Supplemental Information

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3 Supplemental Materials and Methods

4 Gene expression analysis

The National Institutes of Gene Expression Omnibus (GEO) database was used to 5 obtain expression data in all kinds of 6 gene cancers (https://www.ncbi.nlm.nih.gov/geo/). The probe set ID of APOBEC3B in kidney 7 cancer (GSE66270), cervical cancer (GSE63514), non-small cell lung cancer 8 9 (GSE27262) and hepatocellular carcinoma (GSE14520) was 206632 s at. The probe set ID of APOBEC3B in head and neck squamous cell cancer (GSE58911) was 10 8073062. The probe set ID of APOBEC3B in ovarian cancer (GSE12470) was 22344. 11 The probe set ID of APOBEC3B in bladder cancer (GSE37815) was ILMN_1691457. 12 The probe set ID of APOBEC3B in breast cancer (GSE109169) was 3945545. The 13 14 probe set ID of APOBEC3B in anaplastic thyroid cancer (GSE65144) was 15 206632_s_at. The probe set ID of APOBEC3B in papillary thyroid cancer (GSE50901) was 24480. The probe set ID of APOBEC3B and PD-L1 (CD274) in ESCC 16 (GSE17351) and colon cancer (GSE606970 were 206632_s_at and 227458_at, 17 respectively. The probe set ID of APOBEC3B, PD-1 and PD-L1 (CD274) in Renal 18 cell carcinoma (GSE67501) and Melanoma (GSE79691) were ILMN_2219466, 19 ILMN_1806725 and ILMN_1701914, respectively. The probe set ID of mouse 20 APOBEC3 and mouse PD-L1 (CD274) in AOM/DSS induced colon cancer were 21 A_65_P17700 and A_51_P248666, respectively. 22

24 Cell lines

Human esophageal squamous cell carcinoma cell lines (KYSE70, KYSE150), 25 human colon cancer cell line (RKO), human umbilical vein endothelial cell line 26 (HUVEC) and immortalized normal esophageal cell line (HET-1A) were cultured in 27 Roswell Park Memorial Institute (RPMI) 1640 complete medium (Gibco, Grand 28 Island, USA) supplemented with 10% fetal bovine serum (FBS, BI, USA), 100 U/mL 29 penicillin (Solarbio, China) and 100 µg/mL streptomycin (Solarbio, China). Human 30 31 embryonic kidney cell line (HEK-293T) was cultured in Dulbecco Modified Eagle 32 Medium (DMEM) (Gibco, Grand Island, USA) supplemented with 10% FBS, 100 33 µg/mL streptomycin and 100 U/mL penicillin. All cells were incubated in a sterile incubator with 5% CO₂ at 37°C. 34

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36 Plasmid construction and transfection

The full-length nucleic acid sequence of APOBEC3B was optimized by Shanghai Ziben Biotechnology Co., Ltd (Shanghai, China) and cloned into pLVX-Tetone-GP3 vector through *Age* I and *Not* I restriction sites. Subsequently, APOBEC3B overexpression vector and empty vector were transfected into KYSE150 cells with PowerTrans 293 (Sixiang Biological, SX-TR293-001, China) according to the protocol. Finally, KYSE150 cells overexpressing APOBEC3B were induced by doxycycline (dox).

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45 Western blot

46 The total cell lysates were prepared using protein lysis buffer. Then protein was

47 fractionated by 8% SDS PAGE, transferred to polyvinylidene fluoride (PVDF) 48 membrane (Merck Millipore, IPVH00010, USA), and then blocked with 5% defatted milk dissolved in PBS (pH7.2) containing 0.1% Tween 20 for 2 hours at room 49 50 temperature. The PVDF membranes were incubated with antibody of human 51 APOBEC3B (Abcam, ab184990, UK) overnight at 4 °C. The reference antibody was 52 GAPDH (Servicebio, GB11002, China). After incubation of PVDF membranes with secondary antibody (Sangon Biotech, D110011-0100, China), the blots were 53 54 visualized using ECL system (Azure C600, USA).

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56 Cell viability assay

Effect of compounds on the proliferation of cells were determined by MTT assay. 57 Briefly, KYSE70, HEK-293T, HUVEC and HET-1A cells were seeded into 96 plates 58 (3000 cells/well) and grew overnight. Cells were then synchronized by starvation with 59 60 serum-free RPMI 1640 medium or DMEM for 8 hours, followed by treating with different concentrations of compounds in complete medium for 24 hours, 48 hours 61 62 and 72 hours, respectively. MTT (Sigma, USA) dissolved in PBS were then added and cultured for 4 hours at 37°C. Formazan crystals formed by viable cells were dissolved 63 64 by 150 µL of DMSO, and the absorbance was measured by using a multi-functional microplate detector at 490 nm. Cell viability was calculated as the formula: 65

66 Cell viability (%) = (OD_{Experimental group} - OD_{Blank group}) / (OD_{Ctrl group} - OD_{Blank group})
67 ×100%

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69 Microscale Thermophoresis (MST) assay

70 The detailed method was described in materials and methods in the main text. The

71	experimental concentration of APOBEC3A protein (MedChemExpress, HY-P72080,
72	USA) was 5 μ M. The experimental concentration of APOBEC3G protein (Abnova,
73	H00060489-P01, China) was 3 μM.
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75	Fluorescence-based single-stranded DNA cytosine deamination assay
76	The detailed method was described in materials and methods in the main text. The
77	final reaction concentration of APOBEC3A and APOBEC3G was 0.4 μ M.
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79	H&E staining and Immunofluorescence analysis
80	The APOBEC3B antibody in immunofluorescence analysis was purchased from the
81	Absin Bioscience Inc. (Shanghai, China), and the dilution ratio was 1:100 for
82	immunofluorescence analysis. The H&E staining and immunofluorescence analysis
83	were accomplished by the Wuhan Service Biotechnology company in China.
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85	In vivo toxicity analysis
86	The fresh whole blood was taken from mice, quickly added to the buffer containing
87	heparin sodium, and then sent to the laboratory department of hospital for blood
88	routine analysis containing WBC, RBC, HGB, PLT and so on. The serum was
89	collected for blood biochemistry (AST and ALT) analysis according to the protocol.
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91	T cell migration assay
92	The chemotaxis of CD8 ⁺ T cells was measured by transwell assay. The aperture of

93	chamber (Corning, 3421, USA) was 0.5 µm. The peripheral blood mononuclear cells
94	(PBMCs) from human donors were isolated and activated with 100 units IL-2, 1
95	μ g/mL anti-CD3, and 1 μ g/mL anti-CD28 stimulatory antibodies for 2 days. Then,
96	activated PBMCs were harvested, centrifuged and resuspended in serum-free RPMI
97	1640 medium. 200 μ L PBMCs suspensions (1 × 10 ⁵ cells) were seeded into the upper
98	chamber. Then, 600 μ L RPMI 1640 complete medium, supernatant of KYSE70
99	(vehicle group) and supernatant of KYSE70 pretreated with 10 μ M 3,
100	5-diiodotyrosine for 48 hours were added into the lower chamber, respectively. Three
101	days later, the migration number of CD8 ⁺ T cells was analyzed by flow cytometry.
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103	Assessment of disease activity index in colon cancer mice model
104	The disease activity index (DAI) of mice was assessed based on changes in body
105	weight (such as whether body weight increased or decreased), appearance of stool,
106	and hematochezia of stool.
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117 Supplementary Figures and Tables



Figure S1. The expression level of APOBEC3B in normal and tumor tissues of different cancer types from GEO database. Data from GEO database have performed background correction and normalization. The statistical analysis was performed by one-tailed Student's *t* test (**P < 0.01, ***P < 0.001).

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Figure S2. The structure of APOBEC3B. (A) The reported X-ray cocrystal structure 135 136 of APOBEC3B (blue) with its substrate ssDNA (yellow) from PDB (PDB ID: 5TD5). 137 (B) The mutated sites (purple) of APOBEC3B in cocrystal structure. The yellow dot 138 showed the zinc ion in APOBEC3B structure. (C, D) The homology model structure 139 (wild type, green) was superimposed with template structure (blue) with an RMSD of 0.32 Å by MOE. (E) The all-residue RMSD of homology model structure compared 140 141 to template structure. (F) The pocket surface (pink) of wild type APOBEC3B suitable 142 for screening compounds.

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150 Figure S3. The comprehensive workflow chart in this research. The blue part on the

151 left was virtual screening process using computer, and the pink part on the right was

- 152 experimental verification process.
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Figure S4. The interaction between 3, 5-diiodotyrosine and APOBEC3B in cancer 165 166 cells. (A) The mRNA expression level of APOBEC3B in different ESCC cell lines. 167 GAPDH was considered as the reference gene. (B) The mRNA and protein expression levels of APOBEC3B after KYSE150 cells were transfected with expression vector 168 169 and induced by different concentrations of doxycycline (dox). (C, D) The interaction 170 between 3, 5-diiodotyrosine and APOBEC3B were measured within KYSE150-vector 171 (Empty vector was stably expressed in KYSE150 cells) and KYSE150-APOBEC3B 172 (APOBEC3B vector was stably expressed in KYSE150 cells) cells by MST and fluorescence-based ssDNA deaminase analysis. Arrows showed the $K_{\rm D}$ or $IC_{\rm 50}$ 173 174 concentration values. Data are representative of at least three independent 175 experiments.

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181 Figure S5. The interaction of 3, 5-diiodotyrosine with APOBEC3A and APOBEC3G. 182 (A) The curves of 3, 5-diiodotyrosine binding to human APOBEC3A protein and 183 APOBEC3G protein. (B) The curves of 3, 5-diiodotyrosine affecting on APOBEC3A and APOBEC3G deaminase activity. Arrows showed the K_D or IC₅₀ concentration 184 185 values. The absence of label indicated that K_D or IC₅₀ could not be fitted. The data are 186 representative of at least three independent experiments. 187 188 189 190

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Figure S6. The effects of 3, 5-diiodotyrosine on the proliferation of KYSE70 cell and 196 197 expression level of APOBEC3B. (A) Effects of different concentrations (0, 0.01, 0.1, 198 1, 10, 100 μ M) of 3, 5-diiodotyrosine on the proliferation of KYSE70 tumor cell were 199 measured by MTT. (B) The mRNA expression levels of APOBEC3B after 3, 200 5-diiodotyrosine treatment. KYSE70 cells with high expression of APOBEC3B were 201 treated with different concentrations (0, 0.01, 0.1, 1, 10 and 100 µM) of 3, 202 5-diiodotyrosine for 48 hours, and then the mRNA expression levels of APOBEC3B 203 were measured by qRT-PCR. (Mean ± SD were shown for triplicate reactions 204 normalized to GAPDH, *P < 0.05 and ***P < 0.001 by two-tailed Student's t test). 205 Data are representative of at least three independent experiments. 206 207 208

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215 Figure S7. Model establishment and physiological indexes of 4-NQO induced ESCC 216 mice. (A) Water intake, (B) Food intake and (C) body weight of vehicle mice and 217 4-NQO induced ESCC mice (*P < 0.05, **P < 0.01 and ***P < 0.001 by two-tailed 218 Student's t test). (D) Representative physiological state images of vehicle mice and 219 4-NQO induced C57BL/6J mice at 28th weeks. (E) Histopathological condition of 220 vehicle and 4-NQO induced mice at 28 weeks was determined by H&E staining assay 221 (Scale bars: 50 µm). (F) The mRNA expression level of APOBEC3 was detected in 222 esophagus tissues of vehicle and 4-NQO induced ESCC mice at different periods (**P < 0.01, ***P < 0.001). (G) Protein expression of APOBEC3 in esophagus 223 224 tissues of 4-NQO induced ESCC mice at week 28 was detected by 225 immunofluorescence analysis (Scale bars: 20 µm).

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Figure S8. The physiological assessment of mice. (A) Body weight changes of mice (n = 5). (B) Histopathological assessment of esophagus tissues in NS and 3, 5-diiodotyrosine groups were determined by H&E staining assay (Scale bars: 100 μm).



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Figure S9. The effect of 3, 5-diiodotyrosine on cell viability. (A-C) HEK-293T, HUVEC and HET-1A cells were treated with different concentrations of 3, 5-diiodotyrosine for 24, 48 and 72 hours, and cell viability was measured by MTT

analysis. Data are representative of at least three independent experiments.

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Figure S10. Toxicity evaluation of 3, 5-diiodotyrosine *in vivo*. (A) Seven-week-old
naive female C57BL/6J mice were *i.p.* injected with 200 μL normal saline and
different dosages of 3, 5-diiodotyrosine (0.5 mg/kg, 2 mg/kg, and 8 mg/kg),
respectively, every two days for 7 times. (B-E) Blood physiology indexes (WBC,
RBC, HGB and PLT) of mice were analyzed by blood routine assay. (F, G)
Biochemistry indexes of mice (AST and ALT) were analyzed by AST and ALT kit,
respectively (n = 3).

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Figure S11. The expression level of PD-L1 in ESCC cell line and tumor tissue. (A) The expression of PD-L1 in KYSE70 cell after treatment with different concentrations (0, 0.01, 0.1, 1, 10, 100 μ M) of 3, 5-diiodotyrosine for 48 hours was measured by flow cytometry. (B) The mRNA expression of PD-L1 in esophageal tissues of vehicle mice and 4-NQO induced ESCC mice at different periods was detected by qRT-PCR (**P* < 0.05, ***P* < 0.01, ****P* < 0.001).

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Figure S13. The expression levels of APOBEC3 and PD-L1 in colon tissues of vehicle mice and AOM/DSS induced colon cancer mice at different periods. (A, C) The expression levels of APOBEC3 and PD-L1 in colon tissues at 0, 1, 2 and 10 weeks after AOM/DSS induction were analyzed from GEO database (GSE121128) (n = 3). (B, D) The expression levels of APOBEC3 and PD-L1 in colon tissues of AOM / DSS induced colon cancer mice and vehicle at different time points (0, 1, 5, 8, 10 weeks) were analyzed (n = 3, **P* < 0.05, ***P* < 0.01, ****P* < 0.001).

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Figure S14. Model establishment of colon cancer mice induced by AOM/DSS and changes of physiological indexes after 3, 5-diiodotyrosine combined with OPBP-1 treatment. (A-B) The changes of body weight and DAI score in each group (n = 6 or 7, *P < 0.05, **P < 0.01, ***P < 0.001). (C) Colon length in each group. (D) The H&E staining of mice organs in each group after treatment (Scale bars: 100 µm for heart, liver, lung and kidney, 50 µm for spleen). (E) Analysis of hepatic damage by the level of AST and ALT in serum (n = 3).

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Figure S15. The effect of 3, 5-diiodotyrosine on CD8⁺ T cell function. (A) PBMCs 345 346 were isolated and activated with 100 units IL-2, 1 µg/mL anti-CD3, and 1 µg/mL 347 anti-CD28 stimulatory antibodies and directly treated with 10 µM 3, 5-diiodotyrosine 348 for 3 days. Then proportion of IFN- γ^+ CD8⁺ T cells were analyzed by flow cytometry. 349 (B, C) Activated PBMCs were cocultured with KYSE70 cells within the addition of 350 10 µM 3, 5-diiodotyrosine. The proliferation of CD8⁺ T cells and proportion of IFN- γ^+ CD8⁺ T cells were analyzed by flow cytometry. (D) The migration number of 351 352 CD8⁺ T cells was analyzed by flow cytometry. Data are representative of at least three independent experiments (*P < 0.05, **P < 0.01, ***P < 0.001). 353





Figure S16. The expression and prognosis of APOBEC3B in thyroid cancer. (A, B) Expression levels of APOBEC3B in normal and tumor tissues of human anaplastic cancer and papillary thyroid cancer from GEO database were analyzed, *P < 0.05, **P < 0.01. (C, D) The overall survival curve and disease free survival curve in low expression of APOBEC3B and high expression of APOBEC3B in THCA were analyzed from GEPIA database.

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Figure S17. Effects evaluation of 3, 5-diiodotyrosine on thyroid function *in vivo*. (A) Seven-week-old naive female C57BL/6J mice were *i.p.* injected with 200 μ L normal saline and different dosages of 3, 5-diiodotyrosine (0.5 mg/kg, 2 mg/kg, and 8 mg/kg), respectively, every 2 days for 2 weeks. (B-D) The main indexes of thyroid function (*f*T3, *f*T4 and TSH) in mice were analyzed (n = 3).

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389	Table S1.	The primer	sequences	for qRT	-PCR.
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	Gene	Species	Forward	Reverse
	APOBEC3B	Human	CCATCCTCTATGGTCGGAGC	GAGGCTTGAAATACACCTGGC
	IL-7	Human	CCTCCCCTGATCCTTGTTCTG	ACCAATTTCTTTCATGCTGTCCA
	IL-15	Human	ACAGAAGCCAACTGGGTGAAT	TGCTGTTACTTTGCAACTGGG
	GAPDH	Human	GGAGTCCCTGCCACACTCA	GCCCCTCCCCTCTTCAAG
	APOBEC3	Mouse	TGCTACATCTCGGTCCCTTC	TCCTCTTCACTTAGCGGGTC
	PD-L1	Mouse	TCACTTGCTACGGGCGTTTAC	AGTTGCTGTGCTGAGGCTTA
	GAPDH	Mouse	GCATCCACTGGTGCTGCC	TCATCATACTTGGCAGGTTTC
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Reference

Biochemistry,

NO.

PDBID

Notation

1	2NBQ	monomer	-	187-378	-	2016
					F2008 W2288 L230K	2010
2	5COD	monomer	2.08	187-378	Y250S_F308K:	J Biol Chem,
-	50025	include	2.00	107 570	Missing: A242-F249	2015
					F200S, W228S, L230K,	
3	5COH	monomer	1.73	187-378	Y250S, F308K;	J Biol Chem,
					Missing: A242-F249	2015
					F200S, W228S, L230K,	
4	5CQI	monomer	1.68	187-378	Y250S, F308K;	J Biol Chem,
					Missing: A242-F249	2015
					F200S, W228S, L230K,	J Biol Chem,
5	5CQK	monomer	1.88	187-378	Y250S, F308K	2015
					F200S, W228S,	
6	5SXG	monomer	1.93	191-378	L230K, Y250S, F308K;	Sci Rep, 2017
					Missing: D224-M231, A242-F249	
					F200S, W228S,	
7	5SXH	monomer	1.78	191-378	L230K, Y250S, F308K;	Sci Rep, 2017
					Missing: N225-M231, A242-F249	
					F200S, D205G, R212H, Q213K,	
		APOBEC3B-ssD			F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I,	Nat Struct
8	5TD5	APOBEC3B-ssD NA complex	1.72	191-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K;	Nat Struct Mol Biol,
8	5TD5	APOBEC3B-ssD NA complex	1.72	191-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249	Nat Struct Mol Biol, 2017
8	5TD5	APOBEC3B-ssD NA complex	1.72	191-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249	Nat Struct Mol Biol, 2017 Nucleic Acids
8 9	5TD5 5TKM	APOBEC3B-ssD NA complex monomer	1.72 1.90	191-378 1-191	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017
8 9	5TD5 5TKM	APOBEC3B-ssD NA complex monomer	1.72 1.90	191-378 1-191	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017
8 9	5TD5 5TKM	APOBEC3B-ssD NA complex monomer	1.72 1.90	191-378 1-191	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB
8 9 10	5TD5 5TKM 6NFK	APOBEC3B-ssD NA complex monomer monomer	1.72 1.90 1.86	191-378 1-191 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q;	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioady, 2019
8 9 10	5TD5 5TKM 6NFK	APOBEC3B-ssD NA complex monomer	1.72 1.90 1.86	191-378 1-191 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019
8 9	5TD5 5TKM 6NFK	APOBEC3B-ssD NA complex monomer monomer	1.72 1.90 1.86	191-378 1-191 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019
8 9 10	5TD5 5TKM 6NFK	APOBEC3B-ssD NA complex monomer monomer	1.72 1.90 1.86	191-378 1-191 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019
8 9 10	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	1.72 1.90 1.86	191-378 1-191 187-378 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q;	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019
8 9 10	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	 1.72 1.90 1.86 1.73 	191-378 1-191 187-378 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019
8 9 10	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	1.72 1.90 1.86	191-378 1-191 187-378 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, I318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019
8 9 10 11	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	 1.72 1.90 1.86 1.73 2.53 	191-378 1-191 187-378 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G,	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019
 8 9 10 11 12 	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	 1.72 1.90 1.86 1.73 2.53 	191-378 1-191 187-378 187-378	F200S, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y315D, D316Q, P317G, L318R, Y319C, K320Q;	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019
 8 9 10 11 12 	5TD5 5TKM 6NFK 6NFL	APOBEC3B-ssD NA complex monomer monomer	 1.72 1.90 1.86 1.73 2.53 	191-378 1-191 187-378 187-378	F2008, D205G, R212H, Q213K, W228S, L230K, R210G, L209I, Y250S, E255A, F308K; missing: P206-V208, A242-F249 Y83D, W127S, Y162D F200S, W288S, L230K, Y250S, E255Q, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249 F200S, W288S, L230K, Y250S, F308K, Y315D, D316Q, P317G, L318R, Y319C, K320Q; Missing: A242-F249	Nat Struct Mol Biol, 2017 Nucleic Acids Res, 2017 FASEB Bioadv, 2019 FASEB Bioadv, 2019

412 Table S2. Specific information for the crystal structures of human APOBEC3B.

Length

Mutation and missing

Resolution (Å)

Compounds	Mol ID	2D structure	S score	Molecule weight	Log (O/W)	RMSD (Å)	Inhibition rate (%)
SMC111	T1711	N A A A A A A A A A A A A A A A A A A A	-5.47	212.25	2.92	3.35	53.64
SMC115	T2802	S C C C NH	-6.45	301.33	2.31	1.27	25.94
SMC116	T1062	p p t t t t t t t t t t t t t t t t t t	-6.76	305.42	3.56	1.99	32.27
SMC118	T1516	HO CONTRACTOR	-7.07	368.40	3.72	1.53	75.23
SMC121	T1723	HIN NON OH OH OHOHO	-6.87	427.20	-4.09	1.34	41.76
SMC123	T2831	но-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С-С	-7.11	464.62	3.15	2.08	23.67
SMC130	T1653	HO TO INT OF	-5.54	650.98	3.45	2.09	70.19
SMC132	T2815		-7.45	416.38	-0.3	1.95	37.51
SMC139	T3427		-7.16	390.39	1.43	1.97	31.47
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414 Table S3. Structure and inhibition rate of 10 hit compounds in enzyme assay.

415 Inhibition rate indicates that the inhibition effect of compounds on APOBEC3B 416 activity at the concentration of 100μ M.

-7.48

462.36

0.47

1.56

41.25

417 S score indicates the comprehensive score for docking minimum energy.

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SMC140

T3242

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- 421
- 422

423 Table S4. Representative 2D similarity searching results and docking results of

424 SMC130.

	Compounds	Mol ID	2D structure	Molecular name	S score	Molecule weight	RMSD (Å)	Similarity score
	SMC245	T4461	OH I I I I I I I I I I I I I I I I I I I	3,5-Diiodo-L-th yronine	-7.70	525.08	2.76	0.95
	SMC246	T0848		Levodopa	-8.97	197.19	2.00	0.70
	SMC247	T2760		3,5-Diiodotyros ine	-9.08	432.98	0.91	0.79
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445 Table S5. The ssDNA sequences in fluorescence-based single-stranded DNA

-	Gene	Sequence
	APOBEC3A	5'-6-FAM-ATTATTATTATTCTAATGGATTTATTTATTTATTTATTTA
	APOBEC3B	5'-6-FAM-ATTATTATTATTCAAATGGATTTATTTATTTATTTATTTA
_	APOBEC3G	5'-6-FAM-ATTATTATTATTCCAATGGATTTATTTATTTATTTATTTA
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446 **cytosine deamination assay.**

471 Table S6. The detailed DAI scoring criteria.

Score	Range of body weight loss	Stool appearance	Hematochezia
0	None	Normal	Normal
1	1-5%	_	_
2	5-10%	Light diarrhoea	_
3	10-20%	_	_
4	>20%	Severe diarrhoea	Severe hematochezia

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