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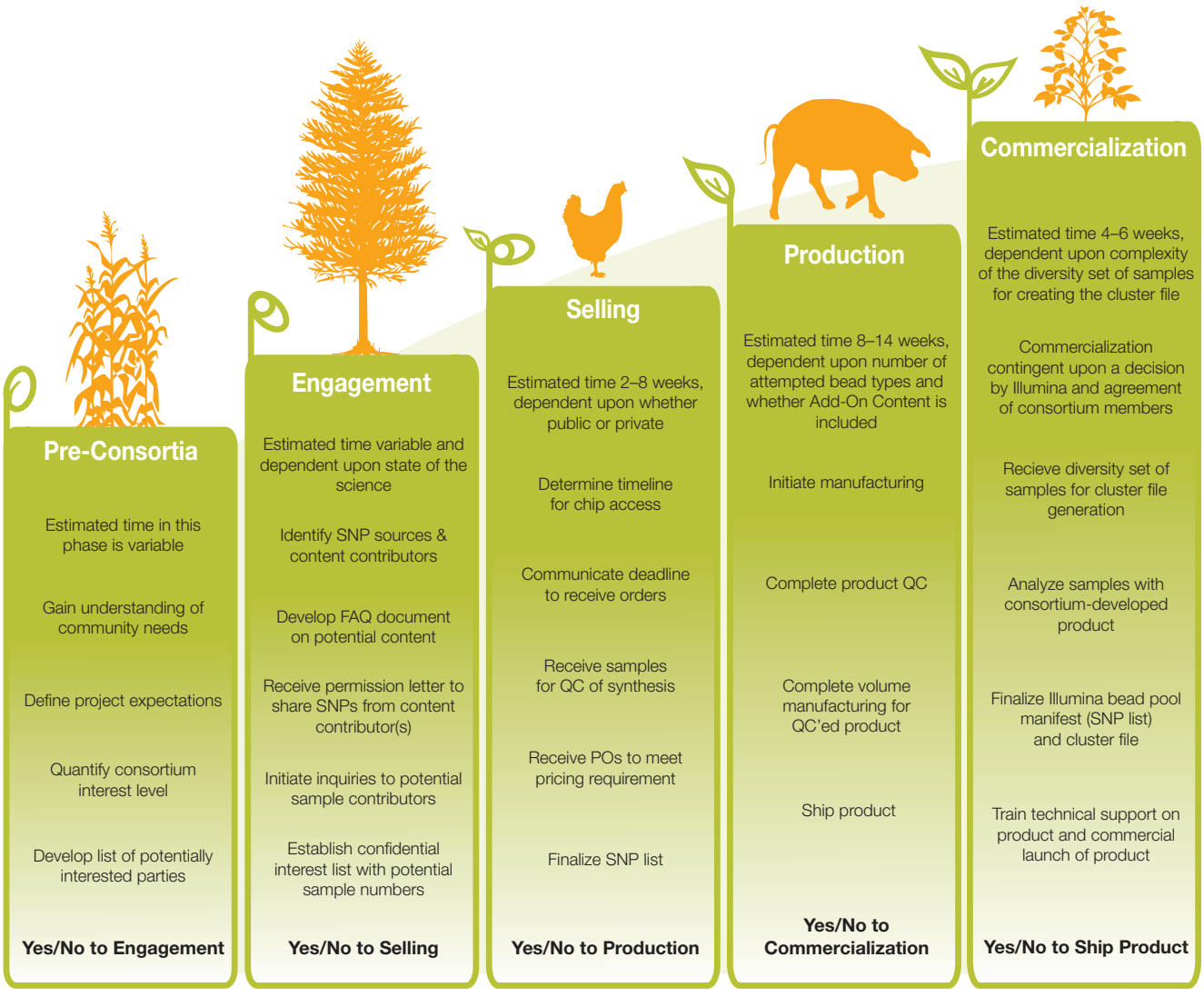
Agriculture Consortia Processes and Milestones

What is an agriculture consortium?

Illumina categorizes projects that facilitate food, feed, (bio) fuel, fiber, forestry, and friends (companion animals) as “agriculture”. The Agriculture Consortium program provides a framework for researchers to pool resources in an effort to develop biomarker/SNP genotyping or sequencing tools for a variety of species. Confidentiality is maintained throughout the process.

What advantage does a consortium offer?

Each species or research community can have unique needs. Within each community, researchers often have overlapping goals that are best addressed by a combined effort and the development of a single tool (or set of common tools). By this collaborative approach, consortia help reduce the barrier of entry for individual researchers to adopt genetic analysis tools into breeding programs.



The process for creating a new product through a consortium occurs over a series of strategic phases. During each phase, a set of milestones must be met before the process can continue on to the next phase. This ensures the greatest probability for success by enabling consortium members to make well-informed decisions along the path to product development. The product may be a base content or an Add-On Content bead pool (or may include both).

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The word “consortium” is frequently used to describe research communities for various species. How does Illumina qualify potential consortia?

Illumina relies on the wider agricultural community to identify species that are a good fit for a consortium approach. In many cases, existing consortia will approach Illumina to inquire about developing a tool through a community effort. Conversely, Illumina will sometimes drive the formation of a consortium if many independent researchers’ inquiries suggest that pooling efforts might be a useful approach. There are a number of flexible options for a consortium approach. The consortium can remain confidential or open, as preferred by consortium members.

Are there particular products that consortia use or can any of the products be accessed?

Typically an iSelect® custom genotyping BeadChip that can meet the research goals of multiple groups is developed. These BeadChips are based on Illumina’s BeadArray™ technology and are compatible with the well-proven Infinium® HD assay. The iSelect platform supports densities of 3,000 to 1,000,000 attempted bead types. Depending upon the content, this means that up to 1,000,000 SNPs and insertions/deletions (indels) can be simultaneously queried per sample.

Benefits, Roles, and Responsibilities

What is the benefit to participants of a consortium approach?

Researchers can typically access a higher density of SNP markers and a lower per-sample price than the budget of a single contributor might otherwise allow. Through the consortium, the cost of bead pool synthesis is spread over more samples than might be possible from a single institution. The minimum order for participating in a consortium is 48 samples, providing that all orders for a private iSelect BeadChip total at least 1,152 samples.

What types of projects are appropriate for an agriculture consortium approach?

The consortium approach can be applied to any agriculture project that may benefit from pooling resources to develop a genotyping tool that will meet the needs of multiple researchers.

Is it mandatory for consortia to be willing to commercialize content in order to participate? What about private consortia?

While several of Illumina’s commercial agriculture genotyping products were developed through consortia, commercializing the content is not a requirement. In addition to non-commercial open consortia, private consortia are an integral part of Illumina’s agriculture program. Illumina maintains strict confidentiality around private consortia, so these projects are not publicized. The only requirement for content (candidate SNPs or indels) in consortia projects is that it can be shared with other members of the consortium. Depending upon the goals of the content contributors, content may be maintained confidentially within a small group or content can be made publicly available. If consortium members are amenable to sharing content publicly, the decision to create a commercial product will be at Illumina’s discretion.

What is the difference between a “content contributor” and a “sample contributor” in a consortium?

Content contributors are typically small subsets of researchers that have driven the discovery efforts of SNP content and genome assembly for a species or species group. Sample contributors include anyone in the research community interested in the targeted species or species group. Illumina requests permission from content contributors to share final content with sample contributors. For sample contributors, Illumina will communicate a deadline by which purchase orders (POs) must be received in order to participate in the consortium. The final sample count for all orders received by the PO deadline will determine the per sample price.

What are the responsibilities of consortium members and users of the tool?

Content contributors should be referenced in any publications, public presentations, press releases, or public announcements resulting from use of the genotyping content. Illumina’s standard terms and conditions for products and services will also apply.

Forming, Joining or Participating in Consortia

Do I need to have my draft genome and all SNPs in hand prior to inquiring about a consortium?

It is not necessary to have all content defined prior to exploring the consortium option with Illumina. In fact, many groups benefit from Illumina’s experience in helping define a streamlined path for discovering, validating, and finalizing content. Depending upon goals for the content (e.g., even-spacing versus gene centric), a draft genome may not be necessary for a community to benefit from the development of a genotyping tool.

What if the timelines of the community change after entering into a consortium with Illumina? For example, what if we evaluate the available data and believe that additional SNP/biomarker discovery is needed prior to finalizing content?

Illumina works closely with content contributors to revisit timelines in order to ensure that goals of the consortium and the research community are best addressed. We offer customers the ability to augment content on existing BeadChips with the latest advances from genome-wide association studies, next-generation whole-genome sequencing, and exome sequencing studies for variant confirmation, fine mapping, and target validation. iSelect+ Add-On Content provides customers with the flexibility to add newly discovered content to a custom array after the initial design period is completed.

What is Add-On Content and how can I use it with a Consortium Project?

Infinium Add-On Content enables customers to incorporate new custom genomic content from new discoveries to an existing Consortium product. The new consortium product + Add-On Content is a unique custom product only available to you (and any others you delegate). The amount of Add-On Content you include is dependent on the amount of base content of the initial consortium product and the remaining available space on the BeadChip. Most consortium products use a 24-sample format that allows space for up to 90,000 total attempted beadtypes.

How do I design my genotyping tool? How are SNPs and insertions/deletions (indels) probes designed?

Researchers can design probes for SNPs or indels for any species using the Assay Design Tool (ADT), available through MyIllumina, Illumina Technical Support, or FastTrack Services. The ADT scores each submitted design to provide a relative confidence level that a probe will successfully query a particular SNP or indel based on the surrounding sequence. The output file finalized by content contributors can then be submitted to the Illumina orders group to place the final order.

How are SNPs selected and content validated?

Research communities considering a high-density genotyping tool often have access to several sources of SNP content with varying levels of validation. The state of the research will dictate whether additional validation might be useful before finalizing the SNP list. Illumina will work with content contributors to identify methods that might reduce risks before finalizing content. Design scores generated by ADT for each potential SNP are well-established indicators of the likelihood that a probe design will be successful.

Access and Pricing

I only need to run one plate (96 samples) and have previously not been able to meet the minimum sample number needed for running an iSelect project with Illumina. How can I benefit from a consortium?

Researchers with as few as 48 samples can benefit from a consortium. Since the bead pool and the BeadChips will be manufactured for the entire consortium at once, as long as the minimum sample order (1,152 samples) is met by the community, individual researchers can order as few as 48 samples' worth of BeadChips.

How many samples can I assay on a BeadChip?

The number of samples that can be assayed on a single BeadChip depends upon the number of attempted bead types (or probes) needed. Most loci in any organism require only a single bead type, but some require two different bead types.

Samples per BeadChip

Attempted Bead Types per Sample	BeadChip Format
3,000 to 90,000	24-sample
90,001 to 250,000	12-sample
250,001 to 1,000,000	4-sample

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What do I need (e.g., reagents, etc.) to run the chips once the consortium BeadChips are shipped to me?

The per-sample price includes BeadChips and all reagents required to run the Infinium HD assay. Illumina recommends a minimum of 200 ng of DNA (> 50 ng/µl as measured by a fluorescent method of quantification) for best results. Access to an Illumina BeadArray Reader, iScan, or HiScan™SQ system is required for BeadChip scanning. For help finding a local service provider or core facility, or for information about Illumina's FastTrack Services, please contact Illumina Technical Support or your local account manager.

What is the consortium price?

Consortium pricing will depend upon the number of total attempted bead types and the number of samples submitted by the deadline determined by the consortium. For any given consortium opportunity, the appropriate density of markers and anticipated sample numbers will differ. Illumina will work directly with content and sample contributors to help identify possible pricing scenarios.

What is the minimum order I can place?

Minimum orders are for 48 samples (the smallest reagent kit configuration), provided that the minimum sample number (1,152) is achieved by the consortium. Re-orders can be placed for up to one year after bead pool manufacture.

Is there a limit to how many samples I can order at the consortium price?

There is no limit to the number of samples that can be ordered, provided the order is in 48-sample increments (47-sample increments for FastTrack Services). The smallest reagent kit configured for a shipment is based on a 48-sample format.

Can I reorder additional BeadChips?

The bead pool is manufactured in liquid phase and is available for a minimum of one year. When orders are filled, the liquid bead pool is stabilized onto BeadChips and processed through quality control, and these BeadChips are under warranty for a minimum of 6 months. This means that the effective time period during which experiments can be run on a bead pool is 18 months. Re-orders can be submitted any time during the lifetime of the bead pool.

Data Analysis and Sharing

My research competes with other interested parties, so I do not want my sample numbers widely publicized. Is it a requirement that other members know about my experiments?

Any information on sample numbers or experiments from each institution will be kept confidential. Individual consortium members can decide whether they are comfortable revealing the goals of their experiment to other consortium participants. Illumina will only divulge the total sample numbers pooled by all participants that will secure the consortium price.

Does Illumina's software discriminate among the three heterozygote and the two homozygote clusters in tetraploid genomes?

Illumina's GenomeStudio® Data Analysis Software currently supports automated calling and genotyping for bi-allelic SNPs and indels that meet the expectations of three possible clusters. Additional functionality includes manual calling and reporting of up to four alleles in up to five clusters. This would support bi-allelic SNPs that occur in tetraploid genomes. Illumina has an ongoing interest in supporting agriculture customers and seeks feedback from customers to help define needs for polyploid genomes.

How do I participate?

Researchers interested in the Agricultural Consortium program can contact a regional agriculture specialist by emailing consortiamanager@illumina.com. A specialist will be able to answer any additional questions and help place orders.

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