Appendix 10

Genetic Analysis of the Combined
Tilly Creek, Bible Springs, Blawn Wash and Four Mile, Utah HMAs

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January 12, 2021

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The following is a report of the genetic analysis of the Combined Tilly Creek, Bible Spring, Blawn Wash, and Four Mile Utah herd Complex.

A few general comments about the genetic variability analysis based upon DNA microsatellites compared to blood typing. The DNA systems are more variable than blood typing systems, thus variation levels will be higher. Variation at microsatellite loci is strongly influenced by allelic diversity and changes in variation will be seen in allelic measures more quickly that at heterozygosity, which is why more allelic diversity measures are calculated. For mean values, there are a greater proportion of rare domestic breeds included in the estimates than for blood typing so relative values for the measures are lower compared to the feral horse values. As well, feral values are relatively higher because the majority of herds tested are of mixed ancestry which results in a relatively greater increase in heterozygosity values based upon the microsatellite data. There are no specific variants related to breed type so similarity is based upon the total data set.

METHODS

A total of 25 samples were received by Texas A&M University, Animal Genetics Lab for 4 Mile, 25 samples from Bible Springs, 30 samples for Tilly Creek, and 25 samples from Blawn Wash on March 28, 2018. DNA was extracted from the samples and tested for variation at 12 equine microsatellite (mSat) systems. These were *AHT*4, *AHT*5 *ASB*2, *ASB*17, *ASB*23, *HMS*3, *HMS*6, *HMS*7, *HTG*4, *HTG*10, *LEX*33, and *VHL*20. These systems were tested using an automated DNA sequencer to separate Polymerase Chain Reaction (PCR) products.
A variety of genetic variability measures were calculated from the gene marker data. The measures were observed heterozygosity *(Ho)* which is the actual number of loci heterozygous per individual; expected heterozygosity *(He)*, which is the predicted number of heterozygous loci based upon gene frequencies; effective number of alleles *(Ae)* which is a measure of marker system diversity; total number of variants *(TWY)*; mean number of alleles per locus (*MNA*); the number of rare alleles observed which are alleles that occur with a frequency of 0.05 or less (*RA*); the percent of rare alleles (*%RA*); and estimated inbreeding level *(Fis)* which is calculated as 1-*Ho/He*.

Genetic markers also can provide information about ancestry in some cases. Genetic resemblance to domestic horse breeds was calculated using Rogers' genetic similarity coefficient, *S*. The resemblance was summarized by use of a restricted maximum likelihood (RML) procedure.

RESULTS AND DISCUSSION

Variants present and allele frequencies are given in Tables 1a to 1d. No variants were observed which have not been seen in horse breeds. Table 2 gives the values for the genetic variability measures of the Combined Utah herds and each of the 4 herds individually. Also shown in Table 2 are values from a representative group of domestic horse breeds. The breeds were selected to cover the range of variability measures in domestic horse populations. Mean values for feral herds (based upon data from 126 herds) and mean values for domestic breeds (based upon 80 domestic horse populations) also are shown.

Mean genetic similarity of the Combined herds and each individual herd to domestic horse breed types are shown in Table 3. A dendrogram of relationship of the Combined UT herds and each of

these four herds individually to a standard set of domestic breeds are shown in Figures 1a-1e. Relationships among Utah HMAs are shown in Figure 2.

Genetic Variants: A total of 82 variants were seen in the Combined UT herds which is higher than the average for domestic breeds and for feral horses. This could partially be due to the large sample size from the four herds combined. Of these, 20 had frequencies below 0.05. This percentage of variants at risk of future loss is near above the average for feral horse populations and that for domestic breeds but is not surprising based upon sampling such a large group. Allelic diversity as represented by *Ae* is high for feral herds as is *MNA*, however, not as high as might be expected based upon *TNV*. All the allelic diversity measures for the individual four herds are less than for the combined population which is as expected. Ra measures are an exception to this trend for Tilly Creek and Bible Springs and are fairly high for the other two herds. This likely is due to the fact that sub-populations are actually what we are looking at and, in each case, animals could be sampled with less common alleles and based upon sample size, lower frequencies are obtained.

Genetic Variation: Genetic variation, as indicated by heterozygosity, in the Combined UT herds is below the feral mean. *Ho* is lower than *He* and the difference may be due to some actual population subdivision within the combined herd area. The higher *He* could be evidence for mixing among subgroups of horses within the area commonly termed the Wahlund Effect). However, the difference between the two heterozygosity estimates is not so great as to suggest a strong degree of subdivision. Heterozygosity values among the four herds are similar with the exception of *Ho* for the Tilly Creek herd which is a good bit higher than the other herds. The remaining three herds had *Ho* values below the feral mean but not so far as to raise concern, especially since total diversity within the area is quite good.

Genetic Similarity: Overall similarity of the Combined UT herds to domestic breeds was somewhat high for feral herds. This is due to the high allelic diversity. Highest mean genetic similarity the Light Racing and Riding breeds while similarity to the other non-Cold Blood groups was lower but not greatly so. The results for all four individual herds are very similar. As seen in Fig. 1, the Combined UT herds fit most closely to two South American Criollo breeds within a major cluster of Thoroughbred related breeds and North American breeds. A similar pattern is seen for each of the four individual herd areas, although the specific Iberian breed(s) paired with the HMA is not always the same. The results suggest mixed origin for the herd with possible Spanish input. However, the Criollo breeds in general have a good deal of genetic diversity and a mixed heritage themselves so the strength of the Spanish association is probably low. The individual trees should not be considered as significant as this really appears to be a single, interbreeding group and not truly four independent populations. Figure 2 shows relationships among the four herds area considered here and six other Utah HMAs. The four herds considered in this report cluster together and are distinct from other herds except Ranger Creek and Cedar Mountain which still are on separate branches of the same cluster. These two herds are not geographically near to the four southwest UT herds. This figure is consistent with the herds being a single population. Figure 3 shows a Principle Coordinates Analysis plot of the individual horses from the four HMAs. There is no distinct clustering of individuals from a single HMA with each other strongly supporting these herds as a single population.

SUMMARY

Blawn Wash and Tilly Creek have been analyzed before, in 2001 and 2002, respectively, utilizing blood typing markers. Based upon this analysis, those results will not be considered here. Current genetic variability levels of this herd complex are good. The variation results suggest that this is a single, interbreeding herd overall, but that there could be some limited population subdivision. This, if true and maintained, could be beneficial to long term maintenance of genetic diversity. The herd arrears to be primarily of mixed breed ancestry.

RECOMMENDATIONS

This herd complex has good genetic diversity, and no action is needed at this time. Another sampling similar to the one used for this report is recommended in about five years to check to make sure diversity is being maintained and to see if evidence of population subdivision is present.

Table 1a. Combined allele frequencies of genetic variants observed in Tilly Creek, Bible Springs, Blawn Wash and Four Mile, Utah HMAs

VHL20															
I	J	K	L	M	N	O	P	Q	R	S					
0.286	0.005	0.000	0.210	0.100	0.081	0.048	0.252	0.019	0.000	0.000					
HTG4															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.290	0.157	0.471	0.038	0.000	0.043	0.000	0.000						
AHT4															
H	I	J	K	L	M	N	O	P	Q	R					
0.119	0.029	0.438	0.043	0.000	0.010	0.000	0.362	0.000	0.000	0.000					
HMS7															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.019	0.000	0.219	0.148	0.462	0.067	0.038	0.048	0.000						
AHT5															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.090	0.252	0.024	0.071	0.276	0.286	0.000	0.000	0.000						
HMS6															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.000	0.171	0.176	0.000	0.224	0.410	0.019	0.000						
ASB2															
B	I	J	K	L	M	N	O	P	Q	R					
0.000	0.195	0.000	0.138	0.000	0.119	0.181	0.119	0.024	0.224	0.000					
HTG10															
H	I	J	K	L	M	N	O	P	Q	R	S	T			
0.000	0.052	0.000	0.000	0.081	0.038	0.019	0.305	0.000	0.024	0.357	0.124	0.000			
HMS3															
H	I	J	K	L	M	N	O	P	Q	R	S				
0.000	0.276	0.000	0.000	0.000	0.019	0.181	0.133	0.348	0.014	0.029	0.000				
ASB17															
D	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
0.000	0.238	0.000	0.000	0.038	0.067	0.000	0.000	0.067	0.338	0.119	0.057	0.024	0.052	0.000	0.000
ASB23															
G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
0.114	0.000	0.095	0.062	0.481	0.100	0.000	0.000	0.000	0.000	0.000	0.024	0.048	0.000	0.076	0.000
LEX33															
F	G	K	L	M	N	O	P	Q	R	S	T				
0.000	0.000	0.129	0.524	0.000	0.000	0.057	0.014	0.162	0.114	0.000	0.000				

Table 1b. Allele frequencies of genetic variants observed in Tilly Creek HMA feral horse herd.

VHL20															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**					
0.216	**0.000**	**0.000**	**0.317**	**0.067**	**0.050**	**0.083**	**0.267**	**0.000**	**0.000**	**0.000**					
HTG4															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.000**	**0.267**	**0.133**	**0.500**	**0.067**	**0.000**	**0.033**	**0.000**	**0.000**						
AHT4															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**					
0.100	**0.033**	**0.317**	**0.067**	**0.000**	**0.017**	**0.000**	**0.466**	**0.000**	**0.000**	**0.000**					
HMS7															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.033**	**0.000**	**0.133**	**0.117**	**0.434**	**0.133**	**0.033**	**0.117**	**0.000**						
AHT5															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.083**	**0.250**	**0.000**	**0.117**	**0.267**	**0.283**	**0.000**	**0.000**	**0.000**						
HMS6															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.000**	**0.000**	**0.083**	**0.083**	**0.000**	**0.367**	**0.434**	**0.033**	**0.000**						
ASB2															
B	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**					
0.000	**0.300**	**0.000**	**0.133**	**0.000**	**0.117**	**0.133**	**0.150**	**0.050**	**0.117**	**0.000**					
HTG10															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**			
0.000	**0.067**	**0.000**	**0.000**	**0.117**	**0.033**	**0.017**	**0.349**	**0.000**	**0.017**	**0.300**	**0.100**	**0.000**			
HMS3															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**				
0.000	**0.300**	**0.000**	**0.000**	**0.000**	**0.033**	**0.300**	**0.150**	**0.200**	**0.000**	**0.017**	**0.000**				
ASB17															
D	**F**	**G**	**H**	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**
0.000	**0.117**	**0.000**	**0.000**	**0.000**	**0.067**	**0.000**	**0.000**	**0.117**	**0.349**	**0.200**	**0.050**	**0.050**	**0.050**	**0.000**	**0.000**
ASB2															
G	**H**	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**	**U**	**V**
0.167	**0.000**	**0.067**	**0.067**	**0.516**	**0.083**	**0.000**	**0.000**	**0.000**	**0.000**	**0.000**	**0.050**	**0.017**	**0.000**	**0.033**	**0.000**
LEX33															
F	**G**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**				
0.000	**0.000**	**0.133**	**0.600**	**0.000**	**0.000**	**0.017**	**0.000**	**0.183**	**0.067**	**0.000**	**0.000**				

Table 1c. Allele frequencies of genetic variants observed in Bible Springs HMA feral horse herd.

VHL20															
I	J	K	L	M	N	O	P	Q	R	S					
0.380	0.000	0.000	0.240	0.140	0.060	0.020	0.160	0.000	0.000	0.000					
HTG4															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.340	0.140	0.460	0.040	0.000	0.020	0.000	0.000						
AHT4															
H	I	J	K	L	M	N	O	P	Q	R					
0.100	0.020	0.500	0.020	0.000	0.020	0.000	0.340	0.000	0.000	0.000					
HMS7															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.040	0.000	0.200	0.080	0.520	0.060	0.040	0.060	0.000						
AHT5															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.160	0.180	0.040	0.100	0.220	0.300	0.000	0.000	0.000						
HMS6															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.000	0.220	0.160	0.000	0.240	0.380	0.000	0.000						
ASB2															
B	I	J	K	L	M	N	O	P	Q	R					
0.000	0.220	0.000	0.080	0.000	0.200	0.080	0.160	0.020	0.240	0.000					
HTG10															
H	I	J	K	L	M	N	O	P	Q	R	S	T			
0.000	0.040	0.000	0.000	0.060	0.060	0.040	0.300	0.000	0.020	0.460	0.020	0.000			
HMS3															
H	I	J	K	L	M	N	O	P	Q	R	S				
0.000	0.200	0.000	0.000	0.000	0.000	0.160	0.160	0.420	0.020	0.040	0.000				
ASB17															
D	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
0.000	0.200	0.000	0.000	0.020	0.040	0.000	0.000	0.120	0.400	0.100	0.080	0.000	0.040	0.000	0.000
ASB2															
G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
0.120	0.000	0.140	0.100	0.380	0.100	0.000	0.000	0.000	0.000	0.000	0.020	0.060	0.000	0.080	0.000
LEX33															
F	G	K	L	M	N	O	P	Q	R	S	T				
0.000	0.000	0.080	0.580	0.000	0.000	0.080	0.000	0.240	0.020	0.000	0.000				

Table 1d. Allele frequencies of genetic variants observed in Blawn Wash HMA feral horse herd.

VHL20															
I	J	K	L	M	N	O	P	Q	R	S					
0.240	0.000	0.000	0.120	0.100	0.120	0.080	0.300	0.040	0.000	0.000					
HTG4															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.280	0.160	0.440	0.020	0.000	0.100	0.000	0.000						
AHT4															
H	I	J	K	L	M	N	O	P	Q	R					
0.220	0.000	0.480	0.060	0.000	0.000	0.000	0.240	0.000	0.000	0.000					
HMS7															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.000	0.240	0.220	0.460	0.020	0.060	0.000	0.000						
AHT5															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.020	0.340	0.000	0.040	0.380	0.220	0.000	0.000	0.000						
HMS6															
I	J	K	L	M	N	O	P	Q	R						
0.000	0.000	0.000	0.260	0.220	0.000	0.100	0.380	0.040	0.000						
ASB2															
B	I	J	K	L	M	N	O	P	Q	R					
0.000	0.200	0.000	0.180	0.000	0.100	0.180	0.080	0.020	0.240	0.000					
HTG10															
H	I	J	K	L	M	N	O	P	Q	R	S	T			
0.000	0.080	0.000	0.000	0.080	0.000	0.000	0.320	0.000	0.020	0.320	0.180	0.000			
HMS3															
H	I	J	K	L	M	N	O	P	Q	R	S				
0.000	0.360	0.000	0.000	0.000	0.020	0.120	0.120	0.380	0.000	0.000	0.000				
ASB17															
D	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
0.000	0.400	0.000	0.000	0.060	0.100	0.000	0.000	0.020	0.240	0.040	0.040	0.020	0.080	0.000	0.000
ASB2															
G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
0.080	0.000	0.080	0.000	0.560	0.160	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.100	0.000
LEX33															
F	G	K	L	M	N	O	P	Q	R	S	T				
0.000	0.000	0.160	0.320	0.000	0.000	0.040	0.060	0.140	0.280	0.000	0.000				

Table 1e. Allele frequencies of genetic variants observed in Four Mile HMA feral horse herd.

VHL20															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**					
0.320	**0.020**	**0.000**	**0.140**	**0.100**	**0.100**	**0.000**	**0.280**	**0.040**	**0.000**	**0.000**					
HTG4															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.000**	**0.280**	**0.200**	**0.480**	**0.020**	**0.000**	**0.020**	**0.000**	**0.000**						
AHT4															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**					
0.060	**0.060**	**0.480**	**0.020**	**0.000**	**0.000**	**0.000**	**0.380**	**0.000**	**0.000**	**0.000**					
HMS7															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.000**	**0.000**	**0.320**	**0.180**	**0.440**	**0.040**	**0.020**	**0.000**	**0.000**						
AHT5															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.100**	**0.240**	**0.060**	**0.020**	**0.240**	**0.340**	**0.000**	**0.000**	**0.000**						
HMS6															
I	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**						
0.000	**0.000**	**0.000**	**0.140**	**0.260**	**0.000**	**0.160**	**0.440**	**0.000**	**0.000**						
ASB2															
B	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**					
0.000	**0.040**	**0.000**	**0.160**	**0.000**	**0.060**	**0.340**	**0.080**	**0.000**	**0.320**	**0.000**					
HTG10															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**			
0.000	**0.020**	**0.000**	**0.000**	**0.060**	**0.060**	**0.020**	**0.240**	**0.000**	**0.040**	**0.360**	**0.200**	**0.000**			
HMS3															
H	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**				
0.000	**0.240**	**0.000**	**0.000**	**0.000**	**0.020**	**0.120**	**0.100**	**0.420**	**0.040**	**0.060**	**0.000**				
ASB17															
D	**F**	**G**	**H**	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**
0.000	**0.260**	**0.000**	**0.000**	**0.080**	**0.060**	**0.000**	**0.000**	**0.000**	**0.360**	**0.120**	**0.060**	**0.020**	**0.040**	**0.000**	**0.000**
ASB2															
G	**H**	**I**	**J**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**	**U**	**V**
0.080	**0.000**	**0.100**	**0.080**	**0.460**	**0.060**	**0.000**	**0.000**	**0.000**	**0.000**	**0.000**	**0.020**	**0.100**	**0.000**	**0.100**	**0.000**
LEX33															
F	**G**	**K**	**L**	**M**	**N**	**O**	**P**	**Q**	**R**	**S**	**T**				
0.000	**0.000**	**0.140**	**0.580**	**0.000**	**0.000**	**0.100**	**0.000**	**0.080**	**0.100**	**0.000**	**0.000**				

Table 2. Genetic variability measures.

	N	*Ho*	*He*	*Fis*	*Ae*	*TNV*	*MNA*	*Ra*	*%Ra*
Combined UT herds	**105**	**0.690**	**0.736**	**0.062**	**4.00**	**82**	**6.56**	**20**	**0.339**
Tilly Creek, UT0449	**30**	**0.728**	**0.722**	**-0.008**	**3.81**	**76**	**6.33**	**20**	**0.263**
Bible Springs, UT0440	**25**	**0.697**	**0.716**	**0.027**	**3.73**	**76**	**6.33**	**21**	**0.276**
Blawn Wash, UT0441	**25**	**0.683**	**0.724**	**0.056**	**3.79**	**70**	**5.83**	**15**	**0.214**
4 Mile, UT0444	**25**	**0.647**	**0.712**	**0.091**	**3.60**	**74**	**6.17**	**17**	**0.230**
Cleveland Bay	47	0.610	0.627	0.027	2.93	59	4.92	16	0.271
American Saddlebred	576	0.740	0.745	0.007	4.25	102	8.50	42	0.412
Andalusian	52	0.722	0.753	0.041	4.26	79	6.58	21	0.266
Arabian	47	0.660	0.727	0.092	3.81	86	7.17	30	0.349
Exmoor Pony	98	0.535	0.627	0.146	2.87	66	5.50	21	0.318
Friesian	304	0.545	0.539	-0.011	2.56	70	5.83	28	0.400
Irish Draught	135	0.802	0.799	-0.003	5.19	102	8.50	28	0.275
Morgan Horse	64	0.715	0.746	0.041	4.19	92	7.67	33	0.359
Suffolk Punch	57	0.683	0.711	0.038	3.88	71	5.92	13	0.183
Tennessee Walker	60	0.666	0.693	0.038	3.66	87	7.25	34	0.391
Thoroughbred	1195	0.734	0.726	-0.011	3.92	69	5.75	18	0.261
Feral Horse Mean	126	0.716	0.710	-0.012	3.87	72.68	6.06	17	0.222
Standard Deviation		0.056	0.059	0.071	0.66	13.02	1.09	7.98	0.088
Minimum		0.496	0.489	-0.284	2.15	37	3.08	0	0
Maximum		0.815	0.798	0.133	5.25	96	8.00	33	0.400
Domestic Horse Mean	80	0.710	0.720	0.012	4.01	80.88	6.74	23.8	0.283
Standard Deviation		0.078	0.071	0.086	0.74	16.79	1.40	10.1	0.082
Minimum		0.347	0.394	-0.312	1.78	26	2.17	0	0
Maximum		0.822	0.799	0.211	5.30	119	9.92	55	0.462

Table 3a. Rogers' genetic similarity of the combined Tilly Creek, Bible Springs, Blawn Wash and Four Mile, Utah HMAs feral horse herds to major groups of domestic horses.

	Mean *S*	Std	Minimum	Maximum
Light Racing and Riding Breeds	**0.777**	**0.018**	**0.753**	**0.796**
Oriental and Arabian Breeds	**0.743**	**0.029**	**0.715**	**0.792**
Old World Iberian Breeds	**0.766**	**0.027**	**0.734**	**0.803**
New World Iberian Breeds	**0.758**	**0.017**	**0.727**	**0.779**
North American Gaited Breeds	**0.767**	**0.029**	**0.736**	**0.802**
Heavy Draft Breeds	**0.695**	**0.038**	**0.650**	**0.763**
True Pony Breeds	**0.715**	**0.019**	**0.691**	**0.735**

Table 3b. Rogers' genetic similarity of the Tilly Creek, UT feral horse herd to major groups of domestic horses.

	Mean *S*	Std	Minimum	Maximum
Light Racing and Riding Breeds	**0.759**	**0.019**	**0.727**	**0.777**
Oriental and Arabian Breeds	**0.725**	**0.032**	**0.692**	**0.778**
Old World Iberian Breeds	**0.752**	**0.028**	**0.717**	**0.791**
New World Iberian Breeds	**0.735**	**0.013**	**0.713**	**0.751**
North American Gaited Breeds	**0.758**	**0.038**	**0.715**	**0.808**
Heavy Draft Breeds	**0.679**	**0.038**	**0.629**	**0.739**
True Pony Breeds	**0.684**	**0.016**	**0.665**	**0.706**

Table 3c. Rogers' genetic similarity of the Bible Springs, UT feral horse herd to major groups of domestic horses.

	Mean *S*	Std	Minimum	Maximum
Light Racing and Riding Breeds	**0.768**	**0.032**	**0.725**	**0.797**
Oriental and Arabian Breeds	**0.738**	**0.038**	**0.689**	**0.797**
Old World Iberian Breeds	**0.756**	**0.029**	**0.719**	**0.796**
New World Iberian Breeds	**0.746**	**0.011**	**0.733**	**0.762**
North American Gaited Breeds	**0.759**	**0.040**	**0.715**	**0.808**
Heavy Draft Breeds	**0.684**	**0.048**	**0.619**	**0.759**
True Pony Breeds	**0.695**	**0.026**	**0.658**	**0.724**

Table 3d. Rogers' genetic similarity of the Blawn Wash, UT feral horse herd to major groups of domestic horses.

	Mean *S*	Std	Minimum	Maximum
Light Racing and Riding Breeds	**0.763**	**0.027**	**0.729**	**0.793**
Oriental and Arabian Breeds	**0.729**	**0.031**	**0.693**	**0.777**
Old World Iberian Breeds	**0.752**	**0.035**	**0.700**	**0.795**
New World Iberian Breeds	**0.735**	**0.025**	**0.688**	**0.763**
North American Gaited Breeds	**0.738**	**0.034**	**0.689**	**0.778**
Heavy Draft Breeds	**0.685**	**0.040**	**0.627**	**0.746**
True Pony Breeds	**0.707**	**0.025**	**0.663**	**0.726**

Table 3e. Rogers' genetic similarity of the Four Mile, UT feral horse herd to major groups of domestic horses.

	Mean *S*	Std	Minimum	Maximum
Light Racing and Riding Breeds	**0.767**	**0.026**	**0.733**	**0.791**
Oriental and Arabian Breeds	**0.724**	**0.038**	**0.680**	**0.781**
Old World Iberian Breeds	**0.755**	**0.033**	**0.723**	**0.804**
New World Iberian Breeds	**0.746**	**0.015**	**0.727**	**0.771**
North American Gaited Breeds	**0.756**	**0.034**	**0.726**	**0.799**
Heavy Draft Breeds	**0.682**	**0.040**	**0.629**	**0.750**
True Pony Breeds	**0.701**	**0.030**	**0.657**	**0.734**

Figure 1a. RML tree of combined Tilly Creek, Bible Springs, Blawn Wash and Four Mile, Utah HMAs genetic similarity to domestic horse breeds.

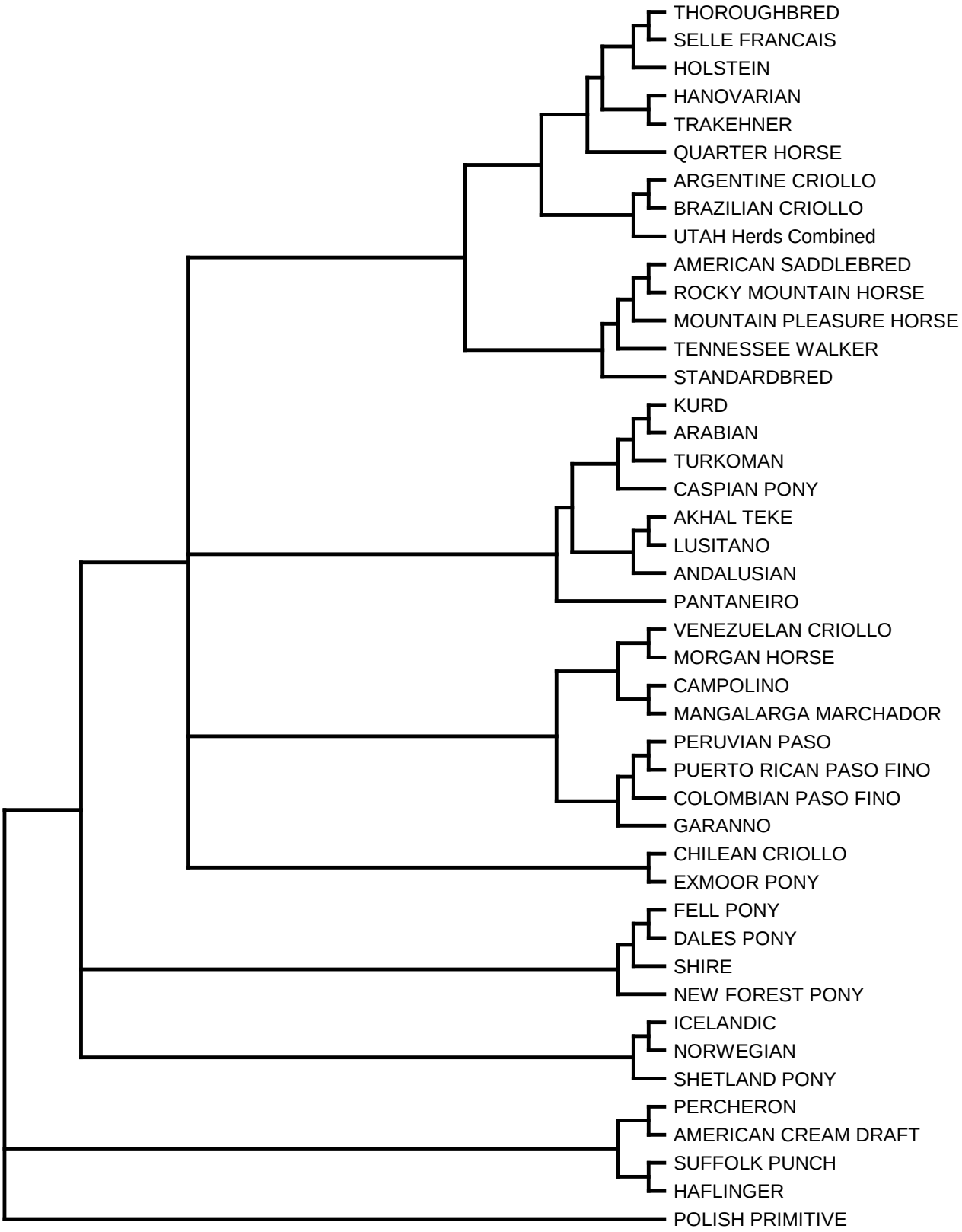


Figure 1b. RML tree of Tilly Creek, UT0449 genetic similarity to domestic horse breeds.

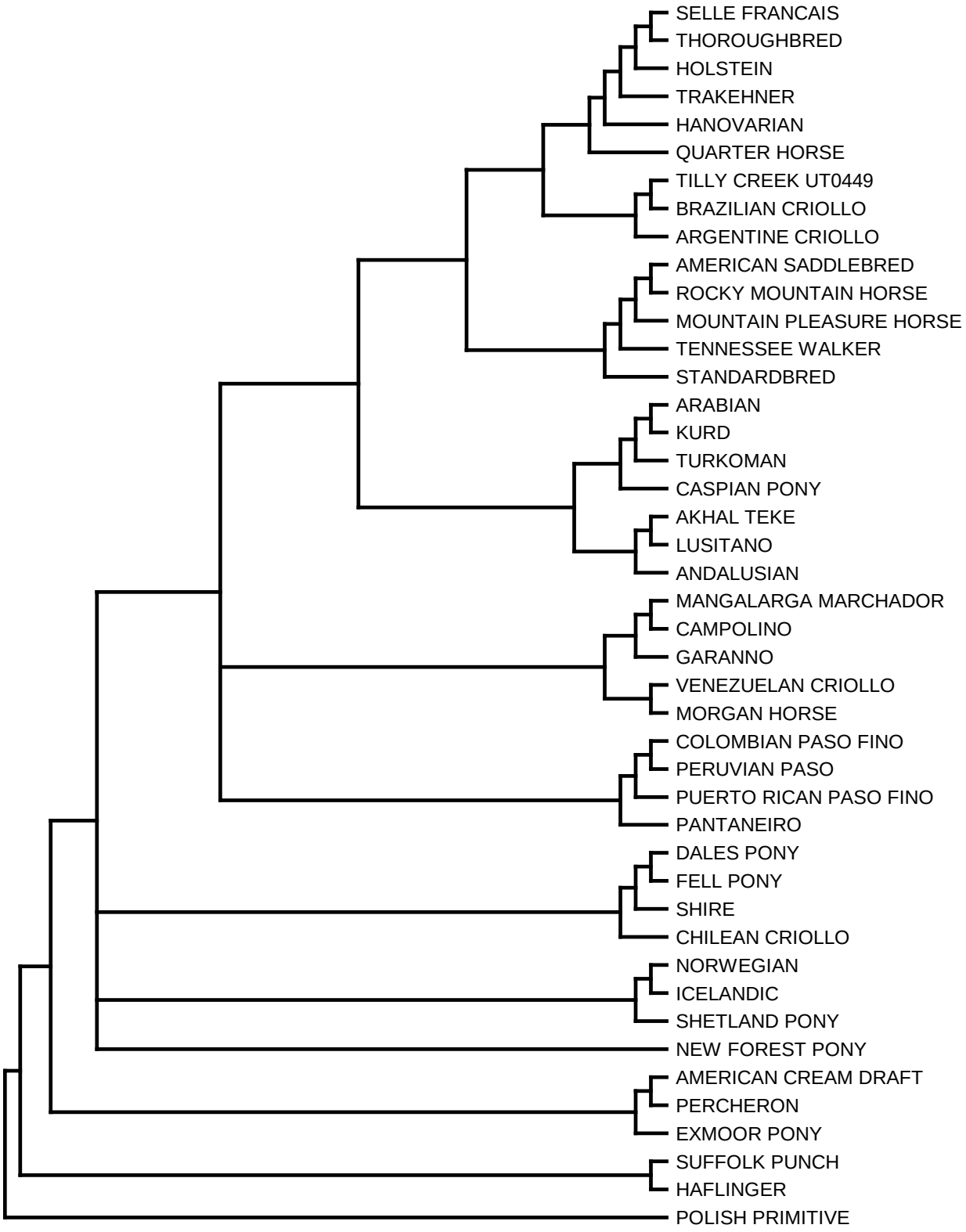


Figure 1c. RML tree of Bible Springs, UT0440 genetic similarity to domestic horse breeds.

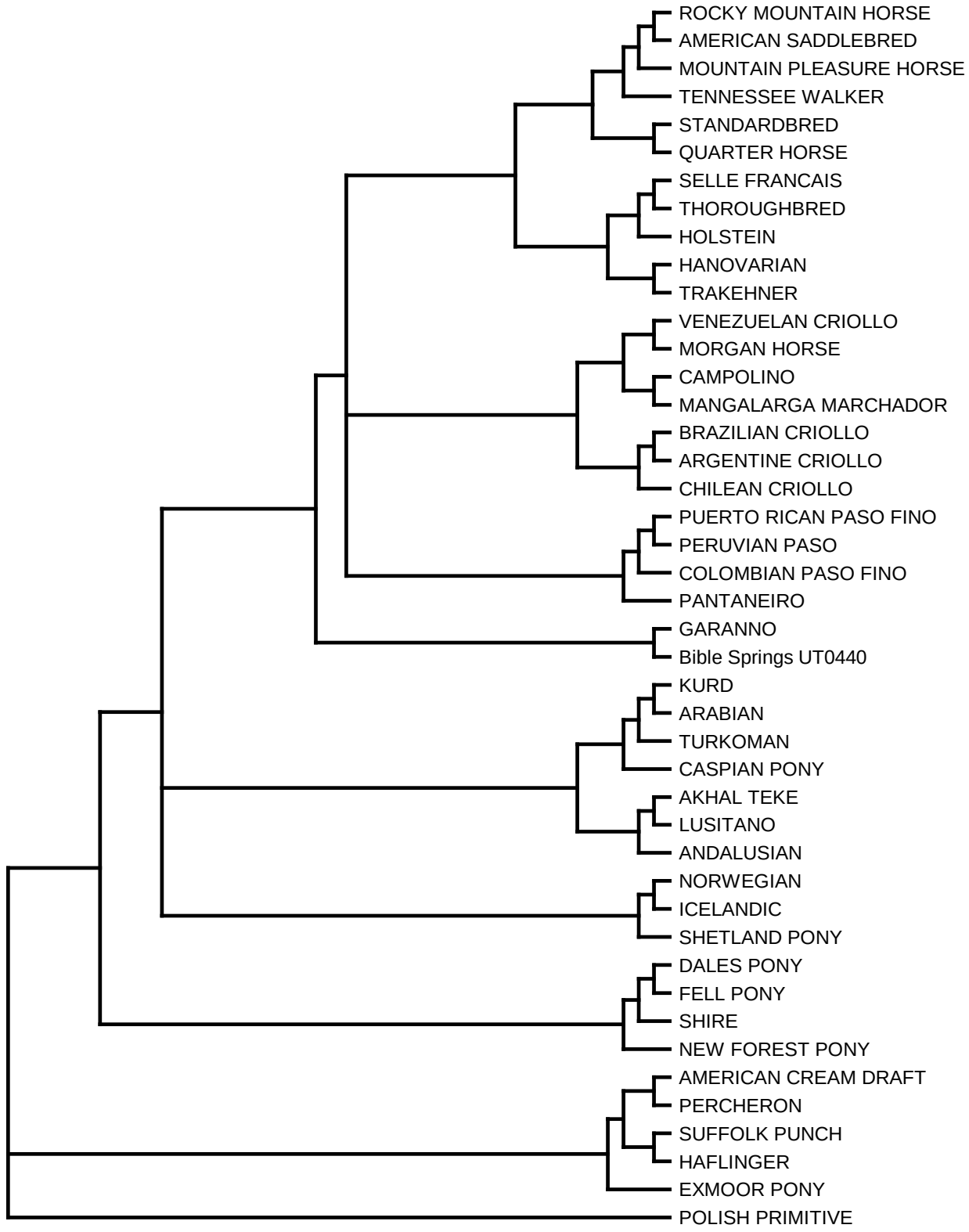


Figure 1d. RML tree of Blawn Wash, UT0441 genetic similarity to domestic horse breeds.

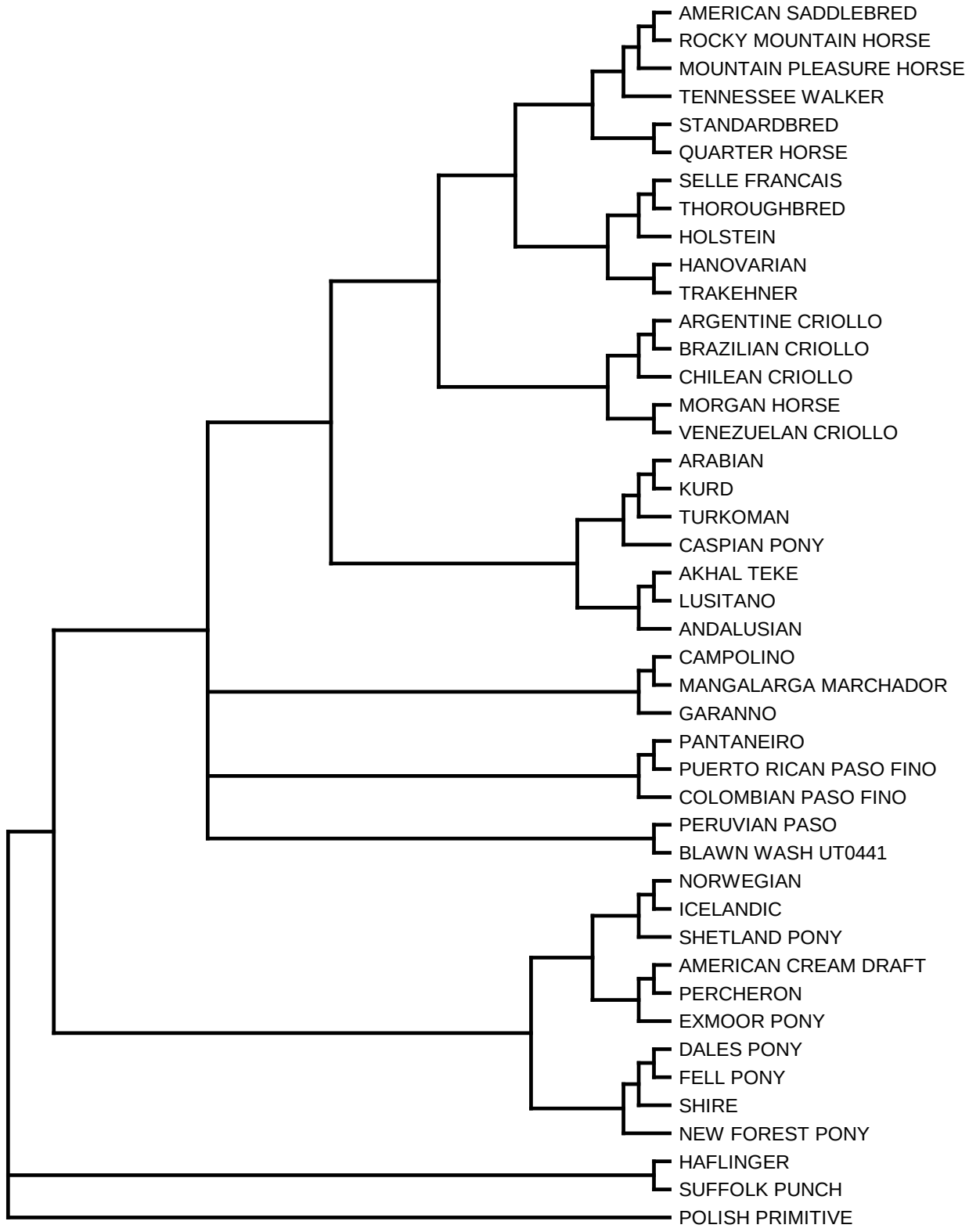


Figure 1e. RML tree of Four Mile, UT0444 genetic similarity to domestic horse breeds.

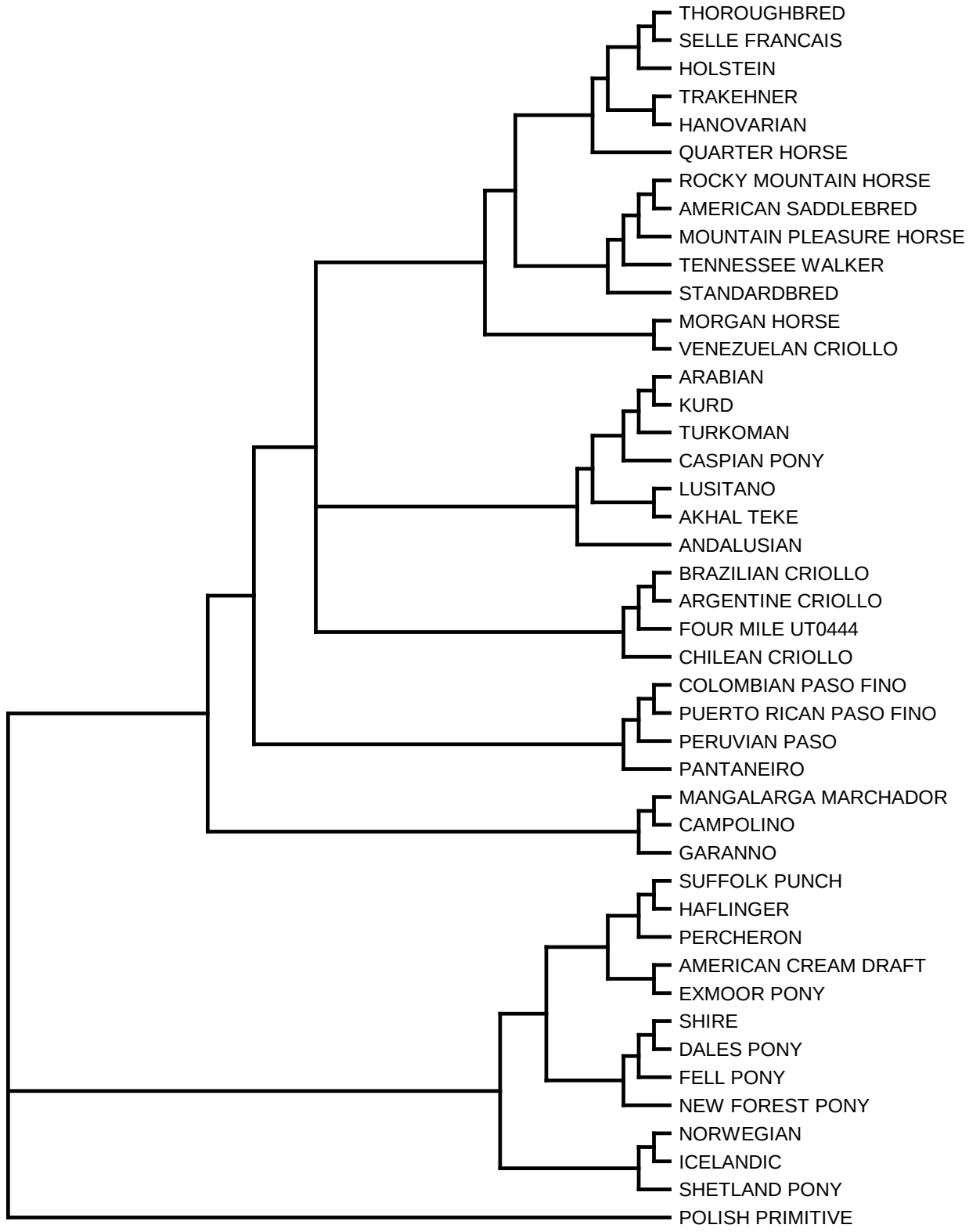


Figure 2. Genetic similarity of Utah herds

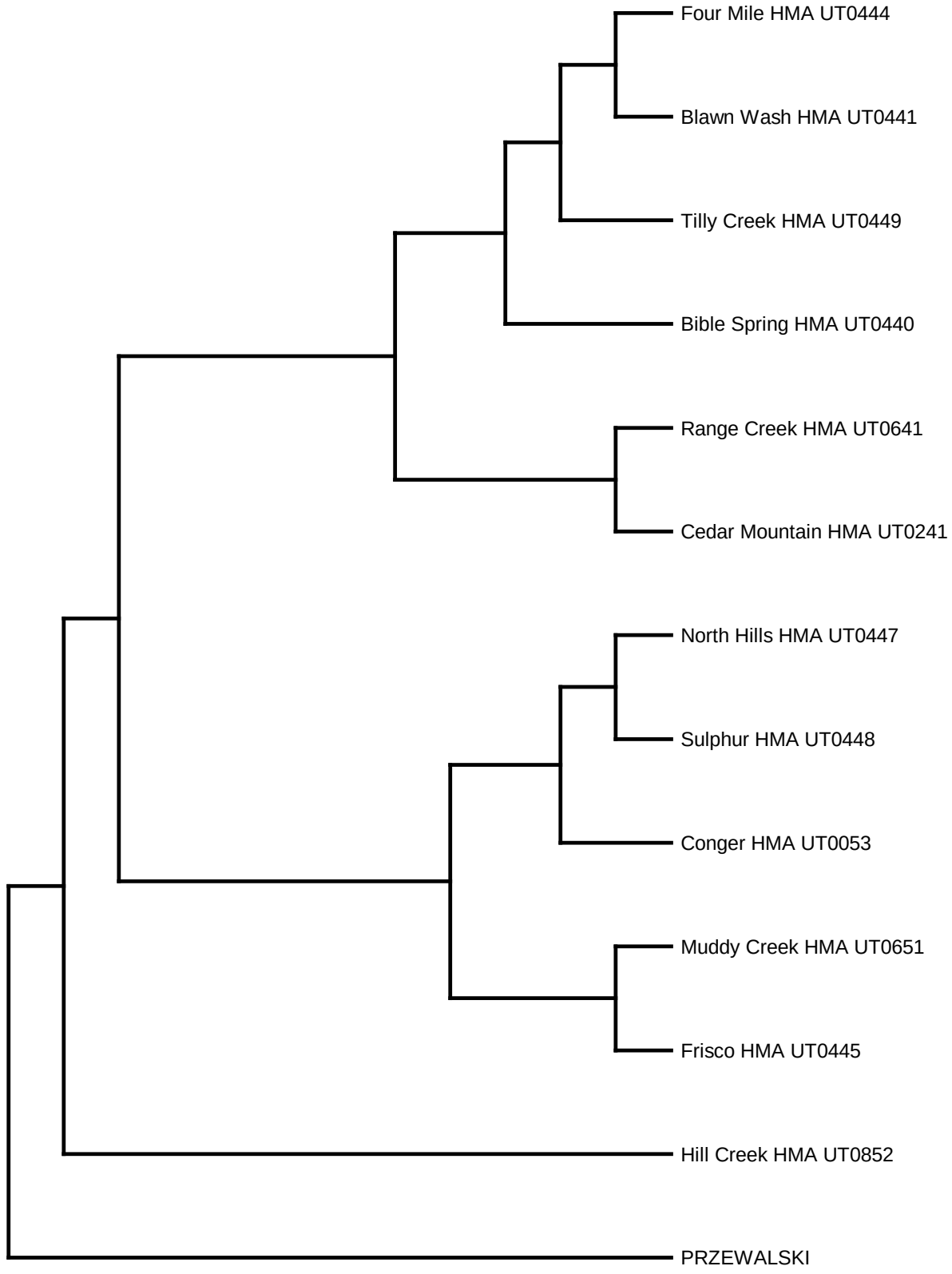
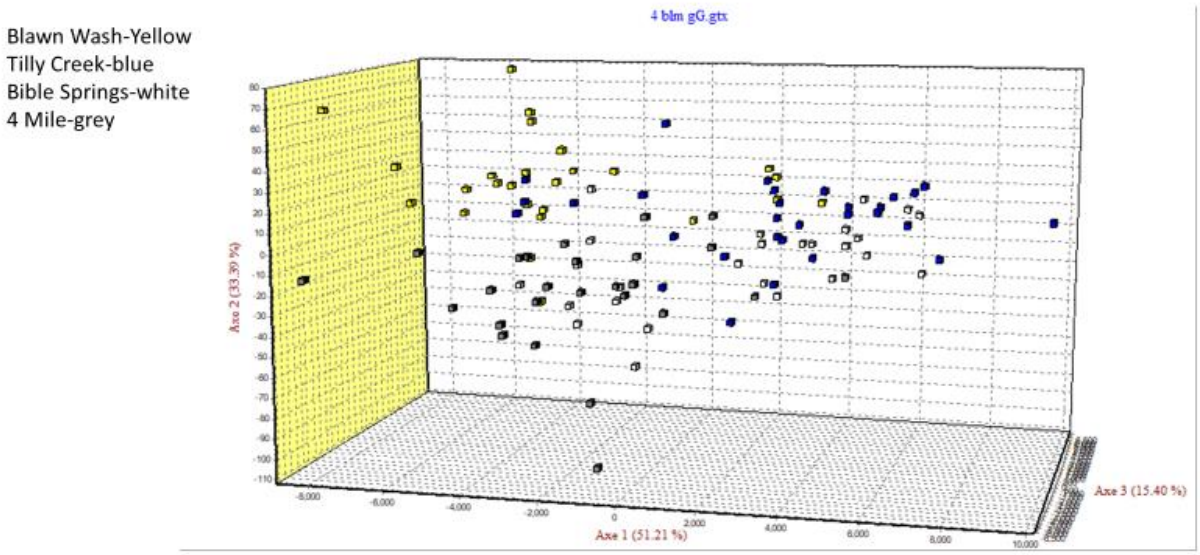


Figure 3. PCA plot of individuals from four southwest Utah HMAs.



Appendix 1a. DNA data for the Tilly Creek, UT herd.

AID	ID	VHL20	HTG4	AHT4	HMS7	AHT5	HMS6	ASB2	HTG10	HMS3	ASB17	ASB23	LEX33	LEX3
104365	6807	MO	KM	KM	LN	NN	MP	KN	MO	IP	NN	IR	LL	FF
104366	6805	LL	LM	OO	NQ	MN	OP	OQ	IO	IN	MQ	KK	KL	LL
104367	6810	LL	LM	JJ	LN	OO	PP	NQ	IR	II	NN	JK	KL	NN
104368	6809	LM	KM	OO	LM	NN	MQ	KN	MO	NR	MM	KU	LR	NN
104369	6798	LN	KK	HJ	LM	KM	MP	NQ	LS	MP	FN	KR	LR	FF
104370	6808	OP	MP	HO	NO	NO	LP	KQ	RS	PP	FF	JU	KO	FF
104371	6817	LN	KP	HJ	MN	OO	PP	MN	NR	OP	FN	KK	KR	NN
104372	6688	LL	KM	OO	JQ	KM	OP	IO	LR	NN	NO	KK	LL	LL
104373	6693	IP	MM	JO	LQ	KO	OO	IM	IO	OP	OR	GG	LQ	HH
104374	6819	LO	KK	IO	MM	MN	OP	KK	OS	IN	FN	KK	KL	NN
104375	6822	IO	KM	HI	MO	KM	PP	KN	SS	II	FN	KL	KK	NN
104376	6690	NP	KM	HH	NQ	KN	MO	IQ	LR	NP	MO	IK	KL	FF
104377	6696	IP	MM	JJ	LN	JK	OP	NO	RR	NP	OO	KS	LQ	HH
104378	6691	IM	LM	JJ	NN	NO	LO	OP	LO	NO	NR	KK	LQ	LL
104379	6689	LM	MM	JO	NN	KO	LO	KP	OR	OP	NN	GK	LL	FF
104380	6679	IP	KM	OO	NN	JO	OP	IM	OO	II	JN	KK	LL	PP
104381	6685	IP	MM	JO	NN	JN	OP	II	OR	OP	NQ	KK	LQ	LL
104382	6694	LP	LM	JO	OQ	KO	OP	IM	OR	NO	NO	JK	LL	FF
104383	6674	IP	MN	JK	JN	MO	OP	IM	RR	IN	JN	IL	LQ	FL
104384	6677	LP	LM	OO	NO	NO	PP	IM	OO	IN	JP	GG	LQ	LL
104385	6682	LP	MN	OO	NN	KK	OP	II	OS	IM	MO	IJ	LQ	LL
104386	6684	II	MM	JJ	NO	KO	PP	IQ	RR	NN	NO	GK	LQ	HL
104387	6675	IP	KN	JO	PQ	KN	OO	IO	LR	IN	NO	GL	LL	LL
104388	6686	LP	MM	OO	NN	KN	PP	II	OO	IO	PQ	KK	LL	LL
104389	6676	IP	LM	JO	LN	JO	LO	OO	QR	NP	NO	KK	QQ	HL
104390	6678	LP	MM	KO	NO	JM	LO	IQ	OO	IO	FR	GK	LL	LL
104391	6683	LP	LM	OO	NO	KO	OP	IM	OR	IN	JP	GK	LQ	LL
104392	6667	LO	KK	KO	MN	NN	MQ	KN	LO	IP	MN	KR	LR	FN
104393	6687	IL	KL	JO	LO	OO	OP	OP	IO	NO	MO	KL	LL	HL
104394	6695	IP	KN	JO	PQ	KN	OO	IO	LR	IN	NO	GL	LL	LL

Appendix 1b. DNA data for the Bible Springs, UT herd.

AID	ID	VHL20	HTG4	AHT4	HMS7	AHT5	HMS6	ASB2	HTG10	HMS3	ASB17	ASB23	LEX33	LEX3
104395	6736	IL	LM	JJ	NN	MO	LO	IO	LR	NO	NP	KL	LO	HP
104396	6731	IP	KN	OO	NQ	KO	OP	IM	OR	IP	JM	JK	QQ	LL
104397	6726	IN	KM	JJ	LN	JM	LP	MP	IR	NP	OR	KS	LQ	HH
104398	6739	LP	LL	JO	NN	MM	PP	MM	RR	IO	MP	KK	LL	FH
104399	6738	IP	KN	KO	NQ	OO	OP	II	OR	IP	FM	JK	LQ	LL
104400	6729	IL	KM	OO	NO	KO	OP	IO	RR	OO	FN	IK	LQ	LL
104401	6740	IP	KM	JO	NO	JJ	LL	IQ	OO	IO	NO	IS	LL	LN
104402	6931	LP	KK	JO	JN	JK	OP	IM	RR	IN	NN	GJ	LL	HL
104403	6933	MM	MM	OO	LM	NN	PP	KM	OQ	PP	FJ	IK	LO	FF
104404	6925	II	MM	JO	MN	KK	MP	NQ	NR	IP	NN	KK	OO	NN
104405	6927	II	KM	HO	NO	JK	OO	IO	OR	OP	FN	GK	LQ	HL
104406	6928	IL	LM	JJ	LN	LO	PP	NQ	LR	IR	FN	JK	LQ	FN
104407	6743	II	MM	JO	LN	JO	OO	OQ	IR	NN	NO	KK	LQ	HH
104408	6705	IP	KM	HJ	LP	JO	LM	NQ	OR	PP	FN	IS	LL	FF
104409	6742	II	MM	JJ	NQ	KO	LL	MM	OR	PP	NN	KL	LQ	HH
104410	6783	MM	MM	JM	MP	LN	LP	IK	MO	IP	MN	IJ	KL	NN
104411	6794	LL	LM	JJ	NN	OO	LP	MM	OR	NP	NN	GL	LQ	HH
104412	6791	II	KM	JJ	LN	NN	MP	NQ	RS	IP	FO	KU	LL	NN
104413	6797	MN	KM	JO	NN	NN	MP	OQ	NR	PP	IP	RU	KL	MM
104414	6796	MN	KM	IO	LM	MN	MM	KO	MR	IQ	MN	IL	KL	MM
104415	6792	PP	KP	HJ	NN	KO	LP	OQ	OO	OP	FO	KU	KL	NN
104416	6751	LL	KL	JJ	NN	NO	OO	IO	OO	NO	NR	GL	LQ	LL
104417	6800	IL	LM	HJ	JN	JO	LO	IQ	RR	NP	NN	GG	LQ	NN
104418	6799	LO	KM	HO	LN	KN	MM	KQ	MO	PR	FM	IU	LR	NN
104419	6801	LM	KK	JO	LL	NO	PP	QQ	LR	PP	FP	KK	LL	NN

Appendix 1c. DNA data for the Blawn Wash, UT herd.

AID	ID	VHL20	HTG4	AHT4	HMS7	AHT5	HMS6	ASB2	HTG10	HMS3	ASB17	ASB23	LEX33	LEX3
104340	6952	PQ	PP	OO	LL	KN	LP	KQ	OS	IN	FF	KK	RR	MN
104341	6961	OP	KM	HH	NP	KK	LM	IK	RS	NP	FJ	IL	LP	IN
104342	6959	NP	KK	HO	MN	KO	LM	MN	OR	IN	IJ	KL	LL	IP
104343	6950	LO	KL	OO	MP	NN	PP	KQ	OR	IP	FN	LL	RR	NN
104344	6958	LN	KM	JJ	MN	OO	LP	NN	II	IP	NN	KK	KR	NN
104345	6947	PQ	MM	HJ	LO	NO	OP	KO	OQ	PP	NR	KK	RR	FF
104346	6960	NP	KM	HJ	MN	NN	MP	NQ	LR	IP	FI	KK	LP	FN
104347	6961	II	LM	JJ	LL	KN	MP	IQ	RS	II	FN	KU	LL	IP
104348	6954	MP	KK	HJ	NN	KK	MP	IQ	RS	PP	FN	LU	KL	FF
104349	6953	IP	MM	JO	LN	OO	MP	MN	OR	IM	IO	KU	KO	IP
104350	6948	IL	MP	HJ	MN	KN	PP	NP	LS	IP	NQ	KK	KK	FF
104351	6947	IP	KM	HJ	MN	KN	MQ	IK	OO	OP	JP	IK	OQ	FN
104352	6949	OP	LL	JO	MN	KN	PP	KQ	LR	IP	FN	KU	LR	MN
104353	6946	MM	KL	HJ	LL	NN	MP	NQ	OR	IP	FJ	KK	LR	FI
104354	6942	LP	KM	JK	NN	MN	LO	OQ	OO	NO	FR	GG	KL	LL
104355	6944	IL	MM	KO	NN	JK	LP	IQ	OO	II	JN	GG	LQ	LL
104356	6941	NP	MM	HJ	LN	OO	LO	MM	OO	PP	FF	IK	LP	NN
104357	6939	NO	KM	HJ	MM	KO	LM	MN	RR	PP	FN	IL	KR	NP
104358	6945	IM	LM	JJ	NN	KN	LO	KO	LR	OP	NR	KK	LQ	FL
104359	6938	IN	MM	JO	MM	NN	LP	KN	RR	IP	FN	KL	KR	IN
104360	6943	II	MM	KO	LN	KM	LO	IK	IR	IO	MO	KS	QQ	HL
104361	6937	MP	KP	JJ	NN	KK	MP	IQ	OS	OP	FP	KL	LR	FM
104362	6940	IL	KM	JJ	LN	NN	MQ	II	RS	IN	FF	KK	RR	FP
104363	6935	IP	LN	OO	NP	OO	LP	IO	IO	NO	FR	KK	QQ	LL
104364	6936	PP	LP	JJ	LN	KN	LP	QQ	SS	II	FF	KU	LL	MN

Appendix 1d. DNA data for the Four Mile, UT herd.

AID	ID	VHL20	HTG4	AHT4	HMS7	AHT5	HMS6	ASB2	HTG10	HMS3	ASB17	ASB23	LEX33	LEX3
104420	6863	MP	LM	JJ	OO	KO	OO	KQ	OS	IP	NQ	KK	LR	FF
104421	6866	IP	KM	JO	LN	NN	PP	NN	RR	PP	FN	KL	KK	NN
104422	6918	IL	LM	JJ	NN	KO	PP	QQ	LR	IP	NN	JK	LO	FN
104423	6920	LN	KK	JO	MM	OO	LP	KN	RS	PP	NN	KK	KK	NN
104424	6921	PP	MM	JO	LN	JK	MP	NQ	OQ	PR	FJ	KU	LO	II
104425	6915	IL	MM	HJ	NP	JN	PP	NQ	OR	PP	NR	KU	LL	LN
104426	6914	PQ	LM	JO	MN	KO	PP	KN	RR	IP	FN	KU	OR	NN
104427	6909	JM	MP	IJ	LL	OO	OP	MM	QS	MO	FF	LU	LL	FI
104428	6913	IP	LM	JO	NN	NN	LM	MQ	OR	PP	JN	IS	LL	LN
104429	6867	NN	KL	OO	MN	KN	MO	QQ	OS	PP	NO	IS	KL	HN
104430	6864	II	MM	JJ	NN	KM	OO	OO	RR	NN	NR	GS	LL	HH
104431	6870	PQ	KN	OO	MN	KN	PP	NQ	RR	IN	OP	GS	LQ	FH
104432	6821	IP	LM	JJ	LN	KL	PP	NQ	RR	IP	FN	JK	KO	FF
104433	6781	MP	KK	JO	LL	NO	LL	NN	SS	IP	NO	KU	LL	FF
104434	6813	IP	KL	JO	LL	NO	MP	NN	SS	II	II	KK	LR	II
104435	6814	II	LM	JJ	LN	OO	LM	QQ	OS	IP	II	KK	LL	FF
104436	6816	LP	MM	JO	MN	KN	MM	NN	NO	NP	FP	JK	OR	NN
104437	6820	MP	LM	OO	LM	JK	PP	QQ	OO	IP	FN	JK	LL	LL
104438	6789	NP	KM	HO	NN	NO	OP	IQ	OO	OO	FO	IK	LL	LL
104439	6780	IP	LM	JO	LM	JN	MP	KO	OR	IR	FF	GK	QR	MM
104440	6806	II	KM	JO	LN	KO	LL	NO	IR	NO	NO	KK	LQ	HH
104441	6811	LN	KK	IK	NN	LO	MM	KN	LM	PQ	FN	KR	LL	MM
104442	6786	IL	KM	JO	LM	OO	MM	IK	RS	IP	JN	IK	KL	FF
104443	6776	LM	KM	IO	LL	LO	MP	KK	MM	QR	FN	IL	LL	MM
104444	6765	II	MM	HJ	NN	JK	OP	NQ	LR	NO	OP	GS	LQ	PP