Human CST Facilitates Genome-wide RAD51 Recruitment to GC-Rich Repetitive Sequences in Response to Replication Stress

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AUTHOR CONTRIBUTIONS

M.C., Q.Z., O.S., P.J., C.H., X.D., M.F., W.C. performed experiments and analyzed data. MC analyzed all ChIP-seq sequences, obtained metaphase FISH data, performed IF experiments and data analysis, assembled figures. Q.Z. obtained RAD51 ChIP results, performed qPCR and data analysis, participated in IF and figure assembly. OS obtained STN1 ChIP results. M.F.M. contributed to the initial conception of the project, gave technical advice, and performed initial ChIP-seq analysis, initial motif discovery experiments, and oncomine Stn1 expression analysis. Q.Z., P.J., C.H., and X.D. contributed to co-IP analysis. L.W. processed ChIP-seq reads. P.Y. directed ChIP-seq reads processing study. W.C. conceived the project, directed the study, participated in cell line establishment, FISH, IF, co-IP experiment execution, and wrote the manuscript.

In the originally published version of this article, Dr. Fadri-Moskwik was omitted. The corrected author list, affiliations, and author contributions are provided here.

The authors regret this error.

