

1 **Supplementary Figure 1. Rarefaction curve of microbial diversity for the microbiota from**
2 **lavage samples.** Rarefaction curves of (a) observed species, (b) Chao1 and (c) phylogenetic
3 diversity for microbiota (mean \pm 95% CI) were plotted at different sequencing depths.

4
5 **Supplementary Figure 2. Shifts of mucosal microbial composition in secretor and non-**
6 **secretor individuals.** (a) Communities clustered using PCoA of the unweighted UniFrac distance
7 matrix. Each colored point corresponds to a sample. (b) Phylum level microbial compositions of
8 *SeSe*, *Sese* and *sese* individuals (mean \pm s.d.). The bacterial community from lavage sample mainly
9 consisted of Bacteroidetes (46.59%), Firmicutes (34.8%), Proteobacteria (14.6%),
10 Verrucomicrobia (1.4%) and Tenericutes (1.4%). Only predominant phyla with relative
11 abundances higher than 1% were depicted in the bar graph. *: Kruskal-Wallis test, FDR-corrected
12 $P < 0.25$. Shifts at the whole-phylum level were observed in *SeSe* individuals, including decreased
13 relative abundances of Bacteroidetes, accompanied by increase of Firmicutes as compared with
14 *Sese* individuals. When compared with *sese* individuals, *SeSe* subjects harbored more Firmicutes
15 and Fusobacteria. In secretors, the trend of lower abundances of Proteobacteria can also be
16 observed.

17
18 **Supplementary Figure 3. Procrustes analysis on the Bray-Curtis PCoA plots derived from**
19 **16S and imputed metagenomic datasets.** The clustering of samples are not consistent using these
20 two datasets ($P = 0.510$), suggesting more profound variations at metagenomic level.

21
22 **Supplementary Figure 4. Relative abundances of metabolic pathways enriched in *Sese* or *sese***
23 **individuals.** The differentially abundant pathways (**Supplementary Dataset 2**) that are not shown

24 in **Figure 1c** are plotted. Compared to *SeSe* individuals, 10 pathways are enriched in *sese*
25 individuals, and 5 are enriched in *Sese* individuals.

26
27 **Supplementary Figure 5. Relative abundances of metabolic pathways enriched in *SeSe***
28 **individuals.** The differentially abundant pathways (**Supplementary Dataset 2**) that are not shown
29 in **Figure 1c** are plotted. In *SeSe* individuals, 20 pathways are enriched compared to *sese*
30 individuals, and 5 are enriched compared to *Sese* individuals.

31
32 **Supplementary Figure 6. Metabolic pathways enriched in *SeSe* individuals.** The 5 KEGG
33 metabolic pathways that are enriched in *SeSe* individuals compared to *Sese* individuals
34 (**Supplementary Figure 4**) are highlighted in light blue; the 20 pathways that are enriched in *SeSe*
35 individuals compared to *sese* individuals (**Supplementary Figure 4**) are highlighted in blue; the 7
36 pathways (**Figure 1c**) that are enriched in *SeSe* individuals compared to both *Sese* and *sese*
37 individuals are highlighted in dark blue.

38
39 **Supplementary Figure 7. Metabolic pathways enriched in *Sese* or *sese* individuals in**
40 **comparison to *SeSe* individuals.** The 5 KEGG metabolic pathways that are enriched in *Sese*
41 individuals (**Supplementary Figure 3**) are highlighted in yellow; the 10 pathways that are enriched
42 in *sese* individuals (**Supplementary Figure 3**) are highlighted in orange; the 5 pathways (**Figure**
43 **1c**) that are enriched in both *Sese* and *sese* individuals are highlighted in red.

44
45 **Supplementary Figure 8. Identification of functional microbial communities.** The hierarchical
46 clustering dendrograms of 97% OTUs based on microbial co-occurrence network using is shown.
47 In the dendrograms, each color represents one FMC, and each branch represents one OTU.

48

49 **Supplementary Table 1. Demographic information of the cohort**

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51 **Supplementary Dataset 1. OTU significance results between *SeSe*, *Sese* and *sese* individuals.**

52 Pair-wise comparison of relative abundances of OTUs in *SeSe*, *Sese* and *sese* individuals. At lower
53 taxonomic levels, we filtered out low-abundance OTUs based on the criteria of 1) present in at least
54 50% of samples and 2) a minimum count of 30 reads. After this step, 419 OTUs remained, and 19
55 (4.5%) of them were concordantly enriched in *SeSe* individuals when compared with either *Sese* or
56 *sese* individuals (Kruskal-Wallis, FDR corrected $P < 0.25$). Consistent with the phylum level
57 variations, these OTUs represented different clades of Firmicutes, namely *Lachnospiraceae*
58 (*Clostridium* spp., *Roseburia* spp. and *Ruminococcus* spp.), *Catabacteriaceae* and
59 *Faecalibacterium* spp.

60

61 **Supplementary Dataset 2. KEGG pathways that differentiate *SeSe*, *Sese* and *sese* individuals**

62

63 **Supplementary Dataset 3. KEGG pathways that differentiate wild-type *FUT2*^{+/-} and *FUT2*^{-/-}
64 mice**

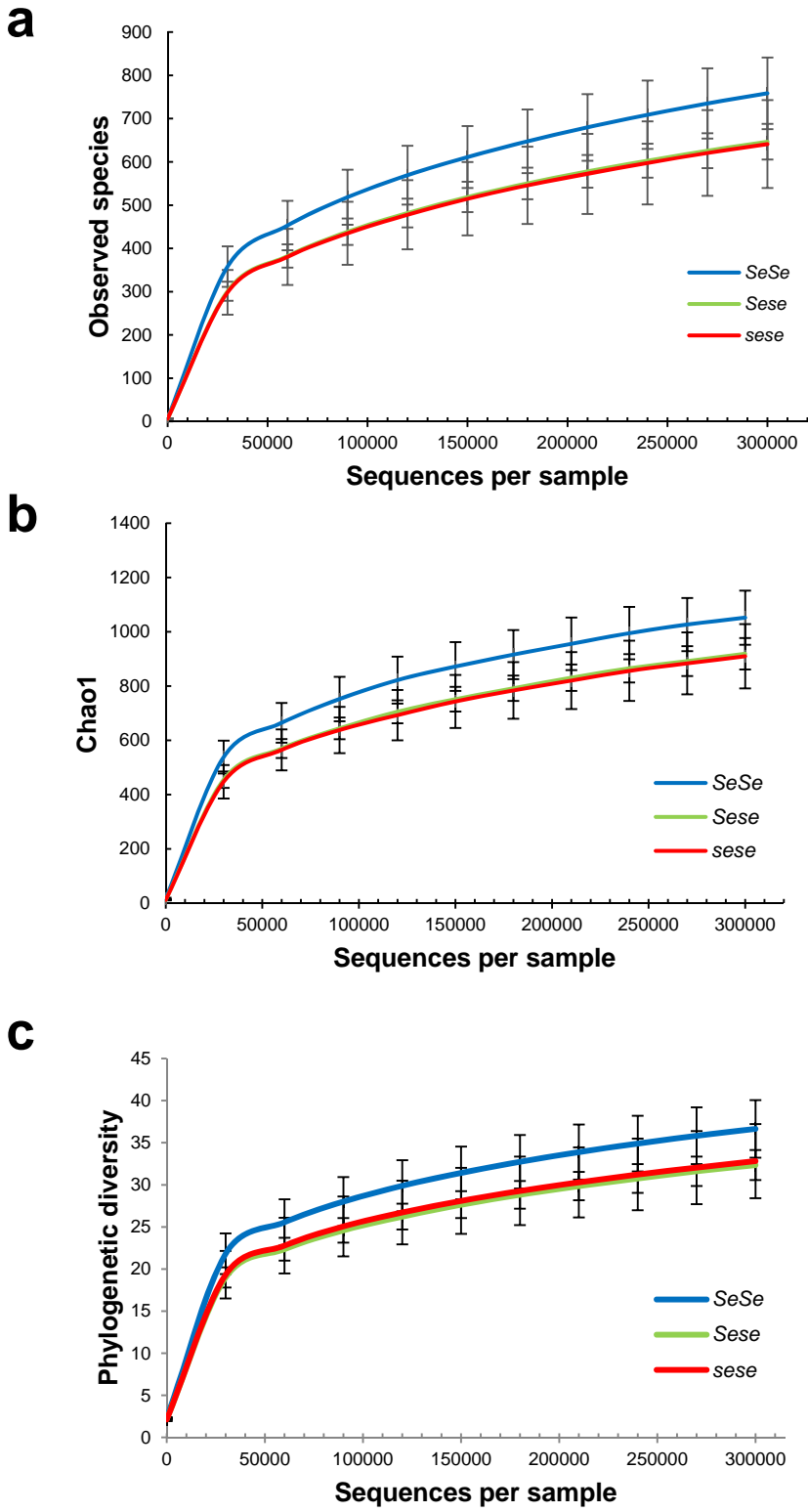
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66 **Supplementary Dataset 4. Module membership and intra-modular connectivity**

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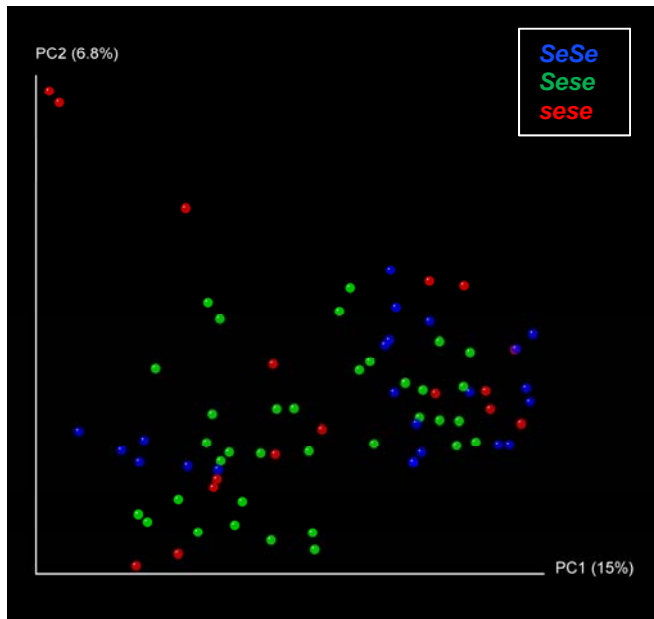
68 **Supplementary Dataset 5. Putative ID of metabolites that differentiate secretors and non-
69 secretors in the human dataset**

Supplementary Figure 1

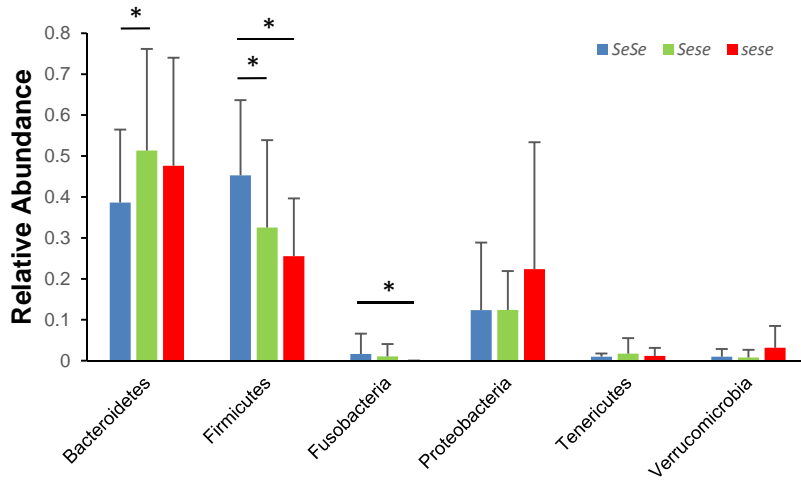


Supplementary Figure 2

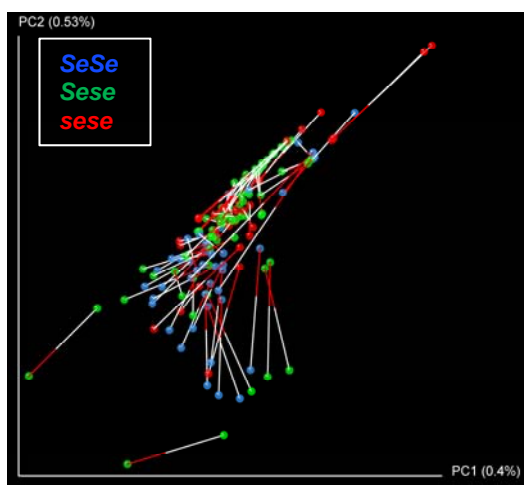
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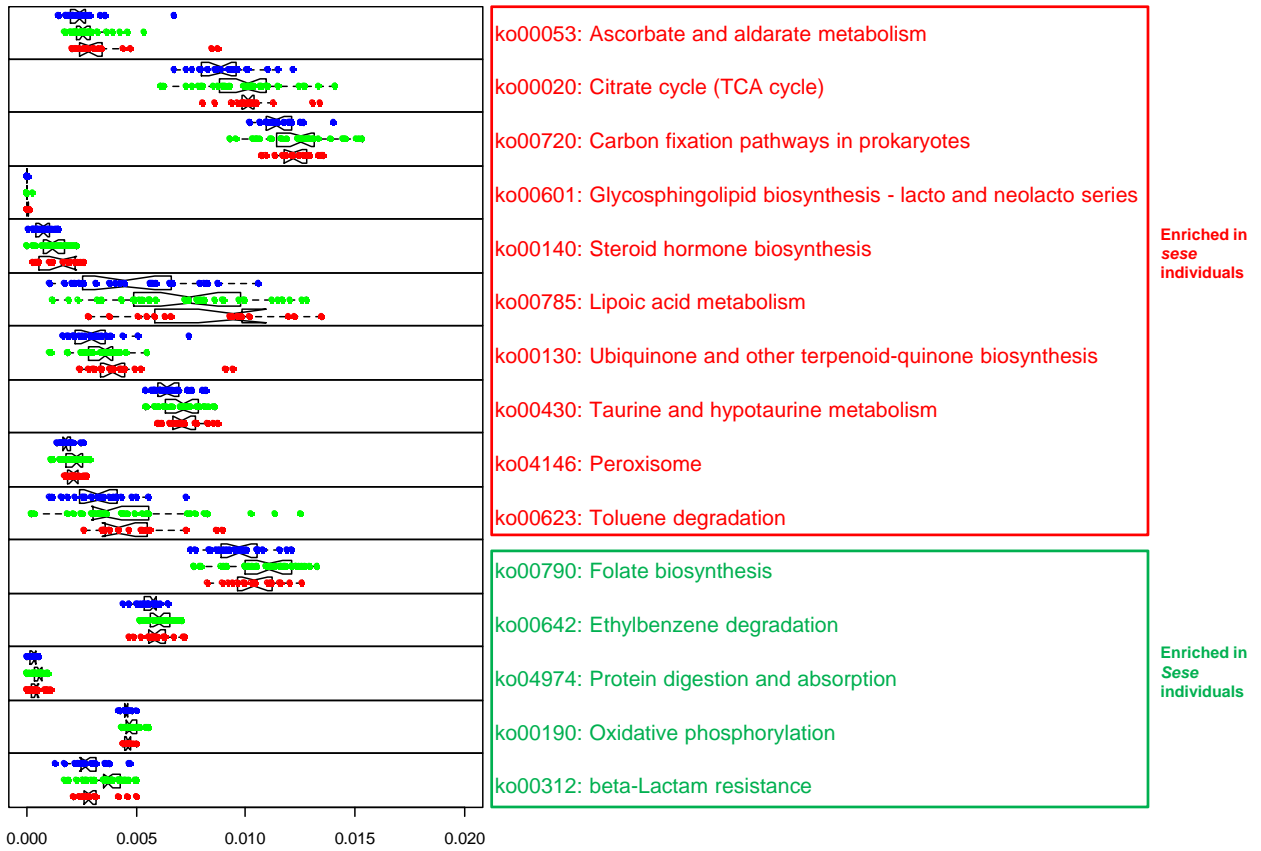
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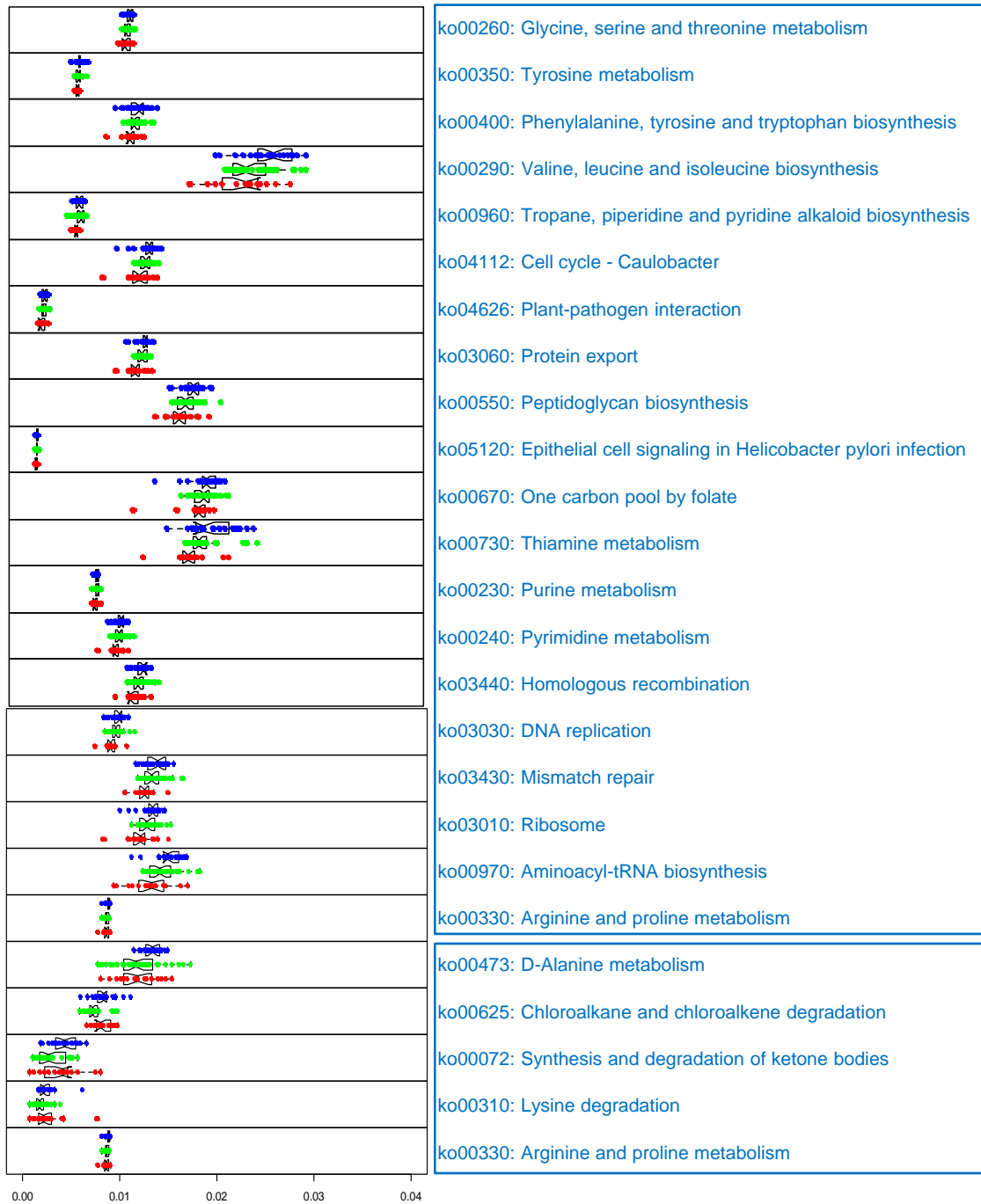
Supplementary Figure 3



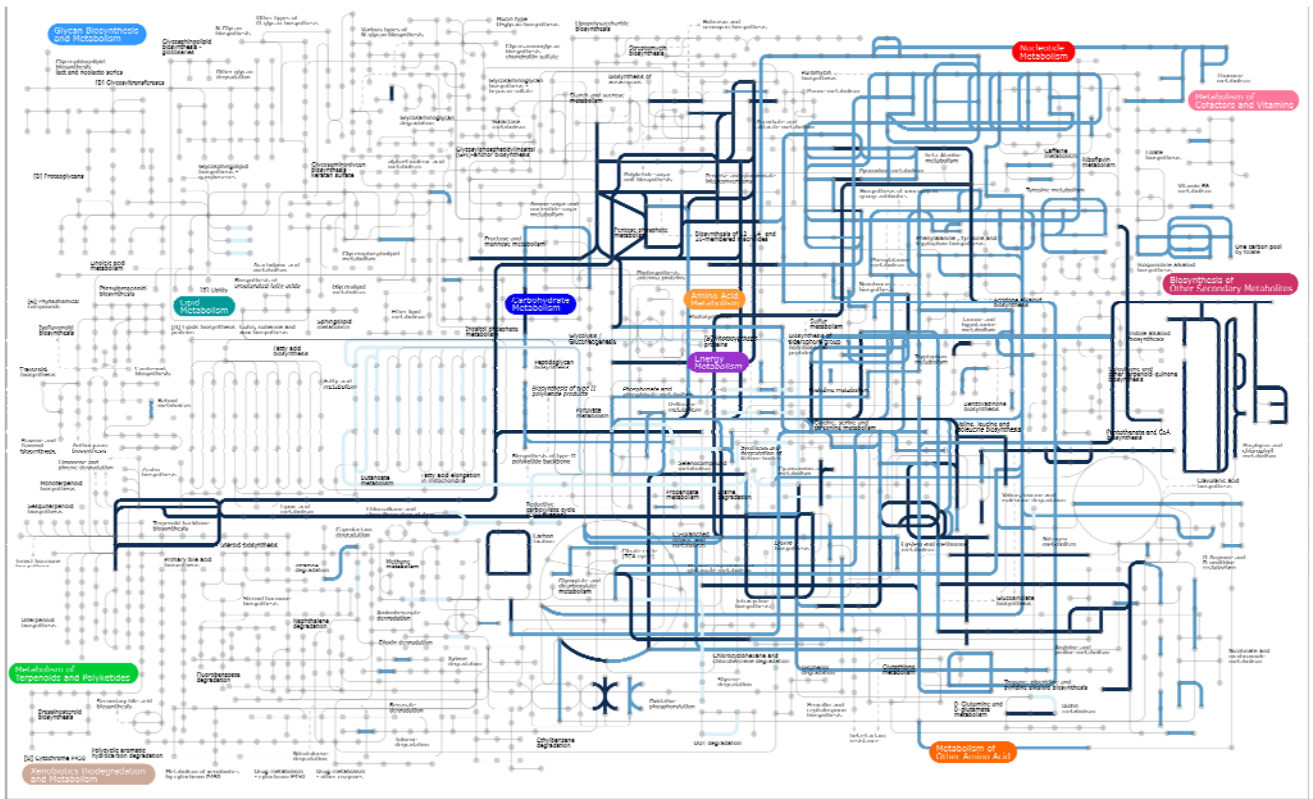
Supplementary Figure 4



Supplementary Figure 5

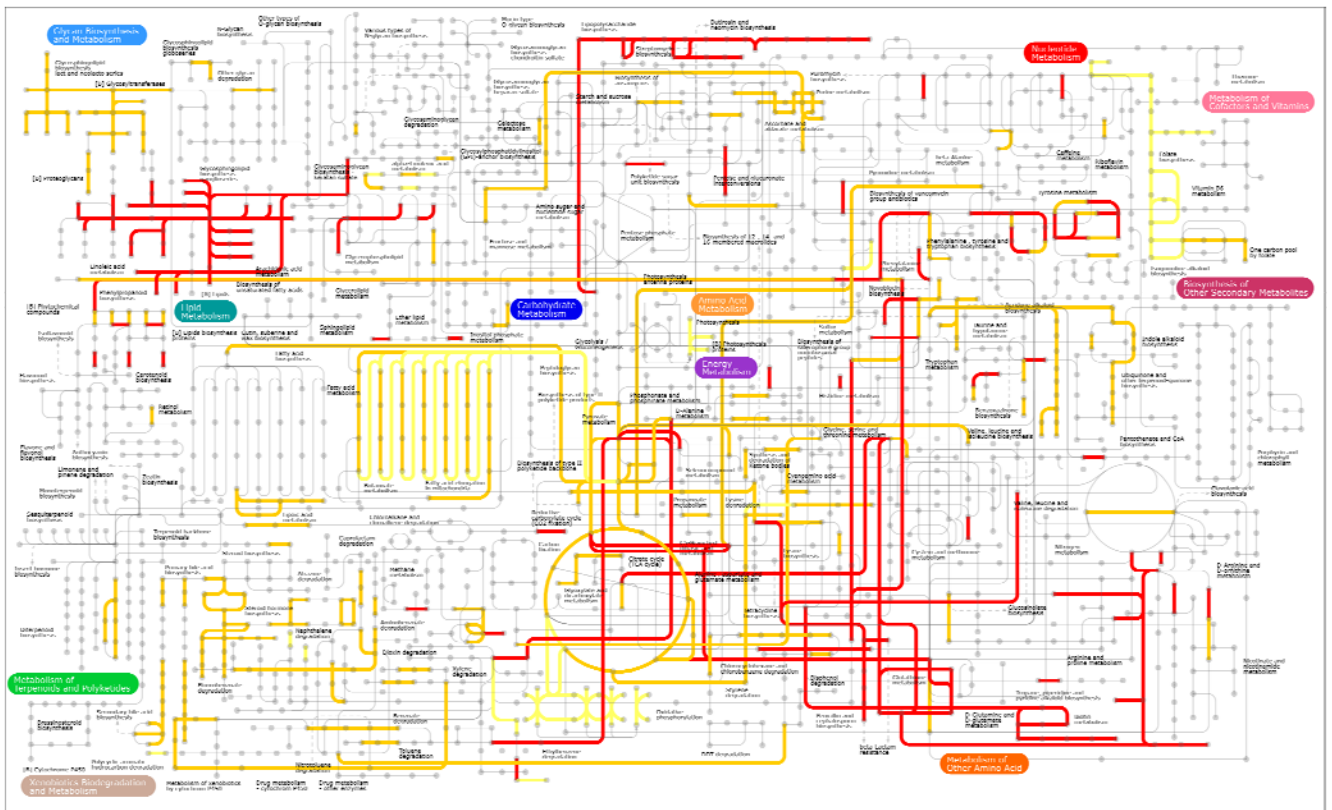


Supplementary Figure 6



- Depleted in Sese
- Depleted in sese
- Depleted in both

Supplementary Figure 7



— Enriched in Sese
— Enriched in sese
— Enriched in both

Supplementary Figure 8

