

Supplementary Material

1 Supplementary Figures and Tables

1.1 Supplementary Table

Supplementary Table 1. Relative potency of the crude supernatants expressing recombinant human immunoglobulin 1 compared to polyclonal anti-AMA-1 (BG98 standard).

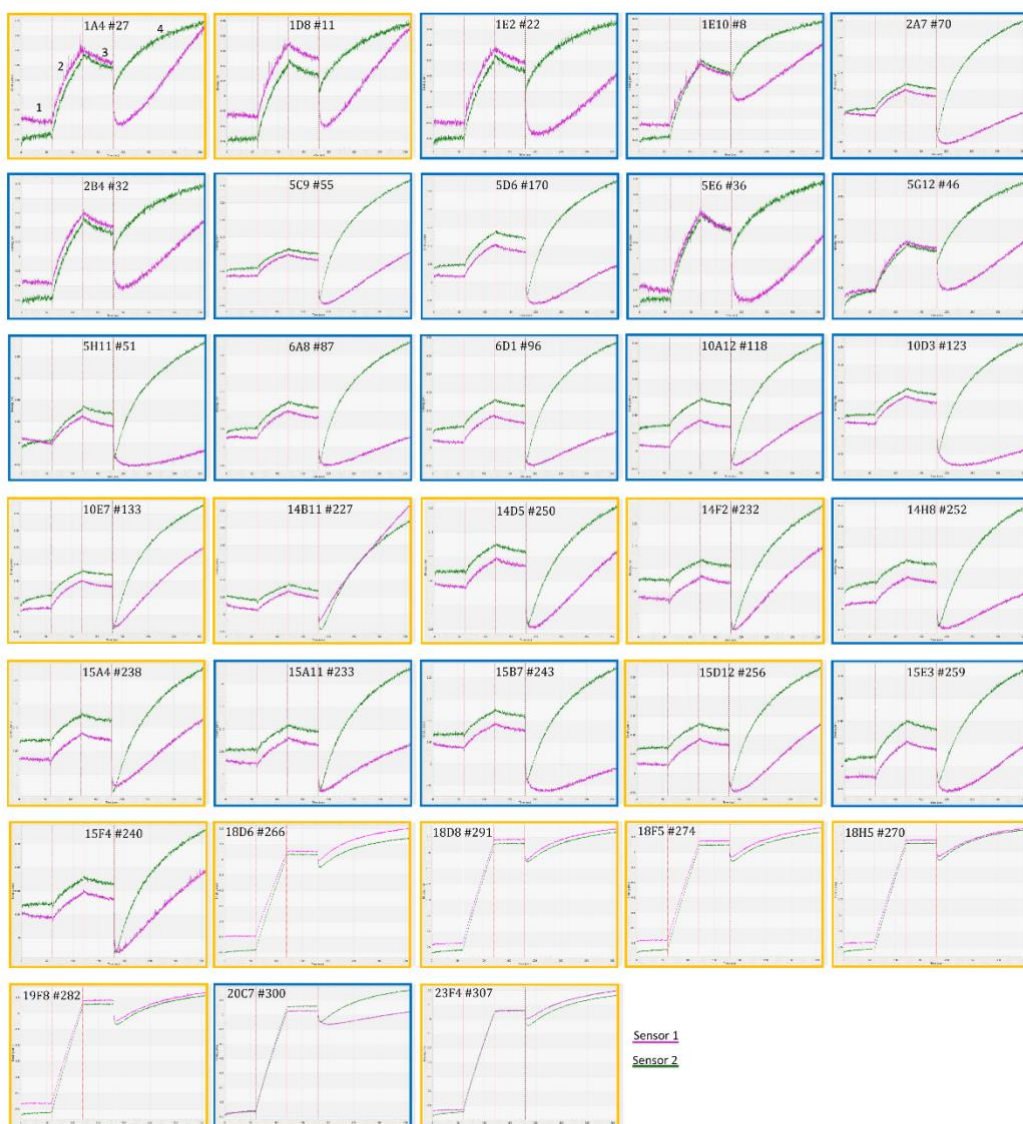
Antigen	Clone	Potency v AMA-1 (fold increase)
RH5	10A12#118	13
RH5	10D3#123	12
RH5	10E7#133	12
RH5	14B11#227	13
RH5	14D5#250	18
RH5	14F2#232	17
RH5	14H8#252	8
RH5	15A11#233	6
RH5	15A4#238	24
RH5	15B7#243	6
RH5	15D12#256	499
RH5	15E3#259	663
RH5	15F4#240	8
RH5	18D6 #266	197
RH5	18D8 #291	967
RH5	18F5 #274	82
RH5	18H5 #270	54
RH5	19F8 #282	473

RH5	20C7#300	73
RH5	23F4#307	46
RH5	1A4#27	23
RH5	1D8#11	1
RH5	1E10#8	44
RH5	1E2#22	9
RH5	2A7#70	81
RH5	2B4#32	25
RH5	5C9#55	11
RH5	5D6#170	14
RH5	5E6#36	867
RH5	5G12#46	80
RH5	5H11#51	21
RH5	6A8#87	5
RH5	6D1#96	9
CyRPA	3A7#22	3
CyRPA	3B3#17	4
CyRPA	3E12#12	8
CyRPA	3G11#15	34
CyRPA	4D12#30	201
CyRPA	4G3#4	13
CyRPA	7B7#7	5
CyRPA	7B9#13	30
CyRPA	8C8#18	8
CyRPA	11D11#36	27

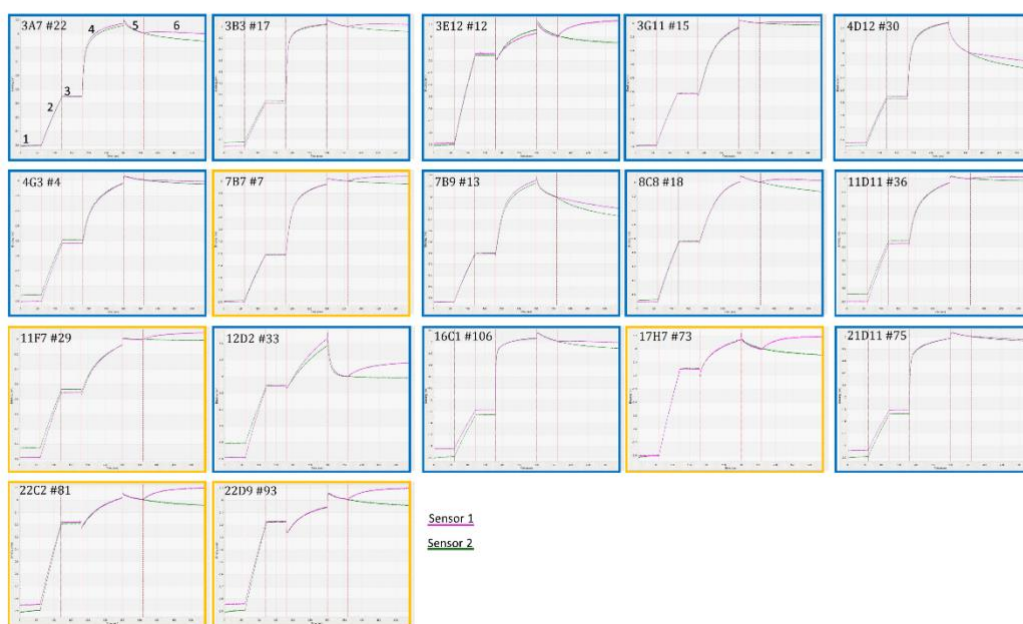
CyRPA	11F7#29	28
CyRPA	12D2#33	9
CyRPA	16C1#106	62
CyRPA	22C2#81	54
CyRPA	22D9#93	146
CyRPA	22D11#75	6
CyRPA	17H7 #73	80

1.2 Supplementary Figures

A

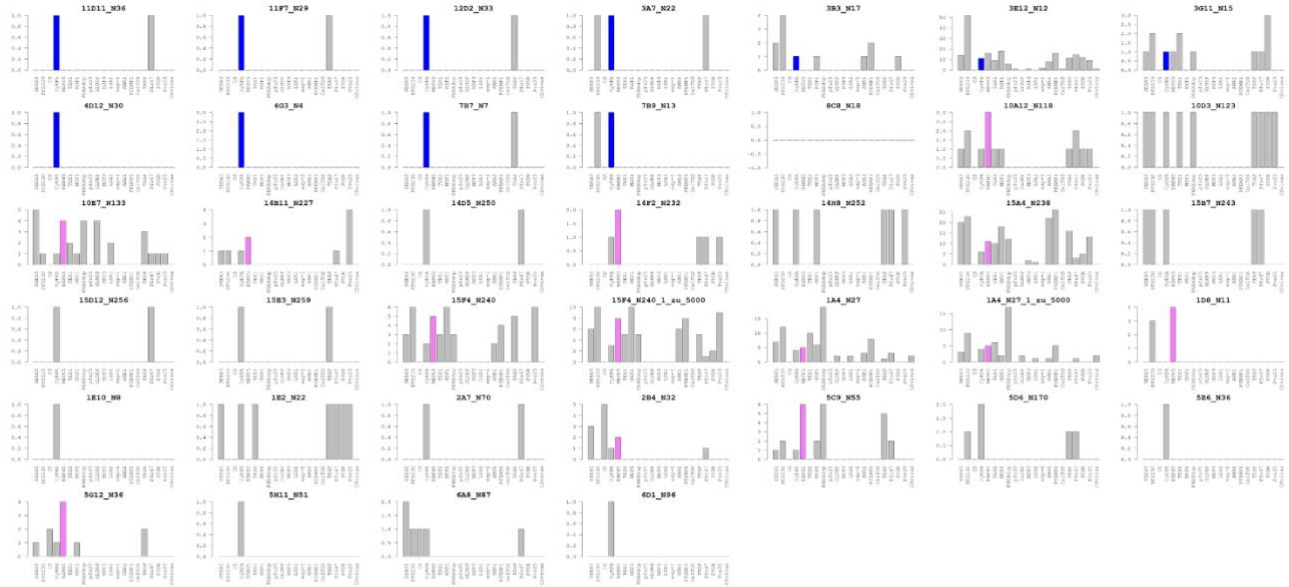
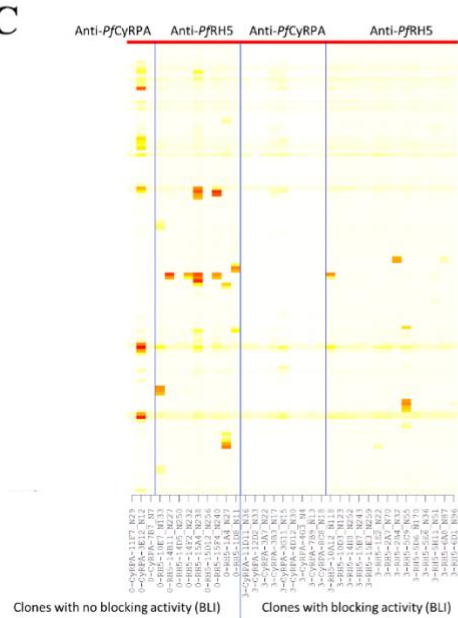


B

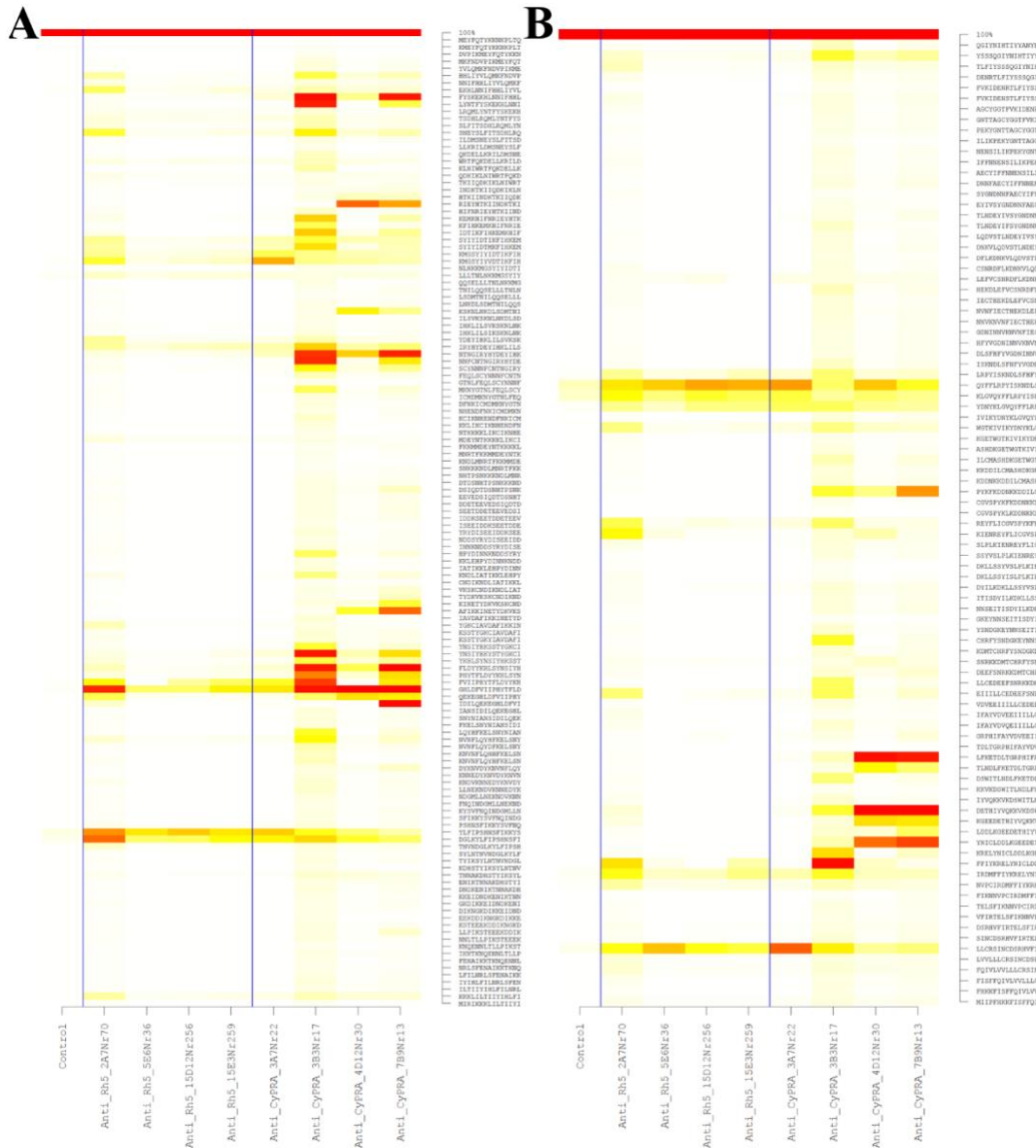


Supplementary Figure 1.

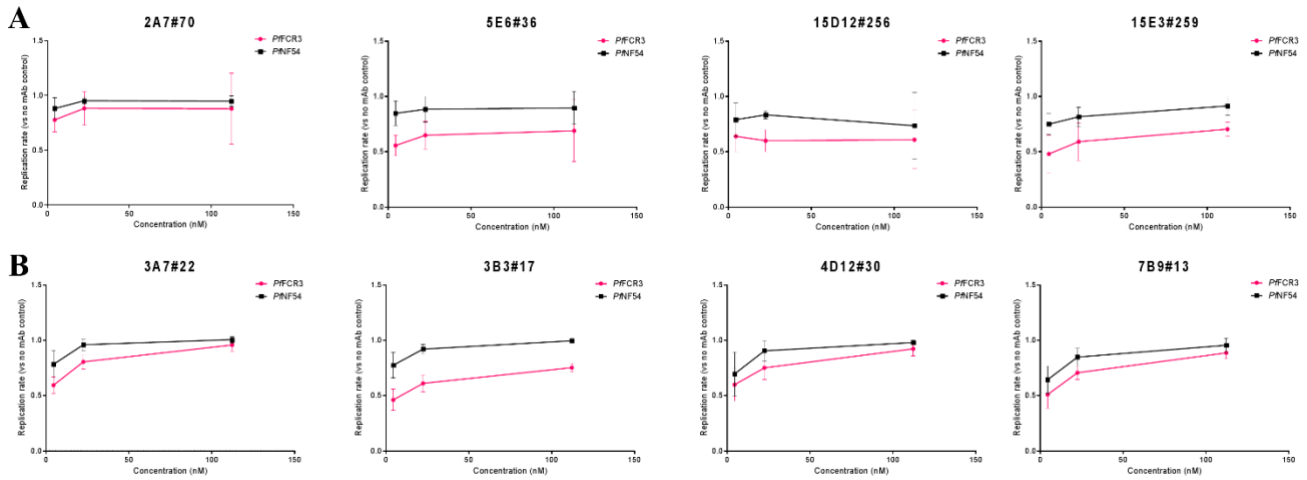
Figure 1. Biolayer interferometry traces of crude hIgG1 clones showing different blocking profiles for (A) *Pf*RH5 clones 1A4#27 and 5E6#36; and (B) *Pf*CyRPA clones 3A7#22 and 3G11#15). For *Pf*RH5 (A) traces show cell culture supernatant containing only *Pf*RH5 recombinant hIgG1 antibodies (green) and cell culture supernatant containing both recombinant *Pf*RH5 (*rPf*RH5) and recombinant human IgG1 antibodies (pink). Antibody 1A4#27 does not block *Pf*RH5 binding to *Pf*CyRPA. Conversely, antibody 5E6#39 blocks binding of *Pf*RH5 to *Pf*CyRPA (step 4). The numbered steps show 1) baseline for both sensors incubated in kinetic buffer; 2) incubation of the sensors with recombinant *Pf*CyRPA-biotin conjugate (*rPf*CyRPA); 3) baseline with the immobilised *rPf*CyRPA-biotin in kinetic buffer; and 4) association of *rPf*RH5 to *Pf*CyRPA. For *Pf*CyRPA (B) traces show incubation of one sensor in kinetic buffer (green) and incubation of the other sensor (pink) with *rPf*RH5 in association step (step 6). The numbered steps show 1) baseline readings for both sensors in kinetic buffer; 2) incubation with biotin-conjugated recombinant *Pf*CyRPA in kinetic buffer; 3) baseline readings for sensors with immobilised *rPf*CyRPA in kinetic buffer; 4) saturation of the sensors with crude antibody cell culture supernatant containing specific anti-*Pf*CyRPA recombinant hIgG1s (pink); 5) baseline with immobilised *Pf*CyRPA-antibody complex in kinetic buffer; 6) One sensor incubated in kinetic buffer (green) and the second in kinetic buffer containing *Pf*RH5 (purple). Clone 3G11#15 shows blocking activity (orange outline) while antibody clone 3A7#22 does not block binding of *rPf*RH5 to *rPf*CyRPA (blue outline). The y-axis shows binding (nm) and x-axis time (sec). Orange boxes indicate clones with no detectable blocking activity. Blue boxes denote clones with blocking activity as determined by biolayer interferometry.

A**B****C**

Supplementary Figure 2. Binding of crude cell supernatant expressing human recombinant IgG1 clones to linear peptide scans of malaria antigens on a peptide microarray. (A) Barplots of counted Signals (>10000) for each antigen. The target antigens for each sample are highlighted (blue: PfCyRPA; violet: PfRH5). (B) Antigen heatmap sorted by blocking activity as determined by biolayer interferometry for *Pf*RH5 showing binding of recombinant IgG1 monoclonals directed against *Pf*RH5 and *Pf*CyRPA. The clones are shown along the x-axis and overlapping peptides on the y-axis. Darker colours indicate brighter fluorescence signals in the array. (C) Antigen heatmap sorted by blocking activity as determined by biolayer interferometry for *Pf*CyRPA. Recombinant IgG1 clones directed against *Pf*RH5 and *Pf*CyRPA are shown on the x-axis of the heatmap with the overlapping peptides shown on the y-axis. Darker colours indicate a brighter fluorescence signal in the array. Raw data are provided in a separate spreadsheet.



Supplementary Figure 3. Binding of human recombinant IgG1 clones to *Pf*CyRPA (A) and *Pf*RH5 (B). Peptide array probed with down-selected purified recombinant IgG1. Darker colours on the heatmap indicate a brighter fluorescence signal in the array. (A) *Pf*RH5 antibody 2A7#70 bound strongly to linear epitopes of the *Pf*RH5 antigen. The other antibodies showed moderate binding to *Pf*RH5. *Pf*CyRPA antibodies recognise several linear epitopes for *Pf*RH5. (B) Recombinant *Pf*CyRPA IgG1 clones bound strongly to recombinant *Pf*CyRPA. Clones 4D12#30 and 7B9#13 recognise similar epitopes.



Supplementary Figure 4. Reduced replication rate of *P. falciparum* NF54 (*PfNF54*) and *PfFCR3* parasites cultured with *PfRH5* and *PfCyRPA* monoclonal antibodies for 1 cycle. Invasion assays were performed with antibodies diluted to 16.4, 3.28, and 0.656 $\mu\text{g/ml}$ (112, 22, 5 nM) to facilitate comparisons with data using cell culture supernatants. Replication rate was calculated by dividing the end parasitaemia from the starting parasitaemia. Comparison of invasion inhibition of A) anti-*PfRH5* and B) anti-*PfCyRPA* antibodies against *PfFCR3* (blue) and *PfNF54* (green). These data show the mean replication rate (and standard deviation) for each strain at different antibody concentrations ($n=3$ experiments).

Variable region sequence alignments

Heavy and light chain variable region sequences and alignments for all clones generated are shown below, CDR-s are shown in [blue](#).

*Pf*CyRPA

Chicken host

Alignments of the variable light and heavy chain amino acid sequences of *Pf*CyRPA hIgG1 clones 3A7#22, 3B3#17, 3E12#12, 3G11#15, 4D12#30, 4G3#4, 7B7#7, 7B9#13, 8C8#18, 11D11#36, 11F7#29, 12D2#33 were derived from chicken immunisations. Heavy chain and light variable region sequence alignments are shown below; CDR-s are highlighted in [blue](#).

VH

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Consensus AVTLDESGGGLQTPGGALSLVCKASGFTF--SSYAMGIVRQAPGKGLEWVAGISND-GSSTGYGPAVKGRATISRDNQGQSTVRLQLNNLRAEDTGTYYCAKSAXXGGXY-SDTXGXIDA WGHGTEIVSS
12D2_VH .....D.....V.....Y.....R.....F.L.T.....A..F.T...DD..H...FS.E.....
4D12_VH .....D.....Y.....R.....F.L.T.....A..F.T...DD..H...FS.E.....
8C8_VH .....G.....Y.....RDS...E.A..A..D.....VNG.SW--TS.P.L.T.....
7B9_VH .....D.....Y.....KS...F.L..ST.....I.....DDN..H...FS.E.....
11D11_VH .....G.....SDY.HG.H.....G--IW...S.....RNSNG.A----YG.D..T.....
7B7_VH .....G.....T.Q.....S.SG--G..AA.....HGVS.CDW-.HST.CV.....
3B3_VH .....G...FSF-N..T.Q.....S.SG--GG.N..A.....L.....HGVS.CDW-.YSV.CV.....
11F7_VH .....R.....C.Q.....A...VAG..Y..ST.....F...E.YDS.CLA..LAAT.....
3E12_VH .....V.....G.T...Y.....I.C...TYRAYCGIAYC.ASG.....
4G3_VH .....ET.....M--.NN.....L..DD..G.A...Q.....A...IRG.AGC.G.-GC.T.TT.....
3G11_VH .....T.....V.....G.T...Y.....I.C...TYRAYCGIAYC.ASG.....
3A7_VH .....T.....G.....E.Q.....D.CIG...Y.....D.....T.RSDYC--ITGLDD.....
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VL

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Consensus ALTQPSSVSANPGETVKITCSGGSX--SYGWIYQKSPGSAVPTVIYYNDKRPSDIPSRFSGSKSGSTGTLTITGVQAEDEVYVYCGSRDS--SNGXFGAGTTTLVL
3E12_VL .....L.G..E.....YN--N..H.....SS.....R.....NS...-K.AA.....
3G11_VL .....S.D-YG.....L.A.TN.....G...N.....R.....GY..SA.IPI.....
11D11_VL .....L...E.....ARY--.....L...EST...N.....T.....R.....NY..ST.TAI.....
12D2_VL .....STY--.....L.....NS...-R.AA.....
4G3_VL .....G--..H.....T.....NDNN.....E.....-SYI.M.....
11F7_VL .....E...D.S--Y.....D.TN.....L...N.....D...I.F.....TYY.I.....
8C8_VL .....E...TSGYG.....NN.....V...I.F.....IIT.A.M.....
3B3_VL .....S-SY.....L.N.Q.....F...N--G.I.....
7B7_VL .....G-SY.....S.....W...-A.I.....
4D12_VL .....STY--N.....NS...-R.VA.....
3A7_VL .....S--D.....E.N.....F...H.....D...F...T--N..A.....
7B9_VL .....S.Y--.....F.NS...-R.AA.....
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Rabbit host

*Pf*CyRPA clones 17H7#73, 16C1#106, 22C2#81, 21D11#75, and 22D9#93 were isolated from rabbit immunisations. Heavy chain and light variable region sequence alignments are shown below; CDR-s are highlighted in [blue](#). Clone 22D9#93 did not contain a full variable heavy chain and is not included in the alignment. It is likely that this antibody binds the target antigen solely through the light chain.

VH

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Consensus Q-SXEESGGRLVTPGXLLTLCTXS GFSLSYYMSWVRQAPGKGLEWIGXIXAGGXTWYASWAKGRFTISKSTTVDLKITSPTTEDATYFCARINXXX--XXXFXL WGXGTLVTSS
17H7_VH .....L.....TP.....V.....Y.A.S.P.F.....GYPG--HSSNS...Q.....
21D11_VH .....V.....GS.....A...N...I.....V.ST.DS...R.....S.....IDSN-NYA.N...P.....
16C1_VH .....EQL.....GS.....A...TI.....T.G.NRNS.....M...L.....DGSSSGVVD.D...Q.....
22C2_VH .....V.....TP.....V.....RNAI.....S..A...I.TS..D.Y.SA.....S..A.....I.....VFG--PSGRAI..P.....
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VL

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Consensus DVVMTQTPASVSAAGGTVTIXCQASQNI--NNXLAWYQQKPGQPPKLLIYEASXLASGVPSRFKSGSGTQFTLTISDLECAADATYYCXYGYXYN--XXXXXFGGGTEVVK
22D9_VL AL.....E.....N.....-YDS.....K..Y.....R.....EY.....GVQ.....QN.Y.SSSNNYIA.....
17H7_VL .....GP.....KR.....-KSY.....HR..D.....R..D.....QS.WE---ADNYN.....
22C2_VL AL.....AS.S.LS.K.VYN.YD.S.....R.....D.....L.GY.G--GSDNG.....
16C1_VL .....S.....N.....SVYN..R.....S.....VV.D..S..A..RG.--SDGTG.....K...E
21D11_VL .....E.....K.....S.--S.L.....GG.N.....S.....A.GW.--SVNFGA.....K...E

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*Pf*RH5

Chicken host

*Pf*RH5 rhIgG1 clones 1A4#27, 1D8#1, 1E10#8, 1E2#22, 2A7#70, 2B4#32, 5C9#55, 5D6#170, 5E6#36, 5G12#46, 5H11#51, 6A8#87, 6D1#96, 10A12#118, 10D3#123, 10E7#133, 14B11#227, 14D5#250, 14F2#232, 14H8#252, 15A11#233, 15A4#238, 15B7#243, 15D12#256, 15E3#259, and 15F4#240 were isolated from chicken immunisations. Heavy and light chain variable region sequences are shown below; CDR-s are highlighted in blue.

VH

```

Consensus AVTLDESGGGLQTPGGGLSLVCKASGFTF--SSYNMxwVRQAPGKGLEWAGIXNX--GSXTGYGPAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKGGTXG-----XXGXGIDAWhGTEIVSS
15E3_VH .....A.....D.....C.Q.....DDD--F.L.A.....S.....K...A...R.YGY.SGC---TGAHA.S.....
5H11_VH .....A.....-R..D.L.....F..S.TSS--GSAN..A.....V.....A..F...SAGGSWTA---AYDASD.....
5D6_VH .....A.....-D.Q.....DAD--S.Y.A..D.....A.....AAGV.WSY---AYFIA.S.....
15D12_VH .....T.....D.S.Q.....DDI--Y.A..A.....K.....A.....ES.G.WCI---GGCNVPY.....
14H8_VH .....A.....-D.S.Q.....D.I--Y.A..AV.....S.....A..F...ES.G.WCI---GGCNVAY.....
14D5_VH .....A.....-D.G.G.....Y...DSG--S.A..T.....GS.....F..RSVYG.SAT---YGCPA.W.....
2A7_VH .....A.....-I.A.N.....Y..Y.NTG--T.Y..T.....S.....AI...CAYMSFC---DHA.D.....
1E10_VH .....T.....V..F.....F..Q.NKA--D.N.....S.....YDGSN-----CCEN.....
10A12_VH .....A.....G.....T.F..F.....S..S.GKT--RS...S...V..K.....R..A-----D.....
1D8_VH .....A.....-DRA.G.....Y...SSS--Y...A.....AA.F.TR..GR.W-----TGDN..T.....
1E2_VH .....A.....-FG.G.....F...SGS--S.W.AT.....DFDN.YCRS--GPCNIDT.....
1A4_VH .....A.....-NA.A.....F.GAVDKT--S.S..S.....DFDN.YCRS--GPCNIDT.....
14B11_VH .....A.....S...F..A.....S..A.G.R--S..S.....R..A-----D.....
14F2_VH .....A.....-D.F..A.....S.GT.GKT--RT...S.....R.....R..A-----D.....
15F4_VH .....A.....F..A.....S..T.G.T--RH..A.....I.....A...R..A-----D.....
15A4_VH .....A.....F..A.....S..T.G.T--RH..A.....I.....A...R..A-----D.....
15A11_VH .....A.....-R.F..A.....S..T.G.T--S..S.....L.....A...R..A-----D.....
15B7_VH .....I.....F..F.....Y..S.Y.GGS.Y.Y..A.M...V.....R..GGPGTN---TND.A.N.....
5E6_VH .....A.....SI--D.SVQ.....A.DDG--GF.V.A.....K.....S.....A..F...DD.STT-----WGG.A..S.....
10E7_VH .....A.....SSYRR..F.....F..R.SST--G.Y..S..Q.....R..AT.SG-----NYRA.S.....
6D1_VH .....A.....VI--I.A.N.....S.DD.RW..A.....L.....DAYRHSDYGNTRYRPNPAA.....
5G12_VH .....A.....I.A.N.....S.DD.RW..A.....L.....DAYRHSDYGNTRYRPNPAA.....
2B4_VH .....A.....I.A.N.....S.DD.RW..A.....L.....TD.....DAYRHSDYGNTRYRPNPAA.....
6A8_VH .....A.....I.A.N.....S.DD.RW..A.....L.....S..TD.....DAYRHSDYGNTRYRPNPAA.....
10D3_VH .....A.....RA.....HA.Y.....S.SGS--GW.D.A.....F...ESDN.CCS---RIYV.S.....
5C9_VH .....A.....VF.....D.A.....S.RKD--RG.D..A.....S.....A...ATCY.CW---RSFHAS.....

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VL

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Consensus  ALTQPSSVSANPGETVKITCSGGGS-----YYGMYQQKSPGSAPTVTIVDNTNRPSDIPSRFSGSLSGSTATLTITGVQAEDEAVYYCYGYDS---TYVGI FGA GTTLTVL
108_VL      .....DD--GS.....R.NQ..T.....V.....RP.NQ.....TRK----ASP.....
15A11_VL    .....S.S---Y.G..F.....L.L.D...N.....A.....V.....A..S---.....
14D5_VL      .....S.S---Y.G..F.....L.L.D...N.....A.....V.....F..NI----SSSA.....
14F2_VL      .....L.....NNYAGS.....G..G.....V.....F..A.....S---.....
2B4_VL      .....L.G.....TYAG-SY.....S.DK.....K.....S.EDN--SGS.....
14B11_VL     .....L.G..D.....NSV-GR.....G.....K...G.....V.....A..S---.....
14H8_VL      .....L.G.....TYA-GS.....N.....G.....V.....A..S---.....
10D3_VL      .....L.G..E.....AGSYA-GS.....N.....K.....K.....F..SA-----D.....
10A12_VL     .....L.G.....SYA-GS.....G.....V.....F..A..S---.....
2A7_VL      .....G.....S.D---A.....Q.I...N.....N.....V.....F..SA.NS--D.....
5H11_VL      .....L.....S---S.....D...N.....K...G..V.....F..S..IG--.....
1E10_VL      .....L.G.....Y.----D.....N.....V.....SR.T---F.....
5G12_VL      .....I.....YA--GS.....A.....S.DK.....G..G.....D.....SK---SSIA.....
5C9_VL      .....I.....YA--GS.....A.....E.....N.....T...S.....D.....NA-----SS.....
15F4_VL      .....L.G.....SA--GS.....G.I.....V.....A.....S.....S.....
15B7_VL      .....E.....IG-----S.....S.DK.....A.....F..G..ITYGF.A.....
15D12_VL     .....L.G..E.....DRTY-----D..F.....N.NK..T.....A.....F..G..G--SIA.....
6D1_VL      .....A..L.....G-----S.....S.DK.....A.....D.....F..SK---SN.....
5E6_VL      .....SY-----H.....S.NQ.....T..VS.....D.....SF..T--NN.....
5D6_VL      .....G-----S.....A.....N.....N.....D...I...GF---SGDS.....
15E3_VL      .....P.....T---SS..F.....Y.....K.....VD.....NE---RGS.....
10E7_VL      .....R-----G..H.....TD.....DDK.....A...N.....RV...I...TW.D--NNDSL.....
1E2_VL      .....L.G..E.....K-----Q.DK.....K...G.....F..G..IS-AG..AV.....
1A4_VL      .....L.G..E.....K-----Q.DK.....K...G.....F..G..IS-AG..AV.....
6A8_VL      .....L.G..E.....N-----K.....K...N.....V.....F..A.G---NSA.....
15A4_VL      .....S.SYY-GR.....G.....V.....A.....S.....S.....

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Rabbit host

*Pj*RH5 rhIgG1 clones 18D6 #266, 18D8 #291, 18F5 #274, 18H5 #270, 19F8 #282, 20C7#300, and 23F4#307 were isolated from rabbit immunisations. Heavy and light chain variable region sequence alignments are shown below; CDR-s are highlighted in blue.

VH

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Consensus  QSVEESGGRLVTPGASLTLTCTASGFSXSSSYMCWVRQAPGKGLEWIGCIYAG--GSTXYASWAKGRFTISKTSSTTVXLMKMTSLTAADTATYFCARXXXGX-----XTXFDLWGPGLVTISS
20C7_VH     .....G..Q..T.....KV...F.GT.Y...L.....AS....-D.N.D...T...A.....T.Q..G.....GNP.YFG--YGAP.Y.N.....
18D6_VH     .....TP.....L-.T.S.G.....M.A.N--SN.F..T.....D...A..AIE.....SDGSGW---NAF.RL...Q....V.....
18F5_VH     .....G.....V...L-.H.Q.....E.....Y.WTS--A.....H.....T...D.....TE.....VGT.I-----GGG...Q....V.....
23F4_VH     .....L.....P.....L-.N..S.....L.NPY--AF.....R..T...G.....TE.....KYRG-----GGY...Q....V.....
18H5_VH     .....D..K.....TI..RGF.V.....A.....NS...Y...N.....D.....ATNN-----DRR.N.....
19F8_VH     .....G..R..EG.....T.F.G..Y.....T.VS...Y...E.....P.....D.....D.WY.DY----TYAS.....
18D8_VH     .....D..K.....F...D.I.....A.....PTNTVHMN.....T.Q.....G.DNDHYSGYGYGT.P.N.....

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VL

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Consensus  DVMVTQTPASVSAAVGGTVTIKCQASQSI--GNXLXWYQQKPGQPPKLLIYSASTLASGVPSRFKSGSGGTQFTLTISDLCEDDAATYYCAGGYNX-XXNXIXFGGGTEVWVK
18D8_VL     .....EP.....-S.Y.A.....R..S.....QTN..CSDSG.Y.A.....
23F4_VL     .....EP.....-SSW.A.....S.....E.....GVQ.....QSV..DGSYGGGA...K...E.....
18D6_VL     .....S.....KVLRA.R.S.F.....A.....W.....H.I.S.....
18F5_VL     .....S.....N..S..KVLRA.R.S.F.....A.....W.....H.I.S.....
18H5_VL     AL.....S.....E...-E.S.....G..N.....E.....VQ.....DSS-NG.RCV...K...E.....
19F8_VL     AL.....-..SN.G.....R...HE..N.ET.....GVQ.....YKGY-NNDDIG.....
20C7_VL     AL.....E.....-..DY.A.....K.....S.....F..E.....A.....QCNN.G-WSYVGG.....

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*Pj*CSP

Chicken host

Clones 2C4#2 6F1#25, and 6F8#32 were isolated from chicken immunisations. Heavy and light chain variable region sequences are shown below, CDR-s are highlighted in blue.

VH

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Consensus AVTLDESGGGLQTPGGALSLVCKASGFTFSSYGMXWRQAPGKGLEFVAGISGXGSGTXYGAAVKGRATISRDNGQSTVRLQLNNLRAEDTGTYYCAKXAYXXXXXXXXXSIDXWGHGTEIVSS
2C4_VH .....NA.I.....Y.....S.RN.E.....I...RS..SGYSDTACT..A.....
6F8_VH .....D.RD...G.M.....GS.YIA.....TI.TIS-TATY..V.....
6F1_VH .....G.....G.....N.....A..YT..S.Y.AP.....A...T.C.WNSCDYDGS...T.....

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VL

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Consensus ALTQPSSVSANPGETVKITCSGSGSYGWYQQKSPGSAVPTVIYXNDKRPSDIPSRFSGSKSGSTXTLTITGVQADDEAVYFCGXYS--XYXGIFGAGTTLTVL
2C4_VL .....GV.....N.NN.....E...A.....S.EG.TYAG.A.....
6F1_VL .....T..L.G.....I.....Y.....G.....E.....G.....S.FV.....
6F8_VL .....NN.....Q.....N.....NW...--T.Y.....

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Rabbit host

Clones 2G12#8, 4E11#20, 4H1#15, and 5B12#21 were isolated from rabbit immunisations. Heavy and light chain variable region sequences are shown below, CDR-s are highlighted in blue.

VH

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Consensus QSVESGGRLVTPGTPLTCTASGFSL-SXYXPMXWRQAPGKGLEWIGVIXXG-GTTYASWAKGRFTISKST-TVDLKXTSPTXEDTATYFCARGGXVX-----XXXFDLWGPGLVTISS
2G12_VH .....TI-.NAD.D.....MNV.-.GIG..T.....R...RI...I.....E.ADV-----NFA.K.....
5B12_VH ..L....G..Q..GS.....FS.S.WIC.....C.VT.S..D..VN...V...ST..T.QM..L.AA.....S.DVS-----ANY.....
4H1_VH .....I.....-NN.G.T.....Y..I.FAT.....M...P.....C..HP.N-----GWFLH.....V..
4E11_VH .....V..L...S.S.S.....SSS-.SA.....I...T.....YYYGDNGYISGT.....

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VL

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Consensus AAVLTQTPSXVSAAVGGTGTINCQASQSI--NSNLAWYQQKPGQPPLLIYXASXLASGVPSRFKSGSGGTQFTLTISDVQCXDAATYYCQGXFYCS-XXDCNAFGGGTEVVVK
2G12_VL DG.M...A.S...V.....LYNSK.....E...S..S..T.....S.....G...A.....L.E.S...-SA..R.....K...E
4H1_VL .QGP...AS.E.....K.....-D.....R...D..K.....D.....D.....VNY.VAFISGN.....
4E11_VL .....P.G.....N...W.....G..N.E.....R...E.....LE.A.....ATDY..-NVAI.V.....
5B12_VL .....P.....S..S.E.VN-.NE.G.....R...L..T.....D.....A.G...-RG..I.....

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