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International Goat Genome Consortium

Developing genotyping tools to improve breeding selection.

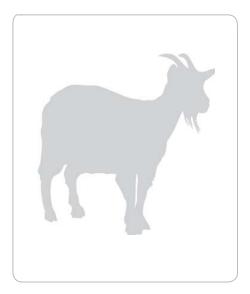## How many SNPs will be on the goat genotyping panel?

SNP content for the goat genotyping panel is still being finalized. It will be designed using 60,000 attempted bead types, with the final SNP number depending upon how many bead types are needed per SNP (some require two, most require only one), and the number of SNPs that pass Illumina quality control for internal redundancy and representation. We expect final content to be between 50,000 and 54,000 SNPs.

For which goat breeds are these SNPs considered appropriate?

Saanen, Alpine, Creole, Boer, Kacang, and Savanna goat breeds were used for SNP discovery. Therefore, one can expect that a high number of SNPs will be polymorphic in these breeds. Based upon experiences in designing other species-specific arrays, a large number of SNPs are expected to also be polymorphic in other breeds.

How were the SNPs discovered?

Several datasets generated by different members of the International Goat Genome Consortium were considered in SNP discovery. These datasets include *de novo* sequencing goat genome scaffolds, SNP discovery datasets from next-generation sequencing, and expressed sequences. SNP discovery data have been aligned on goat genome scaffolds using the BWA software[1,2]. SNP detection is being performed using mpileup from SAMtools[3].

How will the SNPs be selected?

SNPs for the goat genotyping panel are being annotated using expressed sequences together with data from the ovine (sheep) genome. Putative SNPs will be filtered using several criteria, including quality of the flanking sequence, no overlap with known complex regions, alleles identified by at least two reads, minimum six reads for each SNP, minimum estimated allele frequency, representation of genomic regions, and level of intra-specific polymorphism in a maximum number of breeds.

How will the SNP content be validated? How many of the SNPs can I expect to be segregating in my breeds?

Candidate goat SNPs will be validated and optimized for three to six different breeds. For the most up-to-date information, check http://www.goatgenome.org and http://snp.toulouse.inra.fr/~sigenae/50K_goat_snp_chip/index.html.

What will I need (reagents, etc.) to run the goat genotyping panel?

Participants will receive all reagents necessary to run the chips included in their order at the consortium per sample price. For robust results, Illumina recommends a minimum of 200 ng of DNA in a minimum concentration of 50 ng/µl (as measured by a fluorescent method of quantification). Access to an Illumina BeadArray™ Reader, iScan, HiScan™, or HiScanSQ™ system is required for processing the BeadChips. For customers with an instrument automation setup, a 24-sample tip guide is required. Information on service providers and core facilities can be found at www.illumina.com/services.ilmn or by contacting your Illumina Account Manager.

What is the minimum order I can place? Can I order through Illumina FastTrack Services?

The minimum order (considered a reorder of an existing beadpool) is for 288 samples. Illumina strongly recommends processing no fewer than 96 samples in any given project for the most reliable clustering and genotype calling. Orders for BeadChips must be received in multiples of 48 samples (the smallest reagent kit configuration). Projects done through FastTrack Services require a minimum sample order of 564. FastTrack orders must be in multiples of 47 to allow for two control samples per 96-well plate.

What is the consortium price?

Consortium pricing will depend upon the number of samples achieved worldwide by the deadline date determined by the consortium's content drivers. To understand the tiers possible in pricing, please talk to your Illumina Regional Agriculture Specialist or Account Manager. Customers will be invoiced for the per sample price after the deadline for submission of purchase orders.

What are the benefits and responsibilities of accessing this pricing?

Members of the consortium will have reorder privileges at the consortium price for one year from the date of manufacture of the bead pool. The minimum sample number for a reorder is 288 samples. All consortium members must reference the International Goat Genome Consortium, UNCEIA, Capgenes, Valogene, and APIS-GENE in any publications, public presentations, press releases, or public announcements resulting from the use of the consortium SNP content.

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

There is no upper limit on the number of samples that can be ordered for initial shipment. Requests for reorders (during the life of the bead pool) must be for at least 288 samples.

Can I reorder additional BeadChips? For how long?

The bead pool is manufactured in liquid phase and is available for one year from bead pool manufacture. When orders are filled (with a minimum order of 288 samples), the liquid bead pool is stabilized onto BeadChips and processed through quality control, with those BeadChips under warranty for a minimum of six months. Note that the effective time period during which experiments can be run on a bead pool is 18 months from initial manufacture. Reorders for a minimum of 288 samples can be submitted during the life of the bead pool.

I am in competition with other interested parties and do not want my interest in running samples widely publicized. Is it a consortia requirement that other members know about my experiments?

Any information about your orders will be kept confidential. You can decide whether you are comfortable revealing the goals of your experiment to the International Goat Genome Consortium participants. Illumina will only divulge the total sample numbers pooled by all participants when communicating the consortium price.

Will the International Goat Genome Consortium or Illumina be providing a cluster file for the genotyping positions?

The International Goat Genome Consortium may potentially provide a cluster file suitable for use in GenomeStudio™ data analysis software, which will allow calling of three cluster positions at each SNP locus. For the most up-to-date information on support for the goat genotyping panel, see http://www.goatgenome.org.

How do I participate?

Email consortiamanager@illumina.com and we will have a representative contact you to answer any additional questions and help you place your order.

References:

1. Li H. and Durbin R. (2009) Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 25:1754–1760. [PMID: 19451168]
2. Li H. and Durbin R. (2010) Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics 26: 589–595. [PMID: 20080505]
3. SAMtools.sourceforge.net

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