1   Running head: Evaluation of GeneMax Advantage

2

3   **Evaluation of Zoetis GeneMax Advantage genomic predictions in commercial *Bos taurus***

4   **Angus cattle[1]**

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24 **ABSTRACT:** The GeneMax (GMX) Advantage test, developed by Zoetis, uses approximately

25 50,000 single nucleotide polymorphisms (SNP) to predict the genomic potential of a commercial

26 Angus heifer. Genetic predictions are provided for Calving Ease Maternal, Weaning Weight,

27 Heifer Pregnancy, Milk, Mature Weight, Dry Matter Intake, Carcass Weight, Marbling, and

28 Yield. Indices of economically important traits are estimated on an index score (1-100 scale) and

29 are divided into three indices; Cow Advantage index, Feeder Advantage index, and Total

30 Advantage index. The indices provide a genomic prediction of the profitability of the cow's

31 calves. Therefore, test results can inform selection and culling decisions made by commercial

32 beef cattle producers. To measure the accuracy of the trait predictions, data from commercial

33 Angus females and their progeny at the University of Missouri Thompson Research Center was

34 utilized to analyze weaning weight, milk, marbling, fat, ribeye area, and carcass weight. Progeny

35 phenotypic data was matched to the respective dam, then the cow's genomic predictions were

36 compared to the calf's age-adjusted phenotypes using correlation and linear models. All tested

37 GeneMax scores of the dam were significantly correlated with and predicted calf performance.

38 Our predicted effect sizes, except for fat thickness, were similar to those reported by Zoetis. In

39 conclusion, the GeneMax Advantage test accurately ranks animals based on their genetic merit

40 and is an effective selection tool in commercial cowherds.

41

42 **Key words:** genomic prediction, validation, *Bos taurus*, growth, carcass

43

44 **INTRODUCTION**

45

46 Prediction of quantitative traits using DNA markers in beef cattle was first commercialized in the

47 1990s. However, many of these tests relied on a small number of markers and failed validation

48 trials (Van Eenennaam et al., 2007). Genomic prediction, the use of thousands of genome-wide

49 DNA markers (Nejati-Javaremi et al., 1997; Meuwissen et al., 2001), has proven to be a much

50 more efficacious strategy in driving genetic improvement (García-Ruiz et al., 2016; Taylor et al.,

51 2016). Still, many farmers, ranchers (Weaber et al., 2014), extension professionals, and even

52 academics question the effectiveness of genomic prediction in commercial beef cattle.

53 Demonstrations of the ability of genomic tests to accurately predict genetic merit may encourage

54 farmers and ranchers to adopt this technology and accelerate genetic progress in commercial

55 herds. Our objective is to evaluate the effectiveness of the Zoetis GeneMax Advantage (genomic

56 predictions designed for commercial heifers) in predicting the genetic merit of Angus cattle. We

57 hypothesize that, because this test was built using principles of genomic prediction, the dam's

58 GeneMax scores will significantly predict her calves' performance.

59

60 **MATERIALS AND METHODS**

61 An Animal Care and Use Committee protocol is not necessary for this project as DNA samples

62 were collected as part of routine animal production practices. However, the University of

63 Missouri has a demonstration ACUC protocol, number 7491, which covers the procedures used

64 in this research.

65 Phenotypic and pedigree data were collected at the University of Missouri's Thompson Research

66 Center and entered into Angus Genetics Inc. Beef Improvement Records (BIR) program through

67   AngusOnline.org. Pedigree, phenotype, and GeneMax Advantage score information were

68   retrieved as Excel files from AngusOnline.org in June of 2018. Phenotypic records were

69   collected from 1995 to 2018, however only calves born from 2003 to 2011 and from 2014 to

70   2018 had data reported to BIR and genotyped dams (**Figure 1**). Summary statistics are presented

71   in **Table 1**. Excel files were read into R (Team, 2018) and similar files from different years were

72   combined. Packages utilized included readr (Wickham et al., 2018b), ggplot2 (Wickham, 2016),

73   tidyr (Wickham and Henry, 2018), dplyr (Wickham et al., 2018a), and stringr (Wickham, 2018).

74

75   For statistical analyses, the calf phenotype was compared with the dam's GeneMax score. For

76   each of the traits, Pearson and Spearman correlations were calculated.

77

78   To control for potential confounding factors, mixed models were used to evaluate the

79   relationship between calf phenotype and dam's GeneMax Score. We used the model:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Zu} + \boldsymbol{e}$$

80   where, $\boldsymbol{y}$ is the phenotype of the calf; $\boldsymbol{\beta}$ are fixed effects of year of birth, sex, and dam GMX

81   Score; $\boldsymbol{u}$ is the random effect of sire, and $\boldsymbol{e}$ is the residual. Both $\boldsymbol{u}$ and $\boldsymbol{e}$ are $\sim N(0, \boldsymbol{I})$. There were

82   47 bulls who sired calves with weaning weight records, 37 bulls who sired calves with hot

83   carcass weight, marbling, and ribeye area records, and 23 bulls who sired calves with fat

84   thickness records. For each of the traits, three models were compared: a full model including

85   dam GMX Score and the random effect of sire, a reduced model that did not include the effect of

86   sire, and a reduced model that did not include the effect of dam GMX Score. For growth traits,

87   the birth year of the calf was considered the contemporary group. For carcass traits,

88   contemporary group was defined by the harvest date. For each trait, a χ^2 test was run between

89 the first and second models to determine if the inclusion of the random effect of sire was

90 significant. A χ^2 test was also run between the first and third models to determine the

91 significance of the inclusion of the cow's GeneMax Advantage score. For weaning weight, we

92 also fit models that included age-of-dam as a fixed effect factor and dam as a random effect.

93 Further, a model was also executed that included both Weaning Weight (WW) GMX Score and

94 Milk GMX Score. Models containing 1) WW GMX Score, 2) Milk GMX Score, and 3) WW and

95 Milk GMX Scores were compared to see which best fit the data. Because there is a trend over

96 time for weaning weight phenotypes and we do not have a random sample of DNA tested cows,

97 calves born in the early 2000s may have low weaning weights compared to calves born in later

98 years (**Figure 1d**) but ranked high in their own contemporary group (weaning weight ratio,

99 **Figure 1e**). Thus, we also measured the association between the dam's GMX WW scores and

100 GMX Milk scores with the calf's weaning weight ratio (no contemporary group effect was

101 included in these models).

102

103 Estimates of GeneMax Advantage score effects were retrieved from Zoetis technical bulletin

104 GMX-00116 (Zoetis Genetics and Angus Genetics Inc., 2018). Effects were converted from

105 Imperial to scientific units, divided by 10 to represent a 1-point GeneMax score increase, and

106 divided by 2 to change from molecular breeding values to expected progeny differences

107 (transmitting abilities). Our GeneMax score effect estimates were compared to Zoetis' published

108 estimates using a two-tailed Z-test.

109

110 **Results**

111   For each trait evaluated, the Pearson's correlation and Spearman's correlation between the calf's

112   phenotype and the dam's GMX Score were statistically different from zero (**Table 2**). Further,

113   from the six regression models, the dam's GMX Score had a significant effect on the calf's

114   phenotype (**Table 3**). Except for fat thickness, our estimated effect sizes were not statistically

115   different compared with those published by Zoetis (**Table 3**). When weaning weight was

116   adjusted for age-of-dam as a factor and a random effect of dam, the estimated effect of a 1-point

117   change in WW GMX Score increased to 0.29 ± 0.08 kg (p-value = 6.4e-4). Conversely, when

118   Milk GMX Score was evaluated in a model containing age-of-dam, random dam effect, or both,

119   the estimated effect of Milk GMX Score was not different from zero (p-value > 0.9). When

120   weaning weight ratio was the dependent variable to more accurately account for an animal's rank

121   in its contemporary group, WW GMX score was significantly predictive in the simple model

122   with sex and random sire (0.08944 ± 0.02057, p-value = 1.8e-05) and in the more complicated

123   model with age-of-dam and random dam effect (0.1011 ± 0.0321, p-value = 0.002). When Milk

124   GMX Score was compared to weaning weight ratio, the effect was not significant (p-value =

125   0.16). A model containing both GMX WW Score and GMX Milk Score provided a better fit to

126   the data and estimated larger effects for the GMX Scores compared with the models using one

127   GMX Score (**Table 4**). Calf phenotypes were plotted against dam's GMX Score in **Figure 2**.

128

129   **Discussion**

130   In the last ten years, the use of DNA information to produce genomic predictions has changed

131   substantially. For example, when first launched in 2010, the IGENITY MBVs (molecular

132   breeding values) were only based on 384 DNA markers (Weber et al., 2012). However, even the

133   initial genomic predictions (which were use as indicator traits in a multi-step genomic-enhanced

134 EPD analysis) trained with a couple thousand animals accurately predicted genetic merit (Weber

135 et al., 2012). In the last ten years, hundreds of thousands of beef cattle have been genotyped from

136 multiple breeds, increasing the power of these datasets not just for genetic prediction, but also for

137 basic research (Decker, 2015). Since 2015, breed associations have switched to single-step

138 methods, in which pedigree and genomic data are combined in a single analysis (Lourenco et al.,

139 2015). Pedigree information is not typically known for commercial cattle, so a DNA marker

140 effects model is typically used to predict genetic merit for commercial cattle. However, the

141 estimated breeding values produced by a genomic relationship model and a marker effects model

142 are equivalent (Hayes et al., 2009). The marker effects used to calculate GMX scores in the

143 Zoetis GeneMax Advantage test are based off of the American Angus Association single-step

144 BLUP analysis (Zoetis Genetics and Angus Genetics Inc., 2018).

145

146 All traits had relatively weak correlations between the calf's phenotype and the dam's GMX

147 Score. However, this is to be expected as this analysis does not account for Mendelian sampling

148 (random shuffle of genes between generations), contemporary group effects (management and

149 environment effects), sire effects, or the heritability of the trait. Nevertheless, as all correlations

150 were significantly different from zero, it does demonstrate the predictive ability of the GeneMax

151 Advantage test.

152

153 Regression analysis allowed a more sophisticated evaluation of the relationship between a dam's

154 GMX Score and her calf's phenotype. These models accounted for variation due to sex, year of

155 birth or slaughter date, and sire effects. However, this model still did not account for Mendelian

156 sampling or other non-additive genetic effects, including genotype-by-environment effects. The

157   amount of variation due to Mendelian sampling is large and theoretically equal to half of the

158   additive genetic variance. These sources of variation are likely why we still observe substantial

159   spread around the regression lines in **Figure 2**. Genetic predictions are not designed to predict

160   performance of individual animals, but rather the average performance of a large group of

161   progeny out of a parent compared to the progeny average of a different parent or population

162   average. Our results show that the GeneMax Advantage test accurately predicts the average

163   progeny performance for weaning weight, milk, marbling, carcass weight, ribeye area and fat

164   thickness. Our estimates of the effects of GeneMax scores, except for fat thickness, in a

165   validation population were not significantly different from those published by Zoetis.

166

167   Regardless of whether we expressed weaning growth as a weight or as a ratio within

168   contemporary group, WW GMX Score accurately predicted variation in weaning growth.

169   Further, when we adjusted for age-of-dam and accounted for dependency between data with a

170   random dam effect, the magnitude the WW GMX effect increased from 0.18 to 0.29. This larger

171   estimate is closer to that published by Zoetis. However, Milk GMX scores were not predictive of

172   weaning weight ratio or when more complicated models were used. This likely reflects the well-

173   known difficulty of predicting maternal effects (Willham, 1980). For example, in the 2014

174   Angus genomic-enhanced EPD calibration based on 57,550 animals, the correlation between

175   weaning weight and Milk EPD was 0.36. The average of the other traits was 0.66 (range of 0.45

176   to 0.78). In 2016, when 108,211 animals were used to estimate molecular breeding values, the

177   correlation between weaning weight and Milk EPD was 0.37, range of 0.56 to 0.80 for other

178   traits (Albers, 2016). Further, only 491 observations were available when analyzing weaning

179   weight ratio or age-of-dam effects, compared to 781 observations for the models that only fit

180   contemporary group, sex, and sire. Thus, the difficulty of predicting maternal effects and the

181   smaller sample sizes affected the more complicated Milk GMX models.

182

183   We note that the Zoetis GeneMax Advantage prediction is designed to work in high-percentage

184   Angus animals and is not designed for cattle with substantial ancestry from other breeds

185   (Kachman et al., 2013). However, other similar genomic predictions for crossbred cattle should

186   be equally accurate provided they contain the appropriate breeds in a large, multi-breed training

187   population.

188

189   Genetic predictions, whether based on pedigree or genomic relationships, work when trained

190   using ample and appropriately structured data. Models using contemporary group effects and

191   random effects to account for covariance between relatives appropriately separate additive

192   genetic variation from other sources of variation, including management and environment. While

193   genetic predictions were never intended to predict the performance of a single individual, the

194   average progeny performance is accurately predicted by the additive genetic merit of the parent.

195   However, biological variation remains, including non-additive genetic effects and interactions

196   (Smith et al., 2019; Braz et al., 2020) and especially Mendelian sampling (Cole and VanRaden,

197   2011) between full- or half-siblings. The increased adoption of genomic technologies in

198   commercial cattle production has the opportunity to significantly increase long-term genetic gain

199   through more accurate replacement animal selection.

200

201   **Conclusions**

202 Genomic predictions, including the Zoetis GeneMax Advantage, accurately predict a

203 straightbred, commercial Angus animal's genetic merit and the average performance of their

204 offspring. Academics and extension professionals can confidently state to farmers and ranchers

205 that genomic predictions in commercial animals are accurate and effective.

206

207 **Disclosures**

208 The authors declare no competing interests.

209

210 **Literature Cited**

211 Albers, C. 2016. Angus Announces Routine Calibration of GE-EPDs. Angus Media. Available

212 from: http://www.angus.org/pub/newsroom/Releases/032116-recalibration.html

213 Braz, C. U., T. N. Rowan, R. D. Schnabel, and J. E. Decker. 2020. Extensive genome-wide

214 association analyses identify genotype-by-environment interactions of growth traits in

215 Simmental cattle. bioRxiv. doi:10.1101/2020.01.09.900902. Available from:

216 https://doi.org/10.1101/2020.01.09.900902

217 Cole, J. B., and P. M. VanRaden. 2011. Use of Haplotypes to Estimate Mendelian Sampling

218 Effects and Selection Limits. J. Anim. Breed. Genet. 128:1–4. doi:10.1111/j.1439-

219 0388.2011.00922.x. Available from: http://www.ncbi.nlm.nih.gov/pubmed/22059578

220 Decker, J. E. 2015. Agricultural Genomics: Commercial Applications Bring Increased Basic

221 Research Power. G. Gibson, editor. PLoS Genet. 11:3. doi:10.1371/journal.pgen.1005621.

222 Available from: http://dx.plos.org/10.1371/journal.pgen.1005621

223 Van Eenennaam, a L., J. Li, R. M. Thallman, R. L. Quaas, M. E. Dikeman, C. a Gill, D. E.

224 Franke, and M. G. Thomas. 2007. Validation of commercial DNA tests for quantitative beef

225   quality traits. J. Anim. Sci. 85:891–900. doi:10.2527/jas.2006-512. Available from:

226   http://www.ncbi.nlm.nih.gov/pubmed/17178813

227   García-Ruiz, A., J. B. Cole, P. M. VanRaden, G. R. Wiggans, F. J. Ruiz-López, and C. P. Van

228   Tassell. 2016. Changes in genetic selection differentials and generation intervals in US Holstein

229   dairy cattle as a result of genomic selection. Proc. Natl. Acad. Sci.

230   doi:10.1073/PNAS.1519061113.

231   Genetics, Z., and A. G. Inc. 2018. More Informed Commercial Angus Replacement Heifer

232   Decisions with GeneMax® Advantage[TM]. Available from: https://www.zoetisus.com/animal-

233   genetics/beef/pdf/zoetis-gmx-advantage-technical-bulletin-final.pdf

234   Hayes, B. J., P. M. Visscher, and M. E. Goddard. 2009. Increased accuracy of artificial selection

235   by using the realized relationship matrix. Genet. Res. (Camb). doi:10.1017/S0016672308009981.

236   Kachman, S. D., M. L. Spanger, G. L. Bennett, K. J. Hanford, L. A. Kuehn, W. M. Snelling, R.

237   M. Thallman, M. Saatchi, D. J. Garrick, R. D. Schnabel, J. F. Taylor, and E. J. Pollak. 2013.

238   Comparison of molecular breeding values based on within- and across-breed training in beef

239   cattle. Genet. Sel. Evol. 45:30. doi:10.1186/1297-9686-45-30. Available from:

240   http://www.gsejournal.org/content/45/1/30

241   Lourenco, D. A. L., S. Tsuruta, B. O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J. K.

242   Bertrand, T. S. Amen, L. Wang, D. W. Moser, and I. Misztal. 2015. Genetic evaluation using

243   single-step genomic best linear unbiased predictor in American Angus. J. Anim. Sci.

244   doi:10.2527/jas.2014-8836.

245   Meuwissen, T. H. E., B. J. Hayes, and M. E. Goddard. 2001. Prediction of total genetic value

246   using genome-wide dense marker maps. Genetics. 157:1819–1829. Available from:

247   http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1461589&tool=pmcentrez&renderty

248   pe=abstract

249   Nejati-Javaremi, A., C. Smith, and J. P. Gibson. 1997. Effect of Total Allelic Relationship on

250   Accuracy of Evaluation and Response to Selection. J. Anim. Sci. 75:1738–1745.

251   Smith, J. L., M. L. Wilson, S. M. Nilson, T. N. Rowan, D. L. Oldeschulte, R. D. Schnabel, J. E.

252   Decker, and C. M. Seabury. 2019. Genome-wide association and genotype by environment

253   interactions for growth traits in U.S. Gelbvieh cattle. BMC Genomics. 20:926.

254   doi:10.1186/s12864-019-6231-y. Available from:

255   https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-019-6231-y

256   Taylor, J. F., K. H. Taylor, and J. E. Decker. 2016. Holsteins are the genomic selection poster

257   cows. Proc. Natl. Acad. Sci. U. S. A. 113. doi:10.1073/pnas.1608144113.

258   Team, R. D. C. 2018. R: A Language and Environment for Statistical Computing. R. D. C.

259   Team, editor. R Found. Stat. Comput. 1. Available from: http://www.r-project.org

260   Weaber, R. L., J. E. Beever, H. C. Freetly, D. J. Garrick, S. L. Hansen, K. A. Johnson, M. S.

261   Kerley, D. D. Loy, E. Marques, H. L. Neibergs, E. J. Pollak, R. D. Schnabel, C. M. Seabury, D.

262   W. Shike, M. L. Spangler, and J. F. Taylor. 2014. Analysis of US Cow-Calf Producer Survey

263   Data to Assess Knowledge, Awareness and Attitudes Related to Genetic Improvement of Feed

264   Efficiency. In: 10th World Congress on Genetics Applied to Livestock Production. Vancouver,

265   Canada.

266   Weber, K. L., D. J. Drake, J. F. Taylor, D. J. Garrick, L. A. Kuehn, R. M. Thallman, R. D.

267   Schnabel, W. M. Snelling, E. J. Pollak, and a. L. Van Eenennaam. 2012. The accuracies of

268   DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training

269   populations. J. Anim. Sci. 90:4191–4202. doi:10.2527/jas.2011-5020.

270   Wickham, H. 2016. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York.

271   Available from: http://ggplot2.org

272   Wickham, H. 2018. stringr: Simple, Consistent Wrappers for Common String Operations.

273   Available from: https://cran.r-project.org/package=stringr

274   Wickham, H., R. François, L. Henry, and K. Müller. 2018a. dplyr: A Grammar of Data

275   Manipulation. Available from: https://cran.r-project.org/package=dplyr

276   Wickham, H., and L. Henry. 2018. tidyr: Easily Tidy Data with "spread()" and "gather()"

277   Functions. Available from: https://cran.r-project.org/package=tidyr

278   Wickham, H., J. Hester, and R. Francois. 2018b. readr: Read Rectangular Text Data. Available

279   from: https://cran.r-project.org/package=readr

280   Willham, R. L. 1980. Problems in estimating maternal effects. Livest. Prod. Sci. 7:405–418.

281   doi:10.1016/0301-6226(80)90080-9. Available from:

282   https://linkinghub.elsevier.com/retrieve/pii/0301622680900809

283   Zoetis Genetics. (2016). Understanding and using GeneMax Advantage Results. Retrieved

284   September 4, 2018, from https://www.angus.org/AGI/UnderstandingGMXAdvantageResults-08-

285   26-16.pdf

286

287   *Tables and Figures*

288   **Table 1.** Summary statistics of data used for GeneMax Advantage evaluation.

	Number (Number with matched calves)	Mean	Standard Deviation	Median	Minimum	Maximum	Range	Skew	Kurtosis
Weaning Weight, kg	781	263.01	26.3	264.44	178.26	347.45	169.19	-0.17	3.05
Weaning Weight Ratio	491	100.05	9.04	100	67	130	63	-0.08	3.53
Marbling Score	374	6.53	1.14	6.55	3.2	9.2	6	-0.22	3.1
Hot Carcass Weight, kg	376	398.65	40.31	401.88	249.48	504.85	255.37	-0.62	3.93
Fat Thickness, cm	290	1.77	0.48	1.7	0.53	4.14	3.61	1.1	6.33
Ribeye Area, cm^2	374	84.79	9.31	84.52	57.42	112.9	55.48	0.12	2.87
WW GMX Score	554 (231)	45.59	20.39	45	3	97	94	0.19	2.27
Milk GMX Score	554 (231)	51.57	21.17	53	3	97	94	-0.14	2.18
CW GMX Score	554 (196)	49.18	19.41	48	7	95	88	0.11	2.27
Marb GMX Score	555 (196)	64.33	21.2	67	7	98	91	-0.44	2.25
RE GMX Score	556 (196)	50.54	20.07	49	7	97	90	0.19	2.06

| **Fat GMX Score** | 557 (188) | 43.28 | 19.85 | 42 | 3 | 93 | 90 | 0.26 | 2.18 |

289

290

291   **Table 2.** Pearson and Spearman correlation tests between the dam's Zoetis GeneMax Advantage

292   Score (Kalamazoo, MI) and the calf's phenotype.

| GeneMax Trait	Pearson Correlation (95% Confidence Interval)	Pearson Correlation P-value	Spearman Correlation	Spearman Correlation P-value
Weaning Weight	0.178 (0.109 to 0.245)	5.4e-07	0.182	3.0e-07
Maternal Milk	0.183 (0.114 to 0.250)	2.5e-07	0.162	5.3e-06
Marbling	0.273 (0.176 to 0.364)	8.4e-08	0.247	1.3e-06
Carcass Weight	0.125 (0.024 to 0.223)	1.5e-02	0.145	4.8e-03
Fat Thickness	-0.181 (-0.291 to -0.068)	1.9e-03	-0.191	1.1e-03
Ribeye Area	0.120 (0.019 to 0.219)	2.0e-02	0.112	3.0e-02

293

294   **Table 3.** Estimated effects of GMX Scores on production traits. Each row represents a different

295   linear mixed model. Models contained contemporary group and sex as fixed effects and sire as a

296   random effect. Difference from zero P-values from χ^2 test comparing full and reduced model.

297   Difference from Zoetis effects estimated from a Z-test.

| GMX Score	Estimate	Std. Error	t-value	Difference from zero P-value	Zoetis effect	Difference from Zoetis P-value
WW	0.18 kg	0.04 kg	4.43	1.1e-05	0.25 kg	0.08
Milk	0.13 kg	0.04 kg	3.62	3.2e-04	0.14 kg	0.88
Marb	0.01	0.002	4.97	1.1e-06	0.01	0.21
CW	0.20 kg	0.09 kg	2.14	3.3e-02	0.32 kg	0.19
RE	0.06 cm^2	0.02 cm^2	3.10	2.2e-03	0.07 cm^2	0.58
Fat	-0.003 cm	0.001 cm	-2.34	2.0e-02	-0.03 cm	<1.0e-22

298

299   **Table 4.** Estimated effects of dam's WW and Milk GMX Scores on calf's weaning weight. *P*-

300   values from χ^2 test comparing full model with both traits versus reduced models with single trait.

GMX Score	Estimate	Std. Error	t-value	*P*-value
WW	0.20 kg	0.04 kg	4.92	1.0e-06
Milk	0.15 kg	0.04 kg	4.20	3.0e-05
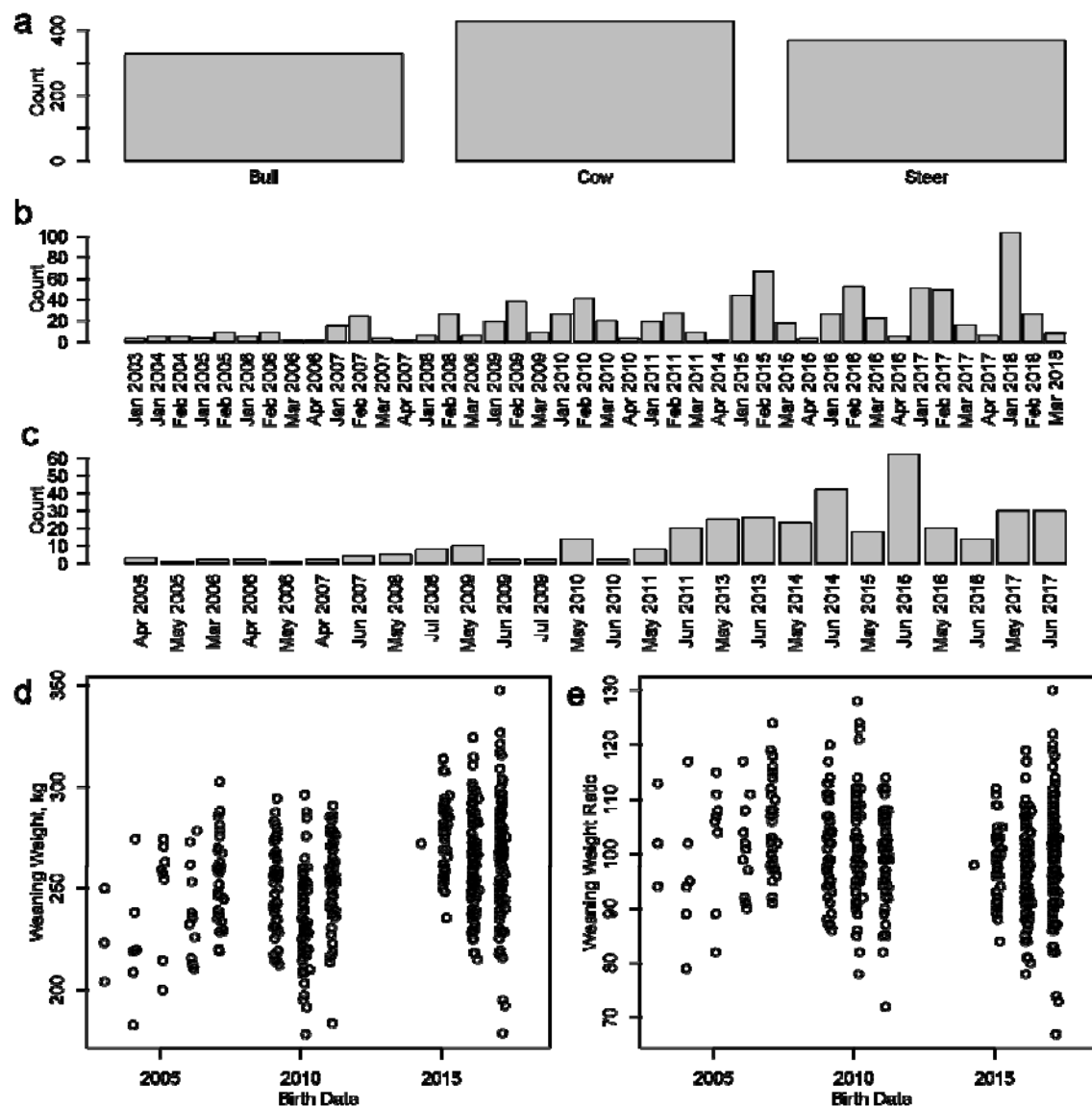
Figure 1. Graphical summary of data available for analysis. a) Counts of animals by sex. An animal can be counted as both a bull and a steer, for example if it was a bull at weaning but castrated prior to entering the feedlot. b) Counts of animals by birth month and year. c) Counts of animals by slaughter month and year. d) Weaning weight plotted against birth date. e) Weaning weight ratio plotted against birth date.

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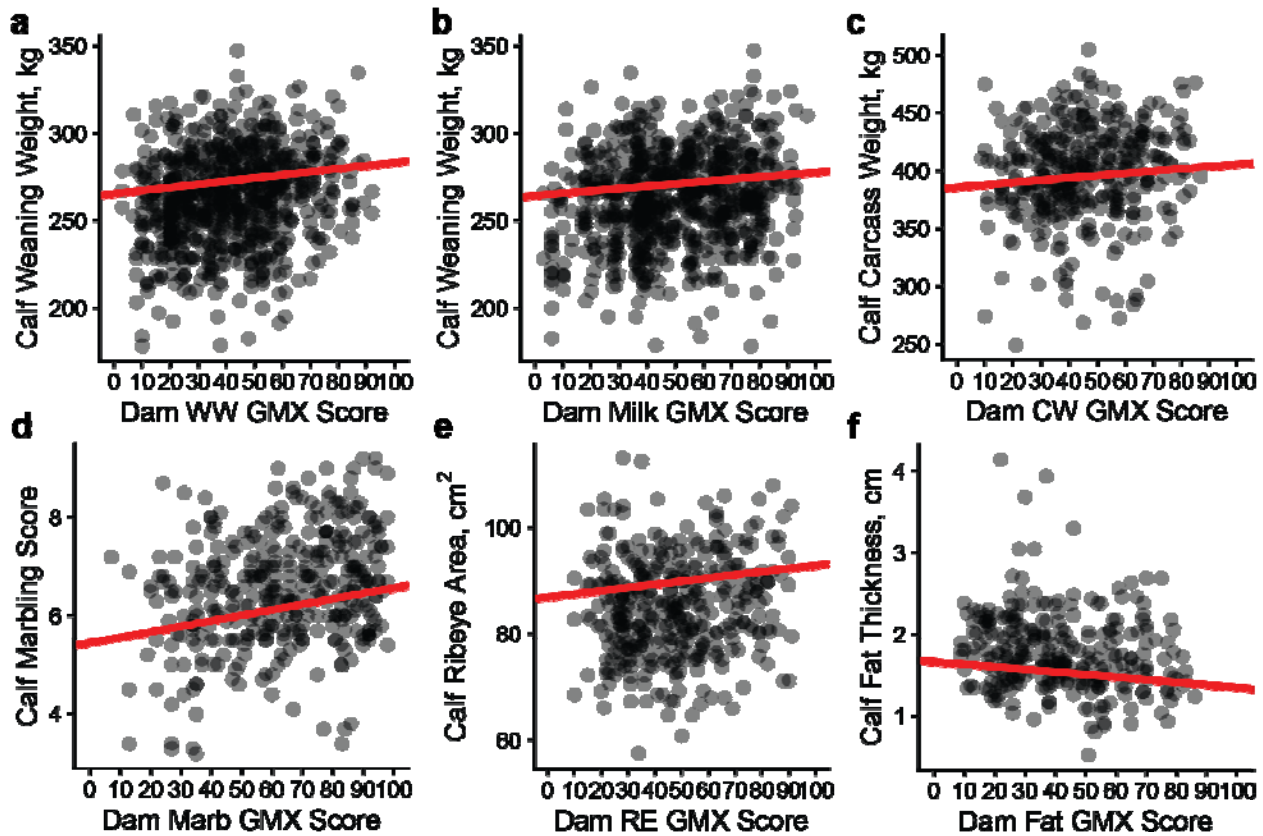
Figure 2. Calf's phenotype plotted against dam's GMX Score. a) Weaning weight versus WW

GMX Score, b) Weaning weight versus Milk GMX Score, c) Carcass weight versus CW GMX

Score, d) Marbling score versus Marb GMX Score, e) Ribeye area versus RE GMX Score, and f)

Fat Thickness versus Fat GMX Score. Red line represents the intercept and slope estimated from

the linear models reported in Table 3.

314