Zika Summary = 1102, 9

```
head(data)
## # A tibble: 6 x 9
##
   date genbank strain
                               genotype host country
                                                              len species check
     <chr>
            <chr>
                     <chr>
                               <chr>
                                        <chr> <chr>
                                                               <chr> <chr> <lgl>
## 1 2014-01 KX447511 1_0015_PF Asian
                                        Human French_Polynesia 10585 Zika_v~ FALSE
## 2 2014-01 KX447520 1_0016_PF Asian
                                        Human French_Polynesia 9725 Zika_v~ FALSE
## 3 2013-11 KX447515 1_0030_PF Asian
                                        Human French_Polynesia 10588 Zika_v~ FALSE
## 4 2014-01 KX447514 1_0035_PF Asian
                                        Human French_Polynesia 10588 Zika_v~ FALSE
## 5 2014-01 KX447517 1_0038_PF Asian
                                        Human French_Polynesia 10654 Zika_v~ FALSE
## 6 2013-12 KX447510 1_0049_PF Asian
                                        Human French_Polynesia 10588 Zika_v~ FALSE
unique(data$genotype)
## [1] "Asian"
                     NA
                                    "West_African" "East_African"
data %>%
 group_by(genotype) %>%
  summarize(n=n())
## # A tibble: 4 x 2
##
   genotype
##
                 <int>
    <chr>
## 1 Asian
                  1066
## 2 East_African
                     2
## 3 West_African
                     2
## 4 <NA>
```

- Genbank Counts:
- genotype asian counts:

```
data %>%
  group_by(host) %>%
  summarize(n=n()) %>%
  knitr::kable(., booktabs=T)
```

```
host n

Anopheles_sinensis 1
Culex_pipiens_quinquefasciatus 1
Howler_Monkey 1
Human 1037
Monkey 5

Mosquito 51
Unknown 6
```

```
data %>%
  group_by(country) %>%
  summarize(n=n()) %>%
  head(.) %>%
  knitr::kable(., booktabs=T)
```

```
Angola 2
Argentina 1
Australia 1
Brazil 243
Cambodia 2
Canada 6
```

1 Flagged Entries

fdata <- data %>% subset(check==TRUE)
fdata %>% knitr::kable(., booktabs=T)

date	genbank	strain
2015-03-01,2015-03	MF073359,MK566202	15098
2015	KU527068,NC_035889	Natal_RGN
2015-05-13,2017-06-29	MF352141,MT078742	PE243
2013-10-25	KX369547,MG827392	PF13/251013-18
2017	$\rm MT507047, MT507048, MT507049, MT507050$	S-542/Yucatan/2017
2016	KU963796,MH055376	SZ-WIV01
2015-12-11	KX156775,MN100039,MN124090,MN124091	ZIKV/Homo_sapiens/PAN/CDC-259249_V1-V3/20
2015-12-01,2015-12,2015	KU501215,KX087101,KX601168,MH158237,MK028857,MK713748	ZIKV/Homo_sapiens/PRI/PRVABC59/2015
2016-02,2016-02-17	KU761560,KU820899	ZJ03