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KDM5A (56) DWQPPFACEVKSFRFTPR---FGSGFPVKDGRRKILPEE (435)
KDM5B (69) DWQPPFACDVKLHFTPR---FGSGFPVRDGKIKLSPEE (451)
KDM5C (51) DWQPPFAVEVDNFRFTPR---FGSGFPVSDSKRHILTPEE (466)
KDM5D (51) DWQPPFAVEVDNFRFTPR---FGSGFPVSNSKQNLSPPEE (456)

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B

Enzyme	(<i>R</i>)-2HG Ki (μ M)	(<i>S</i>)-2HG Ki (μ M)
KDM5A	203 \pm 43	81 \pm 4
KDM5A F68L	144 \pm 37	31 \pm 13
KDM5A R429I	161 \pm 47	68 \pm 33
KDM5B	655 \pm 153	303 \pm 51

Supplementary Figure S5: KDM5A mutants. (A) Sequence alignment of KDM5 residues predicted to be involved in 2OG binding [RefSeq accession numbers: NM_001042603.3 (KDM5A); NM_006618.5 (KDM5B); NM_004187.5 (KDM5C); NM_004653.5 (KDM5D)]. (B) Ki values for (*R*)-2HG and (*S*)-2HG of the indicated KDM5 variants. Results shown are the mean \pm standard deviation of two independent assays.