Supplemental Fig. 1. Change in reconstructed errors according to different reference signature sets. The vertical axis represents the decreased ratio of reconstructed errors by gastric cancer-related signatures and signature 6 (error_s12) compared with that by gastric cancer-related signatures only (error_s11). The reconstructed error for each sample is shown in Supplemental Table 1.
## Supplemental Table 2. Sequencing statistics

| Sample* | Mapped reads | Total reads | Mapping rate (%) | Average depth (×) | Coverage at least 1× (%) | Coverage at least 5× (%) ** |
|---------|--------------|-------------|------------------|------------------|--------------------------|-----------------------------|
| mouse1N† | 686,424,007  | 690,189,248 | 99.5             | 32.4             | 97.9                     | 96.9                        |
| mouse1T† | 1,760,067,996| 1,768,951,232| 99.5             | 77.8             | 98.4                     | 97.5                        |
| mouse2N† | 572,274,358  | 575,959,334 | 99.4             | 27.8             | 96.1                     | 95.6                        |
| mouse2T† | 1,707,299,805| 1,727,069,406| 98.9             | 77.6             | 96.2                     | 95.9                        |
| mouse3N  | 694,786,902  | 878,539,574 | 90.5             | 34.6             | 95.1                     | 94.2                        |
| mouse3T  | 2,096,591,729| 2,679,937,228| 91.4             | 105.0            | 95.4                     | 94.7                        |
| mouse6N  | 673,148,693  | 866,240,228 | 91.8             | 34.2             | 94.9                     | 94.0                        |
| mouse6T  | 1,994,377,732| 2,565,590,330| 91.1             | 99.3             | 95.3                     | 94.6                        |
| mouse7N  | 680,350,881  | 902,993,898 | 91.5             | 34.8             | 95.0                     | 94.1                        |
| mouse7T  | 1,959,871,069| 2,473,695,076| 91.6             | 99.3             | 95.2                     | 94.6                        |
| mouse9N  | 678,122,173  | 877,817,678 | 91.9             | 34.6             | 95.0                     | 94.1                        |
| mouse9T  | 2,058,843,749| 2,628,230,392| 91.1             | 102.8            | 95.5                     | 94.7                        |
| mouse10N | 675,436,008  | 883,001,728 | 91.2             | 34.1             | 95.0                     | 94.1                        |
| mouse10T | 2,027,119,891| 2,602,551,374| 91.6             | 102.2            | 95.3                     | 94.7                        |
| mouse11N | 666,863,094  | 855,346,382 | 91.3             | 33.3             | 94.9                     | 94.0                        |
| mouse11T | 2,114,498,609| 2,738,673,484| 91.8             | 107.0            | 95.3                     | 94.7                        |

*: N: normal tissue; T: tumor tissue.

**: For mouse1 and mouse2: coverage at least 4×.

†: Sequenced by PCR libraries; the other samples were sequenced by PCR-free libraries.
Supplemental Table 3. Number of SNVs and indels detected in eight mouse tumors

Mouse1 and mouse2 were sequenced by PCR libraries; the other samples were sequenced by PCR-free libraries.

| Sample  | SNV  | Indel |
|---------|------|-------|
| mouse1  | 4,416| 474   |
| mouse2  | 5,770| 698   |
| mouse3  | 4,116| 2,807 |
| mouse6  | 164  | 18    |
| mouse7  | 3017 | 257   |
| mouse9  | 1133 | 76    |
| mouse10 | 1511 | 506   |
| mouse11 | 2,226| 732   |
| Total   | 22,353| 5,568 |
Supplemental Fig. 2. Circos plot for eight mouse tumors. Black arrows indicate potential chromothripsis. Outer ring: chromosome loci. Middle ring: absolute copy number, red: amplification; blue: deletion. Inner ring: structural variation, color indicates the chromosome at which the first broken end of SV starts.
Supplemental Fig. 3. B-allele frequencies and copy number status of eight mouse tumors. Black arrows indicate potential chromothripsis.
Supplemental Fig. 4. SVs in DCKO mice. (a) Genes targeted by recurrent SVs. (b) SV status of mouse orthologs of human CFS genes.
Mouse2
Normal
Tumor purity: 0.39
Gata4: 47 copies

Mouse9
Normal
Tumor purity: 0.15
Gata4: 11 copies

Mouse1
Normal
Tumor purity: 0.39
Myc: 7 copies

Mouse7
Normal
Tumor purity: 0.39
Cdk6: 10 copies
Cdk8: 8 copies

Mouse2
Tumor purity: 0.39
5 copies
Cdk6: 10 copies
Cdk8: 8 copies

Mouse3
Normal
Tumor purity: 0.64
Foxa1: 12 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse3
Normal
Tumor purity: 0.64
Mycn: 7 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies

Mouse11
Normal
Tumor purity: 0.21
Sox9: 9 copies

Mouse11
Normal
Tumor purity: 0.21
Mycn: 30 copies

Mouse7
Tumor purity: 0.39
Cnd1: 18 copies
Supplemental Fig. 5. Focal amplifications in putative additional drivers. (a) Focal amplifications and estimated absolute copy number in each putative additional driver. (b) Focal amplification of *FOXA1* in three TCGA gastric cancers (IDs: TCGA-HU-A4GC, TCGA-IN-8462, and TCGA-VQ-AA6D).
**Supplemental Table 7. Focal CNV status of gastrointestinal TFs.** Numbers in the table indicate the absolute copy numbers of genes targeted by focal CNV events.

| Sample  | Gata4  | Gata6  | Klf5  | Sox2 | Sox9 | Foxa1 |
|---------|--------|--------|-------|------|------|-------|
|         | (14qD1)| (18qA1)| (14qE2.2) | (3qA3) | (11qE2) | (12qC1) |
| mouse1  | -      | -      | -      | -    | -    | -     |
| mouse2  | 47     | -      | -      | -    | -    | -     |
| mouse3  | -      | -      | -      | -    | -    | 12    |
| mouse6  | -      | -      | -      | -    | -    | -     |
| mouse7  | -      | -      | -      | -    | -    | -     |
| mouse9  | 11     | -      | -      | -    | -    | -     |
| mouse10 | -      | -      | -      | -    | -    | -     |
| mouse11 | -      | -      | -      | -    | 9    | 1     |
Supplemental Fig. 6. Signature-based hierarchical clustering of mouse and human gastric cancers

All cases were classified into four clusters: signature 6 cluster (c1), signature 5 cluster (c2), signature 1 cluster (c3), and signature 17 cluster (c4). There were no significant differences in clinical features among c2, c3, and c4 (chi-square test, subtype: $p = 0.24$; Lauren class: $p = 0.70$; tumor stage: $p = 0.58$; Kruskal–Wallis rank sum test, age: $p = 0.46$). NA: gray.