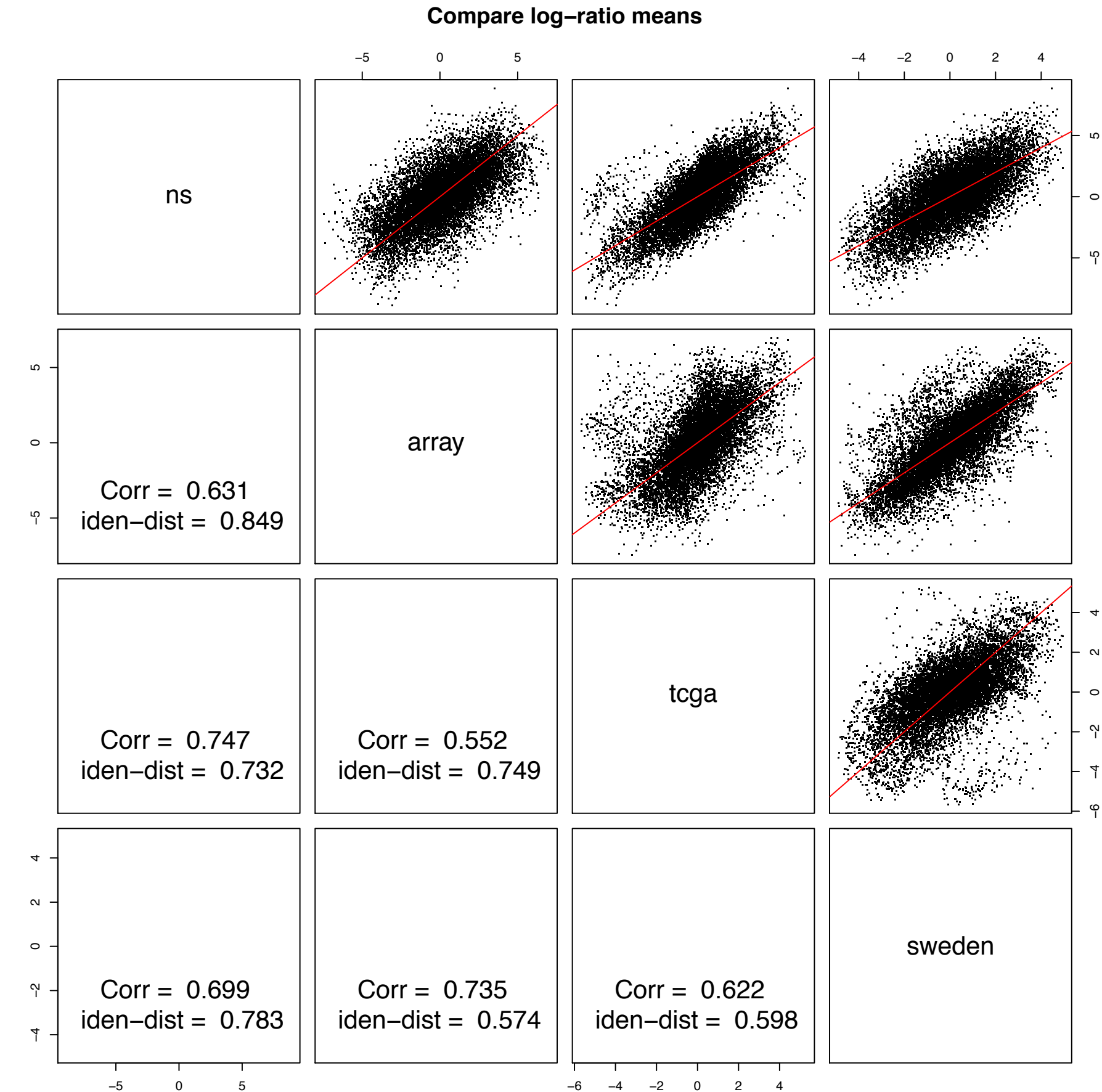
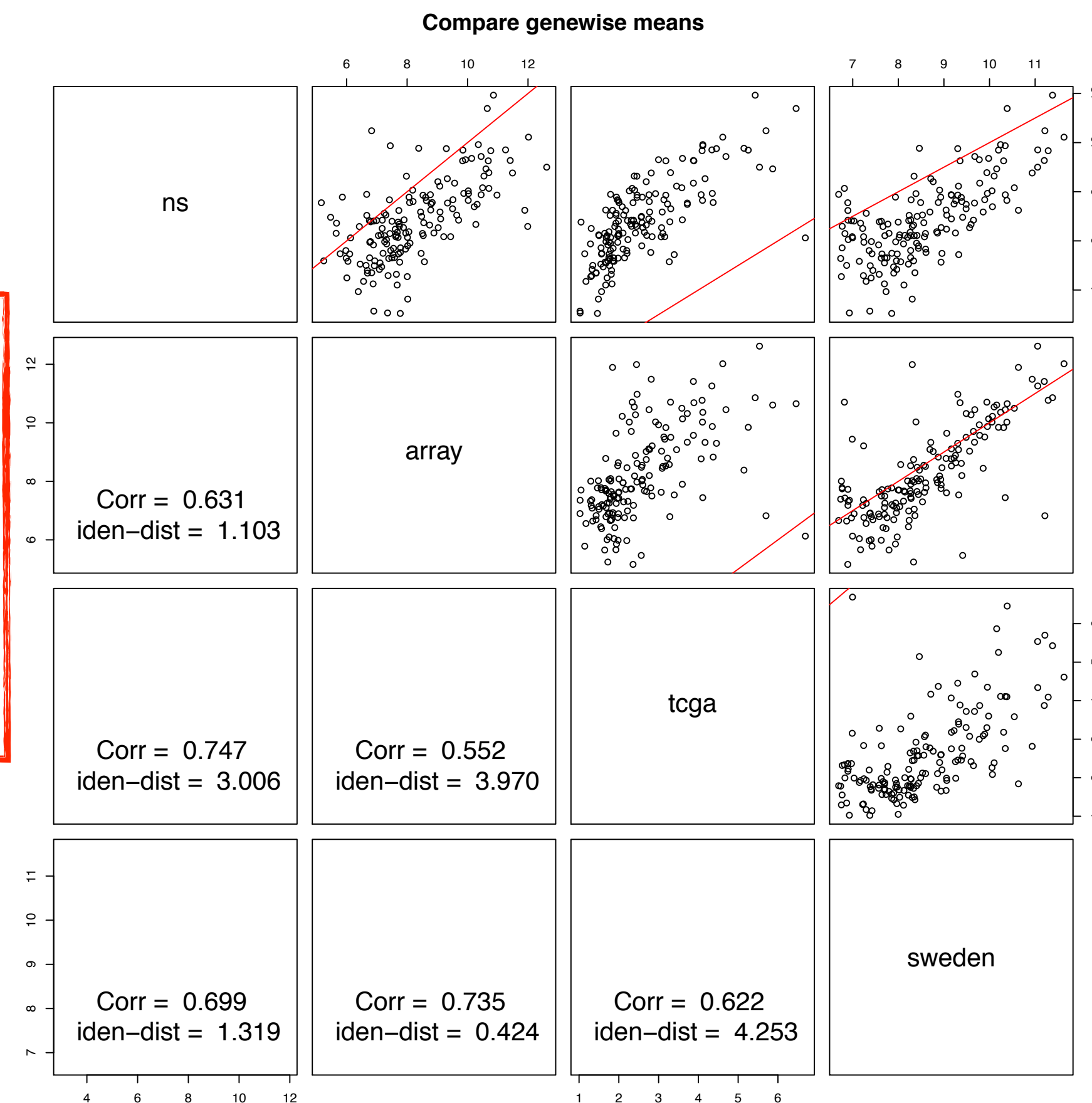


# The solution is trivial.

- We have “standardised features” within every patient to build models

**Log-ratio**

**$\log(\text{gene A}) - \log(\text{gene B})$**



## The solution is trivial?

1. Single-patient prediction
2. Different scaling on genes between datasets
3. Concordance in feature selection/coefficient estimates