Supporting Information

McTavish et al. 10.1073/pnas.1303367110

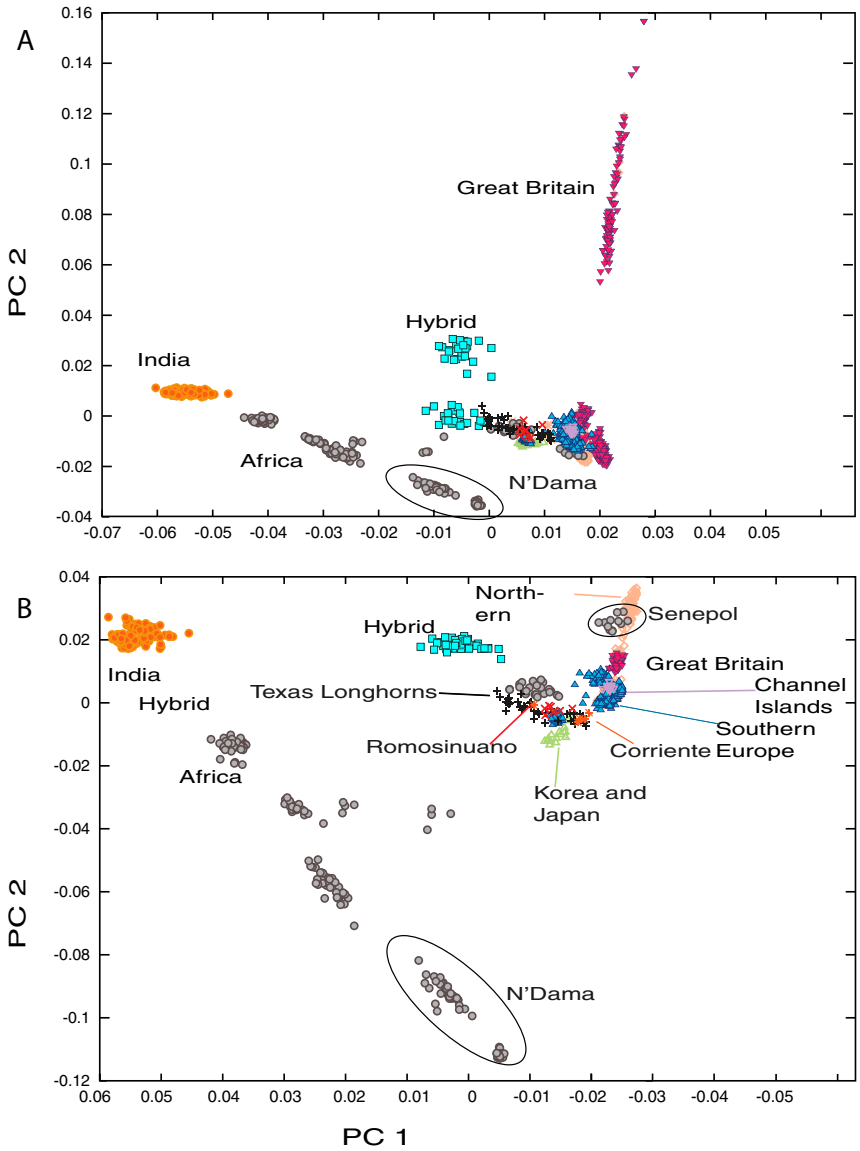

Fig. S1. (*A*) Principal components analysis of genetic variation in 1,369 cattle individuals genotyped at 47,506 single nucleotide polymorphism (SNP) loci. Individuals are grouped by the region of breed origin, as described in Table 1. Ascertainment bias in the SNPs selected for the chip is reflected in greater apparent genomic diversity of British cattle breeds (especially Hereford). (*B*) Principal components analysis based on a subset of individuals shown in *A*; all individuals with a principal component 2 (PC2) score >0.04 in the full analysis were removed before performing the PCA to clarify relationships among the remaining groups.

Table S1. Information for breeds included in analyses

Breed code	Figure legend	Name	Region of origin	Country	Latitude	Longitude	Sample size (50k)	Sample size (1.8k)	Average percent taurine (1.8k, STRUCTURE)	SD	Average heterozygosity (50k)	SD
124	1	Shorthorn	Great Britain	England	52.00	0.75	99	99	1.00	0.003	0.25	0.02
113	2	Maine Anjou	Southern Europe	France	46.00	2.00	5	5	1.00	0.001	0.28	0.00
127	3	White Park	Great Britain	England	52.00	0.75	4	4	0.99	0.002	0.21	0.02
214	4	Kerry	Great Britain	Ireland	53.00	−8.00	3	3	0.98	0.011	0.29	0.00
100	5	Angus	Great Britain	Scotland	55.95	−3.20	90	90	0.99	0.006	0.27	0.02
218	6	Devon	Great Britain	England	52.00	0.75	4	4	0.98	0.009	0.26	0.01
101	7	Hereford	Great Britain	England	52.00	0.75	98	98	0.99	0.010	0.29	0.03
104	8	Simmental	Northern Europe	Switzerland	47.00	8.00	77	78	0.99	0.008	0.28	0.01
129	9	Red Angus	Great Britain	Scotland	55.95	−3.20	15	15	0.99	0.002	0.28	0.01
125	10	Tarentaise	Southern Europe	France	46.00	2.00	5	5	0.99	0.007	0.29	0.01
107	11	Belgian Blue	Northern Europe	Belgium	50.83	4.00	4	4	0.99	0.007	0.30	0.00
212	12	South Devon	Great Britain	England	52.00	0.75	3	3	0.97	0.018	0.27	0.00
114	13	Murray Gray	Australia (via Great Britain)	Australia	−27.00	133.00	4	4	0.98	0.017	0.28	0.01
210	14	English Longhorn	Great Britain	England	52.00	0.75	3	3	1.00	0.001	0.20	0.01
118	15	Red Poll	Great Britain	England	52.00	0.75	5	5	0.98	0.020	0.26	0.01
102	16	Limousin	Southern Europe	France	46.00	2.00	100	100	0.98	0.019	0.29	0.01
217	17	Dexter	Great Britain	Ireland	53.00	−8.00	4	4	0.97	0.024	0.22	0.04
201	18	Finnish Ayrshire	Northern Europe	Finland	64.00	26.00	10	10	0.97	0.013	0.28	0.00
205	19	Guernsey	Channel Islands	Channel Islands	49.47	−2.58	10	10	0.98	0.013	0.25	0.01
211	20	Welsh Black	Great Britain	Wales	51.50	−3.22	2	2	0.99	0.001	0.29	0.00
223	21	Norwegian Red	Northern Europe	Norway	62.00	10.00	21	21	0.98	0.013	0.29	0.01
112	22	Gelbvieh	Northern Europe	Germany	51.00	9.00	8	8	0.96	0.020	0.29	0.01
122	23	Scottish Highland	Great Britain	Scotland	55.95	−3.20	8	8	0.99	0.010	0.25	0.01
117	24	Pinzgauer	Northern Europe	Austria	48.12	16.12	5	5	0.98	0.008	0.29	0.01
120	25	Salers	Southern Europe	France	46.00	2.00	5	5	0.95	0.018	0.27	0.04
221	26	Montbeliard	Southern Europe	France	46.00	2.00	5	5	0.96	0.004	0.28	0.01
109	27	Blonde d'Aquitaine	Southern Europe	France	46.00	2.00	5	5	0.96	0.023	0.29	0.01
216	28	Galloway	Great Britain	Scotland	55.95	−3.20	4	4	0.97	0.011	0.26	0.01
200	29	Holstien	Northern Europe	Netherlands	52.50	5.75	85	100	0.92	0.029	0.30	0.01
215	30	Sussex	Great Britain	England	52.00	0.75	4	4	0.94	0.028	0.25	0.02
103	31	Charolais	Southern Europe	France	46.00	2.00	53	53	0.96	0.031	0.30	0.01
213	32	Belted Galloway	Great Britain	England	52.00	0.75	4	4	0.95	0.032	0.26	0.01
204	33	Brown Swiss	Northern Europe	Switzerland	47.00	8.00	10	10	0.95	0.018	0.26	0.01
116	34	Piedmontese	Southern Europe	Italy	42.83	12.83	29	29	0.94	0.032	0.29	0.01
202	35	Jersey	Channel Islands	Channel Islands	49.25	−2.17	10	10	0.92	0.022	0.24	0.01
119	36	Romagnola	Southern Europe	Italy	42.83	12.83	29	29	0.87	0.027	0.27	0.01
110	37	Chianina	Southern Europe	Italy	42.83	12.83	7	7	0.89	0.045	0.28	0.02
220	38	Marchigiana	Southern Europe	Italy	42.83	12.83	2	4	0.84	0.015	0.27	0.01
121	39	Texas Longhorn	Southwestern United States	USA	32.00	100.00	40	114	0.89	0.068	0.28	0.05

Table S1. Cont.

Breed code	Figure legend	Name	Region of origin	Country	Latitude	Longitude	Sample size (50k)	Sample size (1.8k)	Average percent taurine (1.8k, STRUCTURE)	SD	Average heterozygosity (50k)	SD
901	40	Texas Longhorn cross	Southwestern United States	USA	32.00	100.00	5	5	0.86	0.082	NA	NA
111	41	Corriente	Mexico	Mexico	23.00	−102.00	5	5	0.91	0.034	0.29	0.02
128	42	Romosinuano	Colombia	Colombia	4.00	−72.00	8	8	0.86	0.029	0.27	0.01
106	43	Hanwoo Korean	Asia	Korea	38.50	127.00	7	7	0.86	0.036	0.27	0.00
105	44	Japanese Black	Asia	Japan	36.00	138.00	10	10	0.89	0.021	0.23	0.03
555	45	Santa Gertrudis	Indicine-taurine hybrid (United States)	Brahman/ Shorthorn	NA	NA	24	24	0.68	0.037	0.29	0.01
552	46	Beefmaster	Indicine-taurine hybrid (United States)	Brahman/Hereford/ Shorthorn	NA	NA	24	24	0.67	0.035	0.31	0.01
123	47	Senepol	Africa	Carribean (RedPoll/ N'Dama)	14.00	−14.00	36	37	0.83	0.068	0.28	0.01
500	48	N'Dama	Africa	Guinea	11.00	−10.00	59	59	0.71	0.075	0.21	0.02
222	49	Tuli	Africa	Zimbabawe	−20.00	30.00	4	5	0.64	0.022	0.26	0.01
219	50	Ankole-Watusi	Africa	Uganda	1.00	32.00	5	5	0.45	0.032	0.22	0.01
502	51	N'DamaXBoran	Africa	Ndama/Boran	NA	NA	42	41	0.37	0.024	0.26	0.01
558	52	Sheko	Africa	Ethiopia	8.00	38.00	20	20	0.35	0.030	0.23	0.00
501	53	Boran	Africa	Kenya	1.00	38.00	44	44	0.18	0.022	0.22	0.01
504	54	Nelore	Brazil (via India)	Brazil	−10.00	−55.00	58	60	0.00	0.004	0.15	0.01
503	55	Brahman	United States (via India)	India	20.00	77.00	98	98	0.03	0.028	0.18	0.01
505	56	Guzerat	Brazil (via India)	Brazil	−10.00	−55.00	3	3	0.01	0.006	0.15	0.01
506	57	Sahiwal	India/Pakistan	Pakistan	30.00	70.00	10	10	0.00	0.002	0.15	0.01
507	58	Gir	India	India	20.00	77.00	25	25	0.00	0.003	0.15	0.01

Column labeled "Figure legend" shows label number for Figs. 2 and 3. Sample sizes show the number of individuals included in the analysis after filtering the 50k and 1.8k datasets. "Country" is the country of breed origin or describes the cross for known hybrids. Latitude and longitude coordinates are from CIA World Factbook for the breed's country of origin (1). Average percent taurine was estimated for the 1.8k dataset using STRUCTURE (2) at $K = 2$. Average heterozygosity was calculated for the 50k dataset. NA, not applicable.

1. Central Intelligence Agency (2008) The World Factbook. (Central Intelligence Agency, Washington). Available at https://www.cia.gov/library/publications/the-world-factbook/. Accessed October 5, 2011.
2. Tracy CA, Widom H (1994) Level-spacing distributions and the Airy kernel. *Commun Math Phys* 159:151–174.