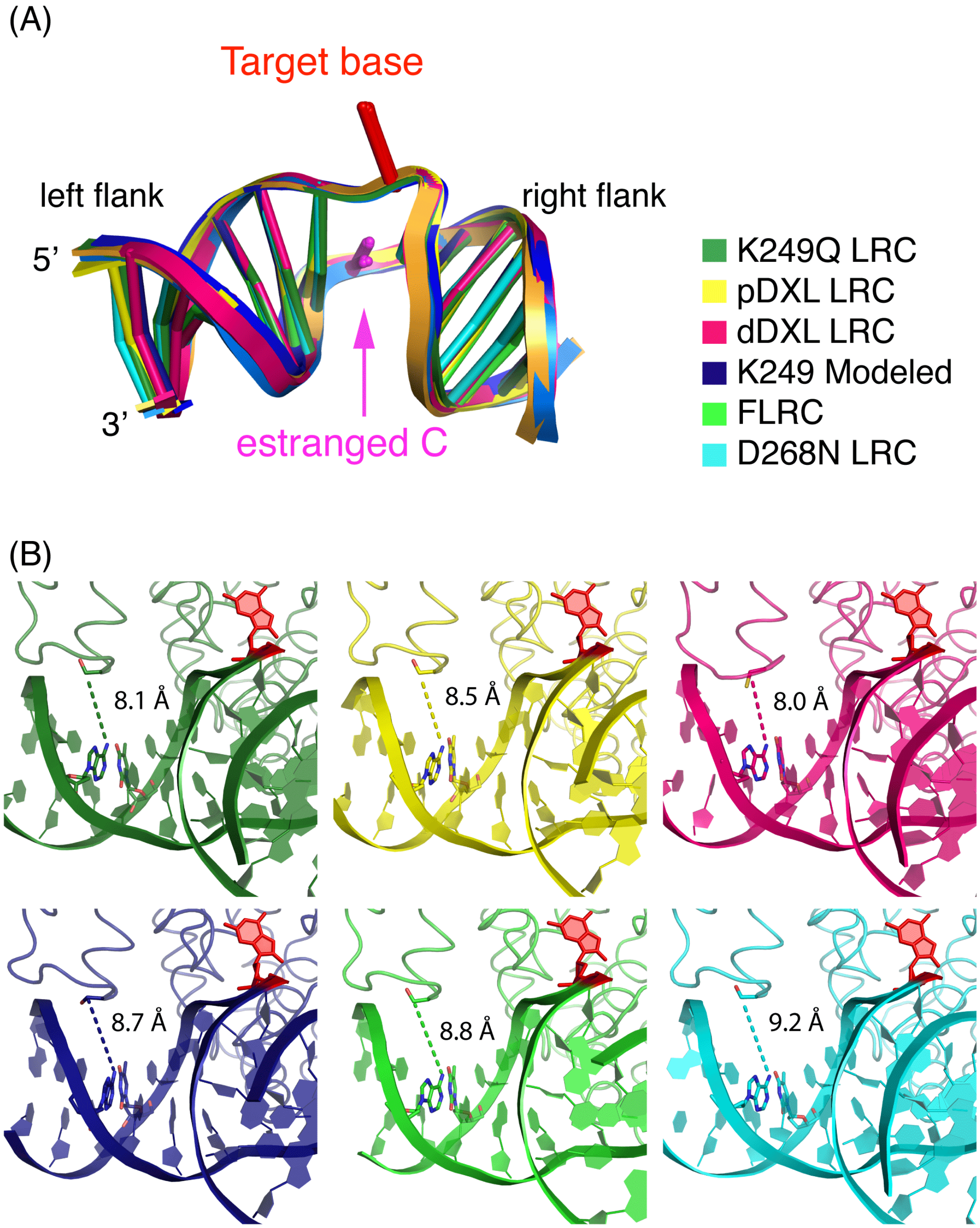

Supplemental Fig. 3. Comparison of the Lesion Recognition Complexes. The DNA portion of the LRC’s are represented in ribbon with the duplexes colored by the specific complex: K249Q (forest green), 1EBM, (1)), K249Q, N149C (pDXL, yellow, 1YQR, (2)), K249Q, S292C (dDXL, hotpink, 2NOL, (3)), K249-modeled and MD simulated LRC (dark blue, see Supp. Materials and Methods), 2’-fluoro-oxoG and WT hOGG1 (green, 3KTU, S. Lee and G.L.V.), and D268N (cyan, 1N3C, (4)). In this overlay, the protein alone was used for the superposition of the structures. Complexes were aligned to the K249Q LRC by a least squares superposition using protein residues 12-300 with the program Coot (5). The target base is colored red and the estranged C is magenta. DNA ribbon and cylinder representation generated with X3DNA (6) and Nuccyl (7) and Pymol (8). *B*, A comparison of distal crosslinking site distances in the hOGG1 LRC's is shown. Complexes are colored according to the key in panel A. Numbers beside structures are the distances from adenine N^6 to the C_β of residue 292. In all cases, the protein is displayed as a ribbon and the DNA is shown in cartoon representation. OxoG is shown in sticks and colored red.

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