

### **Inbreeding Based on DNA Genotyping**

Seven sire lines were used to characterize the Wagyu breed in the United States. Each family consisted of three generations, with four grandget. Grandget offspring that were yet to be registered at the time of this study were identified by one of their parents registration numbers followed by an “o” for offspring. The diagram depicts the relationships among the individuals and the inbreeding of the sires based on DNA genotyping. Levels of inbreeding were calculated for these sires based on the pedigree as listed with the American Wagyu Association and by DNA genotyping of over 50,000 genetic markers/per animal. For calculating inbreeding by pedigree, all known individuals within the pedigree were used. If a pedigree contained unknown ancestors (listed as Japanese cow or Japanese bull), the unknown ancestors were not used for inbreeding calculations. The inbreeding estimates calculated from pedigrees were 0 for TF Itomichi ½, 0 for Kitaguni Junior, 18.7 for TF Kikuhana, 9.4% for Kitateruyasudo, 6.2% for Michifuku, 12.9% for Sanjirou, 12.5% for Takazakura and 9.4% for JVP Fukutsuru 068. The inbreeding listed for each sire (next to their name) is the inbreeding identified by DNA genotyping. This value represents the level of inbreeding represented in the DNA and exceeds the values obtained from the pedigree. This demonstrates that there are common ancestors in the pedigrees of these animals in their distant pedigrees that are not identified with a 5 generation pedigree.

### **Relatedness**

The relatedness of each of these sires to each other is also depicted by this figure. Branches closer together are more closely related than sire branches that are shown that are farther apart.