FLAIRR-seq: A novel method for single molecule resolution of near full-length immunoglobulin heavy chain repertoires

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Abstract:

Current Adaptive Immune Receptor Repertoire Sequencing (AIRR-seq) strategies resolve expressed antibody (Ab) transcripts with limited resolution of the constant region. Here we present a novel near full-length AIRR-seq (FLAIRR-Seq) method that utilizes targeted amplification by 5' rapid amplification of cDNA ends (RACE), combined with single molecule, real-time sequencing to generate highly accurate (>Q40, 99.99%) IG heavy chain transcripts. FLAIRR-seq was benchmarked by comparing IG heavy chain variable (IGHV), diversity (IGHD), and joining (IGHJ) gene usage, complementarity-determining region 3 (CDR3) length, and somatic hypermutation to matched datasets generated with standard 5' RACE AIRR-seq and full-length isoform sequencing. Together these data demonstrate robust, unbiased FLAIRR-seq performance using RNA samples derived from peripheral blood mononuclear cells, purified B cells, and whole blood, which recapitulated results generated by commonly used methods, while additionally resolving novel IG heavy chain constant (IGHC) gene features. FLAIRR-seq data provides, for the first time, simultaneous, single-molecule characterization of IGHV, IGHD, IGHJ, and IGHC region genes and alleles, allele-resolved subisotype definition, and high-resolution identification of class-switch recombination within a clonal lineage. In conjunction with genomic sequencing and genotyping of IGHC genes, FLAIRR-seq of the IgM and IgG repertoires from 10 individuals resulted in the identification of 32 unique IGHC alleles, 28 (87%) of which were previously uncharacterized. Together, these data demonstrate the capabilities of FLAIRR-seq to characterize IGHV, IGHD, IGHJ, and IGHC gene diversity for the most comprehensive view of bulk expressed Ab repertoires to date.

53 **Introduction**

54 Antibodies (Abs) or immunoglobulins (IGs) are the primary effectors of humoral immunity
55 and are found as both membrane-bound receptors on B cells and circulating, secreted proteins
56 (1). Both membrane-bound B cell receptors (BCRs) and secreted Abs act to recognize and bind
57 antigen. All Abs and BCRs are composed of two identical heavy and light chains that are post-
58 translationally associated. The heavy chain is comprised of two distinct domains: (i) the variable
59 domain (Fab), which allows for antigen binding, and (ii) the constant domain (Fc), which
60 modulates downstream effector functions (1, 2). The light chain also includes a variable domain
61 that, once post-translationally associated with the heavy chain variable domain, interacts with
62 cognate antigen (3). In humans, Abs are grouped into discrete isotypes and subisotypes (i.e.,
63 IgM, IgD, IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, and IgE), based on the expression of specific
64 constant (C) genes within the IG heavy chain locus (IGH). Each isotype and subisotype has
65 unique effector properties that together represent the wide diversity of Ab-mediated functions,
66 including binding of Fc receptors (FCR), activation of complement, opsonization, antibody-
67 dependent cellular cytotoxicity (ADCC) and antibody-dependent cellular phagocytosis (ADCP) (4,
68 5).

69 To facilitate the development of diverse Ab repertoires capable of recognizing the wide
70 range of pathogens humans encounter, the IG genomic loci are highly polymorphic and harbor
71 diverse and complex sets of genes that recombine in each B cell to encode up to 10^{13} unique
72 specificities (6). B cells create this expansive catalog of specificities through somatic
73 recombination of the variable (V), diversity (D), and joining (J) genes in IGH, and V and J genes
74 from the corresponding light chain loci, lambda (IGL) and kappa (IGK) (7). During VDJ
75 recombination in IGH, a single D and J gene are first recombined, while the intervening and
76 unselected D and J gene sequences are removed by RAG recombinase (8). After D and J genes
77 are joined, further recombination of a specific V gene to the DJ gene cassette completes the
78 formation of the full VDJ rearrangement. Following transcription of the recombined VDJ, a single

79 constant region gene is spliced together with the VDJ cassette to generate the completed heavy
80 chain transcript (7). Recombination at IGL and IGK occurs similarly, recombining V and J genes
81 only. Heavy and light chain transcripts are independently translated and linked via covalent
82 cysteine bonds resulting in a fully functional protein prior to B cell cell-surface expression or
83 secretion (Figure 1A) (9). Naïve B cells, which develop in the bone marrow from hematopoietic
84 stem cell progenitors, have undergone VDJ recombination but have not yet encountered antigen,
85 and solely express IgM and IgD (10). These naïve B cells then migrate to B cell zones in
86 secondary lymphoid tissues where they encounter antigen, driving further maturation and class
87 switch recombination (CSR) to enable the most effective humoral responses (11). CSR mediates
88 the excision of IGHC genes at the DNA level, which leads to the utilization and linkage of different
89 IGHC genes to the same VDJ, ultimately resulting in class switching to alternate isotypes and
90 subisotypes (11).

91 The IgG isotype class is represented by four subisotypes: IgG1, IgG2, IgG3, and IgG4.
92 Each IgG subisotype circulates at varied frequencies and facilitates unique immune functions. For
93 example, IgG1 is typically the most abundant circulating IgG and mediates proinflammatory
94 responses; IgG2 targets bacterial polysaccharides, providing protection from bacterial pathogens;
95 IgG3 confers protection against intracellular bacterial infections and enables clearing of parasites;
96 and IgG4 contains exclusive structural and functional characteristics often resulting in anti-
97 inflammatory and tolerance-inducing effects (5). Multiple studies have identified Ab-mediated
98 subisotype-specific pathogenicity in the context of autoimmune diseases and cancer highlighting
99 the need for further investigation of subisotype-specific repertoires (12-15).

100 Current Adaptive Immune Receptor Repertoire sequencing (AIRR-seq) methods aim to
101 resolve variable and constant region transcripts to differing extents. Profiling of the variable
102 region, even in part, defines V, D and J gene usage while also providing characterization of
103 complementarity determining regions (CDR) 1, 2, and 3, which are hypervariable and directly
104 interact with target antigen (Figure 1B) (16). CDR3-targeted profiling approaches, such as those

105 used by Adaptive Biotechnologies (17), allow for V, D, and J gene assignments but do not provide
106 complete resolution of the entire variable region (17). Multiplexed primer-based AIRR-seq
107 strategies generate full variable region content but require specific primers to known targets and
108 therefore may miss novel genes and alleles. 5' RACE AIRR-seq methods capture the full-length
109 VDJ exon without variable region-targeted multiplexed primer pools therefore limiting the impact
110 of primer bias and enabling discovery of novel IGHV, IGHD, and IGHJ genes and alleles (18). 5'
111 RACE methods also often prime from the first IGHC exon (CH1), allowing for determination of
112 isotype. Additional methods have been developed that shift amplification strategies by capturing
113 additional IGHC region sequence to enable subisotype resolution; however, these methods
114 sacrifice full and contiguous characterization of the IGHV gene (19). All commonly used AIRR-
115 seq methods are further technically limited by the length restrictions (≤ 600nt) of short-read next
116 generation sequencing. As a result, no current AIRR-seq strategy resolves the complete heavy
117 chain transcript, including all IGHC exons alongside the recombined IGHV, IGHD, and IGHJ
118 genes. Our team has recently shown that population-based polymorphisms within the IGHV,
119 IGHD, IGHJ and IGL loci are far more extensive than previously known; the IGHC region has also
120 been shown to contain genomic diversity, although the extent of this diversity has likely not been
121 fully explored (20-27). Although it is understood that the Fc domain mediates Ab effector
122 functions, there is limited knowledge as to how genetic variation in this region may impact
123 functional capabilities or posttranslational modification (5, 28, 29). As such, there is a growing
124 need to understand genomic variation across the complete Ab molecule. To address these
125 limitations, we have developed novel, end-to-end pipeline to target, profile, and characterize the
126 Ab heavy chain repertoire in the context of isotype (IgG, IgM) and subisotype (IgG1, IgG2, IgG3,
127 IgG4).

128 Here, we present FLAIRR-seq, a novel targeted 5' RACE-based amplification of near full-
129 length IgG and IgM heavy chain transcripts, paired with single molecule real time (SMRT)
130 sequencing, resulting in highly accurate (mean read accuracy ~Q60, 99.9999%), near full-length

131 Ab sequences from RNA derived from whole blood, isolated PBMC, and purified B cells. When
132 analyzed with the Immcantation AIRR-seq tool suite (30, 31), we demonstrate that FLAIRR-seq
133 performs comparably to standard 5'RACE AIRR-seq methods and single-molecule isoform
134 sequencing (Iso-Seq) strategies for characterizing the expressed Ab repertoire. We further
135 highlight the novel features of FLAIRR-seq data, including phased identification of IGHV, IGHD,
136 IGHJ, and IGHC genes, facilitating the profiling of subisotype- and IGHC allele-specific repertoires
137 and CSR characterization.
138

139 **Materials and Methods**

140 **Sample collections**

141 Experiments were conducted using healthy donor peripheral blood mononuclear cells
142 (PBMC), purified B cells from healthy donors, or whole blood collected from hospitalized COVID-
143 19 patients (Supplementary Table 1). Commercially available healthy donor PBMC (STEMCELL
144 Technologies) and a subset of matched purified B cells were utilized to generate AIRR-seq and
145 FLAIRR-seq validation datasets. Full-length isoform sequencing (Iso-Seq) was performed using
146 B cells isolated from the PBMC of a healthy, consented 57-year-old male donor at the University
147 of Louisville (UofL) School of Medicine. The UofL Institutional Review Board approved sample
148 collection (IRB 14.0661). For COVID-19 affected patient samples (n=5), whole blood was
149 collected from the Mount Sinai COVID-19 biobank cohort of hospitalized COVID-19 patients,
150 approved by the Institutional Review Board at the Icahn School of Medicine at Mount Sinai as
151 previously described (32).

152 **PBMC isolation and B cell purification**

153 Frozen healthy donor PBMCs were purchased, thawed, and aliquoted for use in
154 downstream experiments (STEMCELL Technologies). For Iso-Seq analyses, 175mL of venous
155 blood was collected in a final concentration of 6mM K_3EDTA using standard phlebotomy. PBMCs

156 were isolated using Sepmate PBMC Isolation Tubes (STEMCELL Technologies) as previously
157 described (33), with an additional granulocyte depletion step using the RosetteSep Human
158 Granulocyte Depletion Cocktail (STEMCELL Technologies) as directed by the manufacturer. B
159 cells from the freshly collected and frozen healthy donor PBMC were isolated using the EasySep
160 Human Pan-B Cell Enrichment Kit, as described by the manufacturer (STEMCELL Technologies).
161 Briefly, B cells, including plasma cells, were isolated by negative selection using coated magnetic
162 particles. First, the B cell enrichment cocktail was added to the sample and mixed for a 5-minute
163 incubation at room temperature, followed by addition of magnetic particles and further incubation
164 for 5 minutes on the benchtop. The sample tube was then placed on an EasySep magnet
165 (STEMCELL Technologies), and purified B cells were carefully eluted from the magnetic particles
166 and immediately used for RNA extraction.

167 **Genomic DNA and RNA extraction**

168 For the healthy frozen PBMC and matched purified B cells, genomic DNA (gDNA) and
169 RNA were co-extracted using the AllPrep DNA/RNA Mini Kit (Qiagen) according to the
170 manufacturer's instructions. For the freshly processed UofL healthy donor PBMC, purified Pan-B
171 cells were lysed in Buffer RLT Plus, and RNA was extracted with the RNeasy Plus Mini Kit
172 (Qiagen) per the manufacturer's protocol; no gDNA was collected from this sample. COVID-19
173 whole blood-derived RNA was extracted from samples collected in Tempus Blood RNA tubes
174 using the Tempus Spin RNA Isolation Kit (ThermoFisher) as described by the manufacturer. For
175 all samples, concentrations of RNA and gDNA (when appropriate) were assessed using the Qubit
176 4.0 fluorometer, with the RNA HS Assay Kit and Qubit DNA HS Assay Kit, respectively
177 (ThermoFisher Scientific). RNA and gDNA integrity were evaluated using the Bioanalyzer RNA
178 Nano Kit and DNA 1200 Kit, respectively (Agilent Technologies). Extracted RNA and gDNA were
179 stored at -80℃ and -20℃, respectively, until used.

180 **FLAIRR-seq targeted amplification of heavy chain transcripts**

181 Extracted RNA was thawed on ice and converted to first strand complementary DNA
182 (cDNA) using the SMARTer RACE 5'/3' Kit (Takara Bio USA), as described by the manufacturer
183 and a custom oligonucleotide that contained the template switch oligo and a unique molecular
184 identifier (5' TSO-UMI) for template switch during first strand cDNA synthesis. The following
185 reaction conditions were used: (i) a primary master mix was prepared with 4.0 µL 5X First-Strand
186 Buffer, 0.5 µL DTT (100 mM), and 1.0 µL dNTPs (20 mM) per reaction and set aside until needed;
187 (ii) in a separate 0.2-mL PCR tube, 10 µL of sample RNA and 1 µL 5'-CDS Primer A were
188 combined and incubated in a thermal cycler at 72°C (lid temperature: 105°C) for 3 minutes,
189 followed by cooling to 42°C for 2 minutes; (iii) after cooling, tubes were spun briefly to collect
190 contents and 1µL (12µM) of the 5' TSO-UMI was added to the RNA; (iv) 0.5 µL of RNase inhibitor
191 and 2.0 µL of SMARTScribe Reverse Transcriptase were added to the primary master mix tube
192 per sample and 8 µL of the combined master mix was then added to each RNA-containing sample
193 tube. First-strand cDNA synthesis reactions were incubated in a thermal cycler at 42°C (lid
194 temperature: 105°C) for 90 mins, followed by heat inactivation at 70°C for 10 minutes. Total first
195 strand cDNA generated in this reaction was diluted 1:2 with Tricine-EDTA Buffer before moving
196 onto targeted heavy chain transcript amplification.

197 To specifically amplify heavy chain transcripts from total first-strand cDNA, targeted IgG
198 and IgM transcript amplification reactions were performed using barcoded IgG (3' primer binding
199 in the constant region exon 3, CH3) or IgM (3' primer binding in the constant region exon 4, CH4)-
200 specific primers (Supplementary Table 2) and the following conditions: (i) 5 µL of diluted first-
201 strand cDNA was added to 0.2-mL PCR tubes; (ii) a master mix was generated using 10 µL 5X
202 PrimeSTAR GXL Buffer, 4 µL GXL dNTP mixture, 28 µL PCR-grade water, 1 µL PrimeSTAR GXL
203 Polymerase and 1 µL 10x UPM form the SMARTer RACE 5'/3' Kit per reaction; (iii) 44 µL master
204 mix was added to each reaction tube followed by 1 µL of the appropriate barcoded IgG (CH3) or
205 IgM (CH4) primer. Different temperatures were used for annealing of IgG- (63.5°C) and IgM-

206 specific primers (60°C) to account for primer specific melting temperatures and to enhance
207 targeted amplification specificity. Amplification conditions for full-length IgG were: 1 minute at
208 95°C, followed by 35 amplification cycles of 95°C for 30 sec, 63.5°C for 20 sec, and 2 minutes at
209 68°C, followed by a final extension for 3 minutes at 68°C and hold at 4°C. Amplification conditions
210 for full-length IgM were: 1 minute at 95°C, followed by 35 amplification cycles of 95°C for 30 sec,
211 60°C for 20 sec., and 2 minutes at 68°C, followed by a final extension for 3 minutes at 68°C and
212 hold at 4°C. Final amplification reactions were purified using a 1.1x (vol:vol) cleanup with ProNex
213 magnetic beads (Promega) . Successfully amplified products were quantified with Qubit dsDNA
214 HS assay (ThermoFisher Scientific) and length was evaluated with the Fragment Analyzer
215 Genomic DNA HS assay (Agilent). Samples were equimolar pooled in 8-plexes for SMRTbell
216 library preparation and sequencing.

217 **FLAIRR-seq SMRTbell library preparation and sequencing**

218 Eight-plex pools of targeted IgG or IgM amplicons were prepared into SMRTbell
219 sequencing templates according to the "Procedure and Checklist for Iso-Seq Express Template
220 for Sequel and Sequel II systems" protocol starting at the "DNA Damage Repair" step and using
221 the SMRTbell Express Template Prep Kit 2.0, with some modifications (Pacific Biosciences).
222 Briefly, targeted IgG and IgM amplicons underwent enzymatic DNA damage and end repair,
223 followed by ligation with overhang SMRTbell adapters as specified in the protocol. To increase
224 consistency in SMRTbell loading on the Sequel IIe system, we further treated the SMRTbell
225 libraries with a nuclease cocktail to remove unligated amplified products, using the SMRTbell
226 Enzyme Cleanup Kit, as recommended by the manufacturer (Pacific Biosciences). Briefly, after
227 heat-killing the ligase with an incubation at 65°C, samples were treated with a nuclease cocktail
228 at 37°C for 1 hour, and then purified with a 1.1X Pronex cleanup. Final SMRTbell libraries were
229 evaluated for quantity and quality using the Qubit dsDNA HS assay and Fragment Analyzer
230 Genomic DNA assay, respectively. Sequencing of each 8-plex, barcoded sample pool was

231 performed on one SMRTcell 8M using primer v4 and polymerase v2.1 on the Sequel IIe system
232 with 30 hr movies. Demultiplexed, high-fidelity circular consensus sequence reads ("HiFi reads")
233 were generated on the instrument for downstream analyses.

234 **AIRR-seq SMARTer Human BCR IgG/IgM sequencing**

235 Matched healthy donor RNA was used to generate targeted IgG and IgM AIRR-seq
236 libraries using the SMARTer Human BCR IgG IgM H/K/L Profiling Kit (Takara Bio USA) according
237 to the manufacturer's instructions with no modifications. Briefly, for each sample, proprietary IgG
238 and IgM primers were used to amplify heavy chain transcripts following a 5'RACE reaction. AIRR-
239 seq libraries were then quality controlled using the 2100 Bioanalyzer High Sensitivity DNA Assay
240 Kit (Agilent) and the Qubit 3.0 Fluorometer dsDNA High Sensitivity Assay Kit. Sequencing on the
241 MiSeq platform using 300 bp paired-end reads was performed using the 600-cycle MiSeq
242 Reagent Kit v3 (Illumina) according to the manufacturer's instructions, and FASTQ reads were
243 generated using the associated DRAGEN software package (Illumina).

244 **B cell Iso-Seq**

245 RNA extracted from healthy sorted B cells was used to generate Iso-Seq SMRTbell
246 libraries following the "Procedure & Checklist Iso-Seq Express Template Preparation for the
247 Sequel II System" with minor adaptations compared to the manufacturer's instructions. Briefly,
248 Iso-Seq libraries were generated using 500 ng high-quality (RIN > 8) RNA as input into oligo-dT
249 primed cDNA synthesis (NEB). Barcoded primers were incorporated into the cDNA during second
250 strand synthesis. Following double-stranded cDNA amplification, transcripts from two samples
251 sourced from purified B cells and NK cells were equimolar pooled as previously described (33).
252 SMRTbells were generated from the pooled cDNA as described above for the FLAIRR-seq
253 amplification products, including the addition of a nuclease digestion step. Quantity and quality of
254 the final Iso-Seq libraries were performed with the Qubit dsDNA High Sensitivity Assay Kit and
255 Agilent Fragment Analyzer Genomic DNA assay, respectively. This 2-plex Iso-Seq pool was

256 sequenced using primer v4 and polymerase v2.1 on the Sequel IIe system with a 30-hour movie.
257 HiFi reads were generated on instrument before analyses. Demultiplexing of barcoded samples
258 and generation of full-length non-concatemer (FLNC) predicted transcripts were performed using
259 the Iso-Seq v3 pipeline available through SMRTLink (v.10.2). B-cell-derived FLNC reads were
260 mapped to the human genome using the GMAP reference database and reads derived from
261 chromosome 14 were extracted for downstream IGH transcript characterization via Immcantation,
262 as described below.

263 **Immcantation analyses of IgG and IgM repertoires**

264 Analyses of FLAIRR-seq, AIRR-seq, and Iso-seq datasets were performed using
265 Immcantation tools (30, 31). Demultiplexed barcoded HiFi (for SMRT sequencing data) or FASTQ
266 (for AIRR-seq) reads were first processed using the pRESTO tool for quality control, UMI
267 processing, and error profiling (30). For AIRR-seq, pRESTO analysis data from paired-end reads
268 ("R1" and "R2") were trimmed to remove bases with < Q20 read quality and/or <125 bp length
269 using the "FilterSeq trimqual" and "FilterSeq length", respectively. IgG and IgM CH3 or CH4 primer
270 sequences were identified with an error rate of 0.2, and primers identified were then noted in
271 FASTQ headers using "MaskPrimers align". Next, 12 basepair (bp) UMIs were located and
272 extracted using "Maskprimers extract". Sequences found to have the same UMIs were grouped
273 and aligned using "AlignSets muscle," with a consensus sequence generated for each UMI using
274 "BuildConsensus". Mate pairing of AIRR-seq reads was conducted using a reference-guided
275 alignment requiring a minimum of a 5 bp overlap via "AssemblePairs sequential". After collapsing
276 consensus reads with the same UMI ("conscount") using "CollapseSeq"," reads with < 2
277 supporting sequences were removed from downstream analysis. For pRESTO processing of
278 FLAIRR-seq, single HiFi reads ("R1") reads did not require trimming due to > Q20 sequence
279 quality across all bases. 5'TSO-UMI and CH3 or CH4 region primers were identified along with a
280 22 bp UMI with an error rate of 0.3 using "MaskPrimers align". Reads were then grouped and

281 aligned using “AlignSets muscle”. Due to the single molecule nature of FLAIRR-seq reads, no
282 mate pairing was required. Consensus reads were then generated as described above, including
283 removal of sequences with < 2 supporting reads.

284 pRESTO-filtered reads for both AIRR-seq and FLAIRR-seq data were then input into the
285 Change-O tool (Table 1). Iso-seq required no initial processing from pRESTO and was input into
286 Change-O for IG gene reference alignment along with AIRR-seq and FLAIRR-seq data using
287 “igblastn”, clonal clustering using “DefineClones”, and germline reconstruction and conversion
288 using “CreateGermlines.py” and the GRCh38 chromosome 14 germline reference (31). Fully
289 processed and annotated data was then converted into a TSV format for use in downstream
290 analyses. The Alakazam Immcantation tool suite was then used to quantify gene usage analysis,
291 calculate CDR3 length, assess somatic hypermutation frequencies, and analyze clonal diversity
292 (31). SCOPer clonal assignment by spectral clustering was conducted for COVID-19 patient time
293 course samples (34, 35). For clonal lineage tree analysis, the Dowser tool was used to examine
294 clonal diversity and CSR over time (36).

295 **Targeted IG gDNA capture, long-read sequencing, and IGenotyper analyses.**

296 FLAIRR-seq validation samples also underwent IGHC targeted enrichment and long-read
297 sequencing as previously described (37). Briefly, gDNA was mechanically sheared and size
298 selected to include 5-9kb fragments using the BluePippin (Sage Science). Samples were then
299 end repaired and A-tailed using the standard KAPA library preparation protocol (Roche).
300 Universal priming sequences and barcodes were then ligated onto samples for multiplexing
301 (Pacific Biosciences). Barcoded gDNA libraries were captured using IGH-specific probes
302 following a SeqCap protocol (Roche). 26 IGH-enriched samples were purified and pooled together
303 for SMRTbell library prep as described above, including the final nuclease digestion step. Pooled
304 SMRTbells were annealed to primer v4, bound to polymerase v2.0, and sequenced on the Sequel
305 IIe system with 30h movies. After sequencing, HiFi reads were generated and analyzed by the

306 IGenotyper pipeline (37). In brief, IGenotyper was used to detect single nucleotide variants and
307 assemble sequences into haplotype-specific assemblies for downstream IGHC gene genotyping.
308 Alleles were then extracted from assemblies using a bed file containing coordinates for each
309 IGHC gene exon. After sequences were extracted, reads were then aligned to the IMGT database
310 (downloaded on 2/21/22) and assigned as an exact match to IMGT, "novel" if there was no match
311 to the IMGT database or "novel, extended" if a match was detected to a partial allele found in
312 IMGT, but the IMGT allele was a substring of the IGenotyper identified allele (38). This set of
313 alleles was then used as a ground truth dataset.

314 **IGHC gene genotyping with FLAIRR-seq**

315 To genotype IGHC genes and alleles from FLAIRR-seq data, productive reads were
316 filtered by IGHC length (900bp–1100bp) and aligned to the chromosome 14 hg38 reference using
317 minimap2 along with SAMtools to generate sorted and indexed bam files (39, 40). WhatsHap was
318 used to identify, genotype, and phase single nucleotide variants (SNV) (41). Phased SNVs were
319 used to assign each read to a haplotype using MsPAC. Reads from each haplotype and gene
320 were clustered using CD-HIT using a 100% identity clustering threshold parameter, and a single
321 representative read from the largest cluster was aligned to the IGenotyper curated alleles using
322 BLAST (42) to determine the closest matching IGHC gene and allele (38, 43). The representative
323 read was selected based on 100% identity to all other sequences in that cluster.

324 **Inference of IGHV, IGHD, and IGHJ gene haplotypes from FLAIRR-seq data using IGHC**
325 **gene anchors**

326 To test the ability of IGHC genes to be used for the inference of IGHV, IGHD, and IGHJ haplotypes
327 from FLAIRR-seq data, we chose one sample that was heterozygous for both IGHM and IGHJ6
328 (IGHJ6 is standardly used for AIRR-seq haplotype inference). For this sample, we employed
329 TigGER (31, 44-46) to infer novel IGHV alleles, and generate sample-level IGHV genotypes using
330 a Bayesian approach. Rearranged sequences within the Change-O table were then reannotated

taking into account sample genotype and detected novel alleles. Updated annotations were then used to infer haplotypes using RAbHIT version 0.2.4 (47). Both IGHJ6 and IGHM were used as anchor points for haplotyping, and the resulting haplotypes were compared.

Results

Gene usage, CDR3, and SHM profiles characterized from FLAIRR-seq data are comparable to AIRR-seq and Iso-Seq

Current methods for commercially available 5' RACE AIRR-Seq utilize targeted amplification of the variable region and, in some cases, a small portion of the first constant region exon (CH1), in conjunction with short-read sequencing to characterize IG repertoires. However, this minimal examination of the IGHC gene sequence is primarily used to define isotypes. No current method defines both the heavy chain variable and constant regions allowing for both subisotype classification and IGHC allele-level resolution. To address these technical limitations, we developed the FLAIRR-Seq method (Figure 1C), a targeted 5' RACE approach combined with SMRT sequencing to generate highly accurate, near full-length IgG (~1500 bp) and/or IgM (2000 bp) sequences, allowing for direct, simultaneous analysis of the heavy chain variable and constant regions (Figure 1D), including gene/allele identification for IGHV, IGHD, IGHJ and IGHC segments, and isotype- and subisotype-specific repertoire profiling.

To evaluate and validate the capabilities of FLAIRR-seq, matched FLAIRR-seq and AIRR-seq analyses were performed on ten healthy donor PBMC samples. FLAIRR-seq data were filtered from the initial HiFi reads (>Q20) to include only >Q40 reads. The average read quality of these filtered reads was >Q60 (99.9999%), with a pass filter rate ranging from 88%-93% of total reads. AIRR-seq FASTQ bases were trimmed to retain sequences with an average quality of Q20 (99%). These filtered reads were used as input into the Immcantation suite, specifically the pREST-O and Change-O tools, for IGHV, IGHD, and IGHJ gene assignment, and repertoire feature analyses, including identification of clones, extent of somatic hypermutation, and

356 evaluation of CDR3 lengths. As shown in **Table 1,** fewer overall FLAIRR-seq reads were used as
357 input into the Immcantation analyses, after required filtration and read assembly steps (which
358 were not needed for the high-quality single-molecule FLAIRR-seq reads). FLAIRR-seq resulted
359 in comparable or, in many cases, increased number of unique VDJ sequences, clones, and CDR3
360 sequences identified compared to the matched AIRR-seq-derived samples in both the IgG and
361 IgM repertoires. These basic sequencing and initial analysis metrics demonstrated that FLAIRR-
362 seq produced high-quality variable region data for detailed Ab repertoire analyses and is
363 amenable to analysis using existing AIRR-seq analysis tools. While input RNA mass used for
364 FLAIRR-seq was often more than for AIRR-seq, ongoing and future optimization of the method is
365 aimed at reducing RNA input. Furthermore, a comparative cost analysis was performed. To obtain
366 the closest metric to a direct comparison, we calculated the cost per "actionable read", defined as
367 the read number per sample and per method after read and length quality filtration and assembly,
368 but prior to cluster consensus, performed in the pRESTO pipeline. This method was used to
369 represent the total unique single molecule or assembled templates captured by either the
370 FLAIRR-seq or AIRR-seq methods, respectively, that passed all necessary quality control criteria
371 for downstream annotation and analyses irrespective of biologic repertoire diversity or clonality.
372 Lastly, to remove the impact of pooling differences, we used this "per actionable read" cost to
373 calculate the cost for the generation of 15,000 "actionable reads" as our standard price. For AIRR-
374 seq this cost was $25.50 per sample, whereas for FLAIRR-seq, this cost was $33.57 per sample.
375 These costs reflect needed reagents and consumables only, assume instrumentation access and
376 do not include labor. Future optimization for FLAIRR-seq will include integrating a multiplexed
377 array sequencing (MAS) step to concatenate reads and enhance overall depth of sequencing and
378 multiplexing capacity per pool, resulting in decreasing costs per sample (48).

379 While optimizing FLAIRR-seq sample preparation, we examined whether upstream
380 isolation of B cells before FLAIRR-seq molecular preparation would enhance the ability to detect

381 IGHV, IGHD, and IGHJ gene usage. To do this, aliquots of PBMC (n=4) were split into two groups
382 for RNA extraction: (i) RNA derived from bulk PBMC, and (ii) RNA isolated from purified pan B-
383 cells, followed by FLAIRR-seq preparation, SMRT sequencing, and Immcantation analysis of both
384 groups. IGHV, IGHD, and IGHJ gene usage correlations between groups are shown in Figure 2A
385 and demonstrate a significant association (p-values ranging from 0.033 to $4.1e^{-16}$) strongly
386 supporting the conclusion that B cell isolation before RNA extraction was not necessary to achieve
387 comparable gene usage metrics. The limited differences that were observed could be explained
388 by template sampling differences between the two experiments. Due to the strong associations
389 observed and the ease of processing PBMC in bulk, we moved forward with RNA derived directly
390 from PBMC aliquots for the remainder of our analyses.

391 We established FLAIRR-seq performance by comparing its output to the commonly used
392 5' RACE AIRR-seq method. 5' RACE AIRR-seq was chosen as it provides resolution of the
393 complete variable region and a small portion of IGHC, allowing for isotype differentiation.
394 Following matched preparation of both FLAIRR-seq and AIRR-seq libraries from healthy donor
395 PBMC samples (n=10), we compared multiple repertoire features to benchmark FLAIRR-seq
396 performance. First, we evaluated IGHV, IGHD, and IGHJ gene usage frequencies. We observed
397 significant correlations between FLAIRR-seq and AIRR-seq datasets in IGHV, IGHD and IGHJ
398 gene usage for both IgM (V genes: r = 0.93-0.97, $p=<2.2e^{-16}$; D genes: r = 0.98-0.99, $p=<2.2e^{-16}$;
399 J genes: r = 0.94-1.0, p = 0.0028-0.017) and IgG isotypes (V genes: r = 0.90-0.96, $p=<2.2e^{-16}$; D
400 genes: r = 0.87-0.99, $p=<2.2e^{-16}$-$6.1e^{-14}$;J genes: r = 0.89-1.0, p = 0.0028-0.033) (Figure 2B),
401 indicating that FLAIRR-seq comparably resolves IGHV, IGHD, and IGHJ gene usage profiles. To
402 note, IGHJ genes showed lower levels of significance (larger p-values) across all comparisons
403 due to the relatively few genes that make up the IGHJ gene family compared to the more diverse
404 IGHV and IGHD families. We next investigated the performance of both methods in terms of
405 resolving somatic hypermutation (SHM) frequencies (Figure 2C), and complementarity

406 determining region 3 (CDR3) lengths (Figure 2D), which are often used as measures of evaluating
407 B cell affinity maturation. Although we did observe occasional statistically significant differences
408 in the SHM frequency between AIRR-seq and FLAIRR-seq data using the same samples, these
409 differences were not seen across all samples, suggesting that sample-to-sample variation may
410 drive this observation rather than technology-based discrepancies. We found that CDR3 lengths
411 were consistently longer in the FLAIRR-seq datasets for both the IgM and IgG isotypes in most
412 donors. The characterization of unusually long CDR3 regions (> 40 nt) in the IgG sequences with
413 FLAIRR-seq is likely due to the higher contiguity and quality afforded by the longer read lengths,
414 which are less likely to be spanned by short-read 2x300 bp paired-end sequencing strategies.
415 Together, these data demonstrate that FLAIRR-seq achieves comparable gene usage profiles,
416 and improved resolution of long CDR3 sequences.

417 Others have recognized the power of long-read sequencing to resolve B cell repertoires
418 using bulk Iso-Seq methods, allowing for the examination of full-length transcripts from isolated B
419 cells (49). The Iso-Seq method captures full-length transcripts expressing a poly(A) tail without
420 bias through oligo dT-based priming. The trade-offs of this approach are throughput, depth, and
421 cost, as Iso-Seq processing generates a complete transcriptome per sample without enrichment
422 of heavy chain sequences, which then need to be filtered out and analyzed, resulting in a
423 considerable amount of non-repertoire data that is discarded. To investigate whether the
424 untargeted transcriptome-wide Iso-Seq method would resolve a qualitatively different repertoire
425 than FLAIRR-seq, which would have indicated FLAIRR-seq-driven primer bias, we performed
426 matched Iso-Seq and FLAIRR-seq on purified B-cell derived RNA. IGHV, IGHD, and IGHJ gene
427 usage frequencies were compared between Iso-Seq and FLAIRR-seq datasets (Spearman's rank
428 correlation), revealing significant correlations between usage profiles (V genes: $r = 0.94$, $p=2.2e^{-}$
429 ^{16}; D genes: $r = 0.92$, $p =1.4e^{-13}$; J genes: $r = 1.0$, $p = 0.0028$; Figure 2E). These data strongly
430 suggest that FLAIRR-seq has very limited to no primer-driven bias compared to whole

431 transcriptome data. Collectively, this benchmarking dataset confirmed that FLAIRR-seq is
432 comparable other state-of-the-art methods, providing robust characterization of commonly used
433 repertoire metrics, with limited increases in per sample cost.

434 **IGenotyper and FLAIRR-seq provide constant region gene allele identification and allow**
435 **for haplotyping of variable genes**

436 The novel value added by FLAIRR-seq is improved resolution of IGHC, including
437 estimation of IGHC gene and allele usage, subisotype identification, and phasing of variable and
438 constant regions for comprehensive repertoire analysis**.** To evaluate the capabilities and accuracy
439 of IGHC gene and allele identification with FLAIRR-seq, we first established a ground truth dataset
440 of IGHC alleles for all 10 samples by targeted sequencing of the germline IGH locus (Figure 3A)
441 using IGenotyper, as previously described (37). IGHG1, IGHG2, IGHG3, IGHG4 and IGHM alleles
442 called by IGenotyper (see Methods) were assigned to one of three categories, schematized in
443 Figure 3B: (i) "exact match" - alleles documented in the IMGT database; (ii) "novel not in IMGT"
444 – alleles not documented in the IMGT database; or (iii) "extended" – alleles that matched partial
445 alleles in the IMGT database (i.e., those only spanning a subset of exons), but were extended by
446 sequences in our dataset. IGenotyper identified a total of 32 unique IGHG1, IGHG2, IGHG3,
447 IGHG4 and IGHM alleles across all individuals, as schematized in Figure 3C. Among these 32
448 alleles, only 4 were documented in IMGT, the remaining represented novel alleles (n=11) or
449 extensions (n=17) of known alleles. In aggregate, we observed a greater number of IGHG4 alleles
450 than for any of the IGHG genes. Among these alleles were 4 sequences represented by
451 suspected duplications of IGHG4. In fact, we observed 3 IGHG4 gene alleles in 4/10 samples,
452 indicating the presence of gene duplications in these donors; in all cases, these alleles were also
453 identified in the FLAIRR-seq data (see below). Given the relatively small size of this proof-of-
454 concept healthy donor cohort, the identification of 28 (87%) novel or extended alleles underscores

455 the extensive polymorphism In this region and reflects the paucity of information regarding this
456 locus in existing immunogenomics databases.

457 We next used the iGenotyper-derived IGHC gene database as the ground-truth for
458 evaluating the capability of FLAIRR-seq to identify and resolve IGHC gene alleles. Based on our
459 analysis workflow for identifying IGHC alleles from FLAIRR-seq data, we resolved 19/32 (59%)
460 iGenotyper alleles at 100% identity; no additional false-positive alleles were identified. Of the
461 alleles that were not unambiguously resolved by our FLAIRR-seq pipeline, 8 had allele defining
462 single nucleotide variants (SNVs) 3' of the FLAIRR-seq primers. The rate of true-positive allele
463 calls using FLAIRR-seq across all 10 samples ranged from 5% for IGHG1 to 90% for IGHM
464 (Figures 3C and 3D). As a result, the IGHC genotypes inferred by FLAIRR-seq have some
465 limitations, but on the whole allow for much greater resolution of IGHC variation in the expressed
466 repertoire than currently used methods. Future iterations of FLAIRR-seq will include primer
467 optimization to facilitate better sequence coverage in the 3' regions of the IGHC alleles and
468 improve the direct genotyping capabilities of the FLAIRR-seq method.

469 Previous studies have demonstrated the use of IGHJ6 heterozygosity to infer haplotypes
470 of V and D genes from AIRR-seq data (46, 50). However, the frequency of IGHJ6 heterozygotes
471 in the population can vary. Therefore, we wanted to assess the utility of leveraging IGHC
472 polymorphism resolved by FLAIRR-seq for haplotyping IGHV alleles with the publicly available
473 tool RAbHIT(46, 50, 51). We selected a single donor ("1013") from our cohort that was
474 heterozygous for both IGHJ6 (*02 and *03) and IGHM (FL_2 and FL_4). Importantly, we were
475 able to associate each IGHJ6 allele to the respective IGHM allele from the corresponding
476 haplotype (Figure 3E). After defining germline IGHV alleles using TIgGER (31), we generated and
477 compared IGHV haplotype inferences using either IGHJ6 or IGHM alleles as anchor genes using
478 RAbHIT (47)(Figure 3E). Although some allele assignments were ambiguous ("unknown") using
479 both methods, we observed a strong consensus between haplotype inferences using the two

480 anchor genes. For haplotype 1, represented by IGHJ6*03 and IGHM_FL_4, the IGHJ6*03-derived
481 haplotype had 35 IGHV genes for which either an allele or deletion call was made. When using
482 IGHM_FL_4, the same allele/deletion calls were made for 33 of these genes; in addition, using
483 IGHM as the anchor gene, assignments were made for an additional 5 IGHV genes that had
484 "unknown" designations using IGHJ6. Similarly, of the allele/deletion calls made for 36 IGHV
485 genes on haplotype 2 assigned to IGHJ6*02, 33 of these gene had identical assignments to
486 IGHM_FL_2. Together these results indicate that IGHC variants can be utilized for haplotype
487 inference from repertoire data when commonly used IGHJ or IGHD genes are homozygous in
488 individuals of interest.

489 **FLAIRR-seq enables isotype-, subisotype-, and allele-specific repertoire analyses**

490 IGHG and IGHM alleles identified in each sample were used to annotate reads in each
491 respective repertoire. These assignments allowed for partitioning of the repertoire by isotype,
492 subisotype and IGHC allele (Figure 4). To demonstrate this, we utilized the same represtentative
493 sample ("1013") that was heterozygous for all IGHC genes. As shown in Figure 4A, IGHC gene
494 assignments allow for subisotype and allele level frequencies to be estimated as a proportion of
495 the overall IgG and IgM repertoires. In addition, detailed analyses of the repertoire can be
496 conducted within each of these compartments. For example, Figure 4B shows the frequencies of
497 IGHV gene subfamilies for each IGHG and IGHM allele identified in this sample. Using standard
498 AIRR-seq analyses, we would not be able to identify allele-resolved V gene usage or enrichment
499 within subisotype populations, which is important for linking subisotype functionality to particular
500 antigen-specific VDJ clones.

501 Through the partitioning of repertoire sequences by subisotype and IGHC allele, we found
502 that FLAIRR-seq also allowed for trends to be assessed in aggregate across donors. To
503 demonstrate this, we further examined V gene family usage partitioned by IgG subisotype across
504 all 10 healthy donors. This analysis revealed expected patterns, in that IGHV1, IGHV3 and IGHV4

505 subfamily genes were dominant across the 4 subisotypes (Figure 4C). However, we did observe
506 significant variation in subfamily proportions between subisotypes, associated with distinct
507 profiles in specific subisotypes (Figure 4C). Specifically, the estimated frequencies of IGHV1 and
508 IGHV3 were statistically different between subisotypes ($P<0.01$, ANOVA); IGHV1 usage was
509 elevated in IGHG1 and IGHG4, whereas IGHV3 was elevated in IGHG2 and IGHG3. These
510 analyses demonstrate the unique capability of FLAIRR-seq to examine variation in the expressed
511 repertoire at the level of isotype, subisotype, and IGHC allele. As samples sizes increase, we
512 expect that a multitude of additional repertoire features will become accessible to this kind of
513 analysis leading to novel discoveries linking VDJ and IGHC genetic signatures.

514 **FLAIRR-seq identifies subisotype-specific clonal expansion and CSR in longitudinal**
515 **samples.**

516 We wanted to investigate the utility of FLAIRR-seq in clinical samples, particularly to
517 observe changes in immune repertoires over time. Ab responses are highly dynamic, with specific
518 Ab clones expanding upon activation by antigen. We were interested to know if class switch
519 recombination could be captured by FLAIRR-seq, given the capability to identify clones with the
520 subisotype resolved. We had the opportunity to evaluate FLAIRR-seq resolved repertoires over
521 time in four samples collected from one individual over their >13-day hospitalization for severe
522 COVID-19 disease. Blood draws were taken on days 1, 4, 8, and 13 post-hospitalization (Figure
523 5A) and analyzed with FLAIRR-seq across all time points. After initial FLAIRR-seq processing
524 and analysis, we defined unique clones using SCOPer, which clusters sequences based on CDR3
525 similarity and mutations in IGHV and IGHJ genes (34). This analysis allowed for the estimation of
526 subisotype-specific clone counts across the four timepoints examined. Overall, we observed IgG1
527 dominated the repertoire at all four time points, but the proportion of subisotypes fluctuated over
528 time (Figure 5B). Specifically, the IGHG2 and IGHG3-specific repertoires expanded from day 1 to
529 day 4, but then contracted in overall frequency from day 8 to day 13 (Figure 5B). To assess clonal

530 diversity within each subisotype repertoire across time, we calculated the Simpson's diversity
531 index (q=2) using Alakazam (31). All subisotype-specific repertoires became less diverse from
532 day 1 to day 4, suggesting clonal expansion across the IGHG repertoire (Figure 5C). To note,
533 IGHG4 was not included in diversity calculations because IGHG4 would have required higher
534 sequencing depth to ascertain diversity, given the overall lower expression of IgG4 transcripts in
535 this individual. Subisotype-specific repertoire polarity was also assessed by calculating the
536 fraction of clones needed to represent 80% of the total repertoire (Figure 5D), with lower fractions
537 representing more polarized and clonally expended repertoires. Results of this analysis were
538 consistent with the diversity index, demonstrating an increase in clonal expansion (i.e., decreased
539 polarity) at day 4 across IGHG1, IGHG2, and IGHG3 compartments, which returned to baseline
540 at later timepoints.

541 CSR mediates the switching of Abs from one sub/isotype to another. This occurs through
542 the somatic recombination of IGHC genes, which brings the switched/selected IGHC genes
543 adjacent to the recombined IGHV, IGHD, and IGHJ segments, facilitating transcription. The
544 switching of isotypes and subisotypes can result in changes to associated effector functions of
545 the Ab while maintaining antigen-specific variable regions. Given the ability of FLAIRR-seq to
546 resolve clones with subisotype and IGHC allele resolution, as proof-of-concept, we sought to
547 assess whether FLAIRR-seq could allow for more detailed haplotype-level analysis of CSR
548 through the course of infection. To do this, we identified the largest clones in our dataset that were
549 both represented by multiple isotypes and found across timepoints. In total, using SCOper (34),
550 we identified 19 unique clonal lineages that met this criteria. We focused our detailed analysis on
551 one of the largest clones, "9900" (Figure 5E), comprising IGHM, IGHG1, and IGHG2 sequences.
552 On day 1 post-hospitalization, clone 9900 sequences were represented by both IGHM and
553 IGHG2. At day 4, IGHG2 was the only isotype observed, whereas again at day 8, both IGHM and
554 IGHG2 were observed, as well as IGHG1. To visualize CSR, we built a phylogeny using Dowser

555 (36). Highlighted in the red box on the phylogenetic tree shown in Figure 5F, we observe a single
556 subclade that is represented by IGHM, IGHG1, and IGHG2.

557 We were also able to resolve IGHC alleles from this individual, with the exception of
558 IGHG1 alleles which were ambiguous. Critically, both IGHG1 and IGHG2 were heterozygous
559 (Figure 5G). Through the assignment IGHG alleles to haplotypes within this individual using
560 heterozygous V genes (IGHV3-7 and IGHV3-48), we were able to determine that sequences from
561 clone 9900 (Figure 5F) utilized IGHG1 and IGHG2 alleles from the same haplotype, associated
562 with IGHV3-7*07 and IGHV3-48*03 (31). This observation offers direct characterization of CSR
563 events occurring on the same chromosome. When we looked across the remaining clones (n=8)
564 in this dataset that spanned time points and were represented by IGHG1 and IGHG2 subisotypes,
565 we were able to confirm that all of these clones used IGHG alleles from the same haplotype.

566 Together, these data provide demonstrative proof-of-concept evidence that FLAIRR-seq
567 profiling performs robustly on clinical samples, including RNA directly extracted from whole blood.
568 In addition, these data provide novel repertoire resolution extending what would have been
569 possible with standard AIRR-seq methods, including analysis of subisotype-specific repertories,
570 evaluation of clonal expansion, and characterization of CSR in the IgG and IgM repertoires.

571 **Discussion**

572 Here we present the development, validation, and application of FLAIRR-seq, a novel
573 method to resolve near full-length Ab transcripts from bulk PBMC-, isolated B cell- and whole
574 blood-derived total RNA. FLAIRR-seq enables highly accurate, simultaneous resolution of
575 variable and constant regions and suggests that IGHC polymorphism is far more extensive than
576 previously assumed. FLAIRR-seq performed equivalent to or with increased resolution compared
577 to existing standard 5'RACE AIRR-seq methods when resolving V, D, and J gene calls, CDR3
578 lengths, and SHM signatures, suggesting that our CH3/CH4 targeting strategies did not
579 compromise variable region characterization while simultaneously adding the capability to resolve

580 IGHC variation. Little to no primer bias was observed when compared to Ab repertoire profiling
581 from total mRNA Iso-seq methods. FLAIRR-seq provides the novel ability to use IGHC gene
582 usage to identify subisotypes and genotype heavy chain transcripts, linking these data back to
583 evaluate subisotype-specific repertoires, clonal expansion, and CSR. Underscoring the
584 underappreciated extent of IGHC variation, our profiling of a restricted cohort of only 10 individuals
585 from relatively homogenous backgrounds still identified 4 and 7 completely novel IGHC alleles in
586 IgM and IgG, respectively, and extended an additional 17 alleles beyond which had been available
587 in the IMGT database.

588 The unique capabilities of FLAIRR-seq will allow for novel examination of Ab repertoires,
589 including the characterization of variable gene usage and clonotype distribution within unique
590 subisotype subsets. This perspective has the potential to provide key insights into dynamic Ab
591 responses in diseases known to be mediated by subisotype-specific processes or have skewed
592 subisotype distribution as predictive markers of disease, including Myasthenia gravis (mediated
593 by pathogenic autoantibodies across subisotypes that give rise to varied disease pathologies),
594 Acute Rheumatic Fever (associated with elevated IgG3), and melanoma (skewing towards IgG4
595 in late-stage disease thought to be indicative of tolerogenic responses and poor prognosis)(12-
596 14). These subisotype-specific repertoire profiling approaches may be the first step toward
597 identification of unique clones that mediate disease pathogenicity or serve as high-resolution
598 biomarkers to disease progression, as well as open the door for potential functional experiments
599 on subisotype clones of interest, including examining the functional impact of the novel IGHC
600 alleles identified here. Expanded population-based FLAIRR-seq profiling and curation of novel
601 IGHC alleles, particularly in conjunction with IGenotyper targeted genomic assembly efforts in
602 IGH, will be a significant first step in defining the full extent of variation in a region too long
603 assumed to be relatively invariant.

604 The Fc region is known to be critical for modulating differential Ab effector functions. These
605 differential functionalities are currently understood to be regulated by differential posttranslational
606 modifications, such as variable glycosylation (52-55). Future FLAIRR-seq profiling will be a
607 valuable tool to investigate how genomic variation across IGHC genes impacts residue usage
608 and resultant Fc receptor binding, signaling potential, crosslinking, and potential for
609 posttranslational modification, all of which would be expected to alter downstream effector
610 functions, such as ADCC, ADCP, and complement fixation.

611 We further demonstrate that FLAIRR-seq can effectively examine clonal expansion and
612 CSR in longitudinal samples, demonstrating the feasibility of using FLAIRR-seq to resolve Ab
613 repertoire dynamics. This increased resolution will further our understanding of Ab repertoire
614 evolution in the transition of acute to chronic disease states, many of which are associated with
615 overall IgG subisotype distribution changes that are thought to reflect the inflammatory milieu (14,
616 56). One example is advanced melanoma, where late-stage disease is characterized by elevated
617 IgG4 compared to IgG1, which is believed to reflect a more tolerizing, pro-tumor environment (12).
618 FLAIRR-seq examination of these samples may identify specific repertoire distribution patterns
619 that could act as biomarkers of disease progression. Moving forward it is critical to account for all
620 variability within the Ab repertoire for the most comprehensive understanding of repertoire
621 dynamics and the myriad factors impacting Ab effector function. Future efforts will expand
622 FLAIRR-seq methods to target IGHA and IGHE repertoires, as well as implement multiplexed
623 arrays (MAS) sequencing to considerably increase throughput and lower cost (48). Together, the
624 data presented here demonstrate that the FLAIRR-seq method provides a comprehensive
625 characterization of allele-resolved IgG and IgM repertoires, detailing variable region gene usage
626 and measurements of maturation, isotype and subisotype identification, and the unappreciated
627 extent of constant region variation, which will be necessary to fully appreciate the impact of IG
628 genomic variation in health and disease.

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Figure Legends:

Figure 1. Overview of Ab structure and FLAIRR-seq molecular method. (A) Schematic representation of the IGH locus, heavy chain transcript structure, and functional IG protein. (B) Comparative coverage across the heavy chain transcript of commonly used AIRR-seq methods compared with FLAIRR-seq. (C) FLAIRR-seq molecular pipeline: RNA (brown) was converted to first-strand cDNA (red) using the 5' RACE method, incorporating a 5' TSO-UMI (pink) via template switch. Second strand amplification specifically targeted IgG and IgM molecules through priming of the 5' TSO-UMI and the 3' constant region IGH exon 3 (CH3) for IgG, or CH4 for IgM. A 16bp barcode was incorporated into the 3' CH3/CH4 primers to enable sample multiplexing post-amplification. (D) IGV screenshot showing near full-length single molecule structure of IGHG4 FLAIRR-seq transcripts.

Figure 2. FLAIRR-seq shows robust characterization of V, D, and J genes. (A) Spearman ranked correlations and p-values of V, D, and J gene usage frequencies identified by FLAIRR-seq performed on matched total PBMC and purified B cells. (B) Heatmap of Spearman ranked correlations and p-values of V, D and J gene usage frequencies between FLAIRR-seq and AIRR-seq processed samples. (C) Boxplots of somatic hypermutation frequencies defined by FLAIRR-seq or AIRR-seq in IgM- and IgG-specific repertoires. (D) Boxplots of CDR3 length defined by FLAIRR-seq or AIRR-seq analysis in both IgM- and IgG-specific repertoires. (E) Spearman ranked correlation of V, D, and J gene usage frequencies between FLAIRR-seq-based and Iso-

654 Seq-based repertoire profiling. Significant differences between FLAIRR-seq and AIRR-seq data
655 indicated by * ($p < 0.05$) or ** ($p < 0.01$).

656 **Figure 3. FLAIRR-seq provides novel IGHC resolution for allelic discovery and allows**
657 **variable gene haplotyping.** (A) Overview of experimental design and pipeline overviews of
658 genotyping by IGenotyper (gDNA) and FLAIRR-seq (RNA). (B) Schematic depicting IGHC alleles
659 identified by IGenotyper, partitioned by identification as (i) exact matches to documented IMGT
660 alleles, (ii) novel alleles that are not in IMGT, or (iii) extended alleles. (C) Pie chart and stacked
661 bar graph representing the total number of alleles and fraction of each category identified per
662 IGHC gene as identified by either IGenotyper or FLAIRR-seq. Bar charts showing number of
663 IGHC alleles from FLAIRR-seq that were resolved, ambiguous or unresolved when compared to
664 IGenotyper alleles. * Indicates additional allele found due to IGHG4 duplication. (D) Table
665 summarizing novel and extended alleles resolved by IGenotyper data. Extended alleles are
666 denoted by *(allele number)-FL and novel alleles are denoted by FL_(number) alleles resolved
667 by FLAIRR-seq are marked with a dot (•). (E) Venn diagrams showing number of IGHV haplotype
668 allele/deletion calls when using IGHJ6 or IGHM anchors for each haplotype. Tile plots showing
669 IGHV gene haplotypes inferred using either IGHJ6 anchors or IGHM anchors for one sample.
670 Dark gray represents a deletion (DEL), off-white a non-reliable allele annotation (NRA), and light
671 gray represents an unknown allele (Unk). Non-reliable alleles are annotated with an asterisk (*).

672 **Figure 4. FLAIRR-seq resolves subisotype specific repertoire diversity.** (A) Bar plots
673 showing distribution of unique VDJ sequences across isotypes, subisotypes, and subisotype
674 alleles in one representative sample, 1013, characterized by FLAIRR-seq. (B) Circos plots
675 showing V family gene usage frequency within each subisotype allele for sample 1013. (C)
676 Boxplots of V gene family usage frequencies within IGHG1, IGHG2, IGHG3, and IGHG4
677 repertoires across all ten individuals. (D) Principal component analysis of V gene family usage by
678 subisotype; plot includes the first two principal components, and individual repertoires are colored

679 by IGHG subisotype. (E) Boxplots showing sequence frequency of IGHV1 and IGHV3 family
680 genes by subisotype across all 10 samples.

681 **Figure 5. FLAIRR-seq resolves subisotype-specific clonal expansion and facilitates**
682 **haplotype analysis of CSR in a patient hospitalized for COVID-19.** (A) Overview of
683 experimental design: whole blood-derived RNA was collected on days 1, 4, 8 and 13 post-
684 hospitalization and used for FLAIRR-seq profiling. (B) Bar plot showing the percentage of clones
685 represented by each subisotype across timepoints. (C) Simpson's diversity index (q=2) for all
686 clones in each subisotype across four timepoints; IgG4 not included due to low sequence counts.
687 (D) Polarity, or the fraction of clones needed to comprise 80% of the repertoire, reported as
688 fraction of total subisotype-specific repertoires across time. (E) Distribution of a single clone
689 "9900" across isotypes and subisotypes over time, suggesting CSR of this clone. (F) Phylogenetic
690 tree constructed from sequences/members of clone 9900, with the inferred germline sequence
691 as the outgroup (star). Shapes and colors of tips (sequences) indicate time point and
692 isotype/subisotype. The scale bar represents the number of mutations between each node in the
693 tree. The subclade within the red box is represented by multiple time points and subisotypes,
694 providing evidence of CSR. (G) Tile plot showing the assignment of IGHC alleles to their
695 respective haplotypes, based on the frequency of observations in which each IGHC allele was
696 linked to each respective allele of heterozygous V genes, IGHV3-7 and IGHV3-48; light gray
697 denotes IGHC alleles for which haplotype assignment was not possible. Analysis of sequences
698 in (F) revealed that the IGHG1 and IGHG2 alleles represented in the phylogeny came from the
699 same haplotype (IGHG1*02/*07, IGHG2*08, IGHM_FL_2).
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912

Table 1: Comparative analysis metrics between AIRR-seq and FLAIRR-seq on matched samples

Sample ID	Isotype	Method	RNA input (ng)	Input reads into Immcantation[a]	Post assembly /Single reads[b]	Unique VDJc	Unique Clones[d]	Unique CDR3[e]
0007	IgG	AIRR	100	**841627**	15217	3164	1008	1187
		FLAIRR	335	181109	17881	4880	1358	1520
201c	IgG	AIRR	100	**1509063**	25015	4568	1221	1371
		FLAIRR	296	221301	36053	10819	2145	2388
203c	IgG	AIRR	100	**1006965**	23085	5793	1436	1705
		FLAIRR	106	475703	14923	3778	993	1138
602c	IgG	AIRR	100	**1275902**	38078	7736	1542	2217
		FLAIRR	149	344906	33903	9225	1828	2357
705c	IgG	AIRR	100	**1113660**	15358	1362	557	576
		FLAIRR	268	279601	18627	2328	1063	1081
1008	IgG	AIRR	100	**1310350**	56848	12217	3005	3307
		FLAIRR	335	238820	57020	18235	3505	3813
1013	IgG	AIRR	100	**1158222**	25250	5027	1795	1964
		FLAIRR	222	396322	27871	7487	2565	2744
2008	IgG	AIRR	100	**835928**	21681	3900	1235	1368
		FLAIRR	240	418906	16441	4258	1308	1380
4002	IgG	AIRR	100	**632272**	8949	1112	727	772
		FLAIRR	335	398838	19692	5377	1719	1887
5001	IgG	AIRR	100	**695884**	13930	1885	1134	1244
		FLAIRR	335	313843	42845	12146	2226	2381
0007	IgM	AIRR	100	**841627**	12777	9154	7924	8163
		FLAIRR	335	331380	46384	14926	12367	12851
201c	IgM	AIRR	100	**1509063**	26850	17888	14281	14622
		FLAIRR	296	148355	98069	12803	9353	9573
203c	IgM	AIRR	100	**1006965**	24623	18189	16295	16629
		FLAIRR	106	509536	37527	10636	9315	9419
602c	IgM	AIRR	100	**1275902**	12306	8378	7704	7833
		FLAIRR	149	273103	48897	16406	14495	14745
705c	IgM	AIRR	100	**1113660**	19484	14273	12936	13413
		FLAIRR	268	435391	79251	17417	15706	16249
1008	IgM	AIRR	100	**1310350**	20264	12710	7878	8368
		FLAIRR	335	181063	47531	15284	8745	9276
1013	IgM	AIRR	100	**1158222**	12769	9012	8057	8241
		FLAIRR	222	262617	52508	17812	15291	15759
2008	IgM	AIRR	100	**835928**	11608	8551	5838	6206
		FLAIRR	240	502354	47596	14132	10225	10674
4002	IgM	AIRR	100	**632272**	18411	11607	11184	11367
		FLAIRR	335	489287	91732	22379	19000	21532
5001	IgM	FLAIRR	335	**313843**	10018	12146	2226	2381
		FLAIRR	355	171688	18944	6164	4866	5011

([a]) AIRR-seq data reflects total number of un assembled paired end reads (R1+R2) (bold) used as input into analyses.
([b]) Counts of paired reads assembled (R1+R2) in AIRR-seq and single molecules in FLAIRR-seq
([c]) Counts of unique sequences after Immcantation annotation
([d]) Counts of unique clones after clonal clustering
([e]) Counts of sequences containing unique CDR3 sequences

FIGURE 1.

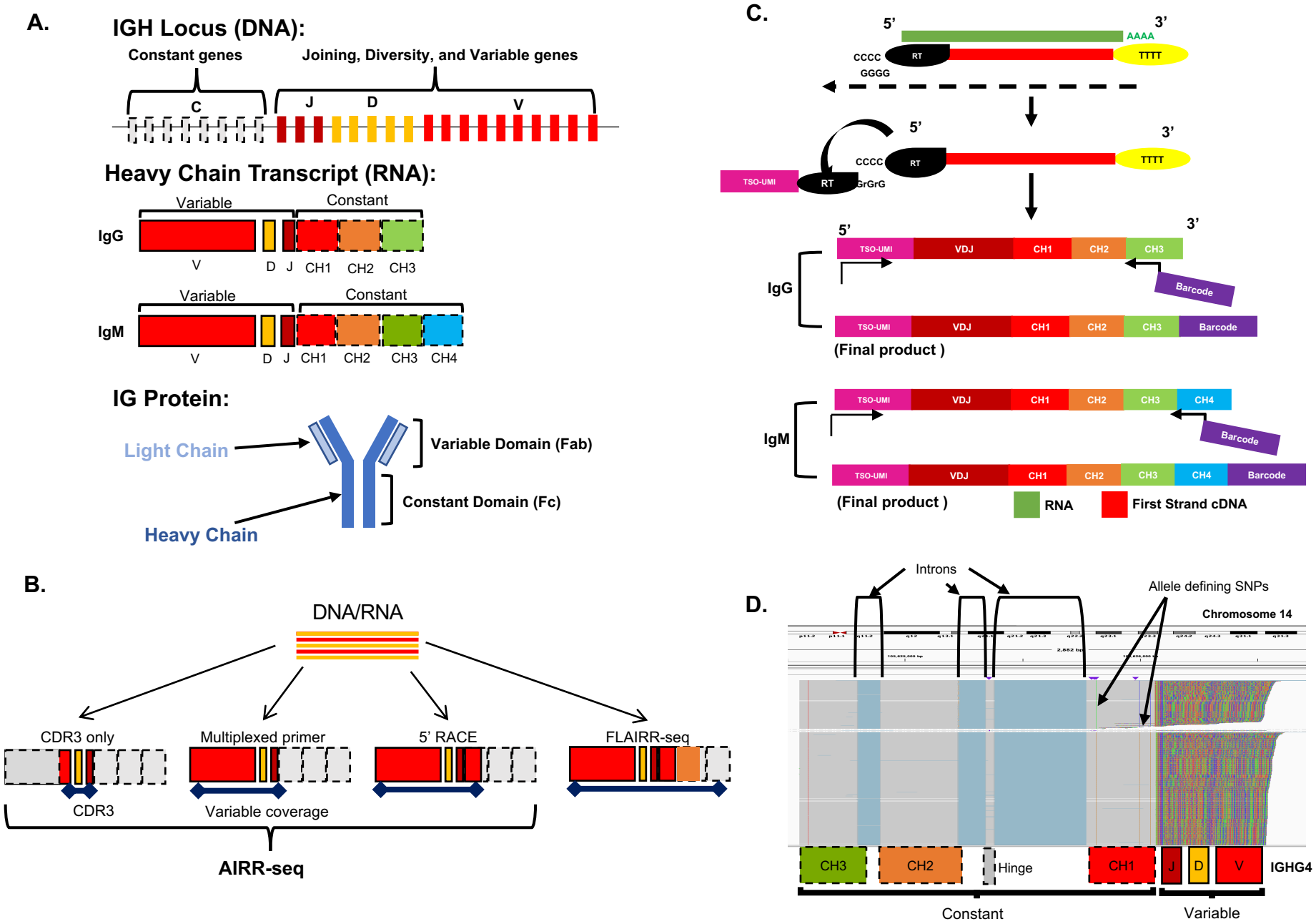

A.
IGH Locus (DNA):
Constant genes
Joining, Diversity, and Variable genes
C
J
D
V
Heavy Chain Transcript (RNA):
Variable
Constant
IgG
V
D
J
CH1
CH2
CH3
Variable
Constant
IgM
V
D
J
CH1
CH2
CH3
CH4
IG Protein:
Light Chain
Variable Domain (Fab)
Constant Domain (Fc)
Heavy Chain
B.
DNA/RNA
CDR3 only
Multiplexed primer
5' RACE
FLAIRR-seq
CDR3
Variable coverage
AIRR-seq
C.
5'
3'
AAAA
CCCC
GGGG
RT
TTTT
TSO-UMI
GrGrG
VDJ
CH1
CH2
CH3
CH4
Barcode
IgG
IgM
(Final product)
RNA
First Strand cDNA
D.
Introns
Allele defining SNPs
Chromosome 14
CH3
CH2
Hinge
CH1
J
D
V
IGHG4
Constant
Variable

FIGURE 2.

A.

IgG BC vs. PBMC FLAIRR-seq

	V		D		J	
	r	p	r	p	r	p
1008	0.95	2.2e−16	0.95	2.2e−16	1.00	0.0028
0007	0.95	2.2e−16	0.95	4.1e−16	0.94	0.017
4002	0.95	2.2e−16	0.98	2.2e−16	0.89	0.033
705c	0.90	2.2e−16	0.97	2.2e−16	0.94	0.017

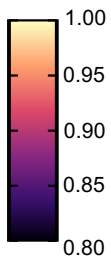
B.

IgM

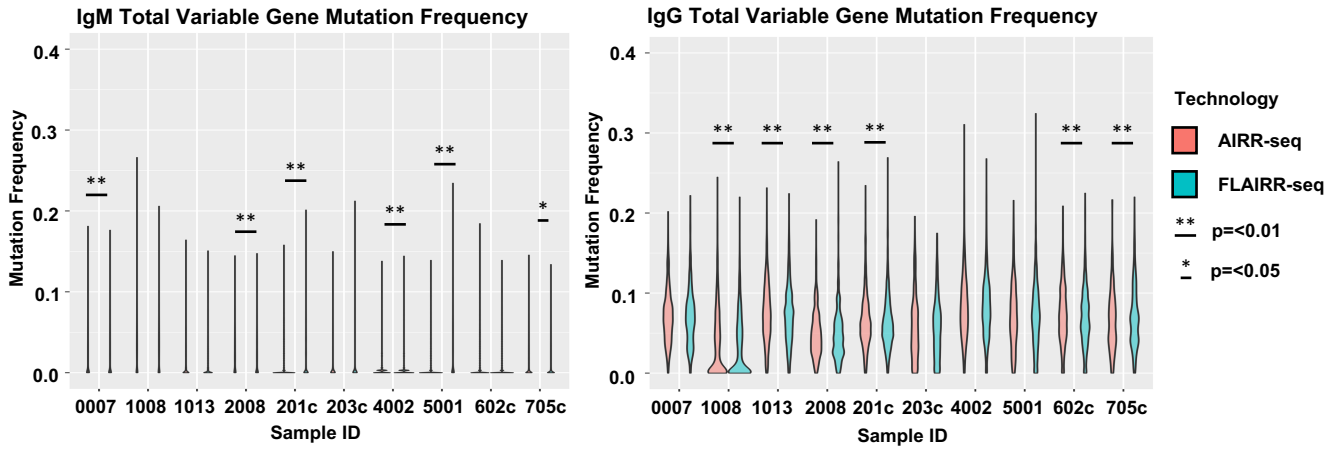
	V		D		J	
	r	p	r	p	r	p
0007	0.94	<2.2e-16	0.99	<2.2e-16	1.00	0.0028
201c	0.97	<2.2e-16	0.98	<2.2e-16	1.00	0.0028
203c	0.93	<2.2e-16	0.99	<2.2e-16	0.94	0.017
602c	0.96	<2.2e-16	0.99	<2.2e-16	1.00	0.0028
705c	0.95	<2.2e-16	0.99	<2.2e-16	0.94	0.017
1008	0.94	<2.2e-16	0.98	<2.2e-16	0.94	0.017
1013	0.96	<2.2e-16	0.99	<2.2e-16	0.94	0.017
2008	0.94	<2.2e-16	0.99	<2.2e-16	1.00	0.0028
4002	0.96	<2.2e-16	0.99	<2.2e-16	1.00	0.0028
5001	0.94	<2.2e-16	0.98	<2.2e-16	1.00	0.0028

IgG

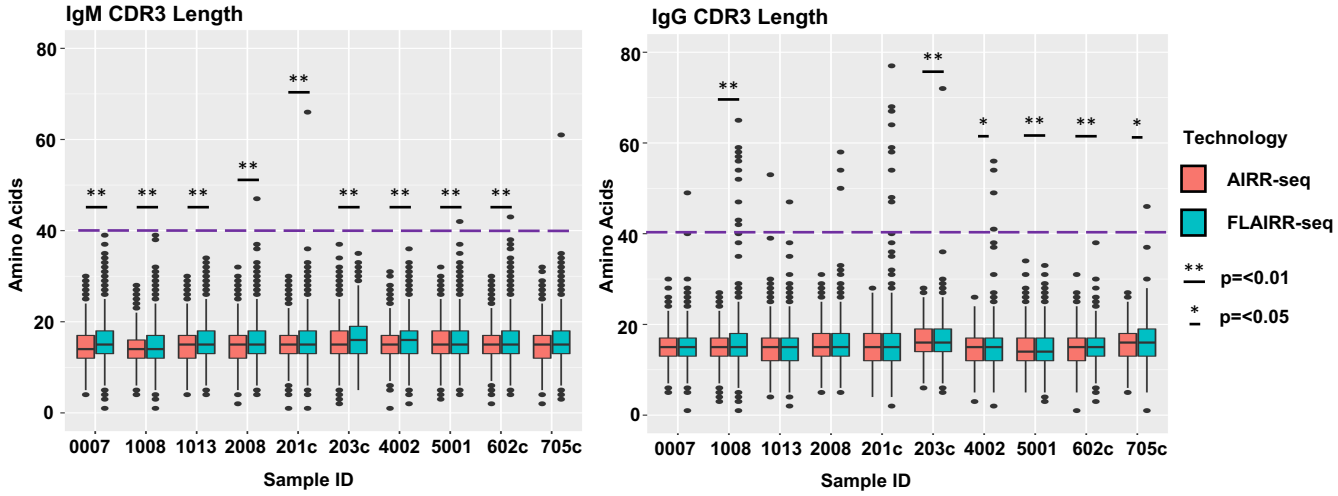
	V		D		J	
	r	p	r	p	r	p
0007	0.93	<2.2e-16	0.94	1.6e-15	0.94	0.017
201c	0.96	<2.2e-16	0.96	<2.2e-16	0.89	0.033
203c	0.91	<2.2e-16	0.93	1.9e-14	0.94	0.017
602c	0.93	<2.2e-16	0.97	<2.2e-16	1.00	0.0028
705c	0.90	<2.2e-16	0.87	3.2e-10	1.00	0.0028
1008	0.95	<2.2e-16	0.99	<2.2e-16	1.00	0.0028
1013	0.95	<2.2e-16	0.95	<2.2e-16	0.89	0.033
2008	0.95	<2.2e-16	0.97	<2.2e-16	0.94	0.017
4002	0.95	<2.2e-16	0.93	6.1e-14	0.93	0.0077
5001	0.95	<2.2e-16	0.95	3.8e-16	1.00	0.0028



C.



D.



E.

Iso-seq vs. FLAIRR-seq

	V		D		J	
	r	p	r	p	r	p
Sorted B cells	0.94	<2.2e-16	0.92	1.4e-13	1.00	0.0028

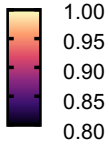


FIGURE 3.

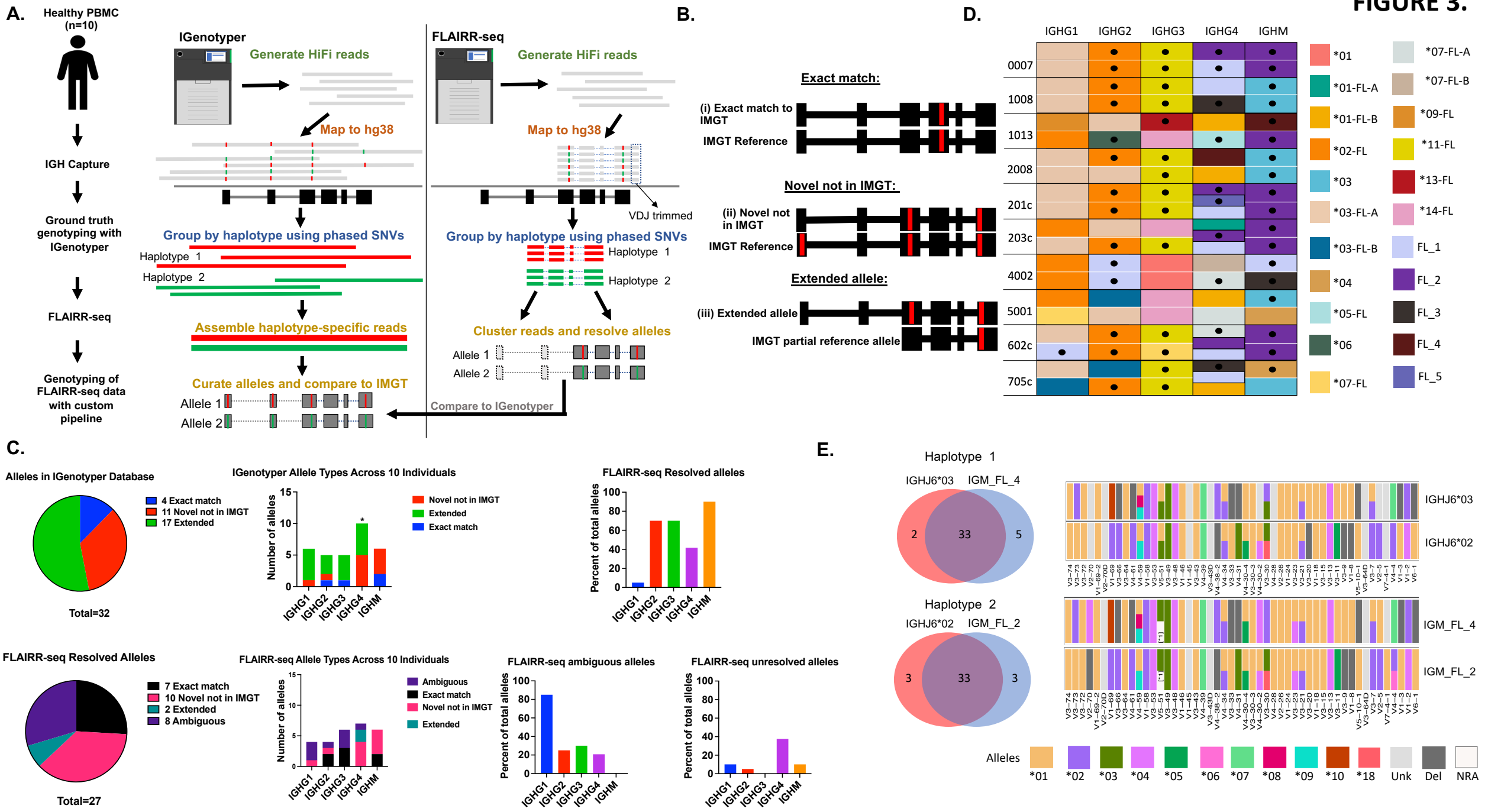

A.
Healthy PBMC (n=10)
IGH Capture
Ground truth genotyping with IGenotyper
FLAIRR-seq
Genotyping of FLAIRR-seq data with custom pipeline
IGenotyper
Generate HiFi reads
Map to hg38
Group by haplotype using phased SNVs
Haplotype 1
Haplotype 2
Assemble haplotype-specific reads
Curate alleles and compare to IMGT
Allele 1
Allele 2
FLAIRR-seq
Generate HiFi reads
Map to hg38
VDJ trimmed
Group by haplotype using phased SNVs
Haplotype 1
Haplotype 2
Cluster reads and resolve alleles
Allele 1
Allele 2
Compare to IGenotyper
B.
Exact match:
(i) Exact match to IMGT
IMGT Reference
Novel not in IMGT:
(ii) Novel not in IMGT
IMGT Reference
Extended allele:
(iii) Extended allele
IMGT partial reference allele
D.
IGHG1
IGHG2
IGHG3
IGHG4
IGHM
0007
1008
1013
2008
201c
203c
4002
5001
602c
705c
*01
*01-FL-A
*01-FL-B
*02-FL
*03
*03-FL-A
*03-FL-B
*04
*05-FL
*06
*07-FL
*07-FL-A
*07-FL-B
*09-FL
*11-FL
*13-FL
*14-FL
FL_1
FL_2
FL_3
FL_4
FL_5
C.
Alleles in IGenotyper Database
4 Exact match
11 Novel not in IMGT
17 Extended
Total=32
IGenotyper Allele Types Across 10 Individuals
Number of alleles
Novel not in IMGT
Extended
Exact match
IGHG1
IGHG2
IGHG3
IGHG4
IGHM
FLAIRR-seq Resolved alleles
Percent of total alleles
FLAIRR-seq Resolved Alleles
7 Exact match
10 Novel not in IMGT
2 Extended
8 Ambiguous
Total=27
FLAIRR-seq Allele Types Across 10 Individuals
Ambiguous
Exact match
Novel not in IMGT
Extended
FLAIRR-seq ambiguous alleles
FLAIRR-seq unresolved alleles
E.
Haplotype 1
IGHJ6*03
IGM_FL_4
2
33
5
Haplotype 2
IGHJ6*02
IGM_FL_2
3
33
3
IGHJ6*03
IGHJ6*02
IGM_FL_4
IGM_FL_2
Alleles
*01
*02
*03
*04
*05
*06
*07
*08
*09
*10
*18
Unk
Del
NRA

FIGURE 4.

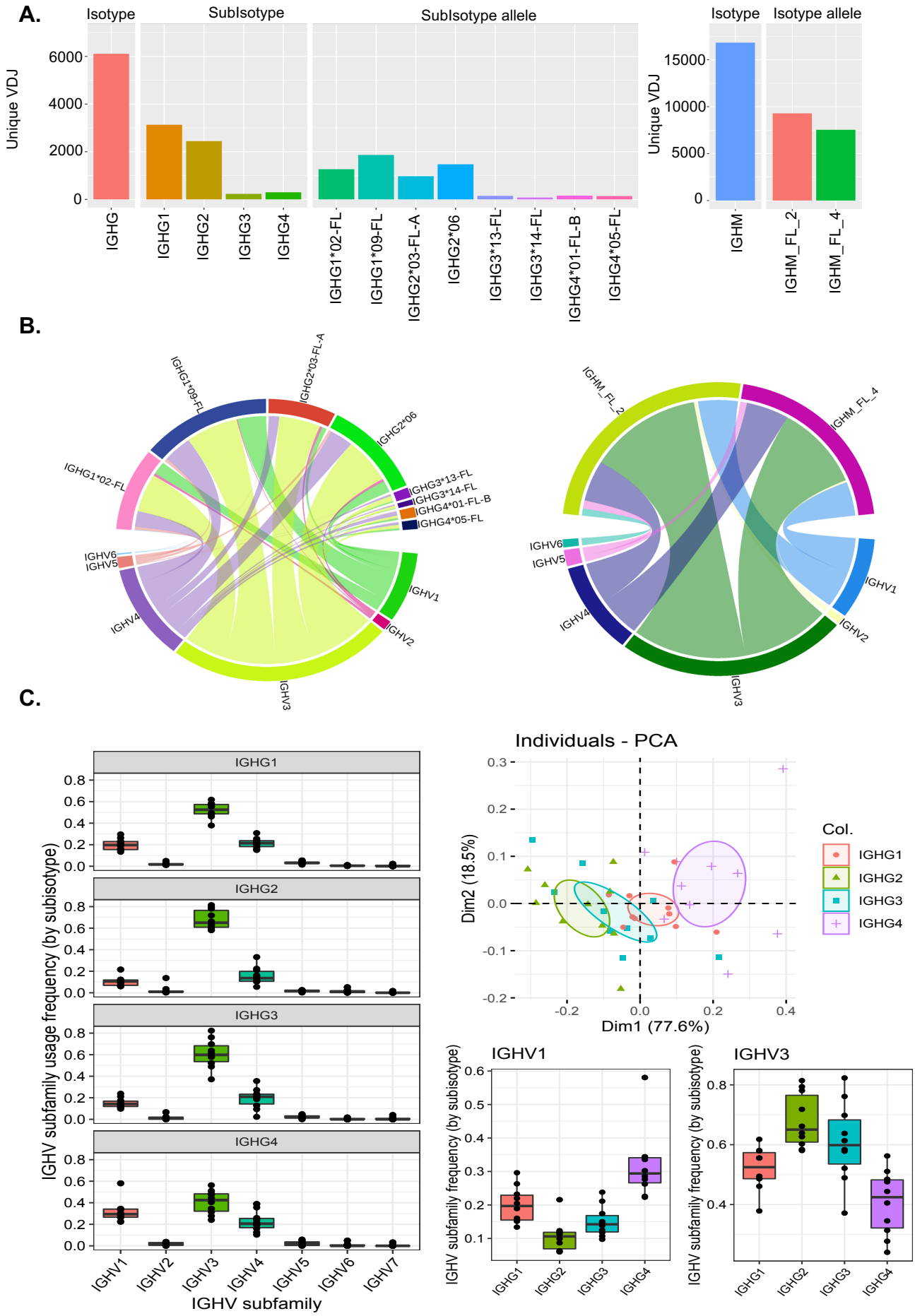
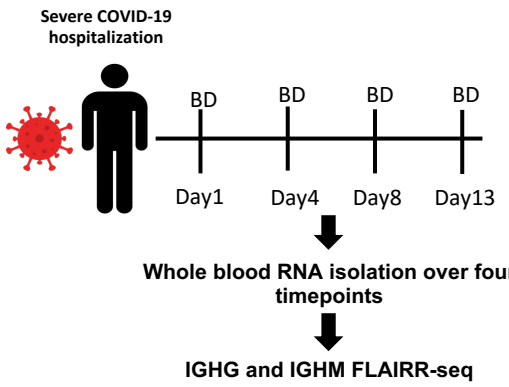
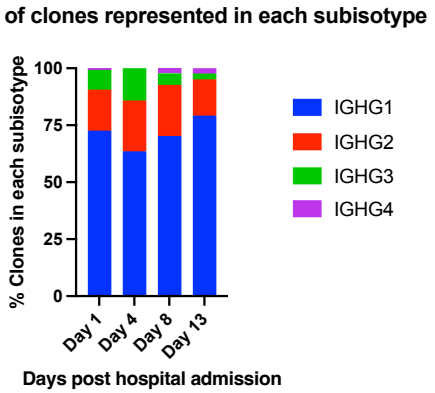
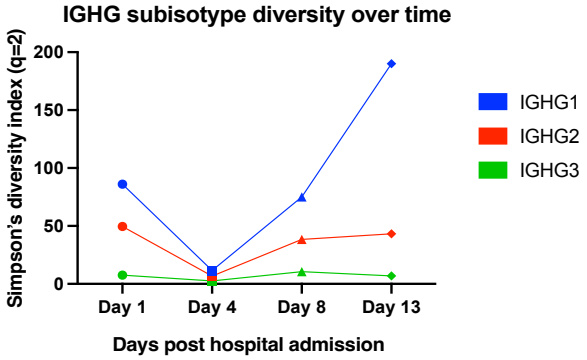
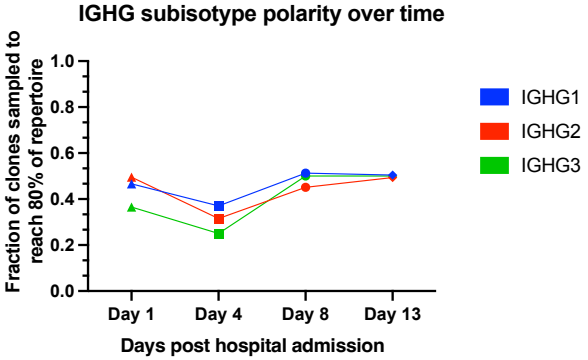

A.
Isotype
SubIsotype
SubIsotype allele
Isotype
Isotype allele
Unique VDJ
IGHG
IGHG1
IGHG2
IGHG3
IGHG4
IGHG1*02-FL
IGHG1*09-FL
IGHG2*03-FL-A
IGHG2*06
IGHG3*13-FL
IGHG3*14-FL
IGHG4*01-FL-B
IGHG4*05-FL
IGHM
IGHM_FL_2
IGHM_FL_4
B.
C.
IGHV subfamily usage frequency (by subisotype)
IGHV subfamily
IGHV1
IGHV2
IGHV3
IGHV4
IGHV5
IGHV6
IGHV7
Individuals - PCA
Dim1 (77.6%)
Dim2 (18.5%)
Col.
IGHV subfamily frequency (by subisotype)

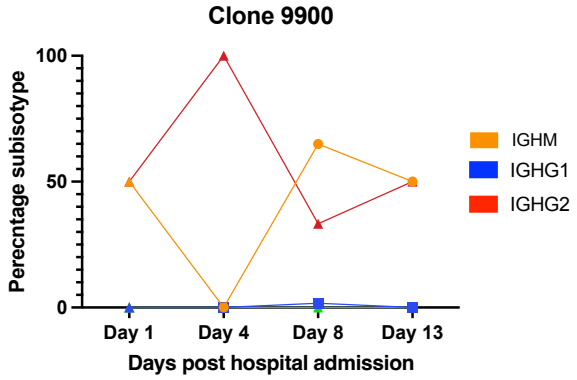
FIGURE 5.

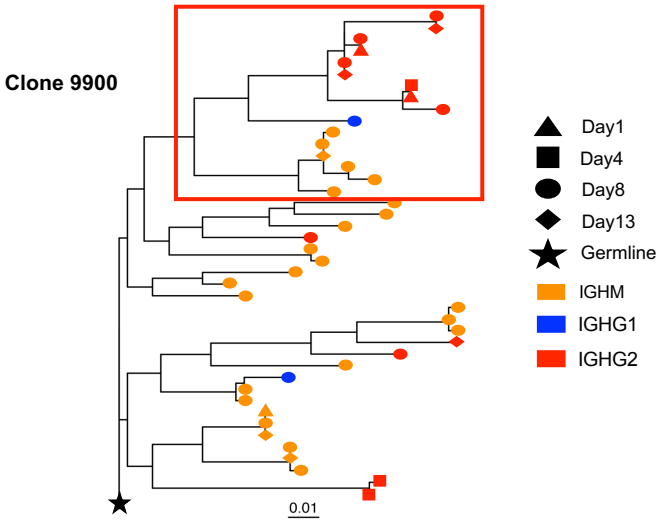

A.
Severe COVID-19 hospitalization
BD
BD
BD
BD
Day1
Day4
Day8
Day13
(Post hospital admission)
Whole blood RNA isolation over four timepoints
IGHG and IGHM FLAIRR-seq

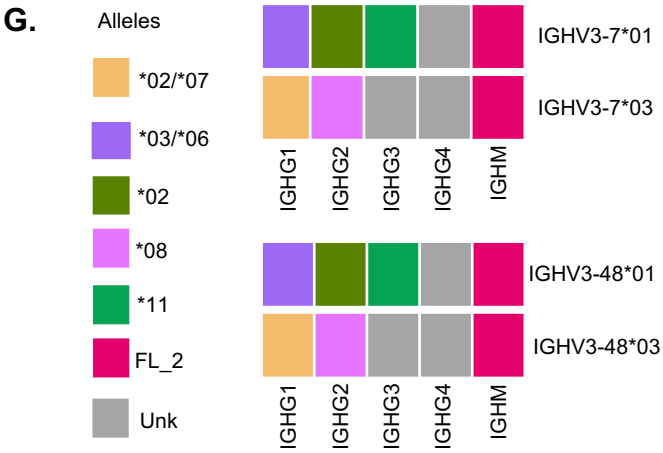

B.
Percentage of clones represented in each subisotype
% Clones in each subisotype
100
75
50
25
0
Day 1
Day 4
Day 8
Day 13
Days post hospital admission
IGHG1
IGHG2
IGHG3
IGHG4


C.
IGHG subisotype diversity over time
Simpson's diversity index (q=2)
200
150
100
50
0
Day 1
Day 4
Day 8
Day 13
Days post hospital admission
IGHG1
IGHG2
IGHG3


D.
IGHG subisotype polarity over time
Fraction of clones sampled to reach 80% of repertoire
1.0
0.8
0.6
0.4
0.2
0.0
Day 1
Day 4
Day 8
Day 13
Days post hospital admission
IGHG1
IGHG2
IGHG3


E.
Clone 9900
Perecntage subisotype
100
50
0
Day 1
Day 4
Day 8
Day 13
Days post hospital admission
IGHM
IGHG1
IGHG2


F.
Clone 9900
0.01
Day1
Day4
Day8
Day13
Germline
IGHM
IGHG1
IGHG2


G.
Alleles
*02/*07
*03/*06
*02
*08
*11
FL_2
Unk
IGHV3-7*01
IGHV3-7*03
IGHV3-48*01
IGHV3-48*03
IGHG1
IGHG2
IGHG3
IGHG4
IGHM