Supplementary Figures and Captions

THE RNA-BINDING PROTEIN FUS/TLS INTERACTS WITH SPO11 AND PROVIDES A LINK WITH PRDM9-DEPENDENT RECOMBINATION HOTSPOTS

Teresa Giannattasio, Erika Testa, Ramona Palombo, Lidia Chellini, Álvaro Crevenna, Petko M. Petkov, Maria Paola Paronetto, and Marco Barchi

[1] University of Rome "Tor Vergata", section of anatomy, via Montpellier, 1, 00133 Rome, Italy; [2] Laboratory of Molecular and Cellular Neurobiology, Fondazione Santa Lucia, CERC, 00143 Rome, Italy; [3] European Molecular Biology Laboratory, Rome, Italy [4] The Jackson Laboratory, Bar Harbor, ME 04609, USA; [5] Institut de Génétique Humaine (IGH), University of Montpellier, Centre National de la Recherche Scientifique, Montpellier, France; [6] Department of Movement, Human and Health Sciences, University of Rome Foro Italico, Piazza Lauro de Bosis 6, 00135 Rome, Italy.

Correspondence: mariapaola.paronetto@uniroma4.it (MPP); marco.barchi@uniroma2.it (MB)

Fig. S1 Analysis of co-localization of SYCP3 and FUS. A) Representative images of zygonema cells, stained by SYCP3 and FUS, acquired using inverted fluorescence microscopy. Magnifications show SYCP3 (green) and FUS (red) single channels. Harrows point to FUS foci and aggregates that co-occur with SYCP3. B) Representative image of a cell at preleptonema/leptonema stained by SYCP3 and FUS and acquired by confocal microscopy. Single channels are in grey, while in merge SYCP3 is red and FUS is grey. C) here the FUS channel in B was rotated clockwise of 180 degrees and overlapped with SYCP3. D-E) Red dots, FUS/SYCP3 Pearson's co-localization coefficient (PCC) calculated in cells at the indicated stage of development. Black dots, Pearson's co-localization coefficient (PCC) calculated in the same set of cells after clockwise rotation of FUS channel of 180 degrees (***$p<0.001$). F) Representative image of SYCP3 and FUS pattern at pachynema. Magnification bars represents 10 μm.

Fig. S2 A) Representative images of SYCP3 (red) and PRDM9 (grey) staining in spermatocytes at the indicated stages of development. Magnification bar represents 10 μm. B) quantification of PRDM9/SYCP3 co-localization and C) FUS/PRDM9 co-localization by Pearson's correlation coefficient (PCC) calculated on a representative group of cells at the indicated stages of development, before (red dots) and after (black dots) rotation of PRDM9 channel. Each dot is a cell. Error bars are mean ± standard error of the mean. Statistical significances (***$p<0.001$) are calculated by two-tail t-test**.** D) percentage of prophase I stage cells in 10 dpp mice testes. Preleptotene (pLe), leptotene (Le), early zygotene (eZ), mid zygotene (mZ) late zygotene (lZ), early pachytene (eP). n. indicates the number of cells.