Supplementary Table 1

Details on experimental conditions for multiplex qIHC staining. Table shows the antibodies used in the current study, antigen retrieval conditions and details on dilution of primary and secondary antibodies. NA-not applicable

Supplementary Table 2

Scoring of Ki67 and MCM2 staining in human gastric samples. Immunohistochemical staining for Ki67 and MCM2 were performed and cells positive for nuclear signals are shown as a percentage of all nuclei in representative areas. Values shown are mean positivity per sample.

Supplementary Table 3

Patient details for TMA used for MCM2 staining. For cores stained with anti-MCM2 and data shown in figure 1A and figure 1C, patient clinical information is provided.

Supplementary Table 4

Patient details for TMA with IM and IGC cores. For cores stained with anti- MCM2/γH2AX and data shown in figure 1B and figure 1D, patient clinical information is provided.

Supplementary Table 5

Patient details for TMA used γH2AX staining. For cores stained with anti-γH2AX and data shown in figure 2A and figure 2C, patient clinical information is provided.

Supplementary Table 6

Patient details for GCEP samples used for γH2AX staining. For GCEP tissues stained with anti-MCM2/γH2AX and data shown in figure 3, patient clinical information is provided.

Supplementary Table 7

Patient details for MCM2 and γH2AX staining of gastric tissues with different extents of inflammation. For gastric tissues stained with anti-MCM2/γH2AX and data shown in figure 4, patient clinical information is provided.

Supplementary Table 8

Patient details for MCM2 and γH2AX staining of IM samples from GCEP with different extents of genomic instability. For IM samples stained with anti-MCM2/γH2AX and data shown in figure 5, patient clinical information is provided.

Supplementary Table 9

Correlation between CD44v9 and γH2AX in IM samples. Pearson's correlation analysis was performed to compare the relationship between CD44v9 and γH2AX staining. Cells positive for γH2AX, CD44v9 or both were subjected to Pearson's correlation analysis and tested for statistical significance. *r* (Pearson's correlation coefficient) was computed for highest biopsy region expressing CD44v9. *Sample ID numbers are matched to patient IDs from figure 5A-D.

Supplementary Table 10

An integrated view of alterations observed in the IM lesions subjected to genomic and IHC analysis. **For the samples used for DDR signalling and cell proliferation analysis (Figure 5A-E), %** CD44v9 expression, mutational accumulation, DNA repair gene mutations, CNAs, promoter hypermethylation and differential hypermethylation of DNA repair genes is shown. CNAs were identified using the GATK4 workflow for allelic copy number variation (ACNV; https://software.broadinstitute.org/gatk/). *Sample ID numbers are matched to patient IDs from figure 5A-D. **NA- Data not available.

Supplemental Appendix

Supplemental Appendix 1

A list of genes found mutated in IM samples. Sample ID numbers are matched to patient IDs from figure 5A-D.

Supplemental Appendix 2

Manually curated list of DNA repair and DNA damage signaling genes

Supplemental Appendix 3

DNA methylation analysis of IM samples. The methylation data from Huang et al (1) was used measure the average β values for the promoter regions of DNA repair genes. The column labelled "Normal" is the average methylation β values of 39 normal gastric samples. Sample ID numbers are matched to patient IDs from figure 5A-D.

References

1. Huang KK, Ramnarayanan K, Zhu F, Srivastava S, Xu C, Tan ALK, et al. Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer Cell. 2018;33(1):137-50 e5.