SUPPLEMENTAL DATA

The Fission Yeast Swi5-Sfr1 Complex, an Activator of Rad51 Recombinase, Forms an Extremely Elongated Dogleg-Shaped Structure*

Yuichi Kokabu[1], Yasuto Murayama[2], Naoyuki Kuwabara[3], Tomotaka Oroguchi[1], Hiroshi Hashimoto[1], Yasuhiro Tsutsui[2], Naohito Nozaki[4], Satoko Akashi[1], Satoru Unzai[1], Toshiyuki Shimizu[3], Hiroshi Iwasaki[2], Mamoru Sato[1], and Mitsunori Ikeguchi[1]

[1]Graduate School of Nanobioscience, Yokohama City University, 1-7-29 Suehiro-cho, Tsurumi-ku, Yokohama, 230-0045, Japan.
[2]Graduate School of Bioscience & Biotechnology, Tokyo Institute of Technology, 4259, Nagatsuda-cho, Midori-ku, Yokohama, 226-8501, Japan.
[3]Graduate School of Pharmaceutical Sciences, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo, 113-0033, Japan.
[4]Bio-Frontier Research Center, Tokyo Institute of Technology, 4259, Nagatsuda-cho, Midori-ku, Yokohama, 226-8501, Japan.

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Figure S1

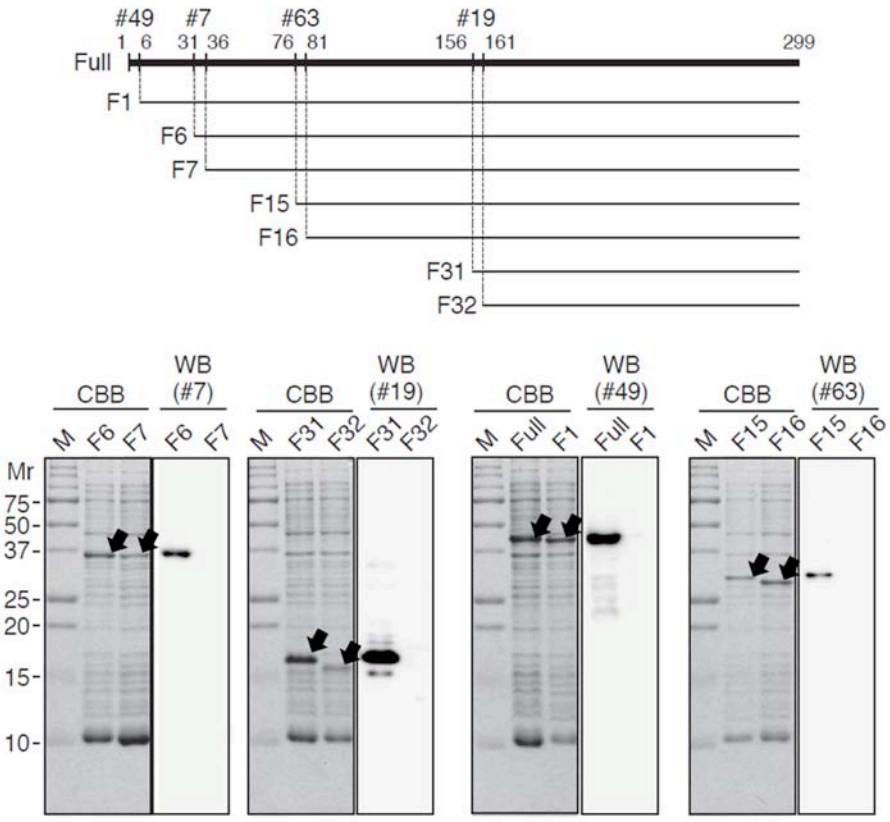

Figure S1. *Determination of the recognition sequence of the monoclonal antibodies.* ***Upper.*** Schematic of the series of the Sfr1 N-terminal truncation constructs. Every five amino acid residues were truncated from the N-terminus (F1 to F40) and the truncated Sfr1 peptides were expressed in a T7 expression system. Only the truncated constructs important for the determination of the recognition sequence are presented in the panel. ***Lower.*** A pair of the important crude extracts of *E. coli* cells expressing the Sfr1 peptides was separated by SDS-PAGE, followed by visualization with Coomassie brilliant blue (CBB) or immunoblotting with four specific antibodies (#7, #19, #49 and #63) Black arrow-heads in the CBB-stained gels correspond to the Sfr1 protein.

Figure S2

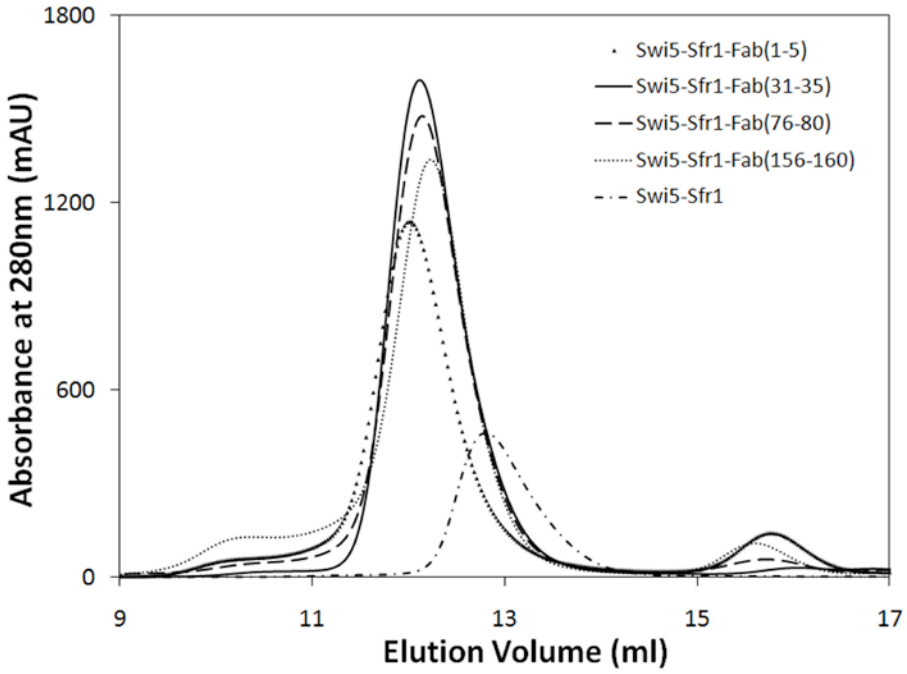

Figure S2. *Swi5-Sfr1 and Fab fragments of Sfr1-specific monoclonal antibodies form stable complexes.* Gel filtration for the Swi5-Sfr1 and Swi5-Sfr1-Fab complexes. Four Fab fragments that bind to distinct sites of Sfr1 were applied. The binding sites of the four Fabs, #7, #19, #49 and #65, correspond to 31-35, 156-160, 1-5, and 76-80 of Sfr1, respectively. Elution profiles for the Swi5-Sfr1-Fab complexes containing Fab (1-5), Fab (31-35), Fab (76-80), and Fab (156-160) are shown in triangles, thin solid lines, dashed lines, and dotted lines, respectively. The elution profile of the Swi5-Sfr1 complex alone is also shown.

Figure S3

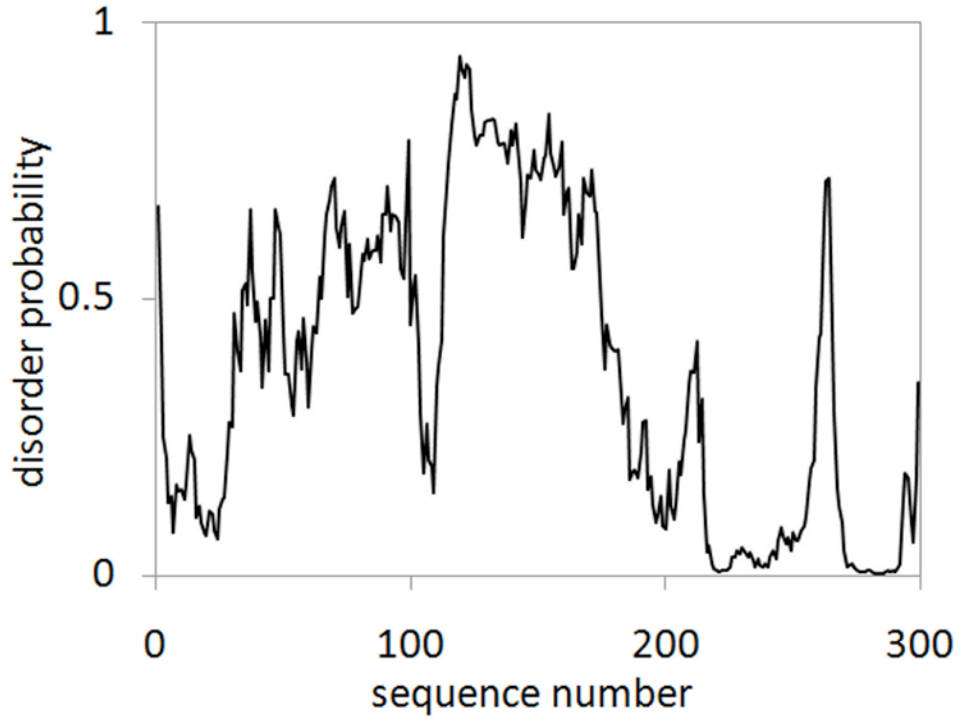

Figure S3. *Disorder probability of Sfr1*. Disorder probability of Sfr1 was calculated from the primary sequence by using DISOPRED. The N-terminal half of Sfr1 has high IDP propensity.