



Microsatellite-based analysis deciphers the uniqueness of three lesser-known Indian cattle populations

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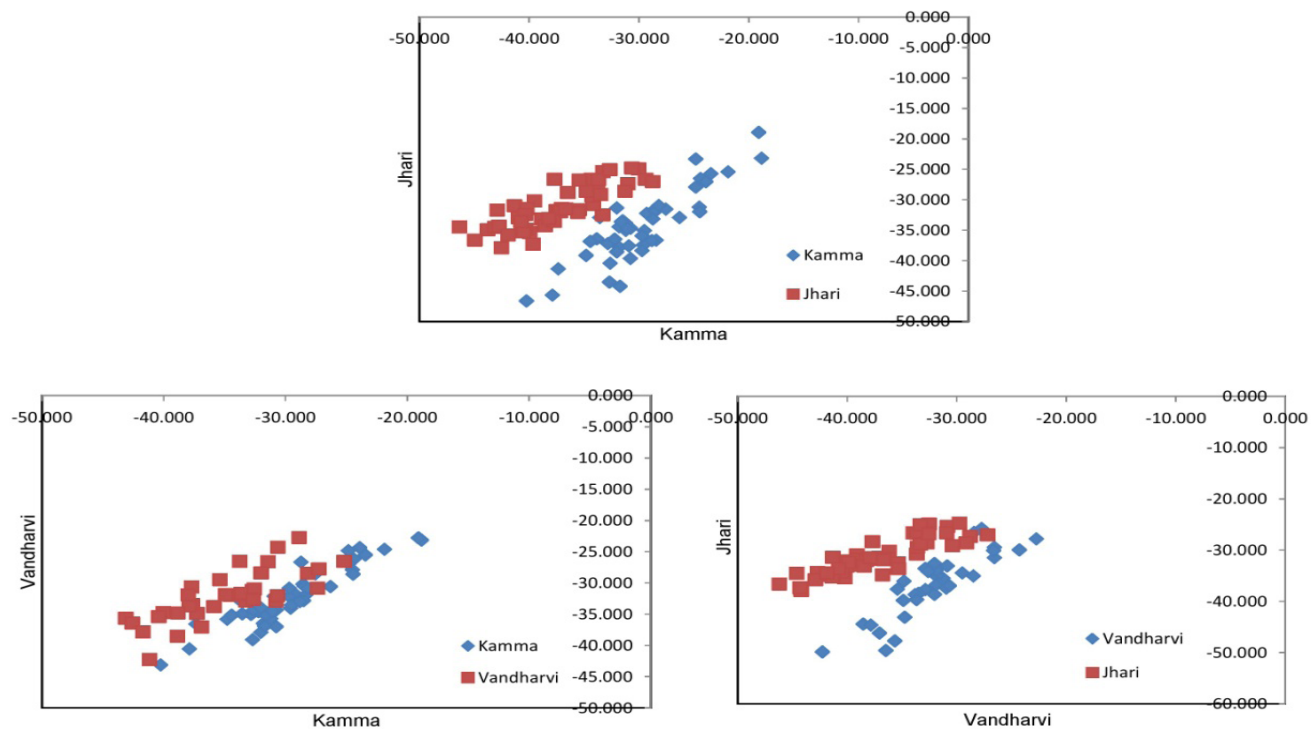
Supplementary Table 1. *F*-Statistics and estimates of gene flow (Nm) for all populations across 25 loci

Locus	F_{IS}	F_{IT}	F_{ST}	Nm
CSSM66	0.008	0.046	0.038	6.288
ETH10	0.188	0.198	0.013	19.640
ILSTS06	0.176	0.203	0.033	7.290
TGLA122	0.064	0.085	0.023	10.678
TGLA227	-0.021	-0.015	0.006	38.746
BM1824	-0.058	-0.046	0.011	21.993
CSSM60	0.024	0.072	0.050	4.799
ILSTS11	-0.083	-0.046	0.034	7.173
INRA05	-0.076	-0.050	0.025	9.948
INRA63	0.008	0.053	0.045	5.295
ETH03	0.020	0.050	0.031	7.836
HEL05	0.521	0.550	0.059	3.954
ILSTS33	-0.125	-0.114	0.010	24.445
INRA35	0.020	0.040	0.021	11.634
ILSTS05	0.014	0.059	0.045	5.271
CSSM08	0.031	0.037	0.007	38.084
CSSM33	-0.036	-0.012	0.022	10.891
TGLA53	-0.052	-0.043	0.008	30.591
CSSM45	0.012	0.031	0.020	12.469
HEL09	0.095	0.141	0.051	4.668
ILSTS54	-0.115	-0.098	0.016	15.801
MM08	-0.061	-0.052	0.009	27.478
MM12	-0.089	-0.084	0.005	54.322
HEL01	0.345	0.458	0.172	1.204
ILSTS34	0.174	0.181	0.009	27.305
Mean	0.039	0.066	0.030	16.312
SE	0.030	0.032	0.007	2.692

Supplementary Table 2. Partitioning of molecular variance within and between cattle populations

Source of variation	d. f.	Sum of squares	Variance components	Percentage of variation	F _{st}	F _{is}	F _{it}	N _m	P
Among populations	2	74.021	0.304	3	0.031*	0.138	0.165	7.744	0.001
Within populations									
Among individuals	128	1372.166	1.303	13					
Within individuals	131	1063.000	8.115	83					
Total	261	2134.479	9.721	100					

*Significant deviation of pair-wise fixation index (F_{ST}) value through 99 permutations from zero ($P < 0.001$); d.f.: degree of freedom.



Supplementary Fig. 1. Population assignment of samples to the populations based on log-likelihood ratio depicting differentiation of population pairs.