Table S6 Cumulative non-exclusion power (1 - Q) calculated for STR considering one and two mismatch criteria (Q_1 and Q_2) in the following cases: two parents known, one parent known, missing parents, and matching samples. Match probability (MP) calculated for matching samples. Markers are listed in order of decreasing gene diversity (h_e). Bold underlined when cumulative 1 - Q reach to 1.0E-4 (Q = 0.999)

Locus Nº	**STR**	**two parents**		**one parent**		**Missing parents**		**Match**		**MP**
		1 - Q_1	**1 - Q_2**	**1- Q_1**	**1 - Q_2**	**1 - Q_1**	**1 - Q_2**	**1- Q_1**	**1 - Q_2**	
1	ETH225	4.1E-01	-	5.9E-01	-	2.3E-01	-	8.0E-02	-	0.07297941
2	BM2113	1.7E-01	6.5E-01	3.5E-01	8.3E-01	5.1E-02	4.0E-01	6.0E-03	1.4E-01	0.00551324
3	TGLA227	8.1E-02	4.0E-01	2.3E-01	6.7E-01	1.5E-02	1.5E-01	**6.0E-04**	2.0E-02	0.00058243
4	TGLA126	3.9E-02	2.3E-01	1.5E-01	5.2E-01	5.0E-03	5.7E-02	7.0E-05	3.0E-03	6.1679E-05
5	RM067	1.9E-02	1.4E-01	1.0E-01	4.0E-01	**8.0E-04**	2.1E-02	7.0E-06	**4.0E-04**	6.9633E-06
6	ETH3	1.1E-02	8.3E-02	7.2E-02	3.1E-01	6.0E-04	9.0E-03	1.0E-06	6.0E-05	9.5781E-07
7	HAUT27	6.0E-03	5.1E-02	5.3E-02	2.5E-01	2.0E-04	3.0E-03	2.0E-07	9.0E-06	1.4179E-07
8	TGLA53	3.0E-03	3.1E-02	3.9E-02	2.0E-01	8.0E-05	2.0E-03	3.0E-08	2.0E-06	2.1429E-08
9	BRR	2.0E-03	1.8E-02	2.8E-02	1.5E-01	3.0E-05	**5.0E-04**	3.0E-09	3.0E-07	2.8508E-09
10	INRA023	1.0E-03	1.1E-02	2.1E-02	1.2E-01	9.0E-06	3.0E-04	4.5E-10	3.6E-08	4.5326E-10
11	BM1824	**6.0E-04**	7.0E-03	1.6E-02	9.5E-02	4.0E-06	1.0E-04	8.0E-11	7.0E-09	7.8866E-11
12	CSRM60	4.0E-04	5.0E-03	1.3E-02	8.1E-02	2.0E-06	5.0E-05	8.0E-11	7.0E-09	1.7891E-11
13	ETH10	3.0E-04	3.0E-03	1.0E-02	6.8E-02	8.0E-07	3.0E-05	4.0E-12	4.0E-10	3.8368E-12
14	BM1818	2.0E-04	2.0E-03	9.0E-03	5.9E-02	5.0E-07	2.0E-05	1.0E-12	1.0E-10	9.9549E-13
15	CSSM66	2.0E-04	2.0E-03	8.0E-03	5.3E-02	3.0E-07	9.0E-06	4.0E-13	4.0E-11	3.5866E-13
16	TGLA122	1.0E-04	1.4E-03	7.0E-03	4.7E-02	2.0E-07	5.0E-06	1.0E-13	2.0E-11	9.3059E-14
17	SPS115	7.0E-05	1.1E-03	6.1E-03	4.3E-02	1.0E-07	3.0E-06	1.0E-13	4.0E-12	3.2339E-14
18	HEL1	6.0E-05	**9.0E-04**	5.9E-03	4.2E-02	1.0E-08	3.0E-06	3.0E-14	3.0E-12	1.8748E-14