Recombinant receptor-binding domains of multiple MERS-coronaviruses induce cross-neutralizing antibodies against divergent human and camel MERS-coronaviruses and antibody-escape mutants

Short title: Cross-neutralization of RBD-based MERS subunit vaccines

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Abstract

Middle East respiratory syndrome coronavirus (MERS-CoV) binds to cellular receptor dipeptidyl peptidase 4 (DPP4) via spike (S) protein receptor-binding domain (RBD). The RBD contains critical neutralizing epitopes and serves as an important vaccine target. Since RBD mutations occur in different MERS-CoV isolates and antibody-escape mutants, cross-neutralization of divergent MERS-CoV strains by RBD-induced antibodies remains unknown. Here, we constructed four recombinant RBD (rRBD) proteins with single or multiple mutations detected in representative human MERS-CoV strains from the 2012, 2013, 2014 and 2015 outbreaks, respectively, and one rRBD protein with multiple changes derived from camel MERS-CoV strains. Like the RBD of prototype EMC2012 (EMC-RBD), all five RBDs maintained good antigenicity and functionality, the ability to bind RBD-specific neutralizing mAbs and the DPP4 receptor, and high immunogenicity, able to elicit S-specific antibodies. They induced potent neutralizing antibodies cross-neutralizing 17 MERS pseudoviruses expressing S proteins of representative human and camel MERS-CoV strains identified during the 2012-2015 outbreaks, 5 mAb-escape MERS-CoV mutants, and 2 live human MERS-CoV strains. We then constructed two RBDs mutated in multiple key residues in the receptor-binding motif (RBM) of RBD and demonstrated their strong cross-reactivity with anti-EMC-RBD antibodies. These RBD mutants with diminished DPP4 binding also led to virus attenuation, suggesting that immunoevasion after RBD immunization is accompanied by loss of viral fitness. Therefore, this study demonstrates that MERS-CoV RBD is an important vaccine target able to induce highly potent and broad-spectrum neutralizing antibodies against infection by divergent circulating human and camel MERS-CoV strains.

45 **Importance**

46 MERS-CoV was first identified in June 2012 and has since spread in humans and camels.
47 Mutations in its spike (S) protein receptor-binding domain (RBD), a key vaccine target, have been
48 identified, raising concerns over the efficacy of RBD-based MERS vaccines against circulating
49 human and camel MERS-CoV strains. Here, we constructed five vaccine candidates, designated
50 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD, and camel-RBD, respectively, containing single
51 or multiple mutations in the RBD of representative human and camel MERS-CoV strains during
52 the 2012-2015 outbreaks. These RBD-based vaccine candidates maintained good functionality,
53 antigenicity and immunogenicity, and they induced strong cross-neutralizing antibodies against
54 infection by divergent pseudotyped and live MERS-CoV strains, as well as antibody-escape
55 MERS-CoV mutants. This study provides impetus for further development of a safe, highly
56 effective, and broad-spectrum RBD-based subunit vaccine to prevent MERS-CoV infection.

57

58 **Keywords:** MERS; MERS-CoV; spike protein; receptor-binding domain; multiple strains;
59 antibody-escape mutants**;** cross-neutralization

60

61 **Introduction**

62 Middle East respiratory syndrome (MERS) is caused by a newly emerged coronavirus, MERS
63 coronavirus (MERS-CoV) (1). This new coronavirus was first identified in Saudi Arabia in June
64 2012 and has since infected at least 1,806 individuals worldwide, with 643 deaths (mortality rate
65 36%), as of September 29, 2016, in 27 countries (http://www.who.int/emergencies/mers-cov/en/).
66 MERS-CoV is derived from zoonotic sources, with bats as its probable original reservoirs and
67 dromedary camels as key intermediate hosts. Thus, animal-to-human transmission of MERS-CoV
68 is believed to be the major route for primary MERS-CoV infection (2-10). Nevertheless, MERS-
69 CoV has gained the ability to infect humans via human-to-human transmission, particularly in
70 healthcare facilities where patients are concentrated and infection prevention control is limited, as
71 seen in the recent "MERS-CoV super-spreading" event in South Korea (11-15). Thus, rapid
72 development of broad-spectrum, effective, and safe vaccines is urgently needed to prevent MERS-
73 CoV infection.
74
75 MERS-CoV spike (S) protein plays a major role in virus infection and pathogenesis by binding to
76 the cellular receptor dipeptidyl peptidase 4 (DPP4) through the receptor-binding domain (RBD) in
77 the S1 subunit, followed by fusion between virus and cell membranes through the S2 subunit (16-
78 19). Our previous studies have demonstrated that the MERS-CoV RBD contains a critical
79 neutralizing domain (CND, residues 377-588), which is able to induce highly potent neutralizing
80 antibodies that protect vaccinated human DPP4-transgenic (hDPP4-Tg)- and adenovirus 5 (Ad5)-
81 hDPP4-transduced mice from challenge with MERS-CoV EMC2012, a prototypic virus strain,
82 suggesting that the MERS-CoV RBD, particularly the fragment containing the identified CND, is
83 a major target for MERS vaccine development (20-28).

As the virus evolved during its spread in humans, key mutations, including L506F, D509G, and D510G, were detected in the RBD of various MERS-CoV strains isolated from different regions and at different times throughout the course of the MERS outbreak from 2012 to 2015 (**Table 1**) (29,30). In addition, the RBD sequences of MERS-CoV from dromedary camels are distinct from those of infected humans (**Table 1**), suggesting that the key residues in RBD susceptible to mutation may play critical roles in MERS-CoV transmission. Furthermore, using RBD-specific neutralizing monoclonal antibodies (mAbs), several important antibody-escape mutations, such as those at residues 511 and 513, have been identified in the MERS-CoV RBD (31-34). This tendency of MERS-CoV RBD to mutate over time may facilitate viral evasion of cross-neutralizing antibodies present in humans and camels previously infected with MERS-CoV or immunized with S protein-based vaccines. In specific, it is essential to investigate whether RBD-based MERS vaccines under development can be effective against MERS-CoV strains now in circulation in humans and camels.

The RBD of MERS-CoV is composed of a core subdomain and an external receptor-binding motif (RBM, residues 484-567). The RBM is the main domain interacting with the DPP4 receptor, and it is defined by a number of key residues, including L506, D509, D510, R511, and E513, which, in the aggregate, determine receptor binding properties and subsequent viral entry into target cells (19,35,36). However, only some of these key residues in the RBM of current MERS-CoV strains have been identified (29,37). Although these key mutations are not fixed in isolated MERS-CoV strains, it is important to note that S protein, particularly the RBM, continues to undergo strong positive selection during virus transmission (38). Consequently, it is possible that key mutations in

the RBM of RBD might accumulate in one single virus in the course of viral evolution, resulting in the emergence of immune escape virus strains. Thus, to improve our understanding of virus escape mutants relative to viral fitness, it is important to establish whether simultaneous changes of multiple key residues in the RBM of RBD will alter the antigenicity, functionality and immunogenicity of the RBD.

In this study, we initially constructed five recombinant RBD proteins, designated 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD and Camel-RBD, respectively. They contain single or multiple mutations in the RBD of representative human MERS-CoV strains circulating in the 2012, 2013, 2014 and 2015 outbreaks, or several mutations noted in the camel RBD. We evaluated whether RBDs with these scattered mutations would maintain their antigenicity, functionality, and immunogenicity. We also evaluated the cross-neutralizing activity of the antibodies induced by these RBDs against divergent human and camel MERS-CoV strains, as well as antibody-escape mutants of MERS-CoV. Two additional RBDs, RBD-FGG and RBD-FGGAA, which contain mutations of 3 and 5 key residues in the RBM of RBD, respectively, were constructed. Our results demonstrate strong cross-reactivity when mice were immunized with wild-type or variant RBDs. They demonstrate that RBD mutations with diminished DPP4 binding also led to virus attenuation, suggesting that immunoevasion after RBD immunization may only result in the context of loss of viral fitness.

Materials and Methods

Ethics statement. Female BALB/c mice at 6-8-weeks were used in this study. The animal studies were carried out in strict accordance with the recommendations in the Guide for the Care and Use

of Laboratory Animals of the National Institutes of Health (NIH), and the protocol was approved by the Committee on the Ethics of Animal Experiments of the New York Blood Center (Permit Number: 194.17).

Sources of sequences. The MERS-CoV S sequences from years 2012 through 2015 were obtained from the GenBank database at the NCBI website (http://www.ncbi.nlm.nih.gov) and aligned with the S protein sequence of MERS-CoV EMC2012 strain to identify key mutations within residues 377-588 of the RBD (**Table 1**).

Construction, expression and purification of recombinant proteins. This was performed as previously described with some modifications (21,39). Briefly, the MERS-CoV EMC-RBD plasmid was constructed by fusing residues 377-588 of EMC2012 RBD with human IgG Fc. This plasmid was used as the template to generate 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD, and Camel-RBD with point or multiple natural mutations, as well as generate RBD-FGG and RBD-FGGAA with simultaneous multiple mutations of key RBM residues, using a QuikChange site- or multisite-directed mutagenesis kit (Agilent Technologies) (**Table 2**). Recombinant S1 of MERS-CoV (EMC2012) (residues 18-725) and camel DPP4 (cDPP4) with a C-terminal His_6 were constructed using the pJW4303 expression vector (26). The aforementioned proteins were harvested from 293T cell culture supernatants. Recombinant human DPP4 protein (residues 39-766) containing a C-terminal His_6 (hDPP4) was expressed in the culture medium of insect cells using the Bac-to-Bac expression system (Invitrogen) (19). The Fc- and His-tagged proteins were purified by Protein A affinity chromatography (GE Healthcare) and Ni-NTA Superflow (Qiagen), respectively.

153

154 **SDS-PAGE and Western blot.** Purified MERS-CoV RBD proteins were subjected to SDS-PAGE
155 and Western blot analysis as previously described (21). Briefly, proteins (boiled or non-boiled)
156 were separated by 10% Tris-Glycine SDS-PAGE and then stained directly by Coomassie Brilliant
157 Blue, or transferred to nitrocellulose membranes. The blots were blocked with 5% non-fat milk-
158 PBST at 4°C overnight, followed by sequential incubation with MERS-CoV RBD-specific
159 antibody (1:1,000) and horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG (1:3,000)
160 (GE Healthcare) for 1 h at room temperature. Binding signals were visualized using ECL Western
161 blot substrate reagents and Amersham Hyperfilm (GE Healthcare).

162 Expression of MERS-CoV spike and HIV-1 p24 in the generated pseudoviruses was
163 identified by Western blot in lysed pseudoviruses using MERS-CoV RBD-specific antibody
164 (1:1,000) and anti-HIV-1 p24 (183-H12-5C, 1:50) mAb as described above (40).

165

166 **Co-immunoprecipitation assay.** Binding between MERS-CoV RBD proteins and hDPP4
167 receptor was performed using a co-immunoprecipitation (Co-IP) assay and Western blot as
168 previously described (21). Briefly, RBDs (10 μg) were incubated with hDPP4 protein (10 μg) or
169 hDPP4-expressing Huh-7 cell lysates (5×10^7/ml) at 4°C for 1 h in the presence of Protein A beads.
170 Protein A beads were washed with lysis buffer and PBS. Proteins were eluted from the beads and
171 assessed for RBD and hDPP4 by Western blot using MERS-CoV RBD-specific antibody (1:1,000)
172 and hDPP4-specific mAb (0.5 μg/ml, R&D Systems), as described above.

173

174 **ELISA.** ELISA was performed to detect binding between MERS-CoV RBD proteins and RBD-
175 specific neutralizing mAbs (21). Briefly, ELISA plates were precoated with RBD proteins (1

176 μg/ml) overnight at 4°C, blocked with 2% non-fat milk-PBST for 2 h at 37°C, and then incubated
177 sequentially with mAbs (1.25 μg/ml) and HRP-conjugated anti-mouse IgG (1:3,000, for mouse
178 mAb) (GE Healthcare) or anti-human IgG-Fab (1:5,000, for human mAbs) (Sigma) for 1 h at
179 37°C. The reaction was visualized by addition of 3,3′,5,5′-tetramethylbenzidine (TMB) substrate
180 (Invitrogen) and stopped by 1N H_2SO_4. Absorbance at 450 nm (A450) was measured using an
181 ELISA plate reader (Tecan).

182 Binding between MERS-CoV RBD and DPP4 proteins was performed using an ELISA
183 protocol similar to that described above, except that the plates were coated with hDPP4 or cDPP4
184 proteins (2 μg/ml) prior to addition of serially diluted rRBD proteins. Binding was detected using
185 RBD-specific mouse antibody (1:1,000), followed by HRP-conjugated anti-mouse IgG (1:3,000).

186 Assays to detect MERS-CoV S-specific antibody responses in mouse sera were performed
187 by coating ELISA plates with MERS-CoV S1 or rRBD protein (1 μg/ml), followed by sequential
188 incubation with serially diluted mouse sera and HRP-conjugated anti-mouse IgG (1:3,000), IgG1
189 (1:2,000) or IgG2a (1:5,000) (Invitrogen) antibodies.

190

191 **Flow cytometry.** To detect the binding between MERS-CoV RBD proteins and hDPP4-
192 expressing Huh-7 cells, cells were incubated with the indicated RBDs (40 μg/ml) for 30 min at
193 room temperature, followed by the addition of FITC-labeled anti-human IgG antibody for 30 min.
194 Cells were analyzed by flow cytometry (26,27).

195

196 **Animal vaccination and sample collection.** This was performed as previously described with
197 some modifications (24). Briefly, mice were subcutaneously (s.c.) immunized with MERS-CoV
198 RBD proteins (10 μg/mouse), or PBS control, plus MF59 adjuvant, and boosted once or twice at 3

199 weeks with the same immunogens and adjuvant. Sera were collected at 10 days after the last
200 immunization.
201
202 **Generation of wild-type and mutant MERS pseudoviruses and pseudovirus neutralization**
203 **assay.** MERS pseudoviruses were generated and pseudovirus-based neutralization assays
204 performed as previously described with some modifications (22,40). Briefly, 293T cells were
205 respectively co-transfected with a plasmid encoding an Env-defective, luciferase-expressing HIV-
206 1 genome (pNL4-3.luc.RE) and plasmids encoding the indicated S proteins (**Table 1**) using the
207 calcium phosphate method. The medium was replaced with fresh DMEM 8 h later, and
208 pseudovirus-containing supernatants were collected 72 h after transfection for single-cycle
209 infection. Wild-type and mutant MERS pseudoviruses were incubated with serially diluted mouse
210 sera at 37°C for 1 h and added to Huh-7 cells, followed by addition of fresh medium 24 h later.
211 The cells were lysed 72 h later in cell lysis buffer (Promega), incubated with luciferase substrate
212 (Promega), and assessed for relative luciferase activity using an Infinite 200 PRO Luminator
213 (Tecan). The 50% MERS pseudovirus neutralizing antibody titer (NT_{50}) was calculated as
214 previously described (41).
215
216 **Measurement of neutralizing antibody titers.** A virus plaque reduction assay was carried out to
217 determine serum neutralizing antibody titers as previously described (42,43). Briefly, sera were
218 serially diluted and incubated with 100 plaque-forming units (PFU) of MERS-CoV EMC2012 or
219 London1-2012 strains at 37°C for 30 min before transferring to Vero cell monolayers. Cultured
220 cells were overlaid with 1% agar-media, and plaques were counted.
221

222 **Statistical analysis.** Statistical significance among different groups was calculated by Student's *t*-
223 test using GraphPad Prism statistical software. *, **, and *** indicate $P < 0.05$, $P < 0.01$, and $P <$
224 0.001, respectively.
225
226 **Results**
227 **Recombinant RBD proteins of representative human and camel MERS-CoV strains in 2012-**
228 **2015 maintained good conformation and antigenicity**
229 The RBD sequences of MERS-CoVs isolated from various infection regions, different time
230 periods (2012-2015), and different hosts (humans and camels) are slightly different from the RBD
231 sequence of EMC2012, the prototype strain. The mutations are summarized in **Table 1**.
232 Accordingly, we initially constructed 5 recombinant RBD (rRBD) proteins (2012-RBD,
233 2013-RBD, 2014-RBD, 2015-RBD and Camel-RBD) containing single and multiple natural
234 mutations in the critical neutralizing domain (CND) of RBD of representative human MERS-CoV
235 strains isolated from 2012 to 2015 and representative camel MERS-CoV strains, respectively
236 (**Table 2, Fig. 1A-B**). These proteins, which were fused with a C-terminal human Fc tag, were
237 characterized by SDS-PAGE and Western blot analysis. Similar to the wild-type RBD (EMC-
238 RBD), the five RBD mutants of native (non-boiled) proteins were twice the molecular weight of
239 those that were boiled (denatured) proteins (**Fig. 1C, top**), suggesting that the Fc tags promoted
240 dimer formation. In addition, all RBD proteins of human and camel MERS-CoVs reacted strongly
241 with antibodies targeting the RBD of MERS-CoV EMC2012 (**Fig. 1C, bottom**).
242 To investigate whether the above rRBD proteins of divergent human and camel MERS-CoV
243 strains maintained good antigenicity, we performed an ELISA to test the binding activity of these
244 proteins to EMC2012 RBD-specific neutralizing mAbs (33,34). All mutant and wild-type RBDs

bound strongly to mouse mAb Mersmab1 and human mAbs m336, m337, and m338 (**Fig. 1D**), demonstrating good antigenicity.

Variant rRBD proteins bound strongly to human DPP4 receptor

A Co-IP assay was initially performed to identify whether the rRBD proteins of representative human and camel MERS-CoV strains circulating in 2012-2015 could bind to DPP4, the receptor of MERS-CoV. Strong reactivity to both proteins was observed in the immunoprecipitated samples containing RBD and hDPP4, or RBD and hDPP4-expressing Huh-7 cell lysates. However, hDPP4 in the absence of RBD was only recognized by anti-hDPP4 antibody, not by anti-MERS-CoV-RBD antibody (**Fig. 2A)**. These data suggest that rRBD proteins of representative human and camel MERS-CoV strains in 2012-2015 bound efficiently to soluble and cell-associated hDPP4 receptors.

ELISA and flow cytometry assays were then carried out to quantify the binding between RBD and DPP4. ELISA results demonstrated that the RBDs from multiple human and camel MERS-CoVs bound to both hDPP4 (**Fig. 2B**) and cDPP4 (**Fig. 2C**) proteins in a dose-dependent manner and that the binding to hDPP4 compared to cDPP4 protein was much stronger. In contrast, no binding was observed between human Fc and hDPP4 or cDPP4 (**Fig. 2B-C**). Results from flow cytometry analysis also revealed strong binding of these rRBD proteins to Huh-7 cell-associated hDPP4 receptor (**Fig. 2D**). Taken together, these results confirm the binding specificity and potency between human or camel MERS-CoV RBDs and the hDPP4 receptor.

Recombinant RBD proteins of representative MERS-CoV strains in 2012-2015 induced highly potent cross-reactive antibody responses

The purified rRBD proteins were then evaluated for their capacity to induce cross-reactive antibody responses in immunized mouse sera. All RBDs elicited similarly high titers of IgG antibodies that cross-reacted potently with S1 protein of MERS-CoV EMC2012 (**Fig. 3A**). Similar to EMC-RBD, 2012-RBD, 2014-RBD, 2015-RBD, and Camel-RBD all induced potent S1-specific IgG1 (Th2) and IgG2a (Th1) antibody responses. In addition, 2013-RBD, which contained 5 mutations spread throughout the RBD, still elicited strong IgG1 and IgG2a antibodies specific to S1 of the EMC2012 strain (**Fig. 3B-C**). In contrast, PBS control only induced background levels of MERS-CoV-specific antibody (**Fig. 3**). These data suggest that RBD proteins of representative human and camel MERS-CoV strains in 2012-2015 are highly immunogenic in inducing cross-reactive antibody responses.

Recombinant RBD proteins of 2012-2015 MERS-CoV strains induced highly potent cross-neutralizing antibodies

An ideal MERS vaccine should induce strong neutralizing antibodies against divergent MERS-CoV strains. Therefore, we generated a series of pseudoviruses expressing S proteins of human and camel MERS-CoV isolates in 2012-2015 with single or multiple natural mutations in the RBD (**Table 1**). We then tested the ability of the aforementioned RBD-immunized mouse sera to prevent infection of these pseudoviruses in Huh-7 cells. All pseudoviruses efficiently expressed MERS-CoV RBD and HIV-1 p24, which are recognized by anti-RBD antibody (**Fig. 4A, top**) and p24-specific antibody (**Fig. 4A, bottom**), and had sufficient infectivity in hDPP4-expressing Huh-7 cells (**Fig. 4B**). As expected, EMC-RBD, the RBD of EMC2012, the prototypic MERS-CoV, induced highly potent neutralizing antibodies that cross-neutralized all 17 pseudoviruses of MERS-CoV strains tested, including those isolated from humans in Saudi Arabia and South Korea

291 in the 2012-2015 outbreaks and those from infected camels (**Fig. 5A**). The RBDs of human
292 MERS-CoV isolates, including 2012-RBD, 2014-RBD, and 2015-RBD, as well as camel MERS-
293 CoV (Camel-RBD), elicited similarly high titers of neutralizing antibodies against these
294 pseudoviruses (**Fig. 5B, 5D-F**). Although 2013-RBD, which contains 5 mutations in multiple sites
295 of RBD from 4 human MERS-CoV strains in 2013, induced slightly lower titers of neutralizing
296 antibodies compared with the other RBDs, these antibodies could still efficiently cross-neutralize
297 all MERS pseudoviruses tested (**Fig. 5C**). In contrast, no specific neutralizing antibody was
298 induced in PBS control mice (**Fig. 5A**). The above results confirm the ability of the test rRBD
299 proteins in inducing strong and cross-neutralizing antibodies against divergent MERS-CoV strains
300 isolated from humans and camels.
301
302 **Recombinant RBD proteins of 2012-2015 MERS-CoV strains induced highly potent cross-**
303 **neutralizing antibodies against MERS-CoV mAb-escape variants**
304 Polyclonal anti-MERS-CoV antibody is expected to neutralize mAb escape variants since many
305 sites on the RBD are targeted in such a preparation. To assess this, we generated 5 pseudoviruses
306 expressing S proteins of mAb-escape mutants with single or multiple mutations in RBD (**Fig. 4**)
307 (31-34) and examined their sensitivity to the antibodies generated in the aforementioned RBD-
308 immunized mice. Except for 2013-RBD, which induced a slightly lower level of neutralizing
309 antibodies, as previously noted, all other RBDs, including EMC-RBD, 2012-RBD, 2014-RBD,
310 2015-RBD, and Camel-RBD, elicited similarly high titers of antibodies able to cross-neutralize all
311 MERS-CoV pseudoviruses tested (**Fig. 6**). Thus, rRBD proteins of MERS-CoV strains isolated
312 from humans and camels in the 2012-2015 outbreaks induce strong, broad-spectrum antibodies
313 capable of cross-neutralizing pseudoviruses of mAb-escape strains of MERS-CoV.

Antibodies induced by rRBD proteins of 2012-2015 MERS-CoV strains cross-neutralized live human MERS-CoV strains EMC2012 and London1-2012

To determine whether RBD immunization also provided protection against infection with infectious MERS-CoV, we infected cells with two representative MERS-CoVs, EMC2012 and London1-2012, isolated in 2012 (1,44). Notably, all RBDs, including EMC-RBD, 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD and Camel-RBD, induced cross-neutralizing antibodies against both human MERS-CoV strains, among which EMC-RBD elicited the highest neutralizing antibodies. Even though relatively lower titers of neutralizing antibodies were induced by 2012-RBD and 2013-RBD compared with other RBD proteins, levels were sufficient to neutralize both test MERS-CoV strains. In contrast, PBS control induced no neutralizing antibodies against MERS-CoV (**Fig. 7**). These data show that infectious viruses, as well as pseudoviruses, were neutralized after immunization with a panel of RBDs.

The MERS-CoV RBD with simultaneous mutations of multiple key residues in the RBM displayed significantly reduced activity of receptor binding and viral entry

The above data demonstrated that RBDs with single or multiple natural mutations derived from representative strains in 2012-2015, which contain scattered mutations in the RBM, had no significant changes in antigenicity, functionality, and neutralizing immunogenicity. To test whether deliberate mutation of multiple key residues in the RBM of the RBD would affect hDPP4-binding ability, we expressed two additional Fc-tagged RBD mutant proteins, RBD-FGG and RBD-FGGAA in the RBM that either occurred naturally, but sporadically (L506F, D509G, or D510G), or were detected in mAb-escape variants (R511A or E513A) (**Table 2**). Similar to wild-

type RBD (EMC-RBD WT), both mutant proteins had high purity, formed conformational dimeric structures (**Fig. 8A, top**), and were recognized by RBD-specific antibodies (**Fig. 8A, bottom**). Then, we tested their binding activity to DPP4 by ELISA and flow cytometry analyses. The results revealed that RBD-FGG and RBD-FGGAA exhibited significantly reduced binding activity to recombinant hDPP4 (**Fig. 8B**), cDPP4 (**Fig. 8C**), and cell-associated hDPP4 (**Fig. 8D**) proteins, with effects most obvious when 5 residues were mutated (**Fig. 8B-D).**

To evaluate the effect of these mutations on S-mediated viral entry, we constructed 2 additional MERS pseudoviruses expressing S proteins with the 3 or 5 aforementioned mutations in RBD and used them to infect Huh-7 cells. These MERS-CoV mutant pseudoviruses were significantly inhibited from entering Huh-7 cells, with the greatest inhibition observed after infection with pseudovirus carrying 5 mutations (**Fig. 8E**).

The MERS-CoV RBD with mutations of multiple key residues in the RBM exhibited significantly reduced antigenicity and neutralizing immunogenicity

To determine whether simultaneous mutations of key residues in the RBM affected antigenicity, we initially evaluated the binding affinity of mutant RBD proteins (RBD-FGG and RBD-FGGAA) to wild-type RBD-specific neutralizing monoclonal and polyclonal antibodies by ELISA. Compared to EMC-RBD WT, the two mutant RBDs exhibited significantly reduced binding to neutralizing mAbs Mersmab1 and m336 (**Fig. 9A**). Both mutant RBDs bound less well than wild-type RBD to polyclonal sera, with the greatest reduction observed when RBD-FGGAA was assayed (**Fig. 9B**).

Then, we further investigated whether RBD-FGG and RBD-FGGAA were as immunogenic as wild-type RBD. First, we examined whether mAbs Mersmab1 and m336 efficiently neutralized

pseudoviruses with RBD-FGG and RBD-FGGAA mutations. The results demonstrated that the pseudoviruses with these mutations were significantly less sensitive to neutralization (ND_{50}) (**Fig. 9C**). Similar results were obtained when the pseudoviruses were exposed to mouse sera containing polyclonal neutralizing antibodies (**Fig. 9D**). After immunization, RBD-FGG and RBD-FGGAA elicited significantly decreased levels of IgG (**Fig. 9E**) and neutralizing antibodies in mouse sera against MERS pseudovirus (EMC2012 WT) (**Fig. 9F**). These results suggest that simultaneous mutations of multiple key residues in the RBM of MERS-CoV RBD resulted in significantly reduced antigenicity and neutralizing immunogenicity, but at the cost of reduced ability to enter cells.

Discussion

Development of safe, effective and broad-spectrum vaccines against MERS-CoV infection is still urgently needed to combat the continuing threat posed by MERS-CoV. Compared with other vaccine types, including those based on viruses and viral vectors, subunit vaccines are safer since viral genomic components are absent (25,28). We previously identified the RBD in the S protein of MERS-CoV as a critical vaccine target and demonstrated that RBD-based MERS vaccines induce highly potent neutralizing antibodies that protect immunized animals against MERS-CoV challenge (20,21,23,24,39).

Studies have revealed the presence of a number of single and multiple mutations in the RBDs of MERS-CoV strains isolated from humans and camels at different time periods during the 2012-2015 outbreaks (**Table 1**) (29,30). Also, analysis of RBD-specific neutralizing mAbs has identified a number of mutations in the RBDs of MERS-CoV mutants that escaped neutralization

383 by these mAbs (31-34). The presence of both natural and antibody-escape mutations in the RBD
384 of MERS-CoV has raised concerns about the capacity of RBDs to induce cross-neutralizing
385 antibodies against different mutant strains of MERS-CoV. Therefore, this study aimed to design
386 and develop RBD subunit vaccines based on different human and camel MERS-CoV strains
387 isolated from 2012 through 2015 and evaluate their cross-neutralizing ability against divergent
388 MERS-CoV strains and mAb-escape mutants.
389
390 Using the RBD sequence of MERS-CoV EMC2012 strain (EMC-RBD) as a prototype, we
391 constructed five mutant RBD proteins, designated 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD
392 and camel RBD that contain single or multiple mutations in the RBD of representative MERS-
393 CoV strains isolated from humans and camels in 2012-2015 (**Tables 1-2**). Our data indicated that
394 all five mutant RBDs maintained good conformation and antigenicity, reacting strongly with
395 polyclonal and mAb neutralizing antibodies that recognize neutralizing epitopes in the RBD of
396 EMC2012 strain (33,34,45). In addition, these RBDs bound strongly to hDPP4 receptor in soluble
397 and cell-associated forms, suggesting good functionality. It should be noted that while the binding
398 between these RBDs and hDPP4 protein was stronger than that between RBDs and cDPP4 protein,
399 the binding between Camel-RBD and hDPP4-expressing Huh-7 cells was enhanced, not reduced.
400 These results suggest that the camel RBD retains its high binding activity to human receptor
401 during evolution, indicating that camels will remain an important reservoir for sporadic human
402 infection.
403
404 MERS vaccines are expected to have broad-spectrum neutralizing ability against different MERS-
405 CoV strains. Indeed, we have found that similar to the prototype EMC-RBD, all five mutant

406 RBDs containing scattered key mutations elicited high-titer antibody responses in immunized
407 mice as assessed by their ability to strongly cross-react with MERS-CoV S protein from the
408 prototype EMC2012 strain. Most importantly, these RBD-induced antibodies could cross-
409 neutralize infection of all MERS-CoV strains tested, including 17 pseudotyped human and camel
410 MERS-CoV strains isolated in the 2012-2015 outbreaks, 5 mAb-escape MERS-CoV mutants, and
411 2 live MERS-CoV strains isolated in the early stage of the 2012 outbreak, thus confirming their
412 ability to induce cross-neutralizing antibodies against divergent circulating MERS-CoV strains.
413 Our other studies have demonstrated that neutralizing antibody titers of ≥ 1:119 (NT_{50}) completely
414 protect highly susceptible hDPP4-transgenic (hDPP4-Tg) mice from lethal MERS-CoV challenge
415 (unpublished data). It is thus expected that immunization with vaccine candidates containing the
416 individual mutant RBDs (2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD, or Camel-RBD), as
417 well as prototype EMC2012-RBD, will protect hDPP4-Tg mice from MERS-CoV infection since
418 all of them induced neutralizing antibody titers of ≥ 1:120 (NT_{50}) against two live MERS-CoV
419 strains (EMC2012 and London1-2012**)**. Therefore, irrespective of these scattered mutations at
420 single or multiple sites of MERS-CoV RBD, the data presented here suggest that RBD-based
421 MERS vaccines will be able to induce sufficient cross-neutralizing antibodies for protection
422 against current circulating strains, as well as other strains that might occur in the future.
423
424 The tertiary structure of MERS-CoV S trimer was modeled based on the recently solved cryo-EM
425 structure of mouse hepatitis virus (MHV) S trimer (**Fig. 10**) (46). Mapping of these naturally
426 occurring scattered mutations in RBD of MERS-CoV on the modeled structure of MERS-CoV S
427 trimer revealed that eight of these residues (506, 509, 510, 520, 522, 529, 530, and 534) are
428 located in the RBM region, whereas the rest are located in the core region of the RBD. Among

these eight RBM residues, three (506, 509, 510) are directly involved in DPP4 binding (35,36). The epitopes covering these three residues have been shown to be critical for the binding of neutralizing monoclonal antibodies (32-34). Two additional key residues (511, 513) in the RBM are also responsible for virus-DPP4 binding and play a role in inducing mAb-escape mutant virus strains (31,32,34). Thus, simultaneous mutations of the above three (506, 509, 510) or five (506, 509, 510, 511, 513) key residues in a single viral strain led to significant changes in the neutralizing immunogenicity of MERS-CoV RBD, facilitating escape of the virus from host immune surveillance. Several reasons explain why this has not happened in nature. First, the chance for simultaneous mutations of these three or five key residues in the RBM of the RBD is significantly lower than that for single mutations. Second, we found that mutating all three or five residues simultaneously significantly reduced viral binding to the DPP4 receptor and, hence, reduced the ability of the virus to enter and infect target cells, a hefty price that the virus cannot afford to pay. Consequently, only scattered mutations of these residues were detected in different viral strains, which led to less significant changes in the neutralizing immunogenicity of each RBD. The other mutated residues play less important roles in receptor binding and in overall neutralizing immunogenicity of the RBD, and are also inconsistently detected in different viral strains. Since these binding and inhibition assays were based on viral RBD protein or pseudoviruses expressing MERS-CoV S protein with the test mutations in the RBD, there exists the possibility that the results might be different when mutations are identified in live MERS-CoV. It is also possible that some live MERS-CoV strains that contain the mutations of key residues in RBD might become resistant to neutralizing antibodies without causing significant reduction of infectivity. Nevertheless, the results presented in this study suggest that it might take much longer for MERS-CoV to acquire immune escape mutations in the RBD than in other

452 regions of the viral S protein since decreased neutralization is accompanied by reduced binding to
453 DPP4. Therefore, the RBD remains a major target site for development of MERS vaccines.
454
455 MERS-CoV RBD contains multiple conformational neutralizing epitopes encompassing key
456 residues that include L506, D509, D510, R511, E513, W535, E536, D539, Y540 and R542
457 (33,34,43,45,47,48); thus, vaccines targeting the RBD are effective against a virus with mutations
458 in one or more epitopes. In contrast, other target sites in the S protein may contain only one single
459 neutralizing epitope. Therefore, vaccines targeting such an epitope would become ineffective if a
460 single mutation occurred. In addition, the RBD is also a critical functional domain, and antibodies
461 targeting the RBD can also block the binding between RBD and viral receptor, in addition to their
462 virus neutralizing activity (26).
463
464 To summarize, we constructed five rRBD proteins respectively covering different mutations in the
465 RBD of MERS-CoV that circulated during the course of the 2012-2015 outbreaks, as well as two
466 mutant RBDs with simultaneous mutations of multiple key residues in the RBM of the RBD.
467 Their antigenicity to bind MERS-CoV RBD-specific neutralizing antibodies, as well as their
468 functionality to bind the DPP4 receptor of MERS-CoV was demonstrated. This study also
469 explored the broad-spectrum capability of the RBDs containing naturally scattered mutations in
470 inducing cross-neutralizing antibodies against human and camel strains isolated from the 2012-
471 2015 outbreaks, as well as antibody-escape mutant strains. Taken together, this study confirms the
472 feasibility of developing an RBD-based MERS vaccine that is safe, effective, and broad-spectrum,
473 with the added ability to cross-neutralize antibodies against infection of current and future
474 divergent MERS-CoV strains.

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Conflict of interest statement

The authors declared no conflict of interest.

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658 **Figure Legends**

659 **Fig. 1. Construction, characterization and antigenicity of human and camel MERS-CoV**
660 **RBD proteins.** (A) Schematic diagram of MERS-CoV S1 subunit. Residues 1-18, signal peptide.
661 RBD, receptor-binding domain, which contains identified critical neutralizing domain covering
662 residues 377-588. (B) Construction of RBDs of divergent human and camel MERS-CoV strains
663 fused with Fc of human IgG. Residues represent single or multiple mutations in the RBD of
664 representative human MERS-CoV strains in 2012-2015, designated 2012-RBD, 2013-RBD, 2014-
665 RBD, and 2015-RBD, respectively, or MERS-CoV from camels (Camel-RBD) in comparison
666 with the RBD of prototype strain EMC2012 (EMC-RBD). (C) SDS-PAGE and Western blot
667 analysis of purified rRBD proteins. Non-boiled (non-denatured) or boiled (denatured) samples (5
668 µg) were subjected to SDS-PAGE (top) or Western blot (bottom), and the binding was tested using
669 MERS-CoV RBD-specific antibody (1:1,000). The molecular weight markers (kDa) are indicated
670 on the left. (D) Detection of antigenicity of rRBD proteins by ELISA. ELISA plates were coated
671 with respective human and camel RBD proteins, or hIgG-Fc control, and then incubated with
672 neutralizing mouse mAb Mersmab1 and human mAbs m336, m337, and m338 (1.25 µg/ml),
673 which recognize conformational epitopes in the RBD of MERS-CoV EMC2012. The data are
674 presented as mean A450 ± standard deviation (SD) (n = 4) of RBDs binding to mAbs.
675
676 **Fig. 2. Detection of binding of human and camel MERS-CoV RBD proteins to DPP4**
677 **receptor.** (A) Co-IP followed by Western blot analysis of binding between human and camel RBD
678 proteins and soluble hDPP4 protein or cell-associated hDPP4 in Huh-7 cells. Recombinant RBD
679 proteins were respectively incubated with hDPP4 protein (left) or Huh-7 cell lysates (right) plus
680 Protein A beads and then detected for binding using MERS-CoV RBD (1:1,000, top) or DPP4 (0.5

μg/ml, bottom)-specific antibodies. The hDPP4 protein only was included as a control. Quantification of binding between rRBD proteins and hDPP4 (B) or cDPP4 (C) protein by ELISA. ELISA plates were coated with hDPP4 or cDPP4 protein (2 μg/ml) and then incubated with dilutions of MERS-CoV RBD proteins or hIgG-Fc control. The data are presented as mean ± SD (n = 4) of RBDs binding to hDPP4 or cDPP4 protein. (D) Quantification of binding between rRBD proteins and cell-associated hDPP4 receptor by flow cytometry analysis. Huh-7 cells were sequentially incubated with rRBD proteins (40 μg/ml), or hIgG-Fc control, and FITC-labeled anti-human IgG antibody, followed by analysis for binding. The data are presented as mean ± SD (n = 4) of RBDs binding to Huh-7-expressed hDPP4 receptor. MFI: median fluorescence intensity.

Fig. 3. Human and camel MERS-CoV RBD proteins induced highly potent cross-reactive antibody responses in immunized mice. PBS was included as control. Sera from 10 days after the 3rd immunization were tested for IgG (A), IgG1 (B), and IgG2a (C) antibody responses specific to S1 of prototype strain of MERS-CoV EMC2012. The antibody titers are expressed as the endpoint dilutions that remain positively detectable, and they are presented as mean antibody titers ± SD of five mice in each group. 2012-RBD, 2013-RBD, 2014-RBD, 2015-RBD, and Camel-RBD represent MERS-CoV strains isolated from humans in 2012-2015 and from camels, respectively. EMC-RBD: RBD of prototype strain of MERS-CoV EMC2012.

Fig. 4. Detection of target proteins and infectivity of MERS pseudoviruses. (A) Packaged MERS pseudoviruses were tested for expression of MERS-CoV S and HIV-1 p24 proteins by Western blot using anti-MERS-CoV RBD (1:1,000, top) and anti-HIV-1 p24 (183-H12-5C, 1:50, bottom) antibodies, respectively. (B) Detection of infectivity of MERS pseudoviruses in DPP4-

704 expressing Huh-7 cells. VSV-G was included as positive control.

705

706 **Fig. 5. Human and camel MERS-CoV RBD proteins induced highly potent cross-**
707 **neutralizing antibodies against divergent human and camel MERS pseudoviruses.** MERS
708 pseudoviruses expressing S proteins of divergent human and camel MERS-CoV strains isolated
709 from 2012 to 2015 with single or multiple mutations in the RBD were tested the ability to cross-
710 neutralize MERS-CoV RBD proteins in Huh-7 cells. Sera of mice immunized with EMC-RBD
711 (A), 2012-RBD (B), 2013-RBD (C), 2014-RBD (D), 2015-RBD (E), and Camel-RBD (F), or PBS
712 control (A), were collected at 10 days after the 3rd immunization and analyzed. Neutralizing
713 activity was expressed as 50% neutralizing antibody titers (NT_{50}). The data are presented as mean
714 ± SD of five mice in each group.

715

716 **Fig. 6. Human and camel MERS-CoV RBD proteins induced highly potent cross-**
717 **neutralizing antibodies against mAb-escape mutants of MERS pseudoviruses.** MERS
718 pseudoviruses expressing RBD mAb-escape variants were generated, as specified above, and
719 tested for cross-neutralizing ability of human and camel RBD proteins in Huh-7 cells. Sera of
720 mice immunized with EMC-RBD (A), 2012-RBD (B), 2013-RBD (C), 2014-RBD (D), 2015-
721 RBD (E), and Camel-RBD (F), or PBS control (A), were collected at 10 days after the 3rd
722 immunization and analyzed. Neutralizing activity was expressed as NT_{50}, and the data are
723 presented as mean ± SD of five mice in each group.

724

725 **Fig. 7. Human and camel MERS-CoV RBD proteins induced cross-neutralizing antibodies**
726 **against different human MERS-CoVs.** Mice were immunized with the indicated RBD or PBS as

727 a control, and sera were collected at 10 days after the 3rd immunization and examined for the
728 presence of antibodies that neutralized MERS-CoV strains EMC2012 and London1-2012 strains
729 in Vero E6 cells. Neutralizing antibody titers are presented as the reciprocal of the highest dilution
730 of sera that resulted in a complete inhibition of virus infectivity in at least 50% of the wells (NT_{50}).
731 The data are from pooled sera of five mice in each group.
732
733 **Figure 8. MERS-CoV RBD with multiple mutations of key residues in the RBM exhibited**
734 **significantly reduced activity of receptor binding and viral entry.** (A) Characterization of
735 mutant MERS-CoV RBD proteins. SDS-PAGE (top) and Western blot (bottom) analyses of the
736 purified mutant RBD proteins respectively containing 3 (RBD-FGG) and 5 (RBD-FGGAA) key
737 mutations in the RBM. Non-boiled and boiled protein samples (5 μg) were subjected to SDS-
738 PAGE (top), or Western blot (bottom), followed by detection by MERS-CoV RBD-specific
739 antibody (1:1,000). EMC-RBD wild-type (WT) was included as a control. The molecular weight
740 markers (kDa) are indicated on the left. Detection of binding affinity between mutant MERS-CoV
741 RBD proteins and hDPP4 (B) or cDPP4 (C) protein by ELISA. The ELISA plates were coated
742 with hDPP4 or cDPP4 protein (2 μg/ml) and then incubated with respective RBD. The data are
743 presented as mean ± SD (n = 4) of RBD binding to hDPP4 or cDPP4 protein. (D) Detection of
744 binding between mutant RBD proteins and Huh-7 cells expressing hDPP4 by flow cytometry
745 analysis. EMC-RBD WT was included as a control. The data are presented as mean ± SD (n = 4)
746 of each RBD (40 μg/ml) binding to hDPP4 in Huh-7 cells. MFI: median fluorescence intensity.
747 For (B)-(D), *** represents $P < 0.001$ between mutant and WT RBDs. (E) Detection of entry of
748 MERS pseudoviruses expressing S proteins with 3 (L506F-D509G-D510G) or 5 (L506F-D509G-
749 D510G-R511A-E513A) mutations in the RBM. The infectivity of EMC2012 WT pseudovirus in
750 Huh-7 cells was set as 100% entry, and the infectivity of the corresponding mutant pseudovirus

751 was expressed as the percentage of entry (%). *** represents $P < 0.001$ between mutant and WT
752 pseudoviruses.
753
754 **Figure 9. MERS-CoV RBD with multiple mutations of key residues in the RBM showed**
755 **reduced antigenicity and neutralizing immunogenicity.** **(i)** Detection of the binding between
756 mutant RBD proteins and RBD-specific neutralizing antibodies by ELISA. rRBD proteins (1
757 μg/ml) were precoated on the ELISA plates, and binding was detected using RBD-specific
758 neutralizing mAbs Mersmab1 and m336 (A), as well as polyclonal antibodies from sera of mice
759 immunized with EMC-RBD wild-type (WT) protein (B). Serum IgG antibody titers are expressed
760 as the endpoint dilutions that remain positively detectable, and the data are presented as mean ±
761 SD (n = 4) of each RBD binding to the antibodies. EMC-RBD WT protein was included as a
762 control. ** and *** represent $P < 0.01$ and $P < 0.001$, respectively, between mutant and WT RBD
763 proteins. **(ii)** Detection of neutralizing activity of MERS-CoV RBD-specific neutralizing mAbs
764 Mersmab1 and m336 (C), as well as polyclonal antibodies from sera of mice immunized with
765 EMC-RBD WT protein (D), against the above mutant and WT pseudoviruses. ND_{50} and NT_{50}
766 represent 50% neutralizing dose (for mAbs) and 50% neutralizing antibody titers (for sera),
767 respectively. ** and *** represent $P < 0.01$ and $P < 0.001$, respectively, between mutant and WT
768 pseudoviruses. **(iii)** Detection of IgG (E) and neutralizing antibodies (F) induced by MERS-CoV
769 RBD mutant proteins, or EMC-RBD WT protein control, by ELISA and MERS pseudovirus
770 neutralization assay, respectively. Sera from 10 days after the 2nd immunization were tested for
771 IgG antibodies specific to EMC-RBD and neutralizing antibodies against EMC2012 WT
772 pseudovirus. The antibody titers are presented as mean ± SD of five mice in each group. The
773 neutralizing antibody titers are expressed as mean NT_{50} ± SD of five mice in each group. * and **

represent $P < 0.05$ and $P < 0.01$, respectively, between mutant and WT RBD proteins.

Figure 10. Distribution of RBD mutation residues in the structural model of MERS-CoV S trimer. Based on the structural homology between MERS-CoV RBD (PDB access code: 4L3N) and the corresponding domain in the trimeric MHV S (PDB access code: 3JCL), the crystal structure of the former was modeled into the cryo-EM structure of the latter. The core structure of MERS-CoV RBD is in cyan, the RBM is in red, and the MERS-CoV RBD residues that have undergone mutations are in blue. The trimeric MHV S protein contains three copies of this domain, with two colored in magenta and the third replaced by MERS-CoV RBD.

784 **Tables**

785 **TABLE 1. Representative MERS-CoV strains isolated in the 2012-2015 outbreaks and their**

786 **mutations in MERS-CoV RBD containing residues 377-588**[a]

GenBank protein ID	Year isolated	Host	Region	MERS-CoV RBD residues 377-588																Mutation
				400	424	431	434	457	460	482	**506**	**509**	**510**	520	522	529	530	534	582	
AFS88936.1	2012	Human	EMC	K	T	A	A	S	S	A	**L**	**D**	**D**	A	Q	I	V	V	N	0
AFY13307.1	2012	Human	England								**F**									1
AGG22542.1	2012	Human	England								**F**									1
AGV08379.1	2012	Human	KSA									**G**								1
AGV08584.1	2012	Human	KSA															A		1
AHI48528.1	2013	Human	KSA			P				V										2
AHI48733.1	2013	Human	KSA				V													1
AHC74088.1	2013	Human	Qatar						F											1
AGV08438.1	2013	Human	KSA																I	1
AID55090.1	2014	Human	KSA		I															1
AID55095.1	2014	Human	KSA		I															1
AID55087.1	2014	Human	KSA												H					1
AKL59401.1	2015	Human	Korea														L			1
ALB08322.1	2015	Human	Korea										**G**							1
ALB08289.1	2015	Human	Korea													T				1
AHY22545.1	2013	Camel	KSA	N																1
AHL18090.1	2013	Camel	Egypt				S													1
AHX00711.1	2013	Camel	KSA					G												1
AHX00721.1	2013	Camel	KSA					G												1
AHY22555.1	2013	Camel	KSA											S						1

787

788 [a]EMC, Erasmus Medical Center; KSA, Saudi Arabia. Key residues in the RBM of the RBD are

789 highlighted in bold.

790

791 **TABLE 2. Constructed MERS-CoV RBD fragments containing single or multiple mutations**
792 **in the RBD of representative MERS-CoV strains isolated in 2012-2015 and multiple key**
793 **mutations in the RBM of the RBD[a]**

794

Proteins	Year isolated	Host	MERS-CoV RBD residues 377-588																	Mutation
			400	424	431	434	457	460	482	**506**	**509**	**510**	**511**	**513**	520	522	530	534	582	
EMC-RBD	2012	Human	K	T	A	A	S	S	A	**L**	**D**	**D**	**R**	**E**	A	Q	V	V	N	
2012-RBD	2012	Human								**F**	**G**							A		3
2013-RBD	2013	Human			P	V		F	V										I	5
2014-RBD	2014	Human		I												H				2
2015-RBD	2015	Human															L			1
Camel-RBD	2013	Camel	N			S	G								S					4
RBD-FGG	2012	Human								**F**	**G**									3
	2015	Human										**G**								
RBD-FGGAA	2012	Human								**F**	**G**									5
	2015	Human										**G**								
		Escape mutants											**A**							
														A						

795

796 [a]EMC-RBD: RBD fragment constructed based on the sequence of MERS-CoV EMC2012
797 (prototype) strain. Key residues in the RBM of the RBD are highlighted in bold.

798
799
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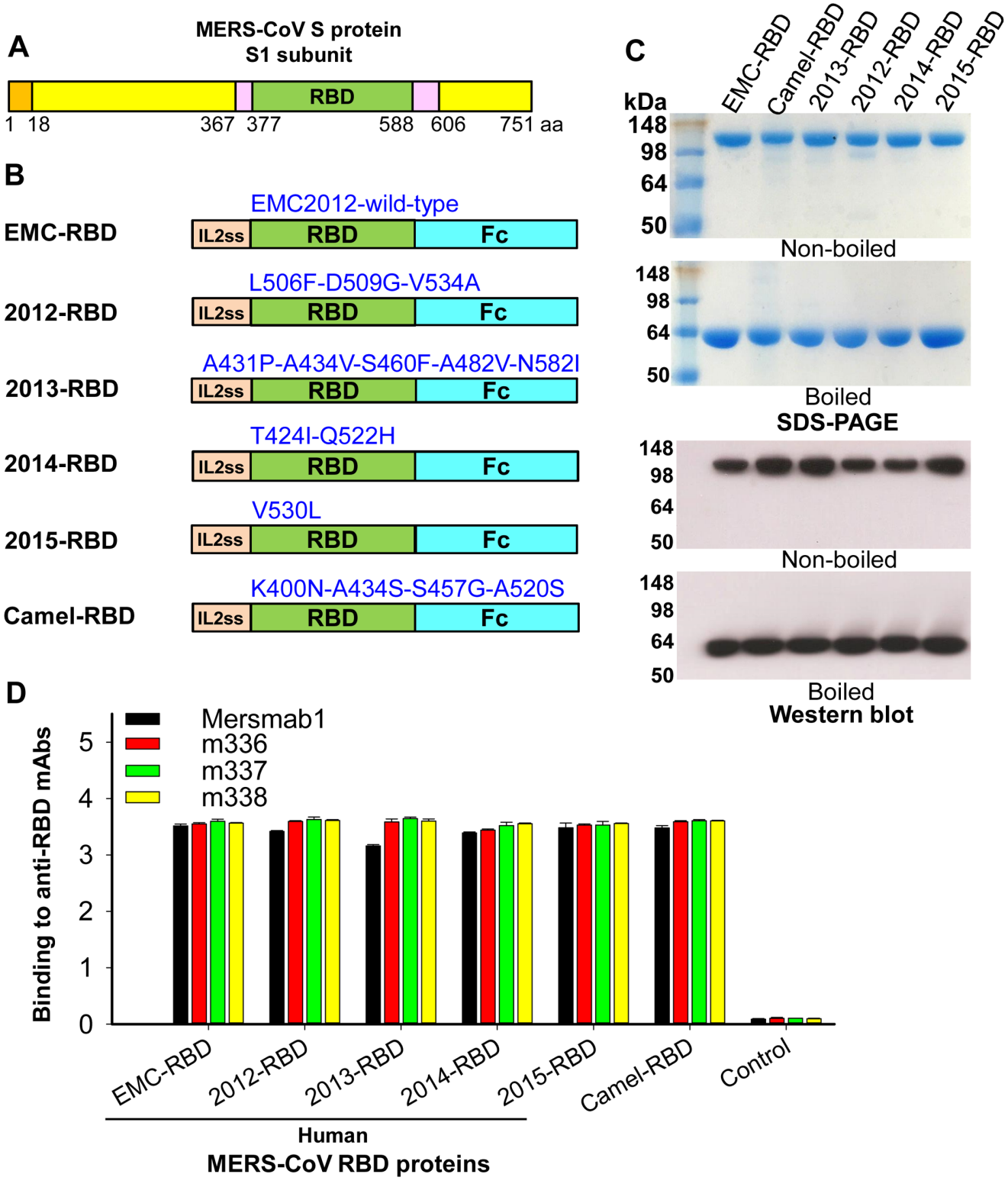
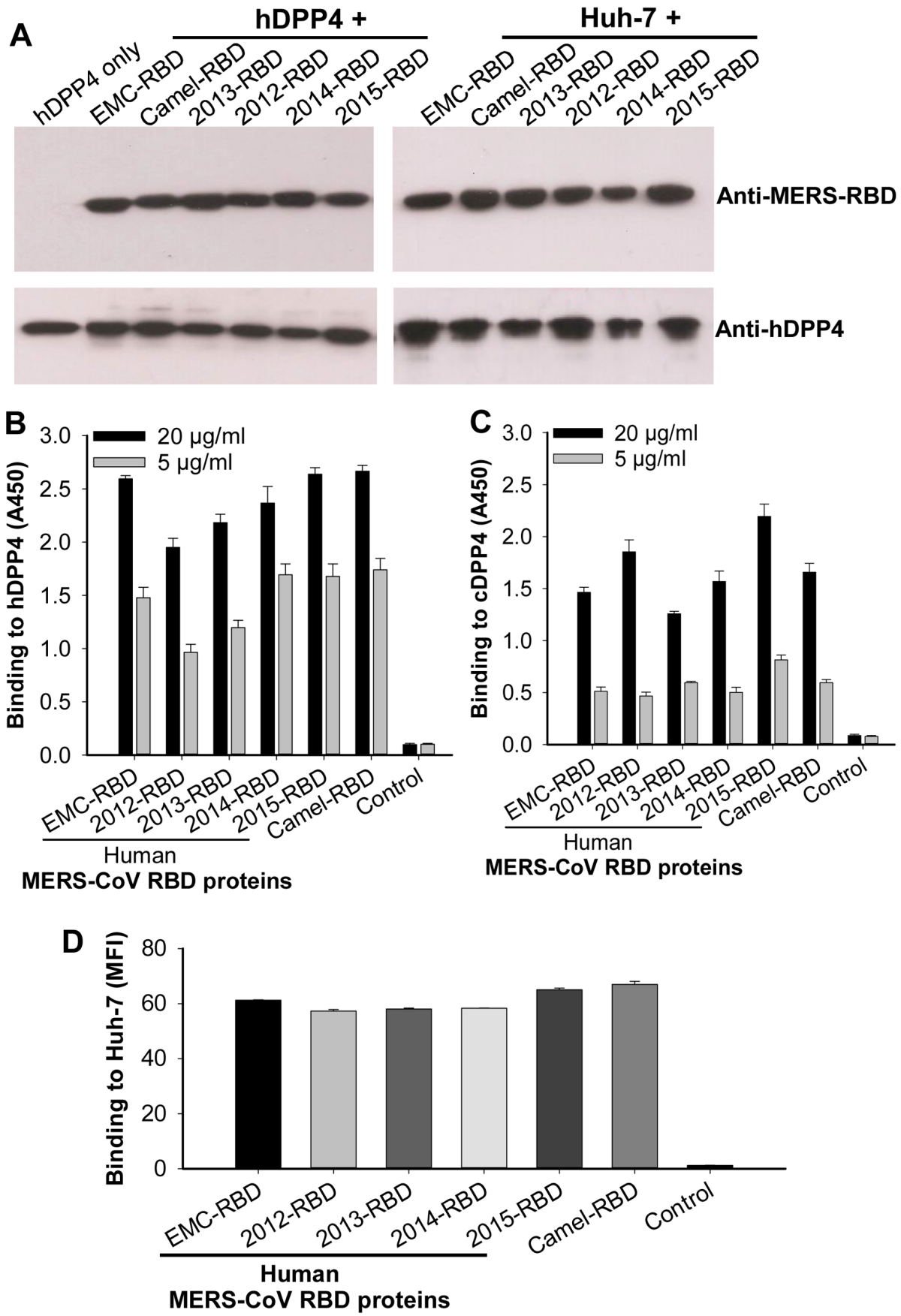
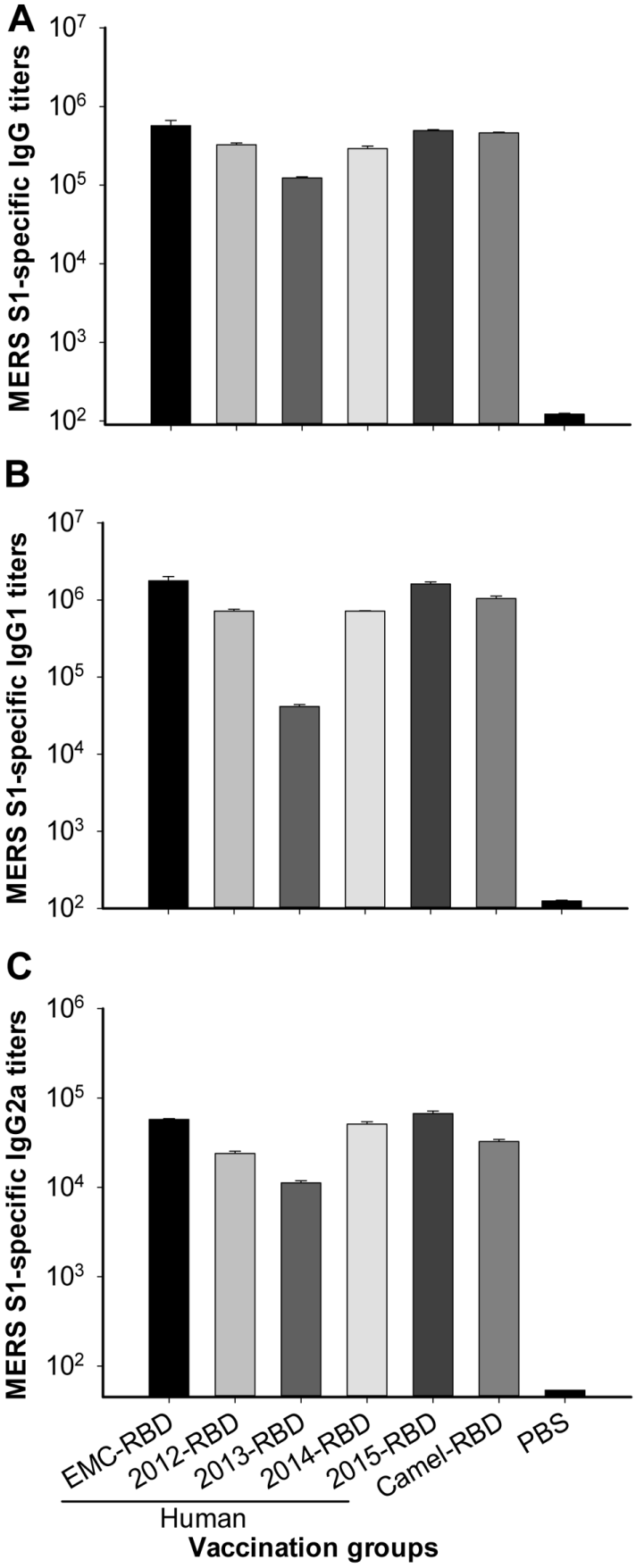
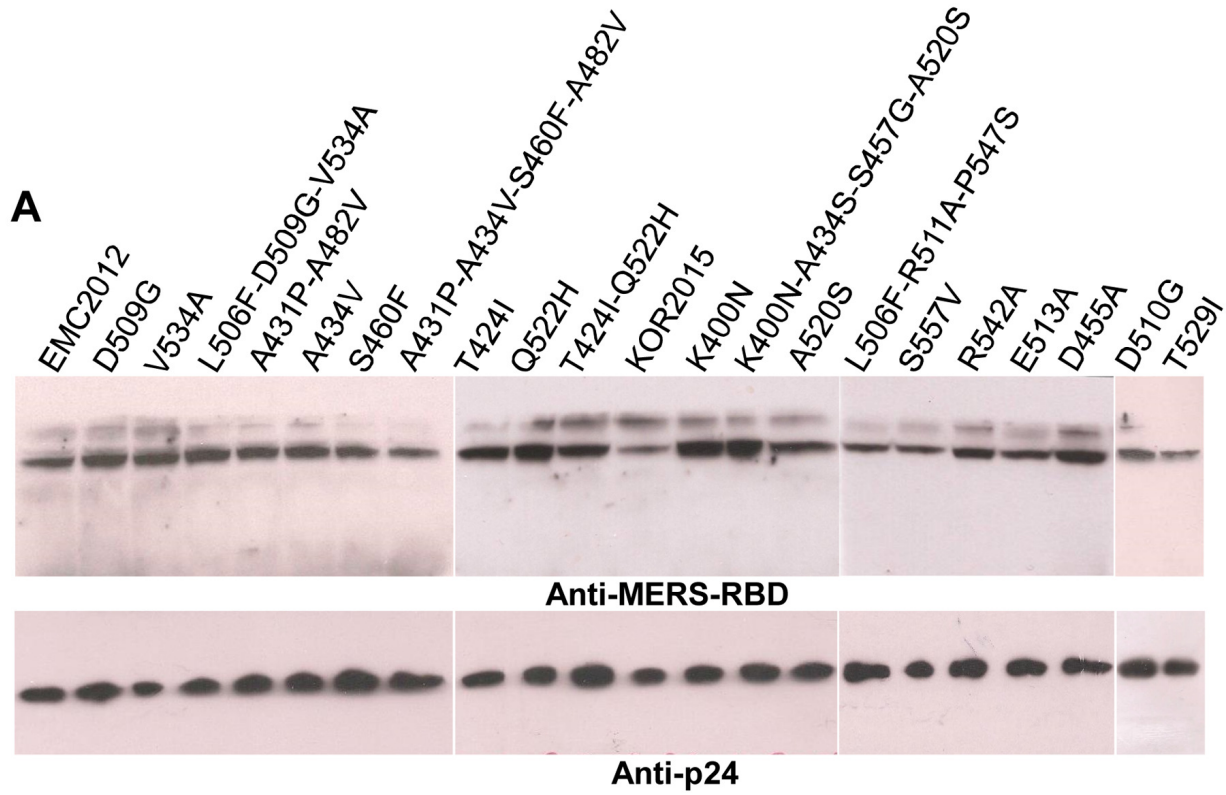
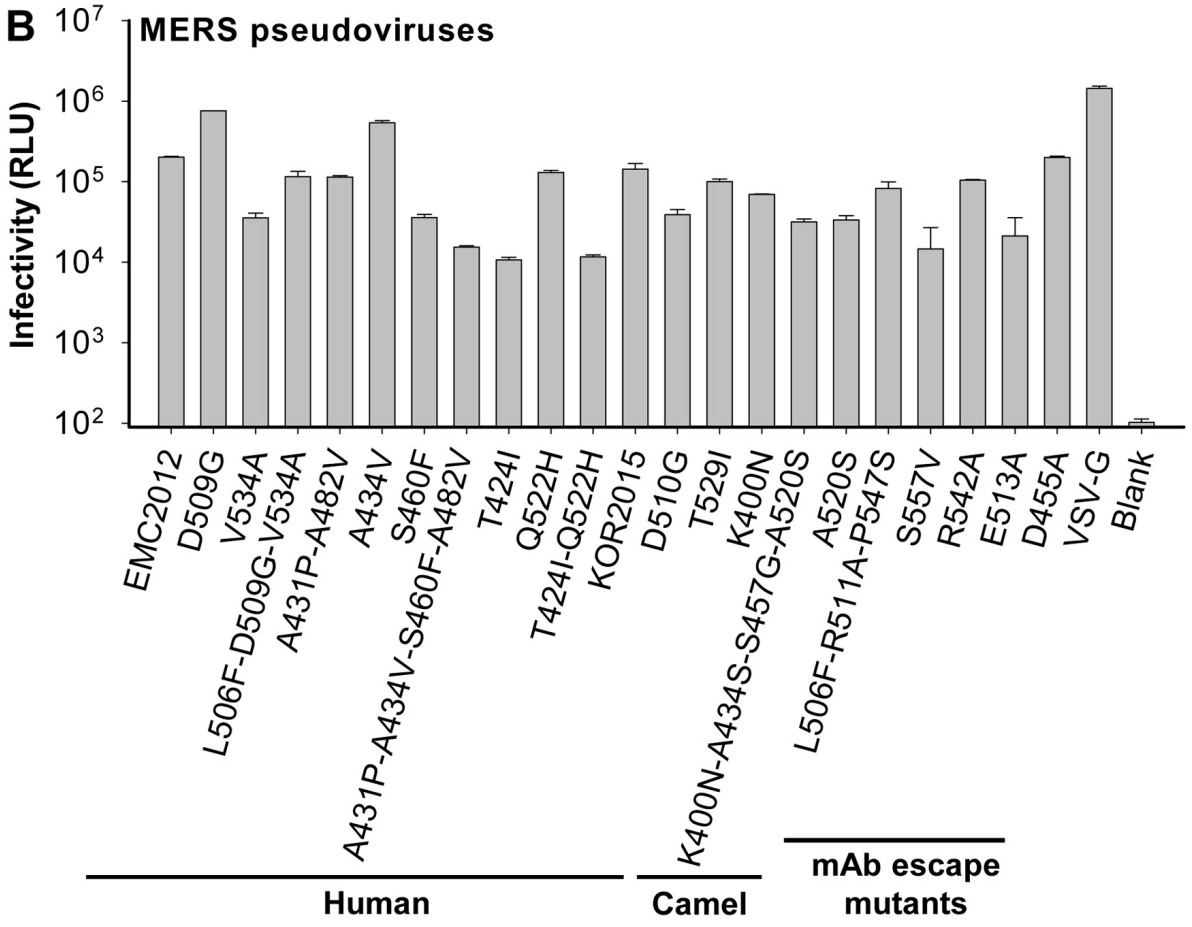
801

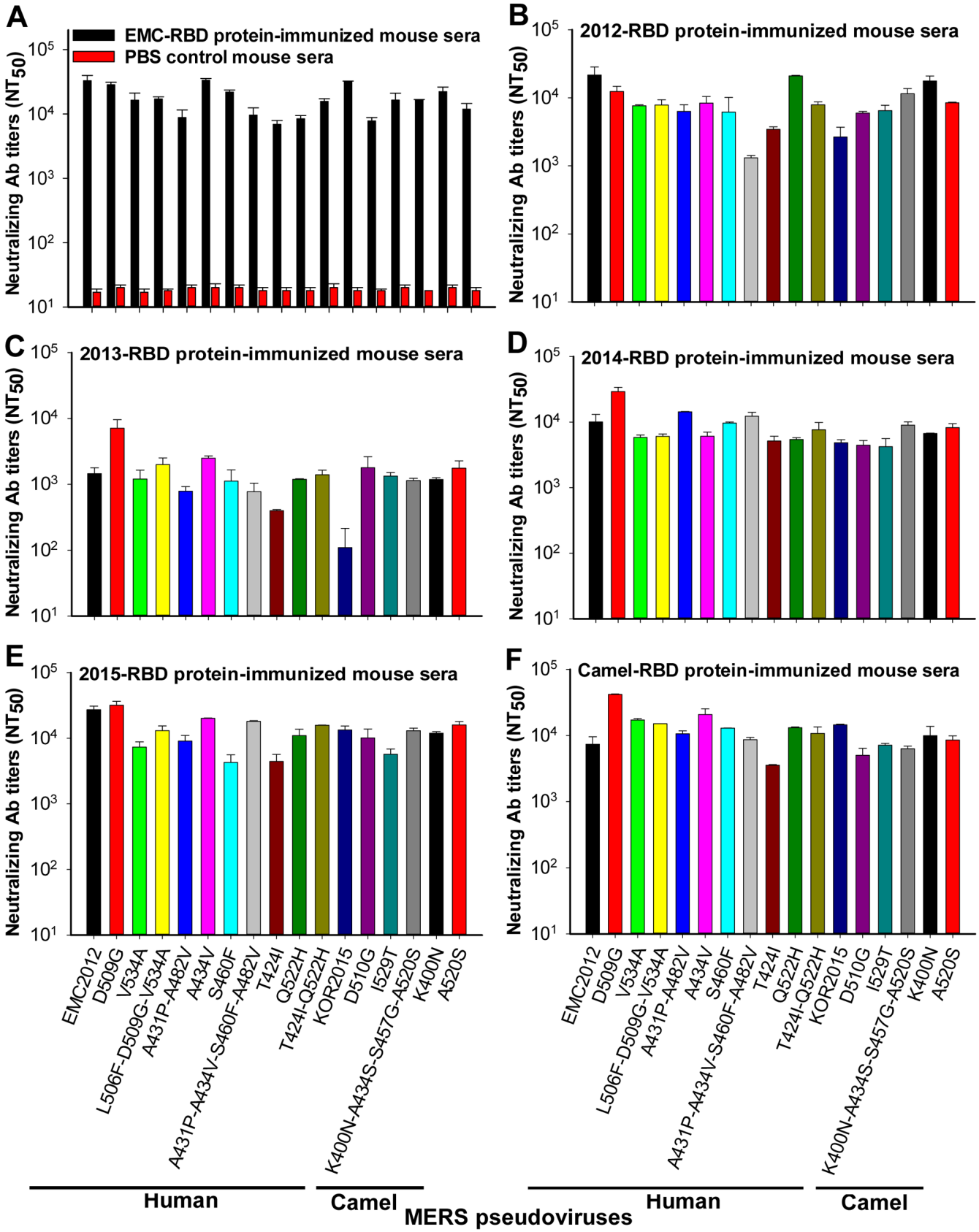


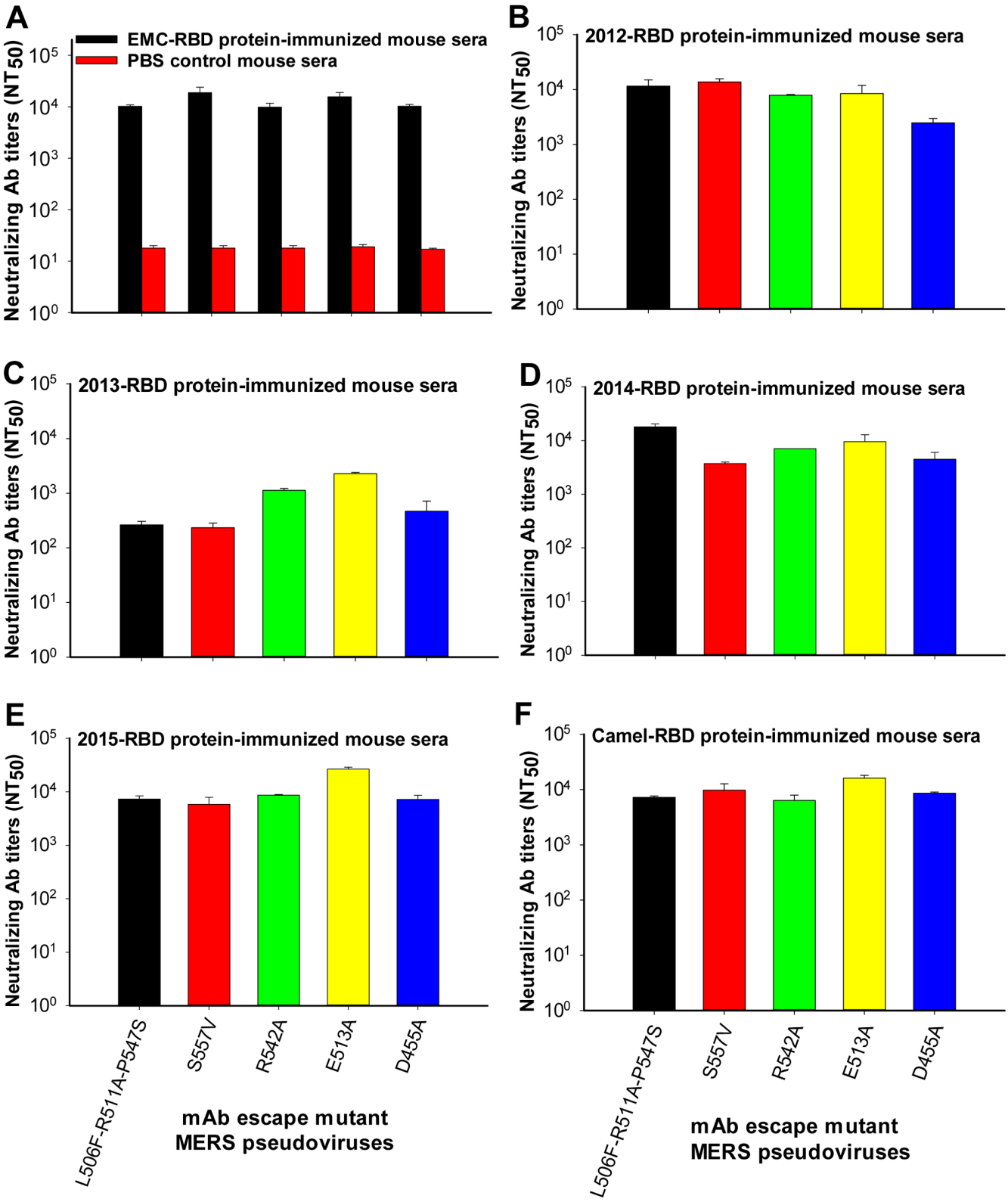


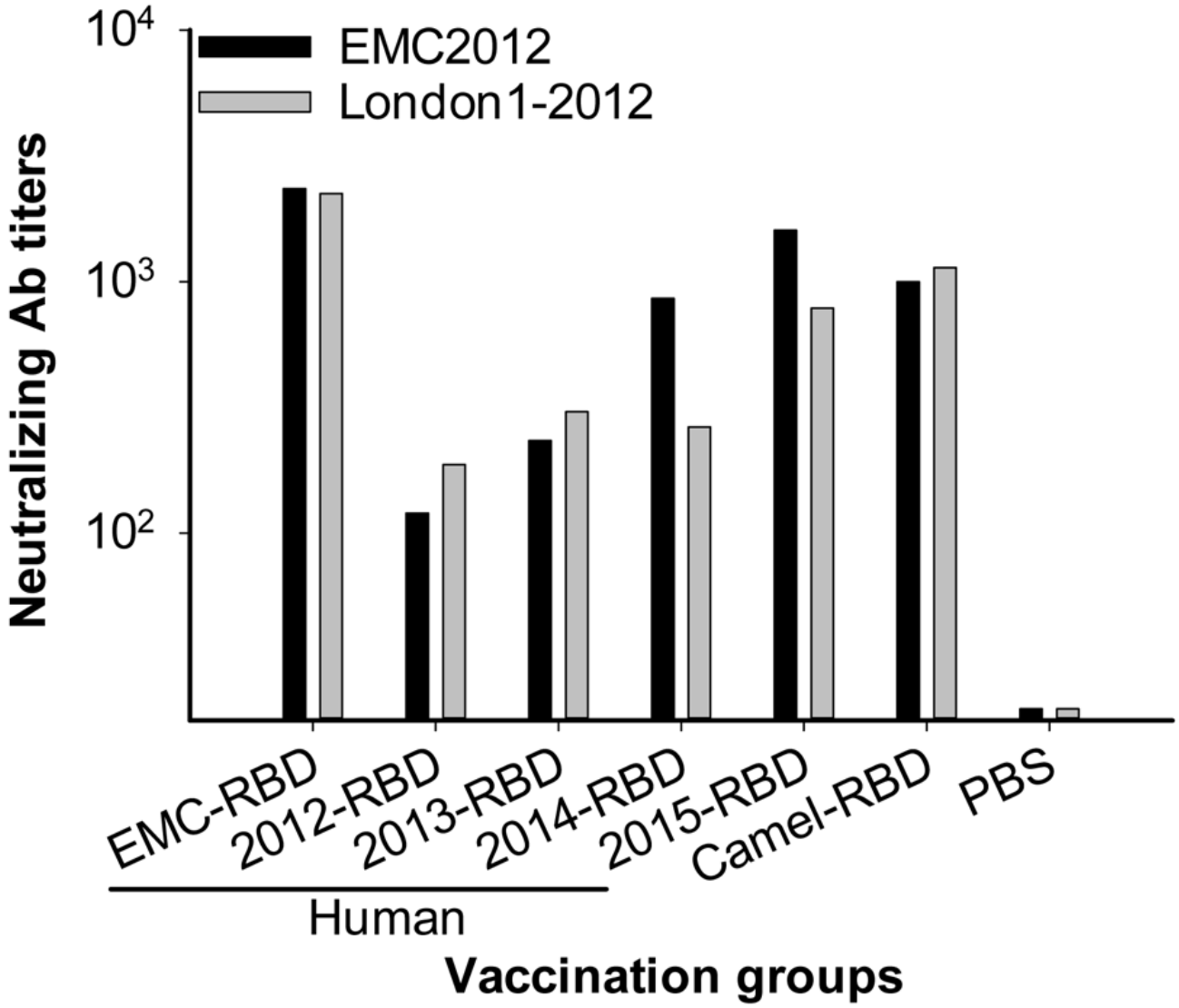












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