GGP

GeneSeek® Genomic Profiler™ Porcine 50K

The Next Generation of Porcine Genotyping

Developed in collaboration with corporate and academic scientists, the second generation GeneSeek® Genomic Profiler (GGP) for Porcine is built on the foundation of the most globally utilized porcine arrays ever developed. The GGP Porcine v2 array features more than 52,000 SNPs specifically chosen for optimal chromosomal spacing and high minor allele frequency values for use in most commercial breeding lines.

The GGP Porcine array also includes several genetic markers that may directly impact disease and performance traits:

Diseases

- Porcine stress syndrome (HAL)
- Rendement napole (RN)
- Resistance marker to *E. coli* (F4 ab/ac)
- PRRS tolerance marker (WUR100000125)

Performance Traits

- Feed intake
- Conversion/weight gain
- Lean growth/fat content
- Meat quality

The average single nucleotide polymorphism (SNP) spacing within the genome is approximately 45 kb (Sus scrofa 11.1) with a higher concentration on the telomeric regions of the chromosome.

Chromosome	Locus Count	Length Covered (bp)	Percentage of Reference Chromosome Covered (%)	Mean Spacing (bp)	Max Spacing (bp)
1	5,038	274,126,849	99.9	54,423	1,595,559
2	3,359	151,357,860	99.6	45,074	804,492
3	2,976	132,538,400	99.8	44,551	814,329
4	3,050	130,772,296	99.9	42,890	693,862
5	2,362	104,255,481	99.7	44,157	976,964
6	3,529	170,724,337	99.9	48,391	1,130,801
7	2,854	121,608,102	99.8	42,625	582,346
8	3,020	138,801,597	99.9	45,976	1,003,318
9	3,233	139,310,738	99.9	43,104	833,250
10	1,609	69,130,541	99.7	42,992	424,450
11	1,890	79,014,180	99.8	41,829	366,195
12	1,422	60,934,130	98.9	42,881	481,381
13	3,770	207,996,524	99.8	55,186	992,494
14	3,382	141,672,876	99.9	41,903	754,202
15	3,003	140,132,670	99.8	46,680	641,725
16	1,886	79,253,250	99.1	42,044	719,342
17	1,486	61,598,438	97.0	41,480	443,493
18	1,328	55,663,571	99.4	41,947	381,185
X	2,318	125,368,167	99.5	54,108	782,122
Y	29	43,151,307	99.1	1,598,197	29,558,799

Accurate Imputation

The GGP Porcine array provides a very robust solution for imputation to higher density arrays such as the GGP Porcine HD (80k) array. The average imputation accuracy is 99.4% across all chromosomes.

Chromosome	Imputation Accuracy (%)
1	99.90
2	99.92
3	99.97
4	99.96
5	99.95
6	99.97
7	99.92
8	99.88
9	99.88
10	99.97
11	99.95
12	99.97
13	99.92
14	99.92
15	99.98
16	99.90
17	99.97
18	99.94
X	100
Average	99.93

Validated Breeds

The GGP Porcine array has been validated in many economically important pig breeds. In addition to spacing, SNPs were selected for high minor allele frequency (MAF) values.

Breed	Number of Polymorphic SNPs	Het Rate Average
Berkshire	46470	0.285
Chester White	47135	0.337
Duroc	43195	0.286
Fengjing	29754	0.191
Guam Feral	33579	0.241
Guinea Hog	28458	0.272
Hampshire	43719	0.275
Hawaiian Feral	47015	0.286
Hereford	42487	0.291
Landrace	47674	0.364
Large Black	26929	0.250
Mangalitsa	23189	0.226
Meishan	28434	0.172
Minzhu	46204	0.314
Ossabaw Island	29204	0.253
Spotted	43565	0.318
Tamworth	42697	0.328
Yorkshire	47791	0.336

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