

## 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      n
##   <chr>      <int>
## 1 Asian      1066
## 2 East_African    2
## 3 West_African    2
## 4 <NA>          32
```

- 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)
```

country	n
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
2015-03-01,2015-03-2015	MF073359,MK566202	15098
	KU527068,NC_035889	Natal_RGN
2015-05-13,2017-06-29	MF352141,MT078742	PE243
2013-10-25	KX369547,MG827392	PF13/251013-18
2017	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-V3/2015
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

## 2 genotypes

Placeholder for later

```
data %>%
  mutate(
    year=substr(date, 0,4)
  ) %>%
  subset(!is.na(year)) %>%
  ggplot(., aes(x=year, fill=genotype)) +
  geom_bar() +
  theme_bw() +
  theme(axis.text.x = element_text(angle=45, hjust=1))+
  labs(title="genotypes")
```

