

t2d-samafs phenotype distribution

2025-01-23

Available traits:

- cystatin_c - log transform
- a2h_ins - log transform
- creatinine - log transform
- adiponectin - log transform
- leptin - log transform
- chol - log transform
- ldl - log transform
- hdl - log transform
- tg - log transform
- bmi - log transform
- hipc - log transform
- waistc - log transform
- whr - log transform
- dbp - log transform
- height
- fast_glu - log transform
- sbp - log transform
- fast_ins - log transform
- a2h_glu - log transform
- weight - log transform

```
# load phenotype file
pheno = read.table("/hpc/dctrl/tt207/meta_analysis_aim/samafs/phs000462.v2.pht002844.v2.p1.c1.T2D_GENES.
                  header = TRUE)
```

```
# traits of interest
traits <- c("height", "fast_glu", "sbp", "fast_ins", "a2h_glu", "a2h_ins",
           "creatinine", "adiponectin", "leptin", "chol", "ldl",
           "hdl", "tg", "bmi", "hipc", "waistc", "whr", "dbp", "weight")
```

```
for (i in seq_along(traits)) {
  current_trait <- traits[i]
  print(current_trait)

  # fit regression model (untransformed)
  par(mfrow = c(1, 2))
  obj <- lm(pheno[[current_trait]] ~ pheno$sex + pheno$age)
  y2 <- obj$residuals
  hist(y2, main = paste("Residuals for", current_trait),
       xlab = paste("Residuals ", current_trait))
  qqnorm(y2, main = paste("Residuals for", current_trait))
}
```

```

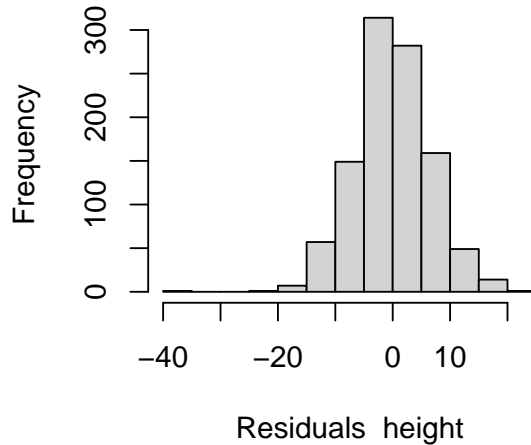
qqline(y2, col = "blue")

# fit regression model (apply log transformation)
obj <- lm(log(pheno[[current_trait]]) ~ pheno$sex + pheno$age)
y2 <- obj$residuals
hist(y2, main = paste("Residuals for \n Log transformed", current_trait),
      xlab = paste("Residuals log", current_trait))
qqnorm(y2, main = paste("Residuals for \n Log transformed", current_trait))
qqline(y2, col = "blue")
}

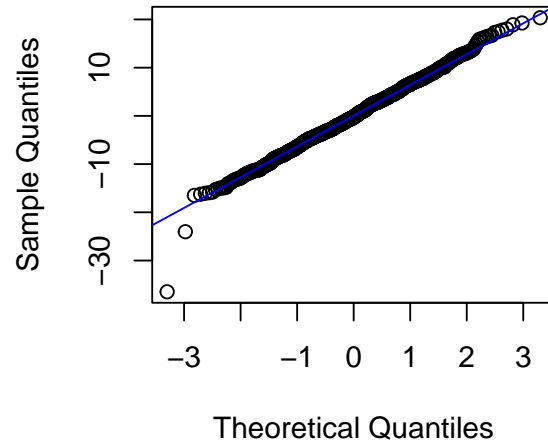
```

```
## [1] "height"
```

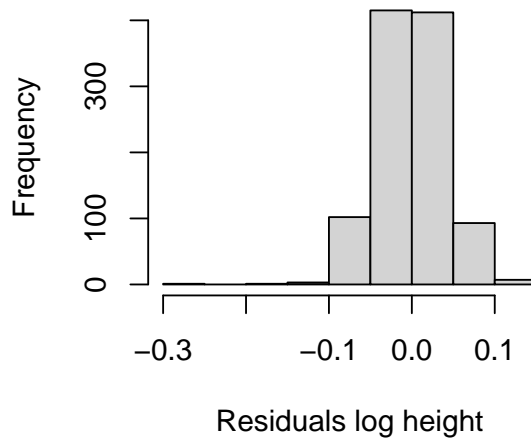
Residuals for height



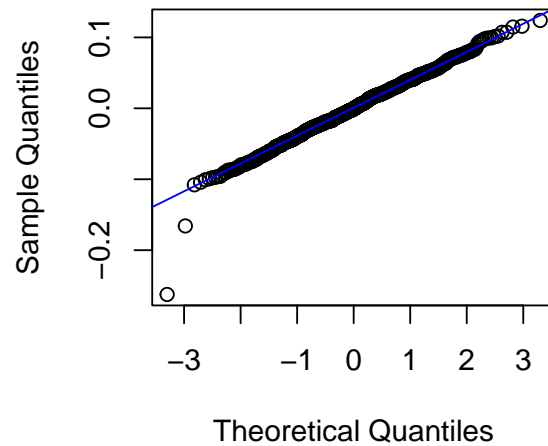
Residuals for height



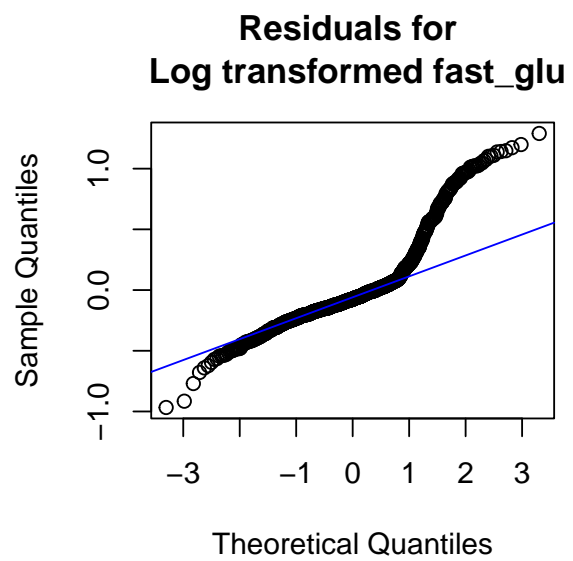
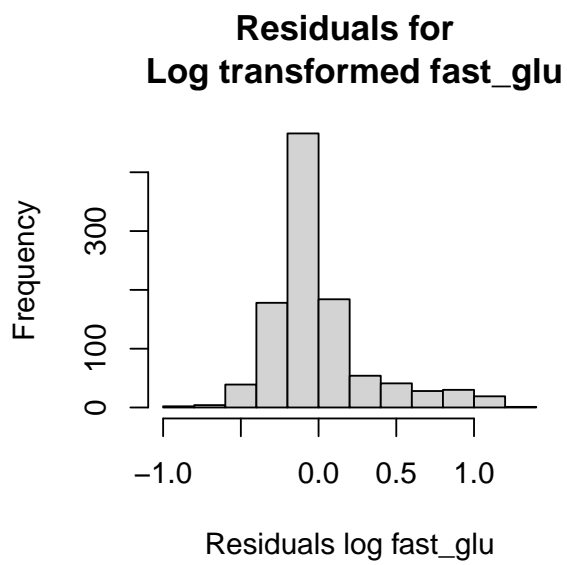
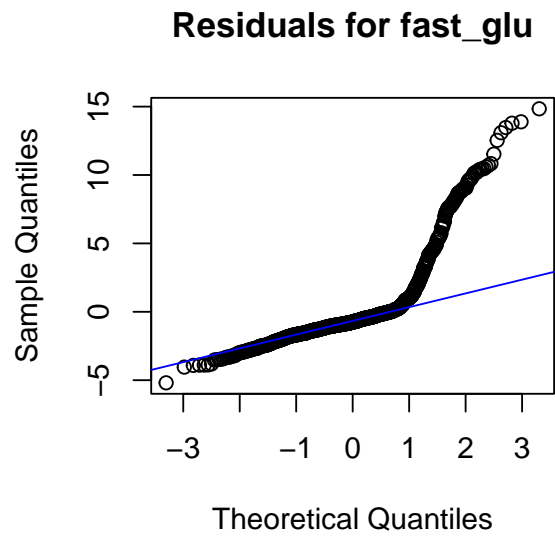
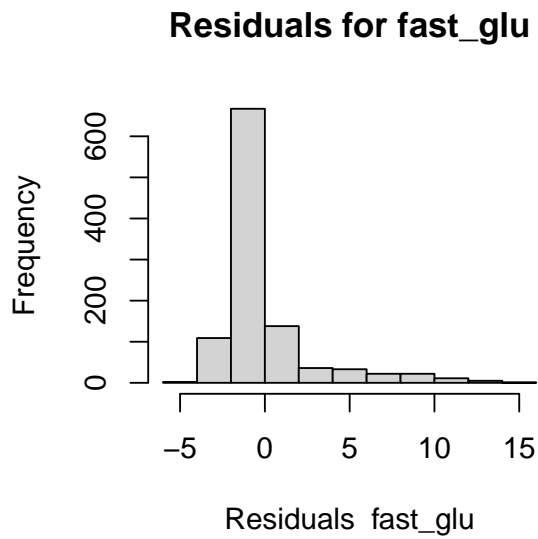
**Residuals for
Log transformed height**



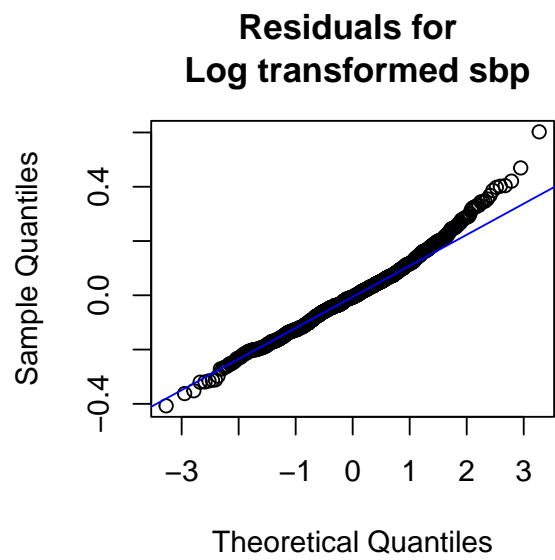
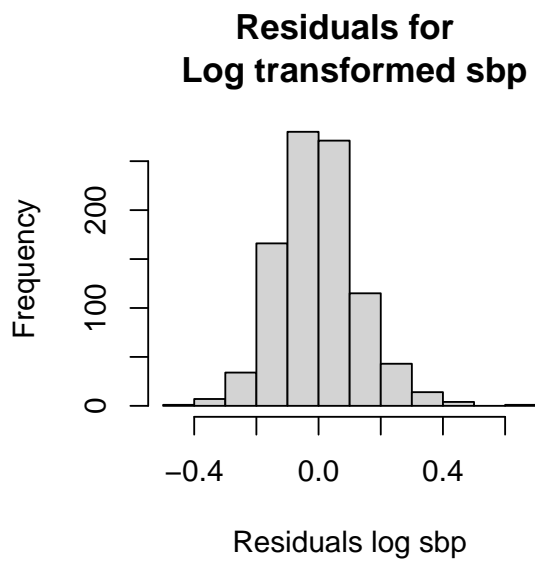
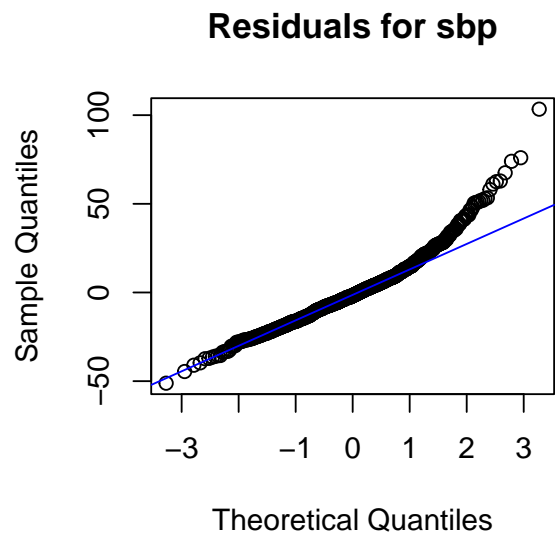
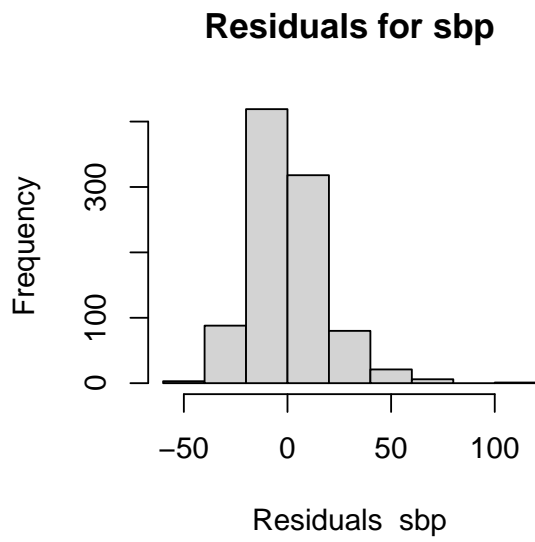
**Residuals for
Log transformed height**



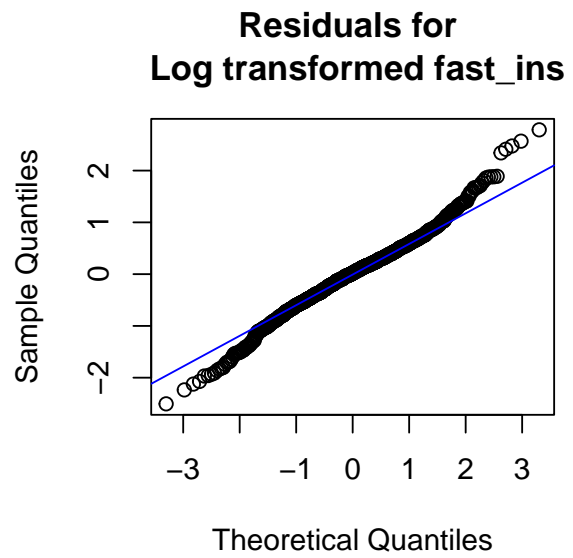
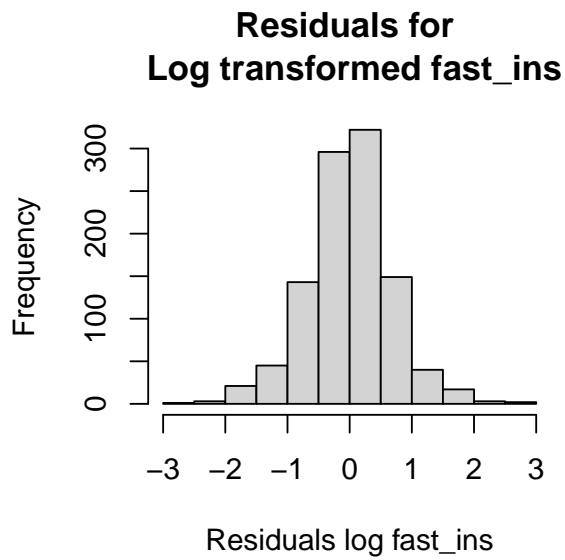
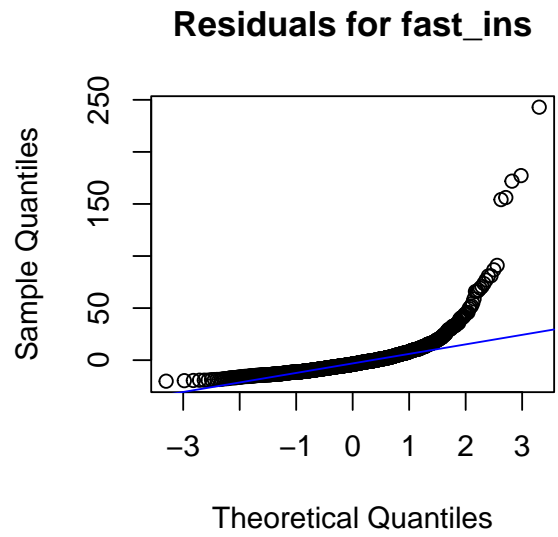
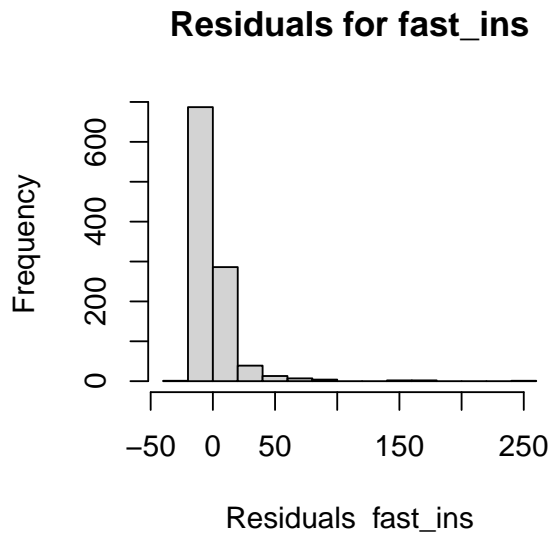
```
## [1] "fast_glu"
```



```
## [1] "sbp"
```

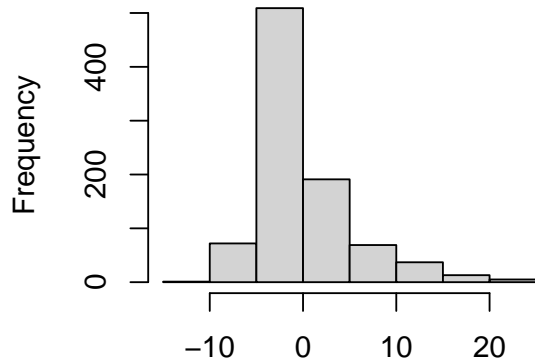


```
## [1] "fast_ins"
```



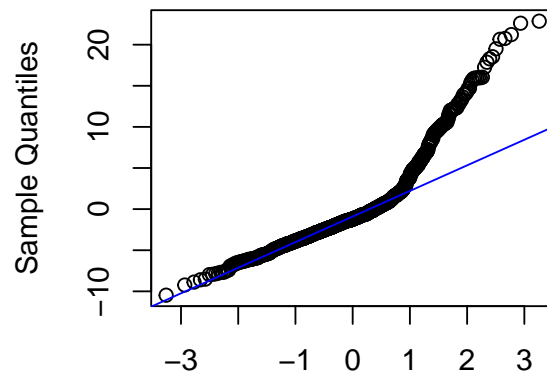
```
## [1] "a2h_glu"
```

Residuals for a2h_glu



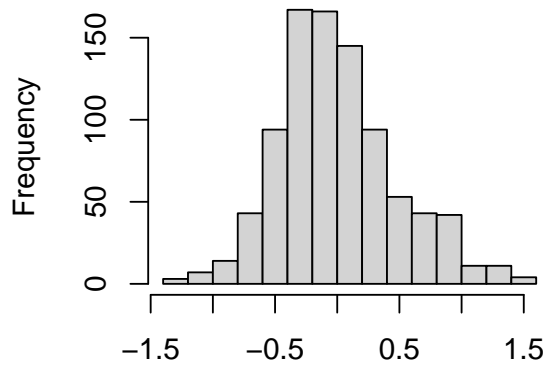
Residuals a2h_glu

Residuals for a2h_glu



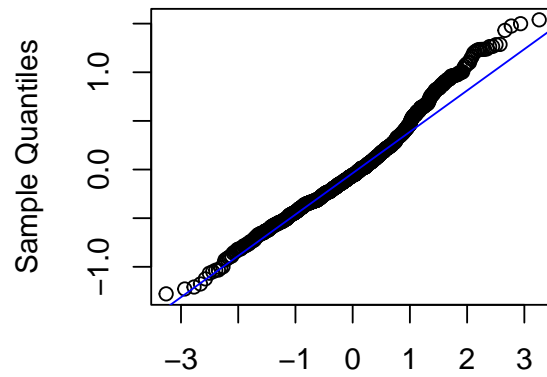
Theoretical Quantiles

**Residuals for
Log transformed a2h_glu**



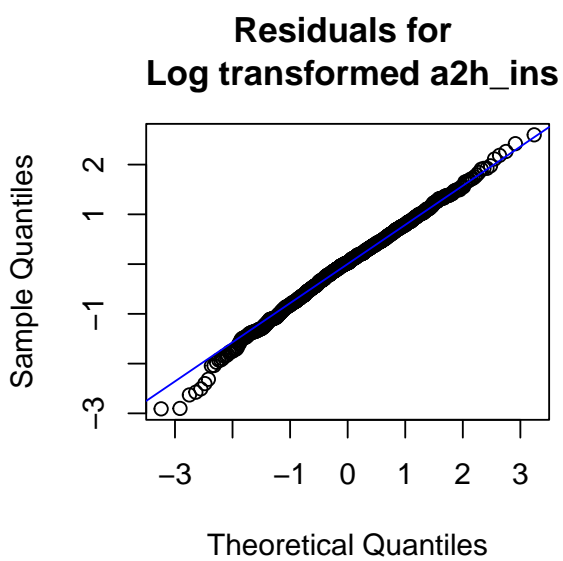
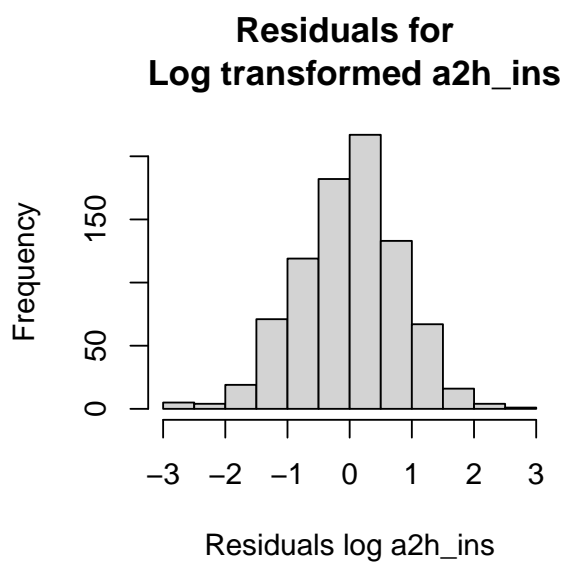
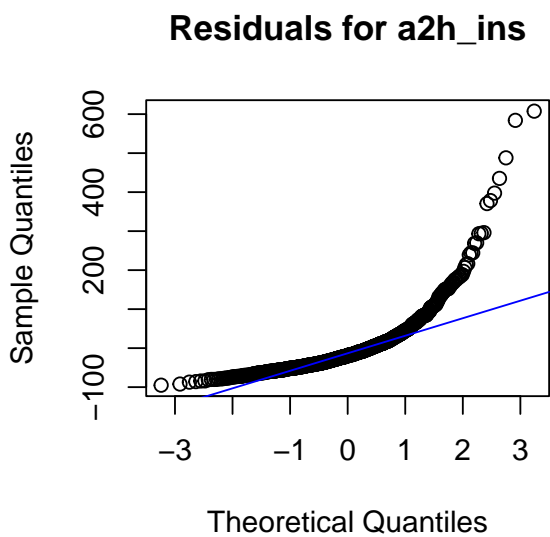
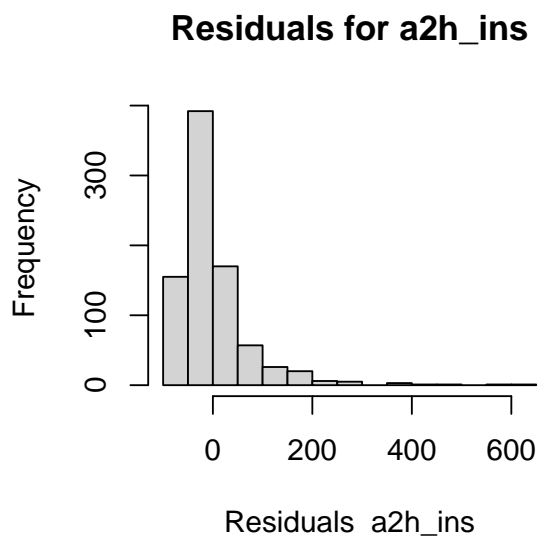
Residuals log a2h_glu

**Residuals for
Log transformed a2h_glu**



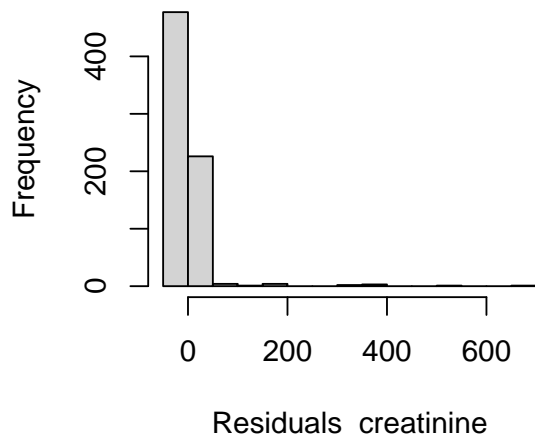
Theoretical Quantiles

```
## [1] "a2h_ins"
```

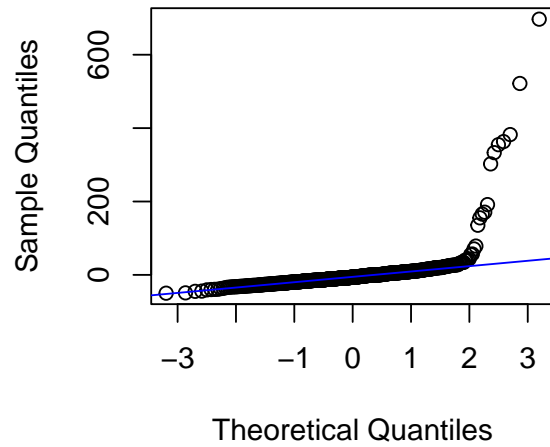


```
## [1] "creatinine"
```

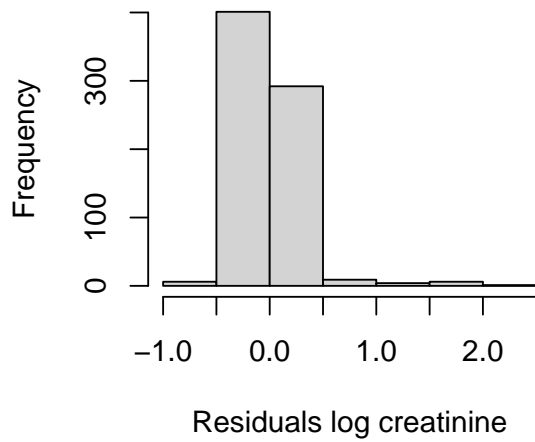
Residuals for creatinine



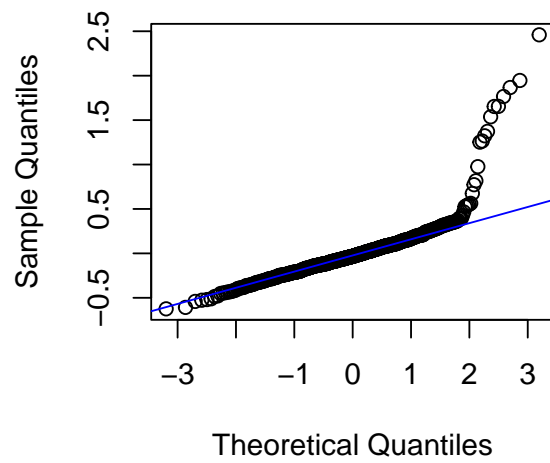
Residuals for creatinine



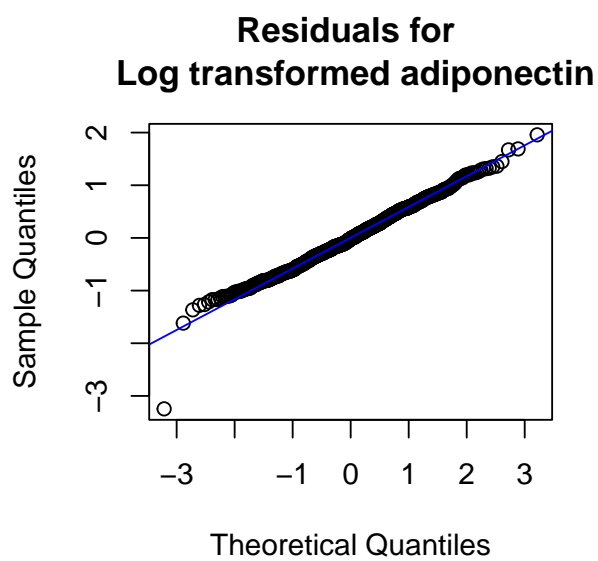
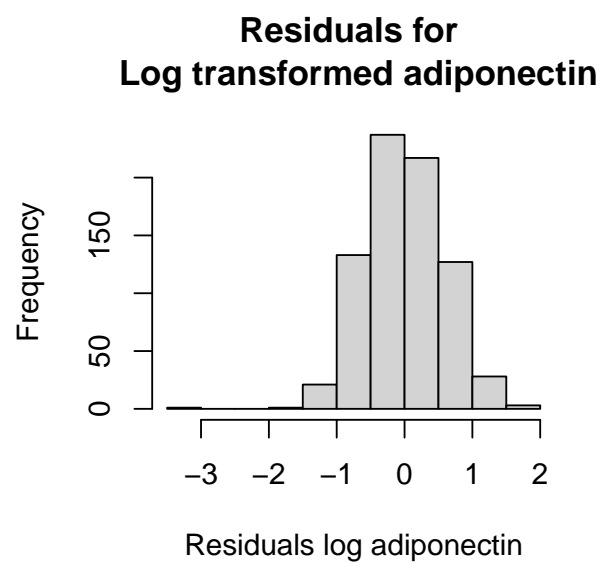
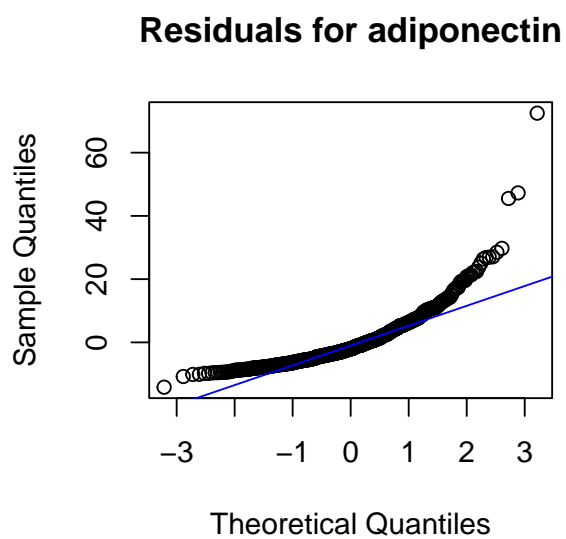
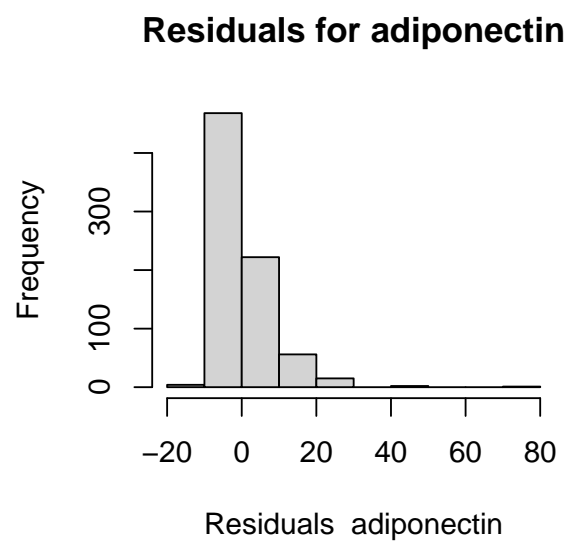
**Residuals for
Log transformed creatinine**



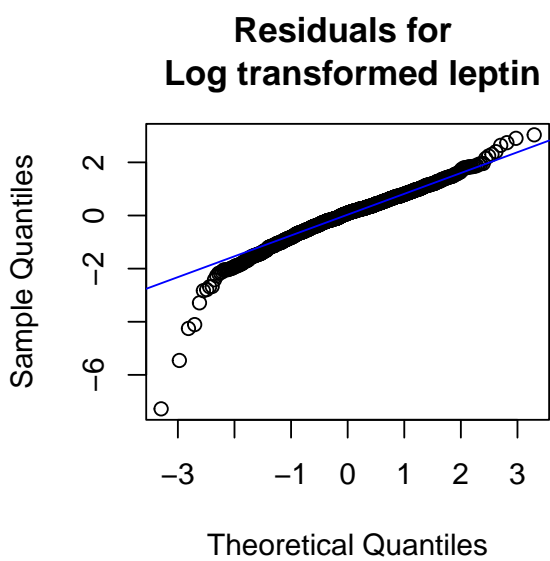
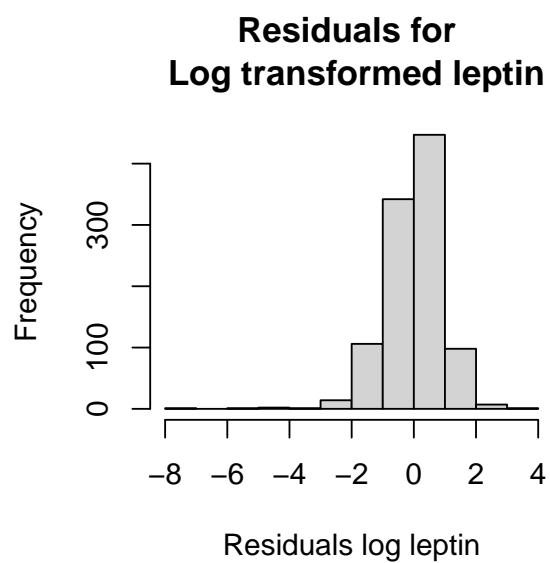
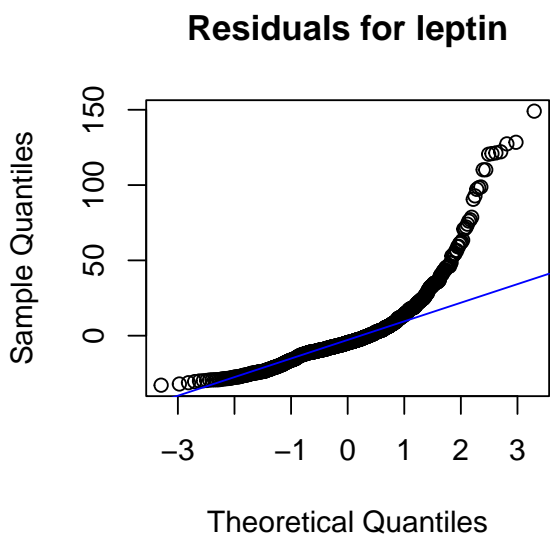
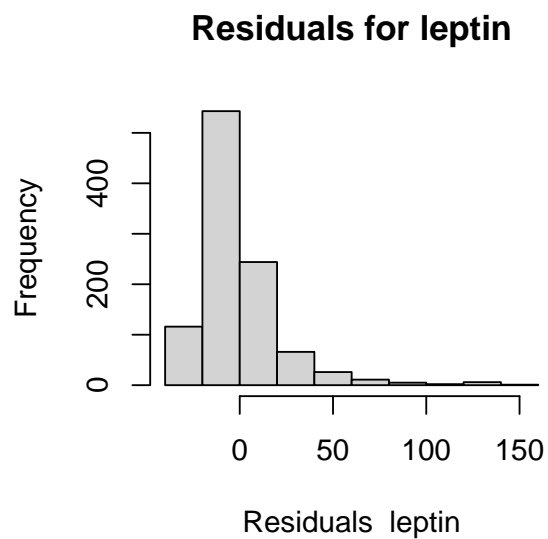
**Residuals for
Log transformed creatinine**



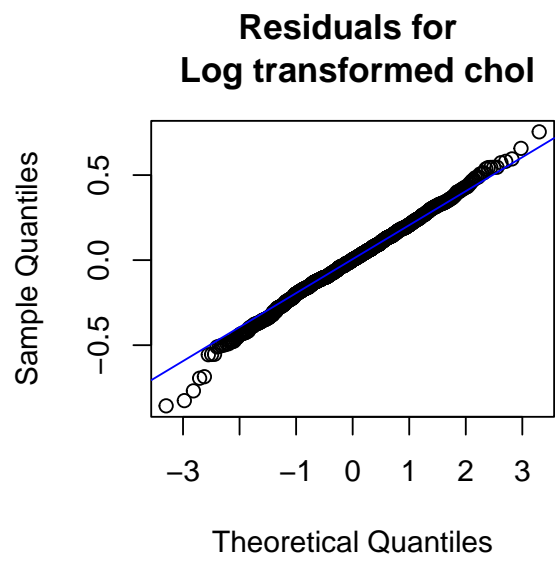
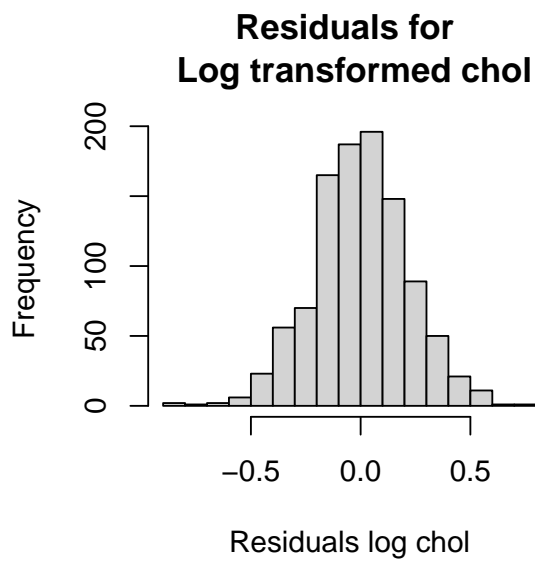
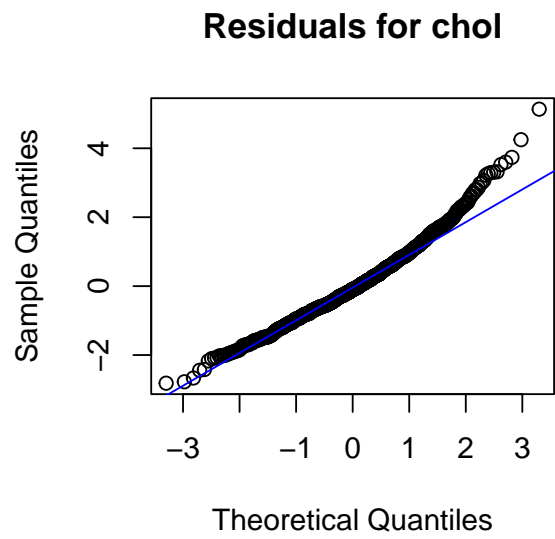
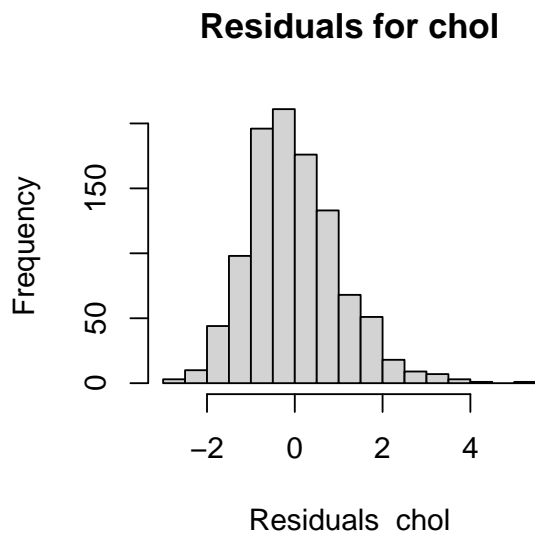
```
## [1] "adiponectin"
```

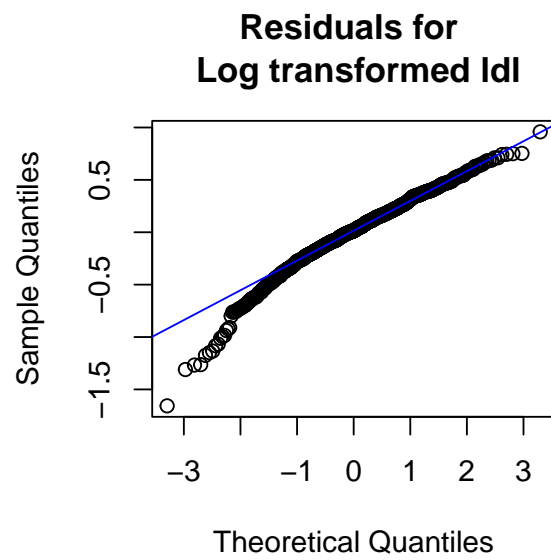
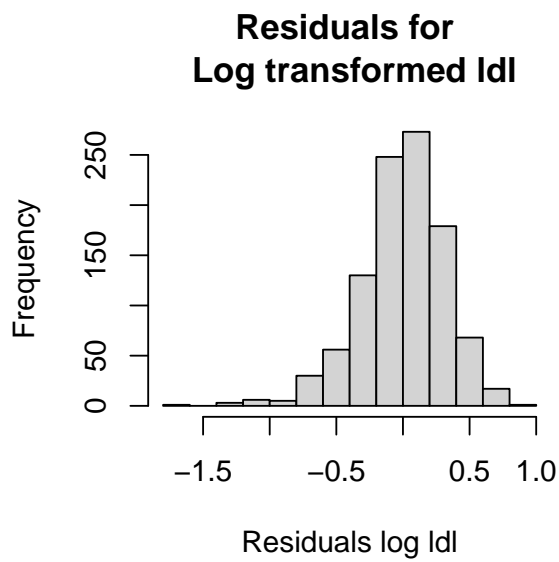
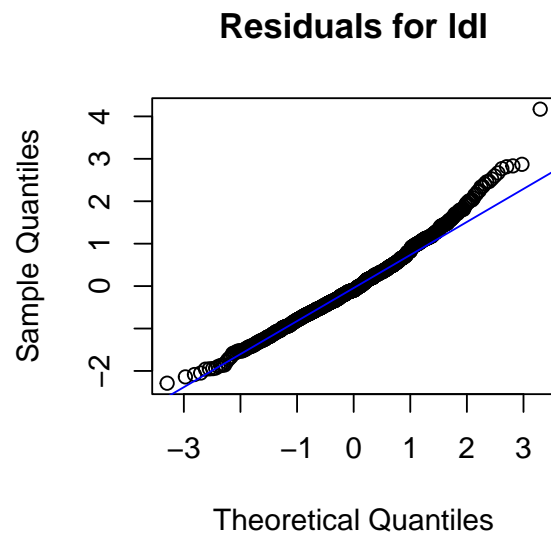
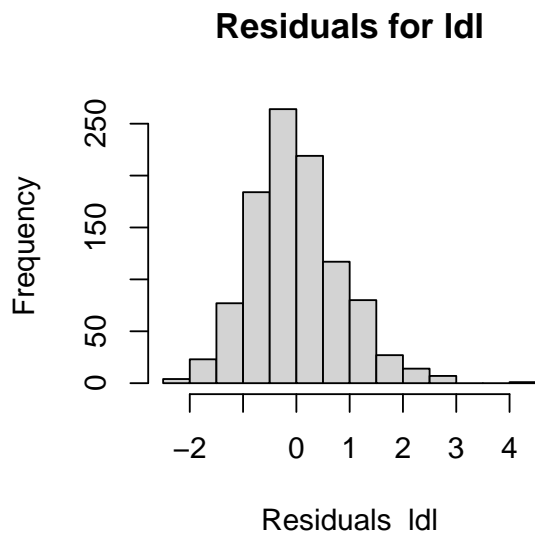
```
## [1] "leptin"
```



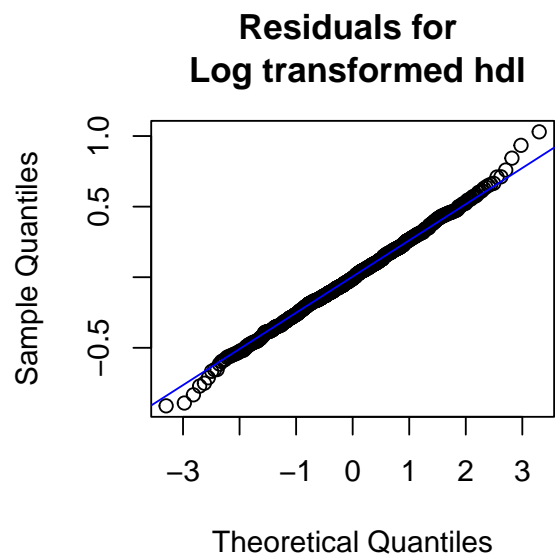
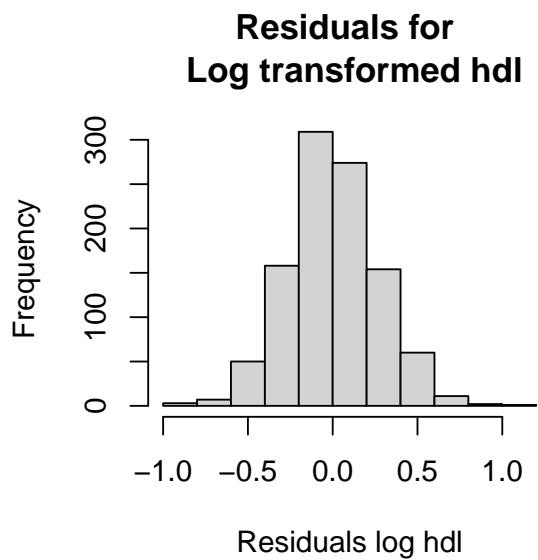
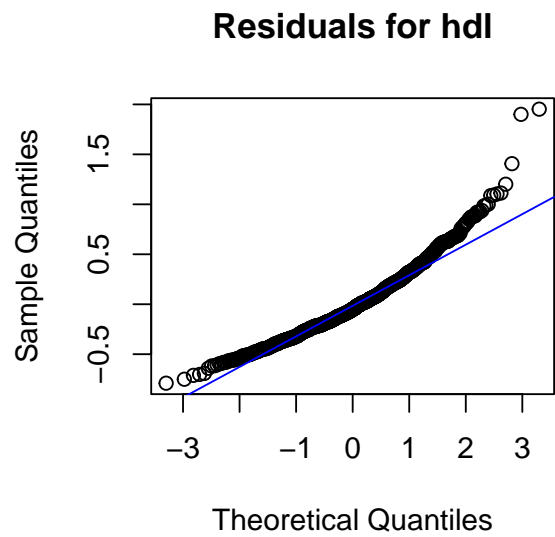
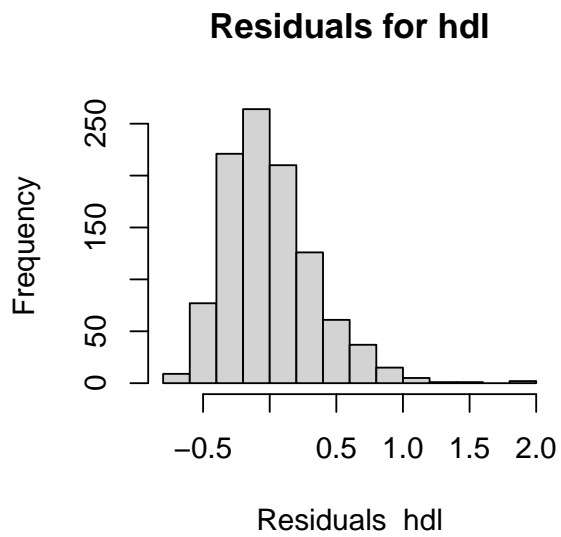
```
## [1] "chol"
```



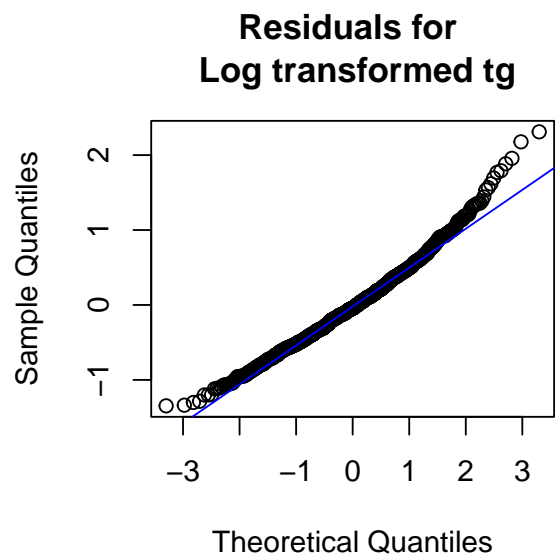
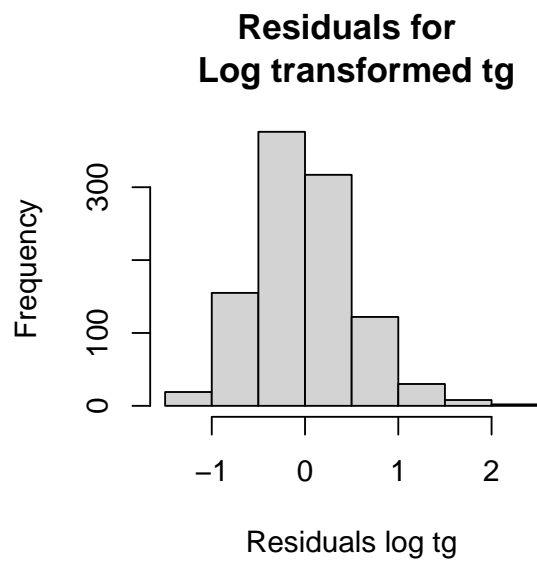
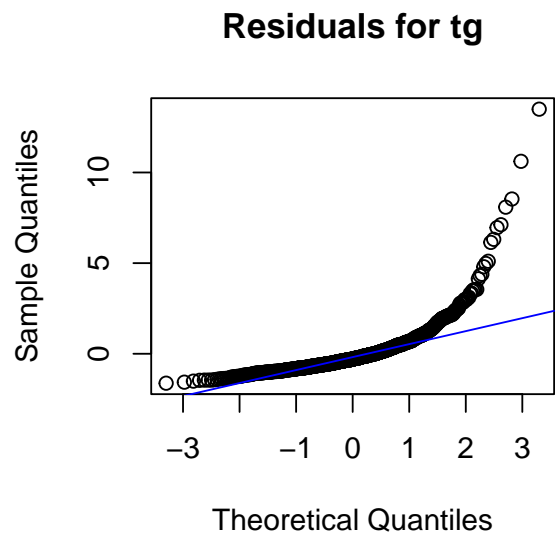
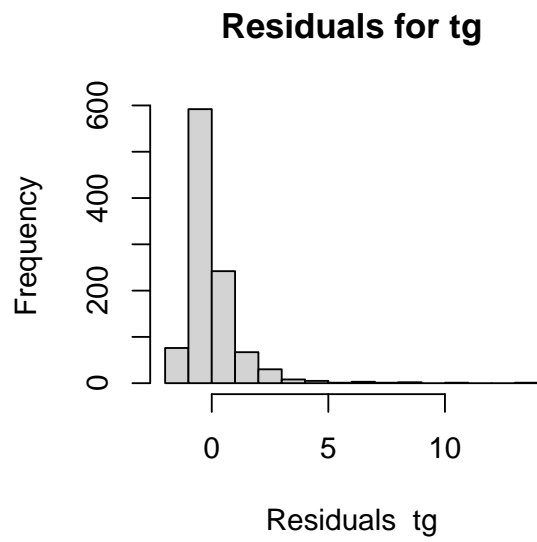
```
## [1] "ld1"
```



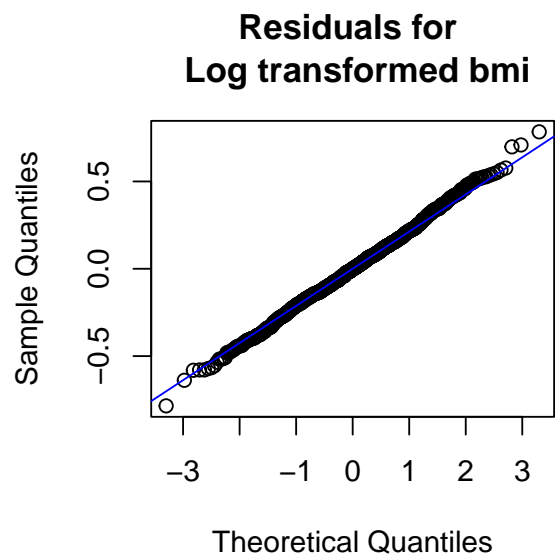
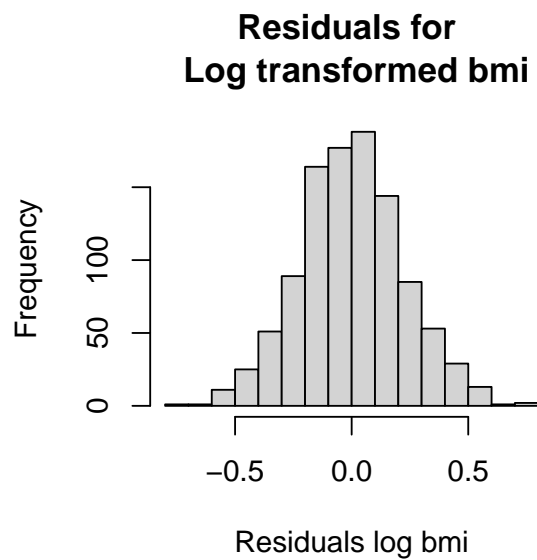
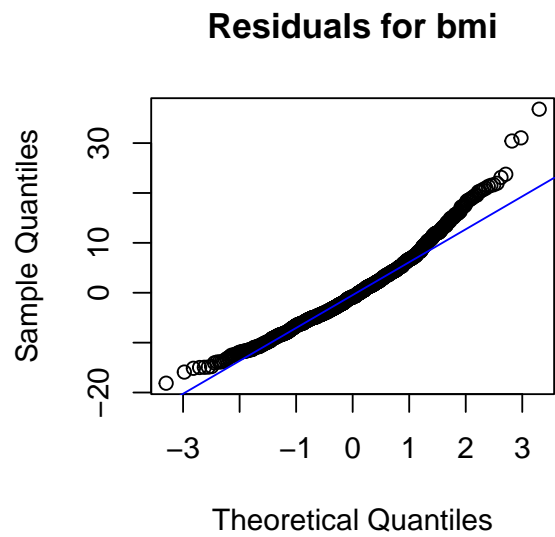
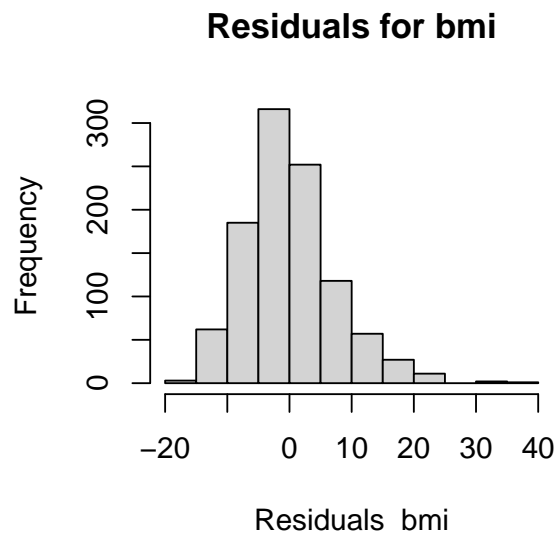
```
## [1] "hdl"
```



```
## [1] "tg"
```

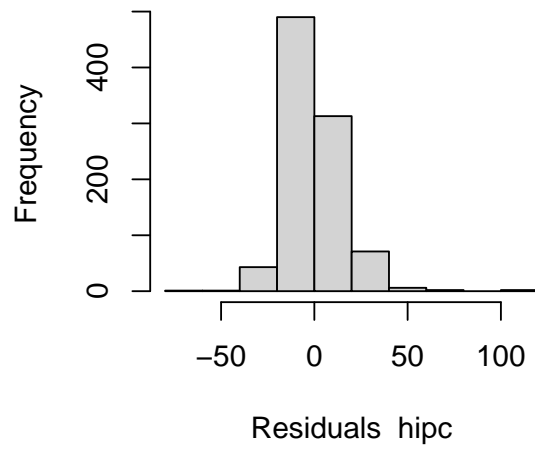


```
## [1] "bmi"
```

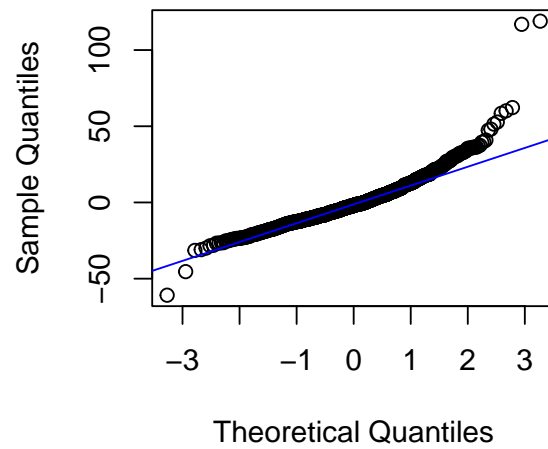


```
## [1] "hipc"
```

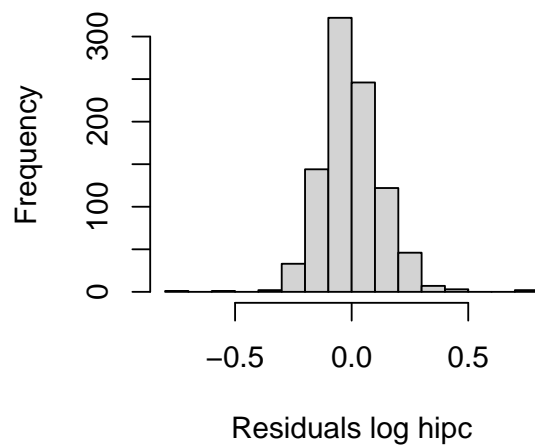
Residuals for hipc



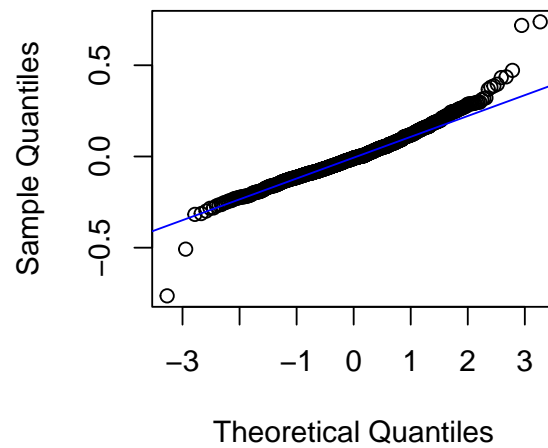
Residuals for hipc



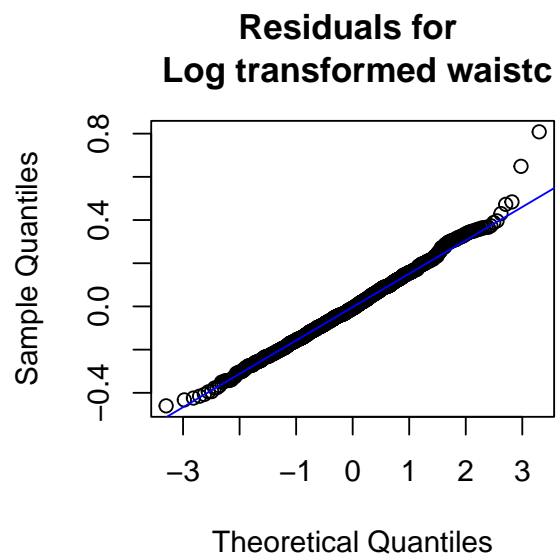
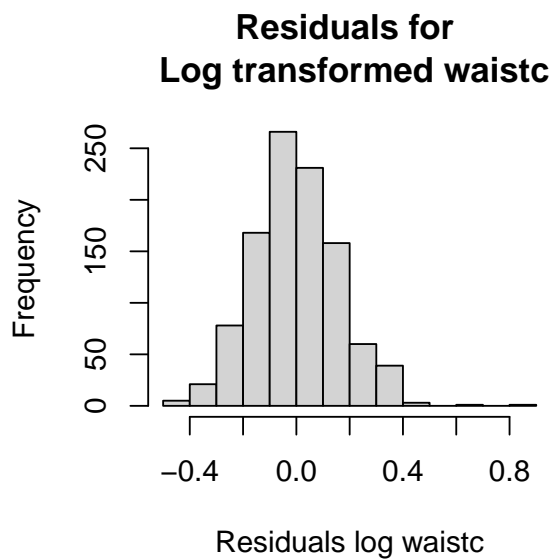
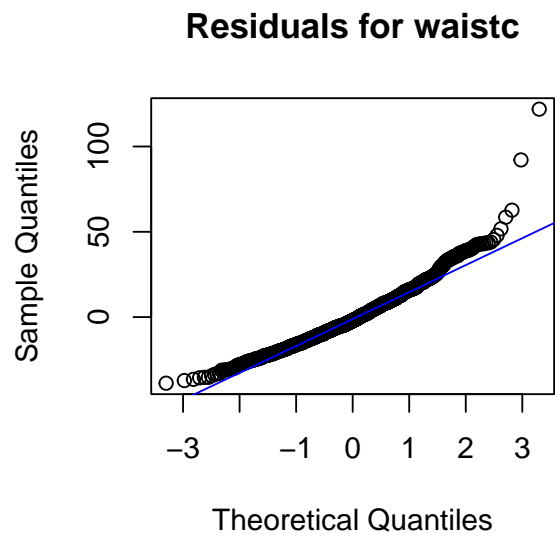
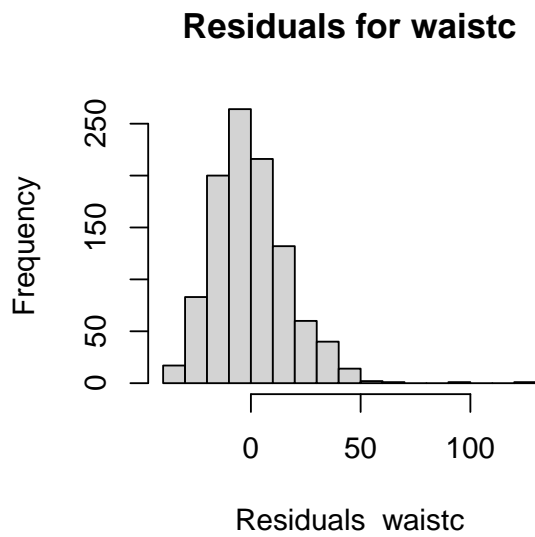
**Residuals for
Log transformed hipc**



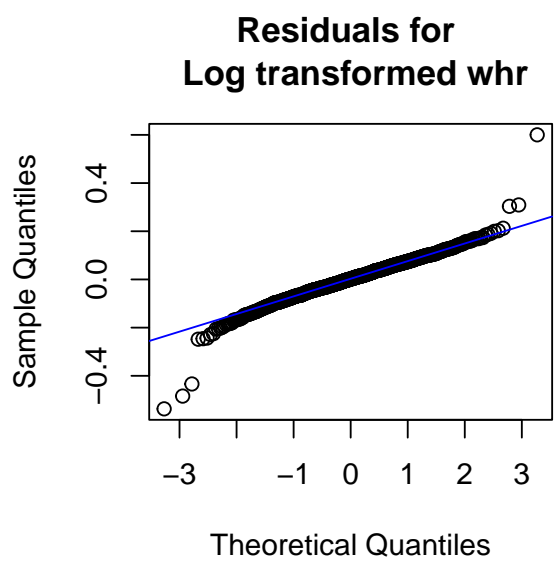
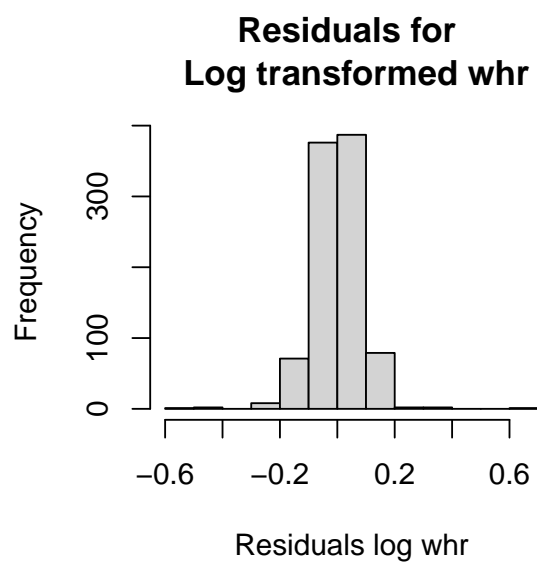
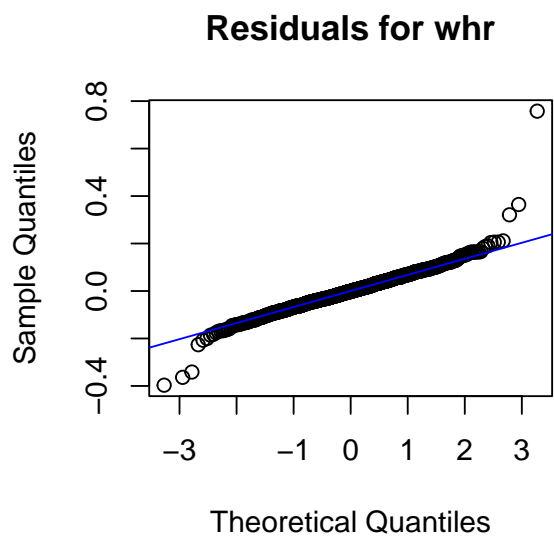
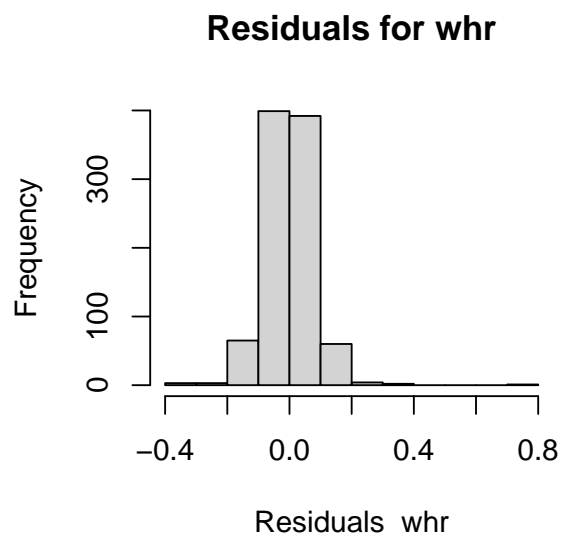
**Residuals for
Log transformed hipc**



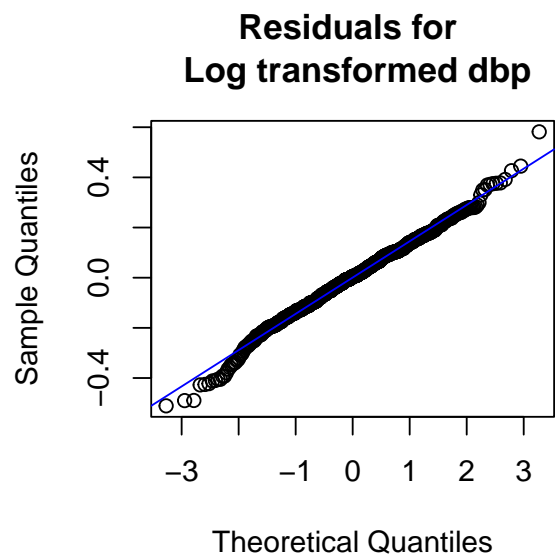
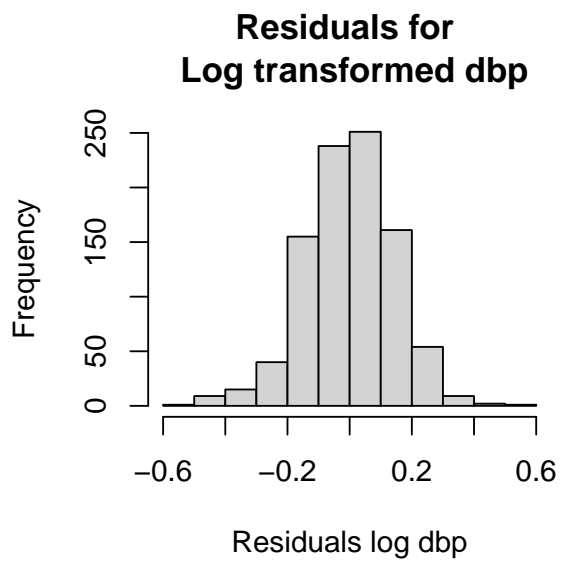
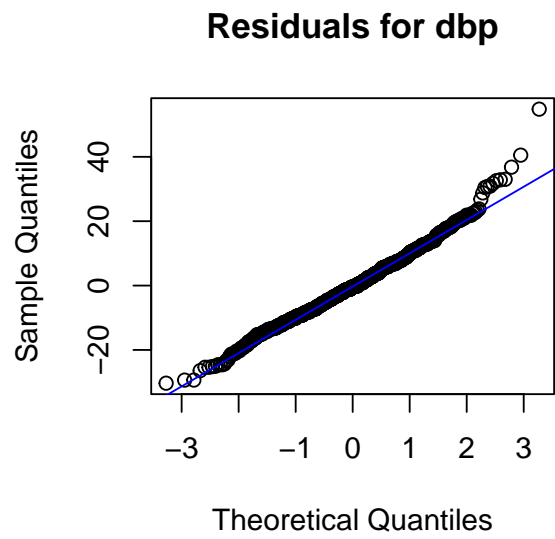
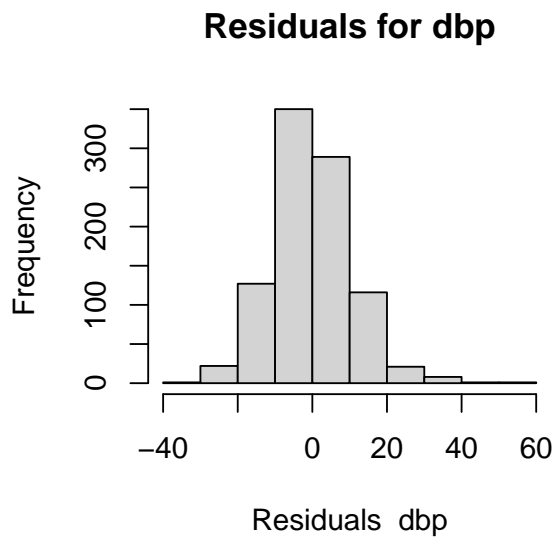
```
## [1] "waistc"
```

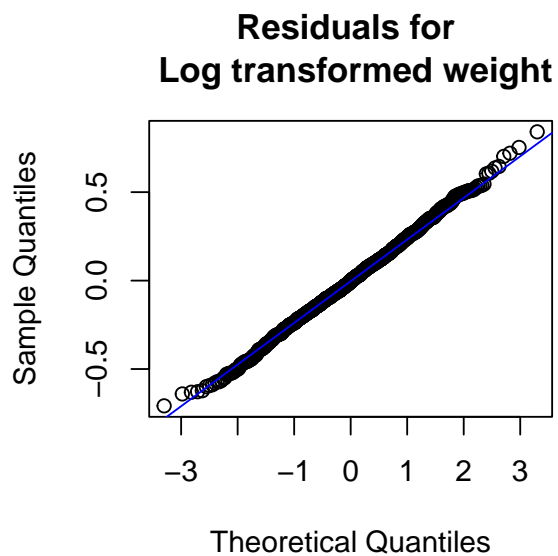
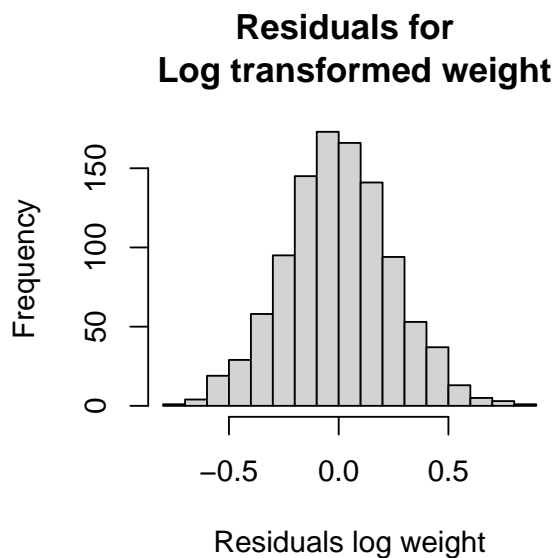
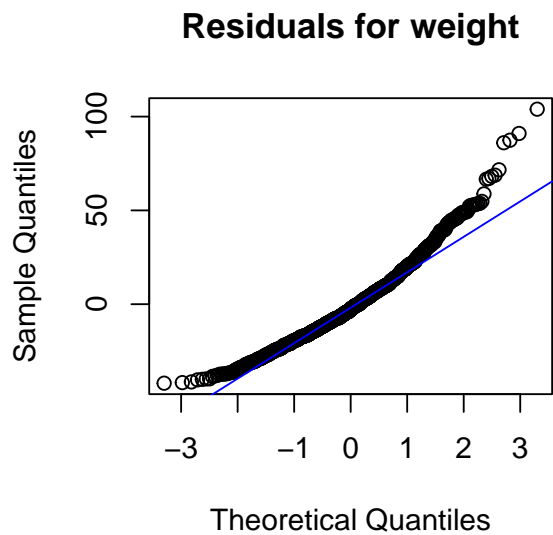
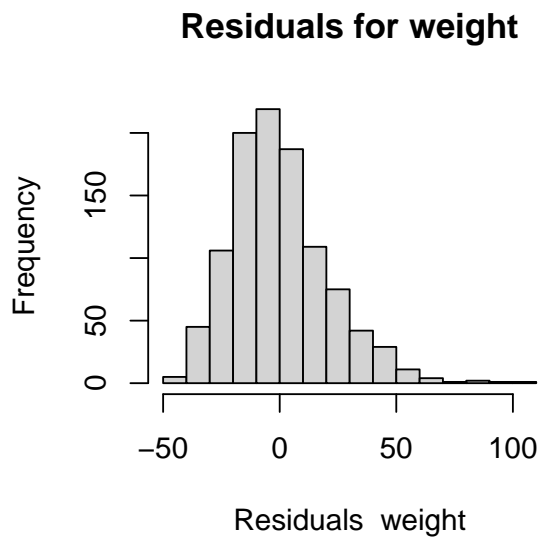
```
## [1] "whr"
```



```
## [1] "dbp"
```



```
## [1] "weight"
```



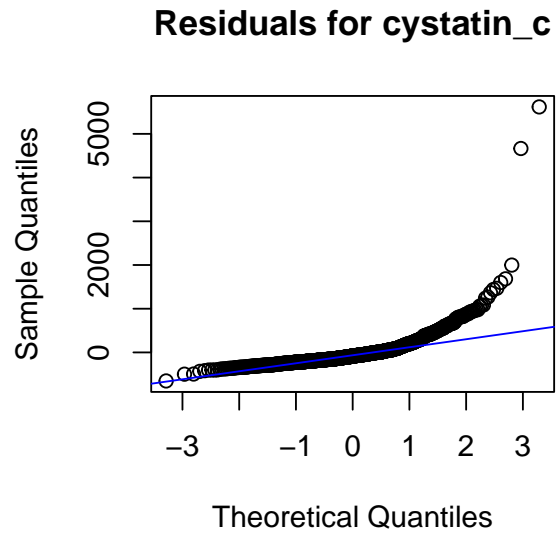
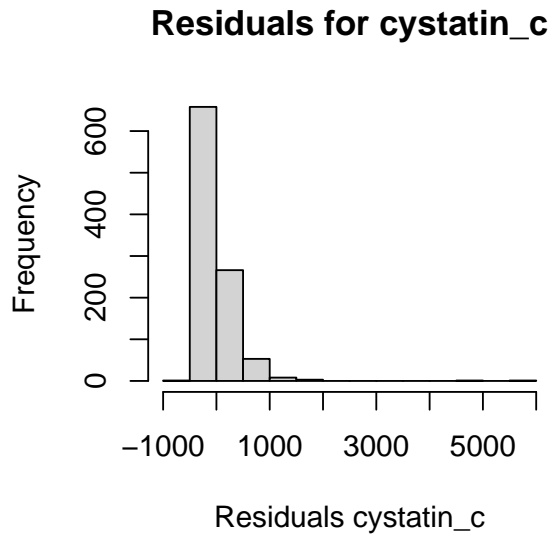
```
cleaned_pheno <- pheno %>%
  filter(!is.na(cystatin_c), !is.nan(cystatin_c), !is.infinite(cystatin_c)) %>%
  filter(!is.na(sex), !is.na(age))
```

```
par(mfrow = c(1, 2))
obj <- lm(as.numeric(cystatin_c) ~ sex + age, data = cleaned_pheno)
```

```
## Warning in eval(predvars, data, env): NAs introduced by coercion
```

```
y2 <- obj$residuals
hist(y2, main = "Residuals for cystatin_c",
     xlab = "Residuals cystatin_c")
```

```
qqnorm(y2, main = "Residuals for cystatin_c")
qqline(y2, col = "blue")
```



```
obj <- lm(log(as.numeric(cystatin_c)) ~ sex + age, data = cleaned_pheno)
```

```
## Warning in eval(predvars, data, env): NAs introduced by coercion
```

```
y2 <- obj$residuals
hist(y2, main = "Residuals for log cystatin_c",
     xlab = "Residuals log cystatin_c")
qqnorm(y2, main = "Residuals for log cystatin_c")
qqline(y2, col = "blue")
```

