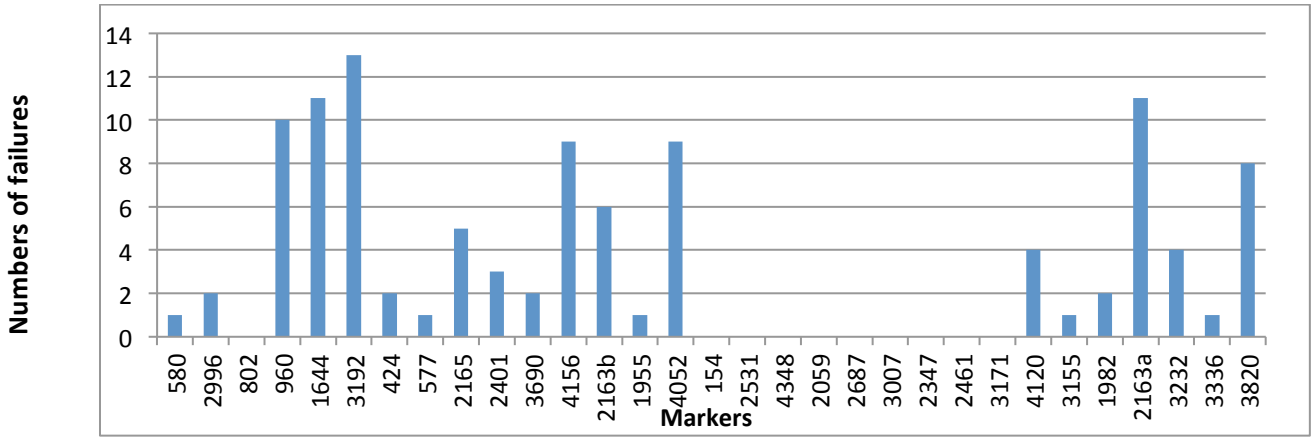
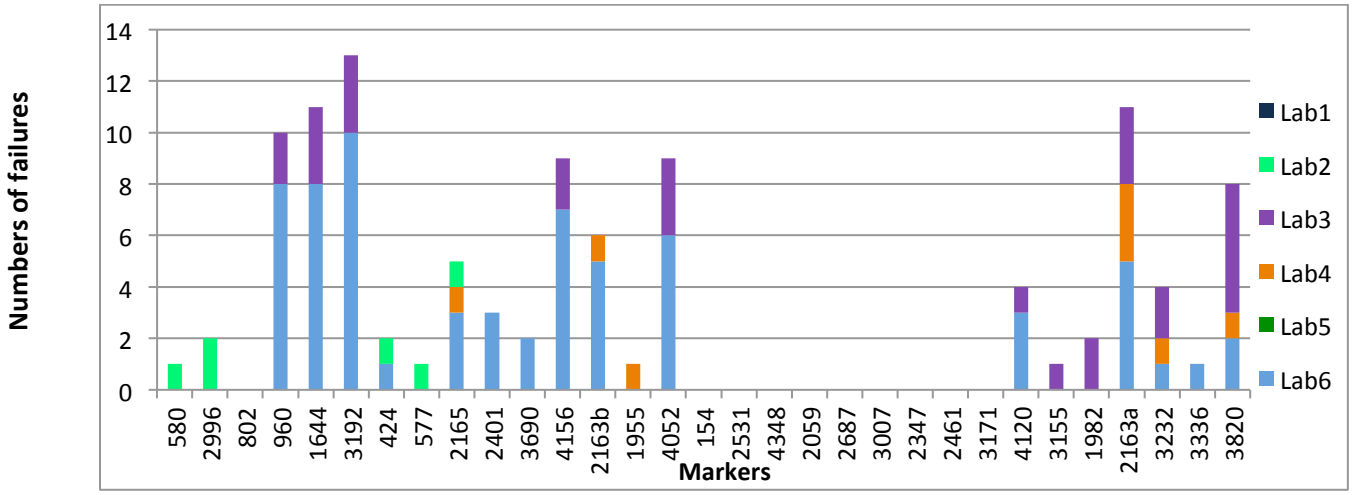
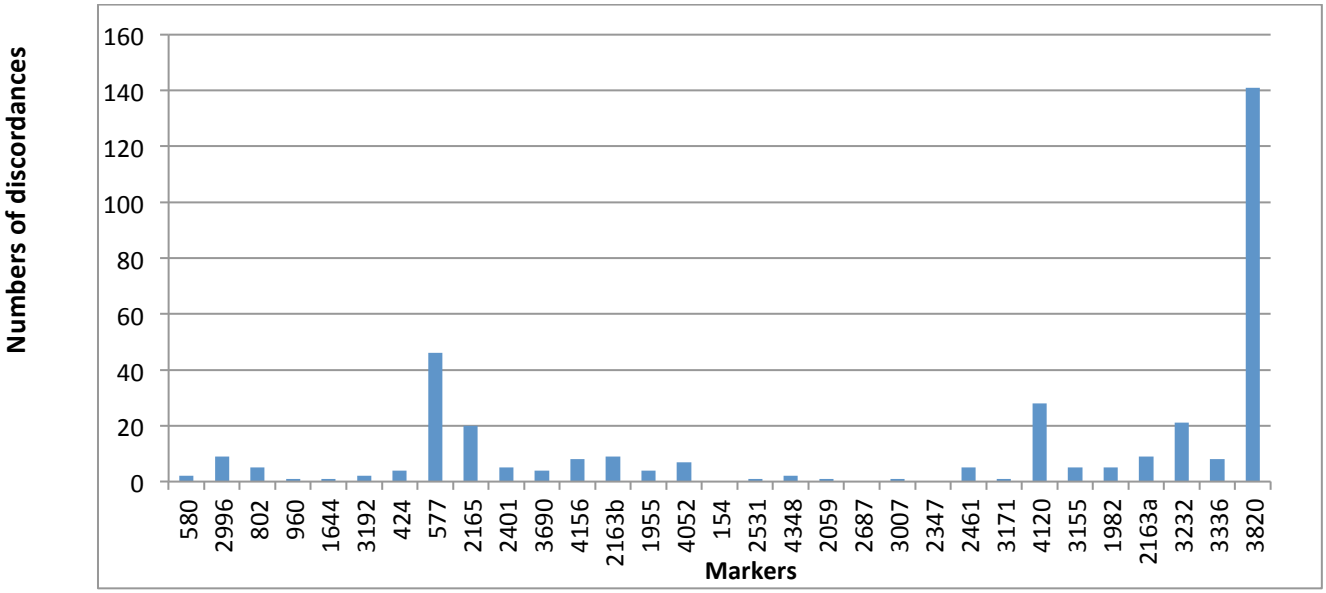
Supplementary information



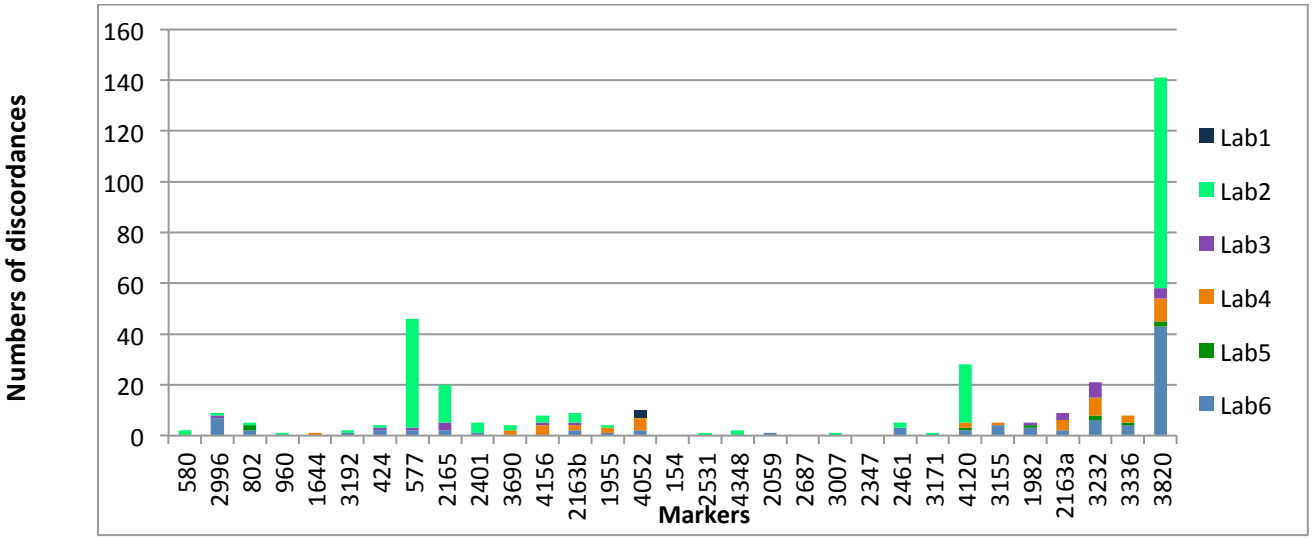
Supplementary Fig. 1a: Typeability of the standard and hypervariable (last seven) markers. Numbers of failures represent the numbers of DNA samples for which an allele of a specific marker was not detected after PCR amplification, on the reproducibility panel of 546 isolates. Note that, for the standard markers, one partner laboratory out of 6 only used the standard 15-locus discriminatory subset, and for the hypervariable markers, typing was done by 5 laboratories out of 6, of which one used only markers 4120 and 3820.



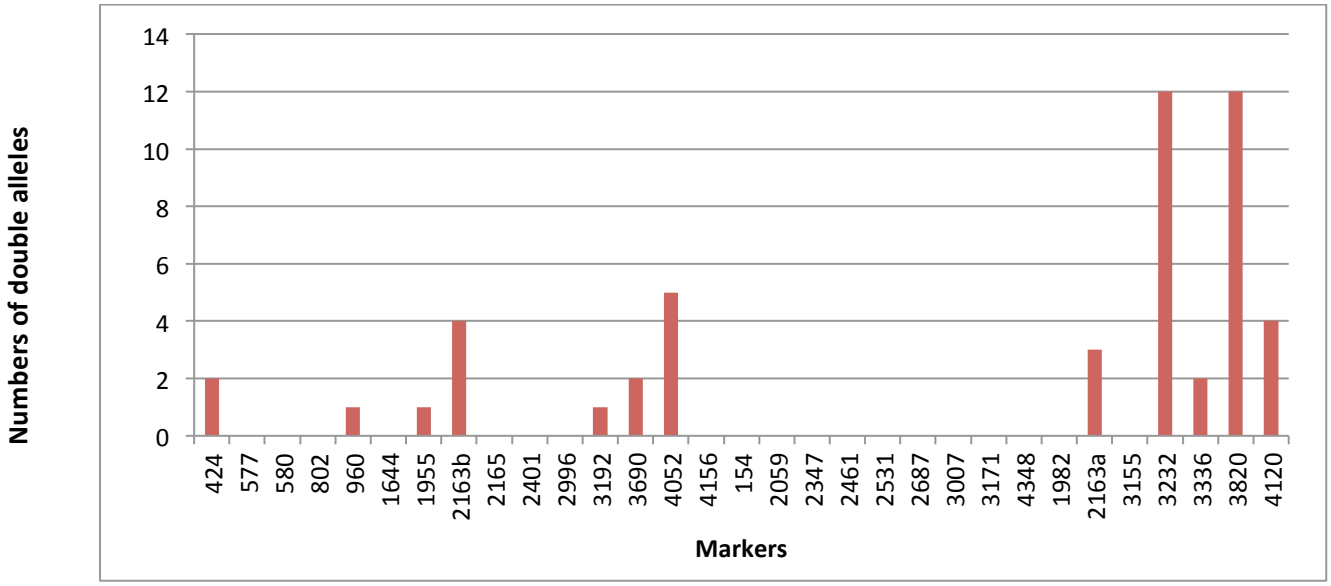
Supplementary Fig. 1b: Typeability of the standard and hypervariable markers (last seven markers). Same as in supplementary Fig. 1a, except that the distribution of failures among the laboratories is shown.



Supplementary Fig. 1c: reproducibility of the standard and hypervariable (last seven) markers. Numbers of discordances per marker represent the numbers of DNA samples for which a discordance was found between Genoscreen and partner laboratories, on the reproducibility panel of 546 isolates. Note that, for the standard markers, one partner laboratory out of 6 only used the standard 15-locus discriminatory subset, and for the hypervariable markers, typing was done by 5 laboratories out of 6, of which one used only markers 4120 and 3820.



Supplementary Fig. 1d: reproducibility of the standard and hypervariable (last seven) markers. Same as in Fig. 1c, except that the distribution of discordances among the laboratories is shown.



Supplementary Fig. 2: numbers of double alleles detected per marker on the global strain panel of 535 isolates.

	Marker																												
Allele	424	577	580	802	960	1644	1955	2163b	2165	2401	2996	3192	3690	4052	4156	154	2059	2347	2461	2531	2687	3007	3171	4348	1982	2163a	3155	3232	3336	3820	4120
0			18												2													3			
1	3			12	27	1	1	1					1				7			4	534	6							1		1
2	10	2	512	10	64	5		14	8	26	1	3	2	12	430	534	527	17	535		1	8		13		5	42	1	1	1	
3s			5																												
3	35	5		498	439	509	10	26	33	5	5	8	469		32	1	1	5		1		510	532	447			7	1			5
4	477	519		15	4	17	100	32	487	504	1	10	57	2	64			512		4		11	3	74	4	1	471	2	9	1	1
5	8	7					402	86	2		111	506	4	2	4			1		518					3	5	12	1	14	1	14
6		1					13	322			25	6		84						5				1	102	66	3	6	3	1	14
7		1					3	38			369			118						2					28	7		10	481	4	8
8							2	7			14	1		280						1					288	15		5	13	3	59
9							1	2			5			23											18	379		22	4	9	51
10											1			8											77	25		16	6	11	314
11														1											6	2		103	1	11	22
12											2																	41		82	13
13							1																		3	1		163		7	8
14s																														1	
14																									5			56		300	7
15																												32		34	3
16s																														1	
16																												22		25	2
17																												8		4	1
18																												5		10	2
19																												4		4	1
20																												2		3	2
21																												2			
22																												8			
23																												1		1	
24																															
25																														6	
Allelic diversity	0,19	0,06	0,08	0,13	0,31	0,08	0,39	0,59	0,15	0,11	0,48	0,10	0,21	0,64	0,33	0,00	0,03	0,08	0,00	0,06	0,00	0,09	0,01	0,28	0,65	0,42	0,22	0,83	0,18	0,63	0,62
No fragment						3		3	4		1				3										1	9		2		2	2
double allele	2				1		1	4				1	2	5												3		12	2	12	4
multi																										5		6		1	1
>1400 bp									1																	12		1			

Supplementary Table 1: Allelic diversities, double alleles and lack of amplification or problematic results observed for the standard and hypervariable (last seven) markers on the global strain panel including 535 isolates. “No fragment” corresponds to no amplification after two independent rounds of PCR. “Double allele” corresponds to two fragments found for one mar ker. “Multi” stands for multi-banded pattern with no clear, typical stutter peak pattern. “>1400bp” indicates fragments with sizes over 1400 bp for which size and allele could not accurately be determined.