

Supplementary Figure Legends

Figure S1. Venn diagrams showing the overlapping between strains sensitive to 5FU and other drugs (valproic acid, bortezomib, micafungin and terbinafine). Three GO biological processes (chromosome organization, chromosome segregation and RNA metabolism) are shown. The two-sided Fisher's exact test was used to calculate P values for the significance of the overlaps.

Figure S2. Sensitivity to 5FU of the *S. pombe* strain deleted for the argonaute gene. The ago1 Δ strain was sensitive to 5FU when compared to the control wild-type (ED668). Data are representative of three independent experiments.

Figure S3. MNase analysis of chromatin from cells treated or not with 5FU. (A) Nucleosome profile after digestion of chromatin with 0, 15, 60 and 240 U/ml of MNase. Samples were separated by gel electrophoresis and quantified by densitometry. (B) DNA protected by nucleosomes obtained from the control or 5FU-treated cells. Values represent mean \pm standard deviation of five independent replicates. No significant differences were found between controls and 5FU-treated cells.

Figure S4. PCR verification of gene deletion strains from Bioneer collection. A total of 18 strains sensitive to 5FU were randomly selected to check whether the appropriated target gene was disrupted. PCR experiments using specific primers for 5' upstream and 3' downstream of the deletion cassette and common primers at the KanMX4 module allowed us to estimate that approximately 90% of the strains had the correct deletion.

Supplementary Table Legends

Table S1. List of the 270 *S. pombe* deletion strains more sensitive to 5FU. Mutants from Bioneer Sets ver 2.0 and upgrade ver 3.0 were used. Genes were grouped according to

GO biological process categories. The absorbance measurements at 595 nm, after the addition of 0, 25, 50 or 150 μ M 5FU were indicated for each time. Controls ED668 and ED666 were also included.