# **SmartGene for Beef**

# Effect of marker genotypes on phenotypic performance

# **Research Report**

by

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On behalf of the SmartGene for Beef Committee

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#### **Executive Summary**

A total of 11,579 animals with genotypes on up to 12 GeneSTAR<sup>®</sup> DNA markers were received from Catapult Genetics for animals recorded in Beef CRC1 and CRC2 progeny test projects. Of these records a total of 8,674 animals were matched to the phenotypic data for the traits of interest in this current study (i.e. tenderness, marbling and feed efficiency) from CRC1 (7 breeds) and CRC2 (2 breeds). Genotypes for the 12 markers were also available on 742 Angus progeny test program animals and of those 399 had phenotypic data for either marble score or net feed intake. Genotypic data for the Shorthorn breed was limited to an initial 340 animals with mainly marbling and net feed intake records.

Allele frequencies were estimated using all genotyped animals for the 12 markers in each breed and dataset. Gene frequencies varied significantly between breeds and markers with some very extreme values estimated (>0.98) which made it difficult to accurately estimate the size of effects and also limits the utility of these markers in evaluation and selection programs for that breed. Most observed gene frequencies were in Hardy-Weinberg equilibrium.

The effects of the 12 markers were estimated using various statistical models and by treating the markers as individual SNP (fitted individually and jointly) or as a combined panel by considering them as "total stars" for each of the three marker complexes.

**Tenderness markers.** The three tenderness markers (T1, T2 and T3) were estimated to have significant effects in tropically adapted breeds for measures of meat tenderness in this data. The markers effects showed shear force reducing (i.e. more tender meat) with increasing number of favourable alleles for each marker and as a total star panel. The effects were consistent also for MSA consumer taste panel score, ST muscle shear force and shear force from tender stretched carcases, but the magnitude of the marker effects for the later two measures were reduced. For the temperate breeds, the T1 and T2 markers were estimated to have significant effects on LD shear force but for T3 the effect was not significant. Tenderness marker T4 was not significantly associated with tenderness measures and varied in direction, with the exception of Brahmans from CRC1 only. The tenderness markers were estimated to explain between 5 and 17% of the sire variance in shear force across the datasets.

**Marbling markers.** In these various datasets, which had low to moderate levels of marbling, none of the four marbling markers were estimated to have significant or consistent effects, when considered as markers or as total stars, on IMF or marble score. The extreme gene frequencies of many of the marbling markers made it difficult to assess the 2 star genotype in most of the breeds studied, however estimates of differences between 0 and 1 stars were also inconsistent. Removing breed and sire from the analytical models in CRC1 data resulted in significant estimates of the effects of the markers and suggests the marbling markers are partly confounded with breed, and in the absence of breed act to explain breed differences in the marbling traits but the degree to which they are able to do this was very small.

**Feed efficiency markers.** The four feed efficiency markers were assessed in six datasets where all animals were feed intake tested on feedlot finishing rations. Results showed two of the feed efficiency markers (N3 and N4) were significant in the CRC1

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temperate breed dataset for net feed intake (NFI) and daily feed intake (DFI) but were not observed to have significant effects in other datasets, and direction of effects for NFI were not consistent. Feed efficiency markers N1 and N2 were not observed to have significant effects on any trait, and their high gene frequency in all populations for the 2 star allele, especially in tropical breeds limit their utility for breeding. When modelled as total stars the effects of the feed efficiency markers were significant in CRC1 temperate breeds for NFI and DFI but in the other datasets were not significant and not consistent in their direction of effects. The effects of the four feed efficiency markers on feed conversion ratio and feedlot average daily gain were not significant. It should be noted that data from the CRC-1 was used to discover the four markers.

The estimated size of effects of these markers together with the marker frequencies from this project, along with a large number of marker genotypes from commercial seedstock animals, are being used in BREEDPLAN to calculate marker enhanced estimated breeding values (denoted EBV<sup>M</sup>) by incorporating traditional measures of phenotype and pedigree with the marker information. First release of trial BREEDPLAN EBV<sup>M</sup> for tenderness in Brahmans is planned for early October 2008. Release for other breeds will follow quickly thereafter.

#### 1.0 Introduction

To combine the traditional systems of genetic evaluation (Animal Model BLUP) with genotypic information (e.g. GeneSTAR markers) requires good estimates of the heritabilities of the traits, the size of the effects of the markers and the gene frequencies in the various populations. Heritability estimates are plentiful in the literature, including many Australian studies, whereas information on marker effects and gene frequencies are not yet plentiful.

To allow the further development of BREEDPLAN towards marker enhanced EBVs, and to establish the effects of the GeneSTAR markers in a number of well recorded Australian purebred cattle populations with specific emphasis on the *Bos indicus* derived breeds of northern Australia, the Queensland government funded the genotyping of approximately 14,000 animals whose DNA was available through the Beef CRC1 and 2 as well as two commercial breed society progeny test programs.

This report presents the results of the analysis performed by the Animal Genetics and Breeding Unit, which merged the genotypic information as provided by Catapult Genetics with the phenotypic data and management information as stored in the CRC1 and CRC2 databases as well as in the National Beef Recording Scheme (NBRS) database (at ABRI) for the progeny test data.

#### 2.0 Phenotypic datasets

The animals genotyped in the SmartGene project came from four different experiments conducted over the past decade. Mean unadjusted phenotypic performance and standard deviations for the target traits of the SmartGene for Beef project (i.e. tenderness, marbling, feed efficiency) are presented in Appendix A by experiment and breed.

2.1 Beef CRC1. This dataset from Beef CRC1 consisted of seven purebred breeds, four temperate breeds (Angus, Hereford, Murray Grey and Shorthorn) and three tropically adapted breeds (Brahman, Santa Gertrudis and Belmont Red). These cattle were born between 1993 and 1998. The basic design of the project and the phenotypic and genetic parameters extracted for these analyses have been described by Upton et al. (2001), Johnston et al. (2003) and Reverter et al. (2003). In brief, the progeny were generated over a number of years in various producer/breeder herds which had only one breed, so herd of origin and breed are confounded. Progeny (both steers and heifers) were purchased by the CRC at weaning and then backgrounded as cohorts in mixed breed groups, finished (either feedlot or pasture) and slaughtered together at the three target market endpoint weights. Daily feed intake was recorded on a sub-set of the feedlot finished groups and comprised of 785 temperate animals (steers only) and 696 tropically adapted animals (steers and heifers). Animals were from all three markets where the mean age at the start of the feed test ranged from 459 days (temperate domestic steers) to 737 days (for tropically adapted Japanese market steers). The average number of days on test for domestic, Korean and Japanese market animals was 53, 57 and 74 days, respectively.

At slaughter all carcases were electrically stimulated and chiller assessment of marble score was done by both AUS\_MEAT and MSA technicians. At 24 h post-mortem a

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sample of the *longissimus lumborum* (LD) and *semitendinosus* (ST) muscles were taken and frozen for later analyses (see Perry *et al.* 2001 for full details). Warner-Bratzler shear force measure of tenderness was taken on a cooked sample (equating to only about two days ageing). Intramuscular fat percentage (IMF%) was determined using either near infra red (NIR) technology or ether extraction. Approximately half the carcases (from June 1996 onwards) were assessed through the MSA consumer taste panel process using a sample of the LD aged for 14 days.

**2.2 Beef CRC2.** These data were from the Beef CRC2 northern breeding project (Burrow *et al.* 2003) and consisted of tropically adapted cattle with purebred Brahman as one group and Tropical Composite (from various pastoral companies) as another. These cattle were born between 1999 and 2003. This data has been described by Barwick *et al.* 2008 and Wolcott *et al.* 2008. Only one herd (Belmont Research Station) had direct comparisons between Brahman and the Tropical Composite. Genotypes were available on both steers and heifers. However, for the traits examined in this project, only steer phenotypes were available. Steers were assembled at weaning into groups that were backgrounded at various locations. At approximately 400 kg liveweight the whole cohort entered the feedlot, were fed for 120 days prior to being slaughtered as a single group, with an average carcase weight of 300-320 kg. HPGs were used from weaning onwards through to finishing. Daily feed intake was recorded on about two thirds of the steers for an average of 71 days and an average age at start of test was 700 days.

At slaughter carcases were not electrically stimulated and the right side of the carcase were normal Achilles tendon hung (NH) and the left sides were tender stretched (TS) using the procedure first described by Hostetler *et al.* (1975). Tender stretching changes the tension on the muscles during cooling and affects meat tenderness, particularly of the higher value loin muscles. After 24 hr post-mortem, a sample of the LD muscle only, from both NH and TS sides, was used for meat quality assessments (as per CRC1 protocols).

**2.3 Angus Australia progeny test**. These data were from the Angus progeny test program conducted using the NSW DPI Trangie Angus herd. Three calf crops were generated during 2002-2004 using 13, 13 and 12 sires, respectively. All males were castrated and carcase data of 415 progeny became available. Steers were backgrounded postweaning and entered the feedlot and were fed for approximately 150 days to an average carcase weight of 370 kg. NFI data were available on a total of 387 steers that were fed for an average of 70 days with an average age at the start of test of 535 days. All steers within a cohort (year location) were slaughtered at the same time and carcase and chiller assessment data were recorded on all steers. The phenotypic data was recorded in the Angus NBRS database and a separate extract was obtained for this study. Genotypic data were provided by Angus Australia.

**2.4 Durham Shorthorn progeny test**. Genotypic data on a sub-set of the Durham Shorthorn steers were available for analysis of feed intake and marbling markers. These were then matched with the phenotypic records. Feed intake were recorded at the Tullimba feedlot for the "domestic" finished steers that entered the feedlot at an average age of 14 months and were feed intake tested under the standard 70d test period. Slaughter and abattoir chiller data were available through the Durham and NBRS databases.

#### 3.0 Genotypic data

Genotypic data was supplied by Catapult Genetics via a series of excel spreadsheets. The files contained an internal DNA identification number for each animal and then the genotypic results for the 12 markers. Results were presented as 0, 1, 2 alleles thus the direction of the "favourable" allele was predetermined. Any genotype that was failed to be called was coded as "NR" (i.e. no-result). The files were merged using a cross-reference file to the phenotypic data on each animal.

#### 3.1 Data quality control

As part of quality control Tables 1-4 presents the number of genotyped animals from each project that were not assigned a genotype (i.e. "NR" call). For CRC1 (Table 1), 63.7 % of the 6844 animals had all 12 markers scored, while 3.2% had five or more markers with no reading. Of the 12 markers, most had a "no-result" call rate of around 5% however there were two exceptions T2 at 15% and M2 at 18%.

 Table 1: Number genotyped animals from of CRC1 with missing marker readings by marker group and in total.

	~,			
Missing			Feed	
markers	Tenderness	Marbling	Efficiency	all traits
0	5560	5337	6207	4359
1	1102	1183	409	1644
2	68	227	93	462
3	71	55	93	117
4	43	42	42	44
>4				218
	6844	6844	6844	6844

In CRC2 (Table 2) only 56.2 % of animals had all 12 markers scored while 7.2% had 5 or more missing markers. Of the 12 markers most had a "no-result" call of around 5% however there were 2 exceptions T2 at 25% and M2 at 19%.

Table 2: Number genotyped animals from of CRC2 with missing marker
readings by marker group and in total.

0	<b>v</b> 0			
Missing			Feed	
markers	Tenderness	Marbling	Efficiency	all traits
0	3266	3612	4258	2661
1	1193	723	268	1305
2	70	298	36	315
3	147	57	138	87
4	59	45	45	24
>4				343
	4735	4735	4735	4735

Table 3: Number genotyped animals from Angus progeny test with mis	ssing
marker readings by trait and in total.	

Missing			Feed	
markers	Tenderness	Marbling	Efficiency	all traits
0	618	674	723	566
1	109	47	19	133
2	6	21		26
3	1			6
4	8			2
>4				9
	742	742	742	742

In the Angus progeny test data (Table 3) 76% of animals had all 12 markers scored but only 1% had 5 or more markers missing. Of the 12 markers most had a "no-result" call of around 2% however there were two exceptions T3 at 16% and M2 at 8%.

#### 3.2 Allele Frequencies

The following tables present number of animals with various genotypes, calculated allele frequencies and significance of deviation from Hardy-Weinberg equilibrium.

Breed/dataset			Tende	rness			Marbli	ng		Feed Efficiency			
		T1	T2	Т3	T4	M1	M2	M3	M4	N1	N2	N3	N4
AA – CRC1	NR	38	235	52	45	93	247	43	52	34	78	95	53
	0	17	365	47	, o	600	707	1070	705	23	53	240	218
	0	000	505	400	040	505	057	1070	705	20	450	240	210
	1	290	527	403	218	505	357	220	513	261	450	605	691
	2	1001	219	844	1074	58	35	13	76	1028	765	406	384
HH - CRC1	NR	32	119	48	23	68	138	33	34	40	52	75	44
	0	19	574	33	0	725	857	802	632	25	0	151	276
	1	311	276	298	0	217	28	183	325	215	78	476	515
	2	661	54	644	1000	13	0	5	32	743	893	321	188
	~	001	04	044	1000	10	U	0	02	740	000	021	100
		10	65	22	10	20	50	21	11	10	27	20	27
311- CKC1		10	250	20	12	29	200	200	044	10	21	07	21
	0	0	352	300	0	297	360	362	214	9	1	87	19
	1	6	10	35	30	89	17	32	170	95	17	190	107
	2	411	0	3	385	12	0	2	29	313	382	120	274
MG –CRC1	NR	13	44	19	12	37	93	15	17	12	22	30	16
	0	5	98	17	7	155	220	383	315	1	71	90	192
	1	101	179	139	113	196	117	34	92	55	224	215	191
	2	314	112	258	301	45	3	1	9	365	116	98	34
	_	011		200	001	10	Ŭ		Ŭ	000	110	00	01
	NR	03	463	142	92	227	528	122	117	96	170	230	140
		11	1320	463	16	1967	2144	2617	1966	58	125	569	705
	1	700	1009	403	204	1007	Z 144 E 4 0	2017	1400	00	700	1400	100
	1	708	992	8/5	301	1007	519	469	1100	020	769	1480	1504
	2	2387	385	1749	2760	128	38	21	146	2449	2156	945	880
											_	_	
Angus PT	NR	15	14	117	10	27	58	0	4	1	5	7	6
	0	3	426	77	2	304	341	545	461	39	16	68	152
	1	107	252	288	70	328	306	193	257	168	181	370	372
	2	617	50	260	660	83	37	14	20	534	540	297	212
SH Durham	NR	4	0	7	2	14	0	2	9	99	5	9	7
	0	2	333	284	1	250	345	324	186	1	3	109	20
	1	14	14	53	28	77	2	18	120	129	25	160	143
	2	327	0	3	316	6	0	3	32	118	21/	60	177
	2	521	0	5	510	0	0	5	52	110	514	09	177
		10	220	22	10	17	000	10	10	10	10	47	10
		12	220	23	12	17	222	10	704	10	10	17	13
	0	156	605	582	195	840	26	855	781	5	0	3	38
	1	427	51	247	432	19	275	5	79	150	18	68	301
	2	281	0	24	237	0	353	0	4	711	842	788	524
SG –CRC1	NR	34	152	32	36	50	227	22	25	27	24	59	30
	0	96	592	530	66	1079	343	1213	1105	15	1	51	65
	1	492	432	518	449	116	507	13	118	227	113	411	427
	2	626	72	168	697	3	171	0	0	979	1110	727	726
	-	020	12	100	007	Ŭ		Ũ	Ŭ	010	1110	121	120
BR = CRC1	NR	31	202	40	30	70	224	37	45	37	55	74	35
		60	440	244	1	1070	562	1240	1001	117	00	210	120
	1	500	44Z	244	4 100	12/0	644	1240	220	E 4 0	100	212	129
		522	595	094	193	130	011	201	338	518	130	080	/1/
	2	870	252	513	1255	4	93	(	27	819	1300	625	610
All Tropical	NR	77	574	95	87	146	673	75	82	74	95	150	78
	0	320	1639	1356	265	3197	932	3308	2967	137	1	266	232
	1	1441	1078	1459	1074	265	1393	225	535	895	267	1059	1445
	2	1777	324	705	2189	7	617	7	31	2509	3252	2140	1860

 Table 4: Number of animals by breed and genotype, CRC1 data and two field data sets

Breed/dataset			Tender	mess			Marblir	ng		Feed Efficiency			
		T1	T2	Т3	T4	M1	M2	M3	M4	N1	N2	N3	N4
AA – CRC1	р	0.124	0.566	0.192	0.091	0.752	0.806	0.906	0.743	0.117	0.219	0.434	0.436
	q	0.876	0.434	0.808	0.909	0.248	0.194	0.094	0.257	0.883	0.781	0.566	0.564
HH – CRC1	р	0.176	0.788	0.187	0.000	0.873	0.984	0.903	0.803	0.135	0.040	0.410	0.545
	q	0.824	0.212	0.813	1.000	0.127	0.016	0.097	0.197	0.865	0.960	0.590	0.455
						_							
SH – CRC1	р	0.007	0.986	0.949	0.036	0.858	0.977	0.955	0.724	0.135	0.024	0.458	0.181
	q	0.993	0.014	0.051	0.964	0.142	0.023	0.045	0.276	0.865	0.976	0.542	0.819
MG –CRC1	р	0.132	0.482	0.209	0.151	0.639	0.819	0.957	0.868	0.068	0.445	0.490	0.689
	q	0.868	0.518	0.791	0.849	0.361	0.181	0.043	0.132	0.932	0.555	0.510	0.311
All Temperate	р	0.126	0.681	0.292	0.063	0.790	0.890	0.918	0.776	0.118	0.167	0.437	0.472
	q	0.874	0.319	0.708	0.937	0.210	0.110	0.082	0.224	0.882	0.833	0.563	0.528
Angus PT	р	0.078	0.758	0.354	0.051	0.655	0.722	0.853	0.799	0.166	0.145	0.344	0.459
	q	0.922	0.242	0.646	0.949	0.345	0.278	0.147	0.201	0.834	0.855	0.656	0.541
SH Durham	р	0.026	0.980	0.913	0.043	0.866	0.997	0.965	0.728	0.264	0.045	0.559	0.269
	q	0.974	0.020	0.087	0.957	0.134	0.003	0.035	0.272	0.736	0.955	0.441	0.731
<b>DU</b> 0004		0.400	0.004		0.470	0.000	0.050	0.007	0.050		0.040		0.040
BH – CRC1	р	0.428	0.961	0.827	0.476	0.989	0.250	0.997	0.950	0.092	0.010	0.043	0.218
	q	0.572	0.039	0.173	0.524	0.011	0.750	0.003	0.050	0.908	0.990	0.957	0.782
00.0004						0.040	0 504	0.005	0.050	0.405	0.047	0.040	
SG –CRC1	р	0.282	0.737	0.649	0.240	0.949	0.584	0.995	0.952	0.105	0.047	0.216	0.229
	q	0.718	0.263	0.351	0.760	0.051	0.416	0.005	0.048	0.895	0.953	0.784	0.771
<b>DD</b> 0D04		0.005	0 574	0.407	0.000	0.054	0.005	0.004	0.004	0.050	0.047	0.054	0.005
BR – CRC1	р	0.225	0.574	0.407	0.069	0.951	0.685	0.924	0.864	0.259	0.047	0.354	0.335
	q	0.775	0.426	0.593	0.931	0.049	0.315	0.076	0.136	0.741	0.953	0.646	0.665
		0.004	0 740	0.500	0.007	0.000	0.554	0.000	0.040	0.405	0.000	0.000	0.070
All Tropical	р	0.294	0.716	0.592	0.227	0.960	0.554	0.966	0.916	0.165	0.038	0.230	0.270
	q	0.706	0.284	0.408	0.773	0.040	0.446	0.034	0.084	0.835	0.962	0.770	0.730

# Table 5: Allele Frequency for Table 5 (p= unfavourable allele), frequencies >0.8 are highlighted (light) and those about 0.9 (dark)

Breed/sex			Tende	rness			Marbli	ing			Feed Efficiency			
		T1	T2	Т3	T4	M1	M2	М3	M4	N1	N2	N3	N4	
BH M	NR	61	216	74	63	59	250	43	62	57	45	47	46	
	0	110	734	669	290	919	28	958	853	7	0	3	29	
	1	455	50	241	457	28	248	5	90	151	15	85	253	
	2	380	6	22	196	0	480	0	1	791	946	871	678	
BH F	NR	23	239	51	30	45	212	32	28	30	29	33	33	
	0	126	743	673	325	956	25	994	916	3	0	4	27	
	1	452	43	278	478	32	273	7	88	132	15	94	253	
	2	432	8	31	200	0	523	0	1	868	989	902	720	
BH all	NR	84	455	125	93	104	462	75	90	87	74	80	79	
	0	236	1477	1342	615	1875	53	1952	1769	10	0	7	56	
	1	907	93	519	935	60	521	12	178	283	30	179	506	
	2	812	14	53	396	0	1003	0	2	1659	1935	1773	1398	
ТС М	NR	73	342	104	76	80	201	65	73	91	67	65	64	
	0	85	501	352	66	989	471	1024	927	56	0	74	108	
	1	453	329	545	364	163	465	142	224	369	39	432	484	
	2	626	65	236	731	5	100	6	13	721	1131	666	581	
TC F	NR	71	307	103	85	90	205	60	82	96	60	65	60	
	0	82	522	350	65	911	460	954	839	43	1	67	79	
	1	431	282	516	372	157	388	141	221	345	45	406	446	
	2	579	52	194	641	5	110	8	21	679	1057	625	578	
TC all	NR	144	649	207	161	170	406	125	155	187	127	130	124	
	0	167	1023	702	131	1900	931	1978	1766	99	1	141	187	
	1	884	611	1061	736	320	853	283	445	714	84	838	930	
	2	1205	117	430	1372	10	210	14	34	1400	2188	1291	1159	

#### Table 6: Number of CRC2 animals by sex and genotype for markers 12 markers

Note: total numbers less than Table 2 because 296 animals were genotyped that were not assigned a breed code (i.e. not delivered to CRC)

Breed/sex			Tende	rness			Marblin	ng			Feed Efficiency			
		T1	T2	Т3	T4	M1	M2	M3	M4	N1	N2	N3	N4	
BH M	р	0.357	0.961	0.847	0.550	0.985	0.201	0.997	0.951	0.087	0.008	0.047	0.162	
	q	0.643	0.039	0.153	0.450	0.015	0.799	0.003	0.049	0.913	0.992	0.953	0.838	
BH F	р	0.349	0.963	0.827	0.562	0.984	0.197	0.997	0.955	0.069	0.007	0.051	0.154	
	q	0.651	0.037	0.173	0.438	0.016	0.803	0.003	0.045	0.931	0.993	0.949	0.847	
BH all	р	0.353	0.962	0.837	0.556	0.984	0.199	0.997	0.953	0.078	0.008	0.049	0.158	
	q	0.647	0.038	0.163	0.444	0.016	0.801	0.003	0.047	0.922	0.992	0.951	0.842	
ТС М	р	0.268	0.744	0.551	0.214	0.925	0.679	0.934	0.893	0.210	0.017	0.247	0.298	
	q	0.732	0.256	0.449	0.786	0.075	0.321	0.066	0.107	0.790	0.983	0.753	0.702	
TC F	р	0.272	0.775	0.574	0.233	0.922	0.683	0.929	0.878	0.202	0.021	0.246	0.274	
	q	0.728	0.225	0.426	0.767	0.078	0.317	0.071	0.122	0.798	0.979	0.754	0.726	
TC all	р	0.270	0.759	0.562	0.223	0.924	0.681	0.932	0.886	0.206	0.019	0.247	0.286	
	q	0.730	0.241	0.438	0.777	0.076	0.319	0.068	0.114	0.794	0.981	0.753	0.714	

Cable 7: Allele Frequenc	y CRC2 datasets (p= uni	favourable allele) frequencies	s >0.9 are highlighted
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**3.2.1 Summary of gene frequencies.** Comparing the allele frequencies of different experiments for the same breed shows only small differences. However significant differences between breeds in allele frequencies exist. These frequencies could be further compared with the frequencies in the NBRS recorded "commercial" populations.

Some noticeable results are the very high frequencies of the "unfavourable" alleles for T2 and T3 in Shorthorn, which is similar to the Brahman frequencies for these two markers. Also worth noting is the allele frequency of 1.0 for the T4 favourable marker in Hereford.

Differences in allele frequencies between the Brahman and Tropical Composite in CRC2 exist. However, no significant difference between sexes within breed was observed.

The CRC1 and CRC2 phenotypic results show the tropically adapted breeds have lower shear force than Brahman. The differences in allele frequency between breed types for the tenderness markers would all support the hypothesis that these markers relate to shear force, the favourable gene (marker) is at a higher frequencies in TC cattle. However it should be noted that using such an argument in reverse could lead to very dubious results.

Brahman gene frequencies for the feed efficiency markers are extreme (>0.9) for three of the four markers. The same can be said for the marbling markers. Such extreme frequencies will mean that it will require a large number of randomly tested animals to establish the marker effects with confidence and even when they can be established for Brahmans they will have little utility as they explain a small amount of the genetic variation as little variation between animals exists.

Breed/dataset			Tenderr	ness			Marbling	g			Feed Ef	ficiency	
		T1	T2	Т3	T4	M1	M2	M3	M4	N1	N2	N3	N4
AA – CRC1	$\chi^2$	0.737	0.514	0.992	0.849	0.016	0.459	0.904	0.389	0.404	0.427	0.862	0.008
	0	20	356	48	11	709	713	1069	714	18	61	235	246
	1	284	546	402	215	467	344	223	494	271	434	614	636
	2	1004	210	845	1076	77	41	12	85	1023	773	401	412
HH – CRC1	y <sup>2</sup>	0.037	0.032	0.979		0.774	0.892	0.282	0.453	0.149	0.427	0.512	0.165
	Ô	31	561	34	0	727	857	806	638	18	2	160	291
	1	288	302	296	0	212	28	174	312	229	75	459	486
	2	673	41	645	1000	15	0	9	38	736	895	330	203
SH – CRC1	$v^2$	0 989	0 965	0 129	0 747	0 262	0 905	0 392	0.831	0 854	0 248	0 771	0 142
	Ô	0.000	352	364	1	293	360	361	216	8	0.2.10	83	13
	1	6	10	39	29	97	17	34	165	98	19	197	119
	2	411	0	1	386	8	0	1	31	312	381	116	268
MG –CRC1	v <sup>2</sup>	0.611	0.302	0 950	0.618	0.352	0.012	0 965	0 761	0 773	0 112	0 400	0.364
	Ô	7	90	18	10	162	228	383	313	2	81	97	198
	1	96	194	137	108	183	101	34	95	53	203	201	179
	2	316	104	259	304	52	11	1	7	366	126	105	40
All Temperate	$v^2$	0 365	0 000	0 000	0 533	0 868	0 590	1 000	0 608	0.055	0 000	0 931	0 4 3 9
Air remperate		0.000 50	1285	263	0.000	1872	2139	2617	1876	0.000 44	85	573	687
	1	690	1200	1276	368	997	529	469	1070	654	849	1476	1540
	2	2396	281	1549	2756	133	33	21	156	2435	2116	950	862
	. 2	0 770	0.000	0.000	0.005	0.000	0.044	0.000	0.077	0.000	0.004	0.000	0.000
AA Prog test	X	0.772	0.322	0.980	0.995	0.929	0.011	0.809	0.077	0.000	0.984	0.008	0.892
	0	4	419	78	Z 70	300	357	547	4/1	20	100	87	100
		104	207	280	70	323	Z/4 52	189	237	205	182	33Z	300
	2	010	43	201	000	60	55	10	30	515	539	310	215
SH Durham	χ <sup>2</sup>	0.001	0.929	0.956	0.904	1.000	0.999	0.000	0.161	0.000	0.016	0.765	0.444
	0	0	333	284	1	250	345	321	179	17	1	106	25
	1	18	14	54	29	77	2	23	134	96	30	167	134
	2	325	0	3	316	6	0	0	25	134	312	66	182
BH – CRC1	x <sup>2</sup>	0.961	0.585	0.937	0.998	0.948	0.008	0.996	0.436	0.625	0.953	0.508	0.819
	Ô	158	606	584	196	840	41	855	779	7	0	2	41
	1	423	49	244	431	19	245	5	83	145	18	71	295
	2	283	1	26	238	0	368	0	2	713	842	787	527
SG –CRC1	x <sup>2</sup>	0.999	0.848	0.076	0.849	0.998	0.778	0.983	0.208	0.904	0.554	0.759	0.977
	Ô	96	596	512	70	1079	348	1213	1108	14	3	55	64
	1	491	425	554	442	116	496	13	112	230	110	402	430
	2	626	76	150	701	3	176	0	3	978	1112	731	725
BR – CRC1	x <sup>2</sup>	0.655	0.130	0.938	0.484	0.937	0.000	0.873	0.995	0.026	0.170	0.000	0.000
-	Ô	74	424	241	7	1277	595	1241	1081	97	3	178	163
	1	510	630	701	187	131	546	204	339	558	130	648	649
	2	876	234	510	1258	3	125	8	27	799	1303	591	644
All Tropical	v <sup>2</sup>	0.526	0 000	0 000	0 000	0 829	0 074	0.311	0 454	0 000	0 165	0 000	0 092
	n n	306	1560	1236	182	3196	901	3305	2961	96	5.105	183	258
	1	1469	1236	1700	1239	268	1454	231	547	976	259	1226	1394
	2	1763	245	585	2106	6	586	4	25	2468	3256	2057	1886
			-			-			-				

# Table 8: Expected numbers by genotypes under Hardy Weinberg equilibrium and significant test $(\chi^2)$ in CRC1 and the Field datasets

Breed/sex			Tenderr	ness			Marbling	9		Feed Ef	ficiency		
		T1	T2	Т3	T4	M1	M2	M3	M4	N1	N2	N3	N4
BH M	χ <sup>2</sup>	0.328	0.000	0.999	0.812	0.899	0.845	0.997	0.684	0.998	0.971	0.835	0.663
	0	121	729	669	285	919	31	958	854	7	0	2	25
	1	434	60	241	467	28	243	5	88	151	15	87	261
	2	391	1	22	191	0	483	0	2	791	946	870	674
BH F	χ <sup>2</sup>	0.899	0.000	0.941	0.602	0.875	0.327	0.994	0.756	0.690	0.972	0.659	0.705
	0	123	736	671	317	956	32	994	917	5	0	3	24
	1	459	57	281	494	31	259	7	86	129	15	97	260
	2	429	1	29	192	0	530	0	2	870	989	901	717
BH all	χ <sup>2</sup>	0.777	0.000	0.947	0.499	0.787	0.338	0.991	0.520	0.857	0.944	0.556	0.464
	0	243	1465	1340	602	1875	62	1952	1771	12	0	5	49
	1	893	116	523	961	59	502	12	174	279	30	183	521
	2	819	2	51	383	0	1012	0	4	1661	1935	1771	1391
TC M	χ <sup>2</sup>	0.970	0.559	0.646	0.075	0.823	0.632	0.905	0.992	0.616	0.845	0.940	0.884
	0	83	495	344	53	990	478	1023	927	50	0	72	104
	1	456	341	561	390	160	452	144	223	380	38	436	491
	2	624	59	228	718	6	107	5	13	715	1131	664	577
TC F	χ <sup>2</sup>	0.990	0.252	0.988	0.535	0.816	0.130	0.547	0.363	0.995	0.771	0.995	0.856
	0	81	514	349	58	912	446	952	834	44	1	66	83
	1	433	299	519	385	154	415	146	231	344	46	407	439
	2	578	44	193	634	6	96	6	16	680	1057	624	582
TC all	$\chi^2$	0.962	0.145	0.721	0.054	0.673	0.781	0.540	0.619	0.807	0.978	0.950	1.000
	0	164	1008	693	111	1903	924	1975	1761	94	1	138	187
	1	889	641	1080	776	314	867	290	454	724	84	844	930
	2	1202	102	421	1352	13	203	11	29	1395	2188	1288	1159

#### Table 9: Expected numbers by genotypes under Hardy Weinberg equilibrium and significant test ( $\chi^2$ ) in CRC2

#### 4.0 Statistical analyses

#### 4.1 Single marker evaluation by breed and dataset.

Initial analyses of the markers were conducted individually for each trait and within breed (with the exception of feed intake traits). In all models, all available phenotypes have been used, including those from animals with missing genotypes (i.e. not genotyped or failed genotyping). This allowed accurate modelling of the systematic fixed effects (e.g. herd, contemporary group) and ensured the correct degrees of freedom for the residual sums of squares. To do this we included an additional term in the model describing, for each individual, if it has a genotype known for a given marker (i.e. yes or no) and then we fitted the marker genotype (i.e. 0, 1, or 2) nested within "yes". For "no", this included all animals with no DNA sample available and also any animal with a failed (i.e. "NR") genotype. Significance tests for all these analyses was done using the F statistic with a significance threshold of P<0.05. Least squares means for genotype were computed for each trait (although when the main

effect of genotype was not significant pair wise tests of significant differences between levels are not appropriate).

The effect of each marker on the nominated trait was estimated for each breed within CRC1 and CRC2 (Brahman and Tropical Composite) as well as the Angus and Shorthorn progeny test data. In the first instance this was pooled across all market and finishing groups of CRC1. Each model fitted the appropriate set of fixed effects (including covariates) for the project (listed below in each section) and each marker was included separately as a fixed effect, commonly with two degrees of freedom. The only exception was the analyses of the NFI data from CRC1 where due the low numbers of total feed intake records the analyses were run in pooled datasets of temperate (Angus, Hereford, Murray Grey, Shorthorn) and tropical breeds (Brahman, Belmont Red and Santa Gertrudis). The model included a term for breed x marker interaction, and if this was non-significant it was removed and the analysis was rerun with just the marker term.

A key design feature of the CRC1 experiment was the splitting of animals into one of three market weight categories. Genotype and gene frequencies for each marker with each market category where computed to check that the allocation process (or chance) did not created differences in gene frequencies, which in turn may have resulted in a confounding of SNP effects and market in the analyses.

#### 4.2 Multiple marker and "stars" evaluations

To increase power to detect significant marker effects the data form CRC1 breeds were combined into three datasets consisting of pooled temperate (TEMP) breeds (Angus, Hereford, Murray Grey and Shorthorn) and tropical (TROP) breeds (Brahman, Belmont Red, Santa Gertrudis) and finally a dataset with all seven breeds (BOTH). Models were run fitting the four markers simultaneously (as either fixed class effects or as single covariates). Marker genotypes were also combined into a numeric variable of "total stars" (also fitted as a fixed class effect and as a linear covariate). The total stars (or panel) were constructed by adding the number of 0, 1, or 2 alleles across the four markers when all were present. Some loss of data occurred and depended on the "NR" rate for each marker and dataset. In the future it should be possible to recover some of this lost information by "filling" the missing genotypes with "predicted" genotypes based on estimated gene frequencies. However this was not done for these analyses. Animal missing one or more of the four markers was included in the analyses with a missing value for "stars" and were pooled with any non-genotyped animals and run as a class nested within breed for each marker.

#### 4.3 Model examination

#### **4.3.1.** Sire and phenotypic variances

Each of the dataset by trait were run with the full fixed effect model with and without SNP or total stars (modelled as fixed effects or covariate) and also with and without sire as a random effect (with no relationships) using Proc Mixed procedure in SAS. The sire model allowed the estimation of the sire variance albeit with limited precision (i.e. generally low numbers) and the residual variance, these were summed to give a phenotypic variance. For the models without sire the residual variance was

estimated. The residual or phenotypic variances where then compared for models with and without SNP.

#### 4.3.2. Residual variance under model reduction

For CRC1 datasets marker information (as SNP and stars and modelled as fixed class effects or as linear covariates) were analysed in a series of models sequentially removing fixed effects and comparing results with previous model. For these models inclusion of non-genotyped animals were nested within breed to ensure differences in gene frequencies within breeds did not influence the estimated SNP solutions. Initial full models were run with and without the covariate (age or carcase weight) to investigate their effect on the estimated SNP effect. Models were then run sequentially removing fixed effects structures and analysing these with and without sire as a random effect. The fixed effects removed where herd (but retaining breed), then breed (and herd), then contemporary group (i.e. leaving only the markers). At each of these stages a base model without markers was also run to allow the percent of variation explained by the markers to be estimated at each stage.

These analyses allowed the assessment of the markers when the amount of assumed information varied (i.e. breed known, sire known, fixed effects known). Full results are tabled with and without sire and summarised in the trait sections below when the model did not include sire.

## 5.0 Trait definitions

#### 5.1 Tenderness traits

Four traits were examined as dependent variables of tenderness:

- 1) Shear force of LD muscle normal hung (LDPF)
- 2) Shear force of LD tender stretch hung (TSPF)
- 3) Shear force of ST muscle (STPF)
- 4) MSA consumer tenderness score (MSATEND)

Phenotypic records were available for CRC1 (traits 1, 3, 4) and CRC2 (traits 1, 2). For CRC1 the data edits and models were as described by Johnston *et al.* (2003) and included fixed effects for herd of origin, kill group and carcase weight as a linear covariate. All carcases were electrically stimulated and lab protocols equated to approximately two days aging of the meat samples.

For CRC2 the data and models for the two genotypes were described by Wolcott *et al.* (2008) and included a number of fixed effects. For these data the records were adjusted for age (using birth month if significant) and carcase weight was not included as a covariate. Also for the tenderness traits it is important to note that HGP were used on all animals and no electrical stimulation was applied.

Tables 10 and 11 present genotype and gene frequencies within each market category for the four tenderness markers. Although large differences exist in the frequencies there were no differences within markets.

Marker	Market	0	1	2	missing	total	р	q
T1	D	7	189	593	26	789	0.129	0.871
	J	12	183	609	30	804	0.129	0.871
	K	14	215	777	22	1006	0.121	0.879
T2	D	327	241	104	143	672	0.666	0.334
	J	368	262	93	111	723	0.690	0.310
	K	452	320	112	144	884	0.692	0.308
T3	D	119	218	453	25	790	0.289	0.711
	J	123	230	442	39	795	0.299	0.701
	K	149	270	563	46	982	0.289	0.711
T4	D	3	97	693	22	793	0.065	0.935
	J	5	101	696	32	802	0.069	0.931
	Κ	5	111	888	24	1004	0.060	0.940

Tabla	1A+ I DDI	markar	gonotypes	and gang	fraguancias	hv morkot	CPC1 Tem	narata braada
Table .	IV. LDI I	inai kei	genotypes	anu gene	nequencies	Dy market –	CKC1 Iem	perate precus

 Table 11: LDPF marker genotypes and gene frequencies by market – CRC1 Tropical breeds

Marker	Market	0	1	2	missing	total	р	q
T1	D	111	438	528	22	1077	0.306	0.694
	J	47	242	315	17	604	0.278	0.722
	Κ	118	555	671	29	1344	0.294	0.706
T2	D	509	308	100	182	917	0.723	0.277
	J	264	191	64	102	519	0.693	0.307
	K	663	401	114	195	1178	0.733	0.267
T3	D	433	424	211	31	1068	0.604	0.396
	J	225	241	133	22	599	0.577	0.423
	K	513	569	258	33	1340	0.595	0.405
T4	D	82	345	650	22	1077	0.236	0.764
	J	52	166	382	21	600	0.225	0.775
	Κ	98	409	837	29	1344	0.225	0.775

#### 5.2 Marbling traits

Two traits were examined as dependent variables of marbling:

- 1) Intramuscular fat percentage determined by NIR or ether extract (IMF)
- 2) MSA marble score (0-9 scores on 0.1 scale) (MSAMARB)

Phenotypic records were available from CRC1 and CRC2 for traits 1 and 2. The CRC1 data was a combination of animals slaughtered for the domestic, Korean and Japanese markets. Age, carcase weight and IMF/Marble scores increased from domestic to Korean to Japanese endpoints as described by Reverter *et al.* 2003. It can be expected that gene markers coding for marble score/IMF would be more expressed in older higher marbling cattle. Therefore above analyses were repeated for traits 1

and 2 with the domestic cohorts excluded, however standard errors of any estimates will increase and the power to detect significant differences is reduced.

CRC1 models for analysing MSA marble score and IMF were described by Johnston (2001) and Reverter *et al.* (2003). The models included fixed effects for herd of origin, kill group and carcase weight as a linear covariate.

For CRC2, the models were described by Wolcott *et al.* (2008) and included a number of fixed effects. For this dataset the records were adjusted for age (using birth month) and carcase weight was not included. All animals were feedlot finished (120 days on feed) to a single market endpoint (approximately 320kg carcase weight).

Angus and Shorthorn progeny test data for marble score was scored by MSA technicians and loaded onto the NBRS breed databases. The records were analysed in a model that included a single contemporary group effect (as defined by BREEDPLAN for abattoir carcase traits) and age at slaughter was included as a linear covariate. Records were therefore not adjusted to the standard BREEDPLAN 300 kg carcase weight basis.

Tables 12 and 13 present genotype and gene frequencies within each market category for the four marbling markers. No differences in frequencies were observed within markets.

Marker	Market	0	1	2	missing	total	р	q
M1	D	548	307	54	344	909	0.772	0.228
	J	555	293	29	228	877	0.800	0.200
	Κ	618	335	40	243	993	0.791	0.209
M2	D	633	178	15	427	826	0.874	0.126
	J	643	139	13	310	795	0.896	0.104
	K	728	161	8	339	897	0.901	0.099
M3	D	800	146	8	299	954	0.915	0.085
	J	762	134	5	204	901	0.920	0.080
	Κ	861	155	6	214	1022	0.918	0.082
M4	D	554	347	44	308	945	0.770	0.230
	J	563	305	42	195	910	0.786	0.214
	Κ	605	377	45	209	1027	0.773	0.227

Table 12: IMF marker genotypes and gene frequencies by market – CRC1 Temperate breeds

Table 13: IMF marke	r genotypes and	l gene frequencies	by market -	<b>CRC1</b> Tropical breeds
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Marker	Market	0	1	2	missing	total	р	q
M1	D	1132	93	3	124	1228	0.960	0.040
	J	567	48	1	57	616	0.959	0.041
	Κ	1265	105	2	127	1372	0.960	0.040
M2	D	314	518	216	304	1048	0.547	0.453
	J	157	253	110	153	520	0.545	0.455
	K	387	521	247	344	1155	0.561	0.439
M3	D	1176	81	2	93	1259	0.966	0.034
	J	579	52	3	39	634	0.954	0.046
	K	1309	81	2	107	1392	0.969	0.031
M4	D	1046	199	11	96	1256	0.912	0.088
	J	531	92	7	43	630	0.916	0.084
	Κ	1171	212	11	105	1394	0.916	0.084

#### 5.3 Feed Intake traits

Four traits were examined as dependent variables of feed efficiency:

- 1) Net or residual feed intake (NFI)
- 2) Daily feed intake (DFI)
- 3) Feed conversion ratio (FCR)
- 4) Average daily gain during feed test (ADG)

Phenotypic records were available for all traits from CRC1 and CRC2. For CRC1 data, the derivation of traits (e.g. NFI) and models were described by Robinson and Oddy (2004). Animals were recorded for feed intake for an average of 60 days and included animals fed for the three market endpoints. Due to lower number of phenotypes in CRC1 data (1472 in total across seven breeds) the analysis was pooled across breeds to form temperate breed and tropical breed datasets. In each of the analyses, breed was fitted along with the interaction term with marker and if not significant (P<0.05) was removed and the analysis re-run. Least squares means for each marker genotype were computed for each trait from the analyses when the breed\*marker term was both included and removed.

For CRC2, the models were described by Barwick *et al.* (2008) and included a number of fixed effects associated with design aspects of the study; however FCR was computed as part of this work and was defined as DFI/ADG. Data were edited to remove extreme FCR records (greater than 18) and the same fixed effect models for DFI were used. Animals were fed for a single market endpoint and were on average in the feeders for 71 days.

Angus and Shorthorn progeny test data for NFI were available for steers tested for feed intake during their feedlot finishing phase. Data were initially processed through the NSW DPI service at Trangie prior to being forwarded to the NBRS databases. The model included a single contemporary group effect (as defined by BREEDPLAN for NFI) and age at the start of test was included as linear covariate.

Tables 14 and 15 present genotype and gene frequencies within each market category for the four feed efficiency markers. Although the numbers of records were quite small the gene frequencies within markets were very similar.

Marker	Market	0	1	2	missing	total	р	q
N1	D	2	14	56	1	72	0.125	0.875
	J	10	47	229	5	286	0.117	0.883
	Κ	4	77	294	2	375	0.113	0.887
N2	D	3	20	50	2	73	0.178	0.822
	J	7	57	212	15	276	0.129	0.871
	Κ	17	85	257	18	359	0.166	0.834
N3	D	8	44	20	1	72	0.417	0.583
	J	49	139	93	10	281	0.422	0.578
	Κ	72	172	109	24	353	0.448	0.552
N4	D	17	33	23	2	73	0.459	0.541
	J	62	137	83	9	282	0.463	0.537
	Κ	94	162	106	15	362	0.483	0.517

#### Table 14: Feed efficiency marker genotypes and gene frequencies by market: CRC1 Temperate breeds

Marker	Market	0	1	2	missing	total	р	q
N1	D	6	31	91	2	128	0.168	0.832
	J	10	56	139	3	205	0.185	0.815
	Κ	11	87	233	5	331	0.165	0.835
N2	D	14	105	11	1	130	0.512	0.488
	J	18	187	3	4	208	0.536	0.464
	Κ	29	298	9	8	336	0.530	0.470
N3	D	22	36	63	9	121	0.331	0.669
	J	24	64	114	6	202	0.277	0.723
	Κ	31	107	185	13	323	0.262	0.738
N4	D	4	58	60	8	122	0.270	0.730
	J	14	86	105	3	205	0.278	0.722
	Κ	26	139	167	4	332	0.288	0.712

#### Table 15: Feed efficiency marker genotypes and gene frequencies by market: CRC1 Tropical breeds

# 6.0 Results

#### 6.1 Tenderness markers

Results for the four tenderness markers are presented in Appendix B.

#### 6.1.1 Estimated markers effects

#### 6.1.1.1 LDPF and STSF

**Marker T1:** Results from the single marker analyses by breed (Table B1) showed a significant reduction of LD shear force for Angus with increasing numbers of stars (i.e. 0 to 2) with a difference between the two homozygotes was around 0.5 kg with the heterozygote being intermediate. In Hereford, the difference between the zero and two star animals was not significant (small numbers of zero star animals) however the difference between one and two was significant and around 0.25 kg, similar to the Angus and Murray Grey. Shorthorn results were not significant and reflect the extreme gene frequency of the T1 marker in this breed.

For tropically adapted breeds (Brahman, Belmont Red, Santa Gertrudis and Tropical Composite; Table B1) the single marker analyses showed a highly significant effect of T1 on LD shear force, the slight exception was the CRC2 Brahman where the effect was only just significant and the difference between zero and two star was considerably smaller than in Tropical Composite. For the tenderstretch data from CRC2 the effect of T1 was considerably reduced and the significance was P=0.06, but the direction of the effect of T1 was still consistent with expectations.

Pooled analyses of CRC1 data for the temperate breeds and also tropical breeds showed T1 was highly significant when fitted jointly with the other 3 markers (Tables B4, B5, B7, B8) or as combined stars as either a fixed effect (Tables B10, B11) or additive covariate (Tables B13 and B14). The regression estimate from the summary Table 16 shows estimates of -0.162 kg shear force/T1 star for both lines.

Joint fitting of T1 with the other 3 markers in CRC2 data showed significant effects of T1 in both Brahman (Tables B16 and B17) and Tropical Composite (Tables B20 and B21) with regression coefficients of -0.15 and -0.19 kg shear force/T1 star respectively (Table 16).

The effects of T1 on ST shear force from single marker analyses (Table B2) were smaller than for the LD muscle and generally not significant with the exception of Angus and for the tropically adapted breeds the direction of the effect, although small, were generally negative (i.e. favourable).

**Marker T2:** The single marker by breed results (Table B1) showed a small but significant effect in Angus and Murray Grey, and the effect of T2 in tropically adapted breeds was significant and slightly larger in magnitude. In Shorthorn and Brahman the effect was not significant due to extreme gene frequencies. However the estimate for the one star showed lower shear force compared to 0 stars in all three

datasets. There seems to be no effect of this marker for Hereford. For the tenderstretch data from CRC2 in Tropical Composite the effect of T2 was reduced compared to normally hung carcases, but still was highly significant.

Pooled analyses of CRC1 data for the temperate breeds and also tropical breeds showed T2 was highly significant when fitted jointly with the other three markers (Tables B4-B16) or as combined stars as either a fixed effect or additive covariate. The regression estimate from the summary Table 16 shows estimates of -0.089 kg and -0.172 kg shear force/T2 star for temperate and tropical lines, respectively.

Joint fitting of T2 with the other three markers in CRC2 data (Tables B16-B23) showed significant effects of T2 but not for Brahmans (as seen in the single marker analyses). For Tropical Composite the estimated effect of the T2 was -0.22 kg/T2 star.

Results for the effect of T2 on ST tenderness were similar to the LD muscle for the tropically adapted breeds but were not significant for any of the temperate breeds.

**Marker T3:** The single marker by breed (Table B1) showed the effect of T3 in tropically adapted breeds could be well established, with larger effects in Brahman (0.7kg) than in the tropically adapted composites (0.35kg). The results were similar for ST with the exception of Belmont Reds that were not significant. For the Taurus breeds the effect of T3 was only significant in Angus and reasonably small in magnitude. No breeds showed significant effects for the ST muscle.

For the tenderstretch data from CRC2 the effect of T3 was reduced (about halved) but was still significant.

Pooled analyses of CRC1 data for the temperate breeds showed T3 was not significant (fitted as either joint markers or stars). For the tropical breeds T3 was highly significant with a regression estimate from the summary Table 16 of -0.117 kg shear force/T3 star.

Joint fitting of T3 with the other three markers in CRC2 data showed significant effects of T3 for Brahman but not for the Tropical Composite. For CRC2 Tropical Composite, the T3 marker was significant as a single marker effect but not significant when fitted jointly, suggesting LD between the markers (maybe with T2 i.e. the other SNP in the Calpain gene) in this genotype. For Brahman the estimated effect of the T3 was -0.27 kg/T3 star.

**Marker T4:** For the single marker and breed analyses the effect of T4 was only significant in one dataset (re: Brahman CRC1) but not in CRC2 Brahmans. The effect of T4 was also not significant for ST muscle with the exception of CRC1 Brahman were the effect of increasing number of stars results in increased shear force. For the tenderstretch data from CRC2 the effect of T4 was also not significant.

Pooled analyses of CRC1 data for the temperate breeds showed T4 was not significant for the temperate breeds (as class or stars). For the tropical breeds T4 was significant when fitted as a class effect (P=0.06) but was not significant when fitted as an additive regression (P=0.86). It appears to be the result of pooling breeds that have

quite different gene frequencies and estimated single marker effects for the T4 marker (Table B1) (also see results from special analyses and Table B33).

For CRC2, joint fitting of T4 with the other three markers did not alter the non-significance of this marker.

**T-STARS**: Combining the 4 tenderness marker genotypes into total number of stars resulted in significant effects when fixed as class effect (e.g. Tables B10-B12) or covariate (e.g. B13-B16) for all datasets. When fitted as a regression on total stars (Table 16), the size of the coefficient was reduced in magnitude compared to some of the individual markers effects. This reduction in magnitude of the coefficient is the result of the small (or positive) effects of the T4 and T3 markers. Tender stretching halved the estimate of size of effect of the markers.

 Table 16: Estimated regression coefficients (kg) for each of the four tenderness

 markers fitted jointly or total stars (T-STARS) from the different datasets.

Dataset	Trait	T1	T2	T3	T4	T-STARS
CRC1 -TEMPERATE	LDPF	-0.162	-0.089	-0.029	0.004	-0.083
CRC1 -TROPICAL	LDPF	-0.162	-0.172	-0.117	0.005	-0.123
CRC1 - BOTH	LDPF	-0.162	-0.131	-0.091	-0.000	-0.110
CRC2 – TROP COMP	LDPF	-0.192	-0.219	-0.070	0.031	-0.111
	TSPF	-0.060	-0.080	-0.054	-0.015	-0.053
CRC2 – BRAHMAN	LDPF	-0.151	0.022	-0.266	-0.010	-0.105
	TSPF	-0.066	-0.001	-0.147	-0.015	-0.058

Bold P<0.05

#### 6.1.1.2: MSA consumer taste panel

In the CRC1 data about half of the total numbers of carcases were assessed by MSA consumer taste panel tests. The consumer tenderness score 0-100 (increasing score indicates more tender meat) was also used as a depended variable in the analysis of the T1-T4 markers and results are presented in Table B3.

**T1, T2, T3:** Single marker analyses by breed showed in all three tropical datasets (while not always significant) an increase in the tenderness score (i.e. more tender) with increasing stars for all three markers. In particular, for T3 there was a large increase in tenderness score for increasing number of stars in Brahman. Whereas for Taurus datasets none of the markers were significant and no overall trends were apparent.

**T4:** The T4 marker had no effect on consumer tenderness similar to the results for LDSF with the exceptions of Brahman where T4 was significant for LDSF but not significant for MSA consumer score. In Belmont Red T4 has a significant effect on consumer score but the score decreased with increasing number of stars.

#### 6.1.2 Model changes

#### **Significance levels**

Changing the fixed effect model had very little effect on the significance levels of the four tenderness markers. This included removing the covariate of slaughter age, removing sire, removing herd, removing breed and finally removing all effects other than the markers, although in many cases the markers were already highly significant prior to reducing the models. The only exceptions were for T3 in CRC1 pooled temperate breeds where the effect of the marker became significant only when breed (and herd) and sire was dropped from the model (Tables B4 and B7). For CRC1 tropical breeds, T4 became highly significant (P<0.001) when dropping breed, herd and sire (Tables B5 and B8).

#### Variances

Based on the variance component estimates in Appendix B the variance explained by the four tenderness markers (when using the full model with markers fit as covariate of number of stars) are presented in Table 17. For CRC1 temperate breeds the heritability estimate for LDPF is low (7%) and the markers explained 7.9 % of the sire variance and 1.3% of the phenotypic variance. Whereas for CRC1 tropical breeds the heritability was moderate (25%) and the markers explained approximately 17% of the sire variance and 3.5% of the phenotypic variance. Similar results were observed for CRC2 breeds, with the exception of Brahmans where the variation explained was lower and reflected the non-significant effect of the T2 marker in this dataset. Fitting sire in the model when estimating the effects of the markers on the variances had little effect and is likely the result of the large number of sires used and the careful allocation of sires across fixed effects.

Table 1	7: Percent	of sire	(Vs),	phenotypic	(Vp)	or	residual	(Ve)	variance
explaine	d by fitting	the four	tende	rness marker	rs using	g th	e full fixe	d effe	cts model
in each d	lataset								

Dataset	Trait	Vs	Vp	Ve
			(+sire)	(-sire)
CRC1 - TEMPERATE	LDPF	7.9	1.3	1.2
CRC1 -TROPICAL	LDPF	17.1	3.5	3.6
CRC2 – TROP COMP	LDPF	9.4	1.7	1.8
	TSPF	19.0	2.7	2.6
CRC2 – BRAHMAN	LDPF	4.9	1.1	1.1
	TSPF	5.3	0.8	1.1

Sequentially removing fixed effects increased the residual variance in CRC1 temperate and tropical data (Tables 18 and 19). For both data, results show that the SNP explained very little of the variation due to herd when herd was not included (i.e. assumed unknown), and breed and contemporary group remained in the model. However when breed (and herd) were removed the SNP explained a large proportion of the variance in LDSF due to breed and increased the amount of residual variance explained by the SNP to 4.3 and 9.4% for temperate and tropical, respectively. Removing all fixed effects (i.e. removing herd, breed and CG) showed the SNP explained almost none of the (large) variance explained by CG.

However when removing fixed effects and re-estimating the effects of SNPs it is possible that the estimated effect of the markers may have changed (even changed sign) and users would need to be made aware of this. It is also likely that the estimated effect (i.e. when breed is removed) will be specific to the exact group of breeds in the sample, and therefore the results would not be transferable across other groups of cattle.

Table 18: CRC1 – Temperate LDPF (kg): Variation explained by four tendernes
markers (SNP) under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect	Sequential increase		explained	Vsnp*	for each
	removed	in model Ve		by SNP		model
		No SNP	+SNP			
Herd + Breed + CG	-	0.431	0.426	-	0.0050	1.2
Breed +CG	Herd	0.040	0.039	2.5	0.0060	1.3
CG	Breed	0.023	0.008	65.2	0.0210	4.3
nil	CG	0.175	0.173	1.1	0.0230	3.4
Herd + Breed + CG Breed +CG CG nil	- Herd Breed CG	0.431 0.040 0.023 0.175	0.426 0.039 0.008 0.173	2.5 65.2 1.1	0.0050 0.0060 0.0210 0.0230	1.2 1.3 4.3 3.4

\* estimated as a difference between model residual variances with and without SNP

# Table 19: CRC1 – Tropical LDPF (kg): Variation explained by four tenderness markers (SNP) under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect	Sequential increase		explained	Vsnp*	for each
	removed	in mode	el Ve	by SNP		model
		No SNP	+SNP			
Herd + Breed + CG	-	0.605	0.5830	-	0.0220	3.6
Breed +CG	Herd	0.030	0.028	6.7	0.0240	3.9
CG	Breed	0.043	0.003	93.0	0.0640	9.4
nil	CG	0.209	0.197	5.7	0.0760	8.6

\* estimated as a difference between model residual variances with and without SNP

#### 6.1.3 Special analyses

Further analyses were performed within breed (Tables B32 and B33) examining the effects of jointly fitting the four tenderness markers as total star regressions. Each analysis was rerun after removing the non-significant markers to examine the effects on the estimated regression coefficients.

For the CRC1 temperate breeds the results showed that for Shorthorn the estimates were inaccurate given the extreme gene frequencies of all 4 tenderness markers. For Angus and Murray Grey the T1 and T2 markers were significant (and appear to act additively) but T3 and T4 were not significant. For Herefords only T1 was significant.

For tropically adapted breeds results for T1, T2, T3 when fitted jointly showed significant (and additive effects) with the exception of T2 in CRC2 Brahmans. However when T4 was then added to the model it had an inconsistent effect. In CRC1

Brahmans (where it was discovered) it had a significant negative effect but not as large as the effects estimated in the single marker analysis (Table B1). This could be due to some linkage or epistatic effects with the other markers. For other breeds, T4 had no observed effect in CRC2 Brahman and Tropical Composite, and positive effects in Santa Gertrudis (P=0.03) and Belmont Red (P=0.19).

#### 6.1.4 Summary of tenderness markers

Tenderness markers T1, T2 and T3 had significant effects in several tropically adapted breeds for LD shear force in normally hung carcases and appear to have consistent effects on MSA consumer taste panel scores. The marker effects appear to be additive in their effects on LDPF. The effects are consistent, but reduced in magnitude, in the ST muscle and also for carcases which have been tenderstretch hung. In the Taurus breeds, the T1 and T2 markers were estimated to have modest effects on LD shear force but for T3 the effect was not significant. Marker T4 does not appear to be a useful marker for tenderness, with the possible exception of Brahmans from CRC1 only. The tenderness markers were estimated to explain between 5 and 17% of the genetic variance in shear force across the datasets and between 0.8 and 3.6% of the phenotypic (or residual) variance.

# 6.2 Marbling results

All results for the four marbling markers on IMF% and MSA marble score are presented in Appendices C and D respectively.

#### 6.2.1 Estimated marbling markers effects

#### 6.2.1.1. IMF

**Marker M1:** Single marker and breed results for the effect of the M1 marker on IMF (Table C1) showed no significant effects in nine out of ten datasets and no constant pattern could be established within breed type. Some of this would be expected due to the extreme gene frequencies and very large standard errors for the estimates of the 2 stars homozygote class. Herefords were the only exception where a significant effect was observed however the least squares estimates indicate a negative effect of increasing number of stars on IMF levels.

Pooled analyses of CRC1 data in temperate and tropical breeds showed M1 was not significant when fitted jointly when considered as class effects (Tables C6-C8) or joint regressions (Tables C9-C11). Summary results of regression coefficient for the joint fitting of markers are presented in Table 20 below. Similar results were also observed for CRC2 Brahman (Tables C25 and C26), Tropical Composite (Tables C21 and C22) and Durham Shorthorns (Tables C29 and C30) for the M1 marker.

**Marker M2:** Single marker and breed results for the effect for the M2 marker showed no significant effects in any of the 10 datasets. The extreme gene frequencies in many of the temperate breeds in CRC1 made it difficult to assess the homozygote 2\* class. However estimates of the 0 to 1\* were better represented in some breeds (Angus and Murray Grey) but showed no significant effects.

Results from pooled CRC1 analyses showed no significant effect of the M2 marker either as class or covariate with similar results in the other three IMF datasets.

**Marker M3:** Single marker and breed results for M3 marker showed the only significant effect in the ten datasets was in CRC1 Angus. The results also reflect the extreme gene frequencies of this marker with all breeds being greater than 0.9 for the unfavourable (i.e. 0) allele.

Pooled analyses of CRC1 data and the joint fitting of the markers in the other dataset showed no significant effects of the M3 marker on IMF with the exception of the pooled CRC1 temperate breeds. In this analysis M3 was significant (P=0.02) when fitted as fixed class effect (Table C6), however the effect was non-significant (P=0.24) when fitted as a regression (Table C9), again reflecting the effect of extreme gene frequency on the estimated effects of this marker.

**Marker M4:** Results for M4 marker reflected the results for the M2 marker with no significant result in either the single or multiple marker analyses or in the single breed or pooled CRC1 datasets.

**M-STARS:** Combining the four marbling marker genotypes into total number of stars for the CRC1 temperate breeds resulted in a significant effect (Table C12) when fitted as class but when small numbers of 5\* and 6\* animals where combined with 4\* class (Table C13) the effect was no longer significant. Number of stars as covariate was also not significant. (Table C18). No significant effects were observed for total stars on IMF in CRC1 tropical breeds (Tables C14, C15) or in CRC2 Brahmans (Tables C25-C28), Tropical Composite (Tables C21-24) or the Durham Shorthorn (Tables C31-C32) data. The summary estimated regression coefficients for total stars as a regression presented in Table 20 show very small coefficient estimates and no consistent direction of effect.

#### 6.2.1.2. MSA MARBLE SCORE

Results for the effects of the 4 marbling markers on MSA marble score (Appendix D) in general mirrored the results for IMF although with lower numbers the power to detect differences declined particularly for those markers at extreme gene frequencies. The Angus and Shorthorn progeny test dataset were also available for these analyses and exhibited higher levels of marbling but none of the four marbling markers had significant effects (or trends) on marble score (Tables D29-D36).

Single marker analyses by breed (Table D1) showed only the one significant result for the M1 and M3 markers and both were in CRC1 Shorthorn where the estimated least squares effect of the 2\* genotype was from a single animal. For M4 only Santa Gertrudis showed a significant result albeit on one degree of freedom. No dataset showed a significant effect for the marker M2 on marble score.

Results from pooled CRC1 datasets (Tables D4-D9) or the fitting jointly of the markers (as class or regression) in the other datasets (Tables D22-D36) showed no significant effects of any of the marbling markers. The summary estimated regression coefficients for each marker are presented in Table 20. In general, the estimated coefficients are very small in magnitude and there is no consistent direction of effects across datasets.

**M-STARS:** Results of combining the four marbling marker genotypes into total number of stars resulted in similar result to IMF. In general the effects of the panel of marbling SNPs were not significant. There were some analyses in CRC1 data where the effects approach significance when the total stars was fitted as a fixed class effect (Tables D10-D15) and genotype classes with extremely low numbers were combined. However in each case when these were re-run as a covariate the results were not significant. For CRC2 Tropical Composite the total stars, fitted as a regression (Table D25), showed increasing levels (P=0.06) of marbling at 0.037 marble score per star (see Table 20). For the two progeny test datasets the effects of total stars on marble score were not significant (Tables D32 and D36).

Dataset	trait	M1	M2	M3	M4	M-STARS
CRC1 - TEMPERATE	IMF (%)	-0.063	-0.057	0.093	-0.033	-0.002
	MSAMARB (score)	0.002	-0.036	0.035	0.012	0.013
CRC1 -TROPICAL	IMF	-0.021	0.009	0.073	0.064	0.019
	MSAMARB	-0.038	0.004	0.044	0.041	-0.000
CRC1 - BOTH	IMF	-0.052	-0.008	0.080	0.004	0.009
	MSAMARB	-0.014	-0.008	0.032	0.022	0.005
CRC2 – TROP COMP	IMF	0.056	-0.083	-0.053	0.019	-0.038
	MSAMARB	-0.023	0.026	0.036	0.029	0.037
CRC2 – BRAHMAN	IMF	-0.110	0.100	-0.564	0.126	0.056
	MSAMARB	0.034	0.025	-0.066	-0.020	0.014
Angus PT	MSAMARB	-0.026	0.087	0.042	-0.068	0.012
Durham PT	IMF	-0.154	-1.442	-0.155	0.053	-0.019
	MSAMARB	-0.132	-1.234	-0.209	0.112	-0.006

Table	20:	Estimated	regression	coefficients	for each	of the	four	marbling	markers
fitted :	join	tly or as tot	al stars (M	-STARS) fro	om the di	fferent	datas	ets.	

Bold P<0.05

#### 6.2.2 Model changes

#### Significance levels

Results show, under full fixed effects models, that removing the covariate (carcase weight or age) or removing sire had no effect on the absence of significance of the marbling markers or stars for either IMF (Appendix C) or marble score (Appendix D) across all datasets. Likewise for CRC1 datasets, removing herd (with and without sire fitted), also had very small effects on the significance levels for IMF or marble score. Some exceptions did exist, for CRC1 temperate M4 became significant for IMF when herd and sire were removed (Tables C6 and C9). For marble score analyses of total stars when low numbers of 4, 5 and 6 star animals were pooled with the 3 star genotypes the effect was significant when fit as a class effect (Table D11) but not as a regression (Table D17).

When breed (and herd) was removed from the models the significance levels changed for many of the analyses and depended in many cases on whether sire was fitted or not. In general fitting sire acted as a proxy for breed and significance levels were often similar to previous analyses that included breed. There were a few exceptions where effects became significant e.g. M2, M3 and M4 in tropical for IMF (Table C7) and marble score (Table D5). However when sire was also removed then many analyses showed significance of the markers. For CRC1 temperate breeds all 4 markers were significant or approached significance for IMF (Tables C6) but not M3 when fitted as a regression (Table C9). Total stars were also now significant as a regression (Table C18). For tropical breed M2, M3 and M4 were significant but not M1 and none of the star regressions were significant (Table C19). The same general trends were observed for marble score with the exception of the markers in temperate breeds.

Further reduction in the model to remove kill group (accounts for group, market, finish and slaughter group) closely mirrored the results of dropping breed (with and without sire).

#### Variance explained

Results presented in Table 21 are the effects on the estimated variances when fitting the 4 marbling markers as total stars (with and without sire in the model as a random effect). In general, the four marbling markers had no effect on the sire variance or the phenotypic variance for either marbling trait. The exception was for MSA marble score in CRC2 Tropical Composite where the markers explained 8% of the sire variance. The occurrence of negative estimates results from the variance (sire or residual) being (slightly) higher in the models when the SNP were not fitted and likely reflect changes in the denominator degrees of freedom used to estimate the residual.

Dataset	trait	Vs	Vp	Ve
			(+sire)	(-sire)
<b>CRC1</b> - TEMPERATE	IMF	-0.5	-0.1	0.3
	MS	0.2	-0.3	-0.4
CRC1 -TROPICAL	IMF	-1.3	-0.1	0.0
	MS	0.0	0.0	0.0
CRC2 – TROP COMP	IMF	-1.6	-0.2	-0.2
	MS	8.3	0.4	0.8
CRC2 – BRAHMAN	IMF	-6.7	0.2	0.0
	MS	0.0	0.0	0.7
Angus PT	MS	-4.4	-0.4	-0.4
Durham PT	IMF	-0.9	-0.6	-0.7
	MS	0.0	-0.5	-0.5

Table2	1: Percent	of sire	(Vs), ph	enotypic	(Vp) c	or residu	ual (Ve)	variance
explaine	d by fitting	the four	marbling	g markers	using	the full f	ixed effe	cts model
in each d	lataset							

Sequentially removing fixed effects increased the residual variance (Tables 22-25). For both lines, results show when herd was not included (i.e. if assumed unknown) but breed and contemporary group were known the SNP explained very little of the variation due to herd. However when breed (and herd) were removed the SNP explained a small amount of the variance in temperate breeds for IMF (0.2%) and MS (0.3%) but none in tropical breeds. Removing all fixed effects (i.e. removing herd, breed and CG) showed the SNP were explaining almost none of the large variance explained by CG.

 Table 22: CRC1 – Temperate IMF (%) Variation explained by four marbling markers

 (SNP) under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect	Sequential increase		explained	Vsnp*	for each
	removed	III IIIOUE	er ve	by SINP		model
		No SNP	+SNP			
Herd + Breed + CG	-	2.007	2.0010	-	0.0060	0.3
Breed +CG	Herd	0.213	0.220	-3.3	-0.0010	0.0
CG	Breed	0.209	0.204	2.4	0.0040	0.2
nil	CG	2.539	2.540	-0.0	0.0030	0.1

\* estimated as a difference between model residual variances with and without SNP

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect	Sequential increase		explained	Vsnp*	for each
	removed	in mode	in model Ve by			model
		No SNP	+SNP			
Herd + Breed + CG	-	0.277	0.2780	-	-0.0010	-0.4
Breed +CG	Herd	0.016	0.015	6.3	0.0000	0.0
CG	Breed	0.042	0.041	2.4	0.0010	0.3
nil	CG	0.223	0.222	0.4	0.0020	0.4

# Table 23:CRC1 – Temperate MSA marble score: Variation explained by the four marbling markers (SNP) under reducing fixed effects models

\* estimated as a difference between model residual variances with and without SNP

# Table 24: CRC1 – Tropical IMF (%): Variation explained by four marbling markers (SNP) under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect removed	Sequential increase in model Ve		explained by SNP	Vsnp*	for each model
		No SNP	+SNP	5		
Herd + Breed + CG	-	0.978	0.9780	-	0.0000	0.0
Breed +CG	Herd	0.014	0.014	0.0	0.0000	0.0
CG	Breed	0.071	0.07	1.4	0.0010	0.1
nil	CG	0.942	0.942	0.0	0.0010	0.0

\* estimated as a difference between model residual variances with and without SNP

# Table 25: CRC1 – Tropical MSA marble score: Variation explained by four marbling markers under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect	Sequential increase		explained	Vsnp*	for each
	removed	in mode	er ve	by SNP		model
		No SNP	+SNP			
Herd + Breed + CG	-	0.236	0.2360	-	0.0000	0.0
Breed +CG	Herd	0	0	-	0.0000	0.0
CG	Breed	0.017	0.017	0.0	0.0000	0.0
nil	CG	0.134	0.134	0.0	0.0000	0.0

\* estimated as a difference between model residual variances with and without SNP

#### 6.2.3 Special analyses

Further analyses were performed dropping certain classes of data or combining datasets to investigate if the estimates of effects for the four marbling markers changed.

#### 6.2.3.1 IMF only export markets

CRC1 data were edited to remove all domestic finished animals to only leave the export market weight finished groups (Korean and Japanese market). This was done

to increase the average level of marbling. Single marker analyses for each breed were run to estimate the size of effects.

Results showed the average IMF% (Table C2) increased by about 0.5% IMF for the tropical breeds and an almost 1% IMF increase for the temperate breeds, however the number of animals per genotype declined in all breeds. In general, the results of marker associations were very similar to the complete IMF dataset.

M1: For the single marker association of M1 the Hereford was the only breed significant, however the trend was for declining IMF with increasing numbers of stars. Murray Grey showed a large increase in IMF from 0 to 1 star. No consistent trend was observed in the other data sets.

M2: No significant effects were estimated in any dataset and no consistent trends were observed across breeds.

**M3:** A significant effect was observed in Angus and Hereford which would indicate a nearly complete recessive gene action (also observed for the full IMF dataset) but given the extreme gene frequencies of this marker across all the temperate breeds this will be difficult to validate.

M4: No significant effect and no consistent trends were observed within breed groups.

#### 6.2.3.2 Removing animals with high numbers of non-called genotypes

Marbling marker genotypes on animals with more than three non-called genotypes (i.e. "NR") out of the 12 total markers were identified in the CRC1 temperate MSA marble score dataset. All the marbling marker genotypes on these animals were then set to missing and the analyses were rerun. A total of 71 animals had their genotypes removed however in no cases did a non-significant marker test become significant.

#### 6.2.3.3 Pooling Angus CRC1, Murray Grey and Angus progeny test data

To increase the power of estimating significant effects, particularly for markers with low frequency alleles, the data were pooled for CRC1 Angus and Murray Grey and the Angus progeny test datasets and were used to examine MSA marbling score in these higher marbling breeds. This combined dataset consisted of 1123 animals with MSA marble score data and 72% of those animals had all four marbling markers genotypes (N=1123) available. The mean MSA marble score was 1.55 (sd = 0.80).

Table 26 show in this combined data the numbers of 2 stars animals were still limited but large numbers existed for the other two genotypes. None of the markers were significant and no trends were observed. Similar results were observed when considering the markers together (Table 27), either as a fixed effect or as a regression on the summed number of stars.

Marker	Model	Pvalue	0	1	2
M1	Frequencies		463	408	71
	Full fixed effects	0.939	1.50	1.52	1.53
MO	Encouchaica		404	275	25
IVIZ	Frequencies		494	525	55
	Full fixed effects	0.869	1.51	1.59	1.54
M3	Frequencies		780	197	16
1010	Full fixed offecto	0.509	1.50	151	1.66
	run nxed effects	0.398	1.30	1.31	1.00
M4	Frequencies		616	352	33
1.1	Eull fixed offects	0.002	1.50	151	1 40
	Full fixed effects	0.983	1.50	1.51	1.49

# Table 26: Least squares means for MSA marble score for the four marbling markers for combined Angus and Murray Grey data.

Table 27: Least squares means and regression coefficients for MSA marble score for
the four marbling markers considered as stars (summing alleles) for combined Angus
Murray Grey data.

	Least squares means							Regression		
Model	Pvalue	0	1	2	3	4	5	6	Pvalue	b
Frequencies		120	260	243	133	41	9	2		
Full fixed effects	0.307	1.54	1.46	1.55	1.45	1.59	1.84	1.22	0.648	0.00923

#### 6.2.3.4 Considering markers as a single combined genotype

To investigate the possible combined effect of the four markers they were concatenated into a single genotype (e.g. 0102) and this was included in the full model. Table 28 lists least squares means and weighted means (by stars) for the CRC1 Angus and Angus Progeny test datasets.

Results were not significant although large differences existed between estimates but there was no consistent trend in the solutions between two Angus dataset.

#### 6.2.4 Summary of marbling markers

None of the four marbling markers were estimated to have consistent effects on IMF or marble score across the various datasets. The extreme gene frequencies of many of the marbling markers made it difficult to assess the 2 star genotypes in most breeds. Reduction of models in CRC1 data showed significant effects of the markers when breed and sire where removed and suggests the marbling markers act as a proxy for breed but the degree to which the breed effects are explained was very low.

			CRC1 - Angus					Angus Progeny Test			
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Genotype	Stars	Ν	LSM	Se	Mean	N	LSM	Se	Mean	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0000	0	64	1.41	0.08	1.41	45	2.02	0.14	2.02	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0001	1	42	1.28	0.10		23	1.86	0.18		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0010	1	22	1.27	0.13		18	2.10	0.19		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0100	1	29	1.22	0.11		26	2.00	0.17		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1000	1	31	1.14	0.11	1.23	33	2.19	0.16	2.05	
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	0002	2	1	-0.85	0.63		0				
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0011	2	11	1.32	0.19		8	1.91	0.27		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0020	2	1	1.10	0.61		2	1.09	0.50		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0101	2	12	1.50	0.18		11	2.05	0.24		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0110	2	5	0.93	0.27		14	2.15	0.22		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0200	2	2	1.11	0.42		2	2.73	0.50		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1001	2	29	1.54	0.11		19	2.01	0.19		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1010	2	16	1.54	0.15		4	1.36	0.37		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1100	2	31	1.42	0.11		29	2.12	0.16		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2000	2	1	0.24	0.62	1.41	10	1.77	0.25	2.01	
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0012	3	1	1.24	0.63		0				
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0102	3	5	1.70	0.28		2	1.81	0.51		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	0111	3	5	1.20	0.27		4	2.19	0.39		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0120	3	1	1.33	0.65		1	1.81	0.71		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0201	3	3	1.46	0.36		3	1.95	0.43		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1002	3	1	1.54	0.60		1	1.10	0.71		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1011	3	8	1.44	0.22		9	1.88	0.25		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1101	3	20	1.19	0.14		22	1.83	0.18		
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	1110	3	4	0.93	0.30		10	2.13	0.24		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1200	3	3	1.27	0.35		6	1.76	0.30		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2001	3	1	1.36	0.68		4	1.65	0.36		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2010	3	0				1	1.82	0.71		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2100	3	2	0.71	0.42	1.29	9	2.44	0.26	1.95	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	0022	4	1	1.43	0.62		0				
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	0112	4	1	0.72	0.59		0				
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0121	4	0				1	3.36	0.70		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1012	4	0				1	1.28	0.71		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1021	4	0				2	2.73	0.52		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1102	4	2	1.22	0.42		2	1.32	0.68		
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1111	4	1	0.83	0.60		3	1.98	0.42		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1201	4	1	1.39	0.58		4	2.11	0.36		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	1210	4	1	1.34	0.61		0				
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	2011	4	1	1.55	0.62		3	2.30	0.42		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	2101	4	1	1.52	0.65		8	2.21	0.27		
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	2110	4	0			1.25	4	1.61	0.36	2.07	
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	0122	5	0				1	2.33	0.71		
2111       5       0       .       1       2.85       0.71         1220       5       1       2.08       0.58       0       .       .         2021       5       1       2.47       0.58       0       .       .         2201       5       1       1.25       0.61       1.59       1       2.02       0.71       2.33         2202       6       0       .       .       1       1.82       0.71         1122       6       1       1.02       0.59       1.02       0       .       1.82	1112	5	1	0.56	0.58		2	2.24	0.51		
1220       5       1       2.08       0.58       0       .       .         2021       5       1       2.47       0.58       0       .       .         2201       5       1       1.25       0.61       1.59       1       2.02       0.71       2.33         2202       6       0       .       .       1       1.82       0.71         1122       6       1       1.02       0.59       1.02       0       .       1.82	2111	5	0				1	2.85	0.71		
2021       5       1       2.47       0.58       0       .       .         2201       5       1       1.25       0.61       1.59       1       2.02       0.71       2.33         2202       6       0       .       .       1       1.82       0.71         1122       6       1       1.02       0.59       1.02       0       .       1.82	1220	5	1	2.08	0.58		0				
2201       5       1       1.25       0.61       1.59       1       2.02       0.71       2.33         2202       6       0       .       .       1       1.82       0.71         1122       6       1       1.02       0.59       1.02       0       .       1.82	2021	5	1	2.47	0.58		0				
2202         6         0         .         1         1.82         0.71           1122         6         1         1.02         0.59         1.02         0         .         1.82	2201	5	1	1.25	0.61	1.59	1	2.02	0.71	2.33	
<u>1122 6 1 1.02</u> 0.59 1.02 0 1.82	2202	6	0				1	1.82	0.71		
	1122	6	1	1.02	0.59	1.02	0			1.82	

#### Table 28: Least squares means<sup>a</sup> for marble score for the four marbling markers considered as a single genotype for CRC1 Angus and Angus progeny test data.

<sup>a</sup> Significance of "genotype" effect: CRC1 (39 df) P=0.16 and Angus PT (39 df) P=0.57.

## 6.3 Feed intake results

All results for the four feed efficiency markers on the feed intake traits are presented in Appendices E-H and comprise of the following datasets: CRC1 temperate, CRC1 tropical, CRC2 Brahman, CRC2 Tropical Composite, Angus and Shorthorn progeny tests.

#### 6.3.1 Estimated feed efficiency marker effects

Results for the four feed efficiency markers on NFI phenotypes are presented in Appendix E.

#### 6.3.1.1 Net feed Intake (NFI)

**Marker N1:** Results for single marker analyses (Table E1) showed for CRC1 temperate breeds the breed\*N1 interaction was significant (P=0.01) but given the high gene frequencies, any trend were difficult to establish. For CRC1 tropical breeds the breed\*N1 term was non-significant and the refitted N1 term approached significance (P=0.08) with the heterozygote genotype class having the lowest least squares mean. A similar result was observed for CRC2 Tropical Composite but CRC2 Brahman, Angus progeny and Shorthorn progeny tests were not significant for N1.

Results from joint fitting of the N1 marker with the other three feed efficiency markers, and also considering as a regression, did not change the results in any dataset with the one exception that in CRC2 Tropical Composite the N1 was significant when fitted as a class effect (Table E26) and approached significance (P=0.07) as a covariate (Table E28).

**Marker N2:** Single marker results show the effect of N2 was not significant in any of the datasets other than for CRC1 temperate breeds and again showed the difficulty of estimating effects for the 0 genotype given the extreme gene frequencies in most breeds. However Angus and Murray Grey had less extreme gene frequencies and the model with the marker\*N2 interaction removed showed the N2 marker was significant (Table E1) with the heterozygote (i.e. 1 star) had the lowest NFI least squares mean.

The only change in significance levels when joint fitting of the N2 marker was that it remained significant when fitted as a fixed class effect for CRC1 temperate breed (Table E2; P=0.006) but not when modelled as a covariate (P=0.45; Table E5)

**Marker N3:** Single marker results show a significant effect of the N3 marker in CRC1 temperate breeds (Table E1) with a trend across the breeds for decreasing NFI with increasing stars. The effect of the N3 marker was not significant in any other dataset and no consistent trends were observed.

Joint analysis showed the effect of N3 remained significant in the CRC1 temperate breeds when fitted as a class and regression effect (Tables E2, E5) with an estimated effect of -0.136 kg/d/N3 star (Table 29). No other dataset changed in the level of significance for the N3 marker when fitted jointly or when considered as a regression.

**Marker N4:** Single marker analyses of N4 showed no significant effects across any of the datasets, However the CRC1 temperate breeds approached significance (P=0.08) with the 0\* genotype having higher NFI least squares mean than the 1 and  $2^*$  genotype classes.

Jointly fitting N4 with the other markers showed in CRC1 temperate breeds the significance remained similar (P=0.09) when fitted as either a class effect or as a regression with a regression coefficient of -0.095 kg/d/N4 star (Table 29). No results changed for the other datasets.

**N-STARS**: Combining the four feed efficiency marker genotypes into total number of stars for CRC1 temperate breeds resulted in significant effects (as both a fixed effect and regression; Tables E8, E11) with an estimated regression coefficient of -0.101 kg/d/star (Table 29). No other dataset was significant, however the Angus Progeny test approached significance with a P=0.07 when the stars were fitted as a class effect (Table E36) but not as a regression (P=0.17; Table E37)). However the solutions suggest a slight positive association of NFI with increasing stars (Table E29).

#### 6.3.1.2 Daily feed intake (DFI)

Full results are also presented for DFI, FCR, and ADG in Appendices F, G, and H but for brevity the description of results is restricted to the significant results from the joint analyses of the four feed efficiency markers fitted as regressions on markers and total stars.

Significant effects were estimated for CRC1 temperate breeds (Table F6) for the N3 and N4 markers with estimated effects of -0.191 and -0.206 kg/d/star, respectively (Table 29) and these results are consistent with the results for these 2 markers on NFI. The effect of total stars was also significant with a -0.176 kg/d/star reduction in daily feed intake.

For CRC1 tropical breeds the same two markers approached significant when fitted as marker regressions but the N4 marker was estimated to have a positive (0.191) effect on DFI. The effect of total stars on DFI was not significant (P=0.64; Table F9).

#### 6.3.1.3 FCR

The only significant effect of the NFI markers on FCR was in CRC1 tropical breeds (Table G6) where the N4 marker had a -0.196 FCR reduction per N4 star, however the overall effect of total stars was not significant (P=0.12; Table G9) (but the regression estimate was negative).

#### 6.3.1.4 ADG

The results for feed efficiency markers on feedlot test ADG showed for CRC1 temperate breed as small but significant effect of total NFI stars on ADG (Table H5). The estimated regression coefficient was -0.016kg/d/star (Table 29). When this result is considered in conjunction with the marker results for NFI and DFI, it suggests the feed efficiency markers are identifying genotypes in this CRC1 dataset that eat less, grow a little slower and visa versa. Whereas results from CRC1 tropical breeds (Table H7) show N4 marker was significant for ADG with a positive (+0.047) coefficient, and is consistent with the result for the effects of the N4 marker on FCR.
		N1	N2	N3	N4	N-STARS
CRC1 - TEMPERATE	NFI (kg/d)	-0.071	-0.062	-0.136	-0.095	-0.101
	NFI-WGS* (kg/d)	-0.045	-0.034	-0.083	-0.024	-0.052
	FCR	-0.032	0.022	-0.072	0.021	-0.015
	DFI (kg/d)	-0.049	-0.184	-0.191	-0.206	-0.176
	ADG (kg/d)	0.004	-0.021	-0.016	-0.021	-0.016
CRC1 -TROPICAL	NFI	0.006	0.102	-0.054	-0.074	-0.035
	NFI-WGS*	0.041	0.134	-0.067	0.008	-0.000
	FCR	-0.105	0.173	0.005	-0.196	-0.075
	DFI	0.025	0.144	-0.178	0.191	0.026
	ADG	0.017	0.001	-0.024	0.047	0.012
CRC1 - BOTH	NFI	-0.031	-0.018	-0.096	-0.081	-0.070
	NFI_WGS*	-0.005	0.004	-0.070	-0.010	-0.028
	FCR	-0.076	0.073	-0.044	-0.073	-0.042
	DFI	-0.014	-0.113	-0.168	-0.026	-0.085
	ADG	0.011	-0.018	-0.017	0.010	-0.003
CRC2 – TROP COMP	NFI	-0.124	-0.270	-0.001	-0.010	-0.036
	FCR	-0.129	0.074	0.154	-0.120	-0.023
	DFI	-0.086	-0.254	-0.106	0.099	-0.012
	ADG	0.012	-0.023	-0.016	0.032	0.011
CRC2 – BRAHMAN	NFI	-0.039	-0.151	-0.072	-0.048	-0.061
	FCR	-0.254	-0.181	0.035	-0.066	-0.129
	DFI	0.191	-0.795	-0.082	-0.075	-0.043
	ADG	0.038	-0.089	-0.023	0.003	0.002
Angus PT	NFI	0.027	0.077	0.054	0.127	0.076
	FCR	0.056	-0.074	0.141	0.029	0.048
	DFI	-0.083	0.177	0.047	0.076	0.056
	ADG	-0.016	0.019	-0.007	-0.013	-0.005
Durham PT		0 1 7 7	0 222	0.020	0.012	0.103
	NFI	0.175	0.255	0.029	0.012	0.105
	NFI FCR	0.175 -0.319	0.233	-0.069	0.012	0.030
	NFI FCR DFI	0.175 -0.319 0.442	0.233 0.122 0.073	-0.069 0.012	0.132	0.030 0.055

Table 29. Estimated regression coefficients for the each of the four feed efficiency markers fitted jointly or total stars (N-STARS) for the different datasets.

\* results from analyses where animals used in WGS were removed (genotypes and phenotypes) Bold P < 0.05

#### 6.3.2 Model changes

#### Significance levels of NFI

Results in Tables (Appendix E) show under full fixed effects models that removing the covariate (age at start of feed test) or sire had no effect on the significance (or not) of the markers or stars for NFI across all datasets. Likewise for CRC1 datasets removing herd (with and without sire fitted) also had very small effects on any of the significance levels. One exception did exist, for CRC1 temperate N4 became non-significant when herd was removed (Table E2 and E5).

When breed (and herd) was removed from the models there was little observed changes in the levels of significance. The one exception was for CRC1 temperate where N2 became highly significant, particularly when modelled as a covariate (Table

E5) and N4 became highly non-significant. The effect of N2 on NFI was still significant when sire was also included in the model.

Further reduction in the model to remove Feed group (accounts for feed group and market) closely mirrored the results of dropping breed (with and without sire). For CRC1 tropical N4 was significant as a covariate (Table E6) and as total star approached significance (P=0.07; Table E12).

#### Variances

Based on the variance component estimates in Appendix E the variance explained by the four feed efficiency markers (when using the full model with markers fit as total stars covariate) are presented in Table 30. For CRC1 temperate and tropical breeds the heritability for NFI were low (0.14 and 0.20, respectively) however for the temperate breeds the markers explained half of the sire variance and 1.8% of the phenotypic variance. For tropical breeds the markers explained none of the sire or phenotypic variance and similar results were observed for CRC2 datasets and the two progeny test datasets. Fitting sire had little effect on the estimates.

### Table 30. Percent of sire (Vs), phenotypic (Vp) or residual (Ve) variance explained in NFI by fitting the four feed efficiency markers using the full fixed effects model in each dataset

Dataset	trait	Vs	Vp	Ve
			(+sire)	(-sire)
<b>CRC1</b> - <b>TEMPERATE</b>	NFI	50.2	1.8	1.4
CRC1 -TROPICAL	NFI	-9.8	-0.2	-0.1
CRC2 – TROP COMP	NFI	0.0	-0.3	-0.3
CRC2 – BRAHMAN	NFI	2.0	-0.1	0.0
Angus PT	NFI	-5.1	-0.1	-0.2
Durham PT	NFI	-6.6	0.0	-0.2

Sequentially removing fixed effects increased the residual variance for CRC1 temperate breeds. The estimated herd effect was very small and the SNP effects were estimated to explain all this effect. The SNP effects were also able to explain about 20% of the (considerable) breed variance and therefore when breed was not known the SNP accounted for 4.4% of the residual variance. The CG had a large effect on the residual variance but this was not picked up by the SNPs. Whereas for tropical the removal of feed group was the only effect that increased the estimated residual variance but there was no variance explained by the SNP with reducing amounts of fixed effect information (Table 31 and 32).

### Table 31. CRC1 – Temperate NFI (kg/d): Variation explained by four feed efficiency markers (SNP) under reducing fixed effects models

	Model			% effect	Cumm	Vsnp/Ve
Basic fixed effects	Effect removed	Sequential in mode	increase el Ve	explained by SNP	Vsnp*	for each model
		No SNP	+SNP	·		
Herd + Breed + CG	-	0.835	0.8230	-	0.0120	1.4
Breed +CG	Herd	0.004	0.000	100.0	0.0160	1.9

CG	Breed	0.136	0.109	19.9	0.0430	4.4
nil	CG	0.441	0.432	2.0	0.0520	3.7

\* estimated as a difference between model residual variances with and without SNP

### Table 32. CRC1 – Tropical NFI (kg/d): Variation explained by four feed efficiency markers under reducing fixed effects models

Model			% effect	Cumm	Vsnp/Ve
Effect	Sequential	increase	explained	Vsnp*	for each
removed	in mode	el Ve	by SNP		model
	No SNP	+SNP			
-	0.681	0.6820	-	-0.0010	-0.1
Herd	0.016	0.017	-6.3	-0.0020	-0.3
Breed	0.004	0.000	100.0	0.0020	0.3
CG	0.327	0.319	2.4	0.0100	1.0
	Model Effect removed - Herd Breed CG	Model Effect Sequential removed in mode No SNP - 0.681 Herd 0.016 Breed 0.004 CG 0.327	Model           Effect         Sequential increase in model Ve           removed         No SNP           -         0.681         0.6820           Herd         0.016         0.017           Breed         0.004         0.000           CG         0.327         0.319	Model         % effect           Effect         Sequential increase         explained           removed         in model Ve         by SNP           No SNP         +SNP         -           -         0.681         0.6820         -           Herd         0.016         0.017         -6.3           Breed         0.004         0.000         100.0           CG         0.327         0.319         2.4	Model         % effect         Cumm           Effect         Sequential increase in model Ve         explained by SNP         Vsnp*           -         0.681         0.6820         -         -0.0010           Herd         0.016         0.017         -6.3         -0.0020           Breed         0.004         0.000         100.0         0.0020           CG         0.327         0.319         2.4         0.0100

\* estimated as a difference between model residual variances with and without SNP

#### 6.3.3 Special analyses

CRC1 analyses were re-run removing the four feed efficiency marker genotypes on the 172 animals involved in the discovery whole genome scan (Tables E14-E25) and another set where both the genotypes and phenotypes on these animals were removed (Table E14b-E25b). Results from the second edited datasets will be discussed. The results for CRC1 Temperate showed N1, N2, N4 were not significant (as joint SNP or as covariates) and N3 was significant as a fixed effect and approached significance (P=0.10) as a covariate. When the SNP were fitted as total stars in the temperate breeds the effect was not significant as a fixed effect (P=0.24) but approached significance as a covariate with an estimate of -0.052 (Table 29). For tropical breed, the N1 marker was significant as a fixed effect and N3 approached significance (P=0.07) but none of the markers were significant when considered as SNP covariates or as total stars.

#### 6.3.4 Summary of feed efficiency markers

Two of the feed efficiency markers (N3 and N4) had significant effect in the CRC1 temperate dataset for NFI and DFI but were not observed to have significant effects in other datasets and direction of effects for NFI were not consistent. The markers N1 and N2 was not observed to have significant effects, and the high gene frequencies of these two markers across all populations for the 2 star allele, especially in the tropical breeds also limits their utility for breeding. Changes to the model in CRC1 data had very little effect on the estimated effects of these markers. The effect of the four feed efficiency markers for feed conversion ratio (FCR) and feedlot average daily gain were not significant.

#### 7.0 Development of marker improved EBVs

Based on the results presented in the study and the CRC-MLA proposed National Genotype Database, AGBU has commenced the development of marker enhanced EBVs  $(EBV^M)$  for the traits studied as part of its enhancements to BREEDPLAN<sup>®</sup>.

The assumptions of these developments are that a national genotype database will be the depository of various quality datasets from animals which have phenotypes and genotypes. This database will provide the estimates of the gene frequencies and gene effects to be used in BREEDPLAN.

BREEDPLAN software will be modified to accommodate, as an additional "phenotype", the derived "Marker Breeding Value" (MBV) which has a variance equal to the covariance with the breeding value and a heritability of basically 1.0. Extension to other traits should be straight forward.

#### 8.0 References

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# **APPENDIX A**

# Phenotypic data description

Dataset	Trait	N	Mean	Std	Min	Max
CRC1						
Temperate	IMF (%)	3594	4.64	2.23	1.23	18.94
	MSA marble score	1454	1.17	0.75	0.00	4.30
	I DPF (ka)	3322	4 12	0.82	2 01	8 75
	STPF (kg)	3357	4.72	0.02	2.01	7.56
	MSA Tondornoss	1222	4.70 60.00	1/ 20	2.00	01 50
	WOA TENUEINESS	1332	00.09	14.09	14.50	91.50
	DFI (kg/d)	785	12.84	1.98	5.53	18.35
	NFI (kg/d)	785	0.01	1.19	-4.03	4.52
	FCR	773	9.70	2.22	5.03	16.99
	ADG (kg/d)	785	1.39	0.39	0.15	2.38
Tropical	IMF (%)	3524	2.88	1.41	0.08	13.19
·	MSA marble score	1808	0.76	0.62	0.00	3.80
		3254	1 55	0 04	2 3/	8 02
	STDE (kg)	3212	4.33 1.73	0.54	2.07	7.24
	MSA Tondornoon	1510	4.73	15 50	2.70	00 00
	WSA Tenuemess	1019	47.40	15.56	4.20	09.00
	DFI (kg/d)	687	11.82	1.99	6.51	18.67
	NFI (kg/d)	687	0.00	1.01	-3.92	3.10
	FCR	678	9.16	1.99	5.26	17.10
	ADG (kg/d)	687	1.35	0.38	0.41	2.78
CRC2						
Brahman	IME (%)	976	2 37	0.87	0.31	6 72
Drannan	MSA marble score	987	0.61	0.07	0.01	2 40
		507	0.01	0.40	0.10	2.40
	LDPF(kg)	961	5.38	1.16	2.55	9.00
	TSPF (kg)	861	4.42	0.58	2.89	6.49
	DFI (kg/d)	704	11.24	1.94	5.97	17.88
	NFI (kg/d)	684	-0.15	1.11	-3.33	6.12
	FCR	634	10.18	2.19	5.08	17.88
	ADG (kg/d)	681	1.13	0.36	0.31	2.07
Tropical	IME (%)	1216	2 91	1 1 1	1 04	14 66
Composite	MSA marble score	1210	0.82	0.55	0.10	3 40
Composite		1000	0.02	0.00	4 ==	0.40
	LDPF (kg)	1206	4.75	1.22	1.57	8.85
	ISPF (kg)	1058	3.91	0.53	2.41	6.00
	DFI (kg/d)	806	13.10	1.95	6.02	20.46
	NFI (kg/d)	802	0.25	1.33	-4.04	8.08
	FCR	791	9.22	1.85	4.55	17.25
	ADG (kg/d)	785	1.47	0.36	0.36	2.90
Field Data						
	MSA marble score	415	1 92	0 74	0.60	4 60
Angus	DEL (ka/d)	387	14 57	1 57	10.00	10 50
	NEL (kg/d)	207	1 60	1.37	5 25	2 10
		301 202	10 60	1.30	-0.00	J. 12 17 01
	ADG (ka/d)	202 207	1 / 1	2.21 0.20	0.02	11.91
Durbom		301	5.00	0.29	0.00	2.23
Duman	IIVIE 70	342	0.ZZ	2.01	0.00	13.10
		342	∠.55	1.17	0.00	0.00
	DFI (Kg/a)	204	13.17	1.52	1.04	17.1
	INFI (Kg/a)	264	-0.52	1.32	-4.09	2.83
		204	1.10	1.40	0.00	14.91
	ADG (Kg/Q)	204	1.70	0.32	0.72	2.02

#### Table A1: Raw trait means for each dataset

### **APPENDIX B**

# TENDERNESS RESULTS

Data	Breed					T1				T2				T3				T4	
		Ν	star	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue
CRC1	AA	1605	0	15	4.53	0.18	0.000	314	4.17	0.04	0.000	42	4.22	0.11	0.045	7	3.93	0.25	0.941
			1	255	4.10	0.05		445	3.99	0.04		344	4.04	0.04		193	4.01	0.05	
			2	841	3.97	0.03		172	3.87	0.05		720	3.97	0.03		903	4.00	0.03	
	MG	369	0	4	4.18	0.31	0.064	80	3.96	0.07	0.011	13	3.93	0.18	0.723	6	3.32	0.25	0.136
			1	84	3.93	0.07		140	3.83	0.05		108	3.82	0.06		93	3.83	0.06	
			2	250	3.77	0.04		94	3.67	0.06		211	3.79	0.04		241	3.81	0.04	
	HH	901	0	14	4.03	0.31	0.000	444	4.13	0.04	0.327	23	4.07	0.16	0.838	0			
			1	242	4.32	0.07		231	4.22	0.05		235	4.17	0.05		0			
			2	537	4.08	0.04		43	4.09	0.12		524	4.16	0.04		801	4.16	0.03	
	SH	447	0	0			0.487	309	4.46	0.05	0.062	313	4.46	0.05	0.588	0			0.284
			1	6	4.20	0.35		7	3.86	0.32		31	4.29	0.16		23	4.24	0.19	
			2	351	4.45	0.05		0				3	4.49	0.50		332	4.46	0.05	
	SG	1127	0	80	4.80	0.18	0.000	514	4.68	0.04	0.000	446	4.68	0.04	0.000	54	4.40	0.11	0.240
			1	418	4.65	0.05		357	4.46	0.05		445	4.48	0.04		375	4.55	0.05	
			2	525	4.46	0.03		60	4.30	0.11		135	4.38	0.07		594	4.60	0.04	
	BR	1341	0	59	4.55	0.10	0.000	383	4.56	0.04	0.000	211	4.61	0.06	0.000	3	5.02	0.45	0.092
			1	443	4.48	0.04		499	4.32	0.04		575	4.39	0.04		162	4.26	0.06	
			2	741	4.27	0.03		218	4.15	0.05		446	4.22	0.04		1074	4.37	0.03	
	BH	786	0	137	5.24	0.08	0.030	539	5.09	0.05	0.022	514	5.12	0.05	0.004	175	5.24	0.07	0.009
			1	374	5.04	0.05		44	4.76	0.14		214	4.96	0.07		383	4.99	0.05	
			2	248	4.98	0.06		0				21	4.52	0.20		201	4.50	0.07	
CRC2	тс	1187	0	77	5.12	0.15	0.000	471	4.80	0.10	0.000	325	4.79	0.11	0.007	65	4.51	0.17	0.361
			1	432	4.75	0.10		315	4.57	0.11		519	4.65	0.10		343	4.71	0.11	
			2	594	4.58	0.10		62	4.28	0.17		228	4.49	0.12		689	4.67	0.10	
	BH	957	0	100	5.47	0.12	0.068	688	5.42	0.07	0.539	626	5.52	0.07	0.000	270	5.45	0.09	0.679
			1	432	5.50	0.08		48	5.23	0.17		229	5.26	0.09		433	5.38	0.08	
			2	356	5.32	0.08		6	5.42	0.45		21	4.75	0.24		183	5.44	0.10	
CRC2	тс	1040	0	67	3.98	0.08	0.130	418	3.98	0.05	0.000	279	3.99	0.06	0.000	57	3.89	0.08	0.679
TS			1	382	3.92	0.05		269	3.85	0.06		461	3.88	0.05		297	3.92	0.05	
			2	522	3.86	0.05		55	3.69	0.08		208	3.78	0.06		617	3.88	0.05	
	BH	857	0	98	4.48	0.06	0.079	627	4.42	0.04	0.460	551	4.47	0.04	0.001	238	4.41	0.05	0.196

Table B1: Least squares means for LD peak force (kg) for each tenderness marker fitted separately by breed

1	384	4.45	0.04	41	4.34	0.09	216	4.33	0.05	387	4.46	0.04
2	314	4.37	0.04	6	4.25	0.22	19	4.17	0.13	169	4.37	0.05

Table B2: Least squares means for ST Peak Force (kg) for each tenderness marker fitted separately for each breed

Data	Breed			T1				T2				Т3				T4			
		Ν	star	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue
CRC1	AA	1606	0	16	5.10	0.15	0.038	313	4.92	0.04	0.604	42	4.73	0.09	0.145	7	5.00	0.22	0.251
			1	260	4.97	0.04		441	4.91	0.03		397	4.91	0.04		192	4.84	0.05	
			2	831	4.88	0.08		174	4.86	0.05		713	4.91	0.02		902	4.92	0.02	
	MG	373	0	5	4.88	0.26	0.646	81	4.69	0.07	0.536	13	4.84	0.17	0.374	6	4.63	0.24	0.771
			1	86	4.62	0.06		142	4.62	0.05		111	4.59	0.06		93	4.59	0.06	
			2	252	4.63	0.04		94	4.59	0.06		213	4.64	0.04		246	4.65	0.04	
	HH	923	0	15	4.66	0.15	0.333	462	4.61	0.03	0.483	24	4.42	0.12	0.358	0			
			1	248	4.54	0.04		235	4.57	0.04		243	4.58	0.04		0			
			2	552	4.60	0.03		42	4.53	0.09		535	4.59	0.03		823			
	SH	455	0	0			0.483	314	4.59	0.03	0.544	322	4.61	0.03	0.383	0			0.491
			1	6	4.45	0.22		7	4.71	0.20		31	4.54	0.10		24	4.67	0.12	
			2	360	4.60	0.03		0				3	4.21	0.31		340	4.59	0.03	
	SG	1151	0	79	4.85	0.07	0.078	520	4.82	0.03	0.000	454	4.80	0.03	0.001	53	4.80	0.09	0.117
			1	423	4.75	0.03		367	4.66	0.04		453	4.64	0.03		386	4.78	0.03	
			2	542	4.69	0.03		61	4.53	0.08		140	4.76	0.06		604	4.69	0.03	
	BR	1372	0	60	4.79	0.07	0.097	393	4.82	0.03	0.016	217	4.79	0.04	0.134	3	4.67	0.32	0.608
			1	460	4.80	0.03		510	4.75	0.03		588	4.77	0.02		163	4.71	0.04	
			2	752	4.73	0.02		222	4.69	0.04		456	4.71	0.03		1103	4.76	0.02	
	BH	790	0	141	4.74	0.05	0.580	545	4.77	0.03	0.734	515	4.80	0.03	0.023	174	4.68	0.04	0.026
			1	380	4.78	0.03		43	4.80	0.09		217	4.69	0.04		381	4.77	0.03	
			2	242	4.74	0.04		0				21	4.59	0.12		208	4.83	0.04	

Data	Breed			T1				T2				Т3				T4			
		Ν	star	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue
CRC1	AA	518	0	2	60.8	8.5	0.722	138	59.9	1.0	0.450	16	63.5	3.1	0.577	4	60.9	6.0	0.850
			1	65	59.5	1.5		166	59.8	1.0		145	60.6	1.1		60	61.4	1.6	
			2	366	60.8	0.7		82	61.8	1.4		262	60.2	0.8		365	60.4	0.7	
	MG	146	0	1	54.1	13.5	0.724	33	57.5	2.5	0.334	8	53.4	5.2	0.085	4	64.7	7.0	0.760
			1	28	61.2	2.6		64	60.8	1.7		48	62.7	1.9		32	59.5	2.4	
			2	105	59.1	1.4		25	56.3	2.8		75	58.0	1.7		98	59.3	1.5	
	HH	500	0	9	59.6	4.4	0.772	243	57.0	0.9	0.127	14	56.5	3.5	0.889	0			
			1	130	57.4	1.2		111	60.0	1.3		119	58.2	1.2		0			
			2	269	58.3	0.9		20	59.1	2.0		264	57.8	0.9		412			
	SH	168	0	0			0.600	123	65.2	1.2	0.400	112	66.1	1.2	0.342	0			0.523
			1	2	70.5	8.6		4	70.3	6.1		13	65.1	3.4		12	68.7	4.0	
			2	136	66.0	1.2		0				2	78.6	9.0		128	66.0	1.2	
	SG	459	0	45	43.8	2.0	0.149	209	45.2	0.9	0.012	197	44.9	1.0	0.046	29	46.4	2.5	0.969
			1	185	46.6	1.0		157	47.6	1.1		190	48.1	1.0		170	47.0	1.1	
			2	212	48.0	1.0		25	53.0	2.7		58	48.8	1.9		244	47.1	0.9	
	BR	656	0	29	49.9	2.5	0.011	202	52.8	1.0	0.053	109	54.0	1.4	0.013	1	59.6	13.1	0.013
			1	231	53.2	0.9		222	55.3	0.9		305	53.2	0.8		89	58.7	1.5	
			2	366	55.9	0.7		103	56.6	1.4		211	56.8	1.0		534	54.1	0.6	
	BH	404	0	89	37.5	1.5	0.282	246	39.0	1.0	0.089	262	37.3	0.9	0.000	86	38.3	1.5	0.793
			1	189	38.9	1.1		16	45.3	3.6		121	41.4	1.3		198	39.5	1.0	
			2	122	40.6	1.3		0				14	56.7	3.5		116	39.1	1.4	

Table B3: Least squares means for MSA Consumer tenderness score for each tenderness marker fitted separately for each breed

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#### Pooled CRC1 – LDPF

#### Section 1: Significance of fitting 4 markers as fixed effects

			S	ignificance	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.008	0.424
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.431
Full	Y	Y	<0.0001	<0.0001	0.36	0.41	0.006	0.419
Full	Ν	Y	< 0.0001	0.0012	0.36	0.40	0.006	0.419
Full	Y	Ν	< 0.0001	0.0013	0.35	0.43	-	0.424
Breed NO herd	Y	Y	< 0.0001	0.0007	0.18	0.24	0.022	0.444
Breed NO herd	Y	Ν	< 0.0001	< 0.0001	0.25	0.28	-	0.464
Breed + kill	Y	Ν	-	-	-	-	-	0.471
NO breed & herd	Y	Y	0.0002	< 0.0001	0.16	0.19	0.026	0.446
NO breed & herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.19	-	0.469
Kill	Y	Ν	-	-	-	-	-	0.494
SNPs only	Ν	Y	0.006	0.0006	< 0.0001	0.45	0.079	0.573
SNPs only	Ν	Ν	0.001	0.0006	< 0.0001	0.12	-	0.642

#### Table B4. Temperate CRC1: LDPF – markers as fixed effects

Table B5. Tropical CRC1: LDPF – markers as fixed effects

			Si	ignificance	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.038	0.571
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.605
Full	Y	Y	<0.0001	<0.0001	<0.0001	0.06	0.032	0.548
Full	Ν	Y	< 0.0001	< 0.0001	< 0.0001	0.06	0.031	0.550
Full	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.02	-	0.577
Breed NO herd	Y	Y	< 0.0001	< 0.0001	< 0.0001	0.11	0.040	0.565
Breed NO herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.02	-	0.604
Breed + kill	Y	Ν	-	-	-	-	-	0.635
NO breed & herd	Y	Y	< 0.0001	< 0.0001	< 0.0001	0.05	0.045	0.565
NO breed & herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.0013	-	0.608
Kill	Y	Ν	-	-	-	-	-	0.678
SNPs only	Ν	Y	< 0.0001	< 0.0001	< 0.0001	0.07	0.082	0.726
SNPs only	Ν	Ν	< 0.0001	< 0.0001	< 0.0001	0.005	-	0.802

Table B6. Both CRC1: LDPF – markers as fixed effects
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			S	lignificance	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.023	0.498
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.519
Full	Y	Y	<.0001	<.0001	<.0001	0.12	0.019	0.485
Full	Ν	Y	<.0001	<.0001	<.0001	0.12	0.019	0.485
Full	Y	Ν	<.0001	<.0001	<.0001	0.04	-	0.502
Breed NO herd	Y	Y	<.0001	<.0001	<.0001	0.22	0.030	0.505
Breed NO herd	Y	Ν	<.0001	<.0001	<.0001	0.06	-	0.533
Breed + kill	Y	Ν	-	-	-	-	-	0.553
NO breed & herd	Y	Y	<.0001	<.0001	<.0001	0.06	0.035	0.506
NO breed & herd	Y	Ν	<.0001	<.0001	<.0001	0.001	-	0.539
Kill	Y	Ν	-	-	-	-	-	0.585
SNPs only	Ν	Y	<.0001	<.0001	<.0001	0.05	0.0923	0.652
SNPs only	Ν	Ν	<.0001	<.0001	<.0001	0.0002	-	0.733

<b>Section 2: Significance</b>	of fitting 4 markers a	s covariate (additive	effect only)
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			S	ignificance	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.008	0.424
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.431
Full	Y	Y	<0.0001	<0.0001	0.32	0.93	0.006	0.420
Full	Ν	Y	< 0.0001	0.0006	0.33	0.94	0.006	0.419
Full	Y	Ν	< 0.0001	0.0007	0.32	0.89	-	0.425
Breed NO herd	Y	Y	< 0.0001	0.0002	0.22	0.88	0.022	0.444
Breed NO herd	Y	Ν	< 0.0001	< 0.0001	0.39	0.82	-	0.464
Breed + kill	Y	Ν	-	-	-	-	-	0.471
NO breed & herd	Y	Y	0.0001	< 0.0001	< 0.0001	0.60	0.030	0.446
NO breed & herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.42	-	0.472
Kill	Y	Ν	-	-	-	-	-	0.494
SNPs only	Ν	Y	0.003	0.0002	0.005	0.38	0.083	0.573

Table B7	Temperate	CRC1.	LDPF -	markers a	as additive	effects
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Table B8 Tropical CRC1: LDPF - markers as additive effects

			S	ignificance	Varia	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.038	0.571
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.605
Full	Y	Y	<0.0001	<0.0001	<0.0001	0.86	0.033	0.549
Full	Ν	Y	< 0.0001	< 0.0001	< 0.0001	0.99	0.032	0.550
Full	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.87	-	0.578
Breed NO herd	Y	Y	< 0.0001	< 0.0001	< 0.0001	0.78	0.042	0.565
Breed NO herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.76	-	0.606
Breed + kill	Y	Ν	-	-	-	-	-	0.635
NO breed & herd	Y	Y	< 0.0001	< 0.0001	< 0.0001	0.14	0.047	0.565
NO breed & herd	Y	Ν	< 0.0001	< 0.0001	< 0.0001	0.009	-	0.611
Kill	Y	Ν	-	-	-	-	-	0.678
SNPs only	Ν	Y	< 0.0001	< 0.0001	< 0.0001	0.64	0.085	0.727
SNPs only	Ν	Ν	< 0.0001	< 0.0001	< 0.0001	0.19	-	0.805

Table B9 Both CRC1: LDPF – markers as additive effects

				Significance	Vari	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Breed+herd+kill	Y	Y	-	-	-	-	0.023	0.498
Breed+herd+kill	Y	Ν	-	-	-	-	-	0.519
Full	Y	Y	<.0001	<.0001	<.0001	>0.99	0.020	0.485
Full	Ν	Y	<.0001	<.0001	<.0001	0.90	0.020	0.486
Full	Y	Ν	<.0001	<.0001	<.0001	0.95	-	0.503
Breed NO herd	Y	Y	<.0001	<.0001	<.0001	0.71	0.032	0.505
Breed NO herd	Y	Ν	<.0001	<.0001	<.0001	0.75	-	0.535
Breed + kill	Y	Ν	-	-	-	-	-	0.553
NO breed & herd	Y	Y	<.0001	<.0001	<.0001	0.10	0.038	0.506
NO breed & herd	Y	Ν	<.0001	<.0001	<.0001	0.007	-	0.541
Kill	Y	Ν	-	-	-	-	-	0.585
SNPs only	Ν	Y	<.0001	<.0001	<.0001	0.13	0.094	0.652
SNPs only	Ν	Ν	<.0001	<.0001	<.0001	0.005	-	0.735

Section	3: Si	gnificance	of fitting	4 markers as	total	STARS (	(class effects)
		0					( )

Table B10. Temperate CRC1: LDPF – markers as stars							
			Variances				
Model	cov	sire	Р	Sire	residual		
Breed+herd+kill	Y	Y	-	0.008	0.424		
Breed+herd+kill	Y	Ν	-	-	0.431		
Full	Y	Y	<.0001	0.007	0.420		
Full	Ν	Y	<.0001	0.007	0.419		
Full	Y	Ν	<.0001	-	0.426		
Breed NO herd	Y	Y	<.0001	0.023	0.444		
Breed NO herd	Y	Ν	<.0001	-	0.465		
Breed + kill	Y	Ν	-	-	0.471		
NO breed & herd	Y	Y	<.0001	0.029	0.445		
NO breed & herd	Y	Ν	<.0001	-	0.471		
Kill	Y	Ν	-	-	0.494		
SNPs only	Ν	Y	<.0001	0.083	0.573		
SNPs only	Ν	Ν	<.0001		0.646		

Table B10. Temperate CRC1: LDPF – markers as stars

Table B11. Tropical CRC1: LDPF – markers as stars

				Variances	
Model	cov	sire	Р	Sire	residual
Breed+herd+kill	Y	Y	-	0.038	0.571
Breed+herd+kill	Y	Ν	-	-	0.605
Full	Y	Y	<.0001	0.031	0.556
Full	Ν	Y	<.0001	0.032	0.550
Full	Y	Ν	<.0001	-	0.583
Breed NO herd	Y	Y	<.0001	0.042	0.571
Breed NO herd	Y	Ν	<.0001	-	0.611
Breed + kill	Y	Ν	-	-	0.635
NO breed & herd	Y	Y	<.0001	0.045	0.571
NO breed & herd	Y	Ν	<.0001	-	0.614
Kill	Y	Ν	-	-	0.678
SNPs only	Ν	Y	<.0001	0.083	0.733
SNPs only	Ν	Ν	<.0001	-	0.811

### Table B12. BOTH CRC1: LDPF – markers as stars

				Varı	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+kill	Y	Y	-	0.023	0.498
Breed+herd+kill	Y	Ν	-	-	0.519
Full	Y	Y	<.0001	0.020	0.488
Full	Ν	Y	<.0001	0.020	0.488
Full	Y	Ν	<.0001	-	0.506
Breed NO herd	Y	Y	<.0001	0.321	0.507
Breed NO herd	Y	Ν	<.0001	-	0.537
Breed + kill	Y	Ν	-	-	0.553
NO breed & herd	Y	Y	<.0001	0.037	0.508
NO breed & herd	Y	Ν	<.0001	-	0.542
Kill	Y	Ν	-	-	0.585
SNPs only	Ν	Y	<.0001	0.088	0.654
SNPs only	Ν	Ν	<.0001	-	0.734

Section 4: Significance	e of fitting 4 markers a	as Total STARS	(additive effect)
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				Variances		
Model	cov	sire	Р	Sire	residual	
Breed+herd+kill	Y	Y	-	0.008	0.424	
Breed+herd+kill	Y	Ν	-	-	0.431	
Full	Y	Y	<.0001	0.007	0.419	
Full	Ν	Y	<.0001	0.007	0.419	
Full	Y	Ν	<.0001	-	0.426	
Breed NO herd	Y	Y	<.0001	0.023	0.444	
Breed NO herd	Y	Ν	<.0001	-	0.465	
Breed + kill	Y	Ν	-	-	0.471	
NO breed & herd	Y	Y	<.0001	0.031	0.446	
NO breed & herd	Y	Ν	<.0001	-	0.473	
Kill	Y	Ν	-	-	0.494	
SNPs only	Ν	Y	<.0001	0.083	0.572	
SNPs only	Ν	Ν	<.0001	-	0.646	

Table B13. Temperate CRC1: LDPF – markers as stars as additive

Table B14. Tropical CRC1: LDPF – markers as stars as additive

				Variances		
Model	cov	sire	Р	Sire	residual	
Breed+herd+kill	Y	Y	-	0.038	0.571	
Breed+herd+kill	Y	Ν	-	-	0.605	
Full	Y	Y	<.0001	0.032	0.556	
Full	Ν	Y	<.0001	0.031	0.556	
Full	Y	Ν	<.0001	-	0.583	
Breed NO herd	Y	Y	<.0001	0.042	0.570	
Breed NO herd	Y	Ν	<.0001	-	0.611	
Breed + kill	Y	Ν	-	-	0.635	
NO breed & herd	Y	Y	<.0001	0.045	0.571	
NO breed & herd	Y	Ν	<.0001	-	0.614	
Kill	Y	Ν	-	-	0.678	
SNPs only	Ν	Y	<.0001	0.084	0.733	
SNPs only	Ν	Ν	<.0001	-	0.811	

Table B15. Both CRC1: LDPF – markers as stars as additive

				Variances		
Model	cov	sire	Р	Sire	residual	
Breed+herd+kill	Y	Y	-	0.023	0.498	
Breed+herd+kill	Y	Ν	-	-	0.519	
Full	Y	Y	<.0001	0.020	0.488	
Full	Ν	Y	<.0001	0.020	0.488	
Full	Y	Ν	<.0001	-	0.505	
Breed NO herd	Y	Y	<.0001	0.322	0.507	
Breed NO herd	Y	Ν	<.0001	-	0.537	
Breed + kill	Y	Ν	-	-	0.553	
NO breed & herd	Y	Y	<.0001	0.037	0.508	
NO breed & herd	Y	Ν	<.0001	-	0.543	
Kill	Y	Ν	-	-	0.585	
SNPs only	Ν	Y	<.0001	0.090	0.654	
SNPs only	Ν	Ν	<.0001	-	0.735	

#### CRC2 – LDPF (AT and TS)

#### Table B16. BRAHMAN: LDPF - 4 markers as fixed class

				Significanc	Var	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.103	1.031
Full no markers	Y	Ν	-	-	-	-	-	1.116
Full	Y	Y	0.02	0.82	0.003	0.52	0.094	1.017
Full	Y	Ν	0.05	0.85	0.002	0.74	-	1.093

Table B17. BRAHMAN: LDPF – 4 markers as covariates

				Significance of marker (P)				iances
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.103	1.031
Full no markers	Y	Ν	-	-	-	-	-	1.116
Full	Y	Y	0.009	0.87	0.004	0.86	0.092	1.016
Full	Y	Ν	0.03	0.89	0.000	0.89	-	1.092

Table B18. BRAHMAN: LDPF – 4 markers as total stars (class)

			Р	Var	iances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.103	1.031
Full no markers	Y	Ν	-	-	1.116
Full	Y	Y	0.05	0.097	1.023
Full	Y	Ν	0.03	-	1.104

Table B19. BRAHMAN: LDPF – 4 markers as total stars covariate

			Р	Variances		
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0.103	1.031	
Full no markers	Y	Ν	-	-	1.116	
Full*	Y	Y	0.005	0.098	1.023	
Full	Y	Ν	0.003	-	1.104	

\* b= -0.1048 (0.03722)

			S	ignificanc	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.085	0.992
Full no markers	Y	Ν	-	-	-	-	-	1.065
Full	Y	Y	0.0004	0.008	0.27	0.42	0.089	0.979
Full	Y	Ν	<.0001	0.01	0.42	0.30	-	1.037

Table B20. TROPICAL COMPOSITE: LDPF – 4 markers as fixed class

Table B21. TROPICAL COMPOSITE: LDPF - 4 markers as covariates

			S	lignificanc	Var	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.085	0.992
Full no markers	Y	Ν	-	-	-	-	-	1.065
Full	Y	Y	0.0004	0.002	0.21	0.59	0.079	0.970
Full	Y	Ν	<.0001	0.003	0.22	0.58	-	1.037

#### Table B22. TROPICAL COMPOSITE: LDPF – 4 markers as total stars (class)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.085	0.992
Full no markers	Y	Ν	-	-	1.065
Full	Y	Y	0.001	0.079	0.978
Full	Y	Ν	0.0003	-	1.046

#### Table B23. TROPICAL COMPOSITE: LDPF – 4 markers as total stars covariate

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.085	0.992
Full no markers	Y	Ν	-	-	1.065
Full*	Y	Y	< 0.0001	0.077	0.981
Full	Y	Ν	< 0.0001	-	1.047
	2				

\* b= -0.1106 (0.02678)

				Significanc	Var	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.019	0.247
Full no markers	Y	Ν	-	-	-	-	-	0.264
Full	Y	Y	0.07	0.96	0.0005	0.17	0.018	0.243
Full	Y	Ν	0.06	0.91	0.0008	0.16	-	0.260

Table B24. BRAHMAN: TSPF - 4 markers as fixed class

Table B25. BRAHMAN: TSPF – 4 markers as covariates

				Significanc	Var	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.019	0.247
Full no markers	Y	Ν	-	-	-	-	-	0.264
Full	Y	Y	0.02	0.99	0.0001	0.60	0.019	0.242
Full	Y	Ν	0.02	0.66	0.0002	0.79	-	0.260

Table B26. BRAHMAN: TSPF – 4 markers as total stars (class)

			Р	Vari	iances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.019	0.247
Full no markers	Y	Ν	-	-	0.264
Full	Y	Y	0.008	0.018	0.244
Full	Y	Ν	0.006	-	0.261

Table B27. BRAHMAN: TSPF – 4 markers as total stars covariate

Table $D_2/$ . DRAHMAN. ISFF – 4 markets as total stars covariate										
		P Variances								
Model	cov	sire		Sire	Residual					
Full no markers	Y	Y	-	0.019	0.247					
Full no markers	Y	Ν	-	-	0.264					
Full*	Y	Y	0.002	0.018	0.245					
Full	Y	Ν	0.001	-	0.262					

\* b= -0.05834 (0.01858)

			_	Significand	Vari	ances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.208
Full no markers	Y	Ν	-	-	-	-	-	0.225
Full	Y	Y	0.08	0.09	0.15	0.49	0.017	0.206
Full	Y	Ν	0.13	0.04	0.05	0.49	-	0.220

Table B28. Tropical Composite: TSPF - 4 markers as fixed class

Table B29. Tropical Composite: TSPF – 4 markers as covariates

				Significanc	Var	iances		
Model	cov	sire	T1	T2	T3	T4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.208
Full no markers	Y	Ν	-	-	-	-	-	0.225
Full	Y	Y	0.03	0.03	0.06	0.63	0.017	0.206
Full	Y	Ν	0.05	0.01	0.02	0.61	-	0.219

Table B30. Tropical Composite TSPF – 4 markers as total stars (class)

			Р	Var	iances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.021	0.208
Full no markers	Y	Ν	-	-	0.225
Full	Y	Y	0.015	0.016	0.207
Full	Y	Ν	0.001	-	0.220

Table B31. Tropical Composite: TSPF – 4 markers as total stars covariate

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.021	0.208
Full no markers	Y	Ν	-	-	0.225
Full*	Y	Y	0.0001	0.017	0.206
Full	Y	Ν	<.0001	-	0.219

\* b= -0.05299 (0.01386)

		Ar	ngus	Here	eford	Murra	y Grey	Shor	thorn
Model	effect	b	Pvalue	b	Pvalue	b	Pvalue	b	Pvalue
All 4	T1	-0.16	<.001	-0.18	<.001	-0.15	0.038	0.19	0.595
markers		(0.04)		(0.05)		(0.07)		(0.36)	
	T2	-0.14	<.0001	0.03	0.455	-0.16	0.004	-0.62	0.096
		(0.04)		(0.05)		(0.06)		(0.37)	
	T3	-0.04	0.348	-0.00	0.956	0.06	0.411	0.04	0.805
		(0.04)		(0.05)		(0.04)		(0.18)	
	T4	-0.03	0.563	0		0.02	0.791	0.24	0.235
		(0.05)				(0.05)		(0.20)	
<b>T</b> 1004	<b>T</b> 1004	0.11	. 0001	0.02	0.051	0.06	0.010	0.10	0.270
11234 geno	11234	-0.11	<.0001	-0.03	0.251	-0.06	0.012	-0.10	0.378
		(0.02)		(0.03)		(0.03)		(0.11)	
T123⊥T4	т123	-0.12	< 0001	-0.04	0.243	-0.08	0.002	-0.18	0.158
1123+14	1123	(0.02)	<.0001	(0.03)	0.245	(0.03)	0.002	(0.13)	0.150
	Т4	-0.04	0.510	0		0.05	0 446	0.23	0 253
	1	(0.03)	0.010	0	•	(0.07)	0.110	(0.20)	0.235
		(0.00)				(0.07)		(0.20)	
T123 geno	T123	-0.12	<.0001	-0.04	0.243	-0.09	0.002	-0.18	0.162
U		(0.02)		(0.03)		(0.03)		(0.13)	
T12 +T3+T4	T12	-0.17	<.0001	-0.05	0.127	-0.16	<.001	-0.17	0.534
		(0.03)		(0.04)		(0.04)		(0.28)	
	T3	-0.03	0.493	0.00	0.930	0.06	0.385	-0.10	0.514
		(0.04)		(0.05)		(0.07)		(0.15)	
	T4	-0.04	0.489	0	0.564	0.02	0.790	0.23	0.261
		(0.05)				(0.07)		(0.20)	
T12 geno	T12	-0.17	<.0001	-0.06	0.126	-0.14	<.001	-0.21	0.439
		(0.03)		(0.04)		(0.04)		(0.27)	

Table B32. LDPF CRC1 temperate breeds- Partial regression coefficients based on number of stars for different combinations of the 4 tenderness markers

		Brah	CRC1	B. Red	d CRC1	Santa	a CRC1	Brah C	RC2	TComp	CRC2
Model	effect	b	Pvalue								
All 4	T1	-0.12	0.016	-0.18	<.0001	-0.18	<.0001	-0.15	0.009	-0.19	<.001
markers		(0.05)		(0.04)		(0.04)		(0.06)		(0.05)	
	T2	-0.21	0.159	-0.16	<.001	-0.19	<.0001	0.02	0.869	-0.22	0.002
		(0.15)		(0.04)		(0.04)		(0.14)		(0.07)	
	T3	-0.18	0.008	-0.10	0.011	-0.13	<.001	-0.27	<.001	-0.07	0.209
		(0.07)		(0.04)		(0.04)		(0.07)		(0.06)	
	T4	-0.11	0.020	0.08	0.227	0.09	0.038	-0.01	0.857	0.03	0.591
		(0.05)		(0.06)		(0.04)		(0.06)		(0.06)	
T1234 geno	T1234	-0.14	<.0001	-0.13	<.0001	-0.12	<.0001	-0.10	0.005	-0.11	<.0001
		(0.03)		(0.02)		(0.02)		(0.04)		(0.03)	
T123+T4	T123	-0.16	<.001	-0.14	<.0001	-0.18	<.0001	-0.17	<.001	-0.15	<.0001
		(0.04)		(0.04)		(0.02)		(0.05)		(0.03)	
	T4	-0.12	0.017	0.08	0.191	0.09	0.030	-0.01	0.839	0.03	0.536
		(0.05)		(0.06)		(0.04)		(0.05)		(0.06)	
T123 geno	T123	-0.16	<.001	-0.14	<.0001	-0.18	<.0001	-0.17	<.001	-0.15	<.0001
		(0.04)		(0.02)		(0.02)		(0.05)		(0.03)	

Table B33: LDPF tropical breeds- Partial regression coefficients based on number of stars for different combinations of the 4 tenderness markers

# **APPENDIX C**

### **IMF% results**

#### SINGLE MARKER results for the 4 marbling markers by dataset and breed

Data	Breed			M1				M2				M3				M4			
		Ν	star	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue
CRC1	AA	1676	0	649	4.94	0.07	0.648	671	5.01	0.07	0.387	998	4.91	0.06	0.031	655	5.00	0.07	0.437
			1	463	4.99	0.08		329	4.86	0.10		203	5.04	0.12		482	4.90	0.08	
			2	55	5.13	0.22		33	4.79	0.28		11	6.14	0.49		68	4.78	0.21	
	MG	427	0	144	5.17	0.17	0.218	211	5.35	0.14	0.682	359	5.38	0.10	0.746	295	5.28	0.11	0.276
			1	185	5.54	0.15		108	5.27	0.20		34	5.10	0.35		89	5.50	0.22	
			2	45	5.28	0.30		3	4.36	1.14		1	5.23	2.00		7	6.37	0.75	
	HH	1027	0	654	4.00	0.05	0.011	786	3.95	0.05	0.921	731	3.91	0.05	0.268	576	4.02	0.05	0.085
			1	202	3.76	0.09		24	3.92	0.27		168	4.03	0.10		296	3.81	0.08	
			2	13	3.32	0.35		0				5	4.55	0.55		29	3.97	0.24	
	SH	464	0	274	4.91	0.09	0.196	336	4.83	0.09	0.463	335	4.89	0.09	0.765	196	4.87	0.11	0.653
			1	85	4.64	0.17		17	5.11	0.37		30	4.90	0.28		162	4.95	0.12	
			2	10	5.37	0.47		0				2	5.71	1.12		27	4.68	0.30	
	SG	1228	0	995	2.69	0.04	0.669	316	2.78	0.06	0.159	1118	2.71	0.04	0.181	1016	2.69	0.04	0.174
			1	106	2.78	0.10		468	2.69	0.05		13	2.31	0.29		112	2.83	0.10	
			2	3	2.95	0.57		154	2.59	0.09		0				0			
	BR	1458	0	1182	3.22	0.04	0.322	516	3.12	0.05	0.079	1144	3.21	0.04	0.983	999	3.19	0.04	0.288
			1	121	3.10	0.11		570	3.28	0.05		196	3.22	0.08		317	3.26	0.07	
			2	3	2.56	0.65		83	3.17	0.13		7	3.22	0.44		25	3.50	0.23	
	BH	838	0	787	2.52	0.04	0.568	26	2.20	0.21	0.131	802	2.52	0.04	0.481	733	2.53	0.04	0.258
			1	19	2.39	0.23		254	2.60	0.07		5	2.84	0.46		74	2.33	0.12	
			2	0				336	2.50	0.06		0				4	2.54	0.48	
CRC2	TC	1197	0	944	2.94	0.04	0.736	449	2.94	0.06	0.325	977	2.93	0.04	0.881	888	2.90	0.04	0.180
			1	159	2.8	0.09		452	2.93	0.06		139	2.97	0.10		212	2.97	0.08	
			2	5	3.15	0.49		89	2.75	0.12		6	3.08	0.43		11	3.43	0.32	
	BH	972	0	877	2.18	0.05	0.256	25	2.02	0.16	0.376	917	2.19	0.05	0.208	815	2.17	0.05	0.309
			1	28	2.02	0.15		237	2.13	0.06		5	1.71	0.38		85	2.27	0.09	
			2	0				454	2.19	0.05		0				1	1.37	0.77	
Durham	SS	342	0	247	5.44	0.16	0.417	340	5.46	0.16	0.262	319	5.41	0.15	0.770	182	5.37	0.17	0.392
			1	76	5.39	0.20		2	3.93	1.32		18	5.38	0.35		119	5.56	0.18	
			2	5	4.54	0.68						3	4.83	0.82		32	5.27	0.27	

Table C1: Least squares means for IMF(%) for each marker fitted separately across breeds

Data	Breed			M1				M2				M3				M4			
		Ν	star	Ν	Est.	SE	Pvalue												
CRC1	AA	1048	0	431	5.85	0.10	0.547	437	5.91	0.10	0.573	647	5.83	0.08	0.008	433	5.92	0.10	0.633
			1	301	6.00	0.12		211	5.77	0.14		130	5.93	0.17		306	5.80	0.12	
			2	24	5.72	0.39		19	5.60	0.43		6	8.14	0.74		45	5.74	0.30	
	MG	280	0	99	6.03	0.23	0.054	142	6.41	0.19	0.668	233	6.45	0.15	0.177	194	6.33	0.16	0.646
			1	120	6.77	0.21		65	6.21	0.30		23	5.75	0.50		57	6.45	0.33	
			2	28	6.21	0.43		2	5.16	1.63						4	7.34	1.15	
	HH	703	0	458	4.99	0.07	0.024	557	4.57	0.06	0.500	516	4.54	0.06	0.047	396	4.68	0.07	0.118
			1	145	4.64	0.21		11	4.87	0.43		114	4.77	0.14		214	4.42	0.10	
			2	9	4.32	0.43						3	6.16	0.78		21	4.47	0.31	
	SH	310	0	185	5.84	0.13	0.174	235	5.72	0.12	0.548	227	5.79	0.12	0.815	145	5.75	0.15	0.583
			1	62	5.44	0.23		13	6.03	0.50		22	5.78	0.39		105	5.91	0.17	
			2	8	6.37	0.61						2	6.63	1.31		17	5.49	0.43	
	SG	794	0	654	3.06	0.05	0.654	205	3.21	0.09	0.127	728	3.07	0.05	0.276	664	3.05	0.05	0.053
			1	66	3.19	0.14		293	3.03	0.07		9	2.66	0.38		71	3.32	0.14	
			2	1	3.04	1.13		106	2.98	0.12									
	BR	895	0	725	3.61	0.05	0.474	325	3.50	0.07	0.100	699	3.60	0.05	0.766	613	3.60	0.05	0.907
			1	73	3.49	0.15		329	3.71	0.07		120	3.69	0.12		193	3.64	0.09	
			2	2	2.75	0.88		54	3.50	0.18		5	3.75	0.57		17	3.68	0.31	
	BH	483	0	453	2.84	0.06	0.941	14	2.31	0.33	0.247	461	2.83	0.06	0.632	425	2.85	0.06	0.338
			1	14	2.81	0.31		152	2.90	0.10		4	3.10	0.56		40	2.62	0.19	
			2					197	2.87	0.09						1	2.00	1.07	

Table C2: Least squares means for IMF(%) -no domestic market CRC1 - for each marker fitted separately

#### CRC1 – base models for IMF%

Table C3. Temperate CKC1. INIT base model variances											
			Vari	ances							
Model	cov	sire	Sire	residual							
Full no markers	Y	Y	0.204	1.824							
Full no markers	Y	Ν	-	2.007							
Breed +kill	Y	Ν	-	2.220							
Kill	Y	Ν	-	2.429							
No fixed effects	Ν	Ν	-	4.968							

#### Table C3. Temperate CRC1: IMF base model variances

#### Table C4. Tropical CRC1: IMF base model variances

			Variances		
Model	cov	sire	Sire	residual	
Full no markers	Y	Y	0.075	0.910	
Full no markers	Y	Ν	-	0.978	
Breed +kill	Y	Ν	-	0.992	
Kill	Y	Ν	-	1.063	
No fixed effects	Ν	Ν	-	2.005	

#### Table C5. BOTH CRC1: IMF base model variances

			Varia	ances
Model	cov	sire	Sire	residual
Full no markers	Y	Y	0.156	1.369
Full no markers	Y	Ν	-	1.501
Breed +kill	Y	Ν	-	1.633
Kill	Y	Ν	-	1.780
No fixed effects	Ν	Ν	-	4.272

#### Section 1: Significant of fitting 4 markers as fixed effects

Tuble Co. Temperate CRC1. IVIT markets as fixed circles											
				Significance	er (P)	Vari	ances				
Model	cov	sire	M1	M2	M3	M4	Sire	residual			
Full no markers	Y	Y	-	-	-	-	0.204	1.824			
Full	Y	Y	0.49	0.69	0.02	0.69	0.206	1.824			
Full	Ν	Y	0.62	0.71	0.01	0.73	0.238	1.884			
Full	Y	Ν	0.49	0.40	0.02	0.51	-	2.007			
Breed NO herd	Y	Y	0.45	0.91	0.10	0.11	0.233	1.980			
Breed NO herd	Y	Ν	0.90	0.75	0.05	0.01	-	2.209			
NO breed & herd	Y	Y	0.46	0.34	0.11	0.23	0.400	1.986			
NO breed & herd	Y	Ν	0.04	0.0003	0.05	0.07	-	2.380			
SNPs only	Ν	Y	0.39	0.31	0.17	0.02	0.365	4.494			
SNPs only	Ν	Ν	0.21	0.04	0.13	0.003	-	4.862			

Table C6. Temperate CRC1: IMF – markers as fixed effects

Table C7. Tropical CRC1: IMF – markers as fixed effects

			Significance of marker (P)				Vari	ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.075	0.910
Full	Y	Y	0.92	0.17	0.60	0.26	0.078	0.911
Full	Ν	Y	0.92	0.15	0.52	0.31	0.077	0.917
Full	Y	Ν	0.79	0.11	0.99	0.33	-	0.981
Breed NO herd	Y	Y	0.93	0.45	0.75	0.16	0.074	0.923
Breed NO herd	Y	Ν	0.46	0.34	0.99	0.24	-	0.994
NO breed & herd	Y	Y	0.97	0.15	0.19	0.04	0.116	0.924
NO breed & herd	Y	Ν	0.72	< 0.0001	0.04	0.006	-	1.033
SNPs only	Ν	Y	0.84	0.008	0.05	0.08	0.112	1.86
SNPs only	Ν	Ν	0.64	0.006	0.02	0.02	-	1.970

Table C8. Both CRC1: IMF – markers as fixed effects

			Significance of marker (P)				Vari	ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.156	1.369
Full	Y	Y	0.37	0.60	0.01	0.91	0.158	1.369
Full	Ν	Y	0.49	0.55	0.006	0.99	0.169	1.392
Full	Y	Ν	0.91	0.37	0.02	0.91	-	1.503
Breed NO herd	Y	Y	0.41	0.71	0.07	0.45	0.174	1.467
Breed NO herd	Y	Ν	0.93	0.67	0.06	0.04	-	1.629
NO breed & herd	Y	Y	0.46	0.19	0.05	0.87	0.298	1.471
NO breed & herd	Y	Ν	0.01	0.0003	0.02	0.45	-	1.744
SNPs only	Ν	Y	0.01	< 0.001	0.03	0.86	0.771	3.218
SNPs only	Ν	Ν	< 0.001	< 0.001	0.0004	0.004	-	3.805

#### Section 2: Significance of fitting 4 markers as covariate (additive only)

Table C9. Temperate CRC1. INIT - markers as additive effects											
				Significance	r (P)	Vari	ances				
Model	cov	sire	M1	M2	M3	M4	Sire	residual			
Full no markers	Y	Y	-	-	-	-	0.204	1.824			
Full	Y	Y	0.25	0.47	0.24	0.54	0.205	1.826			
Full	Ν	Y	0.35	0.48	0.31	0.48	0.237	1.887			
Full	Y	Ν	0.82	0.19	0.07	0.27	-	2.007			
Breed NO herd	Y	Y	0.41	0.85	0.44	0.04	0.232	1.980			
Breed NO herd	Y	Ν	0.99	0.55	0.17	0.004	-	2.209			
NO breed & herd	Y	Y	0.91	0.21	0.67	0.11	0.403	1.987			
NO breed & herd	Y	Ν	0.01	0.0002	0.63	0.03	-	2.383			
SNPs only	Ν	Y	0.78	0.20	0.78	0.007	0.364	4.497			
SNPs only	Ν	Ν	0.20	0.009	0.59	0.0009	-	4.863			

Table C9. Temperate CRC1: IMF – markers as additive effects

Table C10. Tropical CRC1: IMF - markers as additive effects

			Significance of marker (P)				Vari	ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.075	0.910
Full	Y	Y	0.77	0.78	0.34	0.19	0.078	0.911
Full	Ν	Y	0.76	0.75	0.28	0.22	0.078	0.917
Full	Y	Ν	0.58	0.85	0.92	0.23	-	0.981
Breed NO herd	Y	Y	0.78	0.70	0.46	0.16	0.074	0.923
Breed NO herd	Y	Ν	0.30	0.96	0.99	0.25	-	0.993
NO breed & herd	Y	Y	0.91	0.27	0.07	0.03	0.117	0.924
NO breed & herd	Y	Ν	0.47	0.0001	0.01	0.003	-	1.034
SNPs only	Ν	Y	0.82	0.13	0.01	0.05	0.112	1.862
SNPs only	Ν	Ν	0.54	0.001	0.007	0.009	-	1.969

Table C11. Both CRC1: IMF - markers as additive effects

			S	Significance of marker (P)				ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.156	1.369
Full	Y	Y	0.22	0.82	0.15	0.90	0.158	1.369
Full	Ν	Y	0.27	0.89	0.13	0.96	0.168	1.394
Full	Y	Ν	0.73	0.40	0.13	0.71	-	1.504
Breed NO herd	Y	Y	0.41	0.90	0.32	0.22	0.173	1.468
Breed NO herd	Y	Ν	0.85	0.71	0.19	0.02	-	1.629
NO breed & herd	Y	Y	0.89	0.88	0.25	0.63	0.301	1.471
NO breed & herd	Y	Ν	0.001	0.84	0.07	0.54	-	1.748
SNPs only	Ν	Y	0.04	< 0.001	0.04	0.59	0.774	3.219
SNPs only	Ν	Ν	< 0.001	< 0.001	0.0002	0.0008	-	3.808

#### Section 3: Significance of fitting 4 markers as total STARS (class)

				Variances		
Model	cov	sire	Р	Sire	residual	
Full no marker	Y	Y	-	0.204	1.824	
Full	Y	Y	0.009	0.205	1.817	
Full	Ν	Y	0.019	0.237	1.878	
Full	Y	Ν	0.011	-	2.000	
Breed NO herd	Y	Y	0.003	0.238	1.976	
Breed NO herd	Y	Ν	0.004	-	2.212	
NO breed & herd	Y	Y	0.003	0.416	1.978	
NO breed & herd	Y	Ν	0.0006	-	2.417	
SNPs only	Ν	Y	0.036	0.451	4.477	
SNPs only	Ν	Ν	0.029	-	4.954	

Table C12. Temperate CRC1: IMF – markers as stars

Table C13. Temperate CRC1: IMF – markers as stars  $(5^* \text{ and } 6^* = 4^*)$ 

				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.204	1.824
Full	Y	Y	0.36	0.205	1.817
Full	Ν	Y	0.33	0.237	1.884
Full	Y	Ν	0.27	-	2.007
Breed NO herd	Y	Y	0.37	0.237	1.984
Breed NO herd	Y	Ν	0.21	-	2.219
NO breed & herd	Y	Y	0.38	0.416	1.986
NO breed & herd	Y	Ν	0.035	-	2.425
SNPs only	Ν	Y	0.24	0.451	4.485
SNPs only	Ν	Ν	0.13	-	4.961

#### Table C14. Tropical CRC1: IMF – markers as stars

				Variances	
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.075	0.910
Full	Y	Y	0.58	0.076	0.910
Full	Ν	Y	0.59	0.075	0.916
Full	Y	Ν	0.73	-	0.979
Breed NO herd	Y	Y	0.69	0.0724	0.923
Breed NO herd	Y	Ν	0.84	-	0.993
NO breed & herd	Y	Y	0.82	0.143	0.924
NO breed & herd	Y	Ν	0.42	-	1.063
SNPs only	Ν	Y	0.96	0.146	1.864
SNPs only	Ν	Ν	0.74	-	2.005

				Variances	
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.075	0.910
Full	Y	Y	0.38	0.076	0.910
Full	Ν	Y	0.39	0.075	0.915
Full	Y	Ν	0.52	-	0.978
Breed NO herd	Y	Y	0.54	0.0722	0.922
Breed NO herd	Y	Ν	0.69	-	0.992
NO breed & herd	Y	Y	0.79	0.144	0.923
NO breed & herd	Y	Ν	0.34	-	1.062
SNPs only	Ν	Y	0.90	0.146	1.863
SNPs only	Ν	Ν	0.49	-	2.004

Table C15. Tropical CRC1: IMF – markers as stars  $(3^* \text{ and } 4^* = 3^*)$ 

Table C16. BOTH CRC1: IMF – markers as stars class

				Variances		
Model	cov	sire	Р	Sire	residual	
Full no marker	Y	Y	-	0.156	1.369	
Full	Y	Y	0.0016	0.156	1.365	
Full	Ν	Y	<.0001	0.167	1.389	
Full	Y	Ν	0.0025	-	1.498	
Breed NO herd	Y	Y	0.0012	0.175	1.466	
Breed NO herd	Y	Ν	0.0026	-	1.630	
NO breed & herd	Y	Y	0.0007	0.3135	1.467	
NO breed & herd	Y	Ν	0.0002	-	1.775	
SNPs only	Ν	Y	0.0087	1.022	3.194	
SNPs only	Ν	Ν	<.0001	-	4.245	

Table C17. BOTH CRC1: IMF – markers as stars as class  $(5^* \text{ and } 6^* = 4^*)$ 

				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.156	1.369
Full	Y	Y	0.22	0.166	1.392
Full	Ν	Y	0.20	0.167	1.389
Full	Y	Ν	0.20	-	1.501
Breed NO herd	Y	Y	0.50	0.175	1.470
Breed NO herd	Y	Ν	0.41	-	1.633
NO breed & herd	Y	Y	0.42	0.314	1.471
NO breed & herd	Y	Ν	0.06	-	1.779
SNPs only	Ν	Y	0.19	1.024	3.198
SNPs only	Ν	Ν	<.0001	-	4.250

#### Section 4: Significance of fitting 4 markers as total STARS (covariate= additive effect)

Table C18. Temperate CKC1. IVIT – markers as stars regression										
				Varia	ances					
Model	cov	sire	Р	Sire	residual					
Full no marker	Y	Y	-	0.204	1.824					
Full*	Y	Y	0.95	0.205	1.825					
Full	Ν	Y	0.98	0.237	1.885					
Full	Y	Ν	0.99	-	2.001					
Breed NO herd	Y	Y	0.65	0.237	1.985					
Breed NO herd	Y	Ν	0.55	-	2.221					
NO breed & herd	Y	Y	0.66	0.415	1.987					
NO breed & herd	Y	Ν	0.006	-	2.425					
SNPs only	Ν	Y	0.63	0.452	4.487					
SNPs only	Ν	Ν	0.21	-	4.965					
*1. 0.001 <i>C</i> (0.02000)										

Table C18. Temperate CRC1: IMF – markers as stars regression

\*b=-0.0216 (0.03289)

Table C19. Tropical CRC1: IMF – markers as stars covariate

				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.075	0.910
Full*	Y	Y	0.46	0.076	0.910
Full	Ν	Y	0.45	0.075	0.915
Full	Y	Ν	0.87	-	0.978
Breed NO herd	Y	Y	0.55	0.072	0.922
Breed NO herd	Y	Ν	0.94	-	0.992
NO breed & herd	Y	Y	0.74	0.143	0.923
NO breed & herd	Y	Ν	0.23	-	1.062
SNPs only	Ν	Y	0.50	0.146	1.862
SNPs only	Ν	Ν	0.57	-	2.004

b=0.01928 (0.02598)

#### Table C20. BOTH CRC1: IMF – star regression

				Variances			
Model	cov	sire	Р	Sire	residual		
Full no marker	Y	Y	-	0.156	1.369		
Full*	Y	Y	0.68	0.156	1.369		
Full	Ν	Y	0.64	0.166	1.393		
Full	Y	Ν	0.92	-	1.502		
Breed NO herd	Y	Y	0.94	0.175	1.470		
Breed NO herd	Y	Ν	0.54	-	1.634		
NO breed & herd	Y	Y	0.53	0.313	1.471		
NO breed & herd	Y	Ν	0.04	-	1.779		
SNPs only	Ν	Y	0.98	1.036	3.198		
SNPs only	Ν	Ν	0.25	-	4.273		
h 0.000702 (0.00100	))						

b=0.008783 (0.02129)

#### CRC2 – IMF%

ruore cari riopica	i compos	100 11011	i internetit	o do intea e	neeus					
				Significance of marker (P)				Variances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual		
Full no markers	Y	Y	-	-	-	-	0.188	0.762		
Full no markers	Y	Ν	-	-	-	-	-	0.908		
Full	Y	Y	0.74	0.27	0.79	0.31	0.189	0.761		
Full	Y	Ν	0.72	0.33	0.87	0.18	-	0.904		

#### Table C21. Tropical Composite IMF – 4 markers as fixed effects

Table C22. Tropical Composite IMF – 4 markers as covariate

				Significance of marker (P)				Variances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual		
Full no markers	Y	Y	-	-	-	-	0.188	0.762		
Full no markers	Y	Ν	-	-	-	-	-	0.908		
Full	Y	Y	0.53	0.13	0.57	0.79	0.189	0.761		
Full	Y	Ν	0.52	0.23	0.59	0.15	-	0.902		

Table C23. Tropical Composite IMF – 4 markers as total stars (class)

			Р	Var	Variances		
Model	cov	sire		Sire	Residual		
Full no markers	Y	Y	-	0.188	0.762		
Full no markers	Y	Ν	-	-	0.908		
Full	Y	Y	0.70	0.190	0.763		
Full	Y	Ν	0.74	-	0.911		

Table C24. Trop	ical Composite IMF	F – 4 markers as total	stars (covariate)
14010 02 1100	lear composite min		Stars (Co ( arrand)

			P Variances		
Model	cov	sire		Sire Residual	
Full no markers	Y	Y	-	0.188 0.762	
Full no markers	Y	Ν	-	- 0.908	
Full*	Y	Y	0.33	0.191 0.761	
Full	Y	Ν	0.86	- 0.910	

\* b=-0.03829 (0.03922)

				Significanc	Vari	ances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.030	0.513
Full no markers	Y	Ν	-	-	-	-		0.540
Full	Y	Y	0.48	0.16	0.13	0.21	0.035	0.510
Full	Y	Ν	0.40	0.11	0.18	0.27		0.540

Table C25. Brahman CRC2 IMF – 4 markers as fixed effects

Table C26. Brahman CRC2 IMF - 4 markers as covariate

				Significance of marker (P)				Variances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual		
Full no markers	Y	Y	-	-	-	-	0.030	0.513		
Full no markers	Y	Ν	-	-	-	-	-	0.540		
Full	Y	Y	0.46	0.06	0.14	0.22	0.035	0.510		
Full	Y	Ν	0.37	0.21	0.19	0.30	-	0.540		

Table C27. Brahman CRC2 IMF – 4 markers as total stars (class)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.030	0.513
Full no markers	Y	Ν	-	-	0.540
Full	Y	Y	0.68	0.031	0.512
Full	Y	Ν	0.75	-	0.540

Table C28. Brahman CRC2 IMF – 4 markers as total stars (covariate)

			Р	Varia	inces
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.030	0.513
Full no markers	Y	Ν	-	-	0.540
Full*	Y	Y	0.27	0.032	0.511
Full	Y	Ν	0.54	-	0.539
	、 、				

\* b=0.05617 (0.05110)

#### DURHAM PT – IMF%

				Significanc	e of marker	r (P)	Vari	ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.107	1.636
Full no markers	Y	Ν	-	-	-	-	-	1.734
Full	Y	Y	0.35	0.23	0.48	0.36	0.122	1.629
Full	Y	Ν	0.56	0.22	0.54	0.38	-	1.739

#### Table C29. DURHAM IMF - 4 markers as fixed effects

Table C30. DURHAM IMF – 4 markers as covariate

				Significanc	e of marke	r (P)	Vari	iances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.107	1.636
Full no markers	Y	Ν	-	-	-	-	-	1.734
Full	Y	Y	0.38	0.29	0.56	0.66	0.110	1.641
Full	Y	Ν	0.65	0.28	0.48	0.80	-	1.740

Table C31. DURHAM IMF -	4 markers as total stars (	class)
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			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.107 1.636
Full no markers	Y	Ν	-	- 1.734
Full	Y	Y	0.65	0.104 1.652
Full	Y	Ν	0.62	- 1.747

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			Р	Var	Variances		
Model	cov	sire		Sire	Residual		
Full no markers	Y	Y	-	0.107	1.636		
Full no markers	Y	Ν	-	-	1.734		
Full*	Y	Y	0.83	0.108	1.647		
Full	Y	Ν	0.85	-	1.745		

\* b=-0.0185(0.08708)

# **APPENDIX D**

### MSA Marble score results

#### SINGLE MARKER results for the 4 marbling markers by dataset and breed

Data	Breed					M1				M2				M3			Ν	Л4	
		Ν	star	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue	Ν	Est.	SE	Pvalue
CRC1	AA	562	0	243	1.32	0.04	0.855	253	1.35	0.04	0.251	364	1.31	0.03	0.679	274	1.31	0.04	0.896
			1	183	1.35	0.05		131	1.24	0.06		90	1.31	0.07		178	1.33	0.05	
			2	12	1.26	0.18		13	1.35	0.17		7	1.51	0.23		19	1.29	0.14	
	MG	146	0	48	1.07	0.09	0.677	56	1.14	0.09	0.961	126	1.11	0.06	0.318	101	1.07	0.06	0.069
			1	64	1.16	0.08		43	1.10	0.11		7	1.37	0.25		28	1.30	0.13	
			2	10	1.22	0.20		3	1.16	0.38		0				4	1.70	0.33	
	HH	556	0	328	0.86	0.03	0.437	364	0.86	0.03	0.339	386	0.85	0.03	0.976	310	0.85	0.03	0.791
			1	109	0.84	0.05		15	0.99	0.14		72	0.85	0.06		131	0.85	0.05	
			2	4	0.54	0.25		0				3	0.79	0.29		13	0.75	0.14	
	SH	190	0	110	1.41	0.06	0.008	129	1.42	0.05	0.811	135	1.42	0.05	0.009	82	1.44	0.07	0.637
			1	38	1.37	0.10		8	1.48	0.20		8	1.38	0.20		62	1.48	0.08	
			2	1	3.31	0.61		0				1	3.34	0.61		15	1.32	0.15	
	SG	548	0	459	0.69	0.03	0.402	138	0.74	0.05	0.345	522	0.68	0.02	0.203	484	0.66	0.03	0.005
			1	58	0.60	0.07		225	0.66	0.05		7	0.42	0.20		49	0.88	0.08	
			2	1	0.36	0.51		56	0.69	0.04		0				0			
	BR	816	0	668	0.90	0.02	0.819	246	0.89	0.04	0.747	666	0.90	0.02	0.561	580	0.89	0.03	0.753
			1	70	0.86	0.07		351	0.91	0.03		103	0.92	0.06		177	0.91	0.04	
			2	1	0.91	0.56		44	0.95	0.09		3	1.24	0.34		11	1.01	0.17	
	BH	444	0	426	0.53	0.02	0.726	17	0.40	0.11	0.157	433	0.53	0.02	0.320	397	0.53	0.02	0.477
			1	8	0.58	0.15		127	0.57	0.04		2	0.84	0.31		40	0.48	0.07	
			2	0				178	0.49	0.04		0				1	0.12	0.41	
CRC2	тс	1205	0	950	0.92	0.04	0.010	454	0.86	0.05	0.063	982	0.90	0.04	0.369	892	0.88	0.04	0.120
			1	159	0.85	0.06		453	0.94	0.04		140	0.96	0.06		215	0.96	0.05	
			2	5	1.24	0.23		90	0.88	0.06		6	1.00	0.21		11	1.02	0.16	
	BH	983	0	887	0.56	0.02	0.838	25	0.54	0.09	0.742	927	0.56	0.02	0.717	825	0.56	0.02	0.095
			1	28	0.58	0.08		238	0.55	0.03		5	0.48	0.20		86	0.54	0.05	
			2	0				263	0.57	0.02		0				1	-0.34	0.42	
Prog T	AA	415	0	172	2.04	0.10	0.917	185	1.97	0.09	0.513	290	2.08	0.09	0.910	241	2.06	0.10	0.252
			1	161	2.01	0.10		151	2.06	0.10		100	2.00	0.11		146	1.97	0.10	
			2	49	2.06	0.13		19	2.08	0.19		9	2.09	0.25		10	1.76	0.25	
Durham	SS	342	0	247	2.73	0.09	0.535	340	2.74	0.09	0.094	319	2.71	0.09	0.242	182	2.64	0.10	0.395
			1	76	2.65	0.11		2	1.43	0.76		18	2.41	0.20		119	2.78	0.10	
			2	5	2.28	0.39						3	2.40	0.47		32	2.72	0.16	

#### Table D1: Least squares means for MSA Marble score for each marker fitted separately across breeds

#### Pooled CRC1 – MSA marble score

#### **Base models**

#### Table D2. Temperate CRC1: MSA\_MARBLE SCORE base model variances

			ances	
Model	cov	sire	Sire	residual
Full no markers	Y	Y	0.020	0.259
Full no markers	Y	Ν	-	0.277
Breed +kill	Y	Ν	-	0.293
Kill	Y	Ν	-	0.335
No fixed effects	Ν	Ν	-	0.558

#### Table D3. Tropical CRC1: MSA\_MARBLE SCORE base model variances

			Variances			
Model	cov	sire	Sire	residual		
Full no markers	Y	Y	0.021	0.216		
Full no markers	Y	Ν	-	0.236		
Breed +kill	Y	Ν	-	0.236		
Kill	Y	Ν	-	0.253		
No fixed effects	Ν	Ν	-	0.387		
#### Section 1: Significant of fitting 4 markers as fixed effects

			Significance of marker (P)				Vari	ances
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.020	0.259
Full	Y	Y	0.99	0.55	0.26	0.59	0.021	0.260
Full	Ν	Y	0.90	0.52	0.23	0.40	0.024	0.268
Full	Y	Ν	0.38	0.99	0.57	0.76	-	0.279
Breed NO herd	Y	Y	0.88	0.80	0.39	0.80	0.030	0.265
Breed NO herd	Y	Ν	0.93	0.75	0.49	0.74	-	0.294
NO breed & herd	Y	Y	0.70	0.87	0.39	0.97	0.0662	0.266
NO breed & herd	Y	Ν	0.61	0.12	0.42	0.92	-	0.325
SNPs only	Ν	Y	0.33	0.88	0.34	0.75	0.050	0.495
SNPs only	Ν	Ν	0.24	0.37	0.34	0.84	-	0.542

Table D4. Temperate CRC1: MSA\_MARBLE SCORE – markers as fixed effects

Table D5. Tropical CRC1: MSA\_MARBLE SCORE - markers as fixed effects

				Significance	r (P)	Vari	ances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.216
Full	Y	Y	0.69	0.89	0.38	0.44	0.022	0.216
Full	Ν	Y	0.69	0.89	0.38	0.45	0.022	0.216
Full	Y	Ν	0.85	0.80	0.39	0.87	-	0.238
Breed NO herd	Y	Y	0.89	0.89	0.18	0.49	0.018	0.219
Breed NO herd	Y	Ν	0.49	0.64	0.25	0.33	-	0.237
NO breed & herd	Y	Y	0.92	0.13	0.05	0.22	0.027	0.220
NO breed & herd	Y	Ν	0.74	0.0003	0.02	0.04	-	0.246
SNPs only	Ν	Y	0.86	0.002	0.06	0.13	0.020	0.354
SNPs only	Ν	Ν	0.67	<.0001	0.03	0.04	-	0.374

Table D6. Both CRC1: MSA\_MARBLE SCORE - markers as fixed effects

			S	ignificance	: (P)	Vari	ances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.022	0.237
Full	Y	Y	0.86	0.90	0.12	0.32	0.023	0.237
Full	Ν	Y	0.81	0.94	0.10	0.28	0.023	0.239
Full	Y	Ν	0.44	0.99	0.20	0.21	-	0.259
Breed NO herd	Y	Y	0.98	0.80	0.13	0.89	0.025	0.241
Breed NO herd	Y	Ν	0.95	0.57	0.23	0.82	-	0.265
NO breed & herd	Y	Y	0.48	0.44	0.06	0.70	0.048	0.242
NO breed & herd	Y	Ν	0.59	0.01	0.03	0.19	-	0.286
SNPs only	Ν	Y	0.007	< 0.001	0.02	0.26	0.051	0.419
SNPs only	Ν	Ν	< 0.001	< 0.001	0.003	0.01	-	0.465

## Section 2: Significance of fitting 4 markers as covariate (additive only)

				Significanc	r (P)	Vari	ances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.020	0.259
Full	Y	Y	0.94	0.42	0.42	0.69	0.021	0.260
Full	Ν	Y	0.96	0.43	0.52	0.95	0.024	0.269
Full	Y	Ν	0.86	0.33	0.52	0.52	-	0.279
Breed NO herd	Y	Y	0.60	0.66	0.28	0.54	0.030	0.265
Breed NO herd	Y	Ν	0.68	0.67	0.35	0.48	-	0.293
NO breed & herd	Y	Y	0.39	0.57	0.39	0.88	0.066	0.266
NO breed & herd	Y	Ν	0.32	0.03	0.36	0.72	-	0.324
SNPs only	Ν	Y	0.24	0.71	0.41	0.66	0.049	0.494
SNPs only	Ν	Ν	0.21	0.16	0.31	0.80	-	0.541

Table D7. Temperate CRC1: MSA\_MARBLE SCORE - markers as additive effects

Table D8. Tropical CRC1: MSA\_MARBLE SCORE - markers as additive effects

				Significance	r (P)	Vari	ances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.216
Full	Y	Y	0.44	0.86	0.40	0.22	0.022	0.216
Full	Ν	Y	0.44	0.86	0.39	0.22	0.022	0.216
Full	Y	Ν	0.21	0.71	0.61	0.18	-	0.237
Breed NO herd	Y	Y	0.67	0.65	0.38	0.24	0.018	0.219
Breed NO herd	Y	Ν	0.23	0.34	0.47	0.14	-	0.237
NO breed & herd	Y	Y	0.88	0.06	0.07	0.09	0.027	0.220
NO breed & herd	Y	Ν	0.47	0.0001	0.01	0.010	-	0.246
SNPs only	Ν	Y	0.83	0.0009	0.03	0.06	0.020	0.354
SNPs only	Ν	Ν	0.45	<.0001	0.01	0.01	-	0.374

Table D9. Both CRC1: MSA\_MARBLE SCORE – markers as additive effects

			S	bignificance	: (P)	Vari	ances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.022	0.237
Full	Y	Y	0.62	0.73	0.34	0.32	0.023	0.237
Full	Ν	Y	0.63	0.78	0.30	0.43	0.023	0.239
Full	Y	Ν	0.51	0.44	0.55	0.20	-	0.259
Breed NO herd	Y	Y	0.83	0.53	0.21	0.97	0.024	0.241
Breed NO herd	Y	Ν	0.79	0.31	0.31	0.95	-	0.265
NO breed & herd	Y	Y	0.38	0.36	0.10	0.44	0.049	0.242
NO breed & herd	Y	Ν	0.23	0.04	0.02	0.08	-	0.286
SNPs only	Ν	Y	0.003	< 0.001	0.02	0.10	0.051	0.419
SNPs only	Ν	Ν	< 0.001	< 0.001	0.002	0.002	-	0.465

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				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.020	0.259
Full	Y	Y	0.27	0.019	0.259
Full	Ν	Y	0.26	0.023	0.267
Full	Y	Ν	0.27	-	0.277
Breed NO herd	Y	Y	0.12	0.030	0.264
Breed NO herd	Y	Ν	0.09	-	0.292
NO breed & herd	Y	Y	0.08	0.071	0.263
NO breed & herd	Y	Ν	0.01	-	0.333
SNPs only	Ν	Y	0.001	0.063	0.485
SNPs only	Ν	Ν	0.0001	-	0.550

Table D10. Temperate CRC1: MSA\_MARBLE SCORE – markers as stars

Table D11. Temperate CRC1: MSA\_MARBLE SCORE – markers as stars (4\* 5\* 6\* = 3\*)

			Vari	ances
cov	sire	Р	Sire	residual
Y	Y	-	0.020	0.259
Y	Y	0.08	0.020	0.259
Ν	Y	0.08	0.023	0.267
Y	Ν	0.10	-	0.277
Y	Y	0.02	0.030	0.264
Y	Ν	0.02	-	0.292
Y	Y	0.01	0.071	0.263
Y	Ν	0.002	-	0.332
Ν	Y	0.0001	0.063	0.485
Ν	Ν	<.0001	-	0.549
	cov Y Y N Y Y Y Y Y N N	cov sire   Y Y   Y Y   N Y   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N   N Y   N Y   N N   N N	cov sire P   Y Y -   Y Y 0.08   N Y 0.08   Y N 0.10   Y Y 0.02   Y N 0.02   Y Y 0.01   Y N 0.02   Y N 0.002   N Y 0.001   Y N 0.0001   N Y 0.0001	cov sire P Sire   Y Y - 0.020   Y Y 0.08 0.020   N Y 0.08 0.023   Y N 0.10 -   Y Y 0.02 0.030   Y N 0.02 -   Y Y 0.02 -   Y N 0.02 -   Y N 0.02 -   Y N 0.002 -   Y N 0.002 -   N Y 0.0001 0.063   N N <.0001

#### Table D12. Tropical CRC1: MSA\_MARBLE SCORE – markers as stars

				Variances	
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.021	0.216
Full	Y	Y	0.40	0.021	0.216
Full	Ν	Y	0.40	0.021	0.215
Full	Y	Ν	0.60	-	0.236
Breed NO herd	Y	Y	0.58	0.018	0.218
Breed NO herd	Y	Ν	0.65	-	0.236
NO breed & herd	Y	Y	0.58	0.034	0.219
NO breed & herd	Y	Ν	0.13	-	0.253
SNPs only	Ν	Y	0.80	0.033	0.352
SNPs only	Ν	Ν	0.08	-	0.386

				Variances	
Model	cov	sire	Р	Sire residual	
Full no marker	Y	Y	-	0.021 0.216	
Full	Y	Y	0.35	0.021 0.216	
Full	Ν	Y	0.35	0.021 0.215	
Full	Y	Ν	0.49	- 0.236	
Breed NO herd	Y	Y	0.50	0.018 0.218	
Breed NO herd	Y	Ν	0.50	- 0.236	
NO breed & herd	Y	Y	0.59	0.034 0.219	
NO breed & herd	Y	Ν	0.08	- 0.253	
SNPs only	Ν	Y	0.73	0.033 0.352	
SNPs only	Ν	Ν	0.03	- 0.386	

Table D13. Tropical CRC1: MSA\_MARBLE SCORE – markers as stars (4\*, 5\* =3\*)

Table D14. BOTH CRC1: MSA\_MARBLE SCORE – markers as stars class

				Vari	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.022	0.237
Full	Y	Y	0.86	0.022	0.237
Full	Ν	Y	0.84	0.022	0.239
Full	Y	Ν	0.82	-	0.258
Breed NO herd	Y	Y	0.10	0.024	0.240
Breed NO herd	Y	Ν	0.09	-	0.264
NO breed & herd	Y	Y	0.13	0.055	0.240
NO breed & herd	Y	Ν	0.10	-	0.294
SNPs only	Ν	Y	0.008	0.088	0.412
SNPs only	Ν	Ν	<.0001	-	0.500

Table D15. BOTH CRC1: MSA\_MARBLE SCORE – markers as stars class (>3\* =3\*)

				Varia	Variances		
Model	cov	sire	Р	Sire	residual		
Full no marker	Y	Y	-	0.022	0.237		
Full	Y	Y	0.04	0.022	0.236		
Full	Ν	Y	0.04	0.022	0.238		
Full	Y	Ν	0.06	-	0.258		
Breed NO herd	Y	Y	0.02	0.024	0.240		
Breed NO herd	Y	Ν	0.02	-	0.264		
NO breed & herd	Y	Y	0.03	0.055	0.240		
NO breed & herd	Y	Ν	0.04	-	0.294		
SNPs only	Ν	Y	0.001	0.088	0.412		
SNPs only	Ν	Ν	<.0001	-	0.500		

Section 4: Significance of fitting 4 markers as total STARS (covariate= additive effect)

				Vari	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.020	0.259
Full*	Y	Y	0.50	0.020	0.260
Full	Ν	Y	0.68	0.023	0.268
Full	Y	Ν	0.52	-	0.278
Breed NO herd	Y	Y	0.60	0.030	0.265
Breed NO herd	Y	Ν	0.75	-	0.293
NO breed & herd	Y	Y	0.26	0.071	0.264
NO breed & herd	Y	Ν	0.01	-	0.334
SNPs only	Ν	Y	0.20	0.063	0.491
SNPs only	Ν	Ν	0.01	-	0.556
b=0.0127 (0.0190)					

Table D16. Temperate CRC1: MSA\_MARBLE SCORE – markers as stars

Table D17. Temperate CRC1: MSA\_MARBLE SCORE – markers as stars (4\*,5\*,6\* =3\*)

				Variances	
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.020	0.259
Full*	Y	Y	0.53	0.020	0.260
Full	Ν	Y	0.70	0.023	0.268
Full	Y	Ν	0.55	-	0.278
Breed NO herd	Y	Y	0.63	0.030	0.265
Breed NO herd	Y	Ν	0.81	-	0.293
NO breed & herd	Y	Y	0.27	0.071	0.264
NO breed & herd	Y	Ν	0.01	-	0.334
SNPs only	Ν	Y	0.20	0.063	0.491
SNPs only	Ν	Ν	0.01	-	0.556
h=0.0130(0.021)					

b=0.0130 (0.021)

Tuble Die Hopfeur erter hibri hin indele beerte mundeb us sturb	Table D18 Tr	opical CRC1: MSA	MARBLE SCORE -	markers as stars
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				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.021	0.216
Full*	Y	Y	>0.99	0.021	0.216
Full	Ν	Y	>0.99	0.021	0.216
Full	Y	Ν	0.79	-	0.236
Breed NO herd	Y	Y	0.85	0.017	0.218
Breed NO herd	Y	Ν	0.55	-	0.236
NO breed & herd	Y	Y	0.68	0.033	0.219
NO breed & herd	Y	Ν	0.18	-	0.253
SNPs only	Ν	Y	0.56	0.034	0.352
SNPs only	Ν	Ν	0.08	-	0.387

b=-0.00003 (0.0185)

				Variances		
Model	cov	sire	Р	Sire	residual	
Full no marker	Y	Y	-	0.021	0.216	
Full	Y	Y	0.93	0.021	0.216	
Full	Ν	Y	0.93	0.021	0.216	
Full	Y	Ν	0.62	-	0.236	
Breed NO herd	Y	Y	0.79	0.017	0.218	
Breed NO herd	Y	Ν	0.49	-	0.236	
NO breed & herd	Y	Y	0.59	0.033	0.219	
NO breed & herd	Y	Ν	0.11	-	0.253	
SNPs only	Ν	Y	0.53	0.034	0.352	
SNPs only	Ν	Ν	0.06	-	0.387	
0.00101(0.0100)						

Table D19. Tropical CRC1: MSA\_MARBLE SCORE – markers as stars (>3\* =3\*)

-0.00181(0.0192)

Table D20. BOTH CRC1: MSA\_MARBLE SCORE – star regression

				Vari	Variances	
Model	cov	sire	Р	Sire	residual	
Full no marker	Y	Y	-	0.022	0.237	
Full*	Y	Y	0.73	0.022	0.237	
Full	Ν	Y	0.76	0.022	0.239	
Full	Y	Ν	0.92	-	0.258	
Breed NO herd	Y	Y	0.91	0.024	0.241	
Breed NO herd	Y	Ν	0.74	-	0.265	
NO breed & herd	Y	Y	0.56	0.055	0.241	
NO breed & herd	Y	Ν	0.26	-	0.294	
SNPs only	Ν	Y	0.66	0.090	0.413	
SNPs only	Ν	Ν	0.55	-	0.505	
1 0.00460 (0.0100)						

b= 0.00460 (0.0133)

Table D21. BOTH CRC1: MSA\_MARBLE SCORE – star regression (>3\*=3\*)

				Varia	ances
Model	cov	sire	Р	Sire	residual
Full no marker	Y	Y	-	0.022	0.237
Full*	Y	Y	0.80	0.022	0.237
Full	Ν	Y	0.83	0.022	0.239
Full	Y	Ν	>0.99	-	0.258
Breed NO herd	Y	Y	0.98	0.024	0.241
Breed NO herd	Y	Ν	0.65	-	0.265
NO breed & herd	Y	Y	0.64	0.055	0.241
NO breed & herd	Y	Ν	0.38	-	0.294
SNPs only	Ν	Y	0.71	0.090	0.413
SNPs only	Ν	Ν	0.81	-	0.505
1 0 00057 (0 01 11)					

b=0.00357 (0.0141)

## CRC2 – MSA marble score

				Significanc	Var	iances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.024	0.225
Full no markers	Y	Ν	-	-	-	-	-	0.244
Full	Y	Y	0.15	0.23	0.74	0.72	0.022	0.225
Full	Y	Ν	0.16	0.12	0.36	0.17	-	0.242

Table D22. Tropical Composite MSA Marble score – 4 markers as fixed effects

Table D23. Tropical Composite MSA Marble score – 4 markers as covariate

				Significanc	Vari	ances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.024	0.225
Full no markers	Y	Ν	-	-	-	-	-	0.244
Full	Y	Y	0.60	0.34	0.42	0.44	0.022	0.225
Full	Y	Ν	0.38	0.19	0.14	0.06	-	0.242

Table D24. Tropical Composite MSA Marble score – 4 markers as total stars (class)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.024 0.225
Full no markers	Y	Ν	-	- 0.244
Full	Y	Y	0.16	0.022 0.225
Full	Y	Ν	0.02	- 0.243

Table D25. Tropical Composite MSA Marble score – 4 markers as total stars (covariate)

			Р	Varia	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.024	0.225
Full no markers	Y	Ν	-	-	0.244
Full*	Y	Y	0.06	0.022	0.225
Full	Y	Ν	0.006	-	0.243

\* b=0.0366 (0.01926)

				Significanc	Var	Variances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.004	0.131
Full no markers	Y	Ν	-	-	-	-	-	0.134
Full	Y	Y	0.70	0.72	0.72	0.15	0.004	0.131
Full	Y	Ν	0.75	0.79	0.76	0.10	-	0.134

Table D25. Brahman CRC2 MSA Marble score – 4 markers as fixed effects

#### Table D26. Brahman CRC2 MSA Marble score – 4 markers as covariate

				Significanc	Vari	ances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.004	0.131
Full no markers	Y	Ν	-	-	-	-	-	0.134
Full	Y	Y	0.67	0.40	0.74	0.73	0.004	0.131
Full	Y	Ν	0.73	0.49	0.78	0.44	-	0.135

#### Table D27. Brahman CRC2 MSA Marble score – 4 markers as total stars (class)

			Р	Variances		
Model	cov	sire		Sire Residual		
Full no markers	Y	Y	-	0.004 0.131		
Full no markers	Y	Ν	-	- 0.134		
Full	Y	Y	0.58	0.005 0.130		
Full	Y	Ν	0.71	- 0.134		

Table D28. Brahmar	CRC2MSA	Marble score –	4 markers as	s total stars	(covariate)
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			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.004 0.131
Full no markers	Y	Ν	-	- 0.134
Full*	Y	Y	0.62	0.004 0.130
Full	Y	Ν	0.84	- 0.134

\* b=0.01425 (0.028556)

## ANGUS PROGENY TEST – MSA marble score

				Significanc	r (P)	Var	iances	
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.045	0.434
Full no markers	Y	Ν	-	-	-	-	-	0.475
Full	Y	Y	0.91	0.40	0.85	0.49	0.046	0.442
Full	Y	Ν	0.95	0.44	0.88	0.23	-	0.483

Table D29. ANGUS PT MSA Marble score – 4 markers as fixed effects

Table D30. ANGUS PT MSA Marble score – 4 markers as covariate

				Significanc	Vari	ances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.045	0.434
Full no markers	Y	Ν	-	-	-	-	-	0.475
Full	Y	Y	0.66	0.19	0.59	0.34	0.046	0.438
Full	Y	Ν	0.94	0.22	0.98	0.10	-	0.478

Table D31. ANGUS PT MSA Marble score – 4 markers as total stars (class)

			Р	Vari	Variances	
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0.045	0.434	
Full no markers	Y	Ν	-	-	0.475	
Full	Y	Y	0.84	0.047	0.437	
Full	Y	Ν	0.89	-	0.480	

Table D32. ANGUS PT MSA Marble score – 4 markers as total stars (covariate)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.045 0.434
Full no markers	Y	Ν	-	- 0.475
Full*	Y	Y	0.72	0.047 0.434
Full	Y	Ν	0.99	- 0.477

\* b=0.01176 (0.03277)

## DURHAM progeny test – Marble score

				Significanc	Vari	ances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.058	0.520
Full no markers	Y	Ν	-	-	-	-	-	0.573
Full	Y	Y	0.25	0.09	0.29	0.11	0.058	0.518
Full	Y	Ν	0.37	0.08	0.18	0.18	-	0.571

#### Table D33. DURHAM Marble Score – 4 markers as fixed effects

Table D34. DURHAM Marble Score – 4 markers as covariate

				Significanc	Vari	iances		
Model	cov	sire	M1	M2	M3	M4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.058	0.520
Full no markers	Y	Ν	-	-	-	-	-	0.573
Full	Y	Y	0.19	0.12	0.16	0.11	0.058	0.517
Full	Y	Ν	0.29	0.10	0.12	0.18	-	0.570

Table D35. DURHAM Marble Score – 4 markers as total stars (class)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.058	0.520
Full no markers	Y	Ν	-	-	0.573
Full	Y	Y	0.69	0.058	0.525
Full	Y	Ν	0.69	-	0.578

Table D36. DURHAM Marble Score – 4 markers as total stars (covariate)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.058 0.520
Full no markers	Y	Ν	-	- 0.573
Full*	Y	Y	0.90	0.058 0.523
Full	Y	Ν	0.76	- 0.576

\* b=-0.0060(0.04974)

# **APPENDIX E**

# NET FEED INTAKE results

# Single SNP effects for the 4 feed efficiency markers by dataset and breed

Data	Breed				N	1				N2			Ν	3			١	14	
		Ν	star	Ν	Est.	SE	Pvalue												
CRC1	AA	344	0	5	1.01	0.43	0.010	11	0.81	0.30	0.555	64	0.29	0.13	0.732	58	0.30	0.13	0.728
			1	60	0.08	0.13		110	0.13	0.10		148	0.23	0.09		154	0.17	0.09	
			2	253	0.21	0.08		182	0.20	0.09		93	0.07	0.11		99	0.14	0.11	
	MG	87	0	0				16	0.80	0.29		16	0.62	0.28		40	0.27	0.23	
			1	5	1.45	0.46		38	0.01	0.22		48	0.18	0.22		35	-0.03	0.23	
			2	77	0.12	0.20		27	0.09	0.25		16	-0.13	0.29		7	0.29	0.40	
	HH	241	0	10	-0.76	0.30		0				29	-0.44	0.18		68	-0.38	0.13	
			1	49	-0.33	0.15		10	-0.90	0.30		119	-0.47	0.10		120	-0.61	0.10	
			2	166	-0.57	0.09		215	-0.51	0.09		73	-0.69	0.13		36	-0.55	0.17	
	SH	113	0	1	-0.97	0.94		0				20	0.09	0.25		7	0.45	0.39	
			1	24	0.30	0.22		4	-0.01	0.48		40	0.18	0.18		23	0.22	0.22	
			2	83	0.08	0.15		95	0.13	0.09		40	0.05	0.19		70	0.07	0.16	
	NOINT	785	0	16	0.05	0.24	0.411	27	0.61	0.19	0.001	129	0.11	0.10	0.032	173	0.13	0.09	0.083
			1	138	0.09	0.10		162	-0.14	0.09		355	0.03	0.07		332	-0.07	0.07	
			2	579	-0.03	0.06		519	-0.00	0.07		222	-0.14	0.08		212	-0.05	0.08	
	SG	248	0	2	-0.75	0.59	0.234	0			0.392	16	0.28	0.23	0.303	12	0.40	0.25	0.269
			1	55	-0.19	0.14		18	-0.01	0.22		79	-0.10	0.13		79	-0.08	0.12	
			2	181	-0.04	0.10		218	-0.07	0.10		136	-0.07	0.11		145	-0.11	0.11	
	BR	304	0	23	0.50	0.20		0				60	0.30	0.15		23	0.20	0.20	
			1	98	0.07	0.12		40	0.04	0.18		119	0.20	0.12		152	0.17	0.11	
			2	173	0.22	0.11		242	0.21	0.10		103	0.16	0.12		115	0.22	0.12	
	BH	135	0	2	0.65	0.60		0				1	-1.90	0.86		9	-0.08	0.28	
			1	21	0.02	0.20		3	-0.32	0.51		9	-0.10	0.30		52	0.02	0.14	
			2	109	-0.17	0.10		130	-0.12	0.10		123	-0.12	0.10		72	-0.24	0.12	
	NOINT	687	0	27	0.26	0.17	0.079	0			0.412	77	0.13	0.12	0.445	44	0.15	0.13	0.448
			1	174	-0.10	0.08		61	-0.09	0.12		207	-0.01	0.08		283	0.01	0.07	
			2	463	0.02	0.06		590	0.01	0.06		362	-0.01	0.06		332	-0.02	0.06	
CRC2	TC	783	0	39	-0.05	0.18	0.062	0			0.236	48	-0.04	0.17	0.789	55	0.08	0.16	0.785
		-	1	246	0.17	0.10		28	0.27	0.22	-	267	-0.06	0.10	-	316	-0.01	0.10	-
			2	429	-0.03	0.10		711	0.02	0.09		424	0.01	0.10		368	0.04	0.10	
	BH	680	0	5	-0.22	0.46	0.966	0			0.599	2	0.72	0.65	0.227	15	-0.18	0.26	0.828

Table E1: Least squares means for Net Feed Intake	(kg/d) for each	marker fitted separate	v across datasets
	(		,

			1	105	-0.28	0.13		11	-0.12	0.29		54	-0.18	0.16		165	-0.24	0.12	
			2	521	-0.26	0.10		630	-0.27	0.10		584	-0.28	0.10		459	-0.28	0.10	
Angus PT	AA	387	0	20	-1.27	0.31	0.712	8	-1.37	0.44	0.790	36	-1.37	0.25	0.879	73	-1.67	0.21	0.133
			1	88	-1.50	0.21		96	-1.48	0.20		178	-1.44	0.19		187	-1.36	0.18	
			2	262	-1.41	0.18		266	-1.39	0.18		155	-1.38	0.19		108	-1.35	0.20	
Durham	SS	165	0	0			0.465	1	-0.57	0.79	0.151	52	-1.21	0.17	0.739	12	-1.30	0.26	0.540
			1	63	-1.19	0.17		15	-1.51	0.24		77	-1.13	0.15		65	-1.07	0.16	
			2	49	-1.04	0.17		145	-1.12	0.14		31	-1.07	0.19		83	-1.18	0.15	

## Pooled CRC1 – NFI

### Section 1: Significance of fitting 4 SNP as fixed effects

Tuble E2: Temperate	enteri		i indineito do	intea effecti	,			
				Significance	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.835
Full	Y	Y	0.52	0.0006	0.016	0.09	0.026	0.797
Full	Ν	Y	0.54	0.0006	0.017	0.10	0.025	0.797
Full	Y	Ν	0.48	0.0007	0.012	0.08	-	0.820
Breed NO herd	Y	Y	0.22	0.0003	0.01	0.17	0.023	0.796
Breed NO herd	Y	Ν	0.17	0.0003	0.008	0.16	-	0.819
Breed + Feedg	Y	Ν	-	-	-	-	-	0.839
NO breed & herd	Y	Y	0.44	<.0001	0.021	0.14	0.116	0.804
NO breed & herd	Y	Ν	0.38	<.0001	0.02	0.07	-	0.919
Feedg	Y	Ν	-	-	-	-	-	0.975
SNPs only	Ν	Y	0.42	<.0001	0.02	0.09	0.181	1.154
SNPs only	Ν	Ν	0.36	<.0001	0.0068	0.05	-	1.336

## Table E3. Tropical CRC1: NFI – 4 markers as fixed effects

				Significanc	e of marker	(P)	Var	iances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Breed+herd+Feedg	Y	Y	-	-	-	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.681
Full	Y	Y	0.11	0.41	0.48	0.39	0.029	0.654
Full	Ν	Y	0.10	0.37	0.49	0.40	0.027	0.655
Full	Y	Ν	0.10	0.38	0.41	0.42	-	0.680
Breed NO herd	Y	Y	0.16	0.28	0.70	0.26	0.036	0.662
Breed NO herd	Y	Ν	0.15	0.25	0.64	0.27	-	0.696
Breed + Feedg	Y	Ν	-	-	-	-	-	0.697
NO breed & herd	Y	Y	0.14	0.29	0.51	0.23	0.037	0.662
NO breed & herd	Y	Ν	0.14	0.27	0.44	0.23	-	0.696
Feedg	Y	Ν	-	-	-	-	-	0.701
SNPs only	Ν	Y	0.09	0.56	0.65	0.14	0.091	0.926
SNPs only	Ν	Ν	0.07	0.59	0.52	0.11	-	1.01

Table E4. Both CRC1: NFI – 4 markers as fixed class effect

				Significance	of marker	(P)	Var	iances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Breed+herd+Feedg	Y	Y	-	-	-	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.762
Full	Y	Y	0.51	0.0002	0.018	0.037	0.031	0.725
Full	Ν	Y	0.50	0.0002	0.020	0.038	0.030	0.727
Full	Y	Ν	0.48	0.0003	0.015	0.034	-	0.753
Breed NO herd	Y	Y	0.36	<.0001	0.026	0.054	0.035	0.728
Breed NO herd	Y	Ν	0.31	0.0001	0.021	0.048	-	0.762
Breed + Feedg	Y	Ν	-	-	-	-	-	0.772
NO breed & herd	Y	Y	0.66	<.0001	0.018	0.22	0.093	0.731
NO breed & herd	Y	Ν	0.57	<.0001	0.013	0.28	-	0.821
Feedg	Y	Ν	-	-	-	-	-	0.847
SNPs only	Ν	Y	0.52	<.0001	0.025	0.19	0.154	1.045
SNPs only	Ν	Ν	0.34	<.0001	0.016	0.37		1.120

### Section 2: Significance of fitting 4 markers as covariate (additive only)

				Significance	of marker	(P)	Var	iances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Breed+herd+Feedg	Y	Y	-	-	-	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.835
Full	Y	Y	0.36	0.45	0.011	0.086	0.019	0.818
Full	Ν	Y	0.37	0.44	0.01	0.08	0.018	0.818
Full	Y	Ν	0.31	0.40	0.01	0.07	-	0.835
Breed NO herd	Y	Y	0.12	0.34	0.007	0.18	0.017	0.818
Breed NO herd	Y	Ν	0.09	0.30	0.006	0.15	-	0.835
Breed + Feedg	Y	Ν	-	-	-	-	-	0.839
NO breed & herd	Y	Y	0.68	0.003	0.01	0.70	0.105	0.826
NO breed & herd	Y	Ν	0.47	<.0001	0.01	0.33	-	0.931
Feedg	Y	Ν	-	-	-	-	-	0.975
SNPs only	Ν	Y	0.49	0.0002	0.005	0.75	0.173	1.172
SNPs only	Ν	Ν	0.34	<.0001	0.003	0.35	-	1.346

	Table E5.	Temperate	CRC1: NFI -	- markers as	additive	effects
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Table E6. Tropical CRC1: NFI - markers as additive effects

				Significanc	e of marker	: (P)	Vari	iances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Breed+herd+Feedg	Y	Y	-	-	-	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.681
Full	Y	Y	0.92	0.42	0.35	0.18	0.031	0.655
Full	Ν	Y	0.88	0.37	0.36	0.20	0.029	0.657
Full	Y	Ν	0.76	0.39	0.32	0.21	-	0.683
Breed NO herd	Y	Y	0.87	0.28	0.60	0.12	0.038	0.663
Breed NO herd	Y	Ν	0.98	0.27	0.61	0.13	-	0.698
Breed + Feedg	Y	Ν	-	-	-	-	-	0.697
NO breed & herd	Y	Y	0.66	0.30	0.36	0.10	0.038	0.662
NO breed & herd	Y	Ν	0.74	0.29	0.33	0.09	-	0.698
Feedg	Y	Ν	-	-	-	-	-	0.701
SNPs only	Ν	Y	0.82	0.53	0.41	0.05	0.092	0.928
SNPs only	Ν	Ν	0.89	0.60	0.32	0.03	-	1.02

Table E7. Both CRC1: NFI – markers as additive effects

			_	Significance	of marker (	(P)	Var	iances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Breed+herd+Feedg	Y	Y	-	-	-	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.762
Full	Y	Y	0.54	0.78	0.014	0.039	0.029	0.736
Full	Ν	Y	0.57	0.80	0.015	0.042	0.028	0.737
Full	Y	Ν	0.54	0.68	0.011	0.034	-	0.762
Breed NO herd	Y	Y	0.20	0.75	0.021	0.056	0.033	0.740
Breed NO herd	Y	Ν	0.17	0.62	0.016	0.046	-	0.771
Breed + Feedg	Y	Ν	-	-	-	-	-	0.772
NO breed & herd	Y	Y	0.44	0.021	0.016	0.56	0.087	0.743
NO breed & herd	Y	Ν	0.35	0.0006	0.0113	0.96	-	0.828
Feedg	Y	Ν	-	-	-	-	-	0.847
SNPs only	Ν	Y	0.38	0.0018	0.018	0.53	0.148	1.055
SNPs only	Ν	Ν	0.23	<.0001	0.0136	0.98	-	1.203

Section 3: Significance of fitting 4 markers as total STARS (	(class effect)
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<b>^</b>				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	0.835
Full	Y	Y	0.0013	0.015	0.802
Full	Ν	Y	0.0013	0.015	0.801
Full	Y	Ν	0.0008	-	0.815
Breed NO herd	Y	Y	0.0006	0.015	0.801
Breed NO herd	Y	Ν	0.0003	-	0.816
Breed + Feedg	Y	Ν	-	-	0.839
NO breed & herd	Y	Y	0.0009	0.112	0.806
NO breed & herd	Y	Ν	<.0001	-	0.917
Feedg	Y	Ν	-	-	0.975
SNPs only	Ν	Y	0.0007	0.176	1.173
SNPs only	Ν	Ν	<.0001	-	1.349

Table E8	. Temperate	CRC1: NFI -	– markers as star	s (class)
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Table E9. Tropical CRC1: NFI – markers as stars (class)

Table E9. Hopical CKC1. NT1 – markets as stars (class)									
				Vari	ances				
Model	cov	sire	Р	Sire	residual				
Breed+herd+Feedg	Y	Y	-	0.034	0.651				
Breed+herd+Feedg	Y	Ν	-	-	0.681				
Full	Y	Y	0.68	0.036	0.652				
Full	Ν	Y	0.74	0.034	0.655				
Full	Y	Ν	0.70	-	0.684				
Breed NO herd	Y	Y	0.82	0.044	0.662				
Breed NO herd	Y	Ν	0.86	-	0.702				
Breed + Feedg	Y	Ν	-	-	0.697				
NO breed & herd	Y	Y	0.65	0.044	0.661				
NO breed & herd	Y	Ν	0.65	-	0.703				
Feedg	Y	Ν	-	-	0.701				
SNPs only	Ν	Y	0.80	0.096	0.932				
SNPs only	Ν	Ν	0.70	-	1.025				

## Table E10. Both CRC1: NFI – markers as stars (fixed class effects)

				Variances		
Model	cov	sire		Sire	residual	
Breed+herd+Feedg	Y	Y	-	0.034	0.731	
Breed+herd+Feedg	Y	Ν	-	-	0.762	
Full	Y	Y	0.0012	0.029	0.727	
Full	Ν	Y	0.0013	0.027	0.728	
Full	Y	Ν	0.0007	-	0.752	
Breed NO herd	Y	Y	0.0011	0.033	0.730	
Breed NO herd	Y	Ν	0.0005	-	0.762	
Breed + Feedg	Y	Ν	-	-	0.772	
NO breed & herd	Y	Y	0.0004	0.088	0.732	
NO breed & herd	Y	Ν	<.0001	-	0.818	
Feedg	Y	Ν	-	-	0.847	
SNPs only	Ν	Y	0.0002	0.145	1.053	
SNPs only	Ν	Ν	<.0001	-	1.198	

				Vari	iances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	0.835
Full	Y	Y	0.0008	0.015	0.808
Full	Ν	Y	0.0008	0.014	0.808
Full	Y	Ν	0.0005	-	0.823
Breed NO herd	Y	Y	0.0003	0.015	0.808
Breed NO herd	Y	Ν	0.0002	-	0.823
Breed + Feedg	Y	Ν	-	-	0.839
NO breed & herd	Y	Y	0.0035	0.119	0.812
NO breed & herd	Y	Ν	0.0004	-	0.932
Feedg	Y	Ν	-	-	0.975
SNPs only	Ν	Y	0.0003	0.186	1.176
SNPs only	Ν	Ν	<.0001	-	1.364

Table E12.	Tropical	CRC1: NFI	– markers as stars	(covariate)
14010 2121	11001000	011011111		(

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	0.681
Full	Y	Y	0.26	0.038	0.649
Full	Ν	Y	0.30	0.035	0.651
Full	Y	Ν	0.32	-	0.682
Breed NO herd	Y	Y	0.29	0.044	0.658
Breed NO herd	Y	Ν	0.35	-	0.699
Breed + Feedg	Y	Ν	-	-	0.697
NO breed & herd	Y	Y	0.12	0.044	0.659
NO breed & herd	Y	Ν	0.11	-	0.699
Feedg	Y	Ν	-	-	0.701
SNPs only	Ν	Y	0.10	0.096	0.925
SNPs only	Ν	Ν	0.07	-	1.018

## Table E13. Both CRC1: NFI – markers as stars (covariate)

				Variances		
Model	cov	sire	Р	Sire	residual	
Breed+herd+Feedg	Y	Y	-	0.034	0.731	
Breed+herd+Feedg	Y	Ν	-	-	0.762	
Full	Y	Y	0.0013	0.029	0.730	
Full	Ν	Y	0.0017	0.028	0.731	
Full	Y	Ν	0.0008	-	0.756	
Breed NO herd	Y	Y	0.0009	0.033	0.733	
Breed NO herd	Y	Ν	0.0004	-	0.765	
Breed + Feedg	Y	Ν	-	-	0.772	
NO breed & herd	Y	Y	0.001	0.091	0.735	
NO breed & herd	Y	Ν	0.0002	-	0.8243	
Feedg	Y	Ν	-	-	0.847	
SNPs only	Ν	Y	0.0001	0.151	1.054	
SNPs only	Ν	Ν	<.0001	-	1.206	

## Pooled CRC1 – NFI no WGS animal genotypes

Table E14. Temperate CRC1. No Web genotypes NTT – 4 markers as fixed effects								
				Significance of marker (P)				ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.835
Full	Y	Y	0.41	0.22	0.08	0.92	0.026	0.820
Full	Y	Ν	0.39	0.24	0.07	0.88	-	0.844

Table E14. Temperate CRC1: No WGS genotypes NFI – 4 markers as fixed effects

#### Table E15. Tropical CRC1: No WGS genotypes NFI – 4 markers as fixed effects

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.681
Full	Y	Y	0.13	0.25	0.14	0.91	0.027	0.658
Full	Y	Ν	0.11	0.24	0.12	0.90	-	0.682

#### Table E16. Both CRC1: No WGS genotypes NFI – 4 markers as fixed effects

				Significand	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.762
Full	Y	Y	0.75	0.15	0.16	0.86	0.032	0.740
Full	Y	Ν	0.95	0.16	0.15	0.85	-	0.769

#### Table E17. Temperate CRC1: No WGS genotypes NFI – 4 markers as covariates

<b>_</b>								
				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.835
Full	Y	Y	0.46	0.97	0.19	0.70	0.025	0.825
Full	Y	Ν	0.39	0.92	0.17	0.59	-	0.847

#### Table E18. Tropical CRC1: No WGS genotypes NFI – 4 markers as covariates

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.681
Full	Y	Y	0.65	0.34	0.20	0.82	0.031	0.659
Full	Y	Ν	0.51	0.34	0.21	0.80	-	0.682

#### Table E19. Both CRC1: No WGS genotypes NFI – 4 markers as covariates

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.762
Full	Y	Y	0.83	0.64	0.08	0.92	0.032	0.740
Full	Y	Ν	0.84	0.79	0.08	0.83	-	0.769

Table E20. Temperate CRC1: No WGS genotypes NFI – markers as stars (class)

				Variances
Model	cov	sire	Р	Sire residual
Breed+herd+Feedg	Y	Y	-	0.030 0.808
Breed+herd+Feedg	Y	Ν	-	- 0.835
Full	Y	Y	0.41	0.023 0.813
Full	Y	Ν	0.34	- 0.835

Table E21. Tropical CRC1: No WGS genotypes NFI – markers as stars (class)

				Variances
Model	cov	sire	Р	Sire residual
Breed+herd+Feedg	Y	Y	-	0.034 0.651
Breed+herd+Feedg	Y	Ν	-	- 0.681
Full	Y	Y	0.97	0.034 0.658
Full	Y	Ν	0.95	- 0.688

Table E22. Tropical CRC1: No WGS genotypes NFI – markers as stars (class)

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	0.762
Full	Y	Y	0.40	0.031	0.734
Full	Y	Ν	0.33	-	0.762

Table E23. Temperate CRC1: No WGS genotypes NFI - markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.030	0.808
Breed+herd+Feedg	Y	Ν	-	-	0.835
Full	Y	Y	0.17	0.023	0.813
Full	Y	Ν	0.11	-	0.834

Table E24. Tropical CRC1: No WGS genotypes NFI - markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.034	0.651
Breed+herd+Feedg	Y	Ν	-	-	0.681
Full	Y	Y	0.94	0.035	0.654
Full	Y	Ν	0.95	-	0.684

Table E25. Both CRC1: No WGS genotypes NFI - markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.034	0.731
Breed+herd+Feedg	Y	Ν	-	-	0.762
Full	Y	Y	0.31	0.032	0.734
Full	Y	Ν	0.24	-	0.763

## Pooled CRC1 – NFI no WGS phenotypes and no WGS genotypes

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.035	0.567
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.598
Full	Y	Y	0.36	0.15	0.04	0.93	0.037	0.565
Full	Y	Ν	0.39	0.19	0.03	0.84	-	0.598

### Table E14b. Temperate CRC1: No WGS animals NFI - 4 markers as fixed effects

#### Table E15b. Tropical CRC1: No WGS animals NFI – 4 markers as fixed effects

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.475
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.493
Full	Y	Y	0.03	0.14	0.07	0.92	0.008	0.478
Full	Y	Ν	0.03	0.13	0.06	0.90	-	0.485

#### Table E16b. Both CRC1: No WGS animals NFI - 4 markers as fixed effects

				Significan	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.029	0.521
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.547
Full	Y	Y	0.56	0.09	0.10	0.91	0.026	0.523
Full	Y	Ν	0.49	0.11	0.08	0.89	-	0.546

#### Table E17b. Temperate CRC1: No WGS animals NFI – 4 markers as covariates

<b>^</b>				Significand	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.035	0.567
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.598
Full	Y	Y	0.51	0.66	0.10	0.65	0.033	0.573
Full	Y	Ν	0.45	0.57	0.09	0.51	-	0.602

#### Table E18b. Tropical CRC1: No WGS animals NFI - 4 markers as covariates

				Significand	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.021	0.475
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.493
Full	Y	Y	0.47	0.23	0.19	0.88	0.012	0.480
Full	Y	Ν	0.40	0.20	0.16	0.81	-	0.491

#### Table E19b. Both CRC1: No WGS animals NFI - 4 markers as covariates

				Significand	Vari	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.029	0.521
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.547
Full	Y	Y	0.92	0.94	0.05	0.78	0.026	0.524
Full	Y	Ν	0.97	0.99	0.04	0.76	-	0.547

Table E20b. Temperate CRC1: No WGS animals NFI – markers as stars (class)

				Vari	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.035	0.567		
Breed+herd+Feedg	Y	Ν	-	-	0.598		
Full	Y	Y	0.24	0.033	0.563		
Full	Y	Ν	0.34	-	0.592		

#### Table E21b. Tropical CRC1: No WGS animals NFI – markers as stars (class)

				Variances
Model	cov	sire	Р	Sire residual
Breed+herd+Feedg	Y	Y	-	0.021 0.475
Breed+herd+Feedg	Y	Ν	-	- 0.493
Full	Y	Y	0.91	0.020 0.480
Full	Y	Ν	0.89	- 0.498

#### Table E22b. Both CRC1: No WGS animals NFI – markers as stars (class)

				Varı	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.029	0.521
Breed+herd+Feedg	Y	Ν	-	-	0.547
Full	Y	Y	0.23	0.028	0.520
Full	Y	Ν	0.21	-	0.545

#### Table E23b. Temperate CRC1: No WGS animals NFI - markers as stars covariate

				Vari	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.035	0.567		
Breed+herd+Feedg	Y	Ν	-	-	0.598		
Full*	Y	Y	0.07	0.029	0.566		
Full	Y	Ν	0.04	-	0.592		

\* b=-0.0519 (0.029)

Table E24b. Tropical CRC1: No WGS animals NFI - markers as stars covariate

				Varia	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.021	0.475		
Breed+herd+Feedg	Y	Ν	-	-	0.493		
Full*	Y	Y	0.99	0.020	0.477		
Full	Y	Ν	0.89	-	0.500		

b=-0.00018 (0.028)

#### Table E25b. Both CRC1: No WGS animals NFI - markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.029	0.521
Breed+herd+Feedg	Y	Ν	-	-	0.547
Full*	Y	Y	0.31	0.027	0.521
Full	Y	Ν	0.24	-	0.545
h = 0.00772 (0.0000)					

b=-0.02773 (0.0200)

## CRC2 – net feed intake

#### Table E26. TROPICAL COMPOSITE: NFI - 4 markers as fixed effects

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.093	0.991
Full no markers	Y	Ν	-	-	-	-	-	1.069
Full	Y	Y	0.03	0.26	0.96	0.67	0.099	0.984
Full	Y	Ν	0.07	0.28	0.87	0.67	-	1.068

#### Table E27. BRAHMAN: NFI – 4 markers as fixed effects

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.051	0.752
Full no markers	Y	Ν	-	-	-	-	-	0.802
Full	Y	Y	0.92	0.61	0.59	0.77	0.051	0.760
Full	Y	Ν	0.98	0.63	0.25	0.76	-	0.809

#### Table E28. TROPICAL COMPOSITE: NFI – 4 markers as covariates

				Significanc	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.093	0.991
Full no markers	Y	Ν	-	-	-	-	-	1.069
Full	Y	Y	0.07	0.20	0.98	0.87	0.100	0.986
Full	Y	Ν	0.15	0.23	0.96	0.97	-	1.069

#### Table E29. BRAHMAN: NFI – 4 markers as covariates

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.051	0.752
Full no markers	Y	Ν	-	-	-	-	-	0.809
Full	Y	Y	0.68	0.61	0.56	0.51	0.052	0.757
Full	Y	Ν	0.93	0.64	0.22	0.48	-	0.807

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.093	0.991
Full no markers	Y	Ν	-	-	1.069
Full	Y	Y	0.57	0.093	0.994
Full	Y	Ν	0.55	-	1.072

Table E30. TROPICAL COMPOSITE: NFI – 4 markers as total stars (class)

Table E31. BRAHMAN: NFI – 4 markers as 4 markers as total stars (class)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.051	0.752
Full no markers	Y	Ν	-	-	0.802
Full	Y	Y	0.37	0.053	0.752
Full	Y	Ν	0.54	-	0.804

Table E32. TROPICAL COMPOSITE: NFI – 4 markers as total stars (covariate)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.093	0.991
Full no markers	Y	Ν	-	-	1.069
Full*	Y	Y	0.92	0.094	0.992
Full	Y	Ν	0.34	-	1.071
+1 0.00 CA (0.000 A)					

\* b= -0.0364 (0.0384)

Table E33	BRAHMAN <sup>.</sup> NFI	– 4 markers	as total stars (	(covariate)
1 doite 1155.	DIVI 111111 11 1, 1 11 1	+ markers	as total stars	(covariate)

Table E55. BRATHVIAN. NPT – 4 markets as total stars (covariate)									
			Р		Variances				
Model	cov	sire			Sire	Residual			
Full no markers	Y	Y	-		0.051	0.752			
Full no markers	Y	Ν	-		-	0.802			
Full*	Y	Y	0.27		0.050	0.753			
Full	Y	Ν	0.26		-	0.803			
Full no markers Full no markers Full* Full	Y Y Y Y	Y N Y N	- 0.27 0.26		0.051	0.75 0.80 0.75 0.80			

\* b=-0.06094 (0.0552)

# Angus Progeny test - NFI

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.098	1.206
Full no markers	Y	Ν	-	-	-	-	-	1.293
Full	Y	Y	0.74	0.83	0.73	0.22	0.094	1.226
Full	Y	Ν	0.64	0.86	0.78	0.11	-	1.306

## Table E34. NFI – 4 markers as fixed effects

Table E35. NFI – 4 markers as covariates

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.098	1.206
Full no markers	Y	Ν	-	-	-	-	-	1.293
Full	Y	Y	0.81	0.56	0.59	0.20	0.099	1.217
Full	Y	Ν	0.81	0.57	0.93	0.09	-	1.301

Table E36. NFI – 4 markers as total stars (class)

			Р	Vari	iances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.098	1.206
Full no markers	Y	Ν	-	-	1.293
Full	Y	Y	0.07	0.108	1.186
Full	Y	Ν	0.07	-	1.279

Table E37. NFI – 4 markers as total stars (covariate)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.098	1.206
Full no markers	Y	Ν	-	-	1.293
Full*	Y	Y	0.17	0.103	1.203
Full	Y	Ν	0.17	-	1.294

\* b=0.0756 (0.05466)

# Durham progeny test - NFI

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.091	0.511
Full no markers	Y	Ν	-	-	-	-	-	0.596
Full	Y	Y	0.32	0.19	0.95	0.47	0.089	0.520
Full	Y	Ν	0.35	0.10	0.76	0.51	-	0.602

## Table E38. NFI – 4 markers as fixed effects

#### Table E39. NFI – 4 markers as covariates

				Significanc	r (P)	Var	iances	
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.091	0.511
Full no markers	Y	Ν	-	-	-	-	-	0.596
Full	Y	Y	0.36	0.25	0.75	0.91	0.099	0.517
Full	Y	Ν	0.49	0.22	0.50	0.84	-	0.608

#### Table E40. NFI – 4 markers as total stars (class)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.091	0.511
Full no markers	Y	Ν	-	-	0.596
Full	Y	Y	0.24	0.120	0.492
Full	Y	Ν	0.59	-	0.604

#### Table E41. NFI – 4 markers as total stars (covariate)

			Р	Varia	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.091	0.511
Full no markers	Y	Ν	-	-	0.596
Full*	Y	Y	0.14	0.097	0.506
Full	Y	Ν	0.20	-	0.596

\* b=0.1026 (0.06956)

# **APPENDIX F**

# DAILY FEED INTAKE results

## Single SNP effects for the 4 feed efficiency markers by dataset and breed

Data	Breed				1	N1				N2			1	٧3				N4	
		Ν	star	Ν	Est.	SE	Pvalue												
CRC1	AA	344	0	5	14.18	0.72	0.005	11	14.55	0.50	0.490	64	13.69	0.22	0.140	58	13.65	0.22	0.233
			1	60	13.62	0.22		110	13.60	0.17		148	13.55	0.15		154	13.60	0.15	
			2	253	13.53	0.13		182	13.57	0.15		93	13.52	0.19		99	13.45	0.18	
	MG	87	0	0				16	13.16	0.48		16	12.50	0.48		40	12.55	0.37	
			1	5	14.27	0.77		38	12.06	0.37		48	12.38	0.37		35	11.79	0.39	
			2	77	12.01	0.33		27	12.03	0.42		16	11.74	0.48		7	12.28	0.66	
	HH	241	0	10	12.18	0.50		0				29	13.13	0.30		68	12.83	0.22	
			1	49	12.53	0.25		10	12.36	0.50		119	12.56	0.17		120	12.38	0.17	
			2	166	12.54	0.15		215	12.51	0.14		73	12.05	0.22		36	12.31	0.28	
	SH	113	0	1	12.51	1.56		0				20	13.01	0.41		7	14.05	0.65	
			1	24	13.60	0.37		4	13.16	0.80		40	13.53	0.30		23	13.10	0.37	
			2	83	13.30	0.25		95	13.32	0.24		40	13.21	0.31		70	13.38	0.27	
	NOINT	785	0	16	12.89	0.42	0.511	27	13.85	0.33	0.010	129	13.11	0.17	0.049	173	13.17	0.15	0.406
			1	138	13.07	0.17		162	12.84	0.15		355	12.98	0.12		332	12.81	0.12	
			2	579	12.89	0.11		519	12.89	0.12		222	12.70	0.14		212	12.81	0.15	
	SG	248	0	2	13.65	1.09	0.657	0			0.639	16	13.40	0.43	0.338	12	13.52	0.46	0.210
			1	55	12.79	0.29		18	13.11	0.40		79	13.07	0.23		79	12.91	0.23	
			2	181	13.22	0.19		218	13.14	0.19		136	13.12	0.20		145	13.24	0.20	
	BR	304	0	23	12.40	0.37		0				60	12.10	0.27		23	11.41	0.36	
			1	98	11.83	0.23		40	11.82	0.32		119	12.04	0.22		152	11.87	0.21	
			2	173	11.93	0.21		242	11.91	0.19		103	11.63	0.23		115	12.09	0.22	
	BH	135	0	2	10.19	1.11		0				1	11.21	1.57		9	10.23	0.53	
			1	21	10.52	0.37		3	9.83	0.93		9	9.64	0.54		52	10.28	0.25	
			2	109	10.30	0.19		130	10.34	0.18		123	10.38	0.18		72	10.37	0.22	
	NOINT	687	0	27	12.24	0.32	0.155				0.673	77	12.08	0.21	0.242	44	11.61	0.25	0.171
			1	174	11.66	0.14		61	11.71	0.23		207	11.87	0.14		283	11.70	0.12	
			2	463	11.83	0.11		590	11.80	0.10		362	11.73	0.11		332	11.92	0.12	
CRC2	TC	787	0	39	12.64	0.32	0.134	0			0.352	48	12.99	0.30	0.442	59	12.87	0.28	0.457
			1	247	13.23	0.18		28	13.38	0.38		268	13.17	0.18		318	12.97	0.18	
			2	430	13.03	0.17		715	13.05	0.16		427	12.99	0.17		370	13.12	0.17	
	BH	700	0	6	10.59	0.81	0.258	0			0.050	2	10.94	1.22	0.740	15	10.27	0.51	0.666

Table F1: Least squares means for DFI (kg/d) for each marker fitted separately across datasets

			1	107	10.36	0.20		11	11.68	0.54		54	10.81	0.26		169	10.71	0.17	
			2	536	10.69	0.12		647	10.64	0.12		601	10.62	0.12		472	10.62	0.13	
Angus	AA	387	0	20	14.85	0.40	0.511	8	13.82	0.58	0.442	36	14.63	0.33	0.657	73	14.19	0.28	0.183
PT			1	88	14.46	0.27		96	14.49	0.26		178	14.40	0.24		187	14.58	0.24	
			2	262	14.41	0.23		266	14.50	0.23		155	14.51	.0.24		108	14.48	0.26	
Durham	SS	165	0	0			0.211	1	12.97	1.40	0.976	52	12.63	0.30	0.845	12	12.82	0.46	0.851
PT			1	63	12.43	0.30		15	12.66	0.43		77	12.77	0.26		65	12.77	0.28	
			2	49	12.86	0.30		145	12.69	0.24		31	12.64	0.33		83	12.65	0.26	

# Pooled CRC1 – Daily feed intake

### Section 1: Significant of fitting 4 SNP as fixed effects

			_	Significance	Vari	iances						
Model	cov	sire	N1	N2	N3	N4	Sire	residual				
Full no markers	Y	Y	-	-	-	-	0.227	2.132				
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.335				
Full	Y	Y	0.67	0.007	0.05	0.04	0.214	2.071				
Full	Y	Ν	0.61	0.007	0.03	0.03	-	2.262				

#### Table F2. Temperate CRC1: DFI – 4 markers as fixed effects (class)

Table F3. Temperate CRC1: DFI – 4 markers as fixed effects (covariates)

				Significand	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.227	2.132
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.335
Full	Y	Y	0.71	0.18	0.03	0.03	0.208	2.097
Full	Y	Ν	0.61	0.12	0.02	0.02	-	2.283

Table F4. Temperate CRC1: DFI – markers as stars class

				Vari	iances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.227	2.132
Breed+herd+Feedg	Y	Ν	-	-	2.335
Full	Y	Y	0.010	0.198	2.119
Full	Y	Ν	0.003	-	2.295

Table F5. Temperate CRC1: DFI – markers as stars covariate												
				Vari	Variances							
Model	cov	sire	Р	Sire	residual							
Breed+herd+Feedg	Y	Y	-	0.227	2.132							
Breed+herd+Feedg	Y	Ν	-	-	2.335							
Full*	Y	Y	0.0007	0.198	2.120							
Full	Y	Ν	0.0002	-	2.297							

\* b=-0.1760 (0.05139)

				Significanc	Vari	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.050	2.265
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.310
Full	Y	Y	0.14	0.53	0.20	0.14	0.030	2.266
Full	Y	Ν	0.14	0.52	0.18	0.15	-	2.292

Table F6. Tropical CRC1: DFI – 4 markers as fixed effects (class)

Table F7. Tropical CRC1: DFI – 4 markers as fixed effects (covariates)

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.050	2.265
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.310
Full	Y	Y	0.83	0.53	0.09	0.06	0.035	2.267
Full	Y	Ν	0.85	0.52	0.08	0.06	-	2.300

Table F8. Tropical CRC1: DFI – markers as stars class

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.050	2.265
Breed+herd+Feedg	Y	Ν	-	-	2.310
Full	Y	Y	0.51	0.043	2.277
Full	Y	Ν	0.48	-	2.316

Table F9. Tropical CRC1: DFI – markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.050	2.265
Breed+herd+Feedg	Y	Ν	-	-	2.310
Full*	Y	Y	0.64	0.056	2.267
Full	Y	Ν	0.71	-	2.317

\* b=+0.02629 (0.05652)

				Significance	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.150	2.189
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.322
Full	Y	Y	0.65	0.006	0.02	0.09	0.139	2.160
Full	Y	Ν	0.61	0.005	0.01	0.09	-	2.283

Table F10. Both CRC1: DFI – 4 markers as fixed effects (class)

Table F11. Both CRC1: DFI – 4 markers as fixed effects (covariates)

				Significanc	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.150	2.189
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	2.322
Full	Y	Y	0.87	0.33	0.01	0.70	0.140	2.178
Full	Y	Ν	0.76	0.28	0.006	0.66	-	2.302

Table F12. Both CRC1: DFI – markers as stars (class)

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.150	2.189
Breed+herd+Feedg	Y	Ν	-	-	2.322
Full	Y	Y	0.007	0.131	2.185
Full	Y	Ν	0.003	-	2.302

Table F13. Both CRC1: DFI – markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.150	2.189
Breed+herd+Feedg	Y	Ν	-	-	2.322
Full*	Y	Y	0.03	0.139	2.193
Full	Y	Ν	0.01	-	2.317

\*b=-0.08495 (0.03816)

## CRC2 – Daily feed intake

#### Table F14. TROPICAL COMPOSITE: DFI – 4 markers as fixed effects (class)

				Significanc	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.333	2.963
Full no markers	Y	Ν	-	-	-	-	-	3.254
Full	Y	Y	0.08	0.58	0.36	0.64	0.339	2.960
Full	Y	Ν	0.15	0.37	0.49	0.44	-	3.253

Table F15. BRAHMAN: DFI – 4 markers as fixed effects (class)

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.344	2.522
Full no markers	Y	Ν	-	-	-	-	-	2.830
Full	Y	Y	0.46	0.17	0.92	0.41	0.324	2.544
Full	Y	Ν	0.25	0.06	0.69	0.60	-	2.832

Table F16. TROPICAL COMPOSITE: DFI - 4 markers as covariates

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.333	2.963
Full no markers	Y	Ν	-	-	-	-	-	3.254
Full	Y	Y	0.48	0.49	0.35	0.39	0.332	2.975
Full	Y	Ν	0.91	0.32	0.41	0.21	-	3.260

Table F17. BRAHMAN: DFI – 4 markers as covariates

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.344	2.522
Full no markers	Y	Ν	-	-	-	-	-	2.830
Full	Y	Y	0.30	0.17	0.73	0.60	0.321	2.540
Full	Y	Ν	0.14	0.06	0.47	0.92	-	2.825

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.333	2.963
Full no markers	Y	Ν	-	-	3.254
Full	Y	Y	0.48	0.331	2.970
Full	Y	Ν	0.43	-	3.259

Table F18. TROPICAL COMPOSITE: DFI – 4 markers as total stars (class)

Table F19. BRAHMAN: DFI – 4 markers as 4 markers as total stars (class)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.344 2.522
Full no markers	Y	Ν	-	- 2.830
Full	Y	Y	0.98	0.348 2.534
Full	Y	Ν	0.98	- 2.846

Table F20. TROPICAL COMPOSITE: DFI – 4 markers as total stars (covariate)

	Р			Variances		
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0.333	2.963	
Full no markers	Y	Ν	-	-	3.254	
Full*	Y	Y	0.92	0.335	2.971	
Full	Y	Ν	0.86	-	3.263	
	~					

\* b= -0.01215 (0.0667)

Table F21.BRAHMAN:	DFI – 4 ma	rkers as total	stars (	(covariate)
	DII + IIIa	inclib ub totul	stars (	(covariate)

Table 121. DRAINTAIN. DI 1 – 4 markers as total stars (covariate)								
			Р	Var	Variances			
Model	cov	sire		Sire	Residual			
Full no markers	Y	Y	-	0.344	2.522			
Full no markers	Y	Ν	-	-	2.830			
Full*	Y	Y	0.67	0.348	2.526			
Full	Y	Ν	0.94	-	2.837			

\* b=-0.04338 (0.1081)

# ANGUS progeny test- Daily feed intake

Tuble 122. This us 11 D11 + markets as fixed effects (class)								
				Significanc	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	Residual
Full no markers	Y	Y	-	-	-	-	0.360	1.852
Full no markers	Y	Ν	-	-	-	-	-	2.179
Full	Y	Y	0.68	0.39	0.47	0.40	0.339	1.853
Full	Y	Ν	0.43	0.42	0.48	0.17	-	2.149

Table F22. Angus PT DFI – 4 markers as fixed effects (class)

Table F23. Angus PT DFI – 4 markers as covariates

				Significand	Vai	riances		
Model	cov	sire	N1	N2	N3	N4	Sire	Residual
Full no markers	Y	Y	-	-	-	-	0.360	1.852
Full no markers	Y	Ν	-	-	-	-	-	2.179
Full	Y	Y	0.58	0.30	0.71	0.55	0.347	1.851
Full	Y	Ν	0.35	0.46	0.86	0.27		2.155

Table F24. Angus PT DFI – 4 markers as total stars (class)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.360	1.852
Full no markers	Y	Ν	-	-	2.179
Full	Y	Y	0.77	0.345	1.876
Full	Y	Ν	0.42	-	2.181

Table F25. Angus PT DFI – 4 markers as total stars (covariate)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.360	1.852
Full no markers	Y	Ν	-	-	2.179
Full*	Y	Y	0.43	0.367	1.857
Full	Y	Ν	0.64	-	2.185

\* b=0.056(0.07128)

# DURHAM progeny test – Daily feed intake

Tuble 1 20. D'el d'h diff i DTT - Thaixers as fixed effects (class)								
				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	Residual
Full no markers	Y	Y	-	-	-	-	0.186	1.643
Full no markers	Y	Ν	-	-	-	-	-	1.824
Full	Y	Y	0.15	0.73	0.80	0.79	0.265	1.648
Full	Y	Ν	0.15	0.83	0.80	0.79	-	1.889

Table F26. DURHAM PT DFI – 4 markers as fixed effects (class)

Table F27. DURHAM PT DFI – 4 markers as covariates

				Significanc	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	Residual
Full no markers	Y	Y	-	-	-	-	0.186	1.643
Full no markers	Y	Ν	-	-	-	-	-	1.824
Full	Y	Y	0.19	0.84	0.94	0.59	0.258	1.625
Full	Y	Ν	0.20	0.99	0.91	0.58	-	1.860

Table F29. DURHAM PT DFI – 4 markers as total stars (class)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.186	1.643
Full no markers	Y	Ν	-	-	1.824
Full	Y	Y	0.97	0.222	1.688
Full	Y	Ν	0.99	-	1.890

Table F29. DURHAM PT DFI – 4 markers as total stars (covariate)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.186	1.643
Full no markers	Y	Ν	-	-	1.824
Full*	Y	Y	0.65	0.193	1.666
Full	Y	Ν	0.69	-	1.843

\* b=0.055(0.123)

# **APPENDIX G**

# FEED CONVERSION RATIO
# Single SNP effects for the 4 feed efficiency markers by dataset and breed

Data	Breed				1	v1				N2			1	٧3				N4	
		Ν	star	Ν	Est.	SE	Pvalue												
CRC1	AA	342	0	5	9.93	0.58	0.719	11	10.11	0.40	0.676	64	9.92	0.18	0.694	58	9.95	0.17	0.146
			1	60	9.67	0.18		110	9.70	0.13		148	9.93	0.12		154	9.72	0.12	
			2	253	9.86	0.10		182	9.80	0.12		93	9.60	0.15		99	9.86	0.14	
	MG	84	0	0				16	10.08	0.40		16	10.30	0.39		40	9.91	0.30	
			1	5	10.08	0.62		38	10.00	0.30		48	9.98	0.30		35	9.97	0.32	
			2	77	10.02	0.27		27	9.94	0.34		16	10.06	0.38		7	10.81	0.56	
	HH	236	0	10	9.03	0.41		0				29	8.88	0.24		68	9.10	0.18	
			1	49	9.37	0.20		10	8.58	0.40		119	9.18	0.14		120	8.96	0.14	
			2	166	9.02	0.12		215	9.12	0.12		73	9.10	0.18		36	9.44	0.22	
	SH	111	0	1	8.02	1.26		0				20	9.55	0.34		7	10.45	0.52	
			1	24	9.49	0.30		4	9.30	0.64		40	9.23	0.24		23	9.74	0.30	
			2	83	9.43	0.20		95	9.46	0.19		40	9.54	0.25		70	9.22	0.22	
	NOINT	773	0	16	9.49	0.33	0.896	26	9.73	0.26	0.367	127	9.65	0.13	0.569	172	9.66	0.12	0.307
			1	137	9.62	0.13		161	9.46	0.12		349	9.64	0.10		324	9.51	0.10	
			2	568	9.58	0.08		510	9.61	0.09		218	9.53	0.11		209	9.66	0.12	
	SG	246	0	2	7.47	0.93	0.036	0			0.577	16	9.25	0.67	0.208	12	9.06	0.40	0.578
			1	55	8.92	0.22		18	8.79	0.34		79	8.70	0.20		79	8.72	0.19	
			2	181	8.70	0.16		218	9.21	0.16		136	9.05	0.18		145	8.72	0.18	
	BR	303	0	23	9.50	0.31		0				60	9.38	0.23		23	9.71	0.31	
			1	98	9.30	0.19		40	8.94	0.28		119	9.46	0.19		152	9.32	0.18	
			2	173	9.28	0.18		242	9.62	0.17		103	9.57	0.20		115	9.28	0.19	
	BH	129	0	2	12.98	0.95		0				1	8.00	1.35		9	10.81	0.45	
			1	21	9.95	0.33		3	10.83	0.80		9	10.12	0.50		52	10.45	0.22	
			2	109	10.14	0.16		130	10.17	0.15		123	10.67	0.16		72	9.83	0.20	
	NOINT	678	0	27	9.68	0.27	0.499				0.339	77	9.51	0.18	0.782	44	9.83	0.21	0.047
			1	172	9.44	0.13		61	9.24	0.19		206	9.39	0.12		280	9.45	0.11	
			2	457	9.37	0.09		582	9.42	0.09		355	9.42	0.10		327	9.32	0.10	
CRC2	ТС	772	0	38	9.42	0.30	0.438	0			0.731	45	9.13	0.29	0.386	54	9.49	0.26	0.624
			1	241	9.49	0.17		28	9.25	0.36		264	9.29	0.17		311	9.42	0.17	
			2	424	9.31	0.16		700	9.38	0.15		419	9.43	0.15		363	9.31	0.16	

Table G1: Least squares means for FCR (DFI/ADG) for each marker fitted separately

	BH	630	0	6	11.85	0.97	0.335	0			0.817	2	12.56	1.39	0.269	13	10.13	0.60	0.544
			1	93	10.64	0.25		11	10.69	0.62		52	10.36	0.30		155	10.68	0.20	
			2	488	10.50	0.15		588	10.55	0.14		544	10.58	0.15		430	10.51	0.15	
Angus	AA	382	0	20	10.45	0.47	0.961	8	10.36	0.68	0.833	35	10.18	0.38	0.552	73	10.44	0.33	0.947
PT			1	87	10.41	032		95	10.55	0.31		176	10.45	0.28		183	10.43	0.28	
			2	258	10.48	0.27		262	10.42	0.27		153	10.55	0.28		107	10.50	0.31	
Durham	SS	165	0				0.301	1	8.23	1.21	0.922	52	8.21	0.26	0.452	12	7.88	0.39	0.533
PT			1	63	8.45	0.26		15	8.11	0.37		77	8.34	0.22		65	8.24	0.24	
			2	49	8.14	0.26		145	8.25	0.21		31	8.02	0.28		83	8.29	0.22	

## Pooled CRC1 – Feed Conversion ratio

				Significance of marker (P)				Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual		
Full no markers	Y	Y	-	-	-	-	0.009	1.463		
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.471		
Full	Y	Y	0.90	0.54	0.43	0.36	0.014	1.460		
Full	Y	Ν	0.91	0.55	0.43	0.37	-	1.472		

#### Table G2. Temperate CRC1: FCR – 4 markers as fixed effects (class)

Table G3. Temperate CRC1: FCR – 4 markers as fixed effects (covariates)

				Significand	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.009	1.463
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.471
Full	Y	Y	0.76	0.84	0.32	0.78	0.010	1.464
Full	Y	Ν	0.76	0.83	0.32	0.78	-	1.472

Table G4. Temperate CRC1: FCR – markers as stars (class)

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.009	1.463
Breed+herd+Feedg	Y	Ν	-	-	1.471
Full	Y	Y	0.72	0.006	1.473
Full	Y	Ν	0.72	-	1.479

Table G5. Temperate CRC1: FCR – markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.009	1.463
Breed+herd+Feedg	Y	Ν	-	-	1.471
Full*	Y	Y	0.71	0.008	1.469
Full	Y	Ν	0.71	-	1.476

\*b=-0.01513 (0.04049)

					. (			
				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.065	1.619
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.678
Full	Y	Y	0.53	0.39	0.81	0.04	0.049	1.614
Full	Y	Ν	0.61	0.32	0.82	0.05	-	1.658

Table G6. Tropical CRC1: FCR – 4 markers as fixed effects (class)

## Table G7. Tropical CRC1: FCR – 4 markers as fixed effects (covariates)

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.065	1.619
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.678
Full	Y	Y	0.29	0.38	0.95	0.02	0.048	1.613
Full	Y	Ν	0.37	0.31	0.88	0.03	-	1.655

Table G8. Tropical CRC1: FCR – markers as stars (class)

				Variances	
Model	cov	sire	Р	Sire residual	
Breed+herd+Feedg	Y	Y	-	0.065 1.619	
Breed+herd+Feedg	Y	Ν	-	- 1.678	
Full	Y	Y	0.20	0.047 1.625	
Full	Y	Ν	0.18	- 1.667	

Table G9.	Tropical	CRC1: FCR	. – markers as	s stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.065	1.619
Breed+herd+Feedg	Y	Ν	-	-	1.678
Full*	Y	Y	0.12	0.060	1.618
Full	Y	Ν	0.13	-	1.672

\*b=-0.07486 (0.04825)

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.035	1.536
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.568
Full	Y	Y	0.59	0.38	0.66	0.21	0.026	1.537
Full	Y	Ν	0.63	0.37	0.63	0.23	-	1.561

Table G10. Both CRC1: FCR – 4 markers as fixed effects (class)

Table G11. Both CRC1: FCR – 4 markers as fixed effects (covariates)

			Significance of marker (P)					ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.035	1.536
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	1.568
Full	Y	Y	0.29	0.44	0.43	0.20	0.025	1.537
Full	Y	Ν	0.31	0.41	0.40	0.21	-	1.559

Table G12. Both CRC1: FCR – markers as stars (class)

			Vari	ances
cov	sire	Р	Sire	residual
Y	Y	-	0.035	1.536
Y	Ν	-	-	1.568
Y	Y	0.07	0.027	1.537
Y	Ν	0.06	-	1.562
	cov Y Y Y Y Y	covsireYYYNYYYNYN	cov sire P   Y Y -   Y N -   Y Y 0.07   Y N 0.06	cov sire P Sire   Y Y - 0.035   Y N - -   Y Y 0.007 0.027   Y N 0.06 -

Table G13. Both CRC1: FCR – markers as stars covariate

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.035	1.536
Breed+herd+Feedg	Y	Ν	-	-	1.568
Full*	Y	Y	0.18	0.032	1.539
Full	Y	Ν	0.20	-	1.568

\*b=-0.04206 (0.03122)

## CRC2 FCR

#### Table G14. TROPICAL COMPOSITE: FCR – 4 markers as fixed effects (class)

				Significance of marker (P)				ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.046	2.729
Full no markers	Y	Ν	-	-	-	-	-	2.771
Full	Y	Y	0.42	0.83	0.35	0.53	0.057	2.732
Full	Y	Ν	0.51	0.71	0.37	0.54	-	2.783

### Table G15.BRAHMAN: FCR – 4 markers as fixed effects (class)

				Significance of marker (P)				Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual		
Full no markers	Y	Y	-	-	-	-	0.096	3.575		
Full no markers	Y	Ν	-	-	-	-	-	3.663		
Full	Y	Y	0.36	0.76	0.36	0.53	0.086	3.595		
Full	Y	Ν	0.30	0.80	0.33	0.51	-	3.673		

#### Table G16. TROPICAL COMPOSITE: FCR – 4 markers as covariates

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.046	2.729
Full no markers	Y	Ν	-	-	-	-	-	2.771
Full	Y	Y	0.25	0.83	0.15	0.26	0.053	2.725
Full	Y	Ν	0.30	0.72	0.15	0.26	-	2.773

## Table G17. BRAHMAN: FCR-4 markers as covariates

				Significanc	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.096	3.575
Full no markers	Y	Ν	-	-	-	-	-	3.663
Full	Y	Y	0.25	0.77	0.90	0.70	0.094	3.596
Full	Y	Ν	0.21	0.81	0.96	0.68	-	3.681

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.046 2.729
Full no markers	Y	Ν	-	- 2.771
Full	Y	Y	0.95	0.050 2.744
Full	Y	Ν	0.96	- 2.790

Table G18. TROPICAL COMPOSITE: FCR – 4 markers as total stars (class)

Table G19. BRAHMAN: FCR – 4 markers as 4 markers as total stars (class)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.096 3.575
Full no markers	Y	Ν	-	- 3.663
Full	Y	Y	0.32	0.108 3.563
Full	Y	Ν	0.33	- 3.662

Table G20. TROPICAL COMPOSITE: FCR - 4 markers as total stars (covariate)

	Р		Variances		
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.046	2.729
Full no markers	Y	Ν	-	-	2.771
Full*	Y	Y	0.32	0.048	2.734
Full	Y	Ν	0.78	-	2.778
*1 0.00051 (0.06)	107)				

\* b= -0.02251 (0.06197)

Table G21	<b>ΒΡΑΗΜΑΝ</b> · <b>ΕCΡ</b>	_ 4 markers	as total st	ars (covariate)
	DRAIMAN, FUR	= 4 markers	as iotai si	us (covariate)

Table 021. DRAHMAN. FCR-4 markers as total stars (covariate)						
		Р	Variances			
cov	sire		Sire Residual			
Y	Y	-	0.096 3.575			
Y	Ν	-	- 3.663			
Y	Y	0.32	0.095 3.577			
Y	Ν	0.27	- 3.664			
	cov Y Y Y Y Y	covsireYYYNYYYYYNYN	P   cov sire   Y Y   Y N   Y Y   Y Y   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N   Y N			

\* b= -0.1286 (0.1291)

# Angus progeny test – FCR

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.116	2.894
Full no markers	Y	Ν	-	-	-	-	-	2.999
Full	Y	Y	0.93	0.92	0.61	0.97	0.108	2.989
Full	Y	Ν	0.93	0.81	0.54	0.98	-	3.084

Table G22. Angus PT FCR – 4 markers as fixed effects (class)

Table G23. Angus PT FCR – 4 markers as covariates

				Significand	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.116	2.894
Full no markers	Y	Ν	-	-	-	-	-	2.999
Full	Y	Y	0.75	0.71	0.36	0.84	0.109	2.955
Full	Y	Ν	0.77	0.61	0.30	0.88	-	3.052

Table G24. Angus PT FCR – 4 markers as total stars (class)

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.116	2.894
Full no markers	Y	Ν	-	-	2.999
Full	Y	Y	0.22	0.130	2.874
Full	Y	Ν	0.26	-	2.991

Table G25. Angus PT FCR – 4 markers as total stars (covariate)

			Р	Variances
Model	cov	sire		Sire Residual
Full no markers	Y	Y	-	0.116 2.894
Full no markers	Y	Ν	-	- 2.999
Full*	Y	Y	0.56	0.116 2.906
Full	Y	Ν	0.57	- 3.001

\* b=0.04840(0.08226)

# DURHAM progeny test - FCR

14010 0201 2 011		11010	1 markers	us intea ei	ieeus (eiuss	)		
				Significanc	Var	iances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0	1.363
Full no markers	Y	Ν	-	-	-	-	-	1.363
Full	Y	Y	0.32	0.89	0.57	0.50	0	1.416
Full	Y	Ν	0.31	0.89	0.57	0.50	-	1.416

Table G26. DURHAM PT FCR – 4 markers as fixed effects (class)

Table G27. DURHAM PT FCR – 4 markers as covariates

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0	1.363
Full no markers	Y	Ν	-	-	-	-	-	1.363
Full	Y	Y	0.29	0.68	0.62	0.39	0	1.404
Full	Y	Ν	0.29	0.68	0.62	0.39	-	1.404

Table G28. DURHAM PT FCR – 4 markers as total stars (class)

			Р	Vari	iances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0	1.363
Full no markers	Y	Ν	-	-	1.363
Full	Y	Y	0.24	0	1.345
Full	Y	Ν	0.24	-	1.345

Table G29. DURHAM PT FCR – 4 markers as total stars (covariate)

			Р	Variances		
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0	1.363	
Full no markers	Y	Ν	-	-	1.363	
Full*	Y	Y	0.77	0	1.370	
Full	Y	Ν	0.77	-	1.370	
*1 0.0000(0.1000)						

\* b=0.0298(0.1038)

# **APPENDIX H**

# Feedlot ADG

## Single SNP effects for the 4 feed efficiency markers by dataset and breed

Data	Breed				١	N1		N2			N3				N4				
		Ν	star	Ν	Est.	SE	Pvalue												
CRC1	AA	342	0	5	1.467	0.10	0.136	11	1.473	0.07	0.963	64	1.437	0.03	0.203	58	1.432	0.03	0.282
			1	60	1.462	0.03		110	1.458	0.02		148	1.425	0.02		154	1.451	0.02	
			2	253	1.425	0.02		182	1.433	0.02		93	1.450	0.03		99	1.418	0.03	
	MG	84	0	0				16	1.338	0.07		16	1.281	0.07		40	1.305	0.05	
			1	5	1.431	0.11		38	1.256	0.05		48	1.288	0.05		35	1.215	0.05	
			2	77	1.254	0.05		27	1.261	0.06		16	1.211	0.07		7	1.286	0.10	
	HH	236	0	10	1.431	0.07		0				29	1.539	0.04		68	1.472	0.03	
			1	49	1.407	0.03		10	1.480	0.07		119	1.430	0.02		120	1.447	0.02	
			2	166	1.459	0.02		215	1.443	0.02		73	1.410	0.03		36	1.389	0.04	
	SH	111	0	1	1.501	0.22		0				20	1.486	0.06		7	1.444	0.09	
			1	24	1.492	0.05		4	1.501	0.11		40	1.537	0.04		23	1.437	0.05	
			2	83	1.502	0.03		95	1.495	0.03		40	1.464	0.04		70	1.529	0.04	
	NOINT	773	0	16	1.418	0.06	0.975	26	1.470	0.05	0.370	127	1.434	0.02	0.342	172	1.427	0.02	0.501
			1	137	1.415	0.02		161	1.425	0.02		349	1.411	0.02		324	1.410	0.02	
			2	568	1.411	0.01		510	1.407	0.02		218	1.398	0.02		209	1.398	0.02	
	SG	246	0	2	1.961	0.18	0.042	0			0.826	16	1.533	0.07	0.176	12	1.563	0.08	0.911
			1	55	1.518	0.04		18	1.571	0.07		79	1.582	0.04		79	1.564	0.04	
			2	181	1.599	0.03		218	1.593	0.03		136	1.589	0.03		145	1.602	0.03	
	BR	303	0	23	1.346	0.06		0				60	1.361	0.04		23	1.230	0.06	
			1	98	1.330	0.04		40	1.365	0.05		119	1.349	0.04		152	1.328	0.03	
			2	173	1.337	0.03		242	1.326	0.03		103	1.282	0.04		115	1.354	0.04	
	BH	129	0	2	0.767	0.18		0				1	1.487	0.26		9	1.012	0.09	
			1	21	1.087	0.06		3	0.952	0.16		9	0.949	0.10		52	1.032	0.04	
			2	109	1.077	0.03		130	1.073	0.03		123	1.078	0.03		72	1.114	0.04	
	NOINT	678	0	27	1.348	0.05	0.426				0.799	77	1.357	0.04	0.490	44	1.258	0.04	0.029
			1	172	1.309	0.02		61	1.338	0.04		206	1.342	0.02		280	1.315	0.02	
			2	457	1.338	0.02		582	1.329	0.02		355	1.320	0.02		327	1.354	0.02	

Table H1: Least squares means for feed test ADG (kg/d) for each marker fitted separately

CRC2	TC	783	0	39	1.377	0.06	0.607	0			0.503	48	1.394	0.05	0.298	55	1.387	0.05	0.296
			1	246	1.434	0.03		28	1.472	0.07		267	1.454	0.02		316	1.411	0.02	
			2	429	1.434	0.02		711	1.428	0.02		424	1.419	0.02		368	1.446	0.02	
	BH	681	0	5	1.232	0.15	0.098	0			0.218	2	1.051	0.23	0.746	15	1.018	0.09	0.714
			1	105	1.022	0.04		11	1.207	0.10		54	1.117	0.05		165	1.094	0.03	
			2	526	1.090	0.03		633	1.085	0.03		588	1.081	0.03		463	1.089	0.03	
Angus	AA	387	0	20	1.468	0.06	0.674	8	1.379	0.09	0.700	36	1.465	0.05	0.629	73	1.435	0.04	0.816
PT			1	88	1.438	0.04		96	1.426	0.04		178	1.423	0.04		187	1.440	0.04	
			2	262	1.423	0.04		266	1.439	0.04		155	1.431	0.04		108	1.422	0.04	
Durham	SS	165	0				0.076	1	1.580	0.26	0.966	52	1.578	0.06	0.924	12	1.671	0.09	0.507
PT			1	63	1.512	0.06		15	1.605	0.08		77	1.588	0.05		65	1.590	0.05	
			2	49	1.625	0.06		145	1.586	0.05		31	1.602	0.06		83	1.578	0.05	

Table H1: Least squares means for feed test ADG (kg/d) for each marker fitted separately continue

## Pooled CRC1 – Feedlot ADG

<b>^</b>				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.042
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.044
Full	Y	Y	0.97	0.42	0.38	0.28	0.002	0.041
Full	Y	Ν	0.97	0.39	0.32	0.28	-	0.043

Table H2. Temperate CRC1: ADG – 4 markers as fixed effects (class)

Table H3. Temperate CRC1: ADG – 4 markers as fixed effects (covariates)

				Significant	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.042
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.044
Full	Y	Y	0.80	0.26	0.21	0.11	0.002	0.041
Full	Y	Ν	0.87	0.25	0.17	0.11	-	0.043

Table H4. Temperate CRC1: ADG – markers as stars (class)

				Vari	ances
Model	cov	sire	Р	Sire	residual
Breed+herd+Feedg	Y	Y	-	0.002	0.042
Breed+herd+Feedg	Y	Ν	-	-	0.044
Full	Y	Y	0.22	0.002	0.042
Full	Y	Ν	0.20	-	0.044

Table H5. Temperate CRC1: ADG – markers as stars (covariate)

				Vari	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.002	0.042		
Breed+herd+Feedg	Y	Ν	-	-	0.044		
Full*	Y	Y	0.03	0.002	0.042		
Full	Y	Ν	0.02	-	0.044		

\*b=-0.01566 (0.0071)

				Significance of marker (P)				ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.061
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.063
Full	Y	Y	0.33	0.98	0.37	0.02	0.003	0.060
Full	Y	Ν	0.38	0.95	0.44	0.03	-	0.063

Table H6. Tropical CRC1: ADG – 4 markers as fixed effects (class)

## Table H7. Tropical CRC1: ADG – 4 markers as fixed effects (covariates)

				Significand	r (P)	Vari	iances	
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.061
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.063
Full	Y	Y	0.38	0.99	0.16	0.006	0.003	0.060
Full	Y	Ν	0.46	0.95	0.20	0.008	-	0.063

Table H8. Tropical CRC1: ADG – markers as stars (class)

				Variances
Model	cov	sire	Р	Sire residual
Breed+herd+Feedg	Y	Y	-	0.002 0.061
Breed+herd+Feedg	Y	Ν	-	- 0.063
Full	Y	Y	0.13	0.002 0.061
Full	Y	Ν	0.12	- 0.063

Table H9.	Tropical	CRC1: ADG	– markers	as stars (	(covariate)	
					<b>X</b> 7 ·	

			Vari	Variances		
cov	sire	Р	Sire	residual		
Y	Y	-	0.002	0.061		
Y	Ν	-	-	0.063		
Y	Y	0.19	0.002	0.061		
Y	Ν	0.02	-	0.063		
	cov Y Y Y Y Y	covsireYYYNYYYNYN	cov sire P   Y Y -   Y N -   Y Y 0.19   Y N 0.02	cov sire P Sire   Y Y - 0.002   Y N - -   Y Y 0.19 0.002   Y N 0.02 -		

\*b=0.01225 (0.0094)

				Significance of marker (P)				ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.051
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.053
Full	Y	Y	0.47	0.45	0.20	0.50	0.002	0.051
Full	Y	Ν	0.55	0.41	0.19	0.53	-	0.053

Table H10. Both CRC1: ADG – 4 markers as fixed effects (class)

## Table H11. Both CRC1: ADG – 4 markers as fixed effects (covariates)

				Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.002	0.051
Breed+herd+Feedg	Y	Ν	-	-	-	-	-	0.053
Full	Y	Y	0.40	0.32	0.09	0.36	0.002	0.051
Full	Y	Ν	0.49	0.29	0.09	0.40	-	0.053

Table H12. Both CRC1: ADG – markers as stars (class)

				Vari	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.002	0.051		
Breed+herd+Feedg	Y	Ν	-	-	0.053		
Full	Y	Y	0.02	0.002	0.051		
Full	Y	Ν	0.01	-	0.053		

Table H13. Both CRC1: ADG – markers as stars (covariate)

				Varia	Variances		
Model	cov	sire	Р	Sire	residual		
Breed+herd+Feedg	Y	Y	-	0.002	0.051		
Breed+herd+Feedg	Y	Ν	-	-	0.053		
Full*	Y	Y	0.58	0.002	0.051		
Full	Y	Ν	0.48	-	0.053		

\*b=-0.00317 (0.005788)

## CRC2 – FEEDLOT AVERAGE DAILY GAIN

				i manero a		etb (erabb)		
				Significance of marker (P)				ances
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.005	0.106
Full no markers	Y	Ν	-	-	-	-	-	0.111
Full	Y	Y	0.68	0.81	0.18	0.32	0.006	0.106
Full	Y	Ν	0.60	0.50	0.35	0.29	-	0.111

## Table H14. TROPICAL COMPOSITE: ADG – 4 markers as fixed effects (class)

Table H15. BRAHMAN: ADG – 4 markers as fixed effects (class)

				Significanc	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.008	0.095
Full no markers	Y	Ν	-	-	-	-	-	0.103
Full	Y	Y	0.10	0.42	0.85	0.58	0.008	0.095
Full	Y	Ν	0.09	0.25	0.82	0.67	-	0.102

#### Table H16. TROPICAL COMPOSITE: ADG – 4 markers as covariates

				Significanc	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.005	0.106
Full no markers	Y	Ν	-	-	-	-	-	0.111
Full	Y	Y	0.59	0.73	0.44	0.13	0.005	0.107
Full	Y	Ν	0.56	0.46	0.52	0.11	-	0.111

### Table H17. BRAHMAN: ADG - 4 markers as covariates

			_	Significanc	Vari	Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.008	0.095
Full no markers	Y	Ν	-	-	-	-	-	0.103
Full	Y	Y	0.26	0.41	0.61	0.90	0.007	0.096
Full	Y	Ν	0.17	0.24	0.56	0.80	-	0.103

			Р	Vari	ances
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.005	0.106
Full no markers	Y	Ν	-	-	0.111
Full	Y	Y	0.11	0.005	0.105
Full	Y	Ν	0.12	-	0.110

Table H18. TROPICAL COMPOSITE: ADG – 4 markers as total stars (class)

Table H19. BRAHMAN: ADG – 4 markers as 4 markers as total stars (class)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.008	0.095
Full no markers	Y	Ν	-	-	0.103
Full	Y	Y	0.86	0.008	0.096
Full	Y	Ν	082	-	0.103

Table H20. TROPICAL COMPOSITE: ADG - 4 markers as total stars (covariate)

			Р	Vari	Variances	
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0.005	0.106	
Full no markers	Y	Ν	-	-	0.111	
Full*	Y	Y	0.38	0.005	0.106	
Full	Y	Ν	0.38	-	0.111	
*1 0.01070 (0.0100	0)					

\* b= 0.01078 (0.01228)

Table H21	BRAHMAN · ADG – 4 markers as total stars (	(covariate)
1 4010 1121.	Dia markers as total stars (	(covariate)

dual
)95
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03

\* b=0.002477 (0.01964)

## Angus progeny test: ADG

				Significand	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.003	0.048
Full no markers	Y	Ν	-	-	-	-	-	0.051
Full	Y	Y	0.73	0.69	0.54	0.82	0.003	0.049
Full	Y	Ν	0.58	0.74	0.61	0.91	-	0.052

#### Table H22. Angus PT feedlot ADG – 4 markers as fixed effects (class)

Table H23. Angus PT feedlot ADG – 4 markers as covariates

				Significan	Vari	ances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0.003	0.048
Full no markers	Y	Ν	-	-	-	-	-	0.051
Full	Y	Y	0.49	0.47	0.72	0.50	0.003	0.048
Full	Y	Ν	0.33	0.44	0.63	0.70	-	0.051

Table H24. Angus PT feedlot ADG – 4 markers as total stars (class)

			Р	Vari	Variances	
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0.003	0.048	
Full no markers	Y	Ν	-	-	0.051	
Full	Y	Y	0.25	0.003	0.048	
Full	Y	Ν	0.24	-	0.051	

Table H25. Angus PT feedlot ADG – 4 markers as total stars (covariate)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0.003	0.048
Full no markers	Y	Ν	-	-	0.051
Full*	Y	Y	0.63	0.003	0.048
Full	Y	Ν	0.62	-	0.051

\* b=-0.00514(0.01076)

# DURHAM progeny test: ADG

Table 1120. Durham 1 1 Teediot 11DG = 4 markers as fixed effects (class)									
			Significance of marker (P)				Variances		
Model	cov	sire	N1	N2	N3	N4	Sire	residual	
Full no markers	Y	Y	-	-	-	-	0	0.064	
Full no markers	Y	Ν	-	-	-	-	-	0.064	
Full	Y	Y	0.06	0.91	0.81	0.32	0.001	0.065	
Full	Y	Ν	0.06	0.91	0.83	0.32	-	0.065	

Table H26. Durham PT feedlot ADG – 4 markers as fixed effects (class)

Table H27. Durham PT feedlot ADG – 4 markers as covariates

			_	Significanc	Variances			
Model	cov	sire	N1	N2	N3	N4	Sire	residual
Full no markers	Y	Y	-	-	-	-	0	0.064
Full no markers	Y	Ν	-	-	-	-	-	0.064
Full	Y	Y	0.07	0.80	0.66	0.34	0.001	0.064
Full	Y	Ν	0.07	0.79	0.68	0.34	-	0.065

Table H28. Durham PT feedlot ADG – 4 markers as total stars (class)

			Р	Variances	
Model	cov	sire		Sire	Residual
Full no markers	Y	Y	-	0	0.064
Full no markers	Y	Ν	-	-	0.064
Full	Y	Y	0.37	0	0.064
Full	Y	Ν	0.37	-	0.064

Table H29. Durham PT feedlot ADG – 4 markers as total stars (covariate)

			Р	Vari	Variances	
Model	cov	sire		Sire	Residual	
Full no markers	Y	Y	-	0	0.064	
Full no markers	Y	Ν	-	-	0.064	
Full*	Y	Y	0.94	0	0.065	
Full	Y	Ν	0.94	-	0.065	

\* b=0.00167(0.02253)