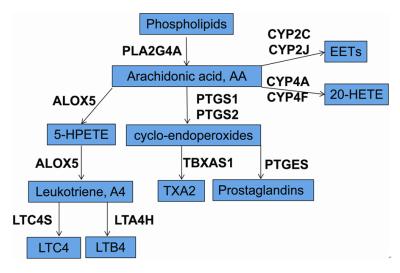
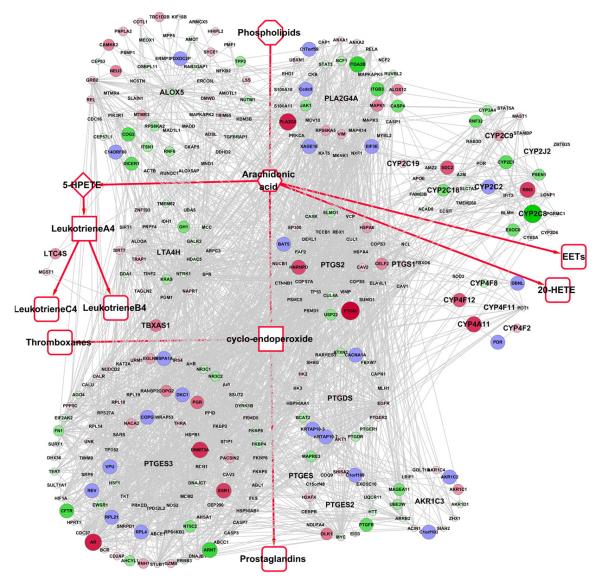
Arachidonic acid metabolism network in esophageal diseases

Supplementary Table 1. DNA sequencing dataset of esophageal cancer from cBioportal

Cancer type	Reference (PMID)	Number of cases	Sequencing method	Abbreviation in cBioportal
Esophageal squamous cell carcinoma	24670651	88	Whole-genome sequencing in 17 ESCC cases and whole-exome sequencing in 71 cases	ICGC, Nature 2014
Esophageal squamous cell carcinoma	24686850	139	Whole exome sequencing or targeted deep sequencing	UCLA, Nat Genet 2014
Esophageal adenocarcinoma	23525077	149	Whole-exome sequencing of 149 EAC tumor- normal pairs, 15 of which have also been subjected to whole-genome sequencing	Broad, Nat Genet 2013
Esophageal carcinoma	NA	186	Whole-genome sequencing	TCGA, Provisional



Supplementary Figure 1. The arachidonic acid metabolism pathway.



Supplementary Figure 2. Expression change and correlation in the AA metabolism PPIN in the GSE9768 dataset after treatment with a mixture of primary bile acids.

Supplementary Table 2. Significant SNPs in esophageal cancer reported in the literature

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Gene symbol	Significant SNP	Cancer type	PubMed ID
PTGS2	rs12042763	269 cases of ESCC	24641411
PLA2G2A	rs11677		
	rs2236771		
PTGS2	rs3218625	1026 cases of ESCC	19347867
PTGS2	-765 G>C	1200 cases of esophageal cancer	19669667
ALOX12	261 Arg> Gln	1026 cases of ESCC	17460548

Arachidonic acid metabolism network in esophageal diseases

```
0%
1.4%
ALOX5
LTC4S
0%
LTA4H
0.7%
PTGS1
0.7%
1.4%
PTGS2
TBXAS1
CYP2C8
0.7%
CYP2C9
0%
0.7%
CYP2C18
0.7%
CYP4A11
0.7%
1.4%
CYP4F2
0%
CYP4F11
0%
1.4%
CYP4F12
PTGES
PTGES3
1.4%
0%
AKR1C3
```

Supplementary Figure 3. Mutation rate of key enzymes in arachidonic acid metabolism from the dataset of Broad, Nat Genet 2013. One block presents one clinical case. Gray color means no alterations, brown color means truncating mutation, green color means missense mutation.

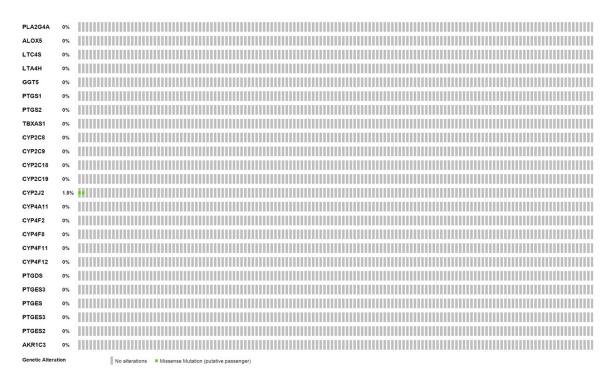
```
PLA2G4A
ALOX5
LTC4S
LTA4H
GGT5
PTGS1
PTGS2
TBXAS1
CYP2C8
CYP2C9
CYP2C18
CYP2C19
CYP2J2
CYP4A11
    CYP4F2
   0%
CYP4F8
    CYP4F11
    CYP4F12
PTGDS
PTGES3
PTGES
PTGES3
    PTGES2
AKR1C3
Genetic Alteration
       No alterations Missense Mutation (putative passenger)
```

Supplementary Figure 4. Mutation rate of key enzymes in arachidonic acid metabolism from the ICGC dataset, Nature 2014. One block presents one clinical case. Gray color means no alterations, green color means missense mutation.

Arachidonic acid metabolism network in esophageal diseases

```
0.9% #
25.
LTC4S
LTA4H
8.5%
1.05
PTGS1
0.5%
os.
PTGS2
108
TBXAS
0.5%
CYP2CE
22%
105
CYP2C18
os.
CYP2.J2
0.5%
CYP4A11
55.
225
CYP4F2
CYP4F8
55.
0.5%
CYP4F11
CYP4F12
145
155
PTGDS
PTGES3
05
PTGES3
05
155
AKR1C3
es |
```

Supplementary Figure 5. Mutation rate of key enzymes in arachidonic acid metabolism from the TCGA dataset, Provisional. One block presents one clinical case. Gray color means no alterations, brown color means truncating mutation, green color means missense mutation.



Supplementary Figure 6. Mutation rate of key enzymes in arachidonic acid metabolism from the UCLA dataset, Nat Genet 2014. One block presents one clinical case. Gray color means no alterations, green color means missense mutation.