KyDab – a comprehensive database of antibody discovery selection campaigns.

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Abstract

Preclinical antibody discovery relies on progressive screening and down-selection of candidate antibodies from large immune repertoires, yet this critical process is poorly represented in existing public databases. Here we introduce KyDab (Kymouse Antibody Database), a well-curated database of antibody discovery selection data generated using standardized workflows on the Kymouse humanized mouse platform. The current release includes 11 Kymouse platform mice immunisation studies covering 51 immunogens, more than 120,000 paired heavy–light chain sequences, and binding measurements for a selected subset of experimentally characterized clones. By capturing full-funnel selection data with consistent metadata and both positive and negative experimental outcomes, KyDab provides a valuable data resource for the development and evaluation of artificial intelligence models for antibody discovery. KyDab is accessible https://kydab.naturalantibody.com, and the database will be continuously updated as new datasets become available.

Introduction

30 Monoclonal antibodies have emerged as the fastest-growing class of biopharmaceuticals, with over
31 150 antibodies approved by the FDA to date[1] . Due to their superior specificity, potency, and safety
32 profiles, antibody-based therapeutics are widely regarded as leading candidates for treating cancer,
33 immune-mediated disorders, and infectious diseases[2]. In recent years, advances in artificial
34 intelligence have begun to reshape antibody drug discovery workflows. Approaches such as virtual
35 screening, affinity maturation, and generative design are increasingly integrated into early discovery,
36 offering opportunities to accelerate development timelines and reduce costs[3]. These methods,
37 however, rely heavily on large, high-quality datasets with experimentally validated outcomes to
38 enable effective model training and benchmarking[4] .
39
40 To support the growing data needs of AI development, several public resources curate large antibody
41 sequence datasets (e.g., Observed Antibody Space;[5]) and structural annotations (e.g., SAbDab;[6]).
42 While these databases provide broad coverage, they do not capture the real-world process of
43 therapeutic antibody discovery as practiced in an industrial setting. Modern discovery pipelines,
44 including phage display, yeast display and animal immunisation, typically generate large pools of
45 clones, followed by multiple stages of down-selection and affinity characterisation using assays such
46 as surface plasmon resonance (SPR). Existing specialised therapeutic antibody databases, such as
47 Thera-SAbDab[7] and IMGT/mAb-KG[8] , focus primarily on the relatively small set of mature,
48 clinically advanced antibodies. To our knowledge, no public resource currently provides full-funnel
49 datasets that reflect the practical selection and screening steps used in real-world antibody discovery
50 workflows.
51
52 Beyond these limitations in dataset representation, another critical gap concerns the scarcity and bias
53 of affinity-characterized antibodies[9] . This is largely due to several factors - manual curation is labor-
54 intensive, affinity values are often presented only as figures or partial tables, and negative screening
55 data are rarely reported. Even in newer structural resources such as SAAINT-DB, which reviewed
56 nearly 10,000 PDB entries, only ~1,400 non-redundant antibody–antigen affinities were identified[10] .
57 Broader protein interaction databases, including SKEMPI v2.0[11] , AbBind[12] , Affinity Benchmark

58 v5.5[13] and PDBbind v2020[14] , catalog tens of thousands of measurements, but fewer than 2,000
59 involve antibody–antigen complexes. Moreover, because many databases draw on overlapping
60 sources, the same affinity measurements are often repeatedly re-curated across databases rather than
61 newly contributed. This scarcity of affinity-resolved antibody data remains a major bottleneck for AI-
62 driven discovery.
63
64 To begin addressing these challenges, we present KyDab (Kymouse Antibody Database), a
65 comprehensive database of antibody discovery selection datasets. KyDab provides systematically
66 curated antibody sequences with comprehensive metadata and, where available, experimentally
67 measured binding data. All datasets originate from Kymouse[15] , a state-of-the-art humanized mouse
68 platform used for therapeutic antibody discovery. Consistent single-cell processing and standardized
69 data analysis pipelines are applied to minimise technical variability and ensure comparability across
70 campaigns. The current release spans 11 immunisation studies, comprising 51 unique immunogens,
71 and 123,527 productive heavy–light chain pairs, with 1,657 clones associated with binding data. By
72 making such campaign data available, KyDab establishes a resource that acts as a real-world
73 benchmark for general-purpose antibody predictors. As such we expect that the database will foster
74 development of more robust algorithms that can be applied in production in therapeutic programs.
75
76 **Materials and Methods**
77 **Antibody Sequence Data**
78 All antibody sequences deposited in this portal were generated from the Kymouse platform[15 16] , a
79 well-established transgenic mouse system for producing antibodies with fully humanized variable
80 regions. Each dataset is accompanied by a dedicated landing page accessible from the KyDab portal
81 homepage, providing flexible download options as well as detailed information on immunisation, cell
82 sorting, and sequencing protocols for each study. Sequences were initially processed and analyzed
83 internally with an in-house bioinformatics pipeline, and subsequently re-annotated using RIOT[17] prior
84 to deposition in the portal to ensure consistent annotation across datasets and to avoid the release of
85 potentially commercially sensitive information.

86

87 **Assay Data**

88 Where available, following sequence analysis, a subset of clones were selected for expression and

89 affinity testing. The specific assays employed in each study are described in the corresponding

90 publications cited on the individual landing pages.

91

92 **Datasets collection**

93 Summary of datasets are provided in **Table 1**.

94

95 **Table 1. Datasets available in the KyDab portal.**

Studies	Immunogens	Binding Assay	Number of antibodies with binding measurements	Total Paired Antibody Sequences
Pertussis	Pertussis toxin WT; Pertussis Toxin R9K E129A mutant	SPR	422	11290
Malaria CSP #1	CSP-based immunogens	SPR	124[a]	18146
Malaria CSP #2	CSP-based nanoparticle immunogens	SPR	110[a]	22427
Malaria CSP #3	CSP-based nanoparticle immunogens	NA	0	6401
SARS-CoV-2 #1	Sarbecovirus/beta coronavirus-based nanoparticles and soluble trimers	NA	0	26379
SARS-CoV-2 #2	SARS-CoV-2 spike nanoparticles/trimer, RBD nanoparticle	HTRF	249	9887
Acinetobacter baumannii #1	OMV cocktail	ELISA	256	7383
RSV #1	Pre-fusion hMPV/RSV F protein-based nanoparticles and trimers	NA	0	10751
RSV #2	Stabilised pre-fusion RSV and hMPV F proteins in nanoparticle and soluble cocktail formats	NA	0	1099
Influenza #1	Stem-only HA immunogens and vaccine control	NA	0	4106
Typhoid #1	Typhoid toxin E133A H160Q mutant	SPR	496	5658

96

97 [a]Binding measurement data were generated by Antibody Dynamics.

98

99 **Availability**

The datasets are available for researchers through our portal :

https://kydab.naturalantibody.com

Results

Overview of the database

All datasets deposited in the portal are generated from mice derived from the Kymouse platform, a transgenic mouse platform developed by Kymab for discovery of therapeutic human monoclonal antibodies. These mice are genetically engineered to produce antibodies with variable heavy and light chain regions (VH and VL) of entirely human origin. Over the past decade, this humanized mouse platform has proven to be robust, stable, and versatile for therapeutic antibody discovery, with several antibodies derived from this platform having advanced to clinical trials[18 19] .

KyDab comprises 11 human antibody studies encompassing 51 unique immunogens generated from the Kymouse platform, targeting a diverse array of viral, bacterial, and parasitic antigens[15 16] . In general, immunogens were either selected from well-established commercial antigen products or designed by structural biologists with expertise in pathogen-specific immunogenic structures. Following immunisation with the respective immunogens, sera were collected and assessed for reactivity using screening assays such as ELISA to evaluate immune responses. Mice demonstrating positive immune responses were selected for further processing.

From each selected mouse, spleen, lymph node, and/or bone marrow cells were harvested and subjected to flow cytometry-based single-cell sorting to isolate antigen-specific B cells for downstream sequencing. The resulting paired VH-VL sequences underwent analysis and down-selection through an in-house bioinformatics pipeline that is similar to the Immcantation framework[20] . Sequences were clustered into lineages based on inferred V and J gene usage and

CDR3 sequence identity, with representative clones from the more expanded lineages preferentially selected. Additional selection criteria included somatic hypermutation frequency, evidence of sequence convergence, developability assessments, and overall sequence diversity. The scale of clone selection varied across studies according to specific research objectives. In most studies, selected clones were recombinantly expressed and further characterized through in vitro affinity assays to assess binding to their corresponding antigens, as illustrated in **Figure 1**. The portal provides comprehensive data including all paired antibody sequences, germline gene annotations, complete metadata (mouse ID, tissue source, immunogen identity), and where available, affinity measurements and antigen sequences in FASTA format. To ensure uniform representation of the data, we post-processed raw read files using RIOT[17] , a sequence annotation tool that translates nucleotide sequences into amino acids and aligns them to the IMGT scheme.

For friendly user experience, KyDab also features simple structured summaries, interactive visualisations, and flexible download options, enabling researchers to access and apply these data with minimal need for additional engineering or background reading.

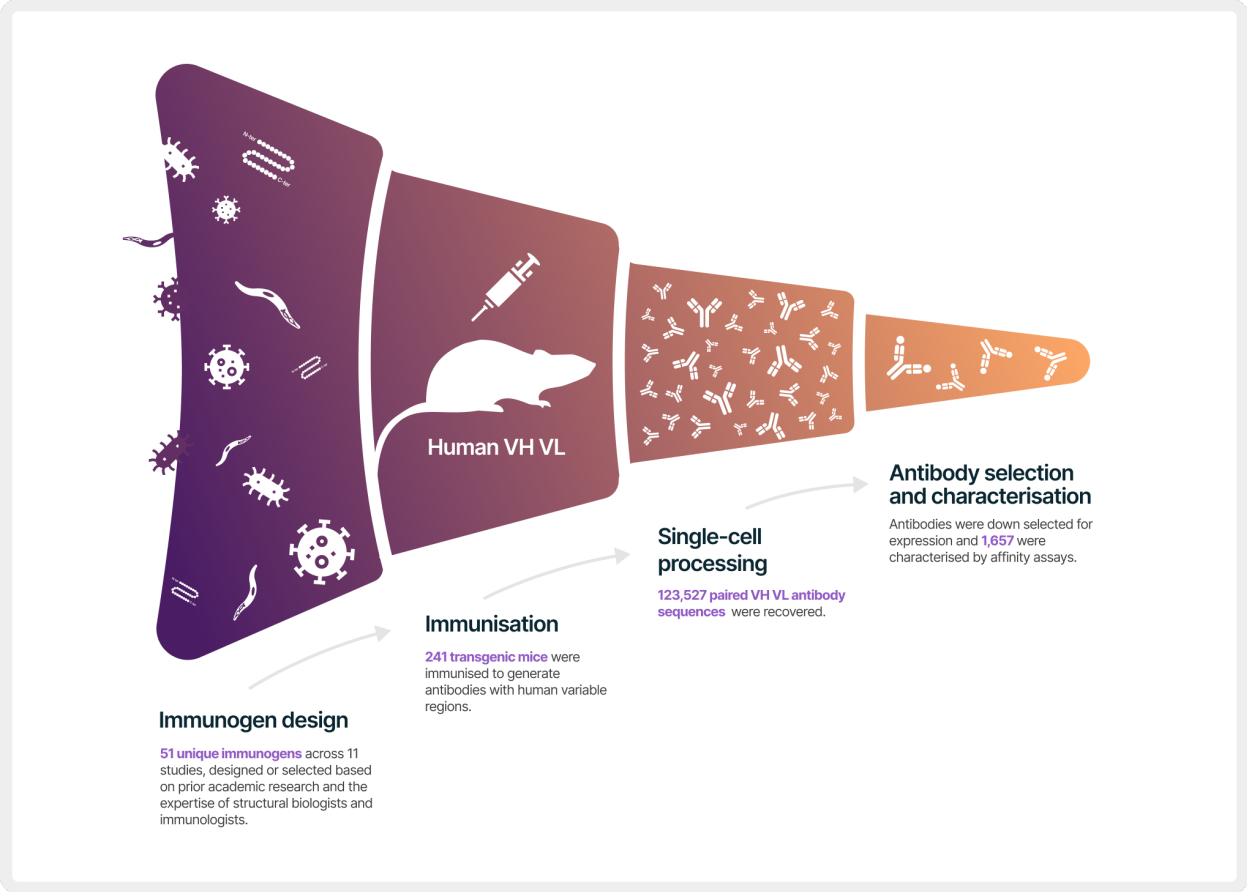

Figure 1. Overview of the KyDab data generation pipeline. All antibodies in KyDab were generated from the Kymouse humanized immune mouse platform. Following immunisation, antigen-responsive mice were selected and lymphoid tissues were harvested for single-cell sorting and sequencing. Resulting sequences were analyzed and down-selected to prioritise high-potential clones, which were often recombinantly expressed and further characterised by in vitro affinity assays. Both positive and negative binding data are made available on KyDab.

Repertoire diversity across datasets

To evaluate the diversity of the antibody repertoires, we performed sequence identity clustering on the heavy and light chain variable regions with respect to IMGT variable region alignment. The raw number of sequences and the resulting cluster counts for each dataset, chain type, and region are detailed in **Table 3**. This analysis focused on the complementarity-determining regions (**CDR1, CDR2, CDR3**) and the framework regions (**FW**) using sequence identity thresholds of 90%, 80%,

160 and 70%. To compare the heterogeneity of antibody responses, we calculated a normalized diversity
161 percentage (number of unique clusters / total sequences), which is plotted in **Figure 2**. The results, as
162 visualized in **Figure 2**, consistently demonstrate that the **CDR3** region of the heavy chain is the most
163 diverse component of the antibody variable domain across all datasets and identity thresholds. For
164 instance, in the top panel of **Figure 2** (90% identity threshold), 8 out of 11 datasets exhibit prominent
165 heavy chain CDR3 diversity, with percentages exceeding 50%, while the light chain regions, by
166 comparison, reflect their more limited contribution to general immune response variability by largely
167 remaining below a 40% diversity threshold across the datasets. In contrast, the FW regions
168 consistently show the lowest diversity (**Figure 2)**, which is expected given their conserved structural
169 role. Furthermore, the data presented in **Table 3** and visualized in **Figure 2** reveal a wide spectrum of
170 diversity profiles among the datasets, reflecting the nature of the specific immune response. The effect
171 of the clustering strictness is also evident when comparing the panels of **Figure 2** from top to bottom;
172 as the identity threshold is relaxed from 90% to 70%, the calculated diversity decreases across all
173 regions due to the merging of sequences into fewer, more heterogeneous clusters. This comparative
174 analysis highlights the varied complexity of antibody repertoires and confirms that our collection
175 encompasses a broad range of immune responses suitable for robust immunological investigation.
176
177 **Table 3. Sequence and Cluster Counts for Antibody Repertoires.** This table provides a detailed
178 breakdown of the total number of sequences (records) and the corresponding number of unique
179 sequence clusters for each IMGT region (cdr1, cdr2, cdr3, fw). Data are presented for both heavy and
180 light chains across all datasets, clustered at sequence identity thresholds of 70%, 80% and 90%.

	IMGT region		**cdr1**			**cdr2**			**cdr3**			**fw**		
	Identity threshold		**70%**	**80%**	**90%**	**70%**	**80%**	**90%**	**70%**	**80%**	**90%**	**70%**	**80%**	**90%**
Dataset	**chain type**	**records**												
Acinetobacter baumannii #1	**heavy**	**6144**	326	529	782	180	305	490	2647	3613	4271	179	410	936
	light	**4711**	251	298	556	154	155	155	664	1028	1531	196	453	1234
Malaria CSP #1	**heavy**	**16643**	1031	1824	2943	872	1515	2583	6097	8400	9970	425	1112	3115
	light	**16425**	899	1180	2072	606	629	658	1517	2501	3905	489	1197	3473
Malaria CSP #2	**heavy**	**21429**	996	1738	2840	878	1535	2592	6498	9073	11251	384	919	2668

	light	**19845**	903	1165	2032	618	645	684	1557	2480	3779	475	1083	2975
Malaria CSP #3	**heavy**	**5884**	467	843	1381	456	789	1284	2228	2855	3306	188	480	1281
	light	**5997**	530	708	1226	371	389	417	758	1234	1890	224	507	1413
Pertussis	**heavy**	**11290**	1215	2203	3517	986	1760	3003	3165	4033	4798	367	1031	3080
	light	**11290**	843	1156	2072	561	582	621	1134	1906	2983	278	748	2383
RSV #1	**heavy**	**10368**	589	1009	1558	432	747	1240	4315	6120	7295	182	507	1469
	light	**9697**	548	751	1271	390	419	460	846	1327	2044	250	606	1730
RSV #2	**heavy**	**1051**	134	229	352	130	205	308	509	595	656	39	90	236
	light	**1011**	129	165	263	124	129	134	242	339	467	59	117	262
SARS-CoV-2 #1	**heavy**	**20189**	1348	2422	3738	986	1699	2858	4500	6351	8080	557	1445	3728
	light	**25970**	1048	1465	2762	431	437	440	1788	3177	5305	431	1188	3998
SARS-CoV-2 #2	**heavy**	**6659**	591	977	1417	314	529	875	810	1040	1359	228	563	1315
	light	**9830**	492	649	1224	215	217	217	621	1091	1766	180	524	1688
Influenza #1	**heavy**	**3949**	493	807	1159	261	453	717	1744	2184	2409	120	345	975
	light	**3852**	361	475	786	239	247	259	481	790	1189	161	380	1153
Typhi #1	**heavy**	**4435**	344	639	1063	416	717	1204	1959	2440	2772	90	195	709
	light	**5005**	345	447	796	269	278	287	674	1124	1706	100	186	543

181

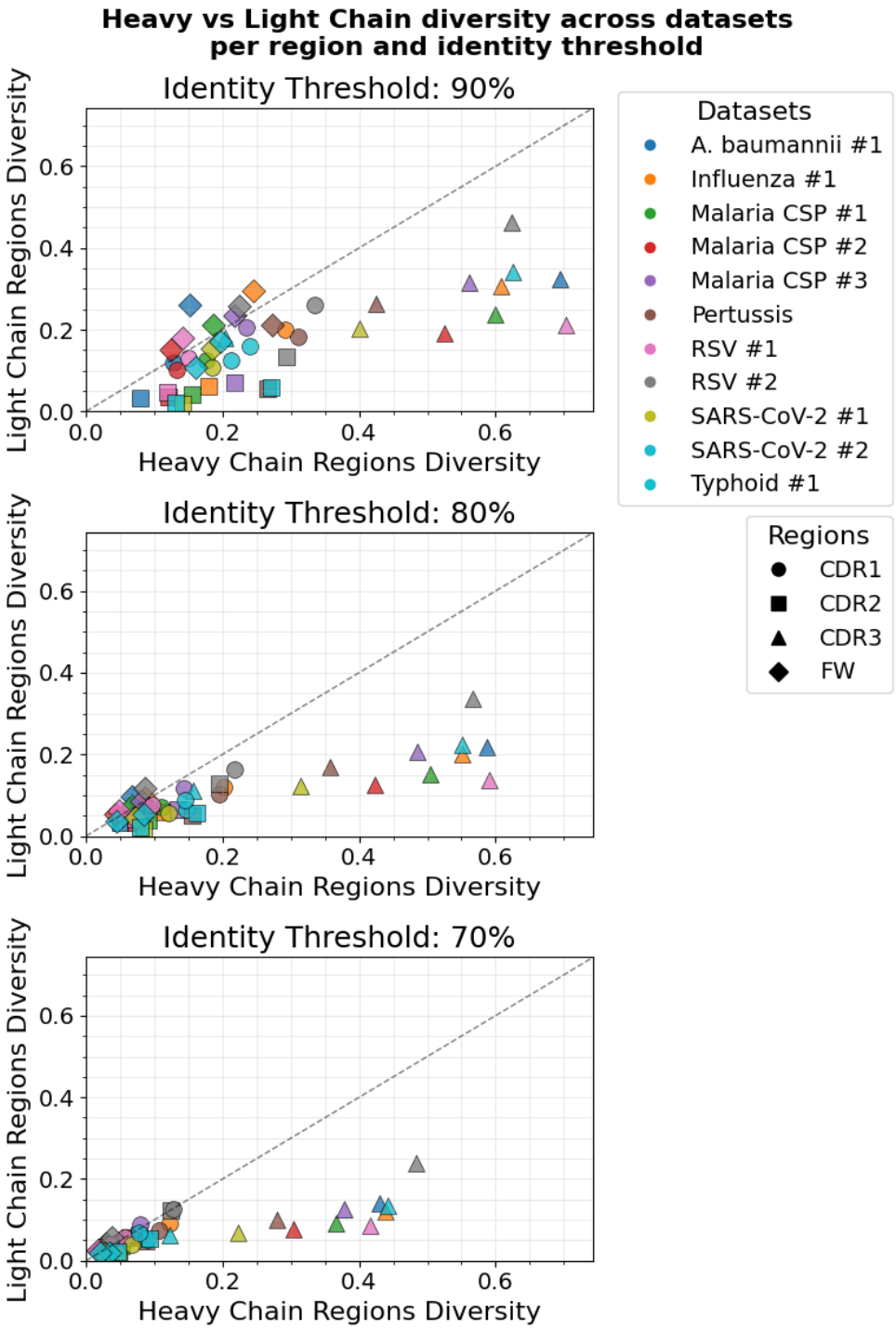

Figure 2. Comparative Diversity of Antibody Regions Across Datasets. The diversity calculated as the ratio of unique clusters to total chain sequences is shown for complementarity-determining regions (CDR1, CDR2, CDR3) and framework regions (FW). The analysis is presented for **11** different antigen-specific datasets at three distinct sequence identity thresholds: **90%** (top), **80%** (middle), and **70%** (bottom). The results highlight the consistently higher diversity of the CDR3 region and the variable diversity profiles across the different datasets.

Discussion

Despite the rapid growth of public antibody databases, there is currently no centralized resource that captures antibody discovery data to such a large scale. Most existing public resources of therapeutic antibody primarily curate clinically successful antibodies from sparse origins, representing only a small fraction of the total discovery funnel and seldom include negative or low-binding clones[7 21] .

KyDab addresses this gap by providing a comprehensive antibody discovery dataset generated under high quality standard and consistent workflows. All data were produced using a well-established humanized mouse platform with standardized immunisation, single-cell sequencing, selection and expression pipelines across multiple studies. This level of upstream consistency is rarely achieved in public antibody resources. Importantly, the dataset reflects the full process of antibody down-selection, from large repertoires of paired VH–VL sequences to a defined high-potential subset advanced to experimental testing. Such data are particularly valuable for AI applications aimed at improving the success rate of experimental validation. In addition, the antigen diversity in KyDab also provides a more challenging and realistic benchmark for evaluating model robustness across targets.

As with all antibody discovery workflows, the dataset reflects biases introduced by bioinformatics-guided down-selection. Sequences advanced to expression are enriched for expanded lineages, higher somatic mutation levels and predicted developability, leading to an overrepresentation of true binders and high-affinity antibodies. Nevertheless, KyDab includes both positive and negative experimental outcomes. The availability of negative data is critical for proper model calibration and for evaluating false-positive behavior in the presence of selection bias.

The long-term goal of AI-driven antibody discovery is to improve success rate, reduce cost and development time by shifting key decision-making steps from experimental screening to

computational prediction. While AI has demonstrated impressive progress in antibody in silico generation, its application to virtual screening and affinity prediction remains constrained by the lack of large, high-quality antibody discovery datasets[3] . By releasing KyDab as an open resource, we aim not only to support this next phase of AI-empowered antibody discovery, but also to demonstrate the value of sharing structured, full-funnel discovery data. We hope this effort will encourage broader data contributions from across the antibody discovery community, particularly from industrial organisations, to enable the development of more robust and generalisable AI models through collective progress.

Disclosure statement

Q.Z., D.M., M.G., S.Y., and M.-M.L.P. are current employees of Sanofi. S.T.R. was a Sanofi employee within the past three years. D.C. and K.K. are current employees of NaturalAntibody.

Funding

This work was funded by the Gates Foundation, INV-040928.

Acknowledgments

The authors thank Donald Drake and Matthew Massett for manuscript review; Aaron Hanley and Josefin Bartholdson-Scott for assistance with dataset preparation; Janet Tse and Juliette Goutorbe for preparing the Terms and Conditions; Jemima Paterson, Andrew Phillips and Jean-Philippe Mametz for support with coordination and digital advice.

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