

Figure S1. Phylogenetic trees of IgA and IgG plasmablast antibody repertoires from four IPAH subjects. The paired, concatenated HC and LC antibody sequences from each single cell were binned and ordered by HC V-gene family and clustered to create phylogenetic trees. Antibodies from clonally expanded lineages are represented by colored tips, with blue representing clonal IgG sequences and red representing clonal IgA. Tips representing non-clonal (singleton) sequences of either isotype are black. Data in the upper right tree are also shown in Figure 2

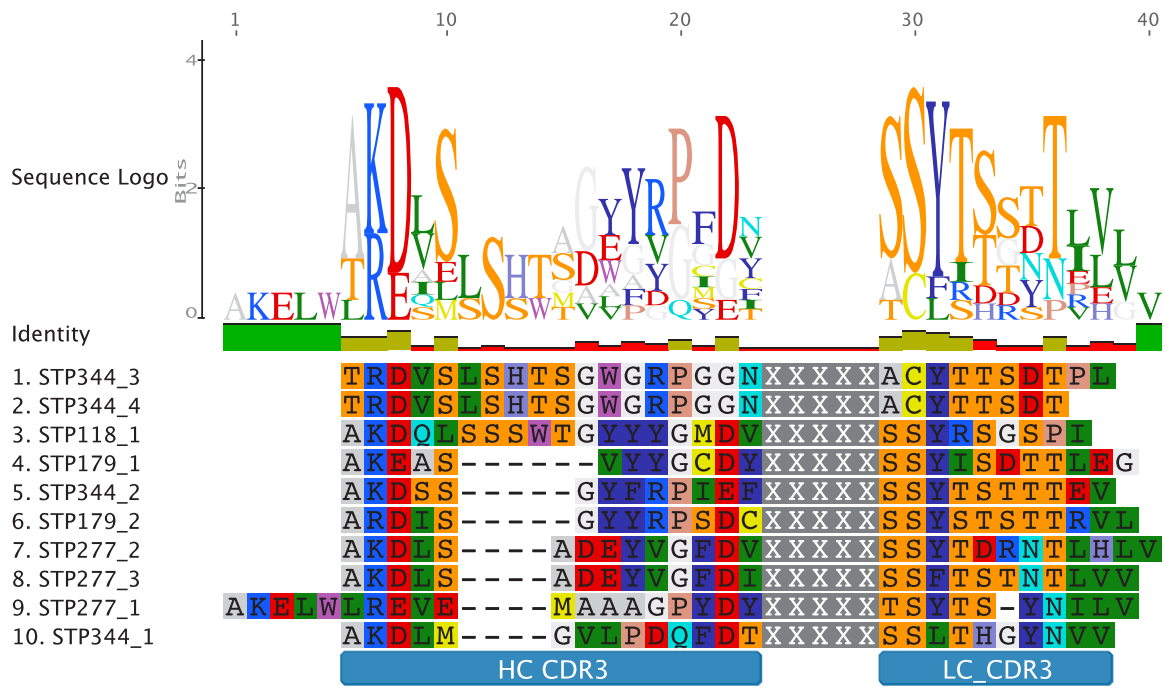


Figure S2. High level of diversity among clones sharing the IGHV3-23 & IGLV2-14 gene segments. HC and LC CDR3 sequences of individual IPAH plasmablasts that share the IGHV3-23 and IGLV2-14 gene segments were concatenated with a 5 amino acid spacer sequence to ensure proper alignment. Concatenated sequences were aligned using a Blosum62 matrix in Geneious V7.1, and a consensus sequence logo was produced. Bits refers to the level of entropy at each amino acid position. Amino acids are colored based on a traditional Rasmol color scheme to indicate similar amino acid properties.

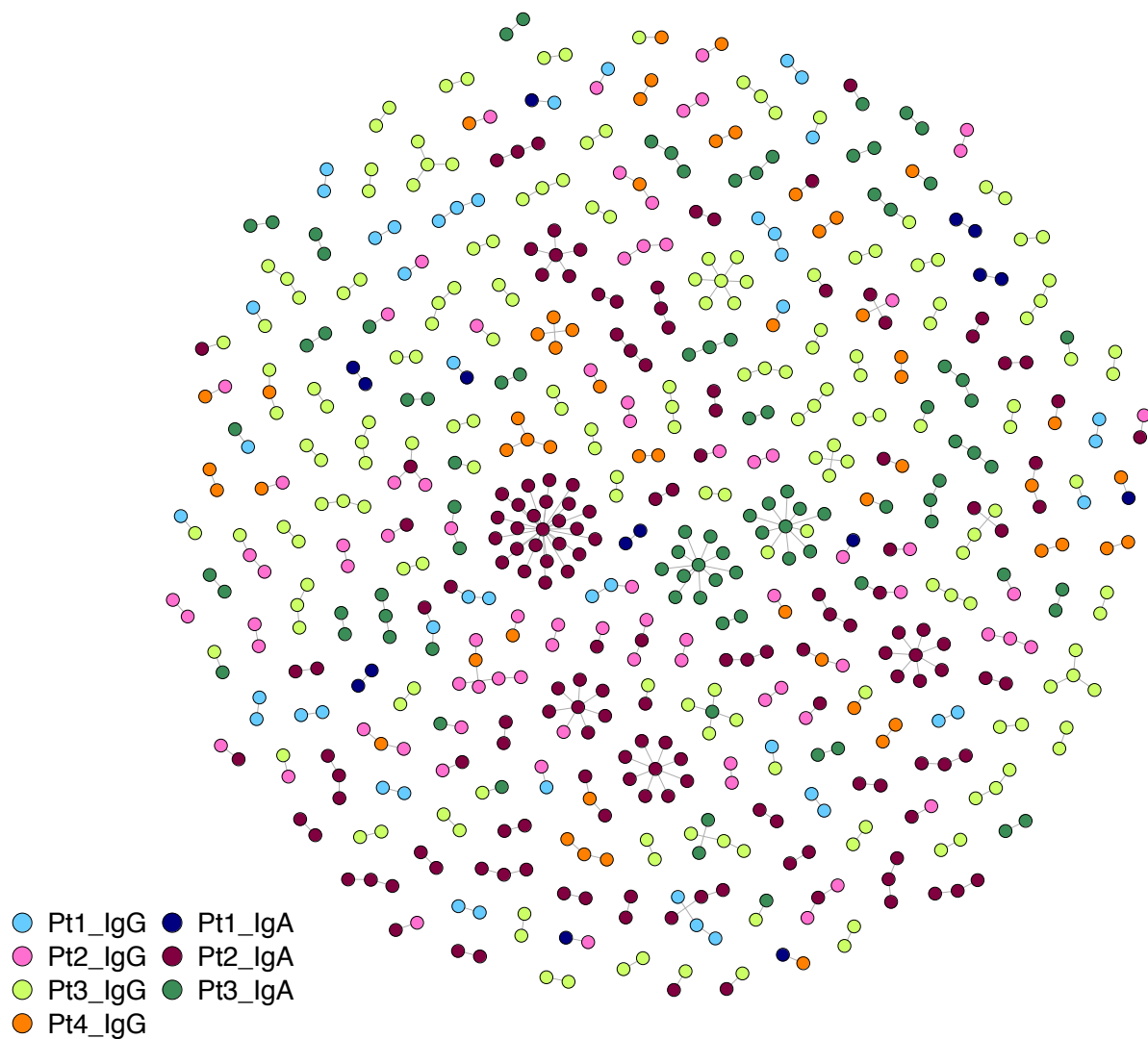


Figure S3. CD-HIT clustering of paired HC CDR3 and LC CDR3 sequences across four IPAH patients. The HC and LC CDR3 amino acid sequences from each single cell were concatenated together, separated by a 5 amino acid spacer sequence. Sequences were clustered using the CD-HIT algorithm, with a cutoff of 0.8 (including the spacer). Networks were visualized using the igraph package for R, with only multi-sequence clusters displayed on the graph.

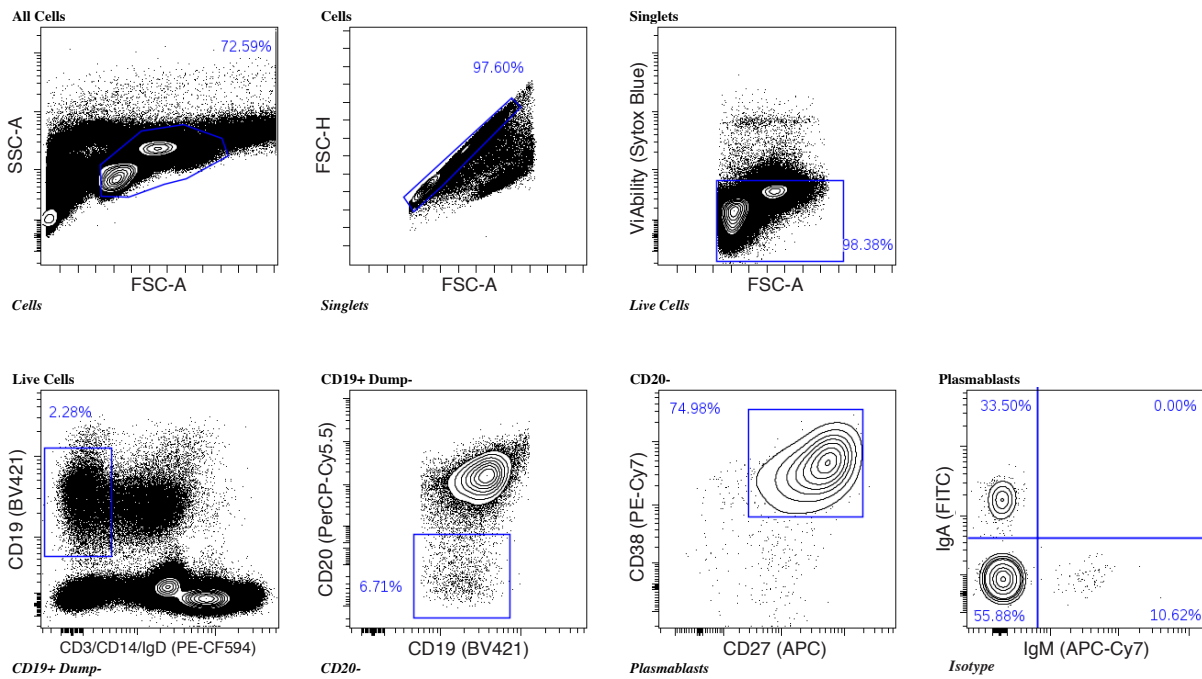


Figure S4. Peripheral blood plasmablast gating hierarchy. Freshly isolated PBMCs from IPAH subjects and healthy controls were stained with fluorescently labeled antibodies in Hank's Balanced Salt Solution (HBSS) with 2% fetal bovine serum prior to flow cytometric analysis. Plasmablasts were defined as CD19⁺CD3⁻CD14⁻IgD⁻CD20^{lo/-}CD27⁺CD38^{hi} live single cells. To convey population hierarchy, labels above each plot indicate prior gating of the population shown and labels below each plot indicate the name of the gate shown in the plot above. Percent labels indicate the percent of the population shown that fall within each gate.

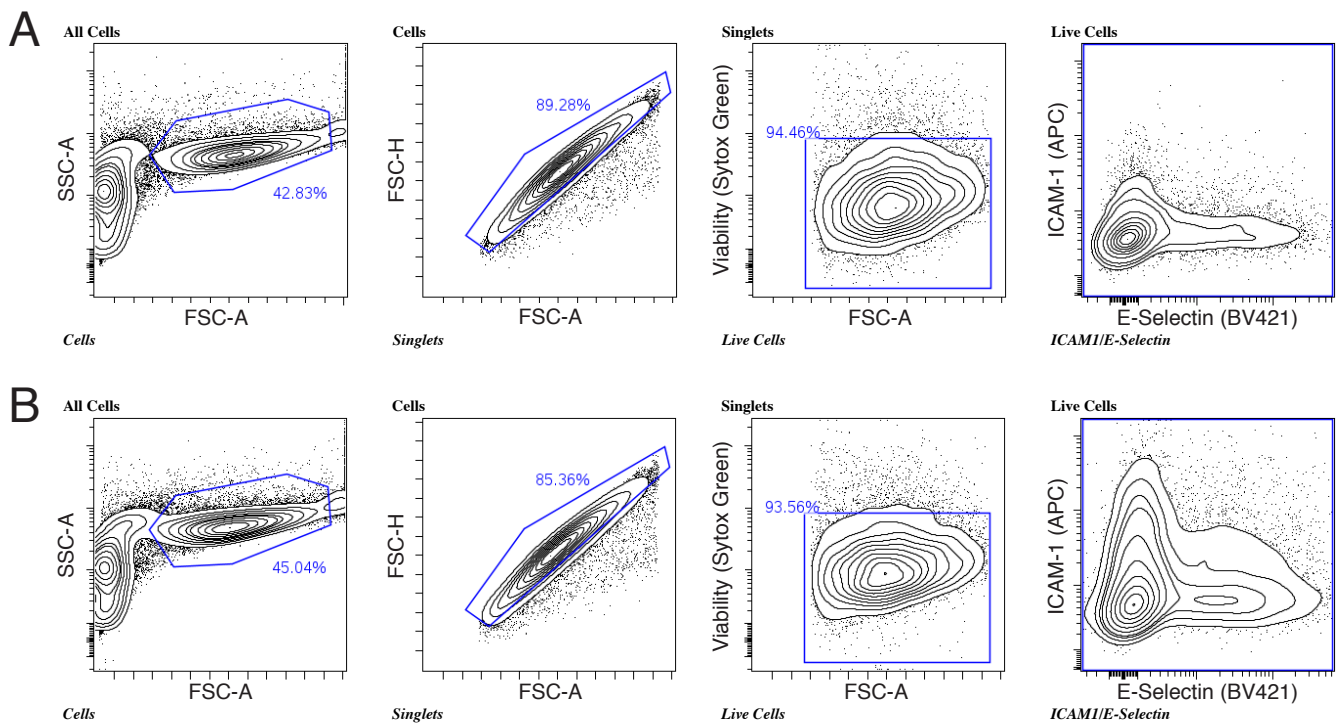


Figure S5. HUVEC stimulation gating hierarchy. HUVECs were harvested during the third to fifth passage and stimulated *in vitro* with (A) control or (B) PAH-derived recombinant mAbs prior to staining in Hank's Balanced Salt Solution with 2% fetal bovine serum. To convey population hierarchy, labels above each plot indicate prior gating of the population shown and labels below each plot indicate the name of the gate shown in the plot above. Percent labels indicate the percent of the population shown that fall within each gate.

Table S1. Univariate relationship between %IgA Plasmablasts and PAH risk markers.

| PAH risk marker | Spearman correlation | p-value* |
|----------------------------------|----------------------|----------|
| Age | 0.086 | 0.679 |
| NYHA functional class | 0.012 | 0.952 |
| Six-minute walk distance | -0.014 | 0.95 |
| NT-proBNP | 0.115 | 0.583 |
| Glomerular filtration rate | 0.055 | 0.793 |
| DLCO | 0.228 | 0.318 |
| Mean pulmonary arterial pressure | 0.049 | 0.822 |
| Right atrial pressure | 0.357 | 0.095 |
| Pulmonary vascular resistance | -0.162 | 0.461 |
| Cardiac index | 0.041 | 0.853 |

* Spearman's correlation test

Table S2. Univariate relationship between %IgA Plasmablasts and Sex, Race, and comorbid conditions.

| | % IgA Plasmablasts median (IQR) | p-value† |
|--|------------------------------------|----------|
| <i>Sex</i> | | |
| Male | 51.5 (17.0) | 0.52 |
| Female | 46.1 (27.4) | |
| <i>Race</i> | | |
| White | 39.6 (31.2) | 0.18 |
| Non-white | 52.1 (15.4) | |
| <i>Essential hypertension</i> | | |
| Yes | 60.3 (37.1) | 0.18 |
| No | 46.2 (18.3) | |
| <i>Renal dysfunction (GFR < 60)</i> | | |
| Yes | 26.2 (35.0) | 0.19 |
| No | 50.9 (10.8) | |
| <i>Diabetes history</i> | | |
| Yes | 41.4 (45.1) | 0.72 |
| No | 46.3 (14.5) | |
| <i>Asthma history</i> | | |
| Yes | 41.8 (53.1) | 0.61 |
| No | 48.6 (17.2) | |

† Wilcoxon rank sum test

Table S3. Clinical comparison of High vs. Low IgA plasmablast subgroups.

| | High IgA PB (n=13) | Low IgA PB n=(12) | p-value[#] |
|--|-------------------------------|------------------------------|----------------------------|
| <i>Female sex, n (%)</i> | 9 (69.2%) | 10 (83.3%) | 0.64 |
| <i>NYHA functional class, n (%)</i> | | | |
| Class I or II | 7 (54%) | 6 (50%) | 0.99 |
| Class III | 5 (38.4%) | 5 (41.7%) | 0.99 |
| Class IV | 1 (7.7%) | 1 (8.3%) | 0.99 |
| <i>Background PAH therapy, n (%)</i> | | | |
| Treatment naïve | 4 (30.8%) | 4 (33.3%) | 0.99 |
| Dual or triple therapy | 4 (30.8%) | 4 (33.3%) | 0.99 |
| Prostanoid therapy | 5 (38.5%) | 6 (50%) | 0.69 |
| <i>Age, years, median (IQR)</i> | 53.1 (33.2) | 62.6 (18.6) | 0.51 |
| <i>6MWD, m, median (IQR)</i> | 465.5 (182.5) | 388.5 (166.5) | 0.22 |
| <i>NT-proBNP, pg/mL, median (IQR)</i> | 129 (244) | 154 (785) | 0.83 |
| <i>DLCO, % predicted, median (IQR)</i> | 75.0 (18.3) | 61 (27.0) | 0.14 |
| <i>Estimated GFR, median (IQR)</i> | 82.3 (28.1) | 53.5 (25.9) | 0.16 |
| <i>RHC measurements, median (IQR)</i> | | | |
| mPAP, mmHg | 40.0 (7.5) | 40 (23.5) | 0.85 |
| RAP, mmHg | 9.5 (6.5) | 9 (5) | 0.97 |
| PVR, Wood units | 7.4 (4.6) | 8.1 (7.2) | 0.46 |
| Cardiac index, ml/min/m ² | 2.2 (0.49) | 2.0 (0.5) | 0.58 |

[#] Fisher's exact test for categorical variables (Sex, NYHA class, therapy); Kruskal-Wallis test for continuous variables.

Table S4. Oligonucleotide sequences used in the study

| Name | Sequence | Step |
|------------|--------------------------------------|------|
| wellID_002 | CACGACCGGTGCTCGATTTAGTACACGTGATAGGG | RT |
| wellID_003 | CACGACCGGTGCTCGATTTAGTACAGATCGTAGGG | RT |
| wellID_005 | CACGACCGGTGCTCGATTTAGTAGTGTAGATAGGG | RT |
| wellID_006 | CACGACCGGTGCTCGATTTAGTCGCACTAGTAGGG | RT |
| wellID_007 | CACGACCGGTGCTCGATTTAGTCTAGCGACTAGGG | RT |
| wellID_008 | CACGACCGGTGCTCGATTTAGTGTGAGTAGTAGGG | RT |
| wellID_010 | CACGACCGGTGCTCGATTTAGACGCGATCGAAGGG | RT |
| wellID_013 | CACGACCGGTGCTCGATTTAGAGTATACATAAGGG | RT |
| wellID_014 | CACGACCGGTGCTCGATTTAGAGTCGAGAGAAGGG | RT |
| wellID_015 | CACGACCGGTGCTCGATTTAGAGTGCTACGAAGGG | RT |
| wellID_017 | CACGACCGGTGCTCGATTTAGCGCAGTACGAAGGG | RT |
| wellID_018 | CACGACCGGTGCTCGATTTAGCGCGTATACAAGGG | RT |
| wellID_020 | CACGACCGGTGCTCGATTTAGCGTACTCAGAAGGG | RT |
| wellID_021 | CACGACCGGTGCTCGATTTAGCTACGCTCTAAGGG | RT |
| wellID_022 | CACGACCGGTGCTCGATTTAGTACGTCATCAAGGG | RT |
| wellID_024 | CACGACCGGTGCTCGATTTAGTCACGCGAGAAGGG | RT |
| wellID_025 | CACGACCGGTGCTCGATTTAGTCGATAGTGAAGGG | RT |
| wellID_026 | CACGACCGGTGCTCGATTTAGTCGCTGCGTAAGGG | RT |
| wellID_030 | CACGACCGGTGCTCGATTTAGTGTGTCGCAAGGG | RT |
| wellID_035 | CACGACCGGTGCTCGATTTAGACTCATCTACAGGG | RT |
| wellID_036 | CACGACCGGTGCTCGATTTAGACTCGCGCACAGGG | RT |
| wellID_037 | CACGACCGGTGCTCGATTTAGAGAGCGTCACAGGG | RT |
| wellID_039 | CACGACCGGTGCTCGATTTAGAGTAGTGATCAGGG | RT |
| wellID_043 | CACGACCGGTGCTCGATTTAGCACGTAGATCAGGG | RT |
| wellID_044 | CACGACCGGTGCTCGATTTAGCACGTGTCGAGGG | RT |
| wellID_046 | CACGACCGGTGCTCGATTTAGCGACACTATCAGGG | RT |
| wellID_047 | CACGACCGGTGCTCGATTTAGCGAGACGCGCAGGG | RT |
| wellID_048 | CACGACCGGTGCTCGATTTAGCGTCGATCTCAGGG | RT |
| wellID_051 | CACGACCGGTGCTCGATTTAGCTCTACGCTCAGGG | RT |
| wellID_055 | CACGACCGGTGCTCGATTTAGTAGCTCTATCAGGG | RT |
| wellID_057 | CACGACCGGTGCTCGATTTAGTCACTCATAACAGGG | RT |
| wellID_058 | CACGACCGGTGCTCGATTTAGTCATCGAGTCAGGG | RT |
| wellID_059 | CACGACCGGTGCTCGATTTAGTCGAGCTCTCAGGG | RT |
| wellID_062 | CACGACCGGTGCTCGATTTAGTGCTATAGACAGGG | RT |
| wellID_069 | CACGACCGGTGCTCGATTTAGATAGCTCTCGAGGG | RT |
| wellID_081 | CACGACCGGTGCTCGATTTAGTAGCATACTGAGGG | RT |
| wellID_082 | CACGACCGGTGCTCGATTTAGTATCTGATAGAGGG | RT |
| wellID_083 | CACGACCGGTGCTCGATTTAGTCTGATCGAGAGGG | RT |
| wellID_089 | CACGACCGGTGCTCGATTTAGTGATCACAGAGGG | RT |

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|------------|-------------------------------------|----|
| wellID_092 | CACGACCGGTGCTCGATTTAGAAGCAGGAAATGGG | RT |
| wellID_093 | CACGACCGGTGCTCGATTTAGAAGTCTGCATTGGG | RT |
| wellID_094 | CACGACCGGTGCTCGATTTAGAATCGGAGCGTGGG | RT |
| wellID_097 | CACGACCGGTGCTCGATTTAGACACGACAACTGGG | RT |
| wellID_100 | CACGACCGGTGCTCGATTTAGACAGTCTTCTGGG | RT |
| wellID_101 | CACGACCGGTGCTCGATTTAGACCCTTGGTGTGGG | RT |
| wellID_104 | CACGACCGGTGCTCGATTTAGACTGCAACCGTGGG | RT |
| wellID_106 | CACGACCGGTGCTCGATTTAGAGACACGTCTTGGG | RT |
| wellID_107 | CACGACCGGTGCTCGATTTAGAGAGGGCGATTGGG | RT |
| wellID_108 | CACGACCGGTGCTCGATTTAGAGCAGCAGTATGGG | RT |
| wellID_109 | CACGACCGGTGCTCGATTTAGAGCCAAATACTGGG | RT |
| wellID_111 | CACGACCGGTGCTCGATTTAGAGCTCGCTCTTGGG | RT |
| wellID_112 | CACGACCGGTGCTCGATTTAGAGGACTTGCCTGGG | RT |
| wellID_113 | CACGACCGGTGCTCGATTTAGAGGTATCGTATGGG | RT |
| wellID_114 | CACGACCGGTGCTCGATTTAGAGTGGATCACTGGG | RT |
| wellID_115 | CACGACCGGTGCTCGATTTAGAGTTGTGCCATGGG | RT |
| wellID_118 | CACGACCGGTGCTCGATTTAGATCCGCCTTGTGGG | RT |
| wellID_119 | CACGACCGGTGCTCGATTTAGATCCTCAACATGGG | RT |
| wellID_122 | CACGACCGGTGCTCGATTTAGCAATCCTGTTTGGG | RT |
| wellID_123 | CACGACCGGTGCTCGATTTAGCAATTCGAGCTGGG | RT |
| wellID_126 | CACGACCGGTGCTCGATTTAGCAGGCGAACTTGGG | RT |
| wellID_127 | CACGACCGGTGCTCGATTTAGCAGTTTCTGTTGGG | RT |
| wellID_129 | CACGACCGGTGCTCGATTTAGCCAATCAACTTGGG | RT |
| wellID_130 | CACGACCGGTGCTCGATTTAGCCACGTGGAATGGG | RT |
| wellID_133 | CACGACCGGTGCTCGATTTAGCCCATACTATTGGG | RT |
| wellID_135 | CACGACCGGTGCTCGATTTAGCCGCTCGTTTTGGG | RT |
| wellID_136 | CACGACCGGTGCTCGATTTAGCCGTTTATCTGGG | RT |
| wellID_143 | CACGACCGGTGCTCGATTTAGCTACCGCTGTTGGG | RT |
| wellID_144 | CACGACCGGTGCTCGATTTAGCTCACGGAAGTGGG | RT |
| wellID_145 | CACGACCGGTGCTCGATTTAGCTCTTCGGATTGGG | RT |
| wellID_146 | CACGACCGGTGCTCGATTTAGCTGCAAGCTGTGGG | RT |
| wellID_153 | CACGACCGGTGCTCGATTTAGGAAGAACAGTTGGG | RT |
| wellID_158 | CACGACCGGTGCTCGATTTAGGACGATATCCTGGG | RT |
| wellID_159 | CACGACCGGTGCTCGATTTAGGAGCACACTTTGGG | RT |
| wellID_162 | CACGACCGGTGCTCGATTTAGGCACTCTGGTTGGG | RT |
| wellID_163 | CACGACCGGTGCTCGATTTAGGCACTTCCAGTGGG | RT |
| wellID_164 | CACGACCGGTGCTCGATTTAGGCAGAGCTACTGGG | RT |
| wellID_167 | CACGACCGGTGCTCGATTTAGGCGACGTTGTTGGG | RT |
| wellID_168 | CACGACCGGTGCTCGATTTAGGCGTTCCTCATGGG | RT |
| wellID_169 | CACGACCGGTGCTCGATTTAGGGACTATACATGGG | RT |
| wellID_171 | CACGACCGGTGCTCGATTTAGGGCATTATTGTGGG | RT |
| wellID_172 | CACGACCGGTGCTCGATTTAGGGCTCGACTATGGG | RT |

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| wellID_174 | CACGACCGGTGCTCGATTTAGGGGTGTTTATTGGG | RT |
| wellID_175 | CACGACCGGTGCTCGATTTAGGGTACGGACATGGG | RT |
| wellID_176 | CACGACCGGTGCTCGATTTAGGGTCAACGATTGGG | RT |
| wellID_177 | CACGACCGGTGCTCGATTTAGGGTTCGGTGTATGGG | RT |
| wellID_178 | CACGACCGGTGCTCGATTTAGGGTGTTACGTGGG | RT |
| wellID_180 | CACGACCGGTGCTCGATTTAGGTTGTGGAGTTGGG | RT |
| wellID_183 | CACGACCGGTGCTCGATTTAGTCAAACAGGATGGG | RT |
| wellID_184 | CACGACCGGTGCTCGATTTAGTCAGGTCTCTTGGG | RT |
| wellID_185 | CACGACCGGTGCTCGATTTAGTCATCCGCAGTGGG | RT |
| wellID_187 | CACGACCGGTGCTCGATTTAGTCCTTTTGGATGGG | RT |
| wellID_191 | CACGACCGGTGCTCGATTTAGTCTCGTTTACTGGG | RT |
| wellID_193 | CACGACCGGTGCTCGATTTAGTGCAACTTCTGGG | RT |
| wellID_203 | CACGACCGGTGCTCGATTTAGTTGGTTCGAGTGGG | RT |
| wellID_205 | CACGACCGGTGCTCGATTTAGTTTACCTGGGTGGG | RT |
| wellID_207 | CACGACCGGTGCTCGATTTAGTTTTGCAACGTGGG | RT |
| OligodTVN20 | TTTTTTTTTTTTTTTTTTTTTVN | RT |
| PCR1_fwd | CACGACCGGTGCTCGATTTAG | PCR1 |
| K_GSP1 | TCTCCCCTGTTGAAGCTCTTTGTG | PCR1 |
| L_GSP1 | TYTGTGGGACTTCCACTGCTC | PCR1 |
| G_GSP1 | TCTTGTCCACCTTGGTGTGCTG | PCR1 |
| A_GSP1 | ATTCGTGTAGTGCTTCACGTG | PCR1 |
| M_GSP1 | CTCTCAGGACTGATGGGAAGC | PCR1 |
| K_GSP2 | TCCCTACACGACGCTCTTCCGATCTGAAGACAGATGGTGCAGCCACAG | PCR2 |
| L_GSP2 | TCCCTACACGACGCTCTTCCGATCTAGAGGAGGGYGGGAACAGAGTGA | PCR2 |
| G_GSP2 | TCCCTACACGACGCTCTTCCGATCTAAGACSGATGGGCCCTTGGTGA | PCR2 |
| A_GSP2 | TCCCTACACGACGCTCTTCCGATCTGAAGACCTGGGGCTGGTCG | PCR2 |
| M_GSP2 | TCCCTACACGACGCTCTTCCGATCTGAGACGAGGGGGAAAAGGGTT | PCR2 |
| PCR2_Fwd | GACTGGAGTTCAGACGTGTGCTCTTCCGATCCACGACCGGTGCTCGATTTAG | PCR2 |
| PCR3_Rev | AATGATACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTT | PCR3 |
| plateID_1 | CAAGCAGAAGACGGCATAACGAGATCGTGATGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_2 | CAAGCAGAAGACGGCATAACGAGATACATCGGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_3 | CAAGCAGAAGACGGCATAACGAGATGCCTAAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_4 | CAAGCAGAAGACGGCATAACGAGATTGGTCAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_5 | CAAGCAGAAGACGGCATAACGAGATCACTGTGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_6 | CAAGCAGAAGACGGCATAACGAGATATTGGCGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_7 | CAAGCAGAAGACGGCATAACGAGATGATCTGGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_8 | CAAGCAGAAGACGGCATAACGAGATTCAAGTGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_9 | CAAGCAGAAGACGGCATAACGAGATCTGATCGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_10 | CAAGCAGAAGACGGCATAACGAGATAAGCTAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_11 | CAAGCAGAAGACGGCATAACGAGATGTAGCCGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_12 | CAAGCAGAAGACGGCATAACGAGATTACAAGGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_13 | CAAGCAGAAGACGGCATAACGAGATTTGACTGTGACTGGAGTTCAGACGTG | PCR3 |

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| plateID_14 | CAAGCAGAAGACGGCATAACGAGATGGAAGTGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_15 | CAAGCAGAAGACGGCATAACGAGATTGACATGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_16 | CAAGCAGAAGACGGCATAACGAGATGGACGGGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_17 | CAAGCAGAAGACGGCATAACGAGATCTCTACGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_18 | CAAGCAGAAGACGGCATAACGAGATGCGGACGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_19 | CAAGCAGAAGACGGCATAACGAGATTTTACGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_20 | CAAGCAGAAGACGGCATAACGAGATGGCCACGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_21 | CAAGCAGAAGACGGCATAACGAGATCGAAACGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_22 | CAAGCAGAAGACGGCATAACGAGATCGTACGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_23 | CAAGCAGAAGACGGCATAACGAGATCCACTCGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_24 | CAAGCAGAAGACGGCATAACGAGATGCTACCGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_25 | CAAGCAGAAGACGGCATAACGAGATATCAGTGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_26 | CAAGCAGAAGACGGCATAACGAGATGCTCATGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_27 | CAAGCAGAAGACGGCATAACGAGATAGGAATGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_28 | CAAGCAGAAGACGGCATAACGAGATCTTTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_29 | CAAGCAGAAGACGGCATAACGAGATTAGTTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_30 | CAAGCAGAAGACGGCATAACGAGATCCGGTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_31 | CAAGCAGAAGACGGCATAACGAGATATCGTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_32 | CAAGCAGAAGACGGCATAACGAGATTGAGTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_33 | CAAGCAGAAGACGGCATAACGAGATCGCCTGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_34 | CAAGCAGAAGACGGCATAACGAGATGCCATGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_35 | CAAGCAGAAGACGGCATAACGAGATAAAATGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_36 | CAAGCAGAAGACGGCATAACGAGATTGTTGGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_37 | CAAGCAGAAGACGGCATAACGAGATATCCGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_38 | CAAGCAGAAGACGGCATAACGAGATAGCTAGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_39 | CAAGCAGAAGACGGCATAACGAGATGTATAGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_40 | CAAGCAGAAGACGGCATAACGAGATTCTGAGGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_41 | CAAGCAGAAGACGGCATAACGAGATGTCGTCGTACTGGAGTTCAGACGTG | PCR3 |
| plateID_42 | CAAGCAGAAGACGGCATAACGAGATCGATTAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_43 | CAAGCAGAAGACGGCATAACGAGATGCTGTAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_44 | CAAGCAGAAGACGGCATAACGAGATATTATAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_45 | CAAGCAGAAGACGGCATAACGAGATGAATGAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_46 | CAAGCAGAAGACGGCATAACGAGATTCGGGAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_47 | CAAGCAGAAGACGGCATAACGAGATCTTCGAGTGACTGGAGTTCAGACGTG | PCR3 |
| plateID_48 | CAAGCAGAAGACGGCATAACGAGATTGCCGAGTGACTGGAGTTCAGACGTG | PCR3 |

Table S5. Recombinant plasmablast antibody characteristics

| mAB | Binding Hits | Origin Isotype | HC V Gene | LC V Gene | HC AA Sequence | LC AA Sequence |
|-------|---|----------------|------------|-----------|---|--|
| PAH1 | Histone H2b, Histone H3 | IgG | IGHV3-7 | IGLV8-61 | DVQLVESGGGLVHLGGSLRLSCAASGFTFSSVWMAWVRQAPGKGLWEWVANINPDGSDRYVDYVSVKGRFTISRDNKATLSLQMNSLTVGDTGIYYCTRDLNWGADWGGTLTVTVSS | QTVVTQEPSPFSVSPGGTTLTCLGSLFSGSVSPITYPSWYQQTPTGQAPRALIYQTNTRSSGVPDRFSGSILGSKAALITGAQADDESYYCVLYMGGGWVFGGGTKLTVL |
| PAH4 | FTCD (LC1) | IgG | IGHV1-8 | IGKV1-5 | QVQLVQSGTEVKKPGASVRVSCRASGYTFTNYDINWVRQAPGGQPEWWMGNPNSGNTGSPQNFRRVMTTRDSTSTAYMELSGLRSEDATVYYCARSPTRIGQWSPGIIRRFDLWGQGLVTVSS | DIQMTQSPSTLSASVGDRTVITCRASQSIRTLAWYQQKPKAPKLLIYEASTLESVPPNFSGSGSGETFTLTISSLQPDFATYYCQYQSTYSLTFGGGKVEIK |
| PAH5 | Histone H1, U1-snRNP A | IgG | IGHV1-18 | IGKV1-5 | RVTLVQSGAELKRPASVKISCKASGYTFGNYGMINWVRQAPGLPEWLGWINCFDGKTFYAKQFQGRVAMTKDSTTTAYLDRSLRSDDTAIYYCARTLLGSDVLGTFDLWGQGTMTVTVSS | DIQMTQSPSTLSASVGDRTVITCRASQSIDSWLAWYQQNPKAPKLLIYKASRLGSEVPSRFSGSGSGETFTLTISSLQPDFATYYCQYQHYDYPWTFGGGKLEVK |
| PAH7 | U-snRNP B/B' protein | IgG | IGHV3-30 | IGKV1-12 | QARLVQSGGGVHPGRRTLTLTCAASGFTFRTFGMHVWRQAPGRGLEWLVAVSHDGKTKYIDAVKRRFHIARDNSNSTLYLMDDPRESDATYFCAKDMWPESSGSGYYFDQWGGQSVVIVSS | DVQMTQSPSFVSAVGDGVTITCRAGQNLNRLAWYQQKPKAPDLYLDVSTLQSGVPSRFSGSGSGRDFTLTISLQPEDSAIYFCQQALVFKTLAWGPPQWRNSFGLGTTVEIK |
| PAH8 | highly polyreactive | IgG | IGHV3-21 | IGKV1-5 | EVQLVESGGGLVKPGGSLRLSCAASGFSFSSYNMIWIRQAPGKGLWEVSSISSSFSIYYADSVKGRFISIRDNAKDSVYLQMNLRRAEDATVYYCARDLKTWCSTNCSAWGRGTLTVTVSS | DIQMTQSPSTLSASVGDRTVITCRANQINTLAWYQQKPKAPNLLVYRASSLERGVPDRFSGSGSGETFTLTVSSLQPDFATYYCQYQYISYPWTFGGGKVEVR |
| PAH9 | PCNA, Jo-1, PL-12, HUVECs, functional assay | IgA | IGHV1-18 | IGKV1-27 | QVQLVQSGAEVKKPGDSVRVSCRASGYTFNTYDINWVRQATGQGLEWWMGNPNSGNRNFQAQKFRGRVTLTRDTSTDAYMELTGLTSEDSAVYYCTTERWDKWAQGYHYHYGMDVWGGGTTVTVSS | DIQMTQSPSSLASVGDSDVTITCRASQDISNLYAWYQQKPKVPLLLIYGASTLQSGVPSRFSGSGSGETFTLTIIGSLQPEDVATYYCQKYSTPRTFGGGKVEIK |
| PAH10 | U1-snRNP A | IgA | IGHV3-53 | IGLV1-47 | EVQLVETGGGLMQPGSLRLSCATSGVTVSSNYMTWVRQAPGKGLWEVSVIYNGDRTYADSVRGRFTISRDNKKTLYLQMDNLRRAEDATVYYCARDDPGAGPGQLYWGQGMPTVTVSS | QSVLTQPPSASGTPGQRVITSCSGSSNIATNYVYVYQQPFGTAPRLLIYINNRPSGVPDRFSAKSGTSASLAISGLRSEADYYCSAWDLRSGPVFVGGGKLAVAL |
| PAH11 | PL-7, PCNA, Mi-2 | IgA | IGHV3-23 | IGKV3-15 | EVQLLESVGGGFLQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLWEVSAISGRVAATTYADSVKGRFTISRDNKNTLYLQINSLRAEDATLYYCAKEESDVRNYYRHWFFDVWGRGTLTVTVSS | EIVMTQSPVTLVSPGERVTLSCRASQSVRSNLAWYQQKPGQAPRLLIYGASTRATGIPSRISGSGSETDFTLTISSLQSEDAIYYCQYQNYWPMCSFGGGKLEIK |
| PAH15 | Sp100, PCNA, PL-12, HUVECs | IgA | IGHV3-30-3 | IGLV6-57 | QVQMVQSGGGVWQGRSLRLSCATSGFTFNRYAMHVVWRQAPGKGLDWVAVISYDGSNKYYADFVKGFRFISIRDNSQNTLYLQMSLSLRPDDTAVYYCVDRSHAPLANPFAFNWRPWFPGWQGTIAVSS | NFMTLQPHSVSGSPGETVTMSCTRSSGAINNYVQVWHRQRPASPIIILYEDYERPPGVPDRFSGSIDSSNSASLTISGLKADEADYYCQSYSDSHSVVFGGGKTLTVL |
| PAH16 | none | IgA | IGHV3-7 | IGKV2-30 | EVRLVESGGGLVQPGGSLRLSCAASGFSFRHYWMSWVRQAPGKGLWEWVANMNQGGNERIYVDYVSVKGRFTISRDNKATLSLFLQMNSLRVEDTAVYYCVGDDYGAHFDPRGRGTLTVTVSS | EVVMTQSPVLPVTLGQPASISCRSSQSLVSRDGNLYLHWFLQRPQQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFLTISRVEAEDVGVYYCMQGSWHPPTWTFGGGKTVDIK |
| PAH17 | none | IgG | IGHV3-30 | IGKV1-12 | QVRLQSGGGGAVEPGRSVTLSCAGSGFTFGSYGMHVVWRQAPGRGLEWLVAVSHDGSVYIYDDVKGFRFTISRDNKNTLYFYMDAPRESDATYFCAKDIRAESGSGYYFDHWGQGSVIVSS | DVQMTQSPSSVSAFVRDRVITICRASQNIIRLAWYQQKPKAPDLIYDASTLYSGVPSRFSGSGSGETFTLTISSLQPEDSAVILSTGQRFPKFNWPGTKVEIK |
| PAH18 | Fibromodulin peptide | IgA | IGHV1-8 | IGKV1-5 | QVQLVQSGAELRQPGASVKVSCRASGYTFTSYDINWVRQAPGGQPEWWMGNPNSANTGFQNFGRVSLTRDVSISTAYMELSGLRFEDATVYYCFVRSPTIRIGKWSPIILRRFEFVWGGGALVTVSP | DIEMTQSPSTLSASVGERVITICRASQYINTLAWYQQKPKAPKLLIYQASILETGVPPTFSGSGSGETFTLTISSLQPDFATYYCQYQNTYSLTFGRGKVEVK |
| PAH19 | Clusterin peptide, PL-12 | IgG | IGHV3-23 | IGLV2-14 | QEQLVQSGAEVKKPGASVKVSKCTSGYTFTNYDINWVRQATGQGLEWWMGNPNSGNTNYAQKFGGRVIMTRDSTGTAYMELSSLSRSDDTAVYYCATEKWEKRGVYIYYGMDVWGGGTTVTVSS | DIQMTQSPSSLASVGDRTVITCRASQGINNLYAWYQQKPKVPLLLIYASTLQSGVPSRFSGSGSGETFTLTISSLQPEDVATYYCQKYSTPRTFGGGKVEIK |