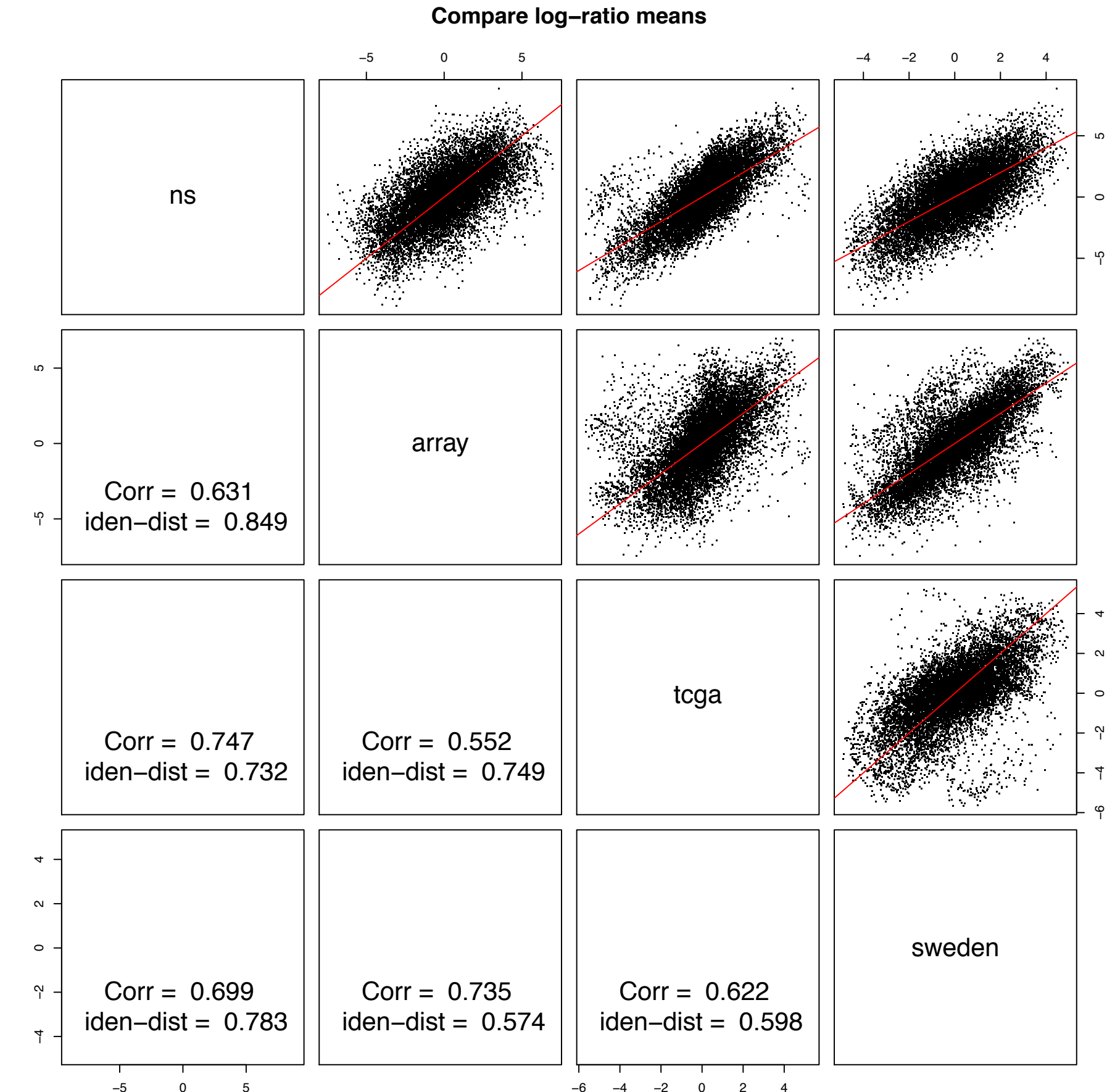
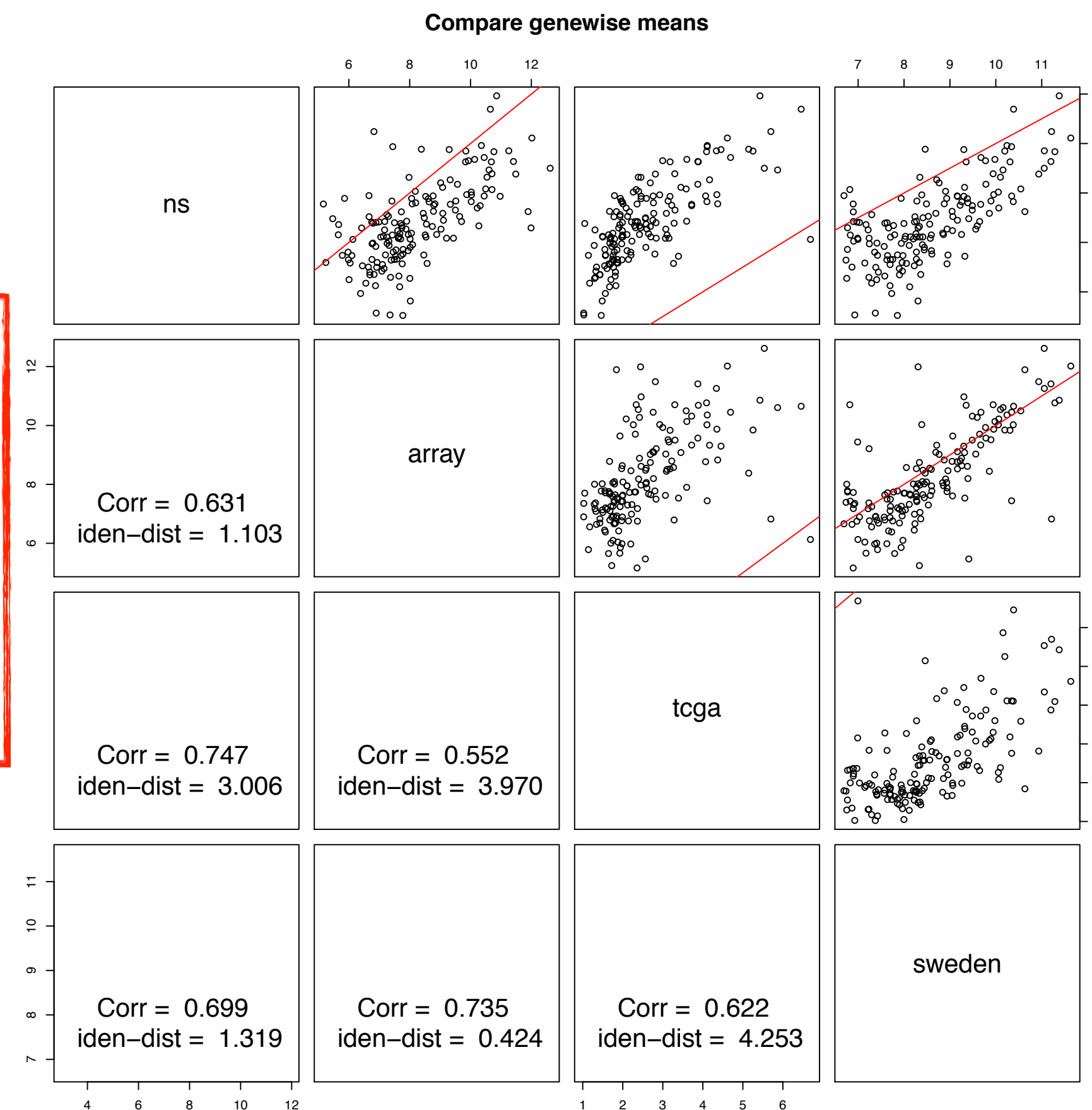


The solution is trivial.

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

Log-ratio
Take the differences between
 $\log(\text{gene A})$ and $\log(\text{gene B})$



The solution is trivial?

- ▶ Some data shifts still remain
- ▶ Lasso offers feature selection but Ridge offers stability in prediction

