Table S4 Exclusion power (Q) estimated for each STR 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 Q values

Locus	two parents	one parent	Missing parents	Match	MP
ETH225	0.5941	0.4152	0.7745	0.9270	0.0730
BM2113	0.5893	0.4103	0.7757	0.9245	0.0755
TGLA227	0.5182	0.3405	0.7022	0.8944	0.1056
TGLA126	0.5175	0.3408	0.7002	0.8941	0.1059
RM067	0.5050	0.3283	0.6915	0.8871	0.1129
BRR	0.4720	0.2851	0.6789	0.8670	0.1330
ETH3	0.4537	0.2811	0.6310	0.8624	0.1376
HAUT27	0.4453	0.2726	0.6342	0.8520	0.1480
TGLA53	0.4395	0.2681	0.6264	0.8489	0.1511
INRA023	0.4273	0.2614	0.6088	0.8410	0.1590
BM1824	0.4004	0.2347	0.5768	0.8260	0.1740
ETH10	0.3637	0.1882	0.5587	0.7856	0.2144
CSRM60	0.3419	0.1814	0.5180	0.7731	0.2269
BM1818	0.3048	0.1524	0.4672	0.7405	0.2595
TGLA122	0.2954	0.1314	0.4767	0.7099	0.3603
SPS115	0.2423	0.1006	0.3929	0.6525	0.3475
CSSM66	0.2074	0.1182	0.3165	0.6397	0.3603
HEL1	0.1272	0.0309	0.2249	0.4203	0.5797