```{r}

#histogram of all AA\_C values

ggplot(data=headscan\_full, aes(x=AA\_C))+

geom\_bar(stat="bin", bins=20, color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

labs(title="Alare to Alare Contour Measurement Distribution",

y="Frequency",

x="Alare to Alare Contour (cm)")

```

mdn = median(AA\_C, na.rm = TRUE),

#boxplot reorderd by median

headscan\_full %>%

ungroup() %>%

mutate(gender= fct\_reorder(gender, AA\_C, FUN=median, na.rm=TRUE)) %>%

ggplot(aes(y=AA\_C, x=gender))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="AA\_C values by Gender",

y="Measurement (cm)",

x="Gender")

#boxplot not reordered by median

ggplot(data=headscan\_full, aes(y=AA\_C, x=gender))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="AA\_C values by Gender",

y="Measurement (cm)",

x="Gender")

#boxplot reorderd by median

headscan\_full %>%

ungroup() %>%

mutate(race\_eth= fct\_reorder(race\_eth, SelDH\_C, FUN=median, na.rm=TRUE)) %>%

ggplot(aes(y=SelDH\_C, x=race\_eth))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

#theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Contour values by Race/Ethnicity",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Race/Ethnicity")

#boxplot not reordered by median

ggplot(data=headscan\_full, aes(y=SelDH\_C, x=race\_eth))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

#theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Contour values by Race/Ethnicity",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Race/Ethnicity")

#boxplot reorderd by median

headscan\_full %>%

ungroup() %>%

mutate(gender= fct\_reorder(gender, SelDH\_C, FUN=median, na.rm=TRUE)) %>%

ggplot(aes(y=SelDH\_C, x=gender))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Contour values by Gender",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Gender")

#boxplot not reordered by median

ggplot(data=headscan\_full, aes(y=SelDH\_C, x=gender))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Contour values by Gender",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Gender")

#boxplot reorderd by median

headscan\_full %>%

ungroup() %>%

mutate(age\_group= fct\_reorder(age\_group, SelDH\_C, FUN=median, na.rm=TRUE)) %>%

ggplot(aes(y=SelDH\_C, x=age\_group))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

#theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Length values by Age Group",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Age Group")

#boxplot not reordered by median

ggplot(data=headscan\_full, aes(y=SelDH\_C, x=age\_group))+

geom\_boxplot(color= "black", fill = "white")+

theme(text=element\_text(family= "Times New Roman"))+

#theme(axis.text.x = element\_text(angle = 20, vjust=0.7))+

labs(title="Sellion to Dorsal Hump Length values by Age Group",

subtitle = "without outliers removed",

y="Measurement (cm)",

x="Age Group")