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The use of accurate pedigrees is important for livestock production systems and research projects. We present the development and attributes of a SNP panel for the assignment of parentage in sheep.

Figure 1: Work Flow for SNP Panel Design

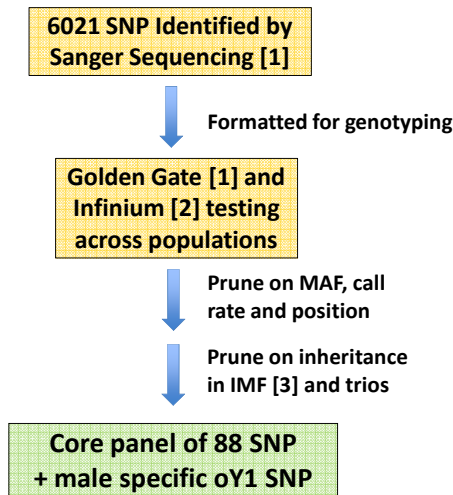


Table 1: SNP ID and Genomic Location for Core SNP

Core SNP	Chr	Mb Pos	Allele	MAF	Core SNP	Chr	Mb Pos	Allele	MAF	Core SNP	Chr	Mb Pos	Allele	MAF
DU290101_408.1	1	7.8	A	0.337	DU194639_560.1	6	56.7	G	0.442	DU426312_454.1	15	44.4	G	0.375
DU518561_359.1	1	14.2	G	0.381	C2925803_293.1	6	100.8	A	0.443	DU301502_402.1	15	73.7	G	0.441
DU351298_316.1	1	69.6	A	0.445	DU337465_337.1	6	106.0	A	0.338	DU241306_191.1	15	78.6	G	0.279
DU232924_365.1	1	95.8	G	0.250	CL635944_160.1	6	115.0	A	0.490	DU324670_456.1	17	10.2	A	0.400
DU271929_382.1	1	97.5	A	0.483	DU467751_524.1	7	10.6	A	0.429	DU206327_107.1	17	14.4	A	0.499
DU502334_443.1	2	19.1	A	0.437	DU499587_509.1	7	74.0	A	0.325	DU378819_632.1	17	22.3	A	0.475
DU469454_586.1	2	26.2	G	0.394	C2920950_468.1	7	74.8	A	0.456	DU511222_139.1	17	27.4	A	0.351
DU425907_184.1	2	50.1	G	0.358	DU530067_219.1	7	100.0	G	0.327	DU300156_445.1	17	38.0	G	0.456
DU501115_497.1	2	62.8	A	0.239	DU213735_493.1	8	6.6	A	0.437	DU463532_137.1	17	56.0	A	0.443
DU492516_411.1	2	63.4	T	0.478	DU411204_551.1	8	13.8	A	0.361	DU492379_209.1	18	3.9	A	0.385
DU470875_383.1	2	91.5	G	0.357	DU189970_325.1	9	86.6	C	0.374	DU488903_267.1	18	21.4	G	0.334
Z50506CS_1	2	100.9	G	0.345	DU471913_499.1	9	91.1	G	0.490	DU325612_517.1	18	25.4	A	0.433
DU191879_495.1	2	157.6	A	0.335	DU364754_308.1	9	93.9	A	0.397	DU440765_491.1	18	60.5	A	0.474
DU480434_533.1	2	192.2	A	0.480	DU372582_268.1	9	94.4	G	0.247	DU453994_399.1	18	61.1	A	0.450
DU260201_585.1	2	226.7	A	0.422	DU468275_284.1	10	33.1	A	0.352	DU264531_279.1	19	0.6	A	0.388
DU503161_123.1	2	237.2	A	0.352	DU310747_445.1	10	38.2	G	0.470	DU258055_237.1	19	57.2	A	0.400
DU425259_620.1	3	21.4	A	0.461	DU256964_582.1	11	1.9	A	0.473	DU411432_523.1	19	57.2	C	0.406
DU231007_156.1	3	59.0	G	0.463	DU433863_261.1	11	15.5	A	0.419	DU183112_480.1	20	31.1	A	0.453
DU225323_218.1	3	91.0	A	0.467	DU417675_79.1	11	19.6	A	0.344	DU442375_141.1	20	48.4	A	0.342
DU260081_579.1	3	108.8	A	0.383	DU508448_227.1	11	25.3	A	0.485	DU380983_440.1	21	28.3	G	0.451
DU394537_289.1	3	181.6	G	0.371	DU326572_241.1	11	59.5	A	0.446	DU383863_376.1	21	38.2	G	0.443
CL635241_413.1	3	181.9	A	0.455	DU314655_578.1	12	26.7	A	0.365	DU196132_525.1	21	42.7	G	0.388
DU408817_431.1	3	205.0	A	0.343	DU310703_497.1	12	75.3	A	0.492	DU413316_575.1	22	13.1	A	0.419
DU202116_405.1	4	58.2	A	0.444	DU275428_276.1	13	10.9	A	0.460	DU302760_528.1	23	11.6	G	0.494
DU460511_423.1	4	61.1	G	0.443	DU435573_466.1	13	30.1	A	0.449	DU313102_671.1	23	17.3	G	0.484
DU305004_417.1	4	70.1	A	0.270	DU411403_398.1	13	41.3	G	0.427	C2920359_258.1	24	3.2	G	0.382
DU369175_467.1	4	73.0	G	0.375	DU462008_263.1	14	44.6	A	0.330	DU455254_479.1	25	0.1	G	0.453
DU446213_412.1	5	12.5	A	0.394	DU223894_556.1	14	57.5	G	0.449	DU512685_259.1	25	1.2	G	0.495
DU444709_372.1	5	56.0	A	0.489	DU381045_479.1	14	60.7	A	0.403	oY1	Y	0.0	G	0.320
DU453259_440.1	5	64.8	G	0.346	DU464373_638.1	15	2.3	A	0.467					

Table 1. The genomic location of each SNP (Chr / Mb Pos) is taken from the genome assembly version OAR2.0 available at [4]. SNP identifiers can be used to obtain additional information about each SNP [4]. The minor allele is given along with its frequency (MAF) in 2384 animals [2].

The genomic position and average minor allele frequency (MAF) of each SNP is given in Table 1. SNP were selected using population allele frequencies obtained from over 70 breeds sampled from 5 continents. The panel is biased towards high MAF markers (Figure 2) to ensure it will be of use across a wide range of breeds.

Figure 2: MAF

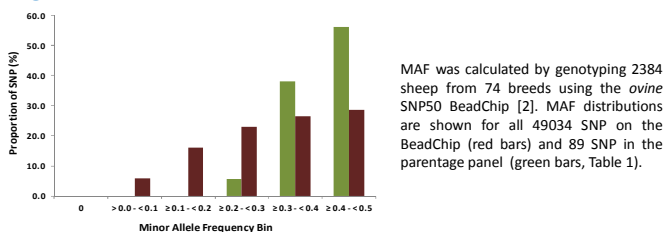
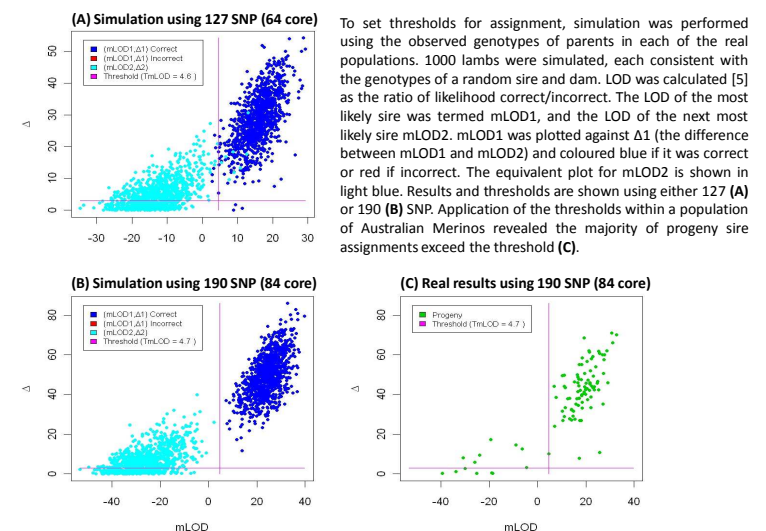


Figure 3: Performance Within an Australian Flock



The core panel of 89 markers was supplemented with additional SNP for testing within Australian flocks that included markers for Horn Poll and disease genes. A total of 6 Sequenom (SQ) multiplexes (383 SNP) were developed and tested for their genotyping accuracy and performance. This sought to identify the minimum number of SNP panels required for achieve high rates of assignment.

Key Points

- * We have identified a technically robust set of SNP suitable for parentage analysis in a wide variety of sheep.
- * Disclosure of the SNP and their attributes is intended to promote uptake by commercial partners.
- * The core panel is being promoted to the International Society of Animal Genetics (ISAG) as the standard for testing in sheep.
- * Using industry Merinos, we find application of 3 SQ plexes (190 SNP) returned high rates of assignment.
- * Wide applicability of the SNP panels opens the way for international level trace-back and product of origin testing.

[1] Kijas et al. (2009) *PLoS ONE* 4:e4668

[2] Kijas et al. (2012) *PLoS Biology* 10:e1001258

[3] Crawford et al. (1995) *Genetics* 140:703-724.

[4] <http://www.livestockgenomics.csiro.au/sheep/oar2.0.php>

[5] Marshall et al. (1998) *Molecular Ecology* 7: 639-655.