Figure S1 Correlation between our E-MAP data and published data. The interaction of 12709/67680 gene pairs in our E-MAP profile are also measured in [9]. The figure shows the correlation between the genetic interaction scores calculated from the two data sets. By using all interactions, the Pearson coefficient is quite low (r=0.37). It’s because the scores of non-interacted pairs are randomly around zero and a great part of gene pairs are non-interacted. We measured the correlation again by using only pairs which satisfy S>2.5 or S<-3. The correlation has been promoted significantly (r=0.65). In this case we could consider the two data sets are consistent.