The solution is trivial.
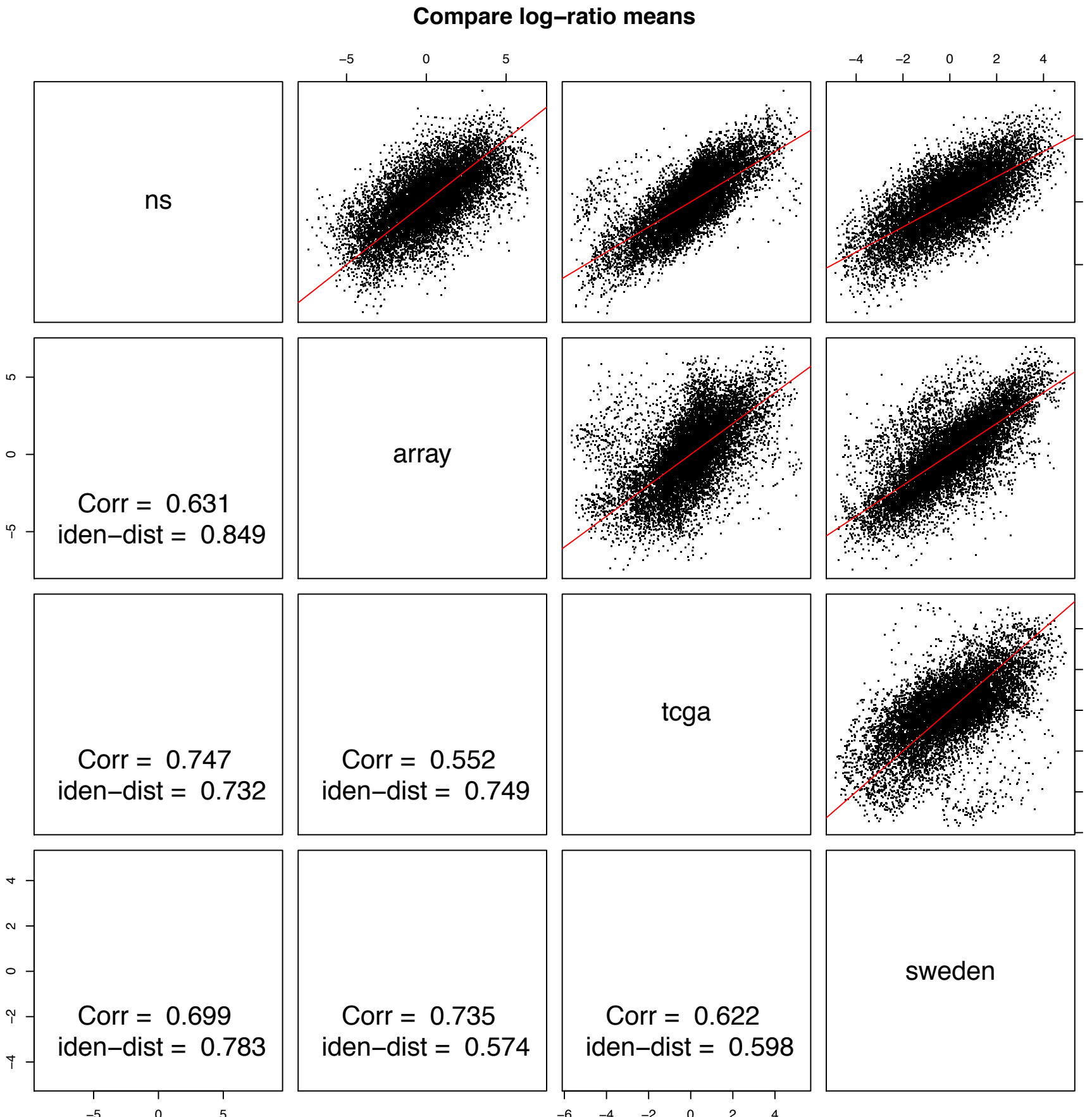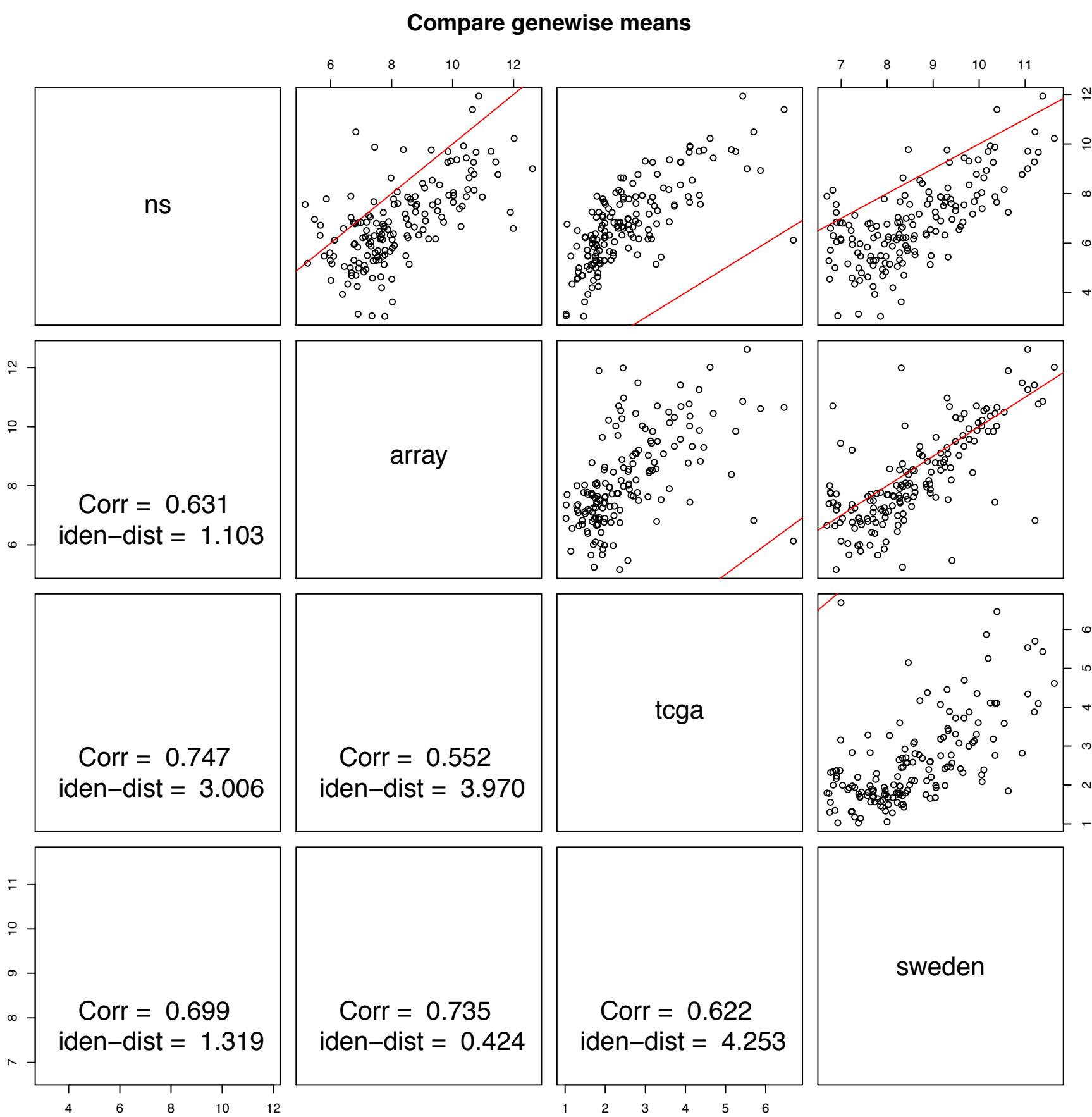
▸ We have "standardised features" within every patient to build models

Log-ratio
Take the differences between log(gene A) and log(gene B)

Compare genewise means

	6 8 10 12		7 8 9 10 11
ns			
	array		
Corr = 0.631 iden−dist = 1.103			
		tcga	
Corr = 0.747 iden−dist = 3.006	Corr = 0.552 iden−dist = 3.970		
			sweden
Corr = 0.699 iden−dist = 1.319	Corr = 0.735 iden−dist = 0.424	Corr = 0.622 iden−dist = 4.253	

Compare log−ratio means

ns			
	array		
Corr = 0.631 iden−dist = 0.849			
		tcga	
Corr = 0.747 iden−dist = 0.732	Corr = 0.552 iden−dist = 0.749		
			sweden
Corr = 0.699 iden−dist = 0.783	Corr = 0.735 iden−dist = 0.574	Corr = 0.622 iden−dist = 0.598	

The solution is trivial?