Supplementary Material

1 Supplementary Figures and Tables

1.1 Supplementary Figures Captions

Supplementary Figure 1. Small intestinal obstruction. Abdominal CT in axial (A) and sagittal (B) sections demonstrated significant intestinal obstruction (arrows).

Supplementary Figure 2. Distribution and panorama of somatic copy number variation. The panorama of somatic copy number variation (A) exhibits shared copy number variations and differences in the genome between the primary and metastatic lesions. The Venn diagram (B) compares the identical and characteristic somatic cellular mutations of primary and metastatic lesions.

Supplementary Figure 3. GO and KEGG pathway enrichment analysis. GO (Gene Ontology) enrichment analysis of differentially expressed genes in small intestinal metastatic lesions (A) and primary breast lesions (B) demonstrates significantly enriched molecular functions in GO categories. KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment analysis illustrated the significantly enriched functional pathways of metastatic (C) and primary (D) lesions. The color and size of the dots represent the P value and number of genes enriched in the pathway, respectively.

1.2 Supplementary Tables

Supplementary Table 1. Representative shared point mutations, insertions and deletions of sample genes before chemotherapy

| Genes | Transcripts | Base changes | Amino acid changes | Functional regions | Mutation frequency of primary tumor (%) | Mutation frequency of metastatic tumor (%) |
|-------|-------------|--------------|--------------------|--------------------|----------------------------------------|------------------------------------------|
| CDH1  | NM_004360.3 | c.1147C>T    | p.Q383*            | EX9                | 43.9                                   | 13.2                                     |
| PIK3CA| NM_006218.2 | c.1624G>A    | p.E542K            | EX10               | 39.6                                   | 13.4                                     |
| AKT1  | NM_00101443 | c.49G>A      | p.E17K             | EX3                | 2.1                                    | -                                        |

Supplementary Table 2. Other representative shared structural variations of the two sample genes before chemotherapy

| Genes | Transcripts | Variation type | Functional regions | Mutation frequency/copy coefficients |
|-------|-------------|----------------|--------------------|---------------------------------------|
|       |             |                |                    | primary tumor | metastatic tumor |
| FGFR1 | NM_023110.2 | Amplification  | 8p11.23            | 1.94        | -               |
| CCND1 | NM_053056.2 | Amplification  | 11q13.3            | 3.42        | 1.84            |
| FGF19 | NM_005117.2 | Amplification  | 11q13.3            | 3.43        | 1.81            |
| FGF4  | NM_002007.2 | Amplification  | 11q13.3            | 3.97        | -               |
| FGF3  | NM_005247.2 | Amplification  | 11q13.3            | 3.95        | -               |