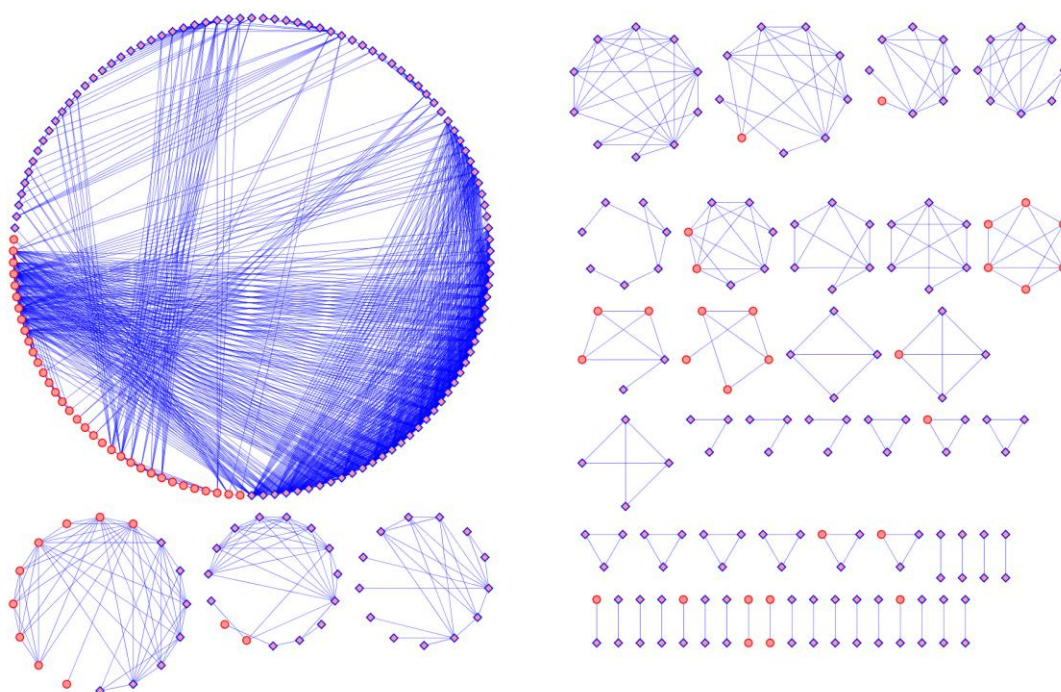


**Fig. S1. Damage size distribution.**

The cumulative distribution for essential and non-essential genes is shown in the figure, where black rectangle represents essential gene and red circle node represents non-essential gene. The inset is in the log-log scale.



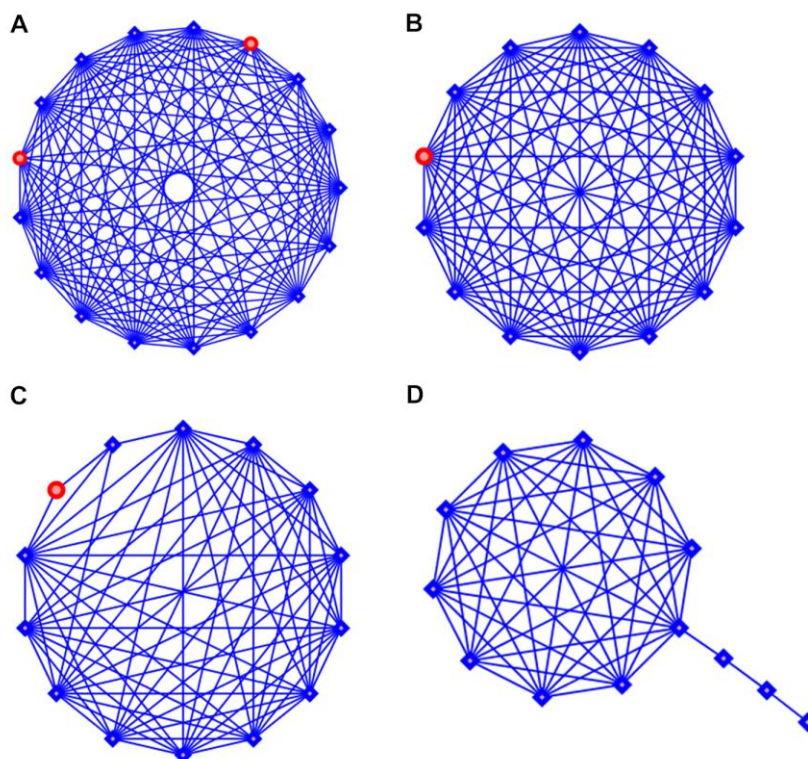
**Fig. S2. Damage list similarity overview.**

Gene pairs with their damage list similarity bigger than 0 are connected. Nodes with red circle border and blue diamond border represent essential and non-essential genes respectively.

## The functional analysis for the largest subnetwork in Fig.2

In this work, we focus on the subnetwork that composed mainly of essential genes. Here, we provide a thorough functional analysis of the largest subnetwork shown in Fig.2.

This subnetwork is composed of 15 non-essential genes and 2 essential genes for the given threshold 0.6 (b3624, b3631, b3632, b0200, b3052, b3628, b3629, b3630, b3198, b3627, b1855, b2040, b3623, b0918, b3619, b3625, and b3626). As we increased the threshold up to 0.9, the subnetwork is totally composed of non-essential genes (as shown in Fig.S3.D). This suggests that the most robust part in this subnetwork is made up of non-essential genes.



**Fig. S3.** (A) The largest subnetwork for the threshold 0.6 as shown in Fig.2. (B) The largest subnetwork for the threshold 0.7. (C) The largest subnetwork for the threshold 0.8. (D) The largest subnetwork for the threshold 0.9. Increasing the threshold remove the essential genes from the subnetwork, indicating non-essential genes are the most robust components.

In this subnetwork, 16 out of 17 genes are from the subsystem Lipopolysaccharide Biosynthesis/Recycling, involved in LPS core biosynthesis. Here are the top five GO functions: GO: 0009103 GO: 0016740 GO: 0005515 GO: 0016757 and GO: 0016020, where their details are given in Table S1.

Table S1. The top five GO functions

Accession	Ontology	Synonyms
GO:0009103	Biological Process	lipopolysaccharide biosynthesis
GO:0016740	Molecular Function	transferase activity
GO:0005515	Molecular Function	protein amino acid binding
GO:0016757	Molecular Function	glycosyltransferase activity
GO:0016020	Cellular Component	membrane

We also analyzed the common damaged genes of this subnetwork: b0622, b2027, b2034, b2035, b2040, b2254, b2255, b2257, b3622, b3623, b3624, b3626, b3627, b3628, b3620, b3631, b3785, b3790, b3793, b3794, and b4481. These common genes are non-essential genes except the gene b3623, and b3793 according to the essential gene list identified through the Keio collection. However, these two genes were considered as non-essential genes in other studies although they may have some important roles, the lack of them may not lead to cell lethality.