1 KDM5A/B promotes HIV-1 latency and KDM5 inhibitors promote HIV-1 lytic reactivation

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28 Abstract

29 Combinational antiretroviral therapy (cART) effectively suppresses HIV-1 infection, 30 replication, and pathogenesis in HIV-1 patients. However, the patient's HIV-1 reservoir still cannot 31 be eliminated by current cART or other therapies. One putative HIV-1 eradication strategy is 32 "shock and kill", which reactivates HIV-1 in latently-infected cells and induces their cytopathic 33 effect or immune clearance to decrease the patients' reservoir size. KDM5A and KDM5B act as 34 the HIV-1 latency-promoting genes, decreasing the HIV-1 viral gene transcription and reactivation 35 in infected cells. Depletion of KDM5 A/B by siRNA knockdown (KD) increases H3K4 36 trimethylation (H3K4me3) in HIV-1 Tat-mediated transactivation. We also found that the KDM5-37 specific inhibitor JQKD82 can increase H3K4me3 at the HIV-1 LTR region during HIV-1 38 reactivation and induce cytopathic effects. We applied the JQKD82 in combination with the non-39 canonical NF-KB activator AZD5582, which synergistically induced HIV-1 reactivation and cell 40 apoptosis in HIV-1 infected cells. These results suggested that the KDM5 inhibition can be a 41 putative HIV-1 latency-reversing strategy for the HIV-1 "shock and kill" eradication therapy.

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49 Introduction

Globally, over 36 million individuals are infected with human immunodeficiency virus type 1 50 51 (HIV-1), and currently, no approved medicine or therapy can eradicate latent HIV-1 proviruses in 52 infected patients. HIV infection dramatically affects patients' immune systems and causes 53 acquired immunodeficiency syndrome (AIDS). Although combination antiretroviral therapy 54 (cART) can suppress viral load below the detection limit in patients' blood and halt disease 55 progression, HIV-1 can still reactivate from latently infected cells in lymphoid tissue that maintain 56 persistent infection in cART-treated patients. The promising shock-and-kill strategy of HIV-1 57 eradication therapy involves combining latency-reversing agents (LRAs) and cART to reactivate 58 the latent HIV-1 in the infected reservoir cells without inducing global T cell activation. During 59 HIV-1 reactivation, the infected cells would be eliminated by the viral cytopathic effect and the 60 cellular immune response from the cytolytic T lymphocytes (CTL) or natural killer (NK) cells [1-61 4]. Unfortunately, most of the currently used LRAs, such as the histone deacetylase (HDAC) inhibitor vorinostat, can induce viral reactivation (as the shock step) but cannot decrease the HIV-62 63 1 latent reservoir size (as the kill step) in the clinical trial setting [2, 5, 6]. The possible reasons for 64 this include that the HIV-1 reservoir cells, such as CD4⁺ T cells or macrophages, are resistant to 65 the killing from CTLs [7-9] or adapt to avoid being killed by NK cells [10, 11]. Furthermore, the 66 latently infected T cells can evade CTL/NK cells in the germinal follicles of lymphoid tissue [12-67 15]. For the future shock-and-kill strategy, we will need to focus on the kill strategies to facilitate 68 the cell death of reservoir cells. Additionally, the putative strategy should activate the CTL/NK 69 immunosurveillance or induce correct cytokine/chemokine to increase the killing of HIV-1 70 infected cells to eliminate the reservoir in the lymphoid tissue [9, 16].

71 Our previous research involved the CRISPR-knockout screening on latently infected cell lines 72 to investigate novel genes that control HIV-1 latency and reactivation [17]. We found that potential 73 latency-promoting genes (LPG) mainly participate in epigenetic regulation and chromatin 74 modification/organization. Notably, the knockdown of certain histone demethylases targeting 75 H3K4 or H3K36 methylation can induce HIV-1 reactivation. Also, the pan-Jumonji histone 76 demethylase inhibitor JIB-04 [18-20] could induce HIV-1 reactivation in the infected T cells or 77 monocytes. These results suggested that H3K4 or H3K36 methylation can be critical to HIV-1 78 reactivation and viral gene expressions. We also found that MINA53, which acts as the H3K36 79 demethylase, can promote HIV-1 latency due to decreased H3K36 trimethylation and inhibit 80 transcription elongation during HIV-1 reactivation [21]. This research focused on other LPG 81 candidates, H3K4 demethylases regulating HIV-1 latency/activation. H3K4 trimethylation 82 (H3K4me3) is located mainly at the transcription start site (TSS) to associate with TAF3 in the 83 TFIID complex [22-25] to facilitate transcription initiation. Previous studies showed that the HIV-84 1 long terminal repeat (LTR) promoter enriched H3K4me3 during HIV-1 Tat-mediated 85 transactivation for viral gene transcription [26-28]. However, the detailed regulatory mechanism 86 of H3K4me3 in HIV-1 LTR for viral gene expression remains unclear. We previously identified 87 one H3K4me3 demethylase, lysine demethylase 5A (KDM5A), as a putative HIV-1 LPG that may 88 decrease the H3K4me3 level of HIV-1 LTR to suppress HIV-1 reactivation. We hypothesize that 89 if we can deplete KDM5A function through gene knockdown or pharmacology inhibition in HIV-90 1 latent infected cells, we can trigger HIV-1 reactivation in infected cells, which can be killed by 91 the induced cytopathic effect or the CTL/NK cell immunosurveillance in the patient's tissue.

KDM5A is one of the KDM5 demethylases (KDM5 A, B, C, and D), which catalyzes
demethylation from H3K4me3 to H3K4me2 and then to the final product H3K4me1 [29-32].

94 Previously reported showed that KDM5A can induce PD-L1 expression [33, 34] that may suppress 95 the immune response for immune escape during HIV-1 infection [35-39]. The other KDM5, KDM5B, has been identified to suppress immune sensing from the STING-GAS signaling [40] 96 97 and RIG-I signaling [41] to decrease innate immunity and antiviral responses. Furthermore, 98 KDM5B can prevent macrophages from releasing inflammatory cytokines like IL12 or TNF- α 99 during L. donovani infection [42]. We hypothesize that KDM5A or KDM5B depletion in HIV-1 100 latently infected cells induces HIV-1 reactivation and stimulates innate immunity to antiviral responses. Furthermore, the H3K4m3 level of proapoptotic genes is usually low to prevent 101 102 accidental cell death during the native state [23], and thus, KDM5A depletion can promote cell 103 apoptosis [43, 44]. Therefore, we expect that inhibition of KDM5A or KDM5B can increase the 104 antiviral responses and proapoptotic genes with HIV-1 reactivation in latently infected cells to 105 eliminate the reservoir by HIV-1 induced cytopathic effects or antiviral-mediated programmed cell 106 death. Above all, this study focuses on the putative KDM5 depletion treatment to achieve the 107 shock-and-kill strategy for future putative HIV-1 eradication therapy.

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109 **Results**

110 Knockdown of KDM5A increases the HIV-1 Tat/LTR-driven transcription.

To identify whether KDM5A depletion increases HIV-1 LTR transcription, we performed KDM5A knockdown (KD) by siRNA in TZM-bl cells, which contain the HIV-1 LTR-driven luciferase reporter [45-47]. First, we used immunoblotting (IB) to identify decreased KDM5A expression with two specific siRNAs for knockdown (**Fig 1A**). Both KDM5A siRNAs decreased KDM5A expression in transfected TZM-bl while increasing the H3K4me3 level and IRF3

116 phosphorylation. Previous studies also suggested that depletion of the KDM5 family (specifically, 117 KDM5B) can increase the IRF3 phosphorylation and transactivation to induce Type I interferon 118 and ISG expression for antiviral responses [40, 41, 48], which can promote cell apoptosis of HIV-119 1 infected cells [49-52]. Also, the phosphorylated IRF3 can associate caspase-8 with Bax, 120 promoting the proapoptotic state for cell death [53]. We used the luciferase reporter assay to 121 identify whether the KDM5A KD affects HIV-1 LTR-driven transcription with or without HIV-1 122 Tat mediation (Fig 1B). We found that KD of siKDM5A#1 increases HIV-1 LTR transcription in 123 the native state of TZM-bl cells. Furthermore, the KD from two different siKDM5A increased 124 HIV-1 Tat-mediated LTR transcription in transfected TZM-bl cells. We also found that KDM5B 125 KD increases the H3K4me3 level, phosphorylation of IRF3 (Fig 1C), and HIV-1 Tat-mediated 126 LTR transcription (Fig 1D), consistent with the results of KDM5A KD in transfected TZM-bl 127 cells. These results suggested that decreasing the KDM5 family, such as KDM5A or KDM5B, can 128 increase HIV-1 reactivation and induce the IRF3-mediated proapoptotic state.

129 KDM5 inhibitor JQKD82 increases HIV-1 reactivation and cell death in latently infected130 cells.

131 Since we showed that KDM5A and KDM5B KD both can promote HIV-1 LTR/Tat-mediated 132 transcription in TZM-bl cells, we went further to investigate whether the inhibition of all KDM5 133 family members (such as KDM5 A, B, C, and D) [30] can promote HIV-1 reactivation in latently 134 infected cells. We used the KDM5 inhibitor JQKD82 [44] to treat the CA5 cell line, the T 135 lymphocyte cell line integrated with the full-length HIV-1 proviral genome and the HIV-1 LTR-136 driven GFP reporter [54, 55]. JQKD82 is the prodrug of KDM5-C49 [56] with the ester 137 metabolized group to inhibit KDM5 demethylase activity with high cellular permeability. We 138 treated the CA5 cells with a low concentration (10 or 25 µM) for 5 days to change the landscape

139 of histone methylation and epigenetic regulation for HIV-1 reactivation. The JQKD82-treated CA5 140 cells showed a significant increase in the GFP expression from HIV-1 reactivation compared to 141 the DMSO solvent control group (Fig 2A-B). These results showed that inhibiting KDM5 142 demethylase activity can directly induce HIV-1 reactivation in latently infected cells. To identify 143 whether KDM5 inhibitor JQKD82 can increase the cell death of HIV-1 infected cells, we treated 144 CA5 cells with JQKD82 for 5 days and stained them with LIVE/DEAD far-red dye to quantify the 145 cell death from the drug effect or HIV-1-induced cytopathic effect [57]. CA5 cells treated with 25 146 µM JQKD82 had higher rates of cell death than untreated CA5 cells or Jurkat parental cells with 147 the same treatment (Fig 2C). The results suggested that the inhibition of KDM5 can decrease cell survival and increase cytopathic effects in HIV-1 latently infected cells. 148

149 We used the chromatin immunoprecipitation (ChIP) qPCR assay to identify whether 150 JQKD82 can increase the H3K4me3 level in the HIV-1 LTR to increase HIV-1 gene transcription 151 for reactivation [26]. We treated CA5 cells for 5 days with DMSO or 25 µM JQKD82 and then 152 harvested HIV-1 LTR-associated nucleosomes from cell lysates by the pull-down of anti-KDM5A 153 or anti-H3K4me3 antibodies. We extracted the nucleosome-associated DNA and performed qPCR 154 with the specific primers targeting the nucleosome binding sites in HIV-1 LTR (Nuc-0 and Nuc-155 1) [17, 58, 59]. The results showed that JQKD82 increases the H3K4me3 level in Nuc-0 and Nuc-156 1 (Fig 2D) at the HIV-1 LTR in CA5 cells compared to the untreated control group. The increase 157 of H3K4me3 in HIV-1 LTR, especially at the Nuc-1 site where the TSS of HIV-1 viral genes [23, 158 24], can promote the transcription initiation to increase HIV-1 viral gene expressions and 159 reactivation in the latently infected cells.

Also, we treated CA5 cells with a high dose of JQKD82 (50 or 100 µM) in a short period (48h),
which also promoted a significant increase in HIV-1 reactivation (Fig S1 A-B). The high dose of

JQKD82 induced significantly higher cell death of CA5 than untreated CA5 cells and Jurkat parental cells under the same treatment (Fig S1C). These results suggested that a high dose of JQKD82 treatment can induce HIV-1 reactivation and cell death of latently infected cells in a short period.

JQKD82 in combination with AZD5582, increases HIV-1 reactivation and cell death in latently infected cells

168 Previous studies indicated that the non-canonical NF-kB activator AZD5582 (AZD) increases 169 HIV-1 reactivation in ex vivo patient samples, humanized mouse models, and SIV-infected 170 macaque models [60]. However, AZD5582 could not decrease the HIV-1 reservoir size in SIV-171 infected macaques. We hypothesized that combining JQKD82 and AZD5582 boosts HIV-1 172 reaction and induces cell death for the shock-and-kill strategy for HIV-1 eradication therapy. We treated CA5 cells with JQKD82 for 3 days and then refreshed the treatment with or without 0.2 173 174 µM AZD5582 for 2 days. Treated cells were harvested, and LIVE/DEAD staining was performed; 175 using FASC, the cells were then analyzed for HIV-1 reactivation from GFP expression and cell 176 death from APC dye signals (Fig 3A). AZD5582 induced ~20% GFP expression from the treated 177 CA5 cells, and JOKD82 further strengthened the AZD5582-mediated HIV-1 reactivation in the 178 treated CA5 cells (Fig 3B). Furthermore, JQKD82 significantly increased the cell death of 179 AZD5582-reactivated CA5 cells compared to the Jurkat cells with the same combination treatment 180 (Fig 3C). We used an IB assay to identify the protein markers for cell responses from the 181 JQKD82/AZD5582-treated Jurkat and CA5 cells (Fig 3D). We found that JQKD82 increases the 182 total H3K4me3 level in both Jurkat and CA5 cells, and JQKD82 can directly increase the HIV-1 183 p55/p24 expression in the treated CA5 cells. With the JQKD82/AZD5582 combination treatment, 184 JQKD82 increased the HIV-1 p55/p24 expression and the PARP cleavage (as the apoptosis marker

[61, 62]) in the AZD5582-reactivated CA5 cells. We also applied a high dose of JQKD82
cotreatment with AZD5582 to Jurkat and CA5 cells for 48 hours (Fig S2A). The
JQKD82/AZD5582 cotreatment increased the HIV-1 reactivation significantly more than a single
JQKD82 or AZD5582 treatment (Fig S2B). The JQKD82/AZD5582 cotreatment also induced
higher cell death in CA5 cells than single-drug treated CA5 cells and the JQKD82/AZD cotreatJurkat cells (Fig S2C). However, the JQKD82/AZD5582 cotreatment also caused high
cytotoxicity in Jurkat parental cells (~20% cell death).

We treated CA5 cells with another prodrug of KDM5-C49, KDM5-C70 [56], cotreated with AZD5582 for 48h. The results suggested that the high concentration of KDM5-C70 can induce HIV-1 reactivation in CA5 cells (**Fig S3A-B**). Also, KDM5-C70 synergistically increased AZD5582-induced HIV-1 reactivation in CA5 cells. However, KDM5-C70 did not significantly increase the cell-killing effect in CA5 cells with or without AZD5582 treatment (**Fig S3C**) compared to JQKD82, which has better cell permeability than KDM5-C70 [44].

198 We performed the DHIV-1 infected primary Tcm model with JQKD82/AZD5582 combination 199 treatment. We identified that the JQK82 and JQKD82/AZD5582 treatment could increase the 200 cellular HIV-1 Gag mRNA level in the primary HIV-1 infected Tcm cells compared to the DMSO 201 control group (Fig 4A). We also treated the s peripheral blood mononuclear cells (PBMCs with 202 CD8⁺ T cell depletion) from HIV-1 aviremic patients with the JQKD82/AZD5582 combination 203 treatment and harvested the cultured supernatant to detect HIV-1 viral RNA release. The results 204 showed that the JQKD82/AZD5582 combination treatment increased HIV-1 viral RNA release from infected PBMCs in 4 donors (Fig 4B), suggesting that JQKD82/AZD5582 can induce HIV-205 206 1 reactivation in HIV-1 aviremic patient' PBMCs. In conclusion, JQKD82 can strengthen 207 AZD5582-mediated HIV-1 reactivation and cell killing in HIV-1 latent infected cells. A low dose of JQKD82, combined with AZD5582, can be a gradual HIV-1 eradication therapy for decreasing
the latently infected cell population and HIV-1 reservoir.

210 Inhibition of KDM5 A/B increases HIV-1 LTR/Tat-mediated transcription in other types of 211 cells.

212 We identified that the inhibition of KDM5 increases HIV-1 reactivation in latently infected 213 CD4⁺ T cells, and we investigated whether the KDM5s regulate the HIV-1 reactivation in the 214 monocyte/macrophage reservoirs. We used HC69 microglia cells containing HIV-1 LTR/Tat-215 driven GFP reporter, mimicking the cell behavior of the HIV-1 latency reservoir in the central 216 nerve system (CNS) [63-65]. We treated HC69 cells with a KDM5 inhibitor, JQKD82, for 5 days 217 and found that JQKD82 significantly increased HIV-1 LTR/Tat-driven GFP expression (Fig 5A-218 **B**), but JOKD82 did not significantly increase the cell death of HC69 cells (Fig 5C). We also used 219 siRNA KD of KDM5A or KDM5B to identify whether H3K4me3 demethylase promotes HIV-1 220 latency in infected microglia. The KD of KDM5A or KDM5B significantly increased HIV-1 221 LTR/Tat-driven GFP in transfected HC69 cells (Fig 5 D-E) but did not cause significant cell death 222 in microglia cells (Fig 5F). These results suggested that inhibition of KDM5A or KDM5B can 223 increase HIV-1 reactivation in the monocyte/macrophage reservoir and need to be combined with 224 other reagents or interventions to eradicate HIV-1 infected microglia cells in CNS.

We also gave JQKD82/AZD5582 combination treatment to U1/HIV cells, the monocytic cell line latently infected by HIV-1 [66-68], for 5 days (**Fig S4A**). The results showed that JQKD82/AZD5582 combination treatment significantly increases HIV-1 Gag protein expression (**Fig S4B**) and mRNA level (**Fig S4C**). These results suggested that JQKD82/AZD5582 combination treatment induces HIV-1 reactivation in latently infected monocytes.

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231 Discussion

232 The results of this study suggested that the depletion of KDM5A or KDM5B can raise HIV-1 233 Tat/LTR mediated transcription to promote HIV-1 reactivation (Fig 1). We hypothesized that 234 KDM5s (Specially KDM5A) can recognize the H3K4me3 at HIV-1 LTR and catalyze the H3K4 235 demethylation to increase the threshold for reactivation and promote latency in HIV-1 infected 236 cells. After KDM5 depletion increases in the H3K4me3 level at HIV-1 LTR sites, H3K4me3 237 facilitates the transcription initiation and HIV-1 Tat/TAR-mediated reactivation. We also found 238 that the KD of KDM5A/B is insufficient to turn on HIV-1 LTR transcription in TZM-bl cells 239 directly. However, KDM5-inhibitor treatment may increase other viral protein expressions, such 240 as HIV-1 Tat, as positive feedback to facilitate the HIV-1 reactivation in the HIV-1 latent CA5 241 cells (Fig 2). In conclusion, the axis of KDM5/H3K4me3/Tat interaction to regulate the 242 transactivation of HIV-1 LTR promoter can be critical for the epigenetic controls of HIV-1 243 reactivation and latency in latently infected cells.

244 In previous studies about the epigenetic control of HIV-1 reactivation, HDAC inhibitors such 245 as valproic acid [69, 70], panobinostat, or SAHA (Vorinostat) [71-73] were used, which could induce HIV-1 reactivation in the latently infected cell line, primary infected cell model, or even in 246 247 ex vivo aviremic ART-treated patients' infected cells. However, these HDAC inhibitors could not 248 pass human clinical as they were being insufficient to progressively reactivate HIV-1 latent 249 infected cells in the lymphoid tissue over a long period [5, 74], failing to terminate HIV-1 infection 250 in resting T cells during HIV-1 reservoir expansion [75, 76], or limiting the cell killing effect [6, 251 77-80] to decrease the reservoir in the patient's body [81]. The future shock-and-kill therapy would 252 need to pursue or combine the different putative drugs to enhance reactivation and promote the 253 killing of HIV-1 reservoirs. Previous studies suggested that KDM5A and KDM5B can associate

with HDAC-complex to perform epigenetic silencing cooperatively [82-85]. KDM5 inhibitors combined with HDAC inhibitors could benefit future HIV-1 eradication by improving the reactivation and cell-killing effects. Also, the depletion of KDM5B can potentially increase antiviral immunity and promote IRF3 signaling (**Fig 1C**), which can increase the IRF3-mediated or antiviral-induced cell death [53, 86-88] to decrease the HIV-1 reservoir expansion and archive the shock-and-kill therapeutic process.

260 JQKD82 is the prodrug with the ester-modified group of the functional metabolite KDM5-261 C49, which can block the α -ketoglutarate catalytic site in the KDM5 Jumonji-C domain [44, 56]. 262 In a previous study, JQKD82 showed better cell permeability and cellular accumulation than other 263 C49-derivatives or prodrugs and significantly increased the global H3K4me3 level in treated cells. 264 In RNA-Seq analysis, the gene expressions after JQKD82-treatment increased in Type I interferon 265 and inflammatory responses [44]. Like other KDM5 inhibitors and depletions, JQKD82 can cause 266 the shut-down cell cycle and promote the proapoptotic state and innate immunity responses [43, 267 44, 89, 90]. We applied the low doses of JQKD82 treatment (below 25 µM) for an extended period 268 (at least 5 days) to HIV-1 latent cells and induced HIV-1 reactivation and their cell death (Fig 2). 269 We also applied the high doses of JQKD82 treatment (beyond 50 µM) to latently infected cells 270 and uninfected parental cells for a short time (48h). This treatment induced HIV-1 reactivation but 271 also caused high cell-killing effects in uninfected parental cells (Fig S1C). These results suggested 272 that intense JQKD82 can cause high cytotoxicity in uninfected cells.

In this study, we used the KDM5 inhibitor, JQKD82, in combination with the non-canonical
NF-κB activator, AZD5582, to synergistically increase HIV-1 reactivation and cell death in
latently infected cells. AZD5582 is a SMAC-mimetic analog that causes inhibitor of apoptosis
proteins (IAPs) self-ubiquitination and degradation [60, 91] to increase p52-RelB nuclear

277 translocation and turn on downstream gene expressions [92]. AZD5582 and other SMAC-mimetic 278 IAP inhibitors can also increase the cellular proapoptotic state for induced HIV-1 cytopathic killing 279 [93-96]. AZD5582 could reactivate HIV-1/SIV in patient cell samples and animal models [60]. 280 However, AZD5582 alone could not decrease the reservoir size in SIV-infected macaques and 281 increase antiviral immunity responses. Our results showed that the combination of JQKD82 and 282 AZD5582 treatment boosted the HIV-1 reactivation and induced apoptosis (Fig 3) in the latently 283 infected cells and did not cause severe cytotoxicity in the uninfected parental cells. We also found 284 that another KDM5-C49 prodrug, KDM5-C70, can synergetically increase AZD5582-induced 285 HIV-1 reactivation, but KDM5-C70 cannot increase the cell-killing effect as JQKD82 treatment 286 (Fig S3). These results suggested that JQKD82 has a better cell permeability and KDM5-inhibitory 287 effect [44], promoting a higher proapoptotic state in HIV-1 latently infected CD4⁺ T cells and 288 monocytes. We also performed JQKD82/AZD5582 combination treatment to the HIV-1 patient's 289 PBMCs (with the depletion of CD8⁺ T cells) and found that JQKD82/AZD5582 can induce HIV-290 1 reactivation and increase the release of HIV-1 viral RNA from 4 donors' infected PBMC (Fig 291 **4B**). In the future, we will test more PBMC samples from different HIV-1 patients to confirm these 292 preclinical results. Also, we will quantify the change in reservoir sizes of JQKD82/AZD5582-293 treated HIV-1 infected PBMCs by the quantitative viral outgrowth assay (QVOA) to validate 294 whether the JQKD82/AZD5582 combination treatment can be the candidate for shock-and-kill 295 therapy.

HIV-1 infected microglia cells are the latency reservoir and cause the abnormal inflammatory state for the pathogenesis of HIV-1-associated neurocognitive disorder (HAND), even under the cART control [97]. In order to understand the HIV-1 reactivation mechanism of microglia and develop a therapy targeting HIV-1 reservoirs in the CNS, we used the immortalizing human 300 primary microglia with HIV-1 LTR/Tat-mediated GFP reporter, HC69 cell line [63-65] to 301 investigate whether the KDM5 depletion can increase HIV-1 reactivation and cytopathic effect. 302 The JQKD82 treatment and KDM5 A/B siRNA KD can increase the HIV-1 LTR/Tat 303 transactivation in HC69 microglia (Fig 3.5). However, the depletion of KDM5, whether by 304 pharmaceutical inhibitors or siRNA knockdown, can not increase the cytopathic effect or cell death 305 in HC69 microglia. HC69 cells contain the HIV-1 LTR/Tat driven GFP reporter, but HC69 cells 306 have the deletion of HIV-1 Gag, Pol, and other accessory viral proteins, which cause single-round 307 infection without generating severe cytopathic effects during HIV-1 reactivation. These results 308 suggested that the KDM5 inhibitors can be a putative LRA for the HIV-1 reactivation in infected 309 microglia, but we need to identify their cell-killing effects in the different HIV-1 infected microglia 310 models.

In this study, we demonstrated that the depletion of KDM5 A/B by siRNA KD or enzymatic
inhibitor JQKD82 increases the H3K4me3 at the HIV-1 LTR site and HIV-1 Tat-mediated viral
gene transcriptions for HIV-1 reactivation. The KDM5 depletion combination with non-canonical
NF-κB activator AZD5582 can significantly increase cell death in HIV-1 infected cells. The
JQKD82/AZD5582 combination treatment can promote the HIV-1 reactivation and proapoptotic
state to eliminate the HIV-1 reservoir for putative HIV-1 cure therapy.

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318 Material and methods

319 Cell culture

TZM-bl, Jurkat, and U1 cell lines were obtained from the National Institutes of Health (NIH)
 AIDS reagent program. The Jurkat-derived CA5 cell line latently infected with replication-

322 competent, full-length HIV-1 genome was provided by Dr. O. Kutsch [54, 55]. TZM-bl and 323 HEK293T (Cat. # CRL-3216, ATCC) cells were cultured in Dulbecco's modified Eagle's medium 324 (DMEM, Cat # D5796, Sigma). All T cell lines were cultured in Roswell Park Memorial Institute 325 (RPMI) 1640 medium (Cat # 11875093, Gibco). Completed cell culture medium contained 10% 326 fetal bovine serum (FBS, Cat. # 10437028, Thermo Fisher), penicillin (100 U/ml) /streptomycin 327 (100 µg/ml) (Cat. # MT30002CI, Corning). Primary peripheral blood mononuclear cells (PBMCs) 328 were maintained and cultured with a completed RPMI medium with 1× minimum essential 329 medium nonessential amino acid (Cat #11140-050, Gibco), 1× sodium pyruvate (Cat #11360-070, 330 Gibco), and 20 mM HEPES (Cat #15630-080, Gibco). Human recombinant IL-2 (rIL-2, Roche) at 331 30 U/ml was supplied to primary cells every 2 days [57]. HC69 and the parental C20 microglia 332 cells were cultured in BrainPhys medium (Cat. #05790, StemCell Technologies) containing N2 333 supplement (Cat. #17502048, Gibco), penicillin (100 U/ml) /streptomycin, 100 µg/mL normocin 334 (Cat. #ant-nr-1, InvivoGen), 25 mM glutamine (Cat. #25030081, Gibco), 1% FBS and 1 µM 335 DEXA (Cat. #D4902, Sigma) freshly added to the cell culture [63-65].

336 Compounds, antibodies, and plasmid

Recombinant human TNF-α (Cat. # 554618) was purchased from BD. Biosciences. KDM5
inhibitor JQKD82 was synthesized and generously gifted by Dr. Jun Qi's lab [44]. AZD-5582 (Cat.
CT-A5582) was purchased from Chemie Tek. KDM5-C70 (M60192-10S) was purchased from
Xcess Biosciences.

Mouse anti-GAPDH antibody (Cat. # sc-32233) was purchased from Santa Cruz Biotechnology. Rabbit anti-phosphorylated IRF3 antibody (Cat. # 4947S), rabbit anti-IRF3 antibody (Cat. # 4302S), rabbit anti-H3 antibody (Cat. # 9715S), rabbit anti-PARP antibody (Cat.

| 344 | # 9542T), goat HRP-conjugated anti-mouse IgG antibody (Cat. # 7076S), and goat HRP- |
|-----|--|
| 345 | conjugated anti-rabbit IgG antibody (Cat. # 7074) were purchased from Cell Signaling Technology |
| 346 | Mouse anti-KDM5A antibody (Cat # 91211) and Mouse anti-H3K4me3 antibody (Cat #61379) |
| 347 | were purchased from Active Motif. HIV-1 Gag p24 IgG1 monoclonal antibody was produced from |
| 348 | the hybridoma cell line (NIH AIDS reagent program). |
| 349 | The pQC-HIV-1 Tat was constructed by subcloning C terminal Flag tag fused HIV-1 Tat into |
| 350 | the pQCXIP retroviral empty vector (Clontech) using NotI and BamHI sites [98]. |
| 351 | Transient transfection |
| 352 | For KDM5A knockdown, 10 nM siRNA (siKDM5A; #1: siRNA ID: s11835: 5'- |
| 353 | CCGCUAAAGUGGAAGCUAUtt-3'; #2: siRNA ID: s11836: 5'-GCGAGUUUGUUGUGACA- |
| 354 | UUtt-3'; siKDM5B #1: siRNA ID: s21145: 5'-GGCAGUAAAGGAAAUCGAAtt ; #2: siRNA Id: |
| 355 | s21146: 5'-GGAAGAUCUUGGACUUAUUtt-3', Ambion by Life technologies; non-targeting |
| 356 | control: Silencer [™] Negative Control No. 4 siRNA, si N.T., Cat. # AM4641, Invitrogen) was |
| 357 | reversely transfected in TZM-BL cells using Lipofectamine [™] RNAiMAX Transfection Reagent |
| 358 | (Cat. # 13778030, Invitrogen). Cells were kept in culture for 48h and continued the further |
| 359 | experiment subjected to IB of KDM5A or KDM5B to evaluate the knockdown efficacy. |
| 360 | For HIV-1 Tat overexpression to induce the HIV-1 LTR-driven reporter assay, we performed |

the transient transfection of pQC-HIV-1 Tat or pQCXIP empty vector control in TZM-BL cells using Fugene6 transfection reagents (Cat. # E2691, Promega). Briefly, cells were seeded and incubated with the mixture of plasmids with Fugene 6 for 24 h, following the manufacturer's protocol. The medium was changed and further cultured for an additional 24h for harvesting and performed following experiments.

366 Luciferase reporter assays

Treated TZM-BL cells were trypsinized and harvested for luciferase activity assay (One-Glo System, Cat. # E6110, Promega) following the manufacturer's protocol. Chemiluminescence was determined by using the was detected using Biotek Cytation5 and analyzed by GEN5 software (Biotek). In the HIV-1 LTR-driven reporter assay, the relative light unit (RLU) of luciferase luminescence was divided by the total protein input (RLU/ μ g) quantified by the BCA assay kit (Cat. #23225, Thermo Scientific). The readouts were normalized with the siNT/pQC-empty vector-transfected TZM-BL group.

374 Protein immunoblotting

375 Protein immunoblotting was performed following our previously published protocols [57, 99]. 376 Briefly, cells were harvested, washed by PBS, and pelleted. Cell pellets were lysed in RIPA buffer 377 (Cat. #20-188, Millipore) containing protease inhibitor cocktail (Cat. # A32965, Thermo Scientific) 378 on ice, followed by brief sonication to prepare cell lysate. The BCA assay kit (Cat. #23225, Thermo 379 Scientific) was used to quantify the total protein amount in cell lysate, which was boiled in the 380 SDS loading buffer with 5% β-mercaptoethanol (Cat. #60-24-2, Acros Organics). The denatured 381 protein samples were separated by Novex[™] WedgeWell[™] 4-20% SDS-PAGE Tris-Glycine gel 382 and transferred to PVDF membrane (iBlot[™] 2 Transfer Stacks, Invitrogen) using iBlot 2 Dry 383 Blotting System (Cat. # IB21001, Thermo Scientific). The membranes were blocked by 5% milk 384 in PBST and probed by the specific primary antibodies at 4°C overnight, followed by the HRP-385 conjugated secondary antibodies. The membranes were developed using the Clarity Max ECL 386 substrate (Cat. # 1705062, Bio-Rad).

387 Cell viability assay

The death of HIV-1-reactivated or compound-treated cells was determined using the LIVE/DEAD Fixable Far Red Dead Cell Stain Kit (Cat. *#* L10120, Invitrogen), following the manufacturer's protocol [57]. In brief, the treated cells were washed and incubated with the working dilution of LIVE/DEAD dye for 30 mins and then washed with PBS. Stained cells were fixed with 4 % paraformaldehyde (Cat. *#* 15714S, Electron Microscopy Sciences), and analyzed the APC signaling by the BD Accuri C6 Plus flow cytometer (BD Biosciences).

394 Flow cytometry

Cells were harvested, washed twice with PBS, fixed by 4% paraformaldehyde, and then resuspended in 2% BSA with PBS for FASC analysis. The cell samples were analyzed using an Accuri C6 Plus flow cytometer (BD Biosciences) with forward versus side scatter (FSC-A versus SSC-A) gating and the corresponding optical filters for the excitation/emission of fluorescence expression. The percentage of fluorescence-positive cells was determined by using the FlowJo V10 software.

401 Chromatin immunoprecipitation (CHIP) assay

402 ChIP assay was conducted as described previously [17, 59, 99, 100]. Cells were cross-403 linked by using 0.5% paraformaldehyde for 10 min, followed by treatment with 125 mM glycine 404 to quench the reaction for 5 min. After washing with cold PBS twice, cells were lysed for 10 min 405 on ice in CE buffer (10 mM HEPES-KOH, 60 mM KCl, 1 mM EDTA, 0.5% NP-40, 1 mM DTT, 406 pH: 7.9 with protease inhibitor cocktail). The nuclei were pelleted by centrifugation at $700 \times g$ for 407 10 min at 4°C and resuspended in SDS lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, 408 Ph: 8.1 with protease inhibitor cocktail). Nuclear lysates were sonicated for 2 min to fragment 409 genomic DNA and subsequently diluted with ChIP dilution buffer (0.01% SDS, 1% Triton X-100,

410 1.2 mM EDTA, 16.7 mM Tris-HCl, 150 mM NaCl, pH: 8.1 with protease inhibitor cocktail). The 411 lysates were incubated overnight at 4°C with specific antibodies or control mouse IgG (Cat. # sc-412 2025, Santa Cruz). Protein A/G beads (Cat. # 88803, Pierce) were pre-blocked with 0.5 mg/ml 413 BSA and 0.125 mg/ml herring sperm DNA (Cat. 15634-017, Invitrogen) for 1 h at room 414 temperature and then added to the lysate-antibody mixture for another incubation at 4°C for 2 h. 415 Beads were washed with the following buffers: low salt wash buffer (0.1% SDS, 1% Triton X-100, 416 2 mM EDTA, 20 mM Tris-HCl, 150 mM NaCl, pH 8.1); high-salt wash buffer (0.1% SDS, 1% 417 Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, 500 mM NaCl, pH 8.1); LiCl buffer (0.25 M LiCl, 418 1% NP-40, 1% Na-deoxycholate, 1 mM EDTA, 10 mM Tris-HCl, pH 8.1); and TE buffer (10 mM 419 Tris-HCl, 0.1 mM EDTA, pH 8.1), and were eluted with fresh elution buffer (1% SDS, 0.1 M 420 NaHCO₃) at room temperature. The eluted samples were incubated at 65°C overnight in the 421 presence of 0.2 M NaCl to disassociate the cross-linking of protein/bound DNA. The eluted 422 samples were then treated with proteinase K (Cat. #EO0491, Thermo Fisher Scientific) for protein 423 digestion at 50°C for 2h, and the DNA species were precipitated by using UltraPureTM 424 Phenol:Chloroform: Isoamyl Alcohol reagent (Cat. # 15593031, Thermo Fisher Scientific) with 425 the manufacturer's protocol. The DNA pellets were dried out and resuspended in water, and the 426 pull-down DNA was quantified by qPCR.

427 Quantitative reverse transcription PCR (RT-qPCR and ChIP-qPCR

428 RT-qPCR assays were performed following the previously published protocol [101]. Total 429 RNAs from harvested cells were extracted using the NucleoSpin RNA extraction kit (Cat. # 430 740955.250, MACHEREY-NAGEL), and ~1 μ g RNA was reversely transcribed using the 431 iScriptTM cDNA Synthesis Kit (Cat. # 1708890, Bio-Rad). Real-time qPCR was conducted using 432 the iTaqTM Universal SYBR® GreenSupermix (Cat. # 1727125, Bio-Rad). The PCR reaction was

433 performed on a Bio-Rad C.F.X. connect qPCR machine under the following conditions: 95 °C for 434 10 m, 50 cycles of 95 °C for 15 s, and 60 °C for 1 m. Relative gene expression was normalized to GAPDH internal control as the $2^{-\Delta\Delta Ct}$ method: $2^{(\Delta CT \text{ of targeted gene - }\Delta CT \text{ of GAPDH})}$. The qPCR primers 435 436 were used in this study as below: HIV-1 Gag (F: CTGAAGCGCGCACGGCAA; R: 5'-CTGAAG 437 CGCGCACGGCAA-3'), ß actin (F: 5'-GGACCTGACTGACTACCTCAT-3'; R: 5'-438 GTAGCACAGCTTCTCCTTAAT-3'), KDM5A (F: 5'-CAACGGAAAGGCACTCTCTC-3'; R: 439 5'-CAAGGCTTCTCGAGGTTTG-3'), KDM5B (F: 5'- ATTCTGTTGGCACATTGAAGACC-440 3'; R: 5'- AGCATACCCTGGGACTCCATAC-3').

441 ChIP-qPCR assays were performed by the elute DNA from the ChIP assay. The fold 442 enrichment from ChIP was normalized to IgG pull-down control in the same treatment as the 2⁻ 443 $^{\Delta\Delta Ct}$ method: 2 ($^{\Delta CT}$ of targeted gene - $^{\Delta CT}$ of IgG pull-down). The PCR primers for the bound nucleosomes of 444 HIV-1 LTR were: Nuc-0 (F: 5'-GAAGGGCTAATTTGGTCCCA -3'; R: 5'-GATGCAGCTCTC 445 GGGCCATG-3'), Nuc-1 (F: 5'-AGTGTGTGCCCGTCTGT-3'; R: 5'-TTGGCGTACTCACCA 446 GTCGC-3').

447 **DHIV-1 preparation**

Envelope-deficient DHIV backbone plasmid was provided by Dr. Vicente Planelles [102].
VSV-G pseudo-typed DHIV viruses were prepared by transfecting HEK293T cells with DHIV
vector and pMD2.G-VSV-G plasmids with Turbofect reagent (Cat. #R0531, Thermos scientific)
following the manuscript protocol. The supernatant containing VSV-DHIV viral particles was
harvested at 48 hours after transfection. Supernatant-containing viruses were centrifuged to
remove cellular debris, filtrated with 0.45-µm membrane filters, and stored at -80°C [57]. Viral
supernatant was tittered by infecting Jurkat cells with serial dilution for 48h and performing anti-

455 HIV-1 Gag immunofluorescence staining. The percentages of HIV-1 Gag positive cells from 456 different dilutions of supernatant were analyzed by FASC. The infectivity of the VSV-G DHIV-1 457 supernatant ranged from $1.7-2.9 \times 10^7$ IU/ml.

458 Establishment of HIV-1 latency in human primary CD4+ T cells

459 A primary CD4+ Tcm cell model of HIV-1 latency established by Dr. Vicente Planelles' 460 group was used as previously described with modifications [57, 102]. The frozen Human primary 461 peripheral blood CD4⁺ T cells (Cat. # 200-0165, Stemcell Technologies) were stimulated on a 96-462 well Nunc-Immuno Maxi Sorp plate precoated with soluble anti-CD3/CD28 antibodies in RPMI 463 complete medium containing TGF-B1 (10 ng/ml), anti-human IL-12 (2 µg/ml), and anti-human IL-464 4 (R&D Systems) (1 µg/ml) for 3 days. After 3-day activation, the naïve cells were considered 465 nonpolarized, differentiated into a TCM-like phenotype, and cultured in RPMI complete medium 466 with Human rIL-2 (30 U/ml). On day 7, the Tcm-like cells were infected with VSV-G pseudo-467 typed DHIV (MOI: 1.0; p24 input 100 ng/ml) through spinoculation with 1×10^6 cells/ml with 8 468 µg/ml polybrene (Cat. # TR-1003-G, Sigma) at 1741g at 37°C for 2 hours. Infected Tcm cells were 469 cultured for 10-day incubation to establish HIV-1 latency. KDM5 inhibitor JQKD82 (10 µM) was 470 treated for DHIV-infected T cm for 3 day and refreshed with JQKD82-treatment with or without 471 0.1 µM AZD-5582. We harvested these cells for RNA extraction and RT-qPCR analysis for 472 detecting HIV-1 Gag mRNA level (β actin mRNA as the internal control).

473 Ex vivo analysis using CD8-depleted PBMCs of aviremic patients

474 Consented HIV-1 positive, cART-treated, aviremic patients (<20 copies per mL) were
475 recruited through the AIDS clinic at the Mayo Clinic to donate whole blood via leukapheresis.
476 Peripheral blood mononuclear cells (PBMCs) were then isolated and cultured in a complete

477 medium supplemented with 30 U/mL interleukin-2 (IL2) and in the presence of 600 nM of 478 Nevirapine (Cat. #, Sigma) for 3 days. PBMCs were subjected to CD8⁺T cells depletion by 479 negative selection using the CD8 MicroBeads (Cat. # 130-045-201, Miltenvi Biotec). CD8⁺ T 480 cells-depleted PBMCs were treated with or without 10 µM JOKD82 for 3 days, and then the 481 JQKD82-untreated were refreshed in the cultured medium with no-treatment (mock), 0.1 µM 482 AZD5582 (AZD), or PMA (100 ng/ml) +ionomycin (0.5 µg/ml) or anti-CD3/CD28 Dynabeads 483 (ratio: 1 bead to 2 cells; Cat. # 11161D, Gibco). The JQKD82-treated cells were changed medium 484 with 10 µM JQKD82 with or without 0.1 µM AZD5582. Supernatants were collected and 485 subjected to the extraction of HIV viral RNAs by using the QIAmp® Viral RNA Kit (Cat. #52904, 486 Qiagen). The ultrasensitive nested qPCR assay was performed to quantify HIV viral RNA copies 487 as previously described [100, 103, 104]. HIV-1 IIIB RNAs were extracted by the NucleoSpin RNA 488 Virus kit (Cat. #740956.10, MACHEREY-NAGEL) and quantified with copy numbers by the 489 Lenti-X qRT-PCR titration kit (Cat. #631235, Takara Bio). A serial dilution of HIV-1 IIIB viruses 490 with known concentrations at a series of dilutions were used to create a standard curve for the 491 absolute quantification of reactivated HIV-1 viruses in supernatants.

492 Statistics

493 Statistical analysis was performed using GraphPad PRISM. Data are presented as mean \pm 494 standard error of the mean (SEM) of biological repeats from at least 3 independent experiments. * 495 p<0.05, ** p<0.01, *** p<0.001, or **** p<0.001 indicated the significant difference analyzed by 496 ANOVA and Tukey's multiple comparison test.

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498

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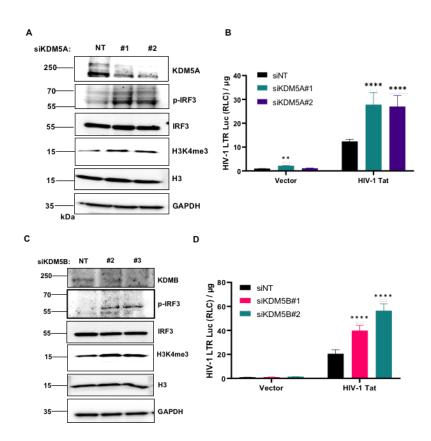


Fig 1 siRNA Knockdown of KDM5A/B increases the HIV-1 Tat/LTR-driven transcription. TZM-bl cells were received from reverse transfection by KDM5A siRNA # 1-2 or KDM5B siRNA #1-2 for 48h, and cells were trypsinized and reverse transfected by pQC empty vector or pQC-HIV-1 Tat for 48h. (A) KDM5A siRNA KD cells were harvested and lysed for IB of anti-KDM5A, p-IRF3/IRF3, GAPDH, and H3K4me3/H3. (**B**) KDM5A siRNA KD Cells with or without HIV-1 Tat overexpression were harvested for luciferase reporter assay. (**C**) KDM5B siRNA KD cells were harvested and lysed for IB of anti-KDM5B, p-IRF3/IRF, GAPDH, and H3K4me3/H3. (**D**) KDM5B siRNA KD cells with or without HIV-1 Tat overexpression were harvested for luciferase reporter assay. (**C**) KDM5B siRNA KD cells were harvested and lysed for IB of anti-KDM5B, p-IRF3/IRF, GAPDH, and H3K4me3/H3. (**D**) KDM5B siRNA KD cells with or without HIV-1 Tat overexpression were harvested for luciferase reporter assay. The readouts of RLU/total protein input (µg) were normalized with the siNT/pQC-empty vector-transfected TZM-bl control group. Results were calculated from at least 3 independent experiments and presented as mean +/- standard error of the mean (SEM). (** p <0.01; **** p<0.0001 by two-way ANOVA and Tukey's multiple comparison test compared to the same treated siNT control).

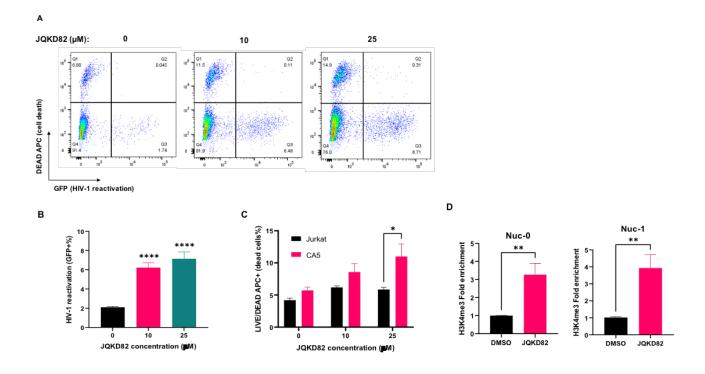


Fig 2 KDM5 inhibitor JQKD82 induces the HIV-1 reactivation, cell death, and H3K4me3 at HIV-1 LTR in the latent infected CA5 cells. (A) CA5 cells were treated with 0, 10, or 25 μ M JQKD82 for 5 days. Cells were harvested for LIVE/DEAD staining and analyzed with FASC to identify the expression of HIV-1 LTR-driven GFP (B) and LIVE/DEAD-APC (C). CA5 cells were treated with DMSO or 25 μ M JQKD82 for 5 days and then harvested to perform the ChIP qPCR assay of H3K4me3 (D) focusing on HIV-1 LTR Nuc-0 and Nuc-1 sites. Results were calculated from at least 3 independent experiments and presented as mean +/- standard error of the mean (SEM). (*p <0.05; ** p <0.01; **** p <0.0001 by one-way/two-way ANOVA and Tukey's multiple comparison test compared to untreated (B, D) or parental cells control group (C)).

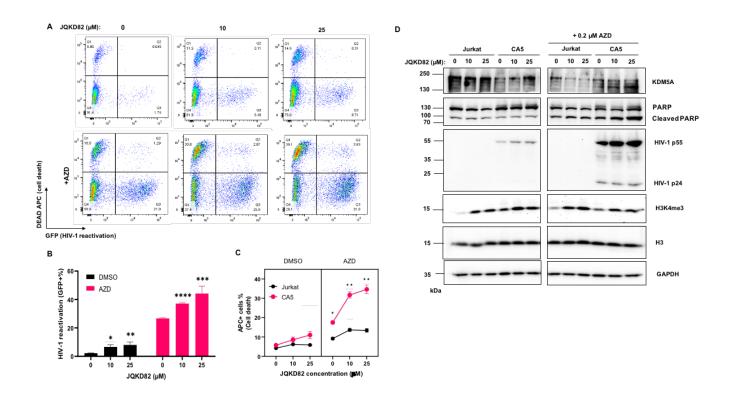


Fig 3 JQKD82/AZD5582 combination treatment synergistically increases the HIV-1 reactivation and cell death in CA5 cells. (A) CA5 cells were treated with 0, 10, or 25 μ M JQKD82 for 3 days and refreshed the JQKD82-treated medium with or without 0.2 μ M AZD5582 for 48h. Cells were performed the LIVE/DEAD staining and analyzed by FASC. (B) Treated CA5 cells were analyzed by the GFP expression from the HIV-1 reactivation. Results were calculated from 3 independent experiments and were presented as mean +/- standard error of the mean (SEM). (*p <0.05; ** p <0.01; *** p < 0.001; **** p <0.0001 by 2-way ANOVA and Tukey's multiple comparison test compared to 0 μ M JQKD82treated control). (C) Treated CA5 and parental Jurkat cells were analyzed for the LIVE/DEAD APC expression. Results were calculated from 3 independent experiments and were presented as mean +/standard error of the mean (SEM). (*p <0.05; ** p <0.01 by 3-way ANOVA and Tukey's multiple comparison test compared to Jurkat cells under the same treatment.). (D) Jurkat and CA5 cells were treated with JQKD82/AZD and harvested for immunoblotting.

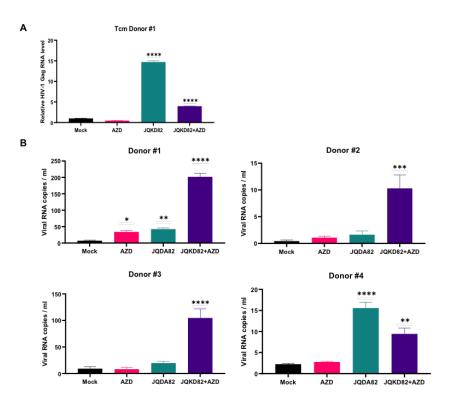


Fig 4 JQKD82/AZD5582 combinatory treatment induced HIV-1 reactivation in the primary T cells and HIV-1 patients' PBMCs. (A) The primary Tcm latency model was established by DHIV-1 infection. The DHIV-1 infected Tcm cells were back to latency and treated with DMSO or 10 μ M JQKD82 for 3 days and then refreshed the treated medium for JQKD82-treated medium for an additional 3 days with or without 0.1 μ M AZD5582. Cells were harvested for RNA extraction and RT-qPCR analysis for HIV-1 Gag mRNA level. (B) The HIV-1 patients' PBMC with CD8⁺ T cell-depletion for Donor #1-4 and treated with DMSO or 10 μ M JQKD82 for 3 days. Then these cells were refreshed with the JQKD82-treated medium for an additional 3 days with or without 0.1 μ M AZD5582. Cultured supernatant was harvested for viral RNA extraction and ultrasensitive nested RT-qPCR analysis and normalized the viral RNA copies with HIV-1 III titration standard curve. Results were calculated from 3 technical repeats and presented as mean +/- standard error of the mean (SEM). (* p<0.05, ** p <0.01; **** p <0.0001 by one-way ANOVA and Tukey's multiple comparison test compared higher to mock control group).

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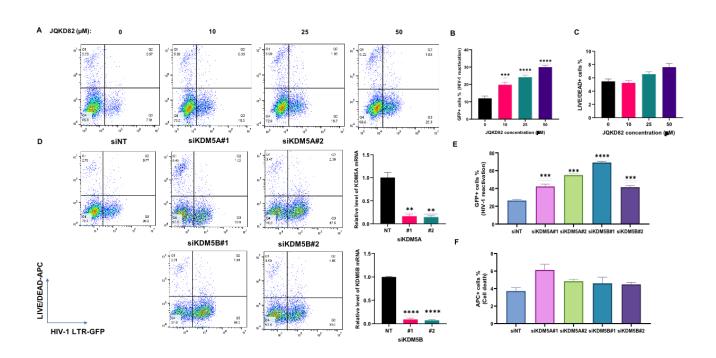


Fig 5 KDM5 inhibitor JQKD82 or siRNA knockdown of KDM5A/B induced the HIV-1 latency reactivation in HC69 microglia cells. (A) HC69 microglial cells were treated with 0, 10, 25, or 50 μ M JQKD82 for 5 days. Cells were harvested for LIVE/DEAD staining and analyzed with FASC to identify the expression of HIV-1 LTR-driven GFP (B) and LIVE/DEAD-APC (C). HC69 microglia cells were received from reverse transfection by KDM5A siRNA # 1-2, or KDM5B siRNA #1-2 for 72hr. The siRNA-transfected cells were harvested for RNA extraction and RT-qPCR to identify the siRNA KD efficiency. Cells were harvested for LIVE/DEAD staining and analyzed with FASC to identify the expression of HIV-1 LTR-driven GFP (E) and cell death (F). Results were calculated from 3 independent experiments and presented as mean +/- standard error of the mean (SEM). (*** p <0.001; **** p <0.0001 by one-way ANOVA and Tukey's multiple comparison test compared to the untreated or SiNT control group).

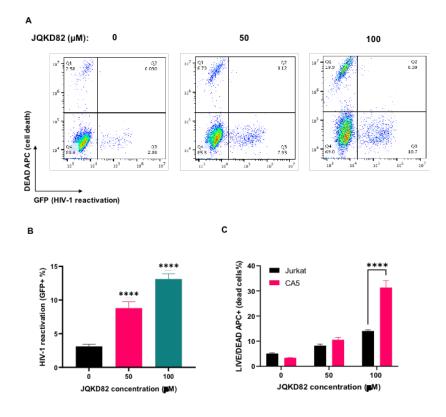


Fig S1 Short-time treatment of JQKD82 in CA5 cells for HIV-1 reactivation and cell killing. CA5 cells were treated with 0, 50, or 100 μ M JQKD82 for 48 h. Cells were harvested for LIVE/DEAD staining and analyzed with FASC to identify the expression of HIV-1 LTR-driven GFP (**A**, **B**) and LIVE/DEAD-APC (**C**). Results were calculated from at least 3 independent experiments and presented as mean +/- standard error of the mean (SEM). (** p <0.01; **** p <0.0001 by one-way/two-way ANOVA and Tukey's multiple comparison test compared to the untreated (**B**) or parental cell control group (**C**)).

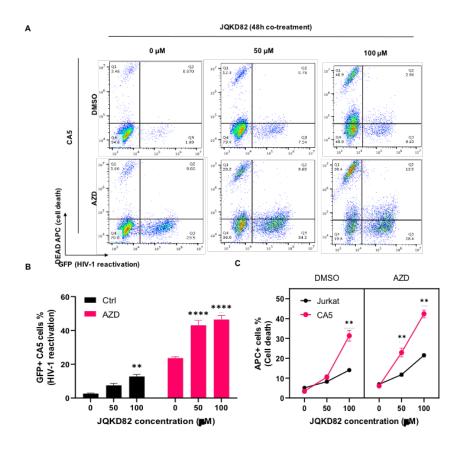


Fig S2 Short-time treatment of JQKD82/AZD5582 in CA5 cells for HIV-1 reactivation and cell killing. (A) CA5 cells were treated with 0, 50, or 100 μ M with or without 0.2 μ M AZD5582 for 48h. Cells were performed the LIVE/DEAD staining and analyzed by FASC. (B) Treated CA5 cells were analyzed by the GFP expression from the HIV-1 reactivation. Results were calculated from 3 independent experiments and were presented as mean +/- standard error of the mean (SEM). (** p <0.01; **** p <0.0001 by 2-way ANOVA and Tukey's multiple comparison test compared to 0 μ M JQKD82 treated group). (C) Treated CA5 cells were analyzed for the LIVE/DEAD APC expression. Results were calculated from 3 independent experiments and were presented as mean +/- standard to 1 μ M JQKD82 treated group). (C) Treated CA5 cells were analyzed for the LIVE/DEAD APC expression. Results were calculated from 3 independent experiments and were presented as mean +/- standard deviation (SEM). (**p <0.01 by 3-way ANOVA and Tukey's multiple comparison test compared to Jurkat cells under the same treatment.).

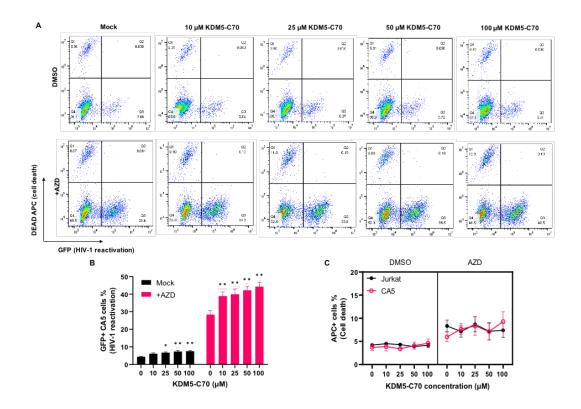


Fig S3 KDM5 inhibitor KDM5-C70 increased the HIV-1 reactivation in CA5 cells. (A) CA5 cells were treated with 0, 10, 25, 50, or 100 μ M KDM5C-70 with or without 0.2 μ M AZD5582 for 48h. Cells were performed the LIVE/DEAD staining and analyzed by FASC. (B) Treated CA5 cells were analyzed by the GFP expression from the HIV-1 reactivation. Results were calculated from 2 independent experiments and were presented as mean +/- standard error of the mean. (* p <0.05; ** p <0.01 by 2-way ANOVA and Tukey's multiple comparison test compared to 0 μ M KDM5-C70 treated group). (C) Treated CA5 and Jurkat parental cells were analyzed for the LIVE/DEAD APC expression. Results were calculated from 2 independent experiments and were presented as mean +/- standard error of the mean +/- standard error of the mean (SEM).

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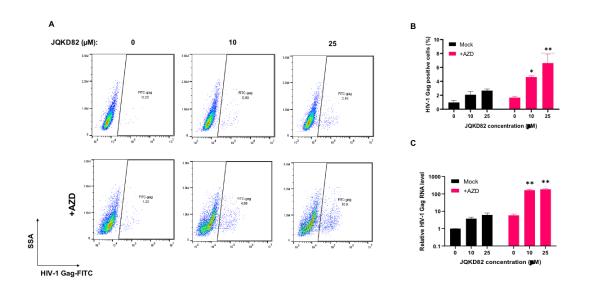


Fig S4 JQKD82/AZD5582 combinatory treatment increases the HIV-1 reactivation in U1/HIV monocyte cell line. (A) U1/HIV cells were treated with 0, 10, or 25 μ M JQKD82 for 3 days and refreshed the treated medium with or without 0.2 μ M AZD5582 for 48h. Cells were performed anti-HIV-1 Gag intracellular staining (B). Treated cells were harvested for RNA extraction and RT-qPCR to detect the HIV-1 Gag mRNA level (C). Results were calculated from at least 2 independent experiments and presented as mean +/- standard deviation (SD). (* p <0.05; ** p < 0.01; by two-way ANOVA and Tukey's multiple comparison test compared to 0 μ M JQKD82-treated control.)