# **1** The potent broadly neutralizing antibody VIR-3434 controls Hepatitis

# 2 **B** and **D** Virus infection and reduces HBsAg in humanized mice

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# 43 **Abstract**

## 44 Background & Aims

Chronic hepatitis B is a major global public health problem, and coinfection with hepatitis delta virus (HDV) worsens disease outcome. Here, we describe a hepatitis B virus (HBV) surface antigen (HBsAg)-targeting monoclonal antibody (mAb) with the potential to promote functional cure of chronic hepatitis B and D to address this unmet medical need.

#### 50 Methods

HBsAg-specific mAbs were isolated from memory B cells of HBV vaccinated individuals. In vitro neutralization was determined against HBV and HDV enveloped with HBsAg representing eight HBV genotypes. Human liver-chimeric mice were treated twice weekly with a candidate mAb starting three weeks post HBV inoculation (spreading phase) or during stable HBV or HBV/HDV coinfection (chronic phase).

56 **Results** 

From a panel of human anti-HBs mAbs, VIR-3434 was selected and engineered for 57 58 pre-clinical development. VIR-3434 targets a putative conserved, conformational 59 epitope within the antigenic loop of HBsAg and neutralized HBV and HDV infection with >12,000-fold higher potency than Hepatitis B Immunoglobulins in vitro. 60 61 Neutralization was pan-genotypic against strains representative of HBV genotypes A-62 H. In the spreading phase of HBV infection in human liver-chimeric mice, a parental 63 mAb of VIR-3434 (HBC34) prevented HBV dissemination and intrahepatic HBV RNA and cccDNA increase. In the chronic phase of HBV infection or co-infection with HDV, 64 HBC34 treatment decreased circulating HBsAg by >1 log and HDV RNA by >2 logs. 65

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## 67 **Conclusions**

This in vitro and in vivo characterization identified the potent anti-HBs mAb VIR-3434,
which reduces circulating HBsAg and HBV/HDV viremia in human liver-chimeric mice.
VIR-3434 is currently in clinical development for treatment of patients with chronic
hepatitis B or D.

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## 73 Lay summary

Chronic infection with hepatitis B virus places approximately 290 million individuals worldwide at risk for severe liver disease and cancer. Currently available treatments result in low rates of functional cure or require lifelong therapy that does not eliminate the risk of liver disease. We isolated and characterized a potent, human antibody that neutralizes hepatitis B and D viruses and reduces infection in a mouse model. This antibody could provide a new treatment for patients with chronic hepatitis B and D.

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## 81 Highlights

Identification of a human mAb VIR-3434 that potently neutralizes HBV and HDV
VIR-3434 targets a conserved, conformational epitope of the HBsAg antigenic loop
VIR-3434 treatment blocks intrahepatic HBV spread in human liver-chimeric mice
VIR-3434 treatment reduces circulating HBsAg and HDV RNA in co-infected mice
Data have enabled clinical development of VIR-3434 against chronic hepatitis B/D

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# 88 Introduction

Chronic infection with HBV is one of the leading causes of liver cirrhosis and hepatocellular carcinoma. Despite a widely available and efficacious vaccine against HBV, approximately 290 million people are currently living with chronic Hepatitis B (CHB) resulting in an estimated 820,000 deaths per year [1].

93 Approved treatments for CHB include nucleos(t)ide reverse transcriptase 94 inhibitors (NRTIs) and pegylated-interferon alpha (PEG-IFN $\alpha$ ); however, neither treatment results in high rates of HBsAg loss. Therapy with NRTIs leads to elimination 95 96 of HBV DNA in circulation but has limited effect on HBsAg levels. Long-term NRTI 97 therapy reduces but does not eliminate the risk of hepatocellular carcinoma and 98 requires lifelong treatment for most patients. Treatment with PEG-IFN $\alpha$  can induce 99 HBsAg loss, but only in a small fraction of patients (<10%) and the treatment is 100 associated with increased flu-like side effects related generally to the 101 immunomodulatory effects of the treatment [2]. Additionally, Hepatitis В Immunoglobulins (HBIG), which are polyclonal human anti-HBs antibodies, purified 102 from the serum of vaccinees, have long been used for preventative indications, 103 104 specifically perinatal mother-to-child HBV transmission and of re-infection after liver transplantation [3]. These limited treatment options underscore the need for novel 105 106 therapies against CHB that are finite and well tolerated. Effective treatments aim at 107 inducing HBV functional cure, which is defined as sustained suppression of HBV DNA 108 and loss of HBsAg off treatment.

HBV is a small, enveloped virus from the *Hepadnaviridae* family, with a relaxedcircular DNA genome packaged into a capsid formed by dimers of the viral core protein.
The capsid is surrounded by a lipid bilayer, into which the three HBV surface antigen

112 proteins (HBsAg) - large (L-HBsAg), middle (M-HBsAg) and small (S-HBsAg) - are 113 embedded. All three surface proteins share the same C-terminal S-HBsAg domain [4]. 114 HBsAg has multiple functions in the viral replication cycle, including facilitating 115 hepatocyte binding and entry by reversible attachment of HBsAg to heparan sulfate 116 proteoglycans (HSPGs) on the surface of hepatocytes [5], followed by non-reversible, 117 high-affinity interaction of the viral preS1 domain of the L-HBsAg with the cellular 118 receptor sodium taurocholate co-transporting polypeptide (NTCP) [6]. HBsAg is also 119 involved in the assembly and secretion of progeny virions and, most importantly, can 120 be secreted in absence of capsid and the HBV genome, forming spherical or filamentous subviral particles (SVPs) that exceed the number of circulating virions by 121 122 3-6 orders of magnitude [4]. Such a high level of circulating HBsAg is thought to 123 represent a viral immunotolerance strategy that can exhaust adaptive immune 124 responses [7]. To circumvent immune exhaustion, removing the tolerogenic HBsAg 125 from circulation could help restore T- and B-cell responses and lead to control of HBV 126 infection [8-10]. An ideal therapeutic strategy may combine immune-stimulatory mechanisms with virus neutralization. 127

HBsAg can be hijacked by HDV, a satellite virus of HBV from the *Kolmioviridae* family with a circular, negative-sense single-strand RNA genome. HDV uses HBsAg for its own envelopment and dissemination and, consequently, the two viruses share the same entry pathway into hepatocytes via NTCP. Therefore, HDV infection occurs only as co- or superinfection with HBV and is associated with the most severe form of viral hepatitis [11, 12]. Here, we characterized a potent and broadly neutralizing mAb that neutralized HBV and HDV infections in vitro, efficiently blocked intrahepatic viral

spread and reduced HBsAg as well as HBV and HDV viremia in human liver-chimericmice.

## 137 Materials and Methods

#### 138 Isolation of anti-HBs monoclonal antibodies (mAbs) from human memory B cells

139 The use of blood cells from healthy human HBV vaccinated donors was approved by the ethical committee "Comitato Etico Canton Ticino" (Switzerland). All participants 140 141 gave written informed consent. Individuals were selected based on high anti-HBs 142 serum antibody titer, as tested by a standard diagnostic method. Total IgG<sup>+</sup> memory B 143 cells were immortalized from peripheral blood mononuclear cells via a previously 144 described method [13]. After 2 weeks of culture, the B cell supernatants were analyzed 145 for their capacity to bind to HBsAg from three serotypes (adw, adr, ayw) by ELISA. To 146 isolate human mAbs, mRNA from B cells of wells with HBsAg binding was reverse transcribed via RT-PCR, cloned, and produced recombinantly as IgG1 via transient 147 148 transfection into mammalian cell lines. MAbs were affinity-purified using HiTrap Protein 149 A columns and sterilized via passage through 0.22 µm filters.

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# 151 For further details regarding the materials and methods used, please refer to

152 supplementary information and CTAT table.

## 153 **Results**

# 154 Isolation and engineering of a potent anti-HBs human mAb from a vaccinated155 donor

156 To identify broadly neutralizing antibodies against HBV, we isolated IgG<sup>+</sup> memory B cells from peripheral blood mononuclear cells of HBV vaccinated donors and 157 158 immortalized them using Epstein-Barr Virus and CpG [13]. The supernatants from B 159 cell cultures were analyzed for binding to HBsAg by ELISA. Selected mAbs were produced as recombinant IgG1 and neutralized HBV more potently than previously 160 161 characterized mAbs against preS1 (Ma18/7 [14]), against HBsAg (17.1.41, 19.79.5 162 [15]) or polyclonal HBV immune globulin (HBIG) (Fig. 1A). To determine binding 163 behavior, we performed a binding competition assay by ELISA. The original B-cell 164 derived mAb HBC34 showed excellent neutralization capacity and did not compete 165 with the other potently neutralizing mAbs, indicating that it recognizes a distinct functional epitope on HBsAg (Fig. S1A). Engineering of the HBC34 Fab light chain 166 167 variable region for improved developability and introducing two sets of mutations in the 168 Fc generated the preclinical lead VIR-3434 (alias HBC34-dev-LS-GAALIE). The LS Fc 169 mutation (M428L N434S) was introduced to extend in vivo half-life via increased 170 binding to neonatal FcR (FcRn) [16-18] and the GAALIE/XX2 Fc (G236A A330L I332E) 171 to augment effector functions [19-21]. Importantly, these mutations in the Fab and Fc of VIR-3434 did not alter HBsAg binding affinity compared to the parental HBC34 172 173 antibody (Fig. 1B).

#### 175 VIR-3434 neutralizes HBV and HDV infection with pan-genotypic activity in vitro

176 To assess the *in vitro* neutralizing activity of VIR-3434 against HBV, primary human 177 hepatocytes (PHH) were infected with HBV in the presence of VIR-3434, Ma18/7 or 178 HBIG (Figs. 1C and S1B). All three antibodies led to a concentration-dependent 179 reduction in HBeAg (Fig. 1C) and HBsAg (Fig. S1B) secretion, indicating the inhibition 180 of HBV infection and replication. VIR-3434 had a >12,000x lower IC<sub>50</sub> value based on 181 HBeAg secretion compared to HBIG (10.9 vs. 138,000 ng/ml) and showed an 182 increased potency (>3x) compared to Ma18/7 (34.9 ng/ml), a mAb that binds to the 183 preS1 region of the L-HBsAg (Fig. 1C) [14]. In addition, VIR-3434 efficiently neutralized 184 HDV (genotype 1, enveloped with HBsAg of HBV genotype A) in Huh7-NTCP cells with 185 an IC<sub>50</sub> value of 1.4 ng/ml, while Ma18/7 and HBIG neutralized with IC<sub>50</sub> values of 13.0 186 ng/ml (>9x higher) and 31,800 ng/ml (>22,000x higher), respectively (Fig. 1D). We next 187 investigated the binding of VIR-3434 to HBsAg from all ten HBV genotypes (A-J) in 188 transiently transfected Expi293 cells. VIR-3434 demonstrated pan-genotypic binding 189 activity, with only genotypes B and F demonstrating lower binding levels (Fig. 1E). In 190 this gualitative assay, this may be due to the lower expression levels of HBsAg that 191 was detected with these genotypes. To evaluate the breadth of neutralization of VIR-192 3434, we generated HDV enveloped with HBsAg from eight different HBV genotypes 193 (A-H). VIR-3434 potently neutralized virus harboring all tested HBsAg genotypes with 194 similar potency (IC50 range 1.4 – 4.2 ng/mL), including genotype B and F (Fig. 1F). 195 Taken together, these data show that VIR-3434 potently and broadly neutralizes HBV 196 and HDV in vitro with pan-genotypic activity.

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#### 198 VIR-3434 targets a conserved epitope on the antigenic loop (AGL) of HBsAg

199 To characterize whether VIR-3434 recognizes a linear or conformational epitope, we 200 analyzed the binding of VIR-3434 to HBsAg preparations produced in yeast or in a 201 human hepatoma cell line (PLC/PRF/5) by Western Blot. VIR-3434 recognized HBsAg 202 only under non-reducing conditions, indicating that VIR-3434 binds to a conformational 203 epitope (Fig. 2A). To further map the epitope, we utilized the Chemical Linkage of 204 Peptides onto Scaffolds (CLIPS) technology (Pepscan), which identifies 205 conformational and discontinuous epitopes by constraining antigen-derived peptides 206 to adopt looped structures that mimic the structure of the peptide in context of the full 207 protein [22]. Motif 1 (114STTSTGPCRTC124) in S-HBsAg was required for VIR-3434 208 binding (Fig. 2B), while a second motif 2 (145GNCTCIPIPSSWAF158) stabilized binding 209 (Fig. 2B). To evaluate conservation of the epitope in circulating HBV strains, 28,331 210 HBV sequences from the HBV database (HBVdb [23]) were aligned to a reference 211 sequence (GenBank ACU26993.1) using pairwise alignments. Remarkably, >99% 212 conservation was observed for 7 out of 11 amino acids in motif 1 and 12 out of 14 213 amino acids in motif 2, with high conservation and/or conservative substitutions for the 214 remaining positions (Fig. 2C, S2A and S2B). Of note, 19 known natural HBV variants 215 or vaccine escape mutants carry mutations within the epitope. VIR-3434 demonstrated 216 binding activity to all but one of the evaluated HBsAg variants by flow cytometry (Fig. 217 2D). However, binding activity to T123N or the vaccine escape variant G145R was 218 decreased, and binding to the T123N/C124R double-mutation was completely 219 abrogated (Fig. 2D) [24, 25]. We next generated HDV enveloped with HBsAg harboring 220 the T123N, T123N/C124R or G145R mutations to assess the ability of VIR-3434 to 221 neutralize these mutants. Despite decreased binding to T123N in flow cytometry (Fig.

2D), VIR-3434 efficiently neutralized this mutant (Fig. 2E). In contrast, the 222 223 T123N/C124R double mutant was not neutralized at the antibody concentrations 224 tested but also demonstrated a 6-fold reduced viral titer during production of the virus 225 stock compared to WT or the other HBsAg mutants (Fig. 2F). The removal of the 226 cysteine at position 124 may destabilize the antigenic loop and possibly result in 227 reduced viral fitness, as observed previously [26]. Additionally, VIR-3434 228 demonstrated decreased neutralization of the G145R variant. Among the 28,331 229 sequences available in the HBVdb, the C124R and G145R mutations were only 230 detected at low frequencies of 0.03% and 0.77%, respectively. Overall, VIR-3434 binds 231 to a highly conserved conformational epitope in the HBsAg antigenic loop, resulting in 232 broad pan-genotypic neutralizing activity.

#### 233 Potential mechanism of VIR-3434-mediated HBV neutralization

234 A hallmark of CHB is the persistence of high HBsAg levels in the blood. The high 235 excess of HBsAg subviral particles (SVPs) may act as a decoy, competing with 236 antibodies binding to infectious virions. We thus assessed the in vitro neutralization 237 capacity of VIR-3434 in the presence of exogenous HBsAg SVPs derived from yeast 238 or PLC cells. Western Blot confirmed that the yeast-derived HBsAg contained only S-239 HBsAq, whereas PLC cell supernatant contained a mixture of S-, M- & L-HBsAq (Fig. 240 S3). Both forms of exogenous HBsAg competed with VIR-3434 neutralization, resulting 241 in a shift (up to 25-fold) of the neutralization IC50 (Fig. 3A). At concentrations exceeding 1 µg/ml, competition could be overcome to achieve complete neutralization, 242 243 even in the presence of 2,000 IU/ml of HBsAg.

244 Next, we set out to investigate the mechanism of action by which VIR-3434 245 inhibits HBV infection. The attachment of HBV to hepatocytes is mediated by i) low-246 affinity binding of HBsAg to HSPGs-cell-surface glycoproteins modified by 247 glycosaminoglycans (GAG) interacting with the preS1 domain and the antigenic loop 248 of HBsAg—and ii) by high-affinity binding of preS1 to the entry receptor NTCP [5]. We 249 exposed HepG2-NTCP cells to HBV in the presence or absence of VIR-3434 and 250 quantified cell-bound virus by quantitative PCR. Neither VIR-3434, the entry inhibitor 251 Myrcludex B [27], nor the preS1-targeting mAb Ma18/7 were able to block binding of 252 HBV to NTCP-expressing cells. Only heparin, a soluble, sulfated GAG could efficiently block attachment of HBV to host cells (Fig. 3B), as previously reported [5]. These data 253 254 indicate that VIR-3434 neutralizes HBV infection not via blocking GAG-mediated 255 attachment but at a later step of infection.

256 We next compared the neutralization capacity of the full VIR-3434 IgG molecule 257 with that of its Fab fragment. While VIR-3434 IgG potently neutralized HBV, VIR-3434 258 Fab did not (Fig. 3C), suggesting that high-avidity bivalent binding of VIR-3434 IgG to virions may be required to block viral entry. However, surface plasmon resonance 259 260 (SPR) experiments showed that VIR-3434 IgG and Fab have comparable or only 261 modestly different apparent affinities to immobilized HBsAg (K<sub>D,app</sub> <1 nM for IgG vs. 262 <1-8 nM for Fab) (Fig. 3D, Suppl. Table S1). Therefore, an alternate explanation is 263 that neutralization by VIR-3434 requires the cross-linking of virions to form antibody-264 antigen immune complexes, which is mediated by full-length IgG but not the Fab 265 fragment. To test this hypothesis, we analyzed the morphology of yeast-derived HBsAg 266 in complex with VIR-3434 by negative stain electron microscopy. The untreated HBsAg control as well as HBsAg incubated with the VIR-3434 Fab contained symmetrical, 267

268 monodispersed, spherical SVPs of ~20 nm diameter (**Fig. 3E**). In contrast, pre-269 incubation of HBsAg with VIR-3434 IgG induced cross-linking of SVPs (**Fig. 3E**). In 270 summary, HBV neutralization requires VIR-3434 as a full-length IgG and is likely 271 mediated via sequestration of virions into SVP-containing immune complexes.

#### 272 HBC34/VIR-3434 prevents HBV spread and decreases circulating HBsAg in vivo

#### 273 in liver-chimeric mice

274 Based on its potent and broad in vitro neutralization capacity, we tested the 275 effectiveness of HBC34/VIR-3434 in an in vivo model of HBV infection. As the specific 276 tropism of HBV for human hepatocytes does not allow infection of wild-type mice, we 277 used a well-established human liver-chimeric mouse model, in which PHH are 278 transplanted into the liver of uPA/SCID beige (USG) mice that lack B and T cells [27, 28]. These mice were infected intraperitoneally with HBV (genotype D) and treated with 279 280 1 mg/kg HBC34 (the parental mAb of VIR-3434 with human Fc) or 1 mg/kg HBIG twice 281 per week or 1 µg/ml oral in drinking water of NRTI Entecavir (ETV) during the viral 282 spreading phase starting at 3 weeks post-infection (Fig. 4A). After 9 weeks of infection 283 (6 weeks of treatment), serum levels of HBV DNA (i.e., viremia) had increased ~3 logs 284 above baseline (BL) in mice that were not treated or were treated with HBIG or a control mAb. ETV reduced HBV viremia to below detectable levels at 3 and 6 weeks of 285 286 treatment, while administration of HBC34 limited HBV viremia to below BL (Figs. 4B 287 and S4A). Serum HBsAg levels increased ~2 logs above BL during the treatment period in the control and HBIG treated groups (Figs. 4C and S4B). HBC34 led to a 288 289 reduction in serum HBsAg levels to ~1 log below BL at 6 weeks of treatment. Although 290 HBC34 binds to the antigenic loop of HBsAg, concentrations of up to 50 µg/ml of

291 HBC34 did not interfere with the assay used for HBsAg guantification (Abbott Architect 292 System) in this study (Fig. S4C). Analysis of livers after 6 weeks of treatment also demonstrated high efficacy of HBC34 to prevent the increase of intrahepatic viral loads 293 (HBV pgRNA, total HBV RNA, and total HBV DNA), as values were comparable to 294 295 those at the start of treatment (Fig. 4D). In contrast, treatment with HBIG at the same 296 dose as HBC34 did not limit the intrahepatic increase of HBV DNA and RNA. HBV core 297 antigen (HBcAg) staining of mouse liver sections from untreated animals showed a 298 dramatic spread of HBV from few infected cells at 3 weeks post-challenge to infection 299 of nearly all liver-resident human hepatocytes after 9 weeks (Fig. 4E). While HBIG 300 showed similar levels of HBcAg positive cells compared to untreated controls, HBC34 301 or ETV treatment limited intrahepatic spread of HBV (Fig. 4E). Given the relatively low 302 potency of HBIG in comparison to HBC34/VIR-3434 (~1,000-12,000x less potent, see 303 Figs. 1A and 1C-D), the lack of efficacy of HBIG in this study was likely due to the sub-304 effective dose of HBIG administered to the mice [29]. Our results show that 305 HBC34/VIR-3434 is highly efficacious in vivo at blocking the infection of new 306 hepatocytes, thereby limiting the increase in viremia and reducing the level of 307 circulating HBsAg.

# 308 HBC34/VIR-3434 reduces HBV and HDV viremia in chronically infected human 309 liver-chimeric mice

We next tested the ability of HBC34/VIR-3434 to reduce HBV infection in human liverchimeric mice with an established infection with high HBV viremia and antigenemia. Mice were infected with HBV for 8 to 12 weeks (see **Fig. 5**) and either not treated or treated with HBC34 (1 mg/kg), with the approved polymerase inhibitor Lamivudine

314 (LAM) at 0.4 mg/ml in drinking water, or with a combination of HBC34 and LAM (Fig. 315 5A). Both drugs alone reduced HBV DNA viremia (~1 log) after 6 weeks of treatment (Figs. 5B and S5A). The combination of HBC34 and LAM showed enhanced 316 317 effectiveness in decreasing viremia compared to the individual agents (greater than 2 318 logs after 2 weeks treatment and at all subsequent timepoints). Treatment with HBC34 319 alone achieved a significant reduction of serum HBsAg levels (nearly 2 logs below BL 320 after 6 weeks of treatment); as expected, serum HBsAg levels in LAM treated mice 321 remained close to BL levels throughout the course of treatment (Figs. 5C and S5B). 322 Notably, the two HBC34 treated animals with lower HBsAg BL levels showed higher 323 reduction and achieved undetectable levels of HBsAg (Fig. S5B).

324 We then investigated the efficacy of HBC34 in the context of HBV/HDV co-325 infection. Human liver-chimeric mice that had been stably co-infected with both HBV 326 and HDV (10 weeks after challenge) were treated with HBC34 (1 mg/kg, 327 intraperitoneally twice per week) either carrying wild-type constant regions of the 328 original human IgG1 or a murine IgG2a, which matches the murine FcγRs expressed 329 in this model (Fig. 5D). Importantly, human or murine HBC34 reduced both HBV (2.7 log or 1 log reduction) and HDV (2.4 log or 2.6 log reduction) viremia within 2-4 weeks 330 331 of treatment (Figs. 5 E-F and S5). In addition, both mAb variants significantly reduced 332 serum HBsAg levels (2.9 log or 2.5 log reduction) (Figs. 5G and S5). Intrahepatic total HBV DNA, HBV RNA transcripts, and HDV RNA did not change substantially in 333 334 HBC34-treated mice, indicating that the mAb treatment did not reduce the number of 335 infected cells in this model (Fig. S5G). Taken together, our data demonstrate that HBC34/VIR-3434 is highly effective in reducing viremia and circulating HBsAg in 336 mouse models of chronic HBV infection and HBV/HDV co-infection. 337

## 338 **Discussion**

339 In acute viral infections, the use of mAbs is well-established in prophylaxis 340 against respiratory syncytial virus infection of neonates or in post-exposure prophylaxis 341 against Rabies virus infection [30]. For early therapy, potent neutralizing mAbs were 342 recently approved against Ebola virus infections [31], and the Coronavirus Disease 343 2019 (Covid-19) pandemic showcased that mAbs provide clear clinical benefits [32]. For therapy targeting chronic viral infections, several ultrapotent, broadly neutralizing 344 mAbs are in clinical development against human immunodeficiency virus 1 [30]. In this 345 346 study, we set out to discover a broadly neutralizing mAb for treatment of CHB. We 347 identified the human mAb VIR-3434 binding with high affinity to HBsAg and neutralizing HBV with broad potency. VIR-3434 had a >12,000-fold higher potency than HBIGs in 348 349 vitro, which are well-established as post-exposure prophylaxis for newborns to HBV+ 350 mothers [33] as well as in preventing re-infection following liver transplantation [34]. In 351 exploratory clinical studies of patients with CHB, a monthly high dose of HBIG reduced 352 HBsAg levels and induced seroconversion to anti-HBs positive after one year in few 353 individuals with low BL HBsAg (<500 IU/ml) [29, 35]. Monoclonal anti-HBs antibody 354 therapies have been previously evaluated and found to be safe in early, small clinical 355 trials. A human anti-HBs AGL mAb, GC1102, effectively lowered HBsAg by 2 to 3 log<sub>10</sub> 356 IU/mL and was well tolerated in a Phase 1 study in patients with CHB, with no evidence of serious sequelae, such as immune complex disease [36]. A mixture of two human 357 anti-HBs AGL mAbs, HBV-AB<sup>XTL</sup> (HepeX-B), significantly reduced HBsAg and HBV-358 359 DNA and had a favorable safety and tolerability profile at up to 4 doses of 80 mg 360 administered weekly, with no signs of immune complex disease or hepatotoxicity in 27

patients with CHB [37]. Thus, anti-HBs mAbs may provide promising treatment options
 for patients with CHB.

We found that VIR-3434 binds to a conformational epitope within the antigenic 363 loop of HBsAg, which forms dimers that protrude from the surface of SVPs and virions 364 365 [38]. The epitope consists of two highly conserved non-overlapping regions. VIR-3434 366 binding and neutralization was confirmed for all HBV genotypes (A-H) and a variety of 367 naturally occurring HBsAg variants. In this study, reduced in vitro activity was observed 368 for 2 of 19 HBsAg variants tested (T123N/C124R and G145R). The T123N/C124R 369 double-mutation was associated with a reduced viral fitness as reflected by a reduced 370 HDV titer in vitro, consistent with published results [26]. G145R is a well-described 371 vaccine-escape mutation, which has been observed in infants born to HBV+ mothers 372 who received the HBV vaccine (with or without HBIGs) [39]. The general prevalence 373 of G145R is low (Suppl. Fig. S2) and correlates with specific genotypes C and G. 374 However, published studies selected G145R upon treatment of HBV-infected liver-375 chimeric mice with HBsAq-specific mAbs [40]. Of note, we did not observe viral rebound in any of the liver-chimeric mice treated with HBC34/VIR-3434 throughout the 376 377 course of the study. The emergence of mAb-selected HBV escape mutants in patients with CHB may be mitigated by combination treatment of mAb with additional 378 379 therapeutic agents (e.g. NRTI) to inhibit ongoing replication during the course of 380 treatment.

381 HBV enters the hepatocyte in a two-step process: initial reversible attachment 382 to HSPGs via the preS1 and AGL regions of HBsAg [5, 41], then the myristoylated 383 preS1 region interacts with the NTCP receptor with high affinity [6]. VIR-3434 neither 384 blocked the interaction of HBsAg with HSPGs nor inhibited viral attachment, indicating

no interference with the preS1 region binding to NTCP. Yet the neutralizing activity of 385 386 VIR-3434 is similar to Ma18/7, currently one of the most potent preS1-specific 387 neutralizing mAbs [42]. Compared to the preS1 epitope of Ma18/7 only present on L-HBsAg of virions and SVP filaments, the epitope of VIR-3434 has higher abundance 388 389 in vivo, as it is present on the AGL in L-, M- and S-HBsAg on virions, filaments, and 390 spherical SVPs. This comparison of neutralization potency and epitope abundance 391 suggests either a much higher affinity of VIR-3434 or a mode of neutralization that 392 does not require blocking every epitope on HBV virions. We further observed that 393 neutralization by VIR-3434 requires the full-length IgG. In contrast, the Fab 394 demonstrated no neutralizing activity despite binding HBsAg with high affinity. Thus, 395 we hypothesize that the cross-linking of virions and SVPs into immune complexes, as 396 we observed in TEM imaging, is likely required for VIR-3434-mediated neutralization.

397 In addition to neutralizing viral entry, the formation of immune complexes leads 398 to the clustering of mAb Fcs that is required for high avidity interaction with low-affinity 399 FcqRs. Fc-mediated effector functions may explain the HBC34/VIR-3434-mediated rapid reduction of HBsAg (up to 2 logs) and HBV viremia (1 log) within 2-6 weeks of 400 401 treatment of chronically HBV-infected human liver-chimeric USG mice. VIR-3434 may 402 opsonize HBsAg SVPs and infectious virions and target them to FcgR-expressing 403 phagocytes, such as monocytes, macrophages, dendritic cells or neutrophils. In a prior 404 study, an anti-HBs mAb (CRL-8017) accelerated the uptake of HBsAg into primary human monocytes, classical dendritic cells, neutrophils, and B cells in vitro [43]. 405 406 Similarly, treatment with an anti-HBs murine mAb (E6F6) led to rapid clearance of 407 serum HBsAg (>2 log) and HBV DNA via Kupffer cells, macrophages, and neutrophils 408 in several mouse models of HBV infection [44]. As interactions with FcgRs mediated

the clearance of HBsAg and virions [44], effector functions are likely pivotal for mAbmediated therapy of CHB.

411 To extend serum half-life, the Fc region of VIR-3434 was engineered to include 412 the LS mutation to increase IgG1 binding to human FcRn in endosomes and thus 413 increase recycling into the serum [16-18]. In addition, the Fc region of VIR-3434 was 414 engineered using the GAALIE/XX2 mutation to increase binding to human activating 415 FcyRIIa and IIIa, while decreasing binding to the inhibitory FcyRIIb [19]. This 416 engineered Fc is designed to boost phagocytosis of HBsAg and HBV virions and 417 augment antigen presentation. Previously, the GAALIE/XX2-modified Fc of an anti-HA stem antibody increased the prophylactic potency against influenza A virus infection 418 419 compared to the mAb carrying a human wild-type Fc in mice transgenic for human 420 FcyRs and FcRn [20]. This increased protection was mediated via fast priming of naïve 421 CD8+ T cells, providing evidence for a mAb-mediated "vaccinal effect". In human 422 transgenic FcyR and FcRn mice, the GAALIE Fc increased protection in therapeutic 423 models of mAbs against SARS-CoV-2 virus infection [21] or cancer metastasis in the 424 lung [19]. While the tested wild-type human and mouse Fcs of HBC34/VIR-3434 both 425 can interact with the murine FcgRs and FcRn, the GAALIE mutation specifically 426 increases binding only to human FcgRs. The USG mouse model lacking T and B cells 427 and carrying myeloid effector cells with mouse FcgRs thus is not suited to address the 428 benefits of the GAALIE Fc. Future studies using primary human immune cells in vitro, 429 mouse models transgenic for human FcgRs and FcRn, and clinical trials will need to 430 determine whether VIR-3434 can induce a vaccinal effect and mediate long-term anti-431 HBV immunity.

432 Beyond HBV monoinfection, more than 12 million chronic HBV carriers are co-433 infected with HDV worldwide and have an even higher risk of developing liver cirrhosis 434 and hepatocellular carcinoma. Current treatment options are limited to PEG-IFNa, 435 which is associated with only a low frequency of sustained responses, and daily 436 injection of the viral entry inhibitor bulevirtide that has gained conditional marketing 437 approval in the EU [11]. Here, we show that VIR-3434 neutralizes HDV infection in vitro 438 and efficiently reduces HDV viremia in human liver-chimeric USG mice. Entry inhibition 439 and removal of HDV virions/HBsAg from circulation support the potential of VIR-3434 440 to be an efficacious treatment for patients chronically co-infected with HBV and HDV.

In conclusion, VIR-3434 is a highly potent, half-life extended and effector 441 442 function-enhanced mAb that binds the antigenic loop present in all forms of HBsAg and 443 neutralizes HBV as well as HDV across all genotypes. VIR-3434 integrates three 444 potential modes of action: (a) inhibition of HBV and HDV entry into new hepatocytes, (b) reduction of circulating HBsAg, and (c) delivering HBsAg to antigen-presenting cells 445 446 that could reinvigorate adaptive T and B cell responses and long-term immunity via a vaccinal effect. Consequently, the half-life extended VIR-3434 provides a promising 447 448 therapeutic option for the treatment of patients chronically infected with HBV or also co-infected with HDV and has the potential to induce a functional cure. 449

450

# **Abbreviations**

Anti-HBs	Antibody directed against HBsAg
AGL	Antigenic loop
BL	Base line
BLI	Bio-layer interferometry
СНВ	Chronic hepatitis B
ETV	Entecavir
FcRn	Neonatal Fc receptor
FcγRs	Fc gamma receptors
HBIG	Hepatitis B immunoglobulins
HBsAg	Hepatitis B surface antigen
HBV	Hepatitis B virus
HDV	Hepatitis delta virus
HSPG	Heparan sulfate proteoglycan
mAb	Monoclonal antibody
NRTIs	Nucleos(t)ide reverse transcriptase inhibitors
NTCP	Sodium taurocholate co-transporting polypeptide
PEG-IFNa	Pegylated-interferon alpha
PHH	Primary human hepatocytes
SD	Standard deviation
SVP	Subviral particle
ТЕМ	Transmission electron microscopy
USG	uPA/SCID beige

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Research (DZIF) TTU Hepatitis provided the infrastructure "Professorship
Translational Virology" to SU.

# 461 **Author contributions**

462 Conceived study: F.A.L., E.C., F.B., M.D., D.C., M.A.S. Isolated and characterized
463 mAbs: E.C., F.B., F.Z., S.B., G.L., S.J., Performed in vitro virological experiments:
464 F.A.L., J.Z., H.K., H.I., A.S. Performed in vivo experiments and virological
465 measurements: T.V., M.L. SPR/EM experiments: L.E.R, D.M.B. Bioinformatic
466 analysis: L.B.S., A.T. Manuscript writing: F.A.L, T.V., F.B., J.N., M.D., D.C., M.A.S.
467 Supervision and manuscript editing: N.P., S.U., A.T., A.L.C., G.S., L.A.P., C.M.H.,
468 M.D., D.C. and M.A.S.

## 469 **Competing interests**

470 F.A.L, E.C., F.B., J.Z, L.E.R., J.N., F.Z., H.K., S.B., G.L., S.J., H.I., L.B.S., N.P., M.L.,

A.T., A.L.C., G.S., L.A.P., C.M.H., D.C., M.A.S are employees of Vir Biotechnology
and may hold shares in Vir Biotechnology. L.A.P. is a former employee and
shareholder in Regeneron Pharmaceuticals. D.M.B. received funding from Vir
Biotechnology. The remaining authors declare that the research was conducted in the
absence of any commercial or financial relationships that could be construed as a
potential conflict of interest. SU is inventor and holder on patents protecting bulevirtide.

#### 477 Data availability statement

478 All source data that support the findings of this study are available from the 479 corresponding authors upon reasonable request.

480

## 482 Figure Legends

483 FIGURE 1. Pan-genotypic neutralization of HBV and HDV infection. (A) HBV 484 neutralization of a panel of human mAbs using HepaRG cells. \*Hepatitis B Immune 485 Globulin (HBIG) was tested at 1000x higher concentrations 5,000, 500, and 50 486 µg/ml. (B) ELISA binding of HBC34 development variants to HBsAg serotype adw. (C) 487 Neutralization of HBV (genotype D) measured via HBeAg secretion as marker of 488 infection of primary human hepatocytes (PHH) in the presence of VIR-3434, Ma18/7 489 mAb or HBIG. (D) Immunostaining for HDAg of Huh7-NTCP cells infected with HDV 490 (genotype 1, enveloped with HBsAg of HBV genotype A) in the presence of respective antibodies. (E) Flow cytometry binding of VIR-3434 to Expi293 cells transfected with 491 492 HBsAg of genotypes A-J. (F) VIR-3434 neutralizing HDV enveloped with HBsAg of 8 different HBV genotypes on Huh7-NTCP cells. 493

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FIGURE 4. HBC34/VIR-3434 prevents HBV spread and decreases circulating 518 519 HBsAg in liver-chimeric mice. (A) Human liver-chimeric USG beige mice were 520 infected with HBV (genotype D). Three weeks post infection, at the onset of viral 521 spreading phase, treatment was started twice weekly at 1 mg/kg intraperitoneally with (i) HBC34 (the parental mAb of VIR-3434), (ii) HBIG or (iii) a control mAb or were 522 treated with Entecavir (ETV) at 1 µg/ml in drinking water. Treatment was continued 523 524 until week 9 post HBV inoculation, when viral infection was spread throughout the 525 human hepatocytes. (B) HBV viremia (HBV DNA) and (C) HBsAg were assessed in 526 serum by qPCR and ELISA, respectively. The mice were sacrificed 9 weeks post 527 infection and intrahepatic HBV pgRNA, total HBV RNA (HBx region), and total HBV DNA (D) were assessed by (RT-)gPCR. Liver sections were immunostained (E) for 528

HBcAg and CK18 as marker for human hepatocytes. In (D), each circle represents one animal. Shown is the median  $\pm$  range. Statistical differences relative to the untreated control were analyzed by one-way ANOVA. p-value \* p ≤ 0.05, \*\* p ≤ 0.01.

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# 548 Supplemental Material Online

- **Detailed Methods** can be found online.
- **Supplemental Figures S1-S5** can be found online.
- **Supplemental Table S1** can be found online.

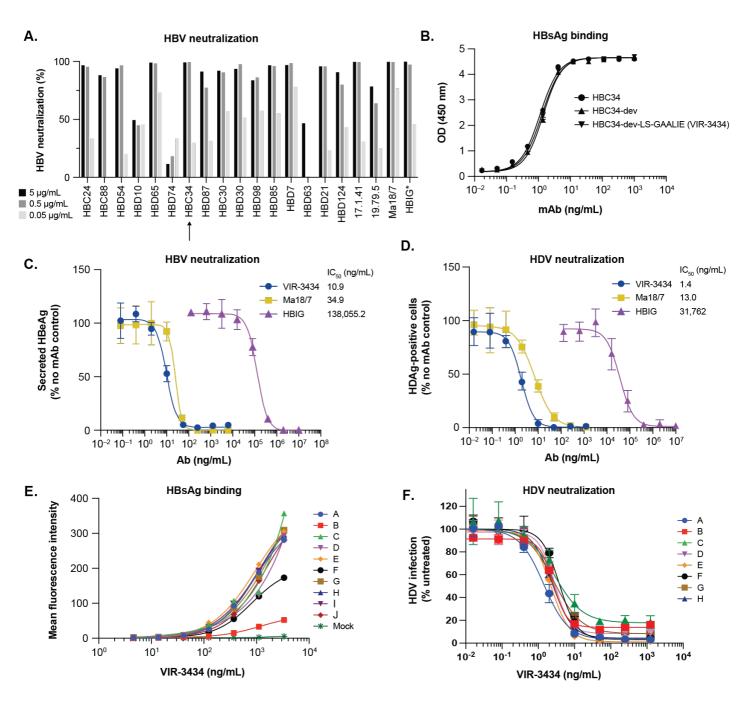
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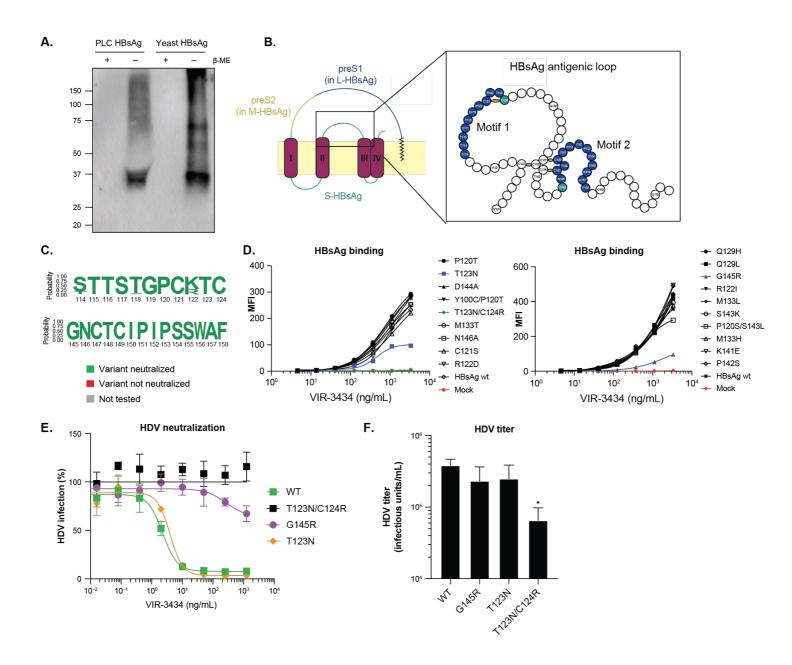


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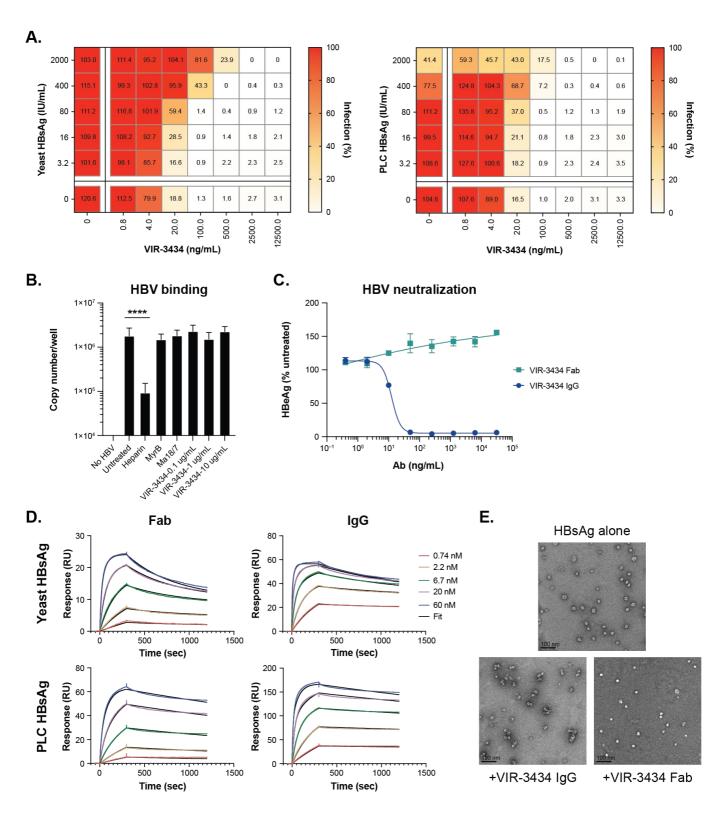


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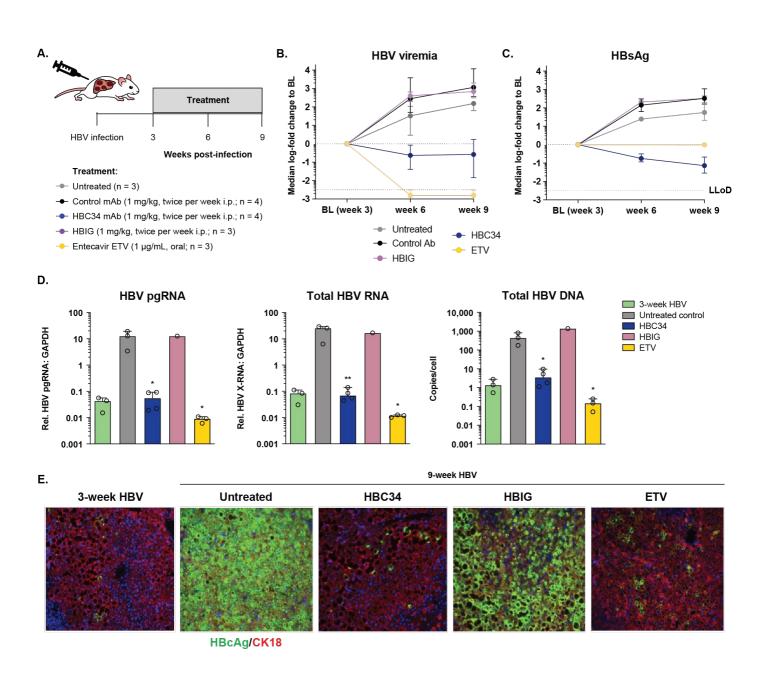


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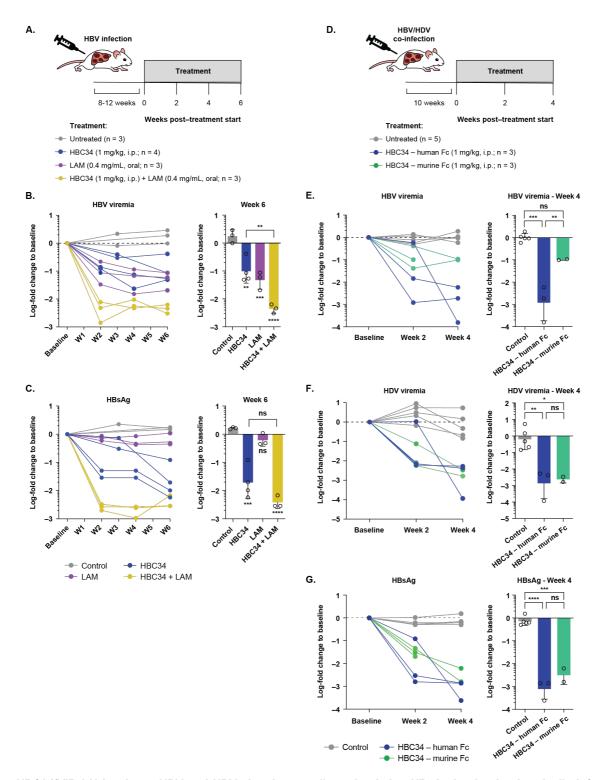


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