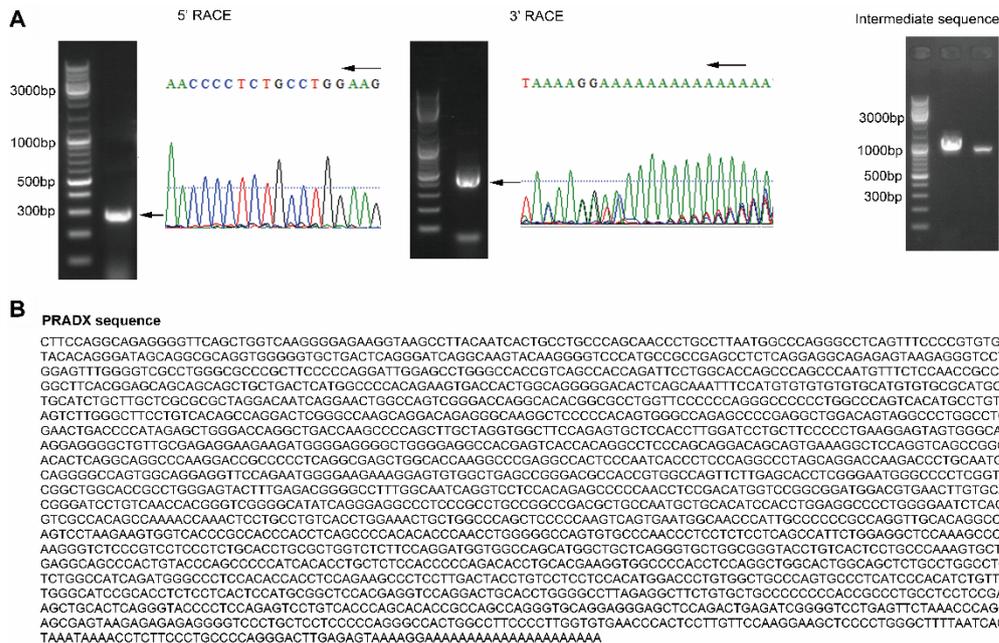


Supplementary materials

1

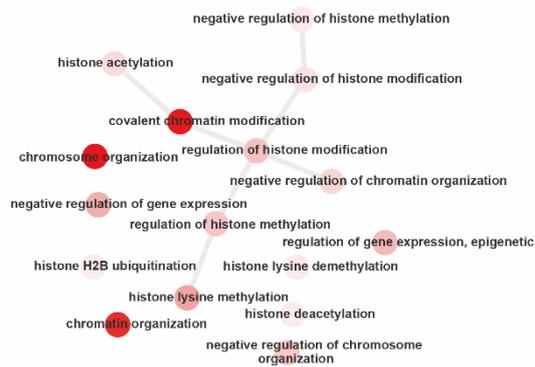


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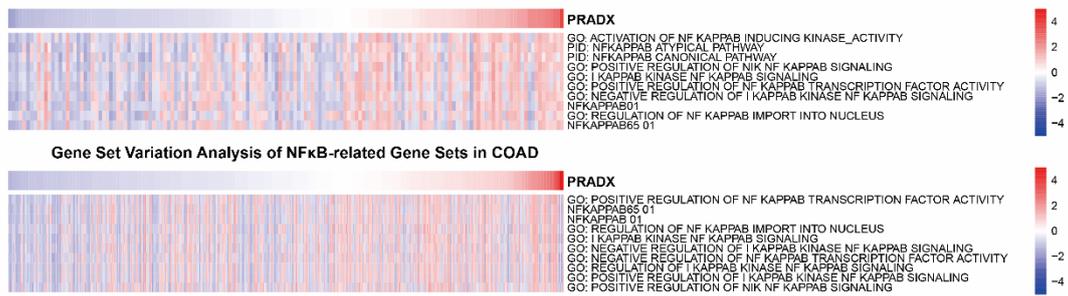
3 **Figure S1** PRADX is a novel lncRNA in cancer cells. **A** Representative images of
 4 PCR products from the 5'RACE (left panel), 3'RACE (middle panel), or intermediate
 5 sequence (right panel). The major PCR product is marked by an arrow, and the
 6 sequence of the PCR product is shown beside it with an arrow indicating the boundary
 7 of PRADX sequence. **B** The full-length sequence of PRADX. **C** The coding potential
 8 was analyzed for the PRADX sequence by 5 different means. **D** Quantification of
 9 PRADX expression was measured by ImageJ software. *** $P < 0.001$.

10

**A GO analysis of co-expression cluster
(Histone Modification related terms)**



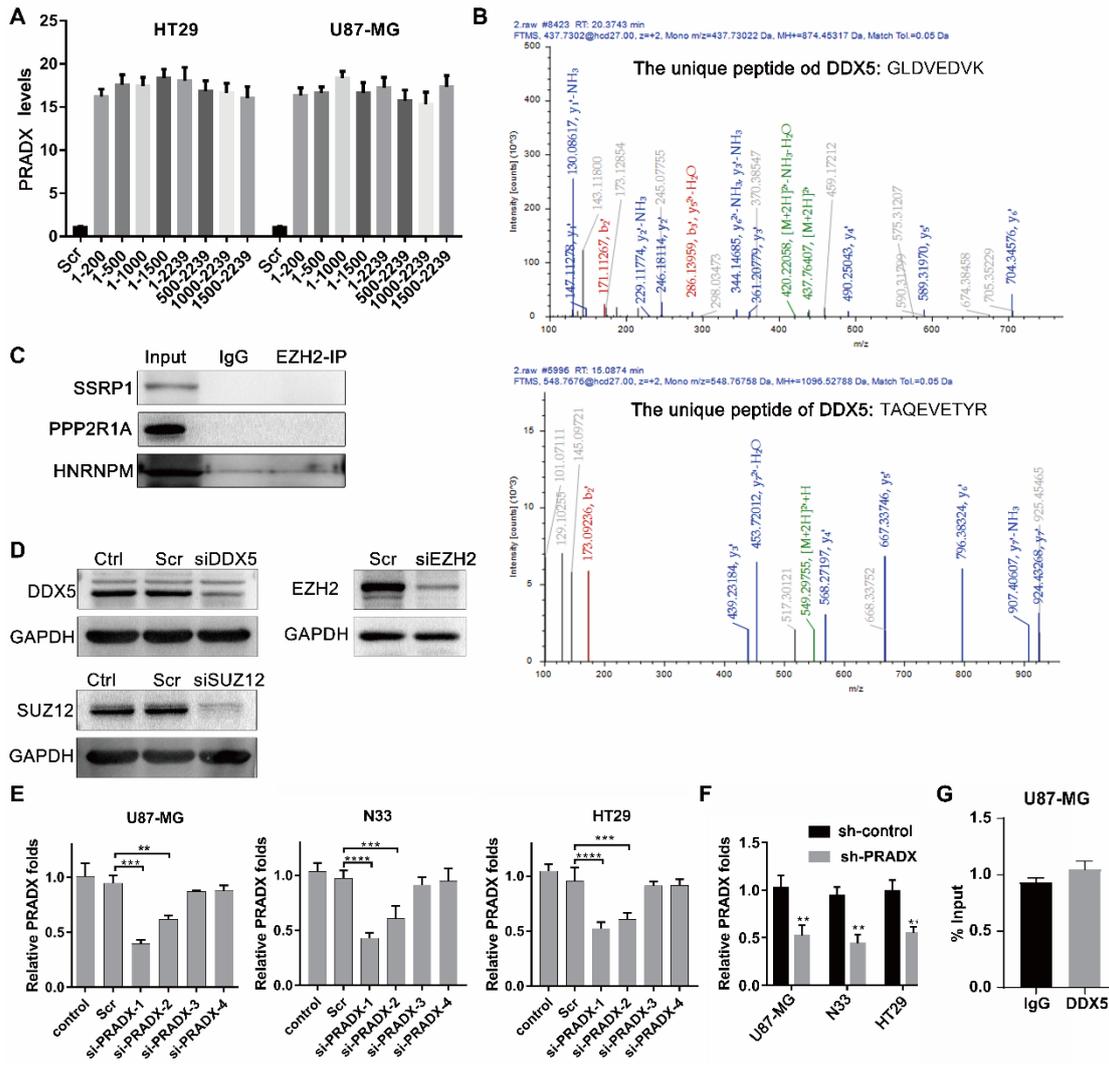
B Gene Set Variation Analysis of NFκB-related Gene Sets in GBM



11

12 **Figure S2** The gene ontology (GO) and gene set variation analyses of PRADX
 13 co-expression cluster. **A** GO analysis of Histone Modification related terms. **B** Gene set
 14 variation analyses showed that NF-κB related genes highly expressed in GBM or
 15 COAD samples with high PRADX expression.

16



17

18 **Figure S3** EZH2 interacts with DDX5. **A** qRT-PCR analysis showing the PRADX

19 levels in HT29 and U87-MG cells transfected with indicating PPADX fragments. **B**

20 Unique peptides of DDX5 were validated by peptide identification spectra. **C** Western

21 blot analysis showed that SSRP1, PPP2R1A or HNRNPM do not bind specifically to

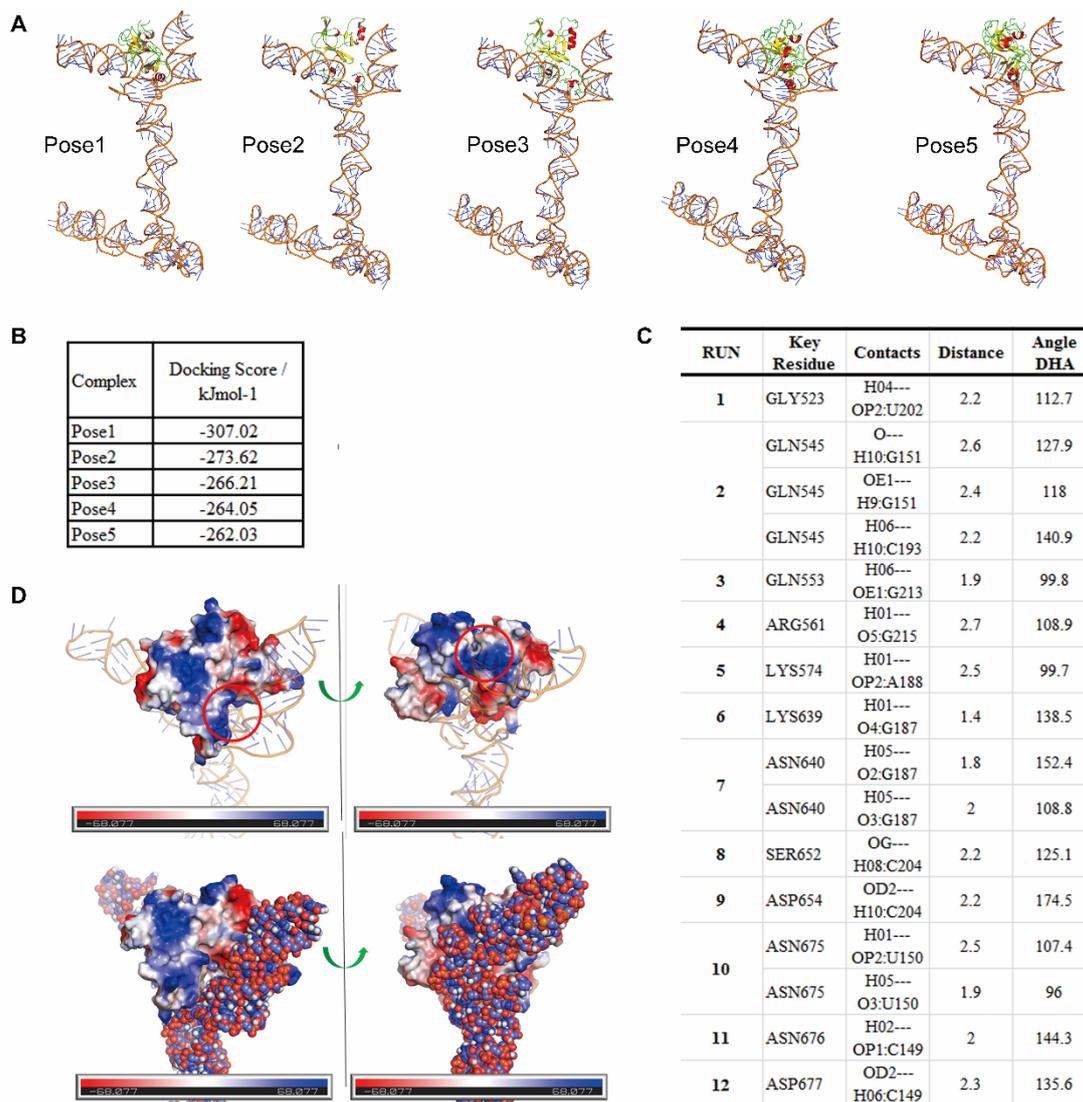
22 EZH2. **D** Western blot analysis showed the efficiency of knocking down DDX5,

23 SUZ12 and EZH2. qRT-PCR analysis showed the efficiency of knocking down

24 PRADX with different siRNAs (**E**) or lenti-shRNA (**F**) in indicated cell lines. **G** RIP

25 assays were utilized to verify that PRADX did not interact with DDX5.

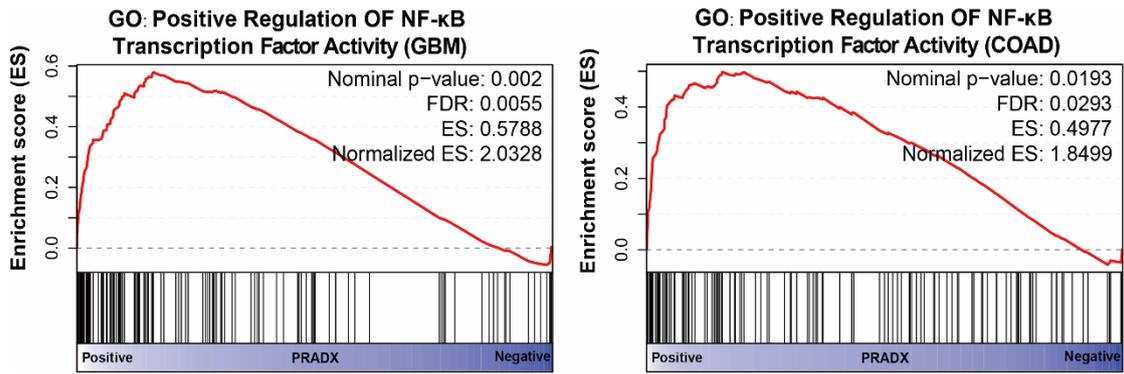
26



27

28 **Figure S4** Molecular simulation study of PRADX and EZH2 (A) Top 5 complex
 29 conformations from molecular docking. (B) Docking Score of top 5 complex
 30 conformations. C Analysis of the hydrogen bond interaction between key residues in
 31 the binding site of EZH2 protein and PRADX. D Electrostatic surface (the up two
 32 graphs) and electrostatic matching (the down two graphs) of PRADX-EZH2.

33

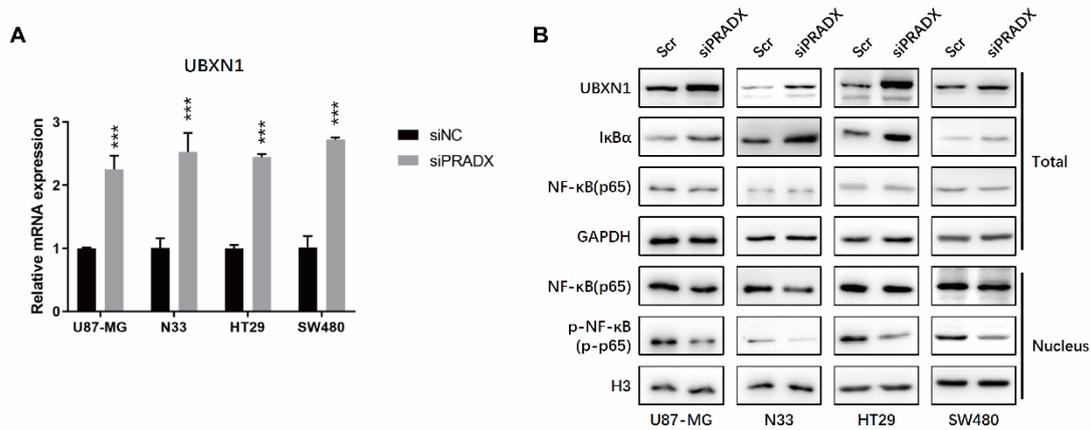


34

35 **Figure S5** GSEA analysis showed that GBM and COADpatients with high PRADX

36 expression were enriched for NF-κB related gene sets.

37



38

39 **Figure S6** The expression of UBXM1 was regulated by PRADX. **A** The mRNA levels

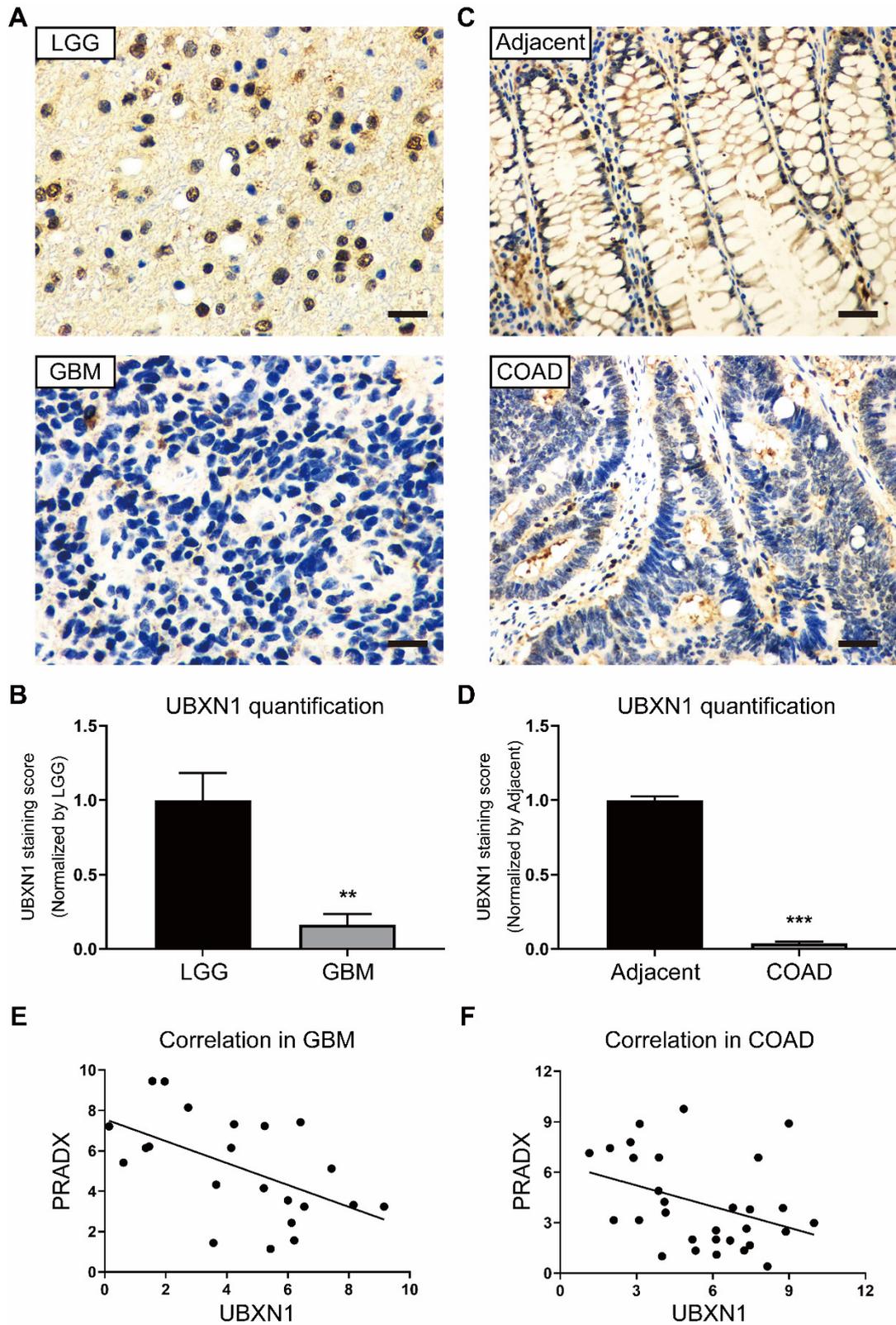
40 of UBXM1 were detected in PRADX knockdown or scramble groups by RT-qPCR. **B**

41 Western blotting results showing the total protein levels of UBXM1, IκBα and NF-κB

42 and the nuclear protein levels of NF-κB and p-NF-κB upon PRADX knockdown or

43 scramble groups.

44



45

46 **Figure S7** Identification of UBXN1 in glioma and COAD tissues. IHC assays were

47 performed to analyze the expression of UBXN1 in LGG (A), GBM (A), adjacent (C),

48 and COAD cancer (C) tissues. Quantitative analysis was measured using ImageJ
49 software (B and D). Scale bar, 20 μm . The quantitative data of PRADX and UBXN1
50 IHC staining in same tissues were used to verify the significant correlation (GBM: $r =$
51 -0.55 , P value = 0.008; COAD: $r = -0.37$, P value = 0.045) (E-F).
52

53 **Table S1** Information of the RT-qPCR primers, ISH-probes, ChIRP-probs, antibodys
54 and siRNA sequence.

55 **Table S2** The differential expressed lncRNAs between tumor and paired adjacent
56 tissues of 12 cancer types.

57 **Table S3** The shared upregulated lncRNAs among 12 cancer types, compared to the
58 matched normal tissues.

59 **Table S4** The univariate COX regression analysis of top 12 lncRNAs in TCGA
60 Pan-cancer Atlas.

61 **Table S5** Gene Ontology analysis of co-expression cluster in TCGA Pan-cancer Atlas.

62 **Table S6** Proteins in the distinct band identified by Mass Spectrometry.

63 **Table S7** PRADX positively associated Gene Ontology and KEGG terms in both
64 GBM and COAD.

65 **Table S8** Gene Set Enrichment Analysis for PRADX high expression patients in
66 GBM.