AmpSeq Terms and Conditions of Service

1. Acceptance of Terms

By accessing or using AmpSeq, LLC ("AmpSeq")'s online customer portal, submitting samples, libraries, metadata, or orders electronically or in writing, issuing a purchase order, requesting services, confirming an order by email, shipping samples, or accepting delivery of services, data, or reports, the customer ("Customer") agrees to be bound by these Terms and Conditions unless otherwise governed by a separately executed Master Service Agreement ("MSA") or Statement of Work ("SOW") signed by AmpSeq.

In the event of any conflict, the following order of precedence shall apply unless expressly agreed otherwise in writing:

- signed MSA
- signed SOW, quote, or order confirmation
- these Terms and Conditions
- any Customer purchase order or procurement terms

Any preprinted, portal-based, procurement, or unilateral Customer terms shall have no force or effect unless expressly accepted in writing by AmpSeq.

2. Scope of Services

AmpSeq provides next-generation sequencing, molecular biology, laboratory processing, and related data analysis services as described in the applicable quote, order confirmation, electronic submission, SOW, or service description.

AmpSeq will perform services using commercially reasonable care and standard operating procedures appropriate for a research service laboratory. Unless expressly stated otherwise in writing, services do not include assay development, regulated validation, clinical reporting, publication support, iterative troubleshooting beyond standard support, or guaranteed scientific outcomes.

The specific scope, deliverables, and turnaround time for each project shall be governed by the applicable quote, order confirmation, electronic submission, or SOW.

Additional service-specific terms may apply as set forth in applicable addendums, which are incorporated by reference into these Terms and Conditions where relevant to the services performed.

3. Research Use Only

All services, workflows, reports, analyses, data, and deliverables provided by AmpSeq are for Research Use Only ("RUO") and are not intended for diagnostic, clinical, therapeutic, prognostic, patient management, donor selection, or regulatory decision-making purposes unless expressly agreed in writing under a separate regulated framework.

Customer shall not use, and shall not permit any third party to use, AmpSeq deliverables for any clinical, diagnostic, therapeutic, or regulatory purpose unless AmpSeq has expressly agreed in writing to provide such services.

4. No Guarantee of Scientific or Experimental Outcome

AmpSeq does not warrant or guarantee any particular scientific, biological, analytical, experimental, or publication outcome, including but not limited to differential expression results, clustering, cell annotation,

variant detection, genome assembly quality, enrichment performance, taxonomic composition, target capture performance, CRISPR edit detection, pathway interpretation, manuscript suitability, or grant utility.

Customer acknowledges that the usefulness and interpretation of sequencing results depend on factors outside AmpSeq's control, including sample quality, contamination, biological variability, experimental design, controls, replication strategy, collection and storage history, library construction strategy, platform compatibility, reference quality, metadata completeness, and downstream analytical choices.

AmpSeq's obligation is limited to performing the agreed technical services using commercially reasonable laboratory and computational practices.

5. Customer Responsibilities and Warranties

Customer is solely responsible for providing accurate and complete order details, sample information, metadata, and project instructions; ensuring that submitted materials comply with AmpSeq's submission requirements; ensuring that submitted materials are lawfully obtained and properly authorized; and determining whether the requested services are appropriate for Customer's intended purpose.

Customer represents and warrants that all submitted samples, libraries, nucleic acids, metadata, and related materials:

- have been lawfully collected, obtained, transferred, and submitted
- are accompanied by all necessary approvals, consents, permits, institutional authorizations, and legal rights
- comply with all applicable laws, regulations, biosafety standards, privacy requirements, and institutional policies
- do not require special handling, containment, security, or regulatory treatment unless expressly disclosed to and accepted by AmpSeq in writing

Customer remains solely responsible for the nature, legality, biosafety classification, and regulatory status of all submitted materials.

6. Sample Identification and Customer-Provided Information

AmpSeq will rely on Customer-provided sample names, identifiers, metadata, concentration values, species information, library information, indexing information, project design details, and instructions as submitted.

Unless expressly agreed in writing, AmpSeq does not independently verify sample identity, species identity, genotype, treatment group, sample pairing, library structure, metadata accuracy, sample sheet correctness, or expected biological composition.

AmpSeq shall not be liable for delays, errors, poor performance, failed analyses, or unusable data resulting from mislabeled samples, swapped or mixed samples, incomplete or inaccurate metadata, incorrect concentration or fragment size information, incorrect library structure or index information, undeclared contaminants or inhibitors, or inaccurate project descriptions.

7. Right to Refuse, Suspend, or Terminate Services

AmpSeq reserves the right, at its sole discretion, to refuse, suspend, delay, or terminate any project, order, or service if submitted materials are unsafe, noncompliant, mislabeled, unsuitable, or inconsistent with the stated order; required information, approvals, or payment arrangements are incomplete; the requested work

would create technical, operational, legal, biosafety, regulatory, or reputational risk; or Customer breaches these Terms and Conditions.

Customer shall remain responsible for all work performed and costs incurred prior to refusal, suspension, delay, or termination.

8. Estimated Output and Performance Variability

Sequencing output, read counts, data yield, mapping rates, alignment rates, duplication rates, on-target rates, coverage metrics, and other technical performance values are estimates only and may vary depending on sample quality, sample composition, library quality, library complexity, fragment size, index balance, sequencing chemistry, platform behavior, run composition, and data processing choices.

Unless expressly stated otherwise in writing, actual sequencing output may vary by plus or minus twenty percent (±20%) from quoted or estimated values, and such variation shall be considered commercially reasonable and shall not constitute nonperformance.

9. Quality Control, Troubleshooting, and Rework

AmpSeq may perform quality control at one or more stages of the workflow, including sample receipt, nucleic acid QC, library QC, post-pooling QC, run QC, and data QC.

If samples or libraries fail internal QC or perform poorly due to factors outside AmpSeq's control, including poor sample integrity, contamination, degradation, inhibitors, low complexity, poor library construction, inaccurate quantification, nonstandard structure, incompatible indexing, or upstream handling issues, AmpSeq is not obligated to repeat services at no cost.

At AmpSeq's discretion, additional sequencing, repeat processing, re-pooling, modified loading, or troubleshooting may be offered to attempt to improve results. Such work may incur additional fees and extended turnaround times.

10. Turnaround Time

Any stated turnaround time ("TAT") is an estimate only and is provided in business days unless otherwise stated.

TAT begins only after all required materials are received, required project information is complete, applicable QC review is completed, and the project is confirmed to proceed. TAT ends when the applicable deliverable is released or made available to Customer.

TAT may be extended due to sample quality or QC issues, missing or inconsistent metadata, order changes, troubleshooting, repeat processing, batching requirements, shared-lane scheduling, supply chain delays, instrument availability, force majeure events, or delayed Customer responses.

Unless expressly included in writing, nucleic acid extraction, data analysis, custom reports, interpretation, and downstream support are separate services with separate turnaround times.

11. Order Changes and Cancellations

If Customer fails to provide timely responses to project-related inquiries, required information, approvals, or instructions, AmpSeq may, at its discretion, pause or delay processing, remove the project from the active queue, adjust applicable turnaround time estimates, and reschedule work based on availability.

AmpSeq shall not be responsible for any delays, performance impacts, or changes in output resulting from such Customer delays.

AmpSeq may store, return, or dispose of materials in accordance with its standard retention policy if Customer does not provide timely direction. Customer remains responsible for all work performed, costs incurred, and any additional charges resulting from project delays, rework, rescheduling, extended storage, or re-initiation of services.

12. Order Changes and Cancellations

Changes or cancellations requested after order confirmation may result in partial or full charges.

AmpSeq reserves the right to bill for labor already performed, reagents already allocated or consumed, instrument time reserved or used, data already generated, custom work already initiated, and administrative or shipping costs already incurred.

Orders may not be cancelled once irreversible processing has begun.

13. Additional Work and Out-of-Scope Requests

Requests outside the original quoted scope may be subject to additional charges and revised timelines, including custom QC or troubleshooting, revised deliverables, custom file formatting, repeated data transfer, re-analysis, revised reports, figure generation, extended consultation, re-pooling, re-sequencing, sample recovery attempts, special handling, and archive retrieval.

14. Pricing, Payment, and Fees

Prices are valid only for the period stated on the quote, order confirmation, or portal order and exclude taxes, shipping, handling, and surcharges unless otherwise stated.

Payment terms are Net 30 unless otherwise agreed in writing.

AmpSeq reserves the right to suspend services, withhold data release, delay shipment or return of materials, and reject future orders for overdue balances or unresolved payment issues.

Late payments may incur a finance charge of 1.5% per month, or the maximum rate permitted by law, whichever is lower, calculated from the due date until paid in full.

Customer shall be responsible for all reasonable costs of collection, including bank fees, wire transfer fees, credit card processing fees if applicable, collection agency fees, and reasonable attorneys' fees.

15. Shipping and Risk of Loss

Customer is responsible for all costs associated with shipping samples or materials to AmpSeq and any return shipment unless otherwise agreed in writing.

All submitted materials are shipped at Customer's risk. AmpSeq shall not be responsible for shipping delays, temperature excursions, package loss, physical damage, leakage, breakage, contamination, degradation, or carrier mishandling caused by third-party carriers or improper packaging.

Customer is encouraged to use appropriate packaging, temperature controls, tracking, and insurance.

16. Sample and Material Storage

Unless otherwise agreed in writing, AmpSeq may retain materials as follows:

- Original biological samples: up to one (1) month following data delivery

- Extracted DNA/RNA samples: up to three (3) months following data delivery
- Final sequencing libraries: up to six (6) months following data delivery
- Residual or intermediate materials: retained at AmpSeq's sole discretion

Storage beyond these standard retention periods is not guaranteed and may be subject to additional fees.

Upon expiration of the applicable retention period, or if Customer fails to provide timely written instructions regarding return shipment, extended storage, or disposition of materials, AmpSeq may destroy or otherwise dispose of such materials without further notice and without liability.

17. Data Delivery, Retention, and Access

Data shall be deemed delivered when AmpSeq provides notice that files are available through sFTP, Box, cloud delivery, secure file transfer, or another designated delivery method.

Unless otherwise agreed in writing, delivered data will be retained for up to 30 days after delivery notice.

Customer is solely responsible for promptly downloading, verifying, storing, backing up, securing, and archiving all delivered files and outputs.

AmpSeq has no obligation to maintain, restore, archive, or re-deliver data after the stated retention period unless otherwise agreed in writing. Archived recovery, if available, may be subject to additional fees and is not guaranteed.

18. Third-Party Platforms, Reagents, and Tools

AmpSeq may use third-party instruments, kits, reagents, software, cloud platforms, consumables, analytical tools, and service providers in performing services.

AmpSeq does not warrant uninterrupted availability, compatibility, or error-free performance of any third-party product, platform, reagent, software, or service and shall not be liable for delays, limitations, or performance issues arising from such third-party dependencies, except to the extent directly caused by AmpSeq's failure to use commercially reasonable care.

19. Bioinformatics and Data Interpretation

Unless expressly included in the applicable quote, order confirmation, or SOW, AmpSeq's services do not include custom downstream interpretation, iterative reanalysis, manuscript support, grant support, regulatory validation, biological consulting, or experimental redesign.

Bioinformatics outputs are provided using standard or agreed workflows, reference resources, software tools, and parameter settings. Customer remains solely responsible for evaluating the suitability, interpretation, and downstream use of all data, reports, and analyses.

20. Confidentiality

AmpSeq shall use commercially reasonable efforts to maintain the confidentiality of Customer's non-public project information and data and shall use such information solely for performing the requested services.

These obligations do not apply to information that becomes public through no fault of AmpSeq, was already known to AmpSeq without restriction, is independently developed without use of Customer's confidential information, or is required to be disclosed by law, court order, subpoena, or governmental process.

AmpSeq may disclose Customer information to its employees, contractors, affiliates, subprocessors, vendors, and service providers who have a need to know such information for performing the services and who are subject to confidentiality obligations.

If Customer requires enhanced confidentiality, security, or data processing terms, such terms must be separately agreed in writing.

21. Intellectual Property

Except as otherwise expressly agreed in writing, Customer retains ownership of Customer-submitted samples, source materials, and pre-existing Customer intellectual property, and AmpSeq retains ownership of its pre-existing and independently developed know-how, methods, workflows, protocols, software, pipelines, templates, tools, QC frameworks, and service methodologies.

Customer shall own the final project-specific raw sequencing data and final deliverables generated specifically for Customer upon full payment.

Nothing in these Terms transfers ownership of AmpSeq's underlying methods, pipelines, software, service know-how, or general improvements.

22. Inspection and Claims Period

Customer shall promptly inspect all deliverables, data, reports, and files upon delivery.

Any claim relating to alleged nonconformity, deficiency, missing deliverables, or technical error must be submitted to AmpSeq in writing within fifteen (15) business days after delivery.

Failure to provide written notice within that period constitutes acceptance of the services and deliverables.

23. Limitation of Liability

To the maximum extent permitted by law, AmpSeq's aggregate liability arising out of or relating to any project, order, service, deliverable, or these Terms and Conditions, whether in contract, tort, negligence, strict liability, or otherwise, shall not exceed the amounts actually paid by Customer to AmpSeq for the specific service giving rise to the claim.

In no event shall AmpSeq be liable for any indirect, incidental, consequential, exemplary, punitive, special, or reliance damages, including loss of data, loss of samples, loss of funding, loss of publication opportunity, loss of research opportunity, loss of profits, project delay, replacement costs, lost time, reputational harm, failed experiments, or missed grant or milestone deadlines, even if advised of the possibility of such damages.

24. Indemnification

Customer shall defend, indemnify, and hold harmless AmpSeq, its affiliates, officers, directors, employees, contractors, and agents from and against any and all claims, demands, liabilities, damages, losses, costs, and expenses, including reasonable attorneys' fees, arising out of or relating to Customer's samples, libraries, materials, metadata, or instructions; Customer's breach of these Terms and Conditions; Customer's downstream use, interpretation, publication, commercialization, or regulatory use of results or data; any allegation that Customer lacked the right or authorization to submit the materials or request the services; or any claim arising from the nature, origin, legality, biosafety, or regulatory status of submitted materials.

25. Force Majeure

AmpSeq shall not be liable for delay, interruption, or failure to perform caused by events beyond its reasonable control, including natural disasters, weather events, public health events, labor disruptions, supply shortages, reagent shortages, instrument failures, utility or internet outages, cyber incidents, transportation disruptions, government actions, or vendor failures.

26. Quote Confidentiality

Any quote, pricing, proposal, statement of work, or similar commercial document provided by AmpSeq is confidential and intended solely for Customer's internal evaluation and purchasing purposes.

Customer agrees not to publish, post, or disclose such materials to third parties without AmpSeq's prior written consent, except as required for internal approval or by law.

27. Entire Agreement; No Reliance

These Terms and Conditions, together with any applicable quote, order confirmation, SOW, or MSA, constitute the entire agreement between the parties and supersede prior discussions, proposals, understandings, or representations.

Customer acknowledges that it has not relied upon any statement, estimate, or representation not expressly set forth in such documents.

28. Governing Law and Venue

These Terms and Conditions shall be governed by and construed in accordance with the laws of the State of Maryland, without regard to conflict-of-law principles.

Any dispute arising out of or relating to these Terms and Conditions or the services provided by AmpSeq shall be brought exclusively in the state or federal courts located in Maryland, and each party consents to personal jurisdiction and venue therein.

Before initiating formal proceedings, the parties agree to attempt in good faith to resolve any dispute through informal business discussions.

Addendum A: Sequencing-Only Services

1. Scope

This addendum applies to all projects in which Customer provides pre-made libraries or requests sequencing-only services.

Unless expressly stated otherwise in writing, sequencing-only services do not include full library optimization, assay redesign, full validation of library structure, primer redesign, index redesign, publication-grade troubleshooting, or guaranteed read distribution per sample.

2. Customer Responsibility for Library Design and Compatibility

Customer is solely responsible for ensuring that submitted libraries are compatible with the requested sequencing platform, chemistry, read length, index configuration, primer requirements, adapter structure, library structure, UMI design, and sequencing strategy.

Unless expressly agreed in writing, AmpSeq does not independently validate full library structure, adapter design, primer compatibility, UMI structure, or sequencing strategy suitability prior to sequencing.

AmpSeq shall not be liable for reduced output, sequencing failure, demultiplexing issues, index misassignment, incompatible read structure, unusable data, or failed downstream analysis resulting from nonstandard, incomplete, incompatible, or inaccurately described library designs.

3. Library Information

Customer must provide complete and accurate library information at submission, including library type, requested platform, read length, fragment size, concentration, molarity, index sequences, index orientation, primer requirements, custom read structure, UMI presence or position, and pooling plan as applicable.

4. Shared-Lane Scheduling and Pooling

Shared-lane sequencing is subject to batching, compatibility with other libraries, run composition, instrument scheduling, lane balancing, operational efficiency, and overall run quality considerations.

AmpSeq reserves the right to determine pooling strategy, loading concentration, sequencing configuration, run timing, and whether a library is suitable for shared-lane placement.

5. Demultiplexing and Index Assignment

Demultiplexing and sample assignment for Customer-prepared libraries are performed based on Customer-provided sample sheet and index information unless otherwise agreed in writing.

AmpSeq is not responsible for read loss, index hopping, cross-assignment, low demultiplexing rate, or incorrect sample attribution resulting from inaccurate sample sheets, reused or overlapping indexes, low edit distance between indexes, incompatible indexing schemes, incorrect i5/i7 orientation, or low-diversity libraries.

6. Non-Standard Libraries and Platform Limitations

Customer acknowledges that short fragments, dimers, long fragments, inaccurate quantification, low complexity, unusual base composition, modified adapters, unusual library structures, and nonstandard chemistry compatibility may adversely affect sequencing performance.

Certain libraries may perform differently across Illumina, AVITI/Element, PacBio, Nanopore, or other platforms. AmpSeq may recommend dedicated runs, alternative platforms, modified loading, custom primers, or alternative sequencing recipes where appropriate.

7. Output Variability

AmpSeq does not guarantee a specific number of reads per sample for sequencing-only services. Total output may vary by ±20% from estimated or quoted values, and read distribution across pooled samples may be uneven.

8. Re-Sequencing

AmpSeq does not guarantee free re-sequencing where reduced output or poor performance results from library quality, library composition, index design, inaccurate Customer-provided information, low diversity, nonstandard structure, pooling variability, platform compatibility limitations, or other factors outside AmpSeq's control.

Addendum B: Bioinformatics and Data Analysis Services

1. Scope

This addendum applies to all projects involving data processing, bioinformatics analysis, computational interpretation, reporting, or custom data deliverables.

2. Workflow Basis

AmpSeq may perform bioinformatics services using standard, semi-standard, or custom workflows, including third-party tools, public references, internally maintained pipelines, and agreed parameter settings.

Unless otherwise stated in writing, AmpSeq may determine the appropriate pipeline version, software tool, parameter set, reference genome or annotation, filtering threshold, QC framework, and reporting format in its professional judgment.

3. No Guarantee of Interpretation

AmpSeq does not guarantee that bioinformatics results will support Customer's hypothesis, be publication-ready, satisfy reviewer expectations, support a patent or regulatory filing, confirm a biological mechanism, or produce a specific number of significant genes, variants, taxa, or pathways.

4. Customer Responsibility for Experimental Context

Customer is responsible for ensuring that project design, metadata, grouping, sample annotation, and biological context provided to AmpSeq are accurate and complete.

AmpSeq is not responsible for analytical limitations arising from insufficient replication, inappropriate controls, unbalanced design, mislabeled samples, missing metadata, poor upstream experimental design, confounding variables, undeclared batch effects, or incompatible reference assumptions.

5. Deliverables

Unless otherwise agreed in writing, deliverables will be determined based on the scope of services for each project and may include, where applicable, processed data files, QC summaries, count matrices, variant tables, alignment metrics, abundance tables, differential analysis outputs, pathway results, summary reports, and standard plots.

AmpSeq is not obligated to provide publication-ready styling, manuscript text, grant-ready interpretation, extensive custom visualization, or raw pipeline source code unless expressly stated in writing.

6. Revisions and Additional Work

Custom reanalysis, revised comparisons, metadata changes after analysis begins, additional plots, alternative statistical comparisons, custom reference building, repeated interpretation calls, manuscript support, and reviewer-response support may incur additional fees.

7. Third-Party Databases and Software

AmpSeq does not guarantee permanence of specific software versions, future reproducibility under changed databases, cross-tool equivalence, or continued availability of third-party resources.

8. Review Period

Customer shall review all bioinformatics deliverables promptly upon delivery. Any request for correction based on alleged technical omission or deliverable mismatch must be made in writing within fifteen (15) business days after delivery.

Addendum C: Sample Submission and Acceptance Policy

1. Customer Submission Obligations

Customer must provide complete and accurate submission information, including as applicable project type, species, sample type, extraction method, concentration, volume, storage buffer, fragment size, library structure, index information, requested sequencing configuration, analysis request, sample identifiers, and grouping metadata.

2. Submission Requirements

Customer is responsible for ensuring that all submitted materials meet AmpSeq's current submission requirements, including concentration range, minimum volume or mass, acceptable buffer, purity, integrity, format, index format, temperature conditions, and packaging requirements.

3. Acceptance Does Not Mean Fitness for Purpose

AmpSeq's acceptance of a sample, library, or material for processing does not guarantee that the material is fit for the requested downstream purpose or that it will perform successfully.

4. Hidden Defects

AmpSeq may perform incoming QC or acceptance review, but such review is limited and does not guarantee detection of all defects. AmpSeq is not responsible for poor performance caused by latent or undetectable issues such as degradation, inhibitors, contamination, low complexity, poor extraction quality, inaccurate quantification, or incompatible chemistry.

5. Hazardous, Infectious, or Regulated Materials

Customer must disclose in advance if submitted materials are or may be infectious, hazardous, biohazardous, toxic, human-derived with special restrictions, regulated under import/export rules, or subject to special biosafety handling.

6. Human Samples and Privacy

Unless otherwise expressly agreed in writing, Customer shall not submit identifiable PHI or patient-identifiable data to AmpSeq. If Customer submits human-derived materials, Customer represents that all required consents, IRB approvals, data use permissions, and legal authorizations have been obtained.

7. Normal Processing Risk

Customer acknowledges that laboratory processing of biological materials inherently involves risk, including sample consumption, depletion, partial loss, processing failure, contamination events despite reasonable care, and inability to recover sufficient material.