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# Agrigenomics Commercial, Collaborative, and Consortia Infinium® Arrays

## Commercial Products

| Species | Array Name[a] | No. of Markers | Add on Available | Description | Link to Data Sheet | Min. Sample Req.[b] |
|---|---|---|---|---|---|---|
| Cow | BovineLD | 7.9K | 80K | Accurate genotyping to understand the impact of genetics on milk production, reproduction, health, and more. | Data Sheet | 48 |
| Cow | Bovine SNP50v2 | 55K | 30K | High-throughput, cost-effective genetic screening in beef and dairy cattle, features evenly spaced SNP probes for genome-wide enabled selection, identification of quantitative trait loci (QTL), evaluation of genetic merit of individuals, and comparative genetic studies. | Data Sheet | 48 |
| Cow | BovineHD | 777K | N/A | Most comprehensive genome-wide bovine genotyping array, providing superior power to interrogate genetic variation across any breed of beef and dairy cattle. | Data Sheet | 48 |
| Dog | CanineHD | 170K | N/A | Enables the interrogation of genetic variation in any domestic dog breed for robust within-breed association and copy number variation studies. | Data Sheet | 48 |
| Corn | MaizeSNP50 | 50K | N/A | Highly polymorphic SNP content subjected to rigorous functional testing across over 30 diverse maize lines. | Data Sheet | 48 |
| Corn | MaizeLD | 3K | 70K | SNP selection is based on a comparison of pairwise distance data for maize inbred lines generated using SNP markers from the Maize SNP50 array and SSR markers previously shown to discern EDV status. | Data Sheet | 48 |
| Pig | Porcine SNP60 | 65K | 25K | Superior solution for interrogating genetic variation in multiple porcine breeds for whole-genome association studies, determination of genetic merit, identification of quantitative trait loci, and comparative genetic studies. | Data Sheet | 48 |
| Sheep | Ovine SNP50 | 54K | N/A | SNPs representing genome-wide selection (estimated one marker per 46 kb on average uniform coverage), identification of QTL, evaluation of genetic merit, cross-breed mapping, linkage disequilibrium studies, comparative genetic studies, and breed characterization for evaluating biodiversity. | Data Sheet | 48 |

a. For more information, visit our Library Prep and Array Kit Selector at www.illumina.com/library-prep-array-kit-selector.html
b. Number of samples that can be processed using the smallest kit configuration.

## GeneSeek Arrays

| Species | Array Name | No. of Markers | Add on Available | Description | Link to Data Sheet | Min. Sample. Req.[c] |
|---|---|---|---|---|---|---|
| Bos indicus | GGP Bos Indicus HD | 74K | N/A | USDA and Australian researcher collaboration. Built on the largest database of influential Nellore sires, plus a global collection of Brahman, Gir, and Girolando samples. Average spacing: ~35 kb | Data Sheet | 288 |
| Bos taurus and B. indicus | GGP Bovine LD (v3) | 26K | N/A | Developed for its imputation accuracy to higher density arrays, both ILMN catalog and GGP. The add-on content includes key diagnostic SNPs plus performance trait SNPs chosen for their expected or demonstrated impact on function. Overlap to the GGP Bovine uHD is essentially 100% and it makes an excellent low to mid density solution for genetic selection programs. Average spacing: 97 kb | Data Sheet | 288 |
| Bos taurus | GGP Bovine 150K | 134K | N/A | USDA collaboration. Includes diagnostic, ISAG parentage, and ILMN Bovine LD, SNP50, HD SNPs on multiple cattle breeds. Average spacing: ~20 kb (vs ~49 kb on ILMN 50K) with a higher concentration on the telomeric regions of the chromosome | Data Sheet | 288 |

# Information Sheet: Genotyping

| Species | Array Name | No. of Markers | Add on Available | Description | Link to Data Sheet | Min. Sample. Req.[c] |
|---|---|---|---|---|---|---|
| Pig | GGP Porcine HD | 70K | N/A | Built from ILMN PorcineSNP60k with additional SNPs provided by Univ. of Wageningen. SNPs selected for prediction accuracy in all the most influential pig breeding schemes globally. Add-on content includes several key diagnostic SNPs for marker assisted selection. ~20 important causative mutations included. Average spacing: 42 kb | Data Sheet | 288 |
| Pig | GGP Porcine LD | 10K | N/A | Designed and developed for imputation accuracy to higher density arrays including the ILMN Porcine60k and GGP Porcine HD. Add-on content includes key diagnostic SNPs for marker assisted selection and causative SNPs. Average spacing: 250 kb | Data Sheet | 288 |
| Horse | GGP Equine | 65K | N/A | Developed with the Equine SNP chip consortium, the GGP Equine array is the most comprehensive solution available for genome-wide genotyping and the standard for Equine research. SNP spacing, minor allele frequency, and call rate have been repeatedly demonstrated to be excellent for horse research and selection studies. Average spacing: ~35 kb | Data Sheet | 288 |
| Mouse | GIGA-MUGA | 140K | N/A | The SNPs were selected to be maximally informative, making the array a highly cost-effective tool for many genotyping applications. The MegaMUGA design criteria make it optimal for detecting heterozygous regions and discriminating between haplotypes in homozygous regions. SNPs were selected to be informative in most mouse populations, including wild mice and multiple Mus species, but with a special emphasis for markers that are informative in the Collaborative Cross and Diversity Outbred population resources. Average spacing: ~25 kb | Data Sheet | 288 |

c. Number of samples that can be processed using the smallest kit configuration.
For more information, visit our web page www.illumina.com/products/ggp-whole-genome-genotyping-arrays.html

# Open Consortia Products[d]

| Species | Consortium Name | No. of Markers | Add on Available | Description | Min. Sample Req.[e] |
|---|---|---|---|---|---|
| Alfalfa | Forage Genetics Alfalfa | 10.5K | 80K | High-density alfalfa genotyping array solution for alfalfa genetics applications. | 288 |
| Apple | Fruitbreedomics Apple20k | 20K | 70K | High-density apple genotyping array solution for fruit breeding applications. | 96 |
| Apple | RosBREED Apple | 9K | 80K | The apple genotyping panel was developed by RosBREED, a multiinstitutional, multinational project dedicated to the improvement of the Rosaceae crops with genomics, developed for use on worldwide breeding germplasm. | 48 |
| Brassica | International Brassica SNP Consortium | 52K | 25K | SNPs extracted and validated in 80 lines from *B.napus*, 4 lines from *B.oleracea*, and 4 lines from *B.rapa*, designed to work in any Brassica A or C genome species. | 48 |
| Cherry | RosBREED Cherry | 6K | 80K | The cherry genotyping panel was developed by RosBREED, a multiinstitutional, multinational project dedicated to the improvement of the rosaceous crops using targeted genomics. | 48 |
| Cotton | International Cotton SNP Consortium | 70K | 20K | The International Cotton SNP Consortium genotyping panel was developed with SNPs from *Gossypium hirsutum*, *G.barbadense*, *G.tomentosum*, and *G.mustelinum*. | 288 |
| Goat | International Goat Genome Consortium | 60K | 30K | Developed by the International Goat Genome Consortium with novel NGS scaffolds and latest genome sequence. Candidate goat SNPs were validated for Alpine, Angora, Boer, Creole, Jinlan, Katjang, Saanen, Savanna, and Skopelos breeds. | 48 |
| Grape | GrapeReSeq Consortium | 20K | 70K | This SNP genotyping tool is useful for mapping and evaluating genetic diversity in the Vitaceae gene pool to support the development of genetic resources and breeding programs that will reduce the use of chemical treatments in viticulture. | 96 |
| Oat | Oat Consortium | 6K | 80K | Private array developed by General Mills and Agriculture and AgriFood Canada, this Consortium is now open to additional interested researchers for oat genomic profiling. | 48 |
| Peach | RosBREED Peach | 9K | 80K | The peach genotyping panel was developed by RosBREED, a multiinstitutional, multinational project dedicated to the improvement of the rosaceous crops using targeted genomics. Suitable for worldwide breeding geoplasms. | 48 |

| Species | Consortium Name | No. of Markers | Add on Available | Description | Min. Sample Req.[e] |
|---|---|---|---|---|---|
| Pepper | UCD TraitGenetics Pepper (Capsicum) Consortium | 19K | 70K | The pepper genotyping panel enables cost-effective genotyping of multiple pepper species. Array contains expertly selected content derived from high-quality sequencing data of 22 pepper lines including sweet blocky peppers and hot peppers. | 192 |
| Potato | SOLCAP Potato 2013 | 10K | 80K | The potato genotyping panel was developed by the Solanaceae Coordinated Agricultural Project (SolCAP). SNP discovery was completed using Sanger-based SNPs from Kennebec, Bintje, and Shepody ESTs, along with SNPs identified by Illumina transcriptome sequencing. | 48 |
| Sheep/Ovine | AgResearch OvineLD Imputation Tool | 6K | 80K | The AgResearch Ovine Imputation Low Density tool consists of approximately 5,000 SNPs intended for imputation to the OvineSNP50 BeadChip. | 96 |
| Soybean | BARSoySNP6k | 6K | 80K | Developed by the Soybean Genomics and Improvement Lab, Beltsville Agricultural Research Center, for quantitative trait locus analysis and for screening the Soybean germplasm. Provides base content with even coverage of the genome. | 192 |
| Tomato | SolCAP Tomato 2013 | 9K | 80K | The SolCAP Tomato genotyping panel was designed by the Solanaceae Coordinated Agricultural Project (SolCAP) and is focused on translating the latest genomic advances to Solanaceae breeding programs. Content is from many lines. | 48 |
| Wheat | US/Australia 9k Wheat Consortium | 9K | 80K | Low density wheat genotyping array that allows the addition of custom content. | 48 |

d. Illumina consortia products are community-driven and are supported as custom products.
e. Number of samples that can be processed using the smallest kit configuration.
For more information on Consortia arrays visit www.illumina.com/applications/agriculture/consortia.html

## Agrigenomics Resources

**GeneSeek Arrays**

GGP Whole-Genome Genotyping Arrays

**Arrays: Custom**

iSelect (SNPs 3k-700k)

**Instruments: Array**

iScan, HiScan, AutoLoader

**Instruments: Sequencing**

MiSeq, NextSeq 500, HiSeq 2500, HiSeq 3000 / 4000

**Library Preparation**

Library Prep Kit Selector
TruSeq Synthetic Long-Read DNA Library Prep Kit
Ribo-Zero rRNA Removal Kit (Plant), ScriptSeq Complete Kit (Plant)
Ribo-Zero Gold rRNA Removal Kit (Human/Mouse/Rat)
TruSeq Stranded Total RNA with Ribo-Zero Globin
TruSeq Stranded Total RNA with Ribo-Zero Plant

**Additional Ag-focused Resources**

Agrigenomics publications
Agrigenomics blog articles
iCommunity articles
Agricultural Greater Good Initiative

## Learn More

For more information on consortia arrays, visit
www.illumina.com/applications/agriculture/consortia.html

For availability of other consortia arrays,
contact consortiamanager@illumina.com.
New products are regularly developed.

For more information on any of these products or to place an order, contact your Genotyping specialist or a local sales representative:

- North America: 800.809.4566
- Europe, Middle East, Africa: +44.1799.534000
- Other regions: www.illumina.com/company/contact-us.html

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