```
## Setting MFI zero values to lower limit of detection
titers2020_calculate_lod <- titers_2020_feature_removed_lod_corrected %>%
  #filter(isotype_antigen == 'IgE_Total') %>%
  group_by(isotype_antigen) %>%
  mutate(
         lod_new = min(ab_titer[ab_titer > 0], na.rm = TRUE),
         MFI_na_removed = if_else(ab_titer == 0 | is.na(ab_titer) == TRUE, lod_new, ab_titer)
         ) %>%
  ungroup()

## Calculate Overall median using MFI at day post boost 0
df_d0_median_2020  <- titers2020_calculate_lod %>%
  filter(planned_day_relative_to_boost == 0) %>%
  group_by(isotype_antigen) %>%
  summarise(
    MFI_median_d0 = median(MFI_na_removed),
  ) %>%
  ungroup()

titers_2020_new_raw   <-  left_join(titers2020_calculate_lod , df_d0_median_2020 , by = "isotype_antigen
  mutate(
    MFI_normalized = MFI_na_removed / MFI_median_d0,
  )
```

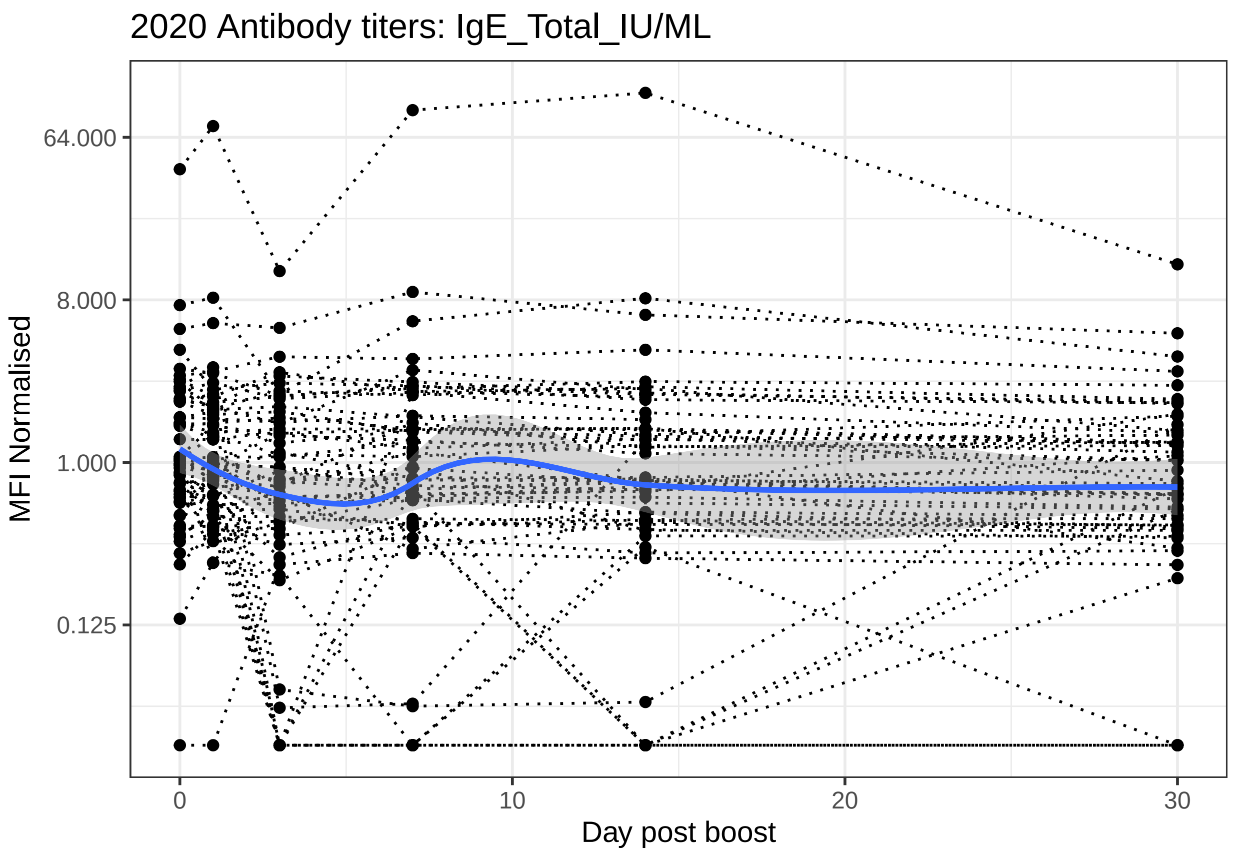
Plot longitudinal data after median based normalisation

```
#for(select_ia in c('IgE_Total_IU/ML'))
for(select_ia in unique(titers_2020_new_raw$isotype_antigen))
{
plot1 <- titers_2020_new_raw %>%
  mutate(subject_id = as.character(subject_id)) %>%
  filter(isotype_antigen == select_ia, planned_day_relative_to_boost < 50) %>%
    ggplot(aes(x=planned_day_relative_to_boost, y=MFI_normalized, )) +
      geom_line(aes(group=subject_id),linetype = "dotted") +
      geom_point() +
      labs(x = "Day post boost", y = "MFI Normalised") +
      geom_smooth(size = 1) +
      theme_bw() +
      theme(strip.background = element_blank(), strip.placement = "outside") +
      ggtitle(paste0("2020 Antibody titers: ", select_ia)) +
      scale_y_continuous(trans = 'log2', labels=scaleFUN)

plot(plot1)
}
```

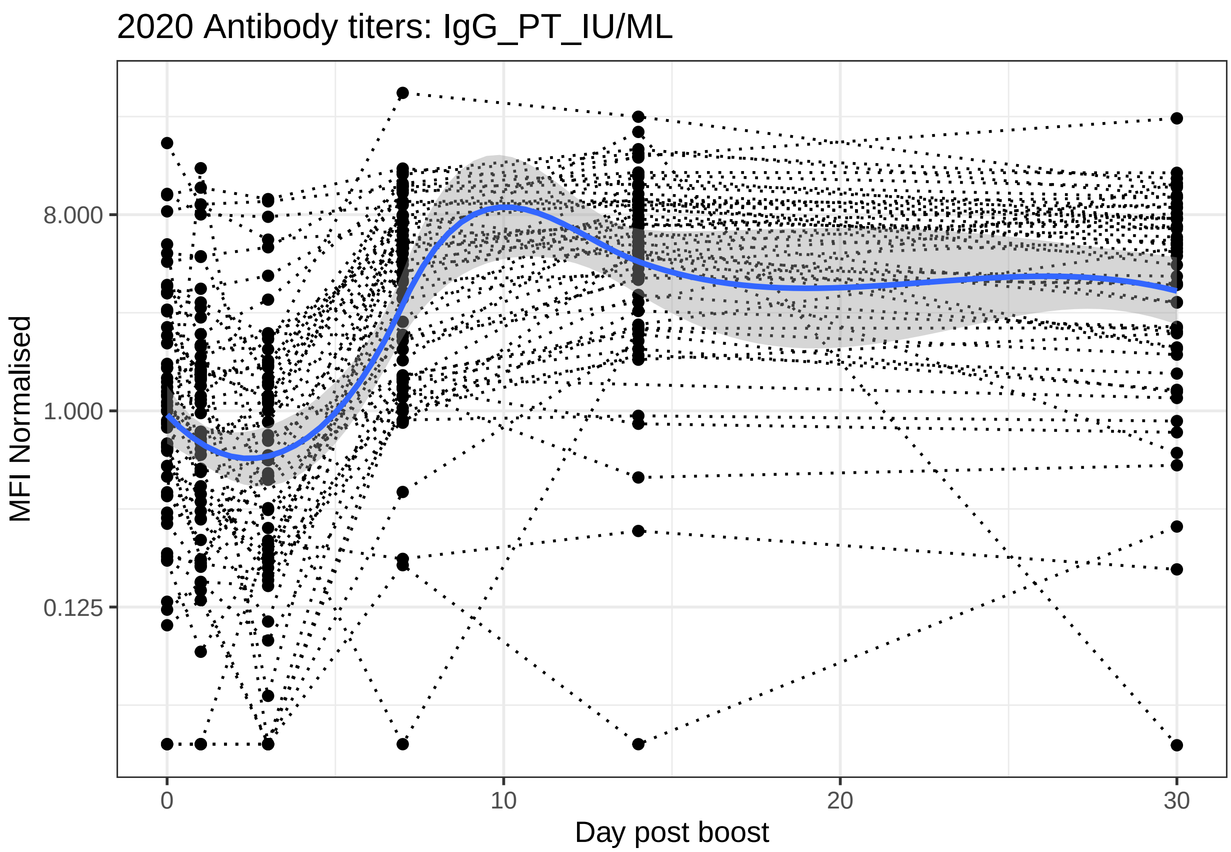
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



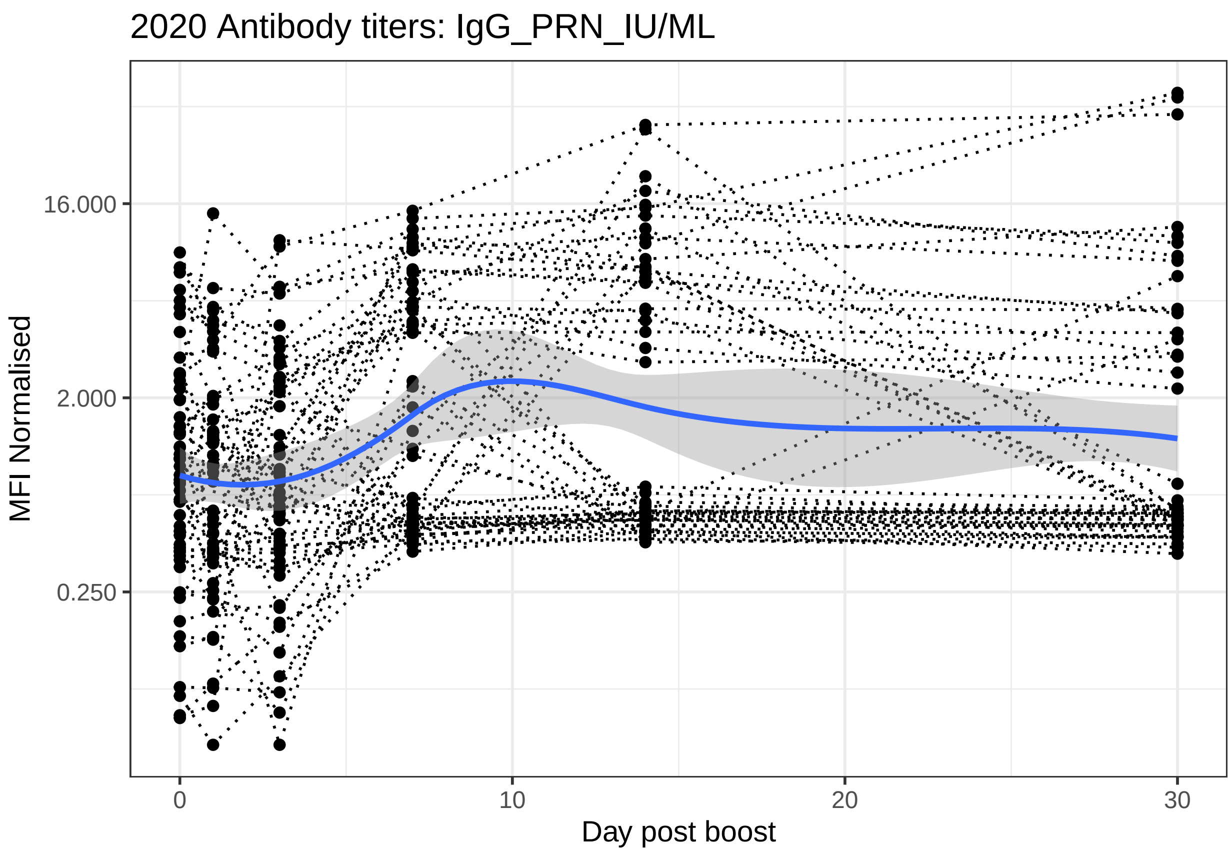
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



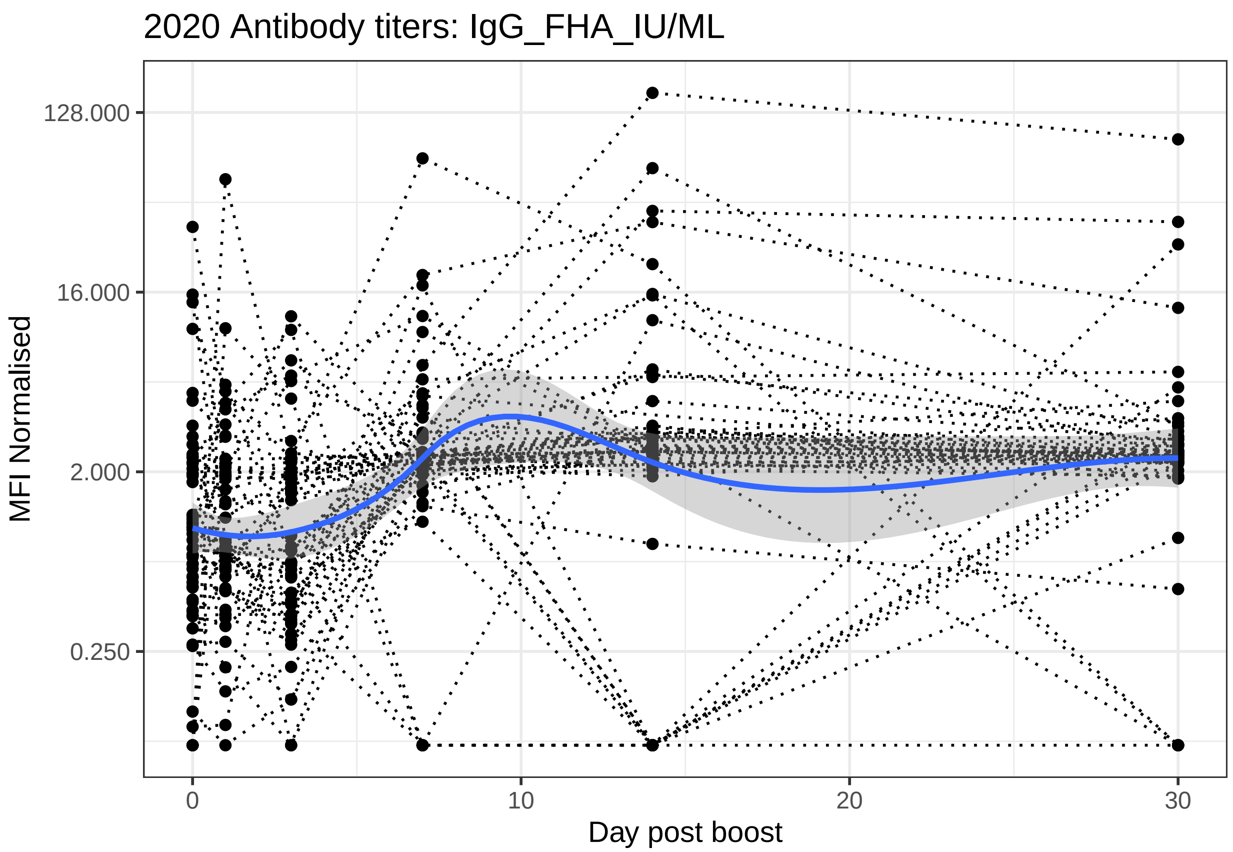
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



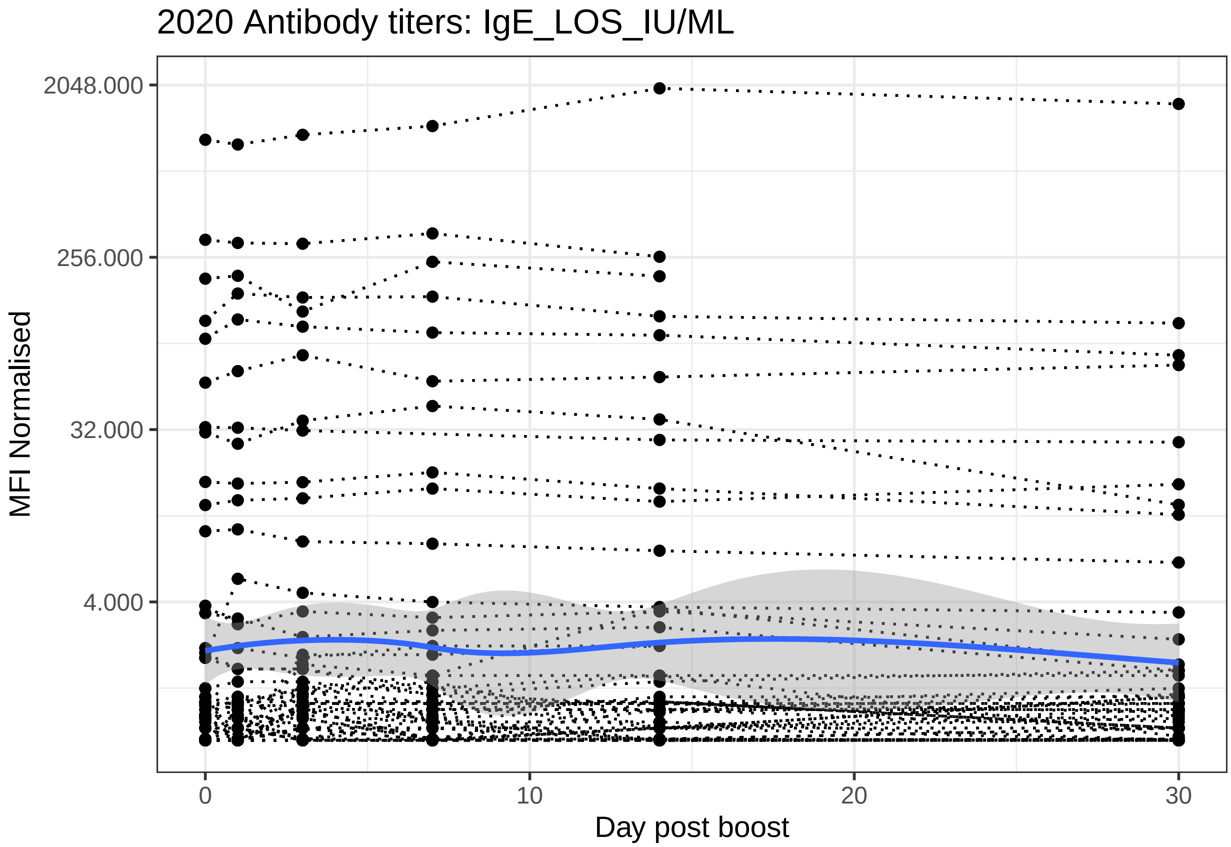
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



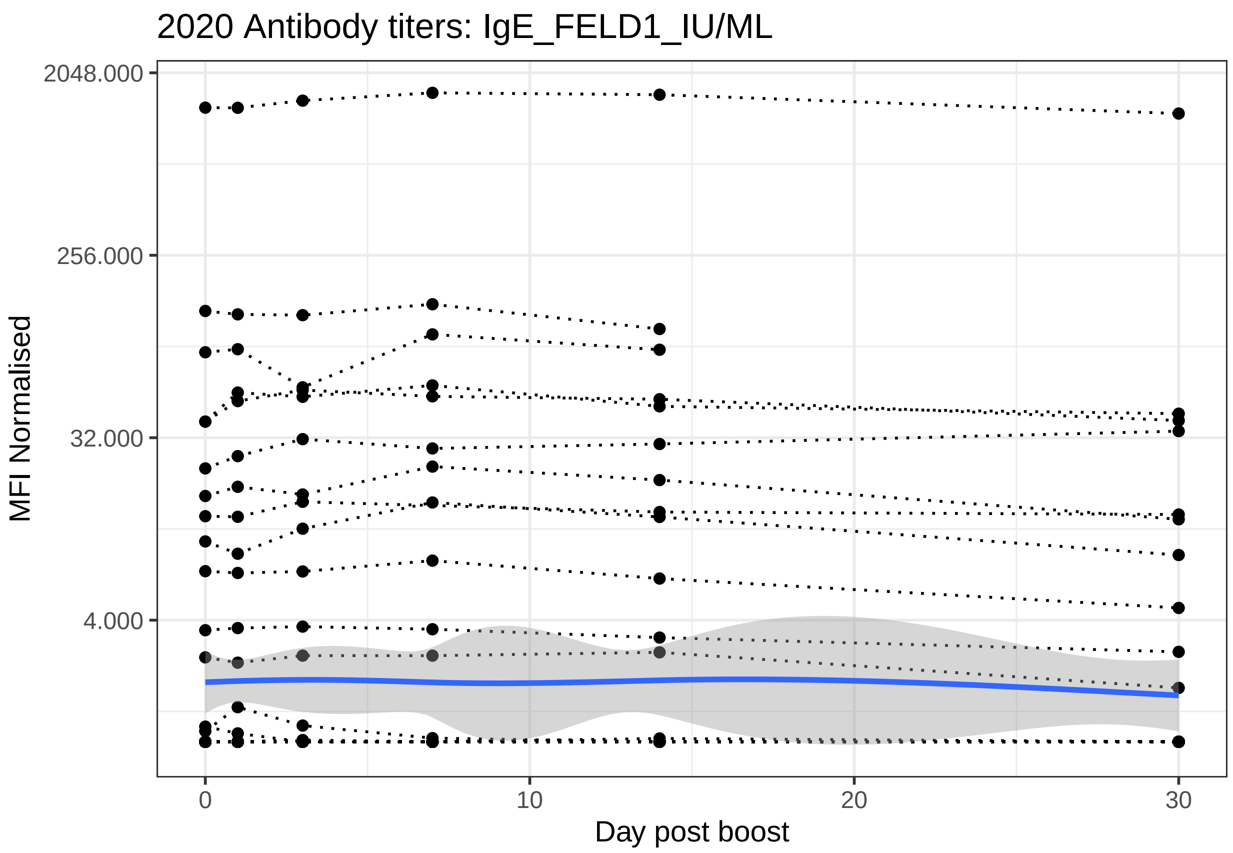
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



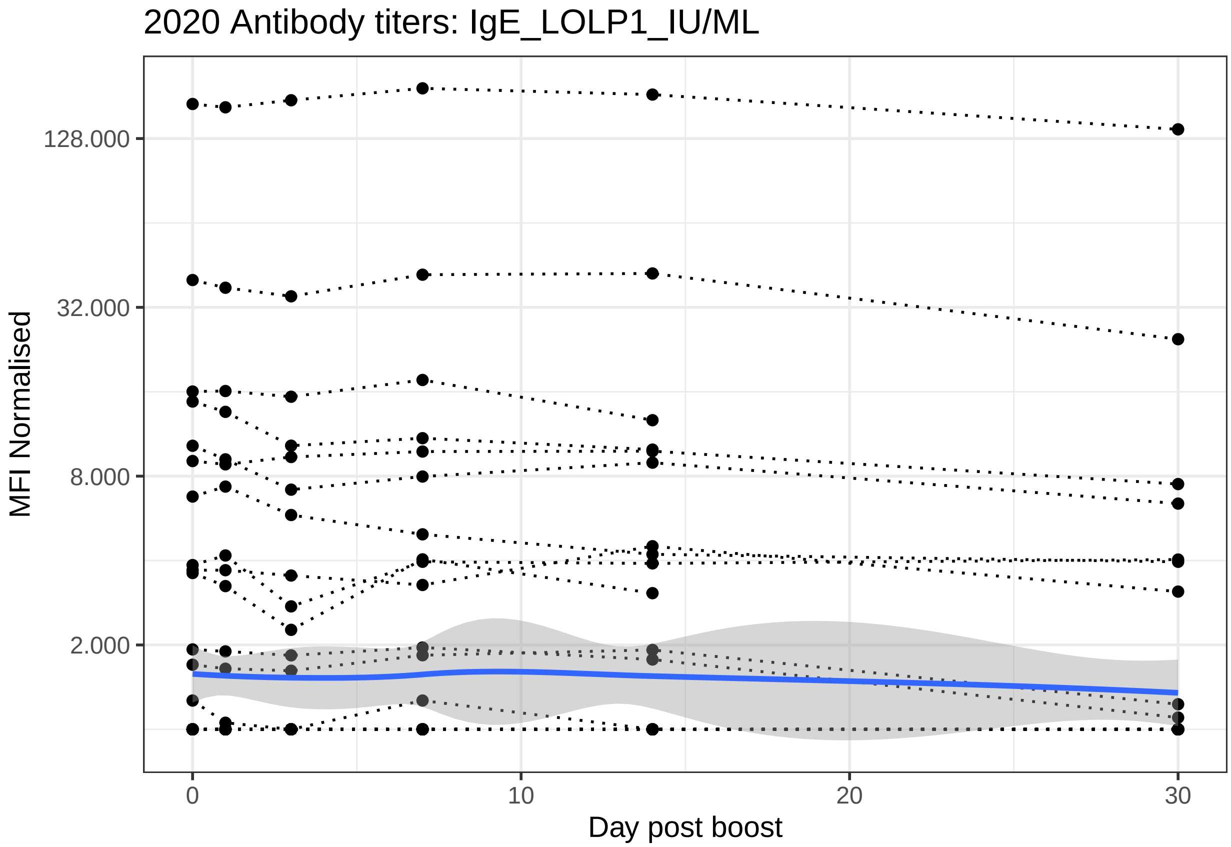
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



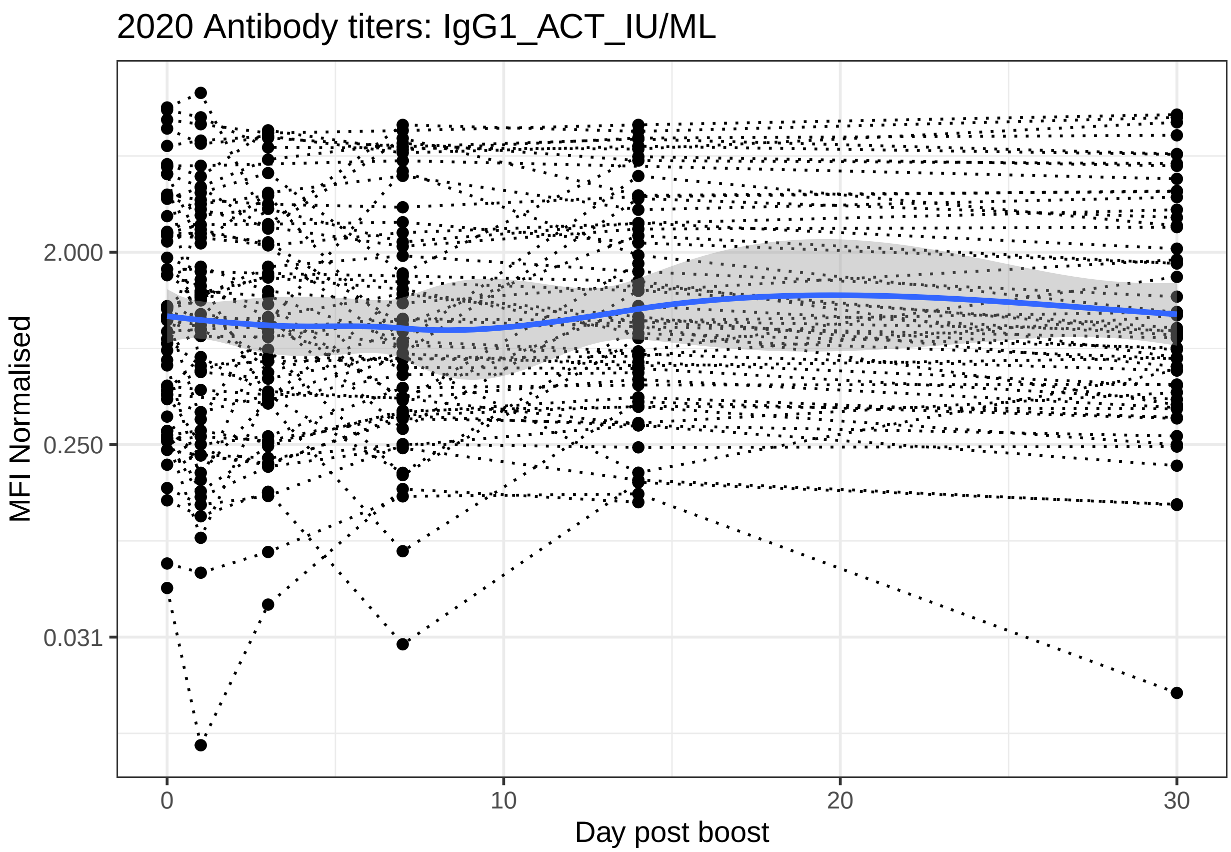
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



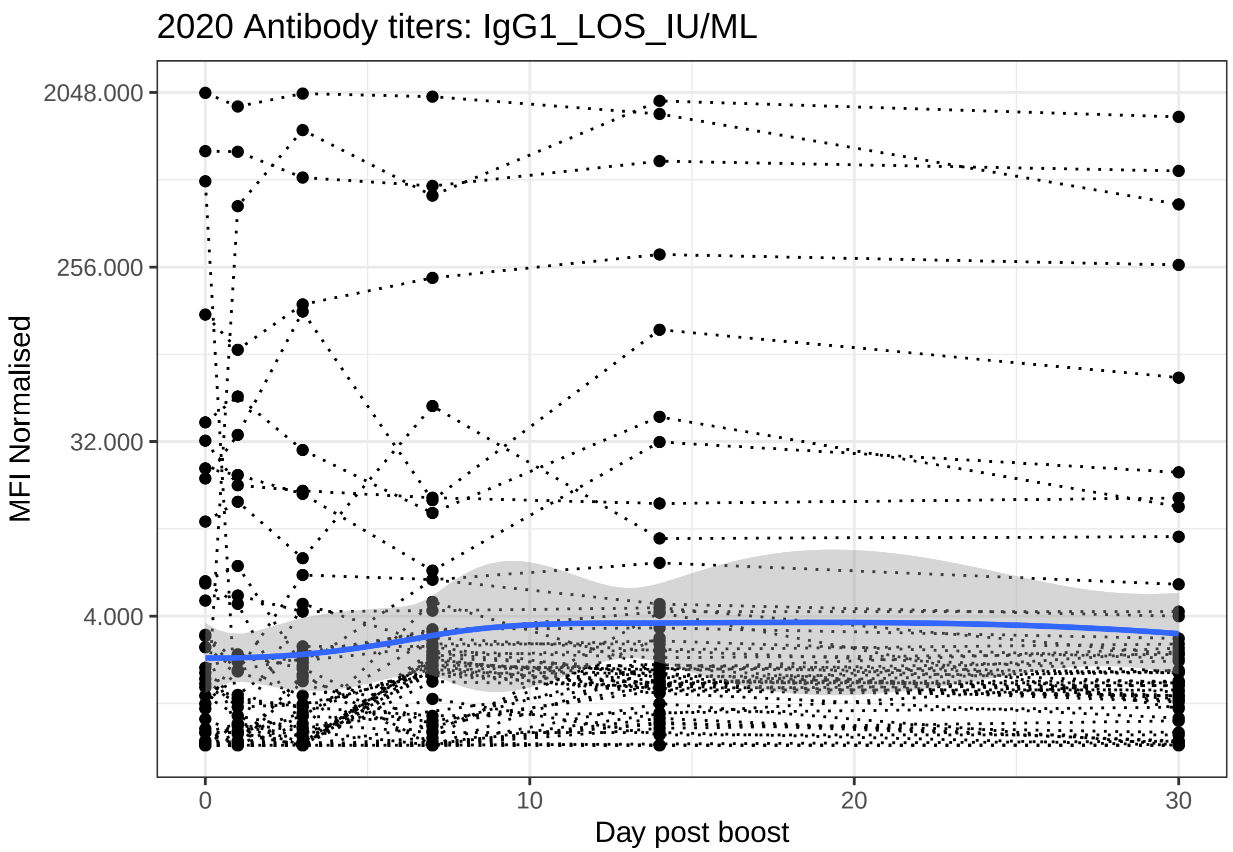
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



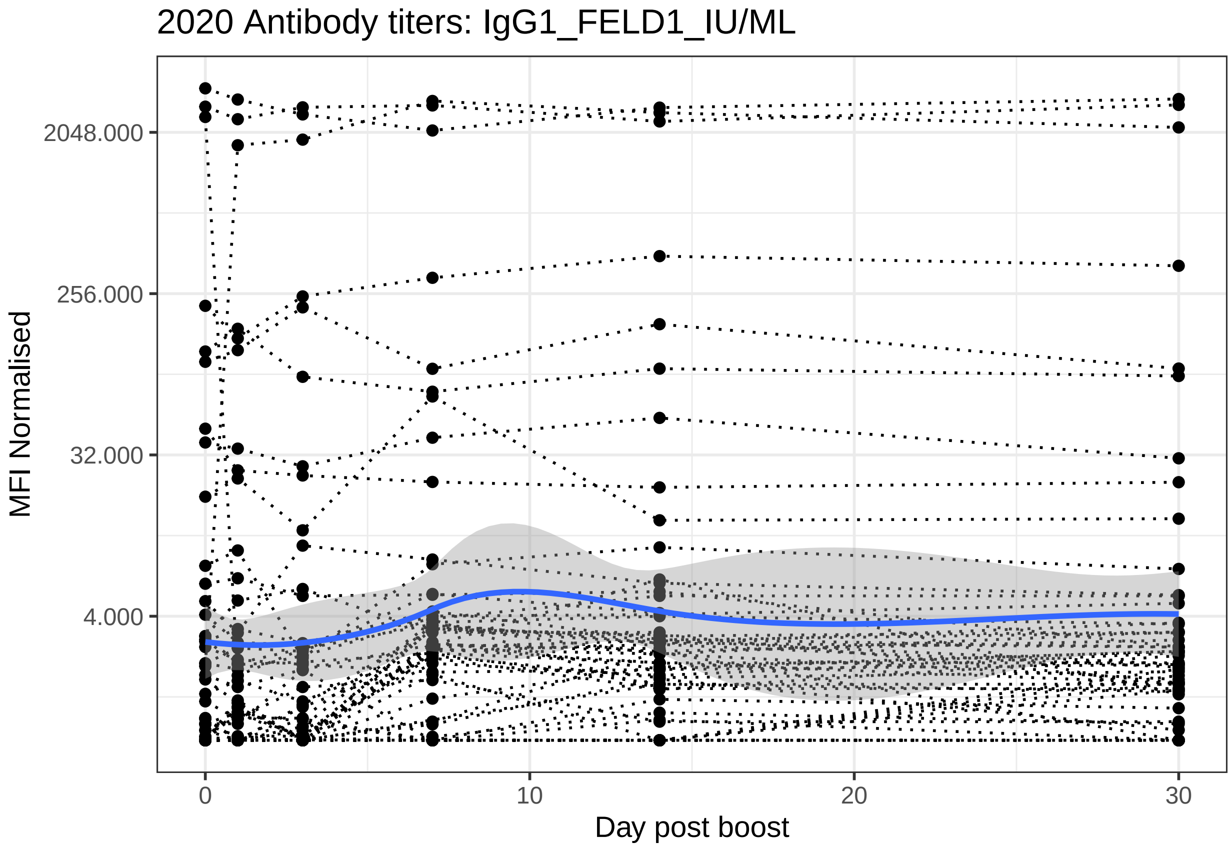
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



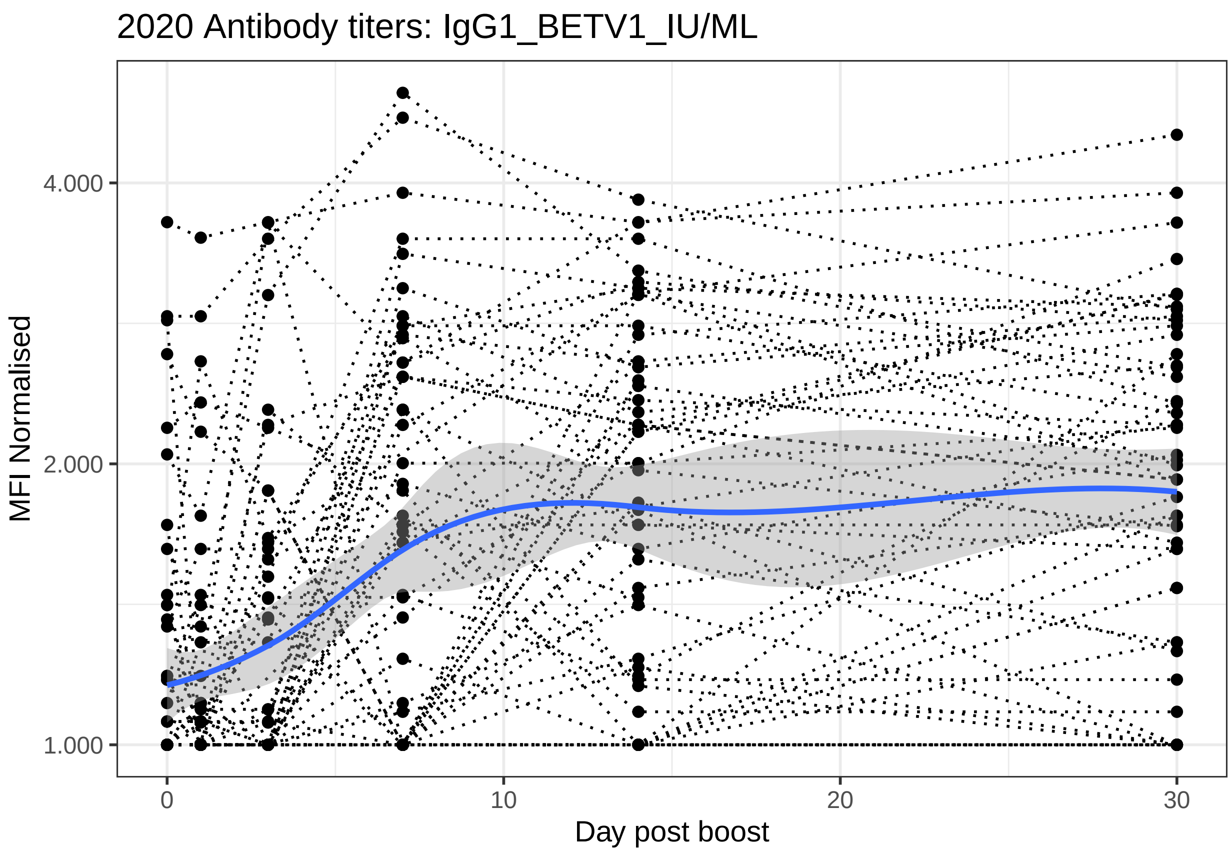
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



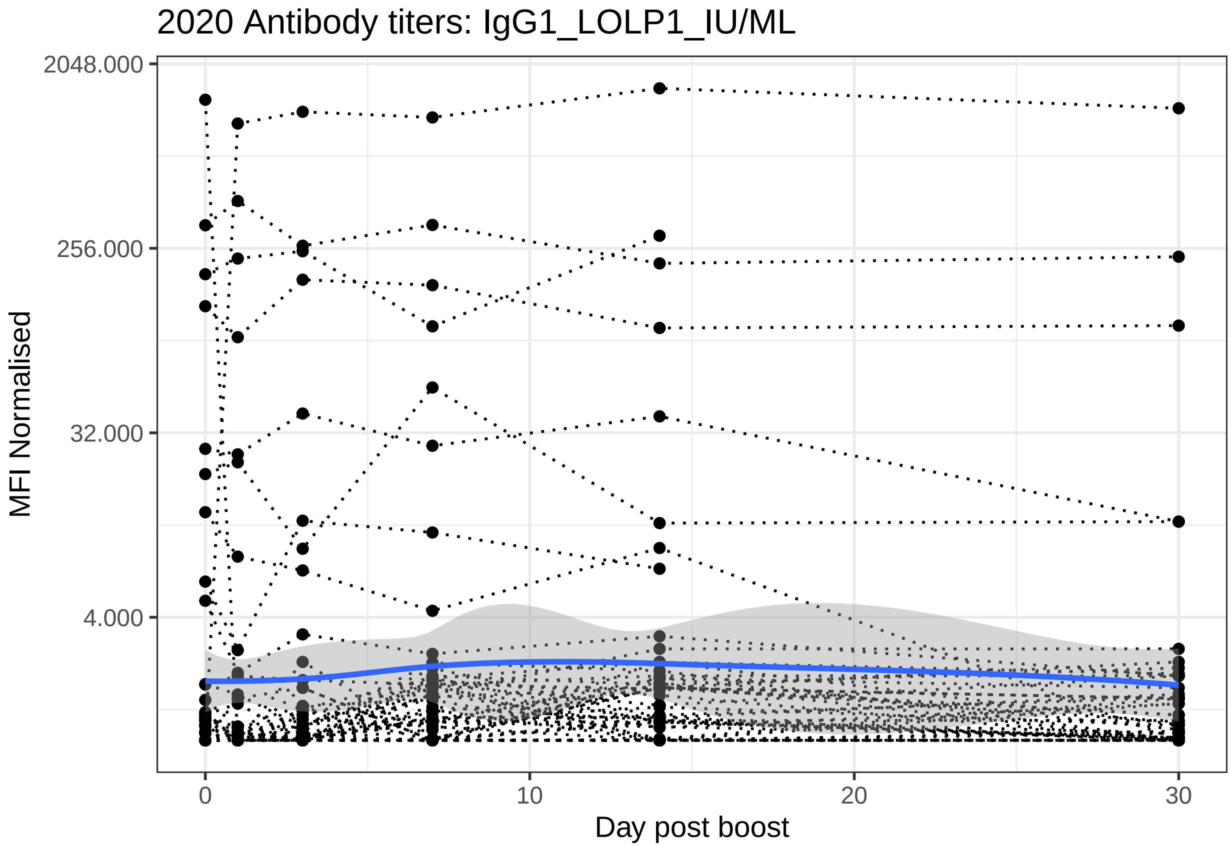
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



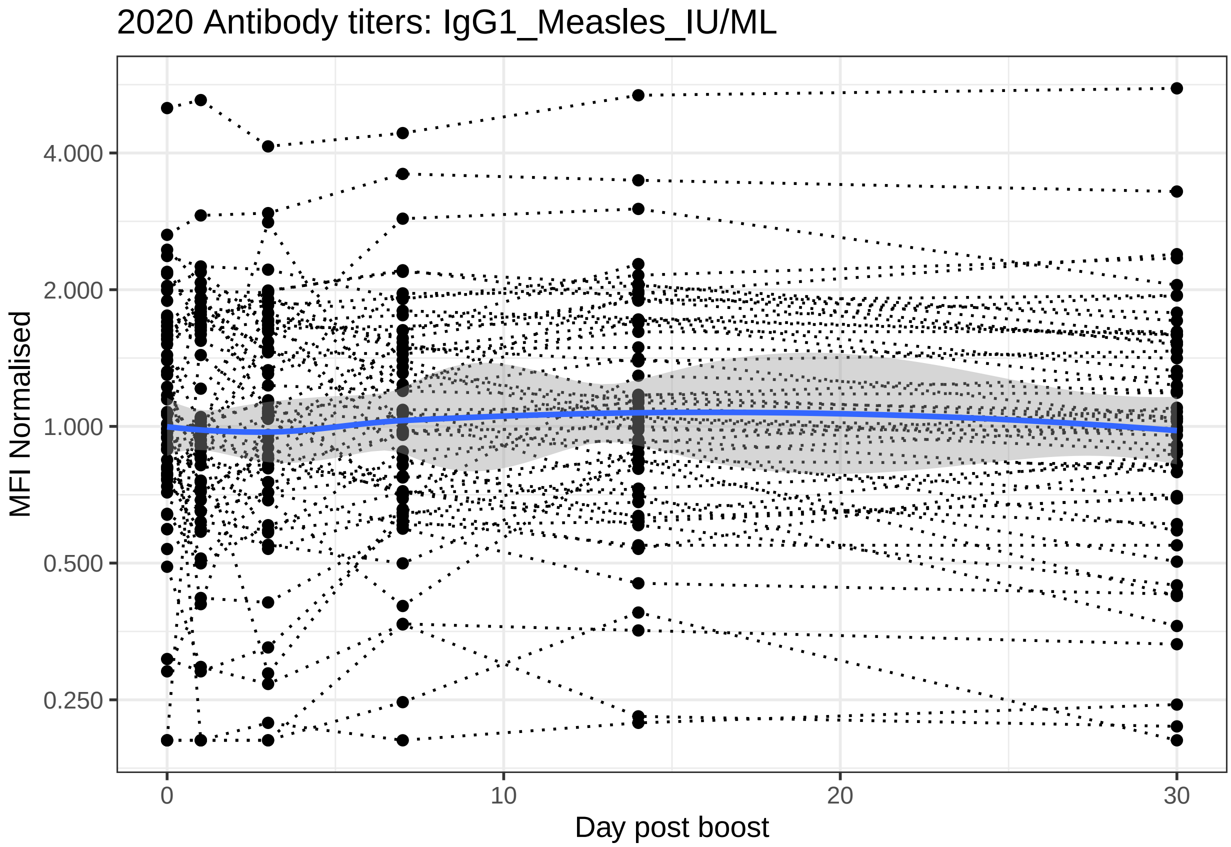
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



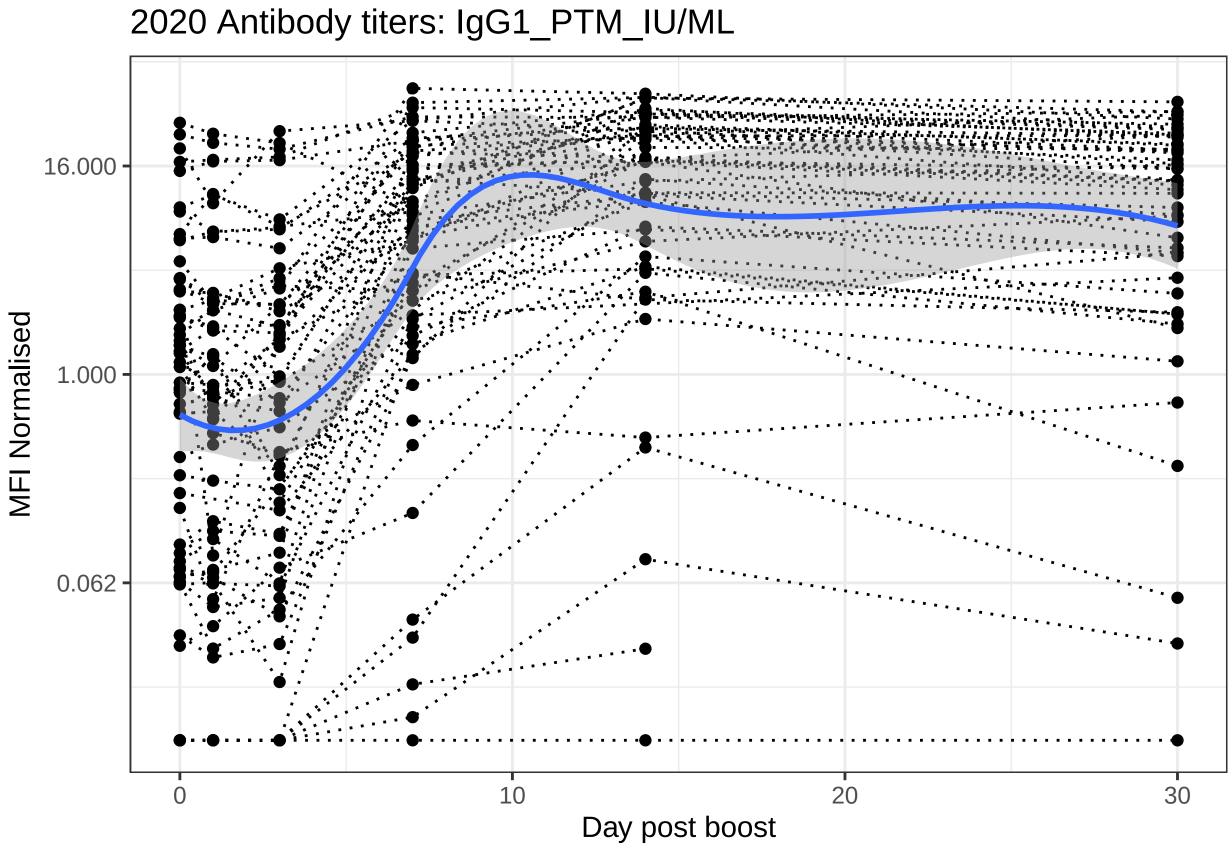
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



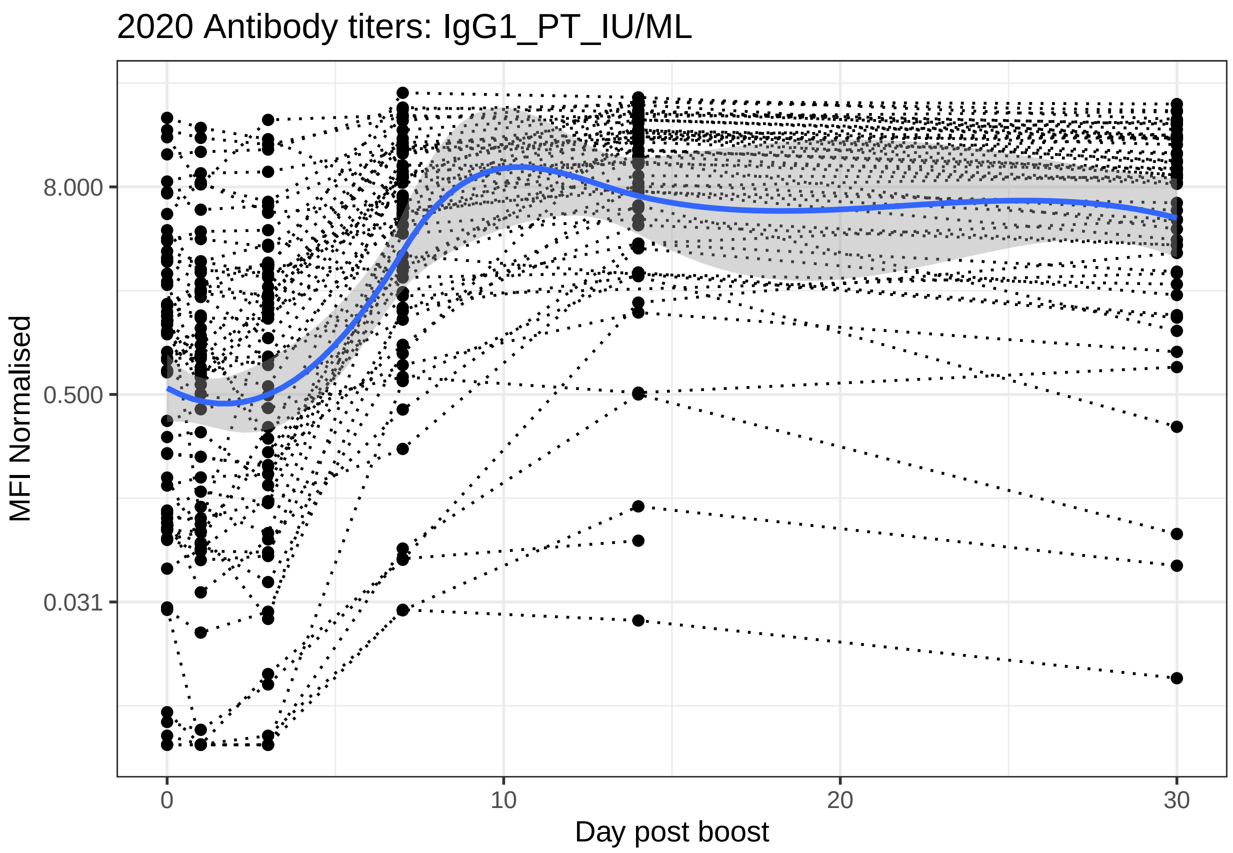
```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



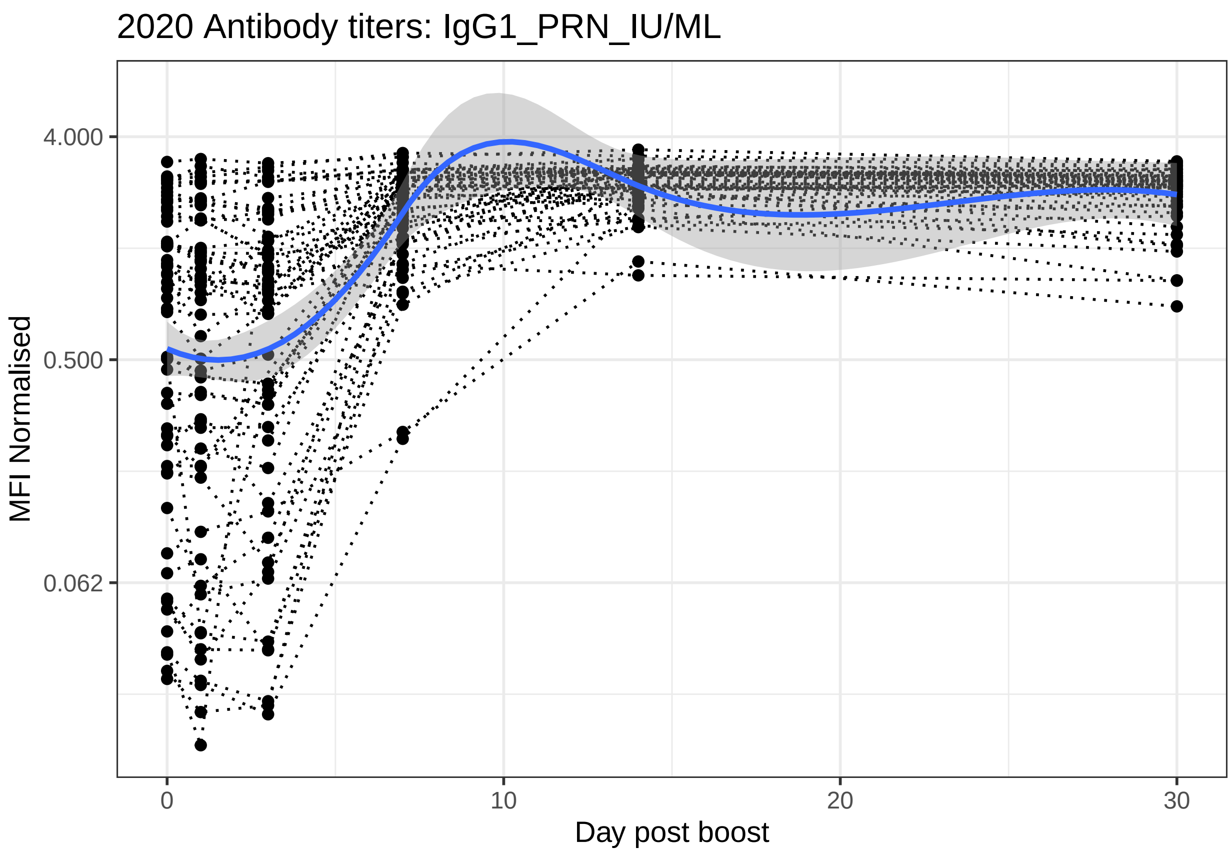
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



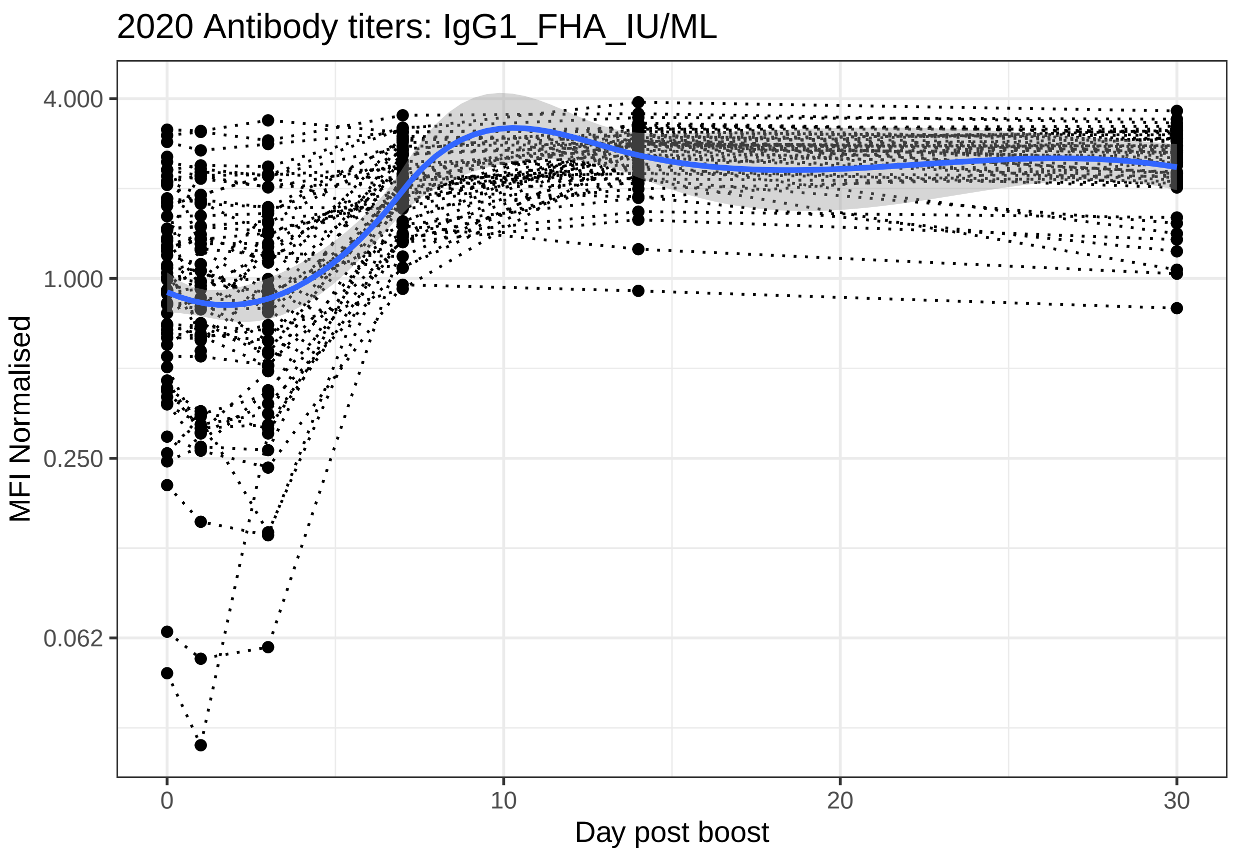
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



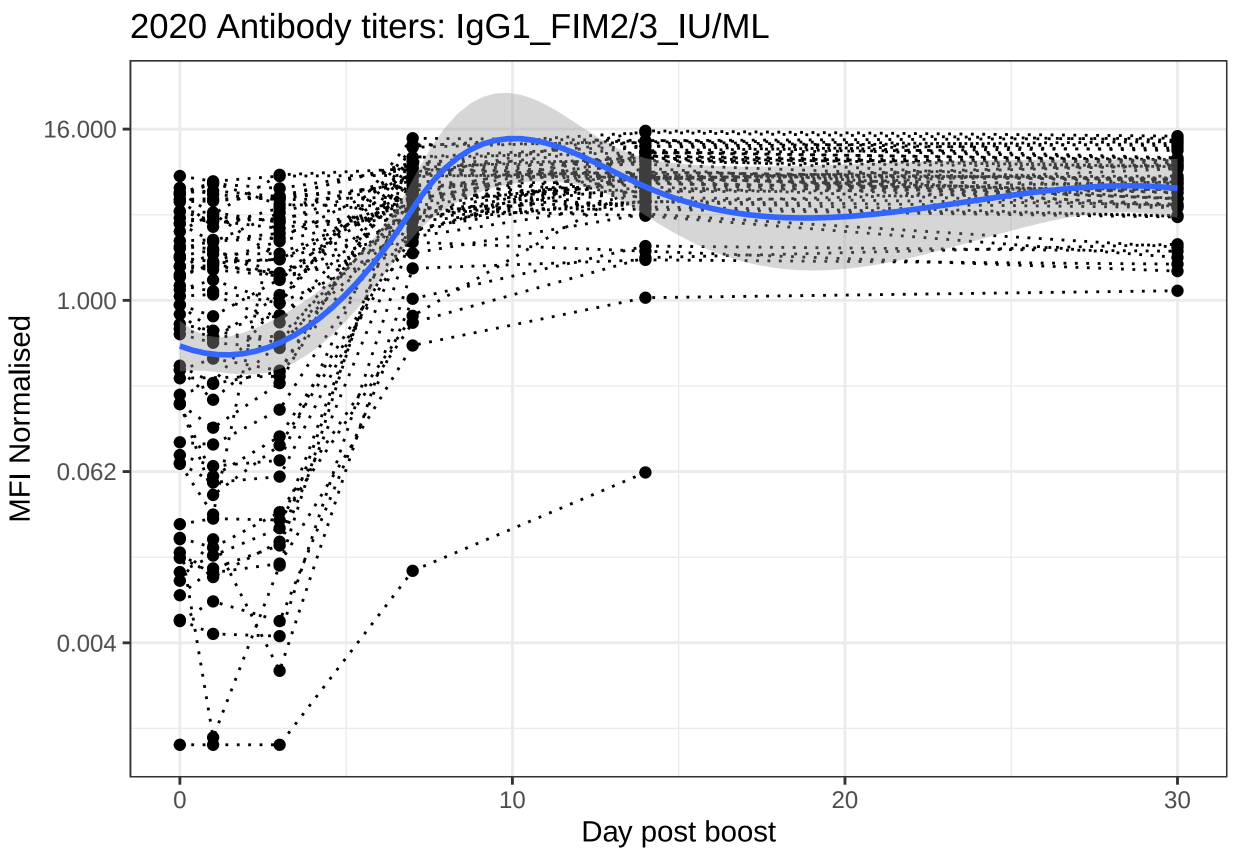
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



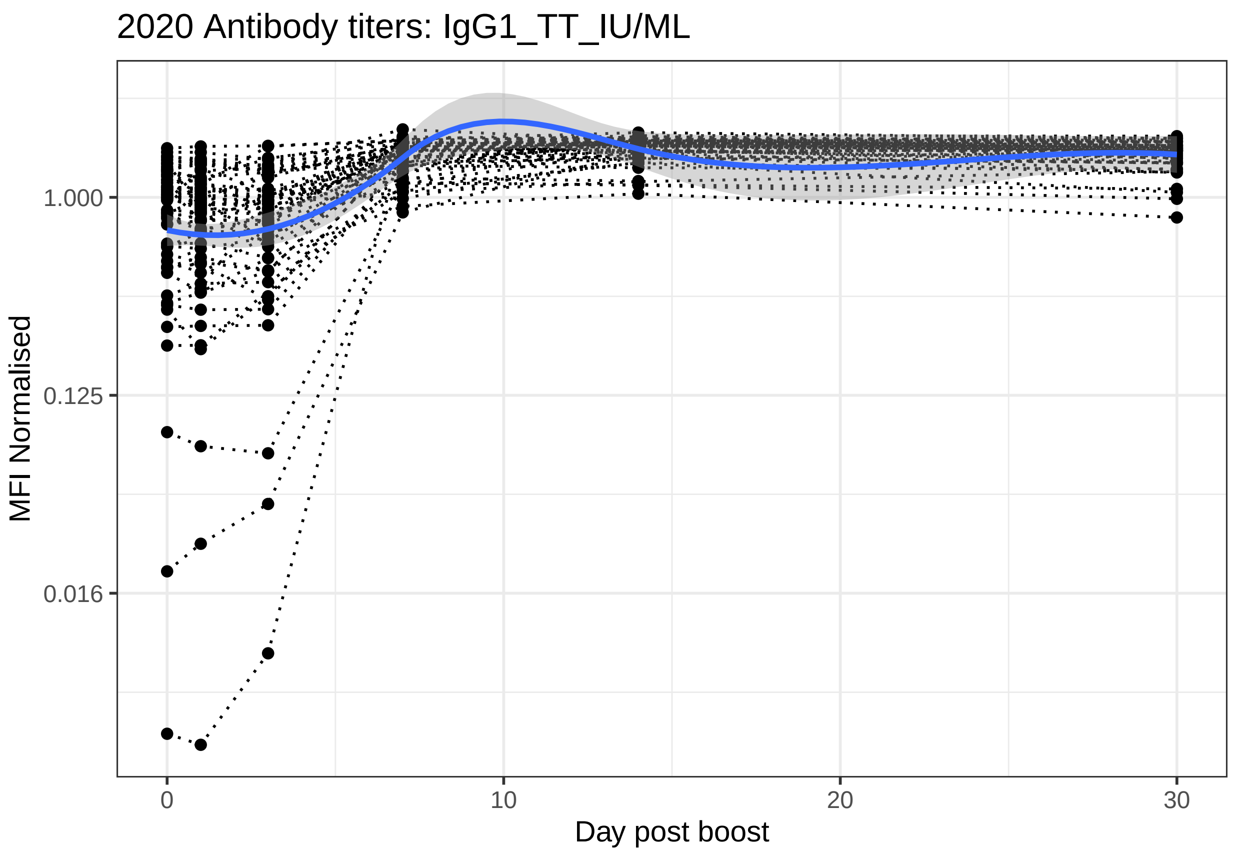
```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



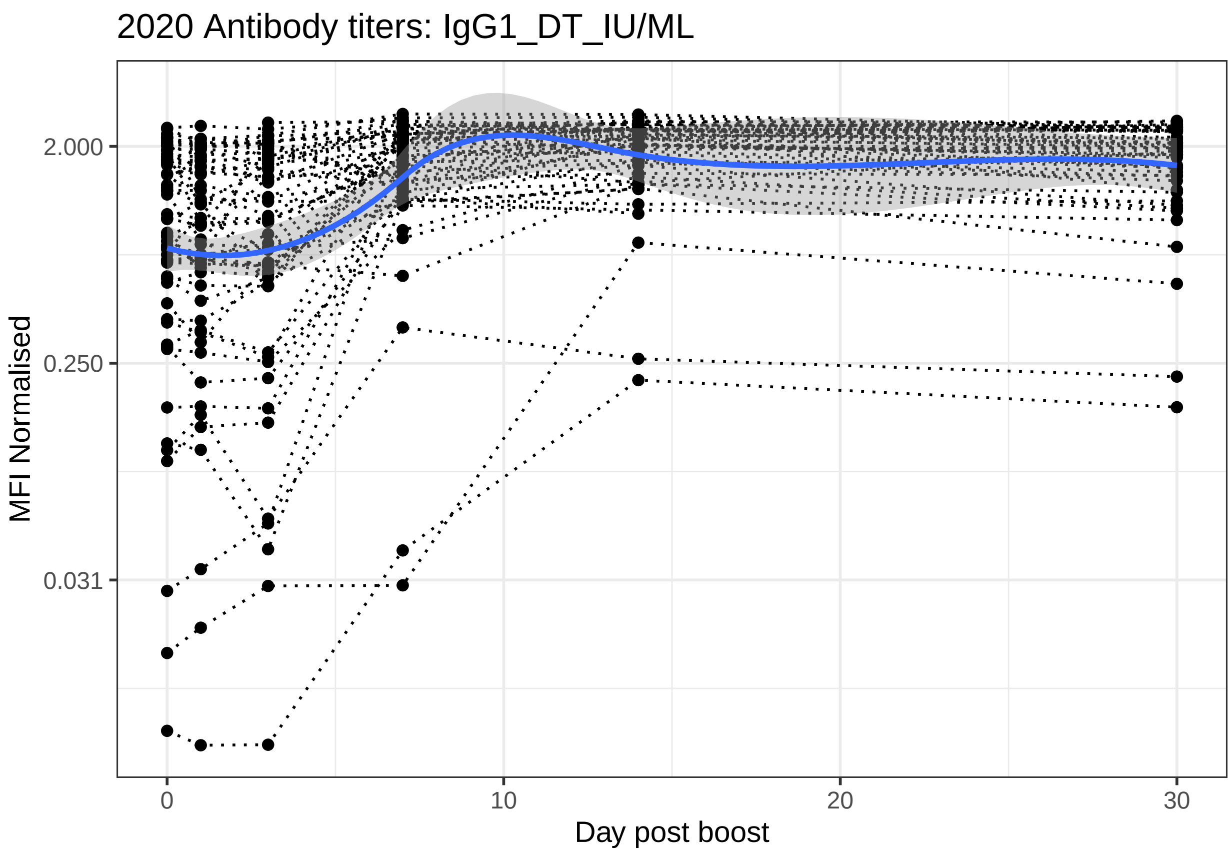
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



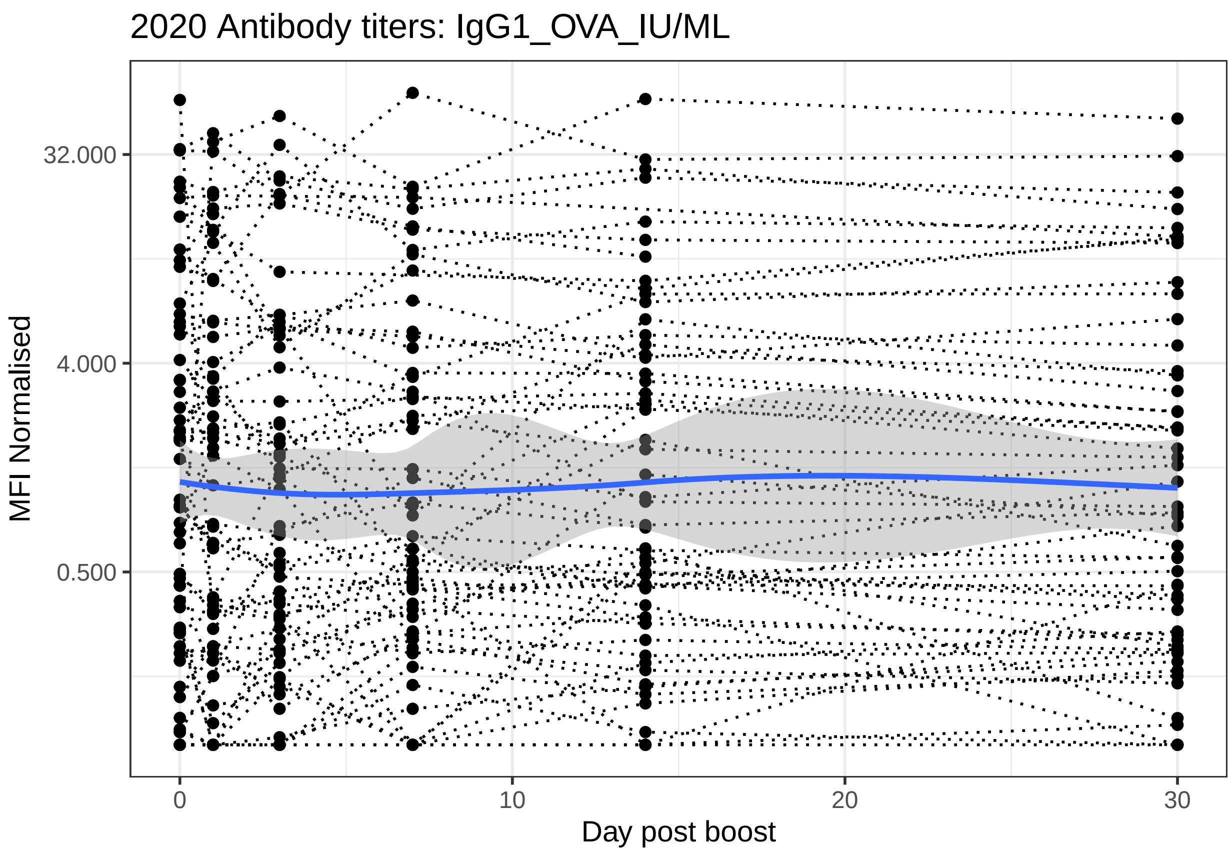
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



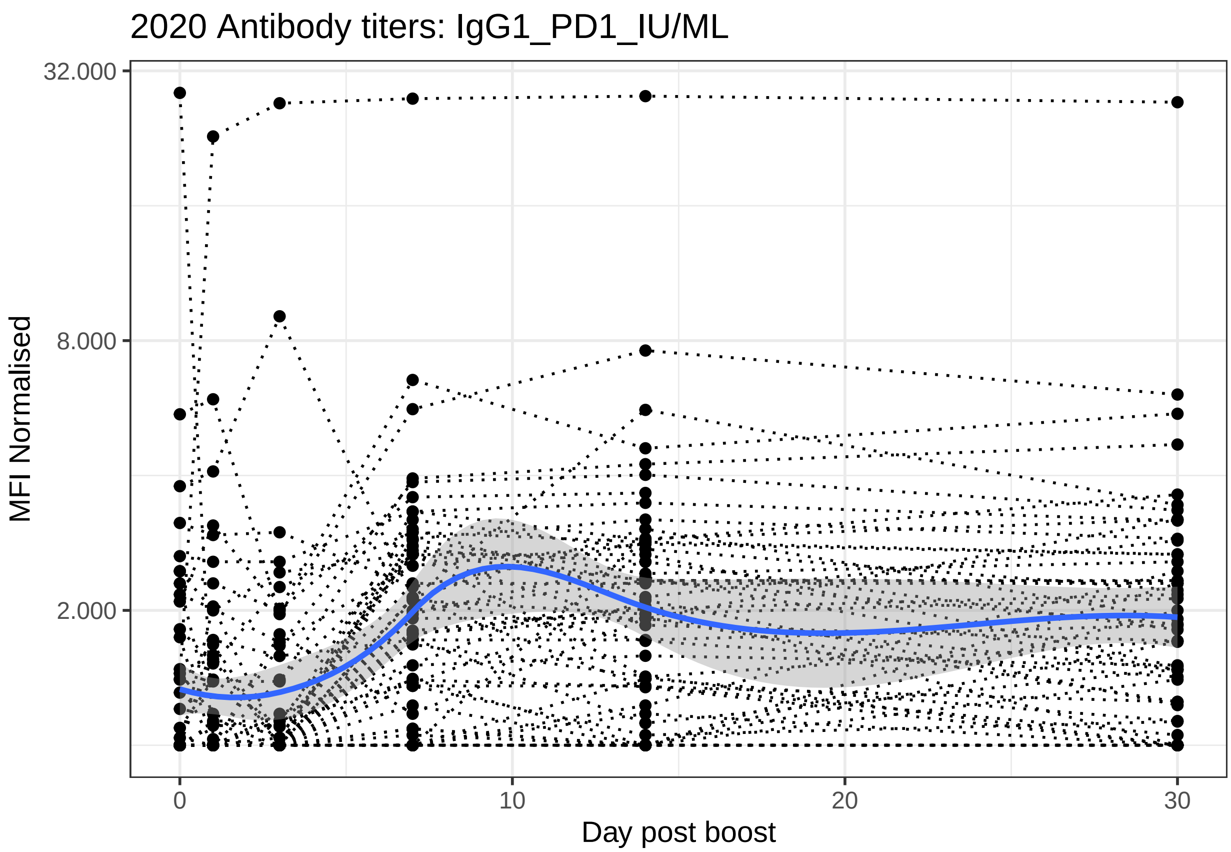
```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



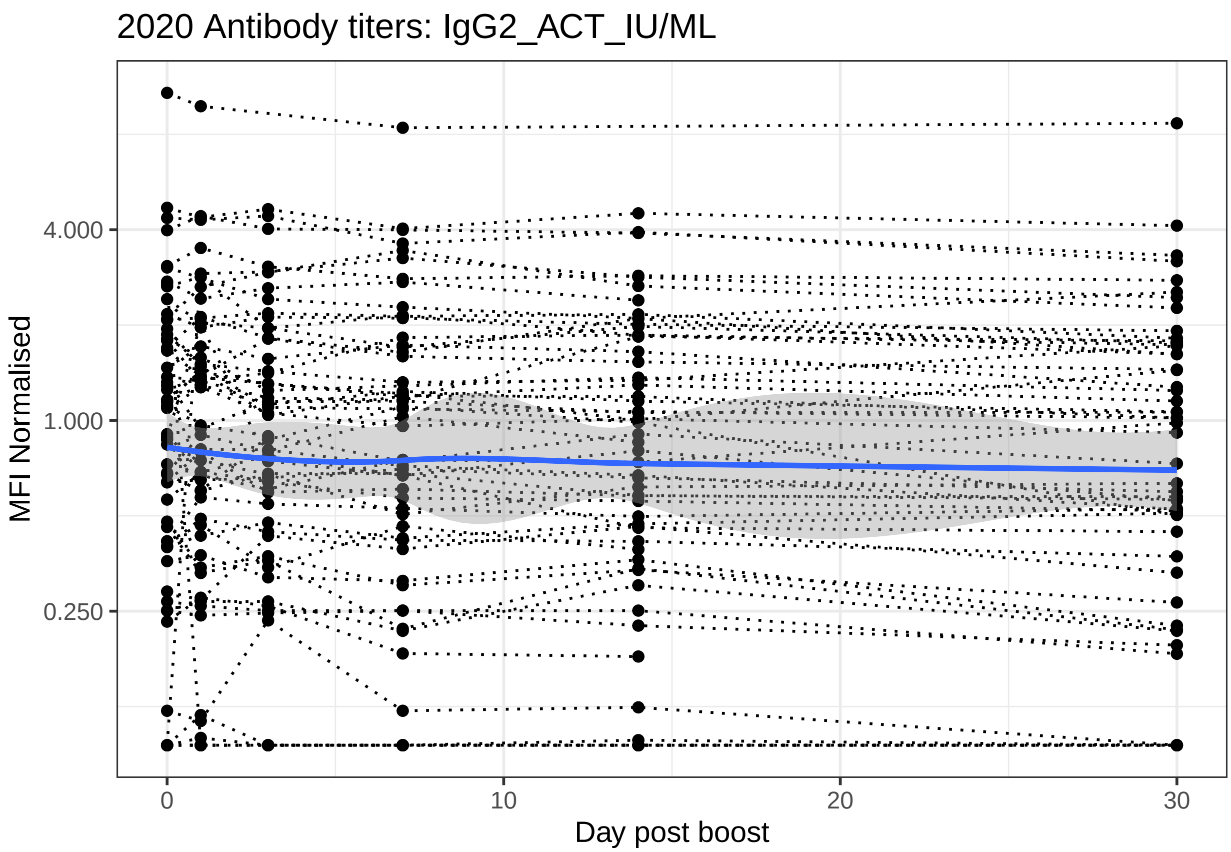
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



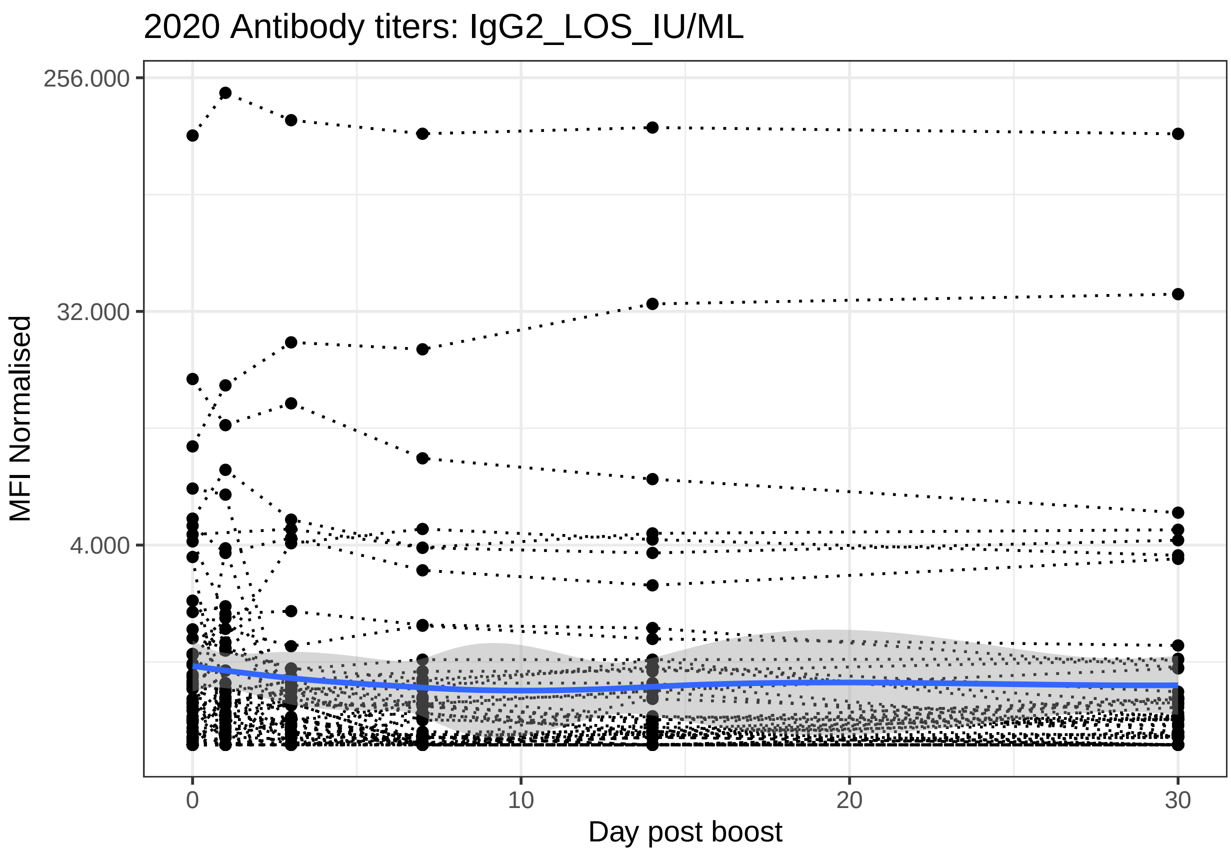
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



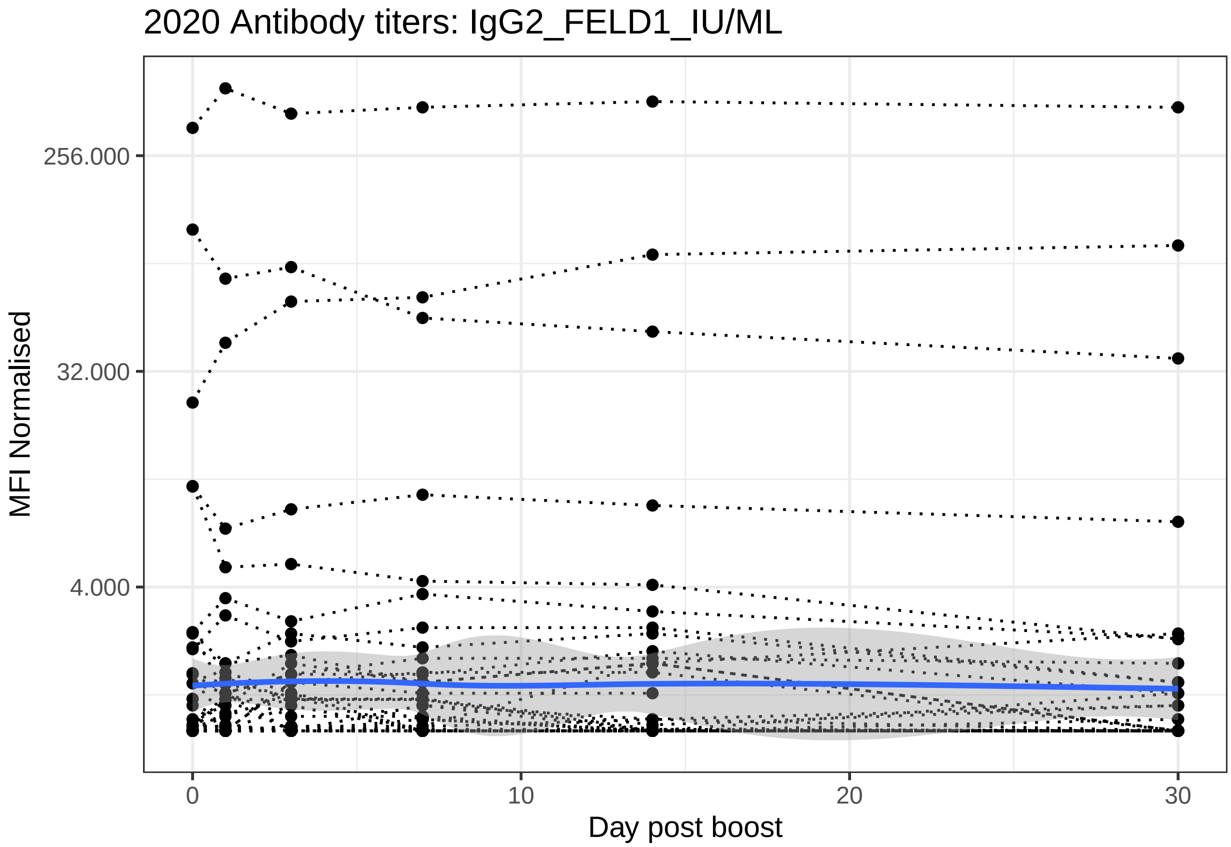
```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



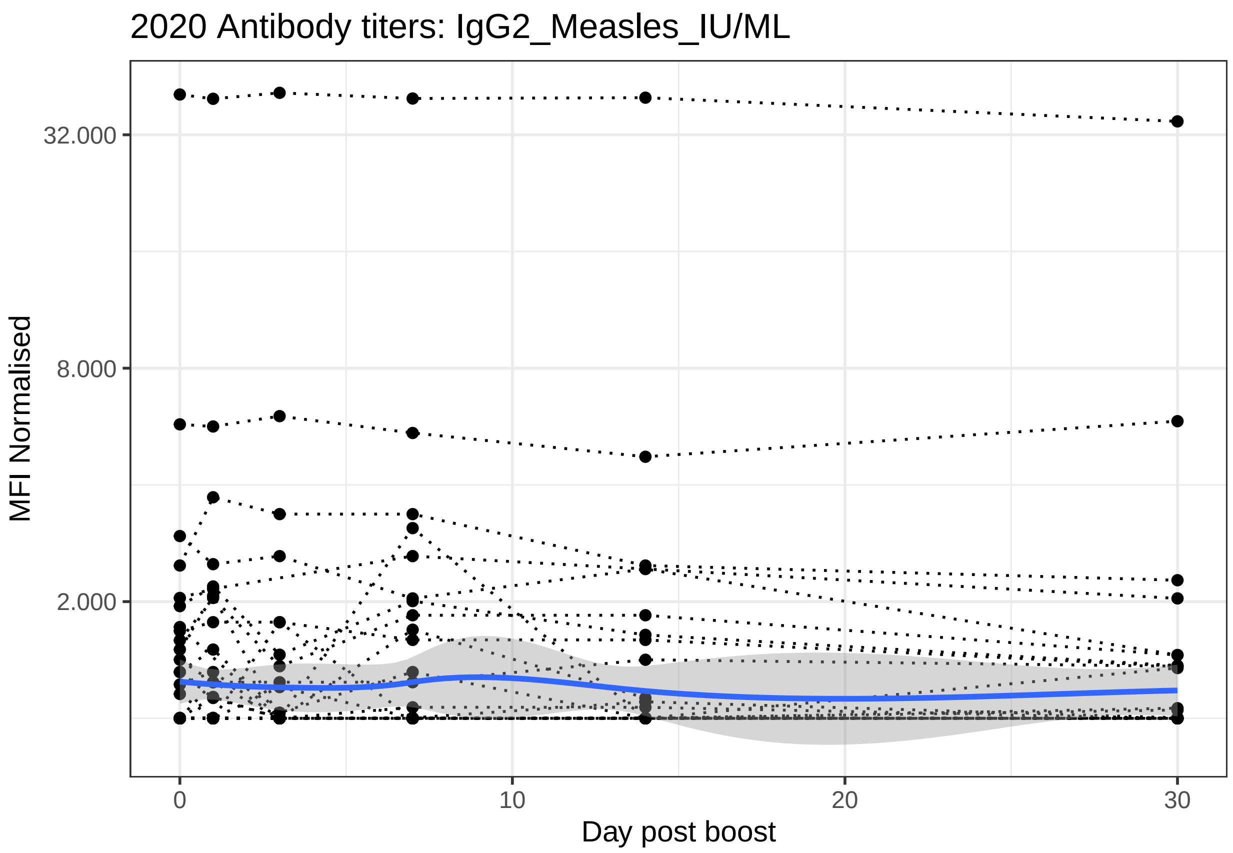
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



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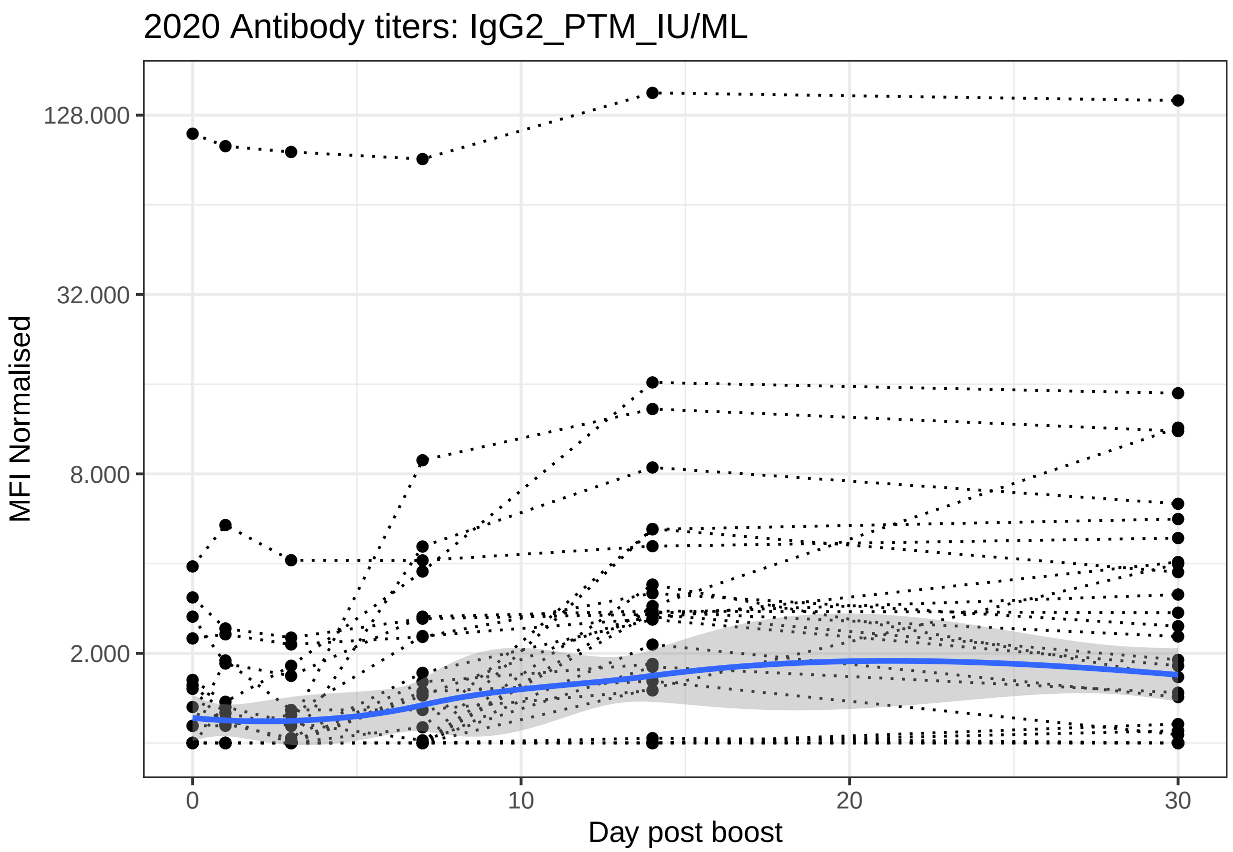

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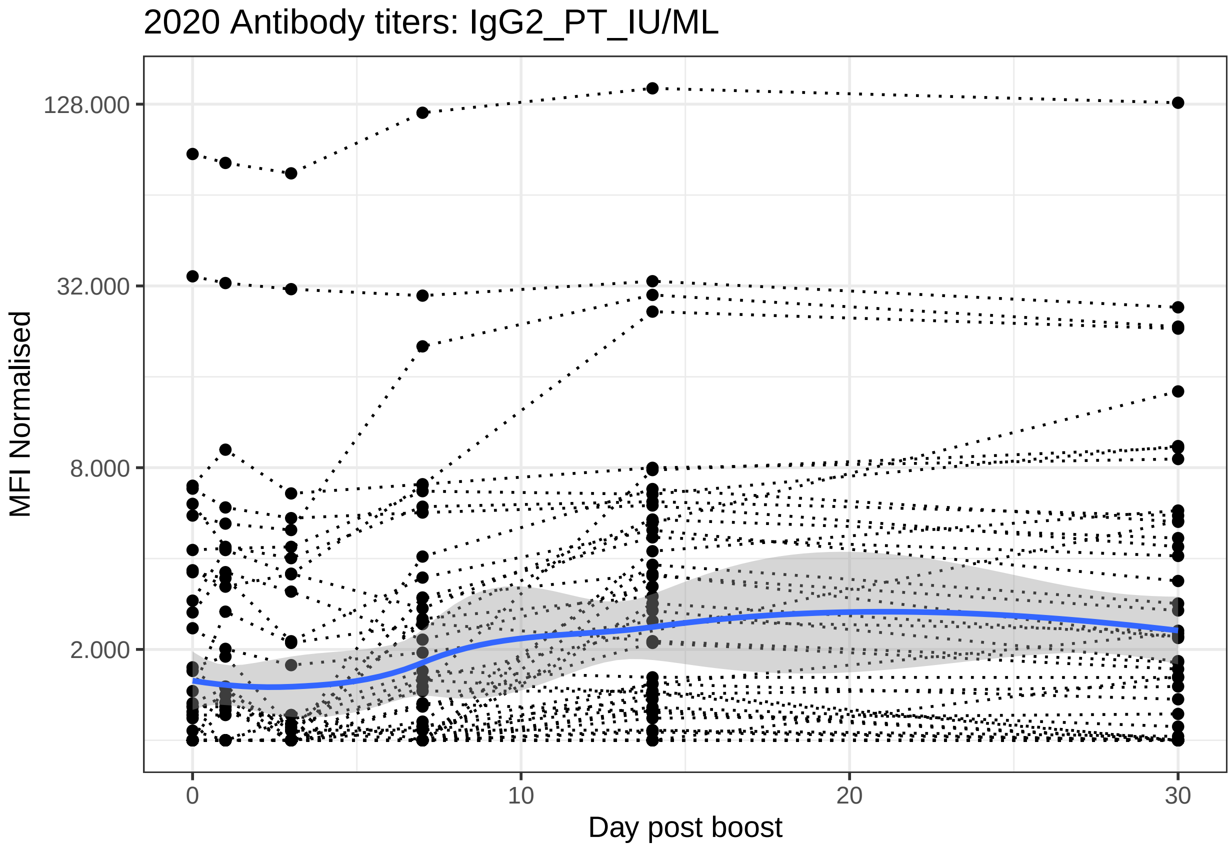

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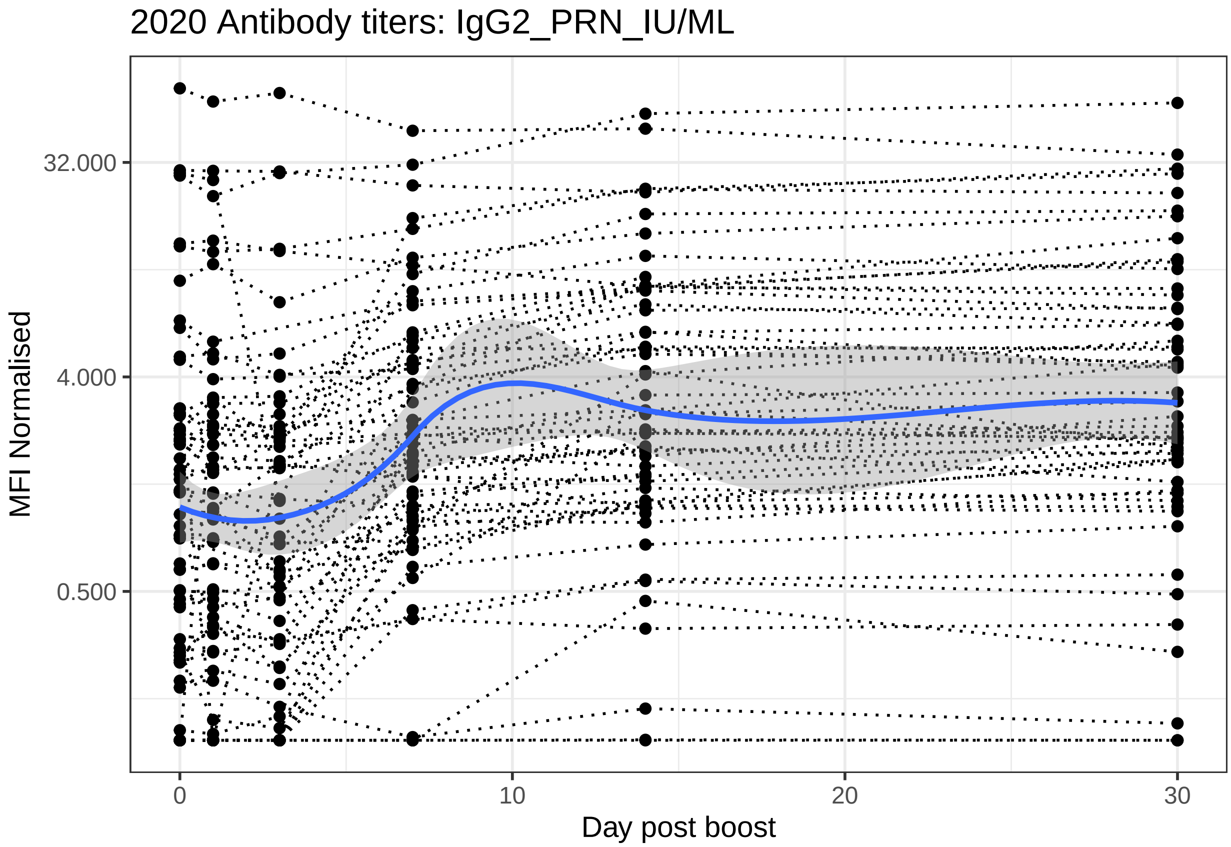

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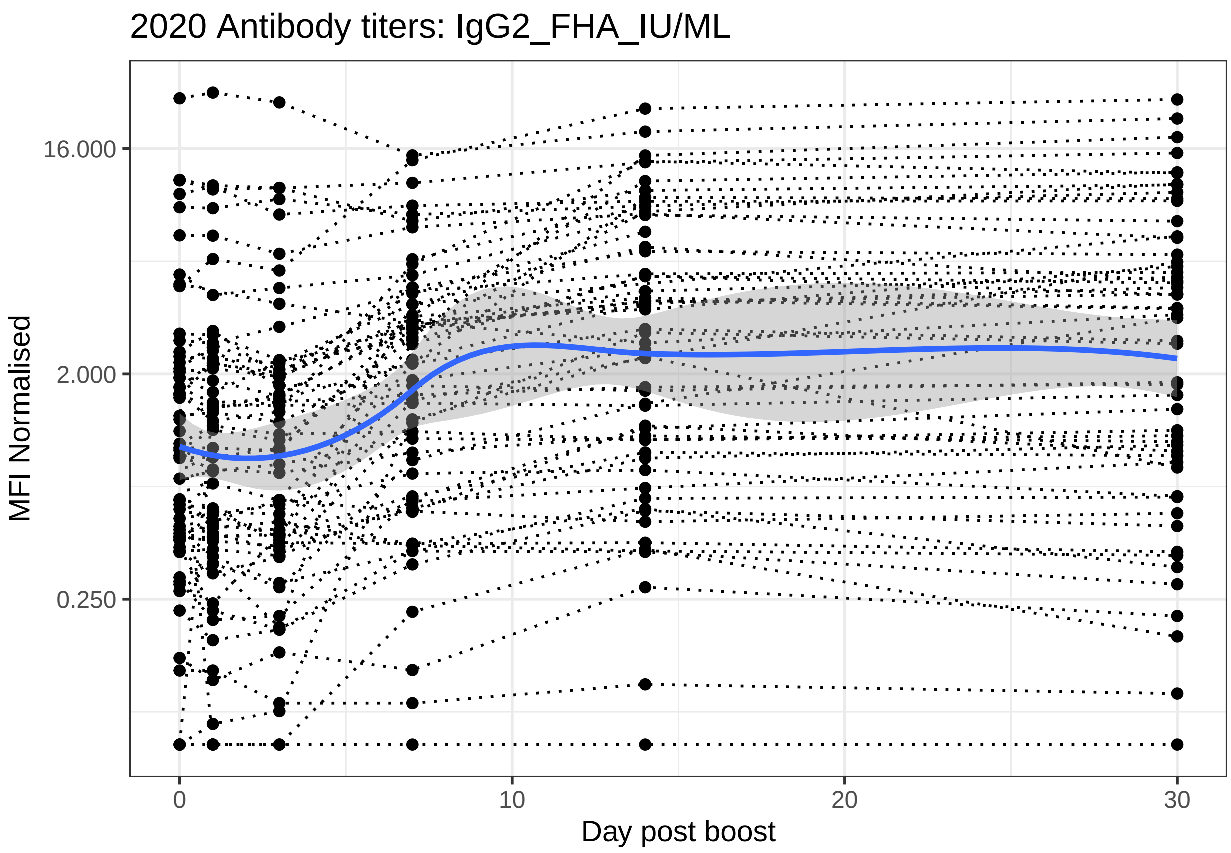

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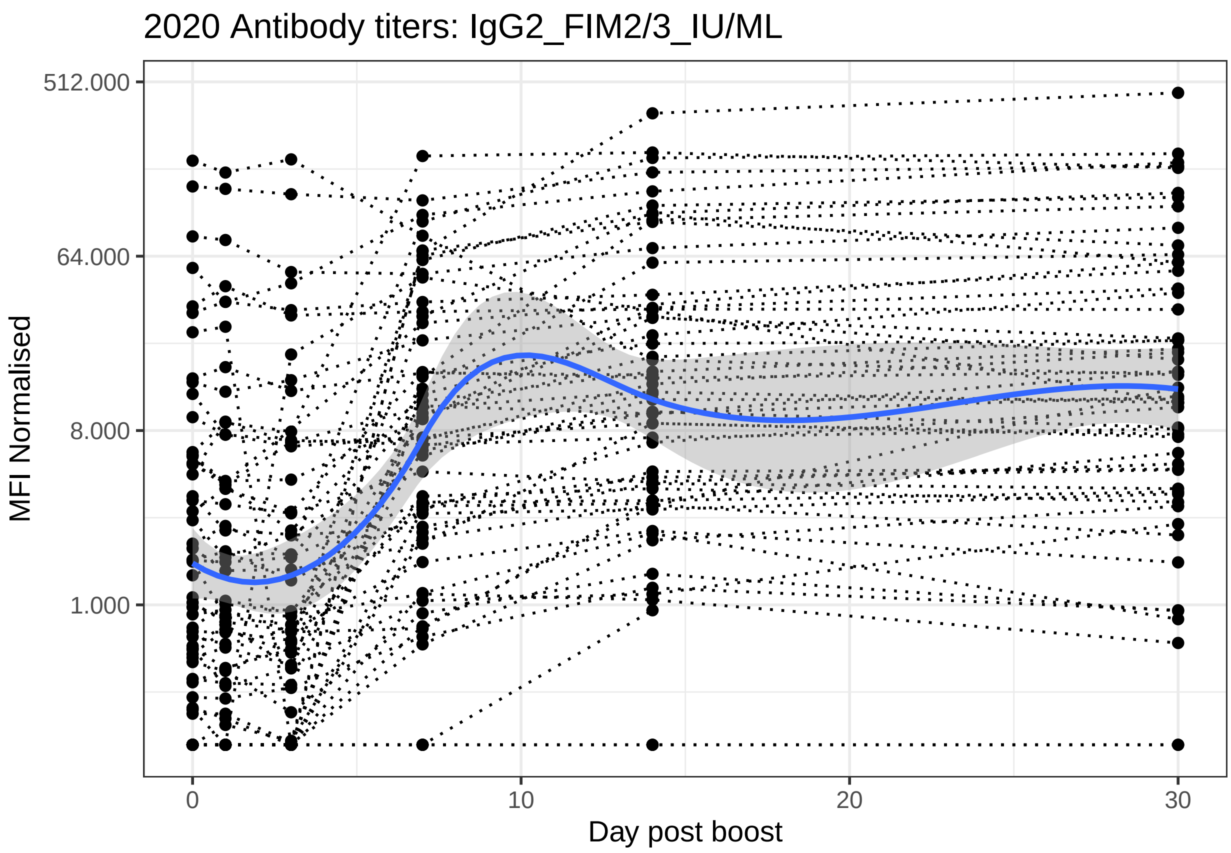

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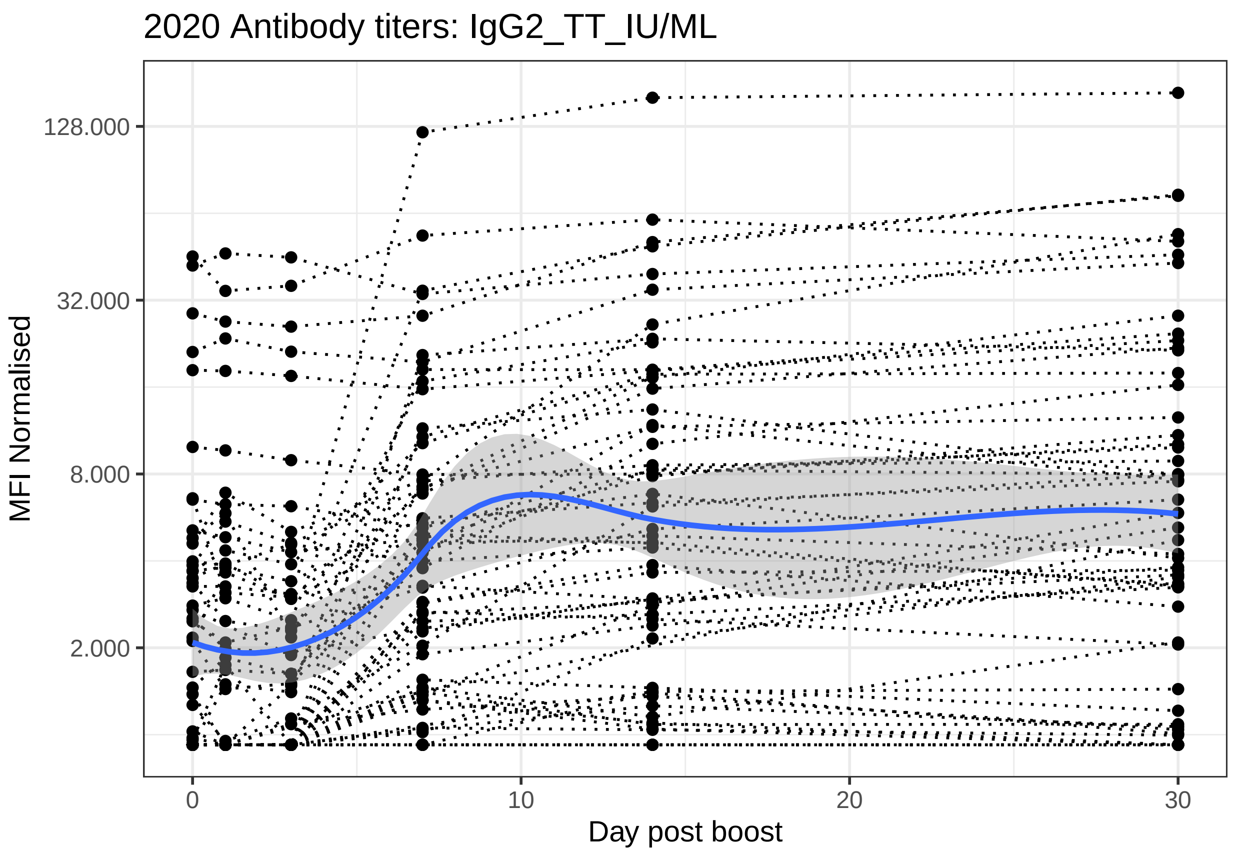

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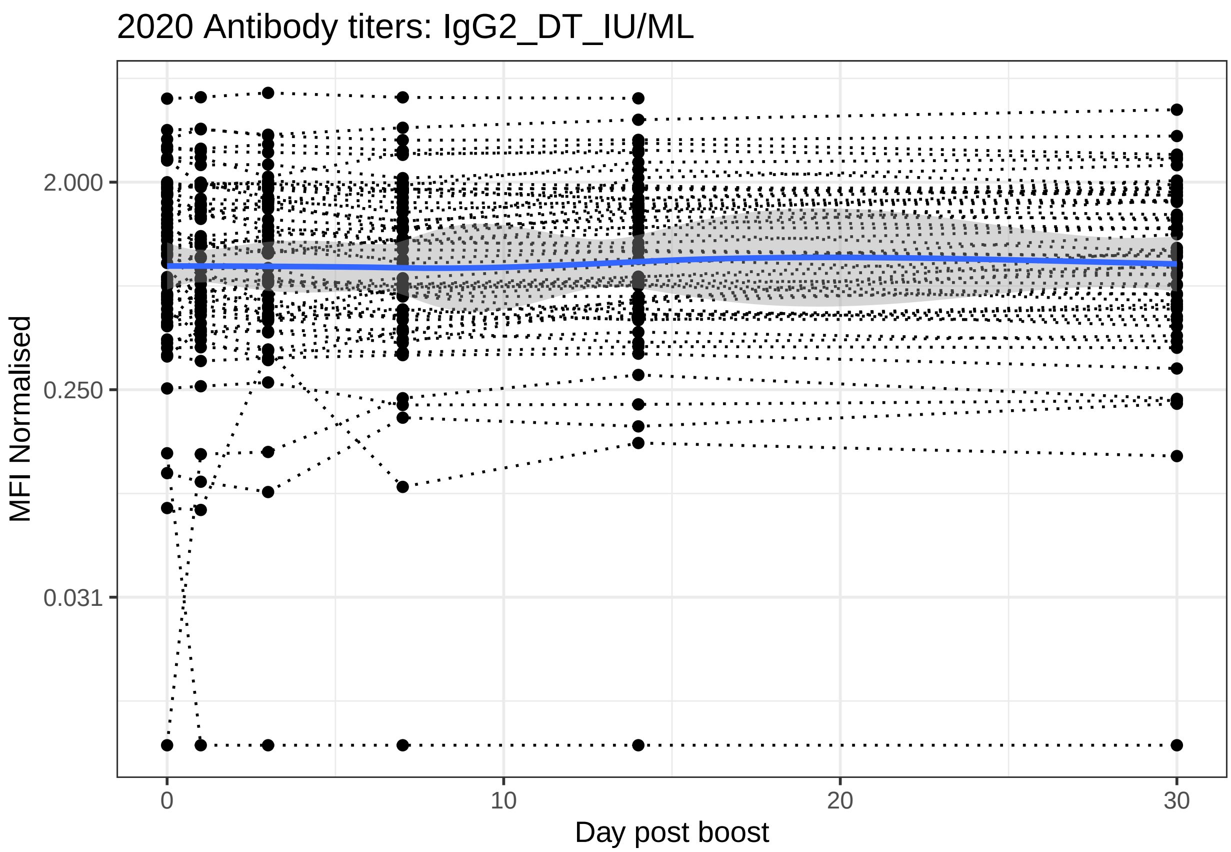

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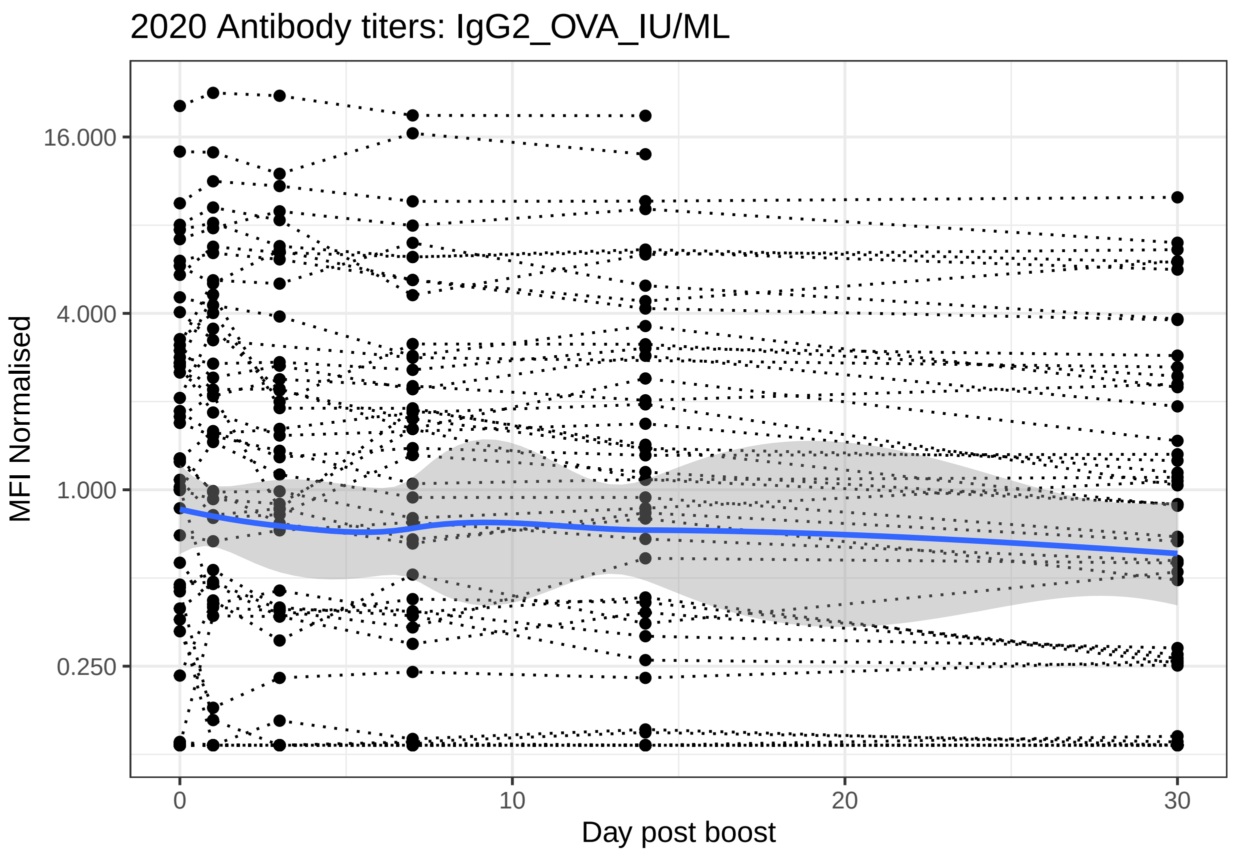

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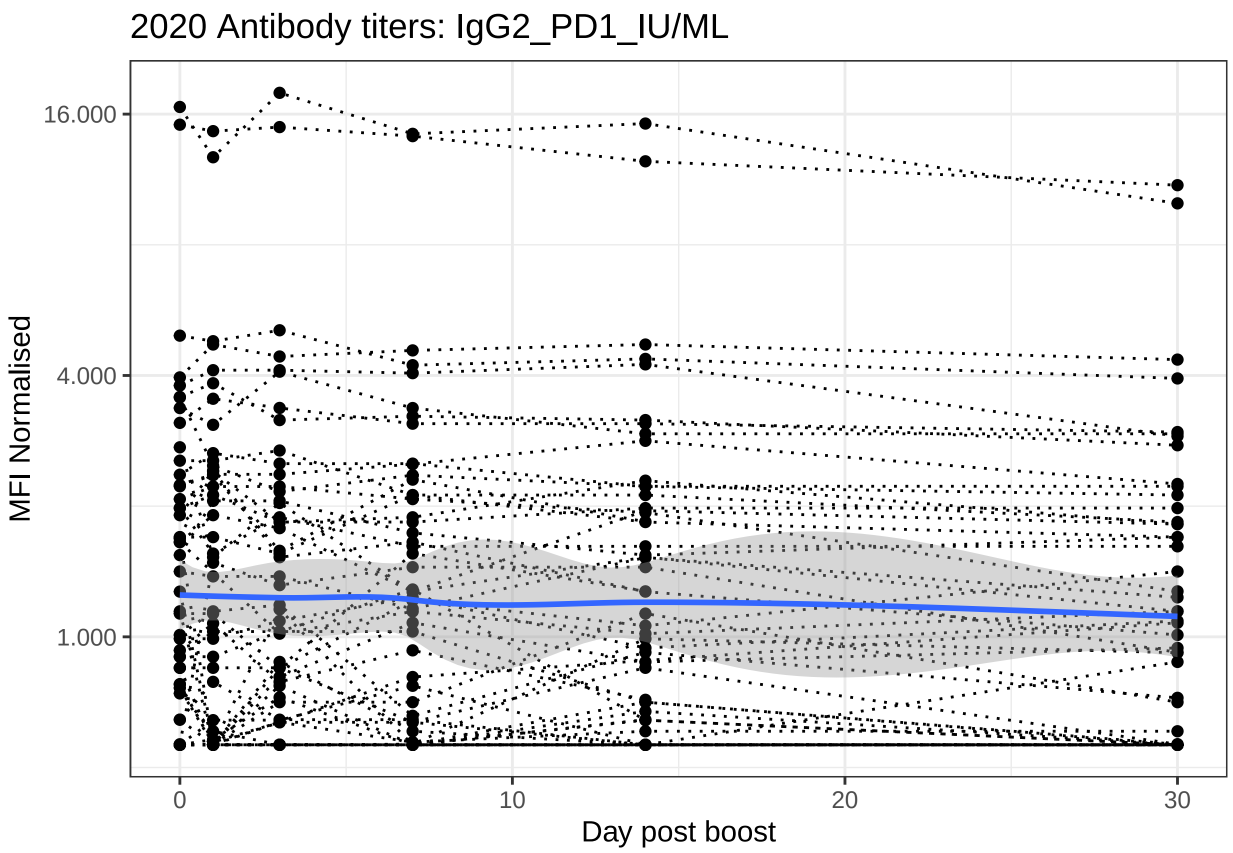

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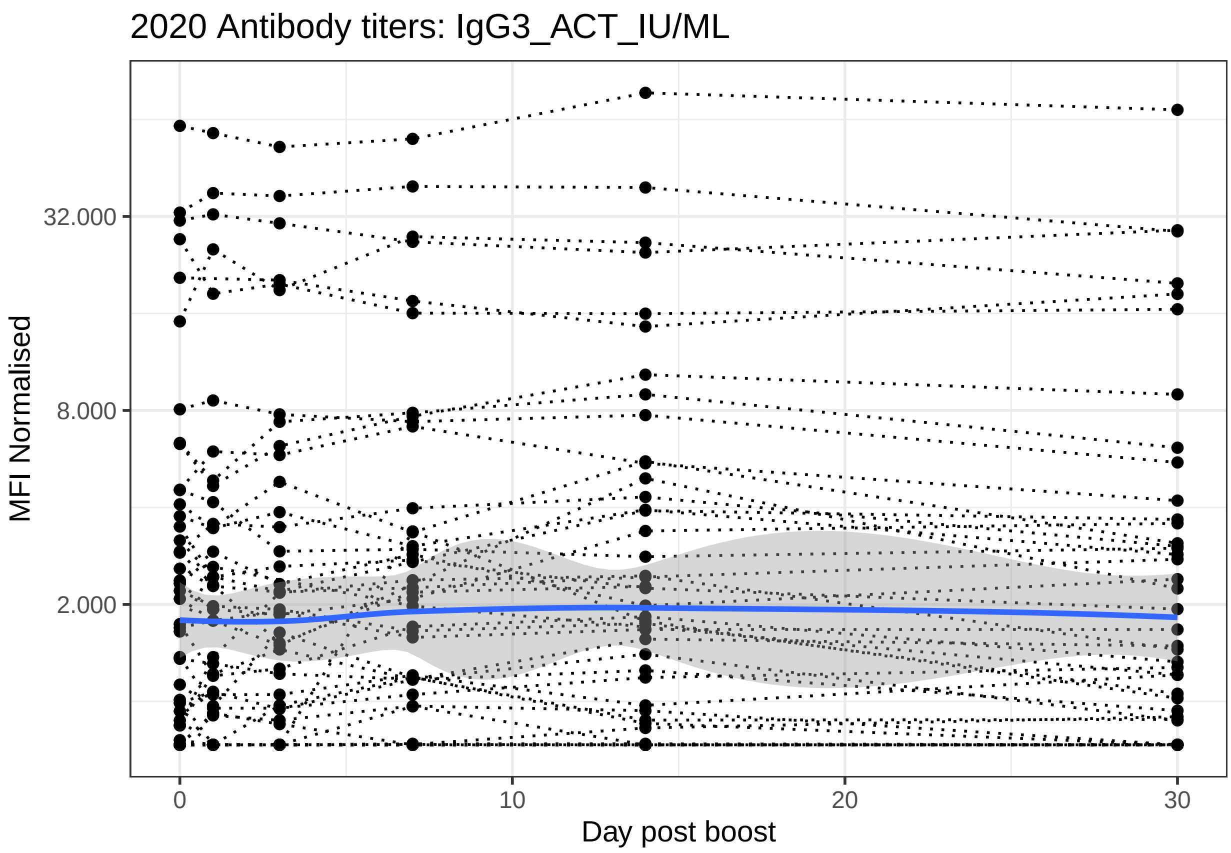

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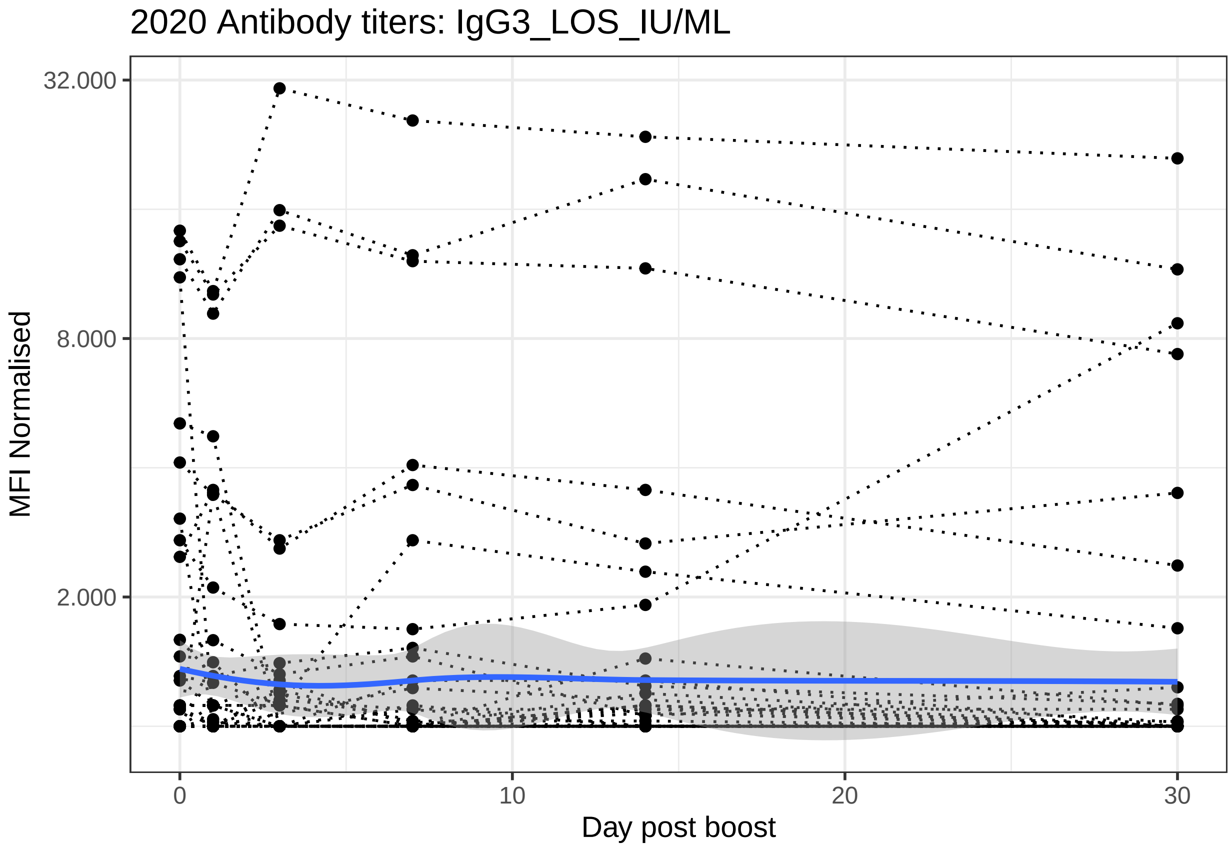

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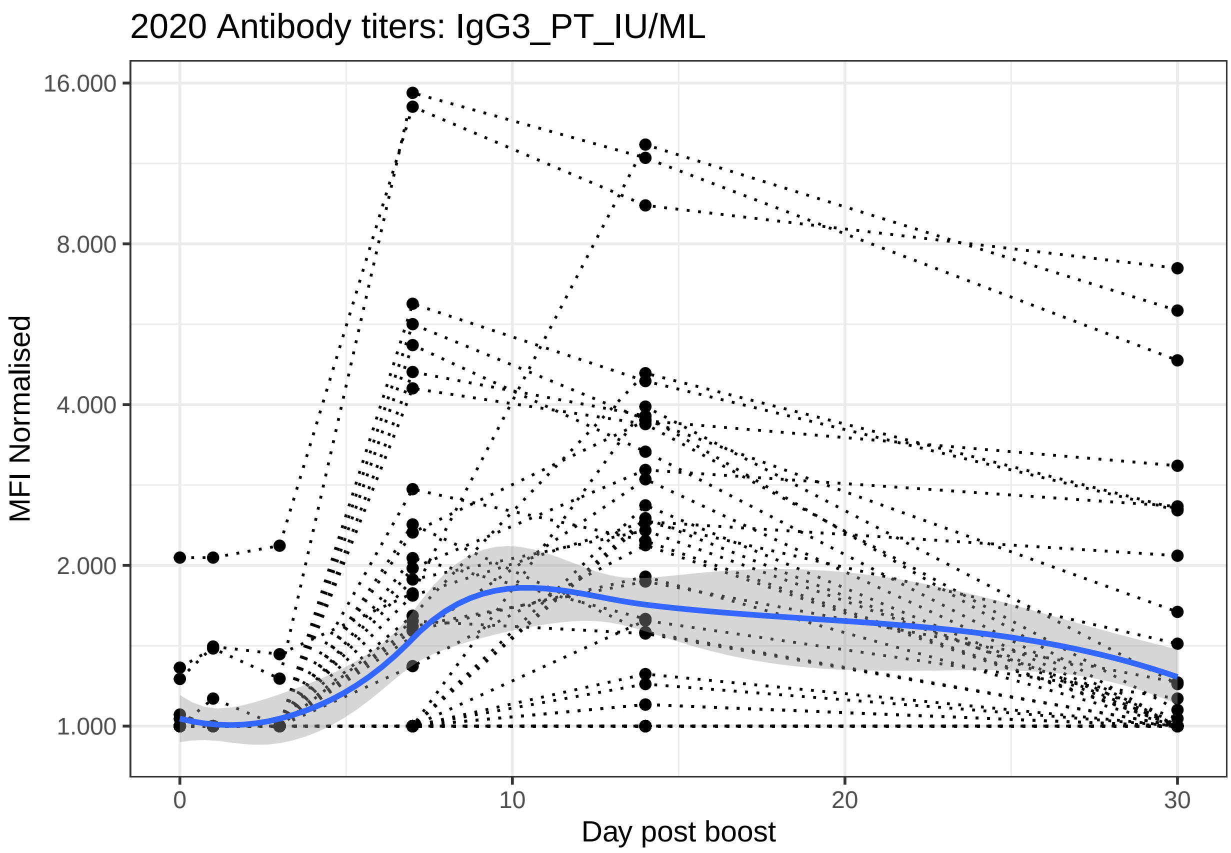

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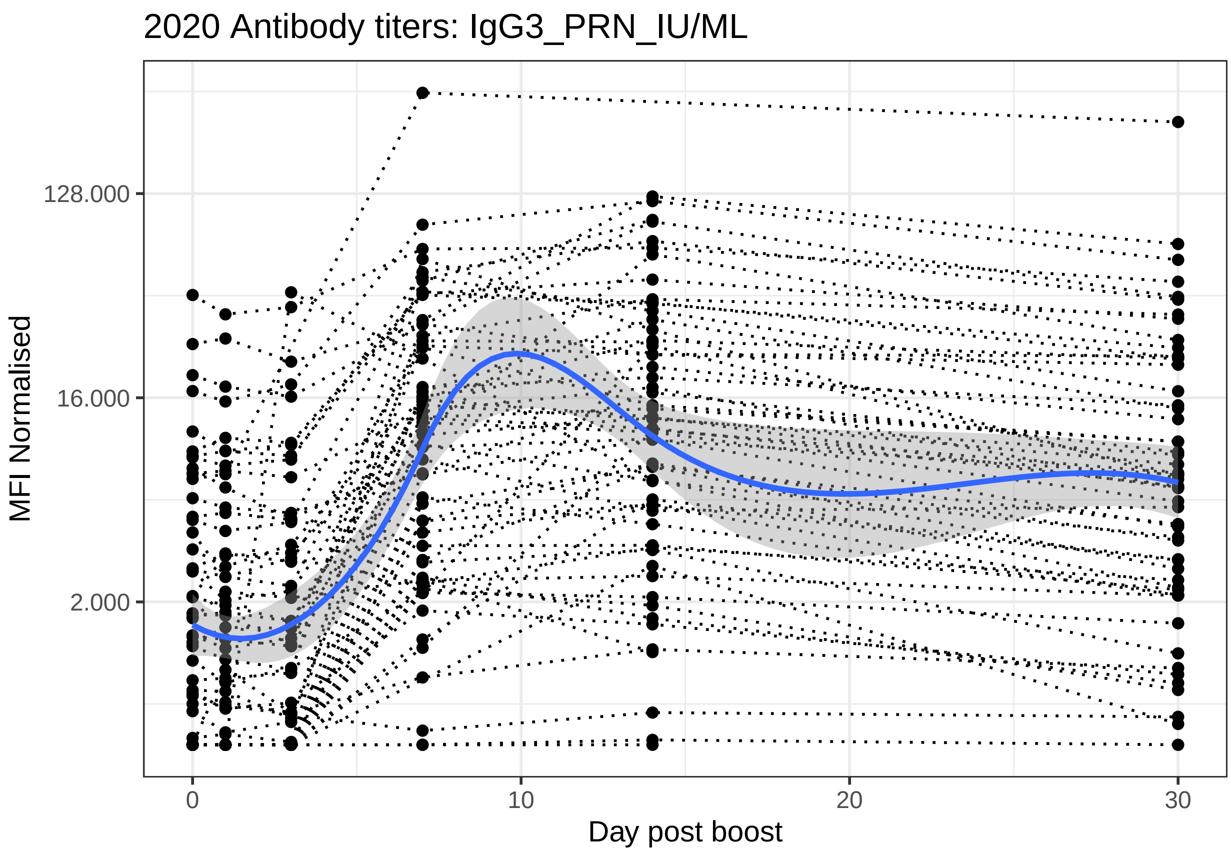

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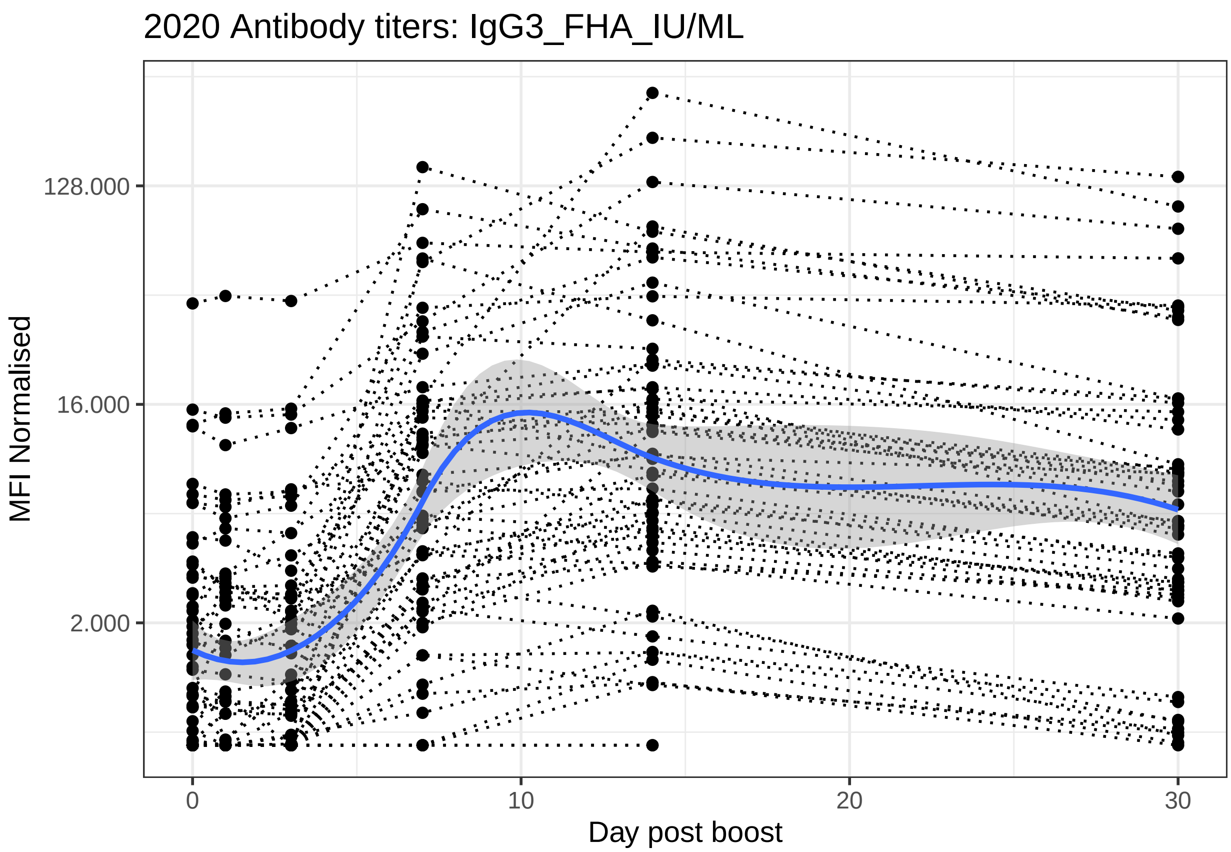

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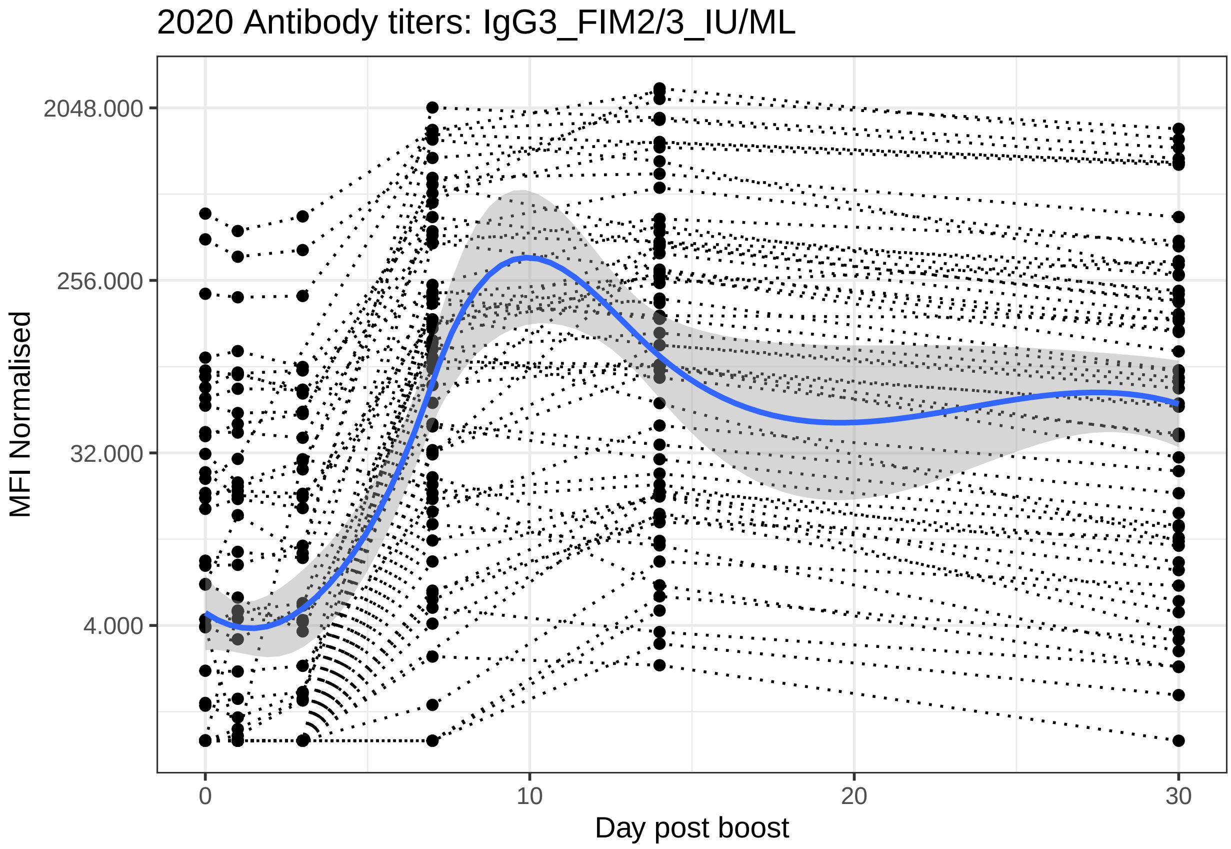

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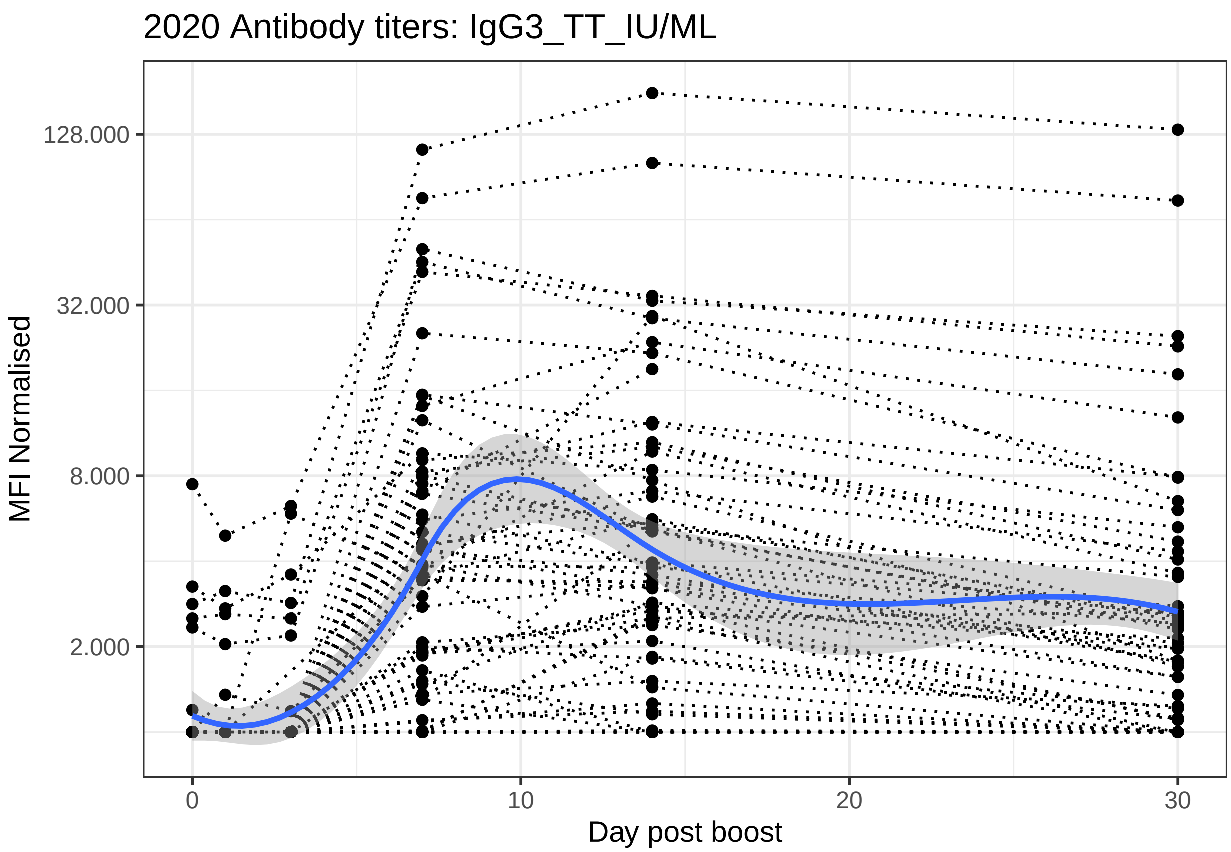

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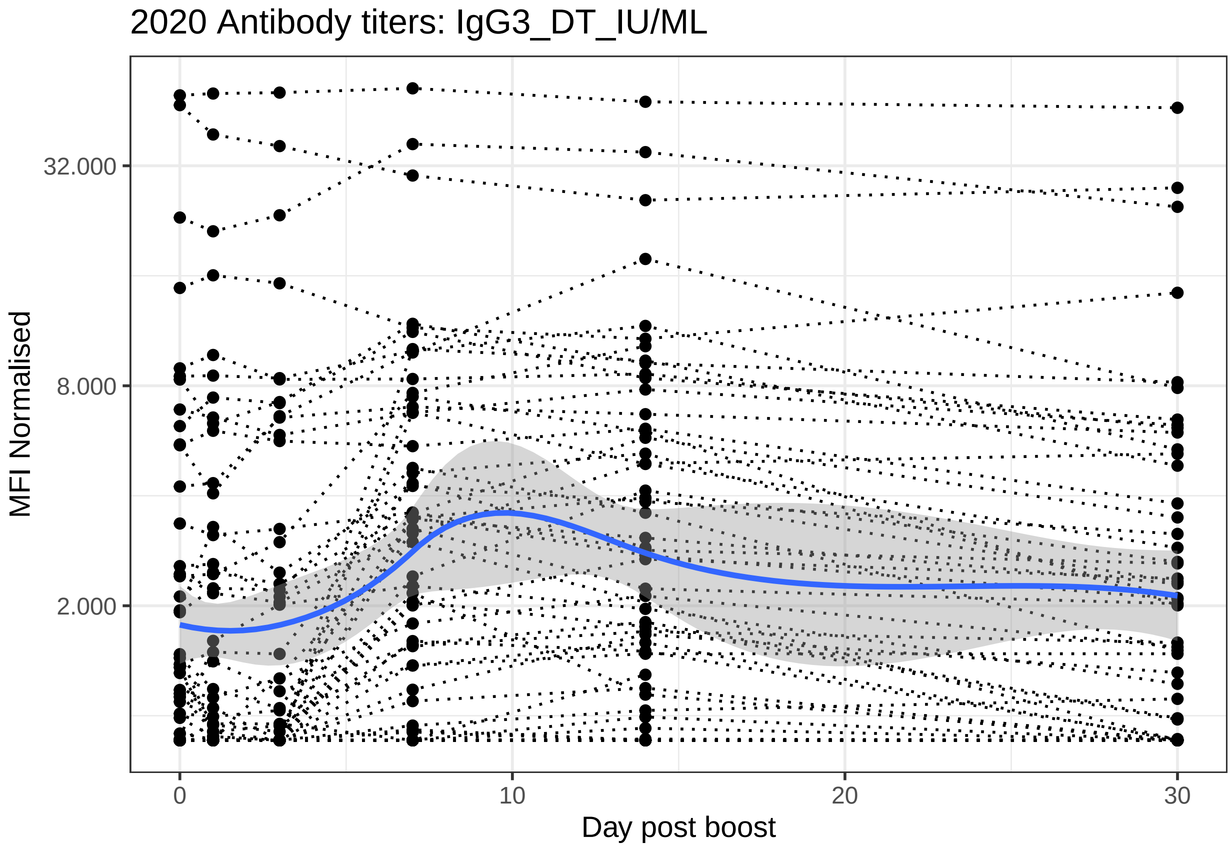

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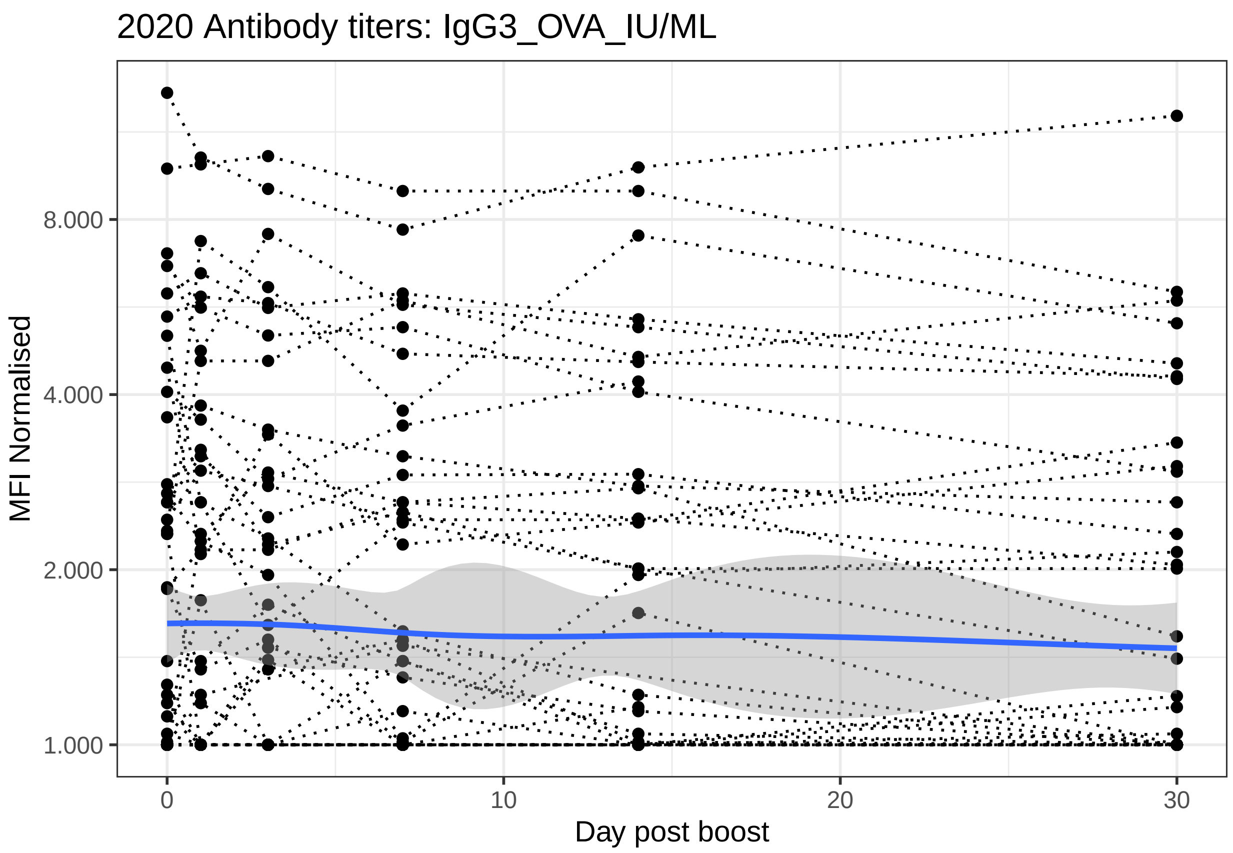

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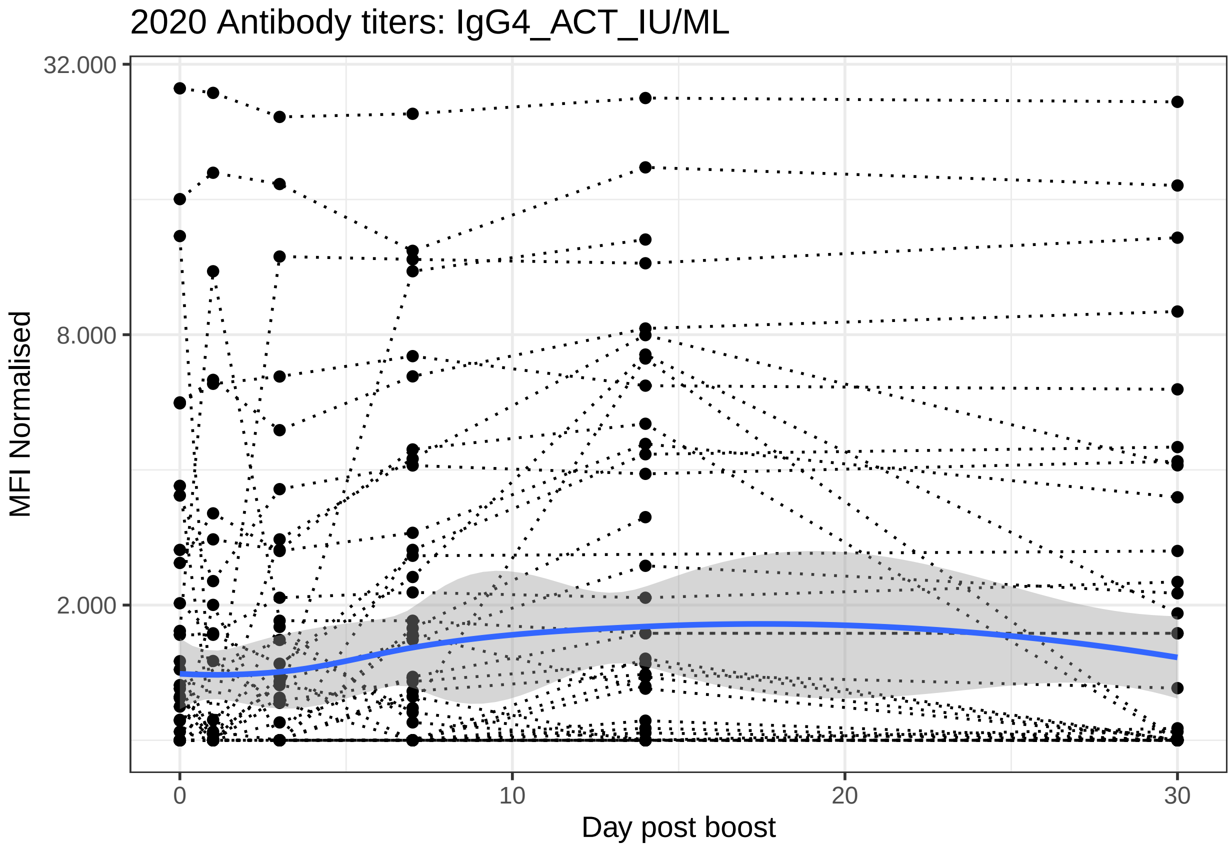

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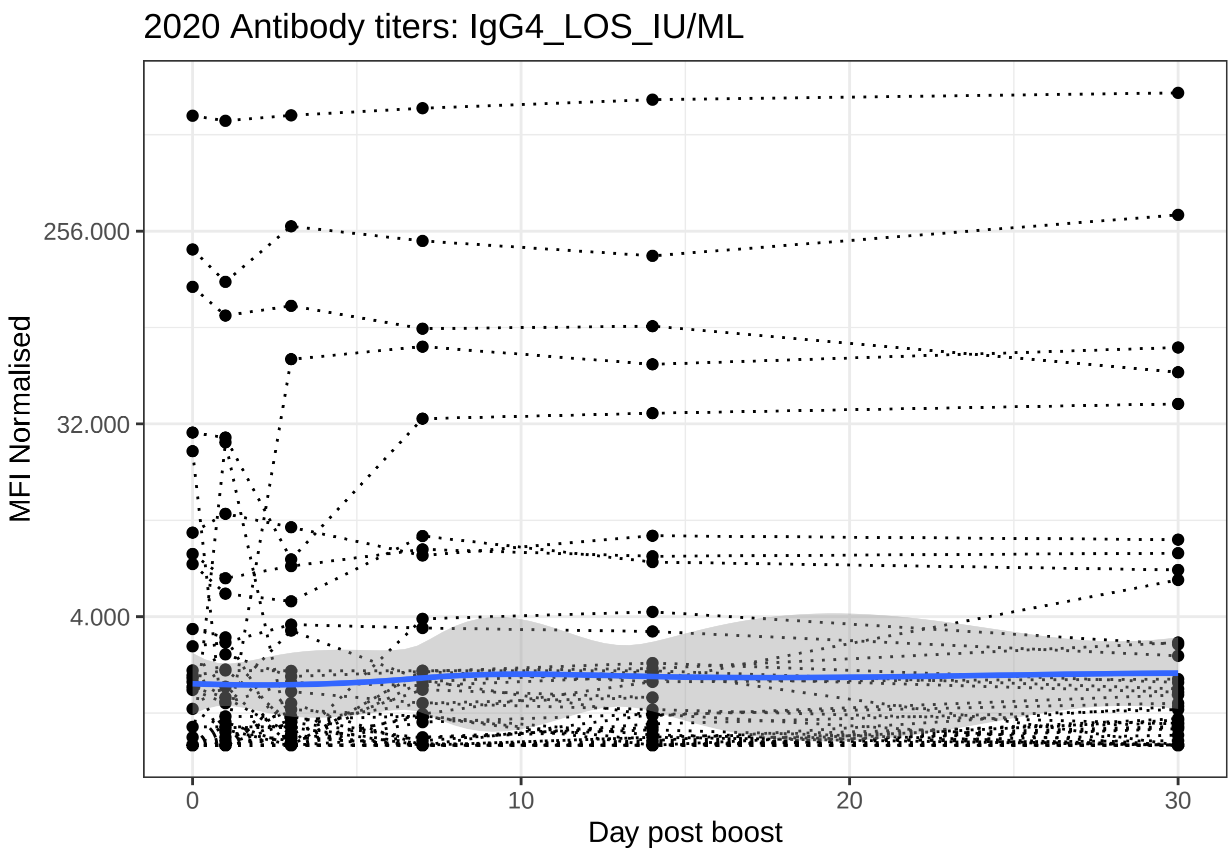

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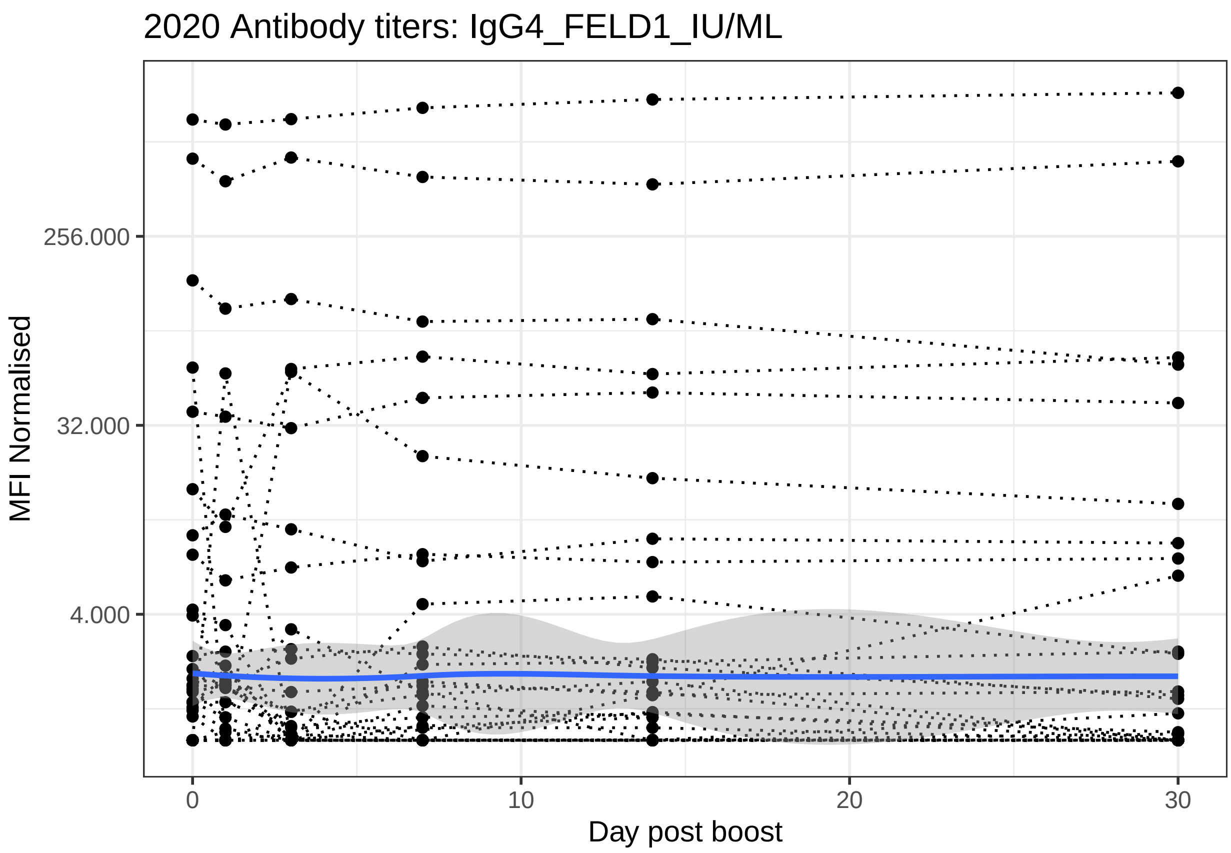

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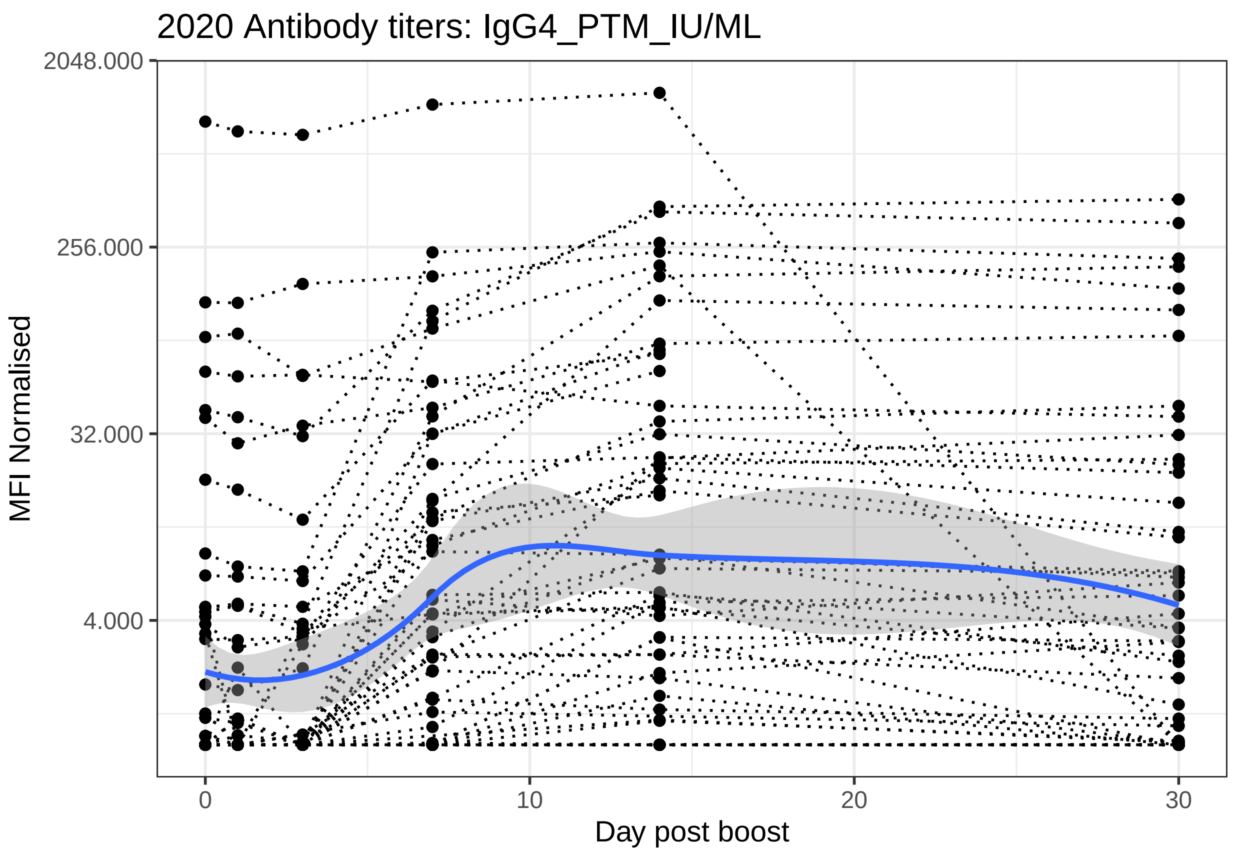

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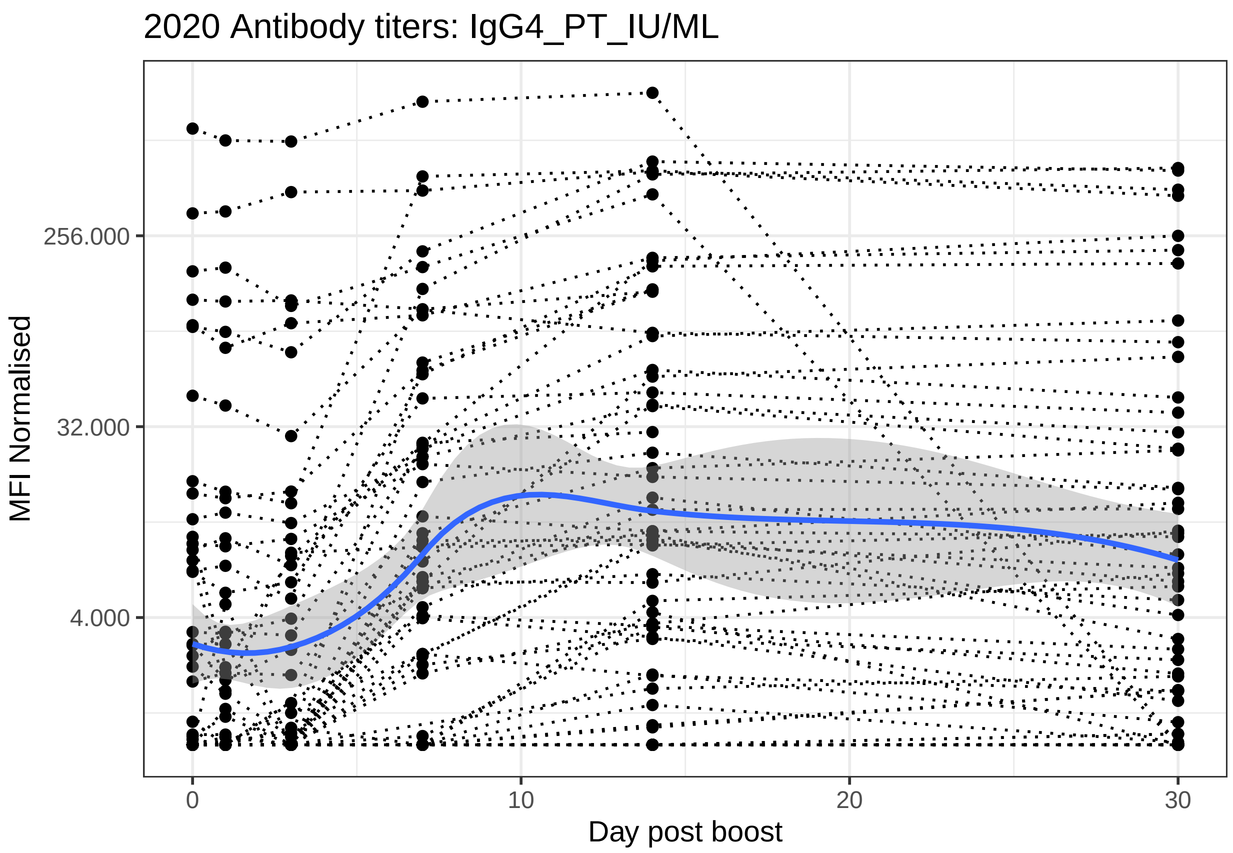

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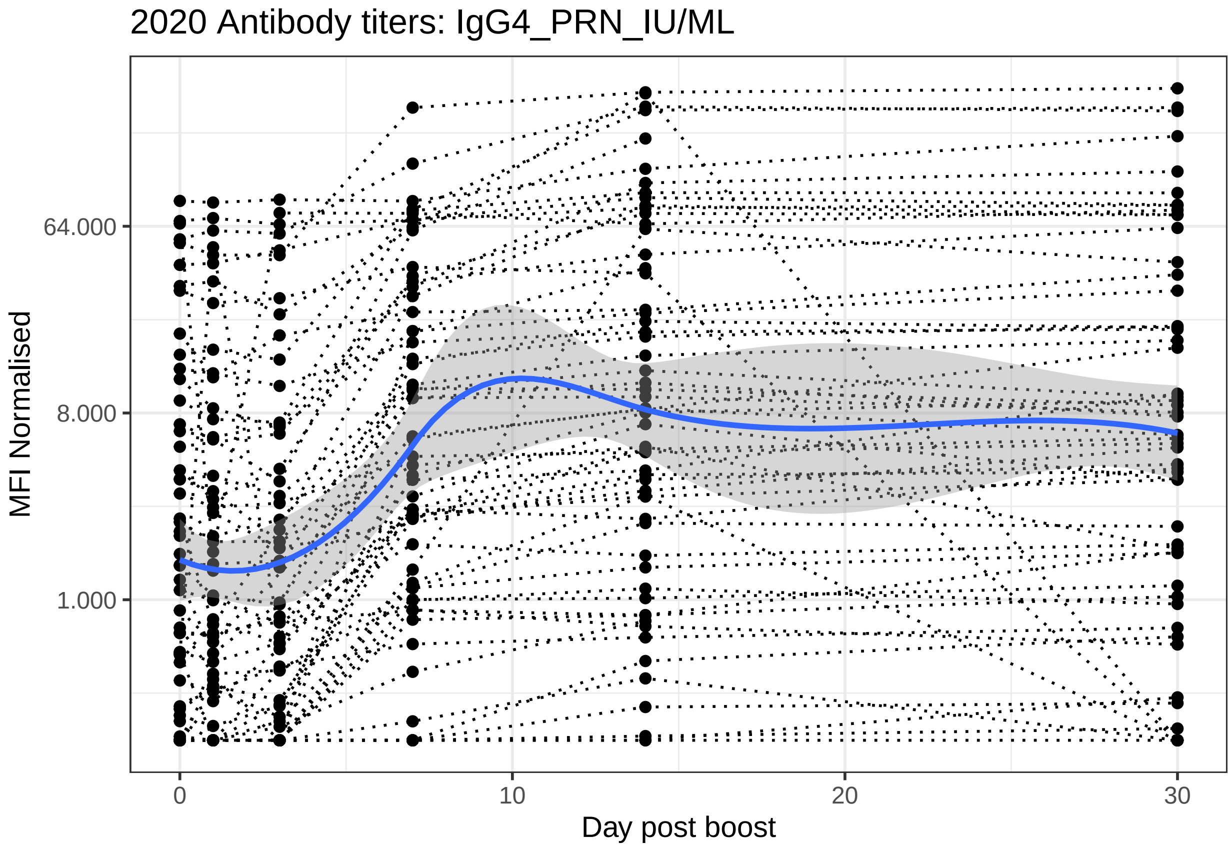

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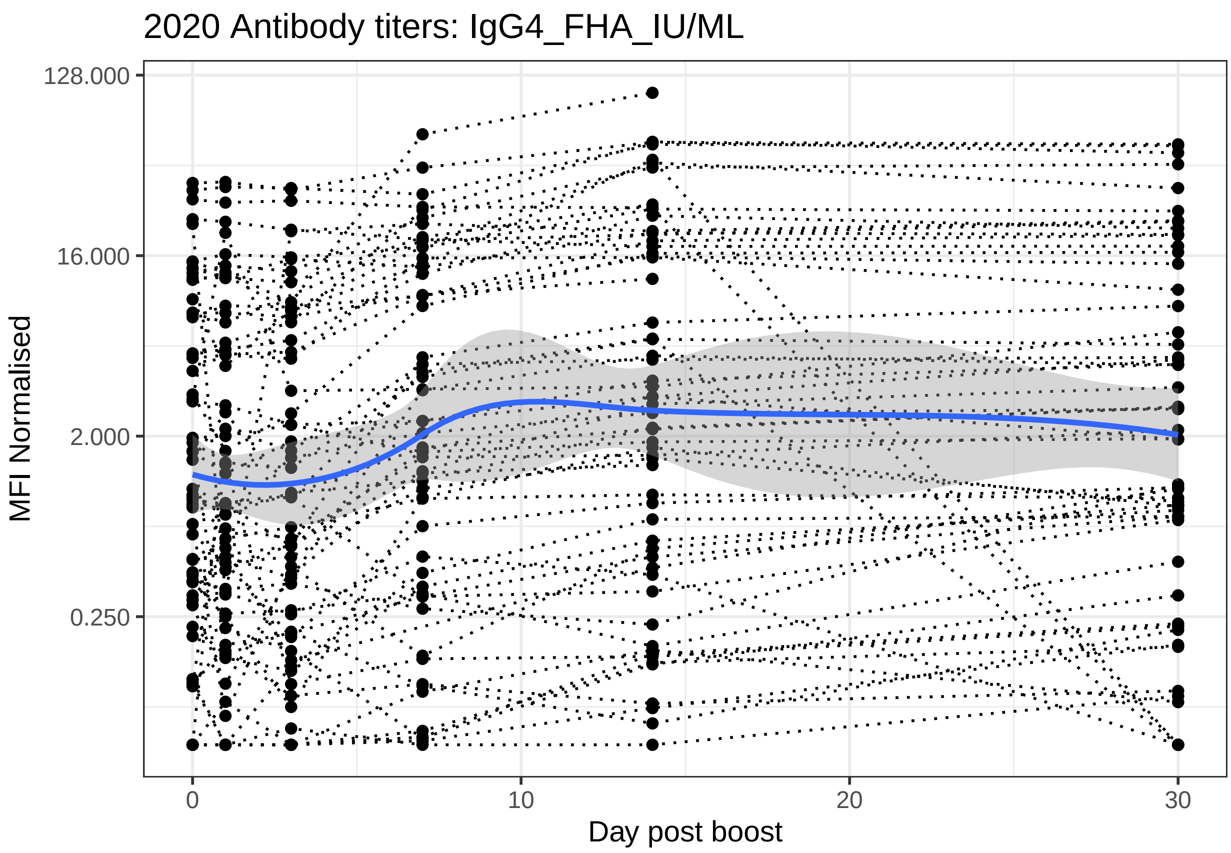

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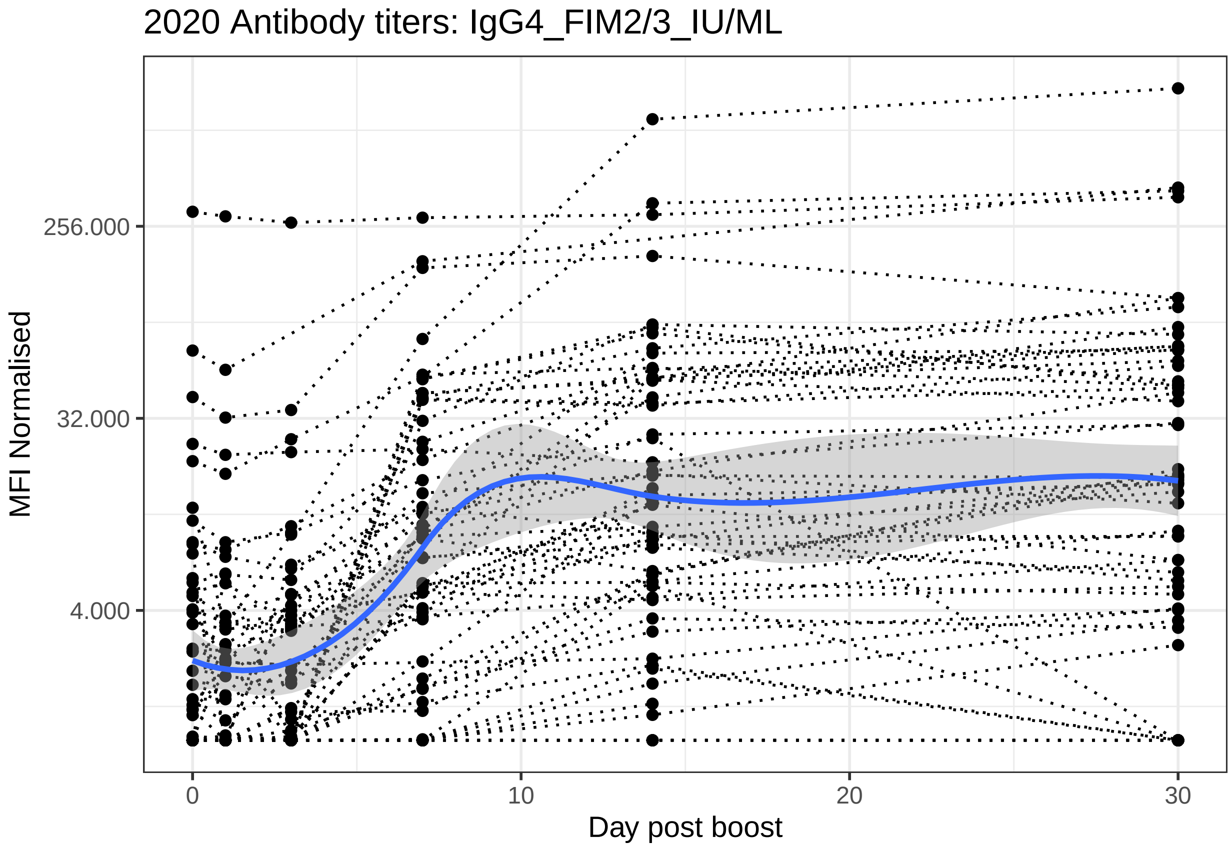

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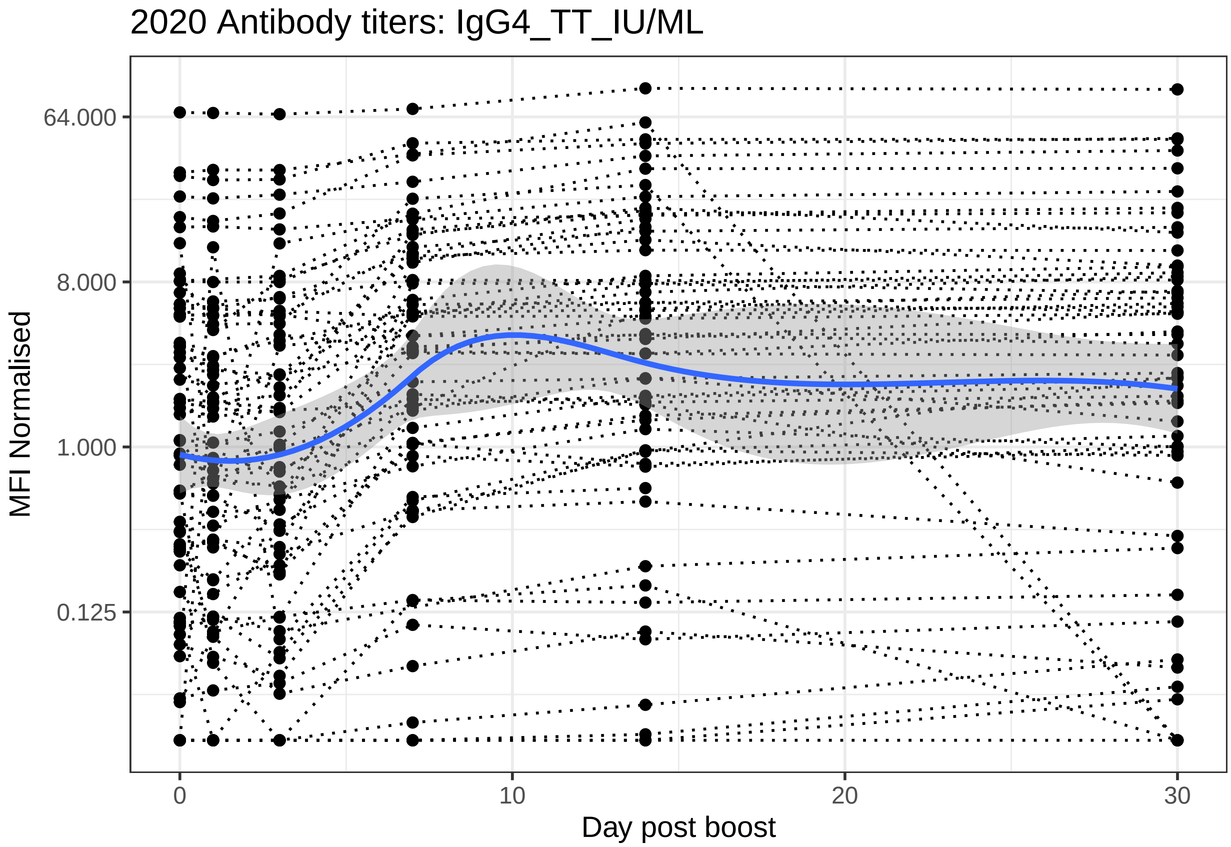

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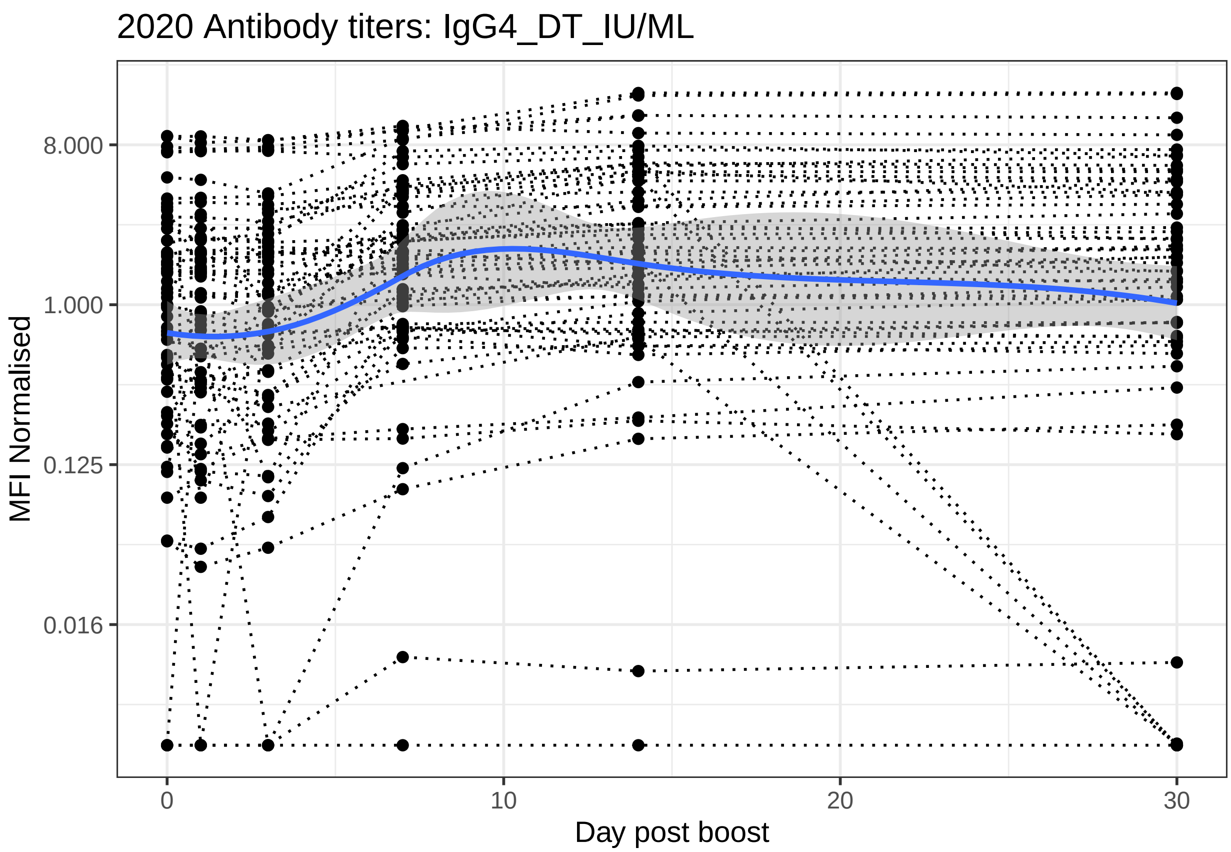

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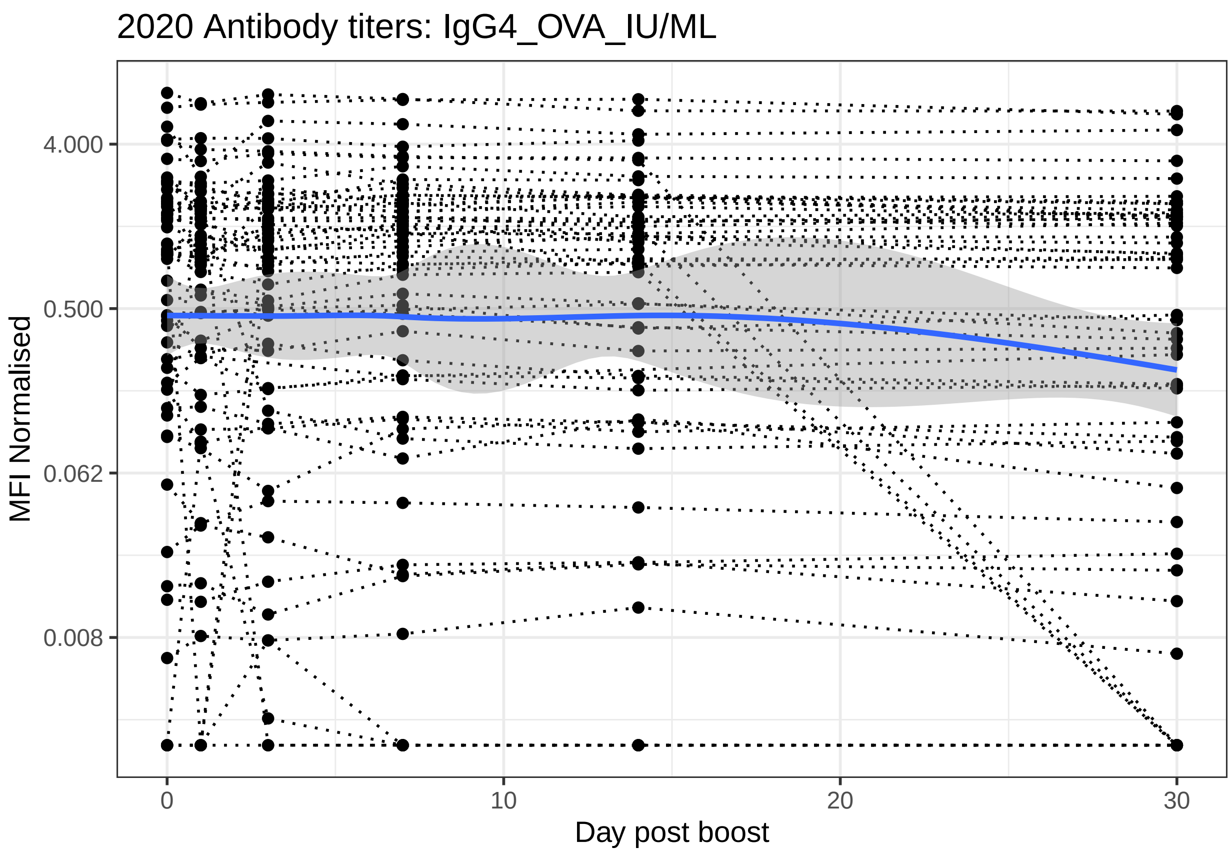

### Output/final dataframe for database porpose

```
titers_2020_new <- titers_2020_new_raw %>%
  mutate(ab_titer_normalised = MFI_normalized,
         ab_titer = ab_titer_original) %>%
  select(specimen_id, isotype, antigen, unit, is_antigen_specific, ab_titer, ab_titer_normalised, lower_

write.csv(titers_2020_new,"titers_2020_new.csv")
```

“‘