Supporting Information

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Table S1. Transfer frequency of the 30 Erm^R insertions

Insertion	Coordinates of the Erm^R Insertion on the NEM316 Chromosome (bp)	Transfer Frequency ($\times 10^{-8}$)	Standard Deviation
I-1	144,753	ND*	—
I-2	297,448	0.11	0.10
I-3	332,423	ND	—
I-4	376,913	ND	—
I-5	656,967	0.17	0.09
I-6	658,284	0.69	0.23
I-7	761,268	2.35	0.56
I-8	818,056	1.25	0.16
I-9	821,759	1.03	0.23
I-10	846,720	0.09	0.09
I-11	967,298	0.06	0.06
I-12	986,348	0.87	0.11
I-13	1,064,640	1.71	0.18
I-14	1,073,073	0.06	0.04
I-15	1,080,795	0.12	0.08
I-16	1,124,410	0.06	0.01
I-17	1,159,993	0.05	0.03
I-18	1,213,207	2.33	0.25
I-19	1,272,413	1.28	0.31
I-20	1,304,385	0.06	0.04
I-21	1,355,312	ND	—
I-22	1,458,647	ND	—
I-23	1,527,989	0.03	0.03
I-24	1,619,215	0.04	0.03
I-25	1,665,129	ND	—
I-26	1,784,976	ND	—
I-27	1,836,262	ND	—
I-28	1,928,182	0.01	0.02
I-29	1,942,706	ND	—
I-30	2,105,767	ND	—

*No transconjugant detected ($<10^{-11}$)

Table S2. Conserved regions among the eight *S. agalactiae* chromosomes

Reference	Region of Low Polymorphism Shared by the Indicated Genome
2603 V/R	
	18RS21
	Region 1: 1348.5–1065.5
	Region 2: 1232.5–1241
	CJB111
	Region 1: 44–173.5
	Region 2: 180–433
	Region 3: 480–494.5
	Region 4: 499.5–674.5
	Region 5: 717-1029
	Region 6: 1232.5–1241
	Region 7: 1348.5–1369
	Region 8: 1608.5–1688
	A909
	Region 1: 154.5–173.5
	Region 2: 180–411
	Region 3: 476–674.5
	Region 4: 698.5–1019
	Region 5: 1348.5–1369
	Region 6: 1494–1728.5
	H36B
	Region 1: 154.5–173.5
	Region 2: 180–411
	Region 3: 459–674.5
	Region 4: 698.5–1019
	Region 5: 1348.5–1369
	Region 6: 1422.5–1435
	Region 7: 1483–1487.5
	Region 8: 1640–1728.5
	NEM316
	Region 1: 1798.5–16.5
	Region 2: 44–53
	Region 3: 297–328.5
	Region 4: 336.5–411
	Region 5: 512–674.5
	Region 6: 717–795
	Region 7: 987.5–1065.5
	Region 8: 1228–1241
	Region 9: 1348.5–1369
	Region 10: 1422–1495
	Region 11: 1507.5–1522
	Region 12: 1541–1572.5
	Region 13: 1678–1688
	515
	Region 1: 1798.5–44
	Region 2: 512–529.5
	Region 3: 534.5–547.5
	Region 5: 599.5–674.5
	Region 6: 987.5–1052.5
	Region 7: 1288–1241
	Region 8: 1348.5–1384.5
	Region 9: 1422–1495
	Region 10: 1507.5–1522
	Region 11: 1547–1572.5
	Region 12: 1678.5–1688
	COH1
	Region 1: 433–438.5
	Region 2: 445–455.5
	Region 3: 599.5–700.5
	Region 4: 947-1019
	Region 5: 1232.5–1335
	Region 6: 1348.5–1369
	Region 7: 1424–1448

Reference	Region of Low Polymorphism Shared by the Indicated Genome
	Region 8: 1499.5–1679.5
	Region 9: 1702.5–1798.5
	Region 10: 2100–2114
	Region 11: 2119–2128.5
18RS21	
	CJB111
	Region 1: 44–173.5
	Region 2: 180–433
	Region 3: 480.5–494.5
	Region 4: 499.5–674.5
	Region 5: 717-1029
	Region 6: 1066–1081
	Region 7: 1103.5–1124
	Region 8: 1232.5–1241
	Region 9: 1348.5–1369
	Region 10: 1608.5–1688
	A909
	Region 1: 154.5–173.5
	Region 2: 180–411
	Region 3: 476–674.5
	Region 4: 698.5–1019
	Region 5: 1124–1132.5
	Region 6: 1157–1167.5
	Region 7: 1342–1369
	Region 8: 1494–1728.5
	H36B
	Region 1: 154.5–173.5
	Region 2: 180–411
	Region 3: 459–674.5
	Region 4: 698.5–1019
	Region 5: 1103.5–1132.5
	Region 6: 1342–1369
	Region 7: 1422–1435
	Region 8: 1483–1487.5
	Region 9: 1640–1728.5
	NEM316
	Region 1: 1798.5–16.5
	Region 2: 44–53
	Region 3: 297–328.5
	Region 4: 336.5–411
	Region 5: 512–674.5
	Region 6: 717–795
	Region 7: 987.5–1081
	Region 8: 1103.5–1167.5
	Region 9: 1232.5–1241
	Region 10: 1348.5–1369
	Region 11: 1422–1495
	Region 12: 1507.5–1522
	Region 13: 1541–1572.5
	Region 14: 1678–1688
	515
	Region 1: 1798.5–44
	Region 2: 512–529.5
	Region 3: 534.5–547.5
	Region 4: 599.5–674.5
	Region 5: 987.5–1052.5
	Region 6: 1069.5–1081
	Region 7: 1124–1132.5
	Region 8: 1157–1167.5
	Region 9: 1232.5–1241
	Region 10: 1342–1384.5
	Region 11: 1422–1495
	Region 12: 1507.5–1522
	Region 13: 1547–1572.5

Reference	Region of Low Polymorphism Shared by the Indicated Genome
	Region 14: 1678–1688
	COH1
	Region 1: 433–438.5
	Region 2: 445–455.5
	Region 3: 599.5–700.5
	Region 4: 946.5–1019
	Region 5: 1103.5–1145.5
	Region 6: 1232.5–1369
	Region 7: 1424–1448
	Region 8: 1499.5–1679.5
	Region 9: 1702.5–1798.5
	Region 10: 2100–2114
	Region 11: 2119–2128.5
CJB111	
	A909
	Region 1: 154.5–411
	Region 2: 480–494.5
	Region 3: 499.5–700.5
	Region 4: 717-1019
	Region 5: 1319.5–1335
	Region 6: 1348.5–1495
	Region 7: 1608.5–1688
	Region 8: 1728.5–1878.5
	Region 9: 2019–2115.5
	H36B
	Region 1: 154.5–411
	Region 2: 480–494.5
	Region 3: 499.5–700.5
	Region 4: 717-1019
	Region 5: 1103.5–1124
	Region 6: 1319.5–1335
	Region 7: 1348.5–1369
	Region 8: 1487.5–1608.5
	Region 9: 1640–1688
	Region 10: 1728.5–1878.5
	Region 11: 2019–2115.5
	NEM316
	Region 1: 44–53
	Region 2: 297–328.5
	Region 3: 336.5–411
	Region 4: 512–795
	Region 5: 987.5–1029
	Region 6: 1065.5–1124
	Region 7: 1232.5–1243.5
	Region 8: 1319.5–1369
	Region 9: 1678–1688
	515
	Region 1: 512–529.5
	Region 2: 534.5–547.5
	Region 3: 599.5–700.5
	Region 4: 987.5–1029
	Region 5: 1069.5–1081
	Region 6: 1232.5–1243.5
	Region 7: 1319.5–1335
	Region 8: 1348.5–1369
	Region 9: 1541–1547
	Region 10: 1678–1688
	COH1
	Region 1: 0–9
	Region 2: 599.5–674.5
	Region 3: 946.5–1019
	Region 4: 1103.5–1124
	Region 5: 1233–1241
	Region 6: 1348.5–1369

Reference	Region of Low Polymorphism Shared by the Indicated Genome
	Region 7: 1608.5–1679.5
A909	H36B Region 1: 1640–459 Region 2: 476-1103.5 Region 3: 1124–1132.5 Region 4: 1184.5–1369 Region 5: 1487.5–1495 NEM316 Region 1: 297–328.5 Region 2: 336.5–411 Region 3: 512–700.5 Region 4: 717–795 Region 5: 987.5–1019 Region 6: 1124–1132.5 Region 7: 1157–1167.5 Region 8: 1311.5–1335 Region 9: 1348.5–1369 Region 10: 1507.5–1522 Region 11: 1541–1572.5 Region 12: 1678–1688 515 Region 1: 512–529.5 Region 2: 534.5–547.5 Region 3: 599.5–700.5 Region 4: 987.5–1019 Region 5: 1124–1132.5 Region 6: 1157–1167.5 Region 7: 1311.5–1369 Region 8: 1507.5–1522 Region 9: 1547–1572.5 Region 10: 1678–1688 COH1 Region 1: 599.5–674.5 Region 2: 946.5–1019 Region 3: 1124–1132.5 Region 4: 1342–1369 Region 5: 1499.5–1679.5 Region 6: 1702.5–1728.5
H36B	NEM316 Region 1: 297–328.5 Region 2: 336.5–411 Region 3: 512–700.5 Region 4: 717–795 Region 5: 987.5–1019 Region 6: 1103.5–1132.5 Region 7: 1311.5–1335 Region 8: 1348.5–1369 Region 9: 1422–1435 Region 10: 1483–1487.5 Region 11: 1678–1688 515 Region 1: 512–529.5 Region 2: 534.5–547.5 Region 3: 599.5–700.5 Region 4: 987.5–1019 Region 5: 1124–1132.5 Region 6: 1311.5–1369 Region 7: 1422–1435 Region 8: 1483–1487.5 Region 9: 1541–1547 Region 10: 1678–1688 COH1

Reference	Region of Low Polymorphism Shared by the Indicated Genome
	Region 1: 599.5–674.5 Region 2: 946.5–1019 Region 3: 1103.5–1132.5 Region 4: 1342–1369 Region 5: 1424–1435 Region 6: 1640–1679.5 Region 7: 1702.5–1728.5
NEM316	515 Region 1: 1547–16.5 Region 2: 218.5–228 Region 3: 443–447 Region 4: 470.5–529.5 Region 5: 534.5–547.5 Region 6: 599.5–700.5 Region 7: 795-1052.5 Region 8: 1069.5–1081 Region 9: 1124–1132.5 Region 10: 1157–1167.5 Region 11: 1228–1335 Region 12: 1348.5–1369 Region 13: 1422–1541 COH1 Region 1: 470.5–503 Region 2: 599.5–674.5 Region 3: 987.5–1019 Region 4: 1103.5–1132.5 Region 5: 1232.5–1241 Region 6: 1348.5–1369 Region 7: 1424–1448 Region 8: 1507.5–1522 Region 9: 1541–1572.5 Region 10: 2100–2114 Region 11: 2119–2128.5
515	COH1 Region 1: 392.5–407.5 Region 2: 470.5–503 Region 3: 599.5–674.5 Region 4: 987.5–1019 Region 5: 1124–1132.5 Region 6: 1232.5–1241 Region 7: 1342–1369 Region 8: 1424–1448 Region 9: 1507.5–1522 Region 10: 1547–1572.5 Region 11: 2100–2114 Region 12: 2119–2128.5

The chromosomal coordinates relative to strain 2603 V/R in kb are indicated. Previously described genomic islands (absent in at least one strain) and ribosomal RNA operons (conserved in all strains) are not taken into account.

Table S3. Bacterial strains and plasmids

Strains and Plasmids	Relevant Genotype and Resistance Profile[*] or Characteristics
Strains	
NEM316	ST23; III; Isolated from neonate[†]
A909RF	ST7; Ia; Isolated from neonate[‡], spontaneous mutant for Rif and Fus
A909RF *recA*$^-$	*recA*$^-$; Tet
BM110	ST17; III; Tet; Isolated from neonate[§]
BM132	ST19; III; Rif, Fus[¶]
304–36	ST67; NT[b]; Bovine mastitis; France
411–07	ST61; NT; Bovine mastitis; France[‖]
553–08	ST2; NT; Goat mastitis; France
CCH268	ST10; III; Carriage, adult; France[‖]
Dak30	ST26; V; Carriage, adult; Senegal
Ban43	ST328; V; Carriage ,adult; Central African Republic
2.22	ST246; Ib; Fish; Israël[**,††]
043–14	ST340; NT; Bovine mastitis; Great Britain
SS1218	ST260; Ib; Bigmouth Buffalo; USA
NEM1575	ST17; III; Neonate; France[‖]
Mad74	ST2; Ia; Carriage, adult; Spain
Ban29	ST188; III; Carriage adult; Central African Republic
CCH263	ST23; Ia; Urine, adult; France[‖]
CCH350	ST23; NT; Blood, adult; France[‖]
Plasmids	
pGhost8	Tet; Thermosensitive derivative of pGK12[‡‡]
pCAM45	Em, Km; ColE1 replicon, thermosensitive derivative of pGK12, Himar1[§§]

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[*] Abbreviations: Em, resistance to erythromycin; Fus, resistance to fusidic acid; Km, resistance to kanamycin; NT, non-typeable; Rif, resistance to rifampicin; Tet, resistance to tetracycline.

[†] Glaser P, *et al*. (2002) Genome sequence of *Streptococcus agalactiae*, a pathogen causing invasive neonatal disease. *Mol Microbiol.* 45:1499–1513.

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[**] Eldar A, *et al*. (1997) Restriction fragment length polymorphisms of 16S rDNA and of whole rRNA genes (ribotyping) of S*treptococcus iniae* strains from the United States and Israel. *FEMS Microbiol Lett* 151:155–62.

[††] Vandamme P, Devriese LA, Pot B, Kersters K, Melin P. (1997) *Streptococcus difficile* is a nonhemolytic group B, type Ib *Streptococcus*. *Int J Syst Bacteriol* 47:81–85.

[‡‡] Biswas I, Gruss A, Ehrlich SD, Maguin E. (1993) High-efficiency gene inactivation and replacement system for gram-positive bacteria. *J Bacteriol* 175:3628–3635.

[§§] May JP, Walker CA, Maskell DJ, Slater JD. (2004) Development of an *in vivo* Himar1 transposon mutagenesis system for use in *Streptococcus equi* subsp. equi. *FEMS Microbiol Lett* 238:401–409.

Table S4. Oligonucleotide primers

Name	Forward Probe	Reverse Probe
Determination of the Erm^R marker insertion		
Himar	CAAACATGAGAGCTTAGTACGTG	AACACACTCTTAAGTTTGCTTC
RecA inactivation		
RecA	GAATTCGGTGATGAACGTCGAAA	GGATCCCATACGAGCTTGCAAAC
gbs1121 inactivations		
gbs1121	GGATCCATGGCAATCTAGCAGAT	GAATTCCCTGCATGCTTGTCCGA
Characterization of transconjugants*		
0183	TTGGCTTATGTCAAAAGGTT	TATGACCAGAGGTCCCTAGA
0235	CGCTACCCTAGTGAGTTGTC	CAGAAACAAGTCGGTCTTTC
0262	ATAAAAGGCGTGCAATTAGA	AACACCAAATTAGCCAAATAA
0286	GATTCAACTTTAGCAGGACG	TTACTCCAAGGGCTATTTCA
0318	CAGAATGGACAGAACCATTT	ACCAAACCACCATAAGAATG
0355	TATTGAAGAAACAAAGCCGT	ATCATAGCGCATACGAGAAT
0358	AATAGCGTTACTGCGGATAC	TTCGTTGATTTTACCTTCTAA
0411	GCTCAAGAATGGTTAGATGG	TTTGCTCCAGACTTTCTCAT
0423	TTAGGTTTTGTAACGGCATT	TCATTTCTTACGTGGTCTGA
0442	CCTGGTACTCATGAACGACT	CTTCAATAACCATCCCCATA
0449	GACATGTGGTGTCCTTGA	AAAGTCTCTATAGCAAACTCCAT
0502	CTTCTCAAAATGAGTCCGTC	GAAACAACTTTCAAACCTGC
0514	TATGGCGTCACAAGACAATA	TGAGTCAGAGACATATTGCG
0535	GGAAAACAAAAGCAAGTTGA	TCACAACATCCAAACGAATA
0542	TGGGTTTTGAATTAGAGGAA	TAGAAATAACGGGAAGACGA
0654	TGAACGCATCTGTTCTATTG	TACCAAAGCTGAGCAGTACA
0674	GAAATTACAGGTCCAGCATC	CTAGCCCTACAACCATTTTG
0684	CTTTAGGAGTTCTGCGTCAC	TTTACCTAATTTGCGATGGT
0743	TCTTTTAATCGATGCTGGTT	TTGCTTAAGTGTCCAAGGAT
0747	GCACTTGAGTCGAGAACAAT	TTTCTGTTGCGATAGCTTTT
0788	TAAAAGGAGCAAGAGATGGA	ATGCCATCTGAACTCATACC
0807	TCAAAATGCGGAATTAGACT	CTAAATCACGCGCTAAATCT
0832	AAAGGCACTCAGTCGTAGAG	TATTTATTGACTGGACGCAA
0864	AACCAGGAGTTGATATGTGG	CATAGTTAGGCACCATAGGC
0890	GAAAAAGAGCGTGCAGTATT	AGCATAAGCTCCGATGATAA
0900	GGACAAGACTACGAACAAGC	TACCGTATTTGTTACGGAGG
0927	CCAGATAAGGGAGATATCGTT	AAAGAGAGCATCAATCGAAC
0930	GTCTAACTGAGCACGGTTTC	CTCCCATACGAGATGCTAAG
0948	CAAAATGGACTTCGTGCTAT	AGAACGACCAGTTTGAGAAA
0968	TCGGTGATATCATTAATTCAAA	AGTTGGGCTAACTTTTGATG
1044	ACTGACGCAAATGAATTTTT	AAAGGCCAATTAATGACAAA
1076	ATCGCCCTTGATTTAGTACA	TCTATTCAAAGACCAGGTGA
1082	TGTCAAAATAGGAATGGAGC	TTTCGTTATAGGTCTTCCCA
1091	GAAGCTTTTCCGGATTTTAT	AGCATGAAAGTCAGCATCTT
1105	CAGAATAACCTTCCAAGTGC	CTTGGTAGACATTGTTGGGT
1108	TTAATCAAGCATTACGGACA	ATAAAAGTCACTTCCGCATC
1163	CAAGCTTATTTTCTCATGTTCA	CACCTTACTTTTGGCGTATT
1167	TCGAAAAAGCTAGTTCCAAA	TGGAGAAAAACTCAAGATGC
1180	TGACAACCGTTTACTTGAGTT	TAGTTGAGGTGCTATTTCGAG
1198	GGAAAACAGCTACAAGTTGG	GCTTCGTAGTCAACATCTGA
1231	GAATCGTTTATCCTCCAAGA	CTACCAAAGAAGCCACGATA
1379	TGAAGAATATCAGTTTCCCG	CCATTTGCCAAGGACTAATA
1410	TTTTGGACACCGTACTTTCT	TGTAAACTAGCAGCATCACG
1445	ATGGAGCAAAAGTCCTGTTA	TTTCTAAATGCAAGATGGGT
1494	CACCTTTTAGACGAACGAAC	AACTCAGCCAAAGTACGTGT
1581	TCAGACACAATTTGGTGGTA	TTGTATCATTTGCACGATGT
1606	GGGTTATCATCACAACGATT	GACCTCAAATGGATTAGCTG
1627	GCTATTGGGGTTAGTGACAG	ATCCTTGTCAGCGTATCCTT
SNP mapping in a collection of 14 additional strains		
0588	CTTCGCTGAATGTTTAGGTT	ATTGCATGTAAATAGCGGTT
0589	TGATGGAAAAGGCTCTCTTA	TTTCACACGTCTATCAACCA
0594	GCTTGCCTTAAACAAATTGA	AATGAAGAGGCCATTACAAC
0595	TTCTTTCCTTACTTGCAGGA	TCTAAAATGATATCCGCAGAA
0596	ACCAAGATGCAACATTCTTT	TTGTTGAATCCTTCAGCTTC
0597	TCAGGCTAAAGATGGAAGG	CATAAGGGATCTCTTCGCTA
0598	CATATTTGGAGACGAGGAAA	TTTGCTGTTTTAGTTGTCCA
0601	GATGTTTCAGCAGGTGTCTT	AAAATTGGCAAGATTATCCA

Name	Forward Probe	Reverse Probe
0602	TTATATTTGGGATTTGGGTG	TGACCCATCGACTAATAAGG
0605	AGGTTTGTTAGTCATGGACG	CACAAAAAGCAATTCCTACC
0608	AGCTTCTACTGGTGAACACG	TACGCCATCTTCAGTACCTT
0610	AGTTACCCGAATTGTTGATG	CCGAATCATGTCCTCAGTAT
0612	CCACAGAGAAGGACAGAAAG	ATGGTATCTGTTCTCGCATC
0615	TTTGGTTTTAGGGATTACGA	TTTTTAGGTTTATCGCCTGT
0628	GCGACTGGAATGAGTATTGT	GTAATTCCAACACAAACGGT
0630	TCGTTTAATTTTCTTAGCGG	CAATGTAAAAACGGTCACCT
0636	TTCCTTATCTTTTAGTGGCG	GTCGTTTTTCCTGAATTTTG
0641	GGATATTGGAGTCGTTTTTG	TCTCCGACTTTCCAATTAAA
0642	TACCTTTTCATGGAGATTGG	TGGATAGTGATATGCGACTG
0645	GAGGACAGGGTAATGTTCAG	AGAAAGAACGGTTGACTTGA
0646	GCAAGAGCTTTACAAGAGGA	TAAAAAGCTTACGAGCCAAG
0653	AGAGGTTCCTGAGCAATACA	TGACAAGAACAACAAAACCA
1019	GCGCTATGGTGTTTATTCTT	CTATAATCGGTTTTTGTGCC
1020	CTTCCAAGTGTTGAAAGAGC	CTACGCAAAGTTTGAAGGTT
1022	AAGCTATCGGACAAATCAAA	TTTTTGCCATAATCTCCAAT
1024	GAAAATTCAGCTCTCACCAC	GAATTTCTGGTTTAACTGCG
1029	GGAAAAGTCTCGATTTGATG	GACTTTTGCCATGCTAATTC
1032	CAAGCTAAAGAAGATTGCGT	CATGTACTACCATGCCACAG
1035	TAATATTAGGGGAGCAAGCA	TCGATAGATAAAGTCCCCCT
1036	CCAACAAGTAACCCAGAGAA	TCTAAAAAGCGGGATACTTG
1038	CCGGTGATTTTATCCATTTA	CAACATCATTTGACGGTGTA
1040	ATGGCAACTACGACAAAAAC	CAACAATGCGATCTAAAACA
1416	TCTGCATCAGGTGTTGATTA	CATCAAAACGATCCATCTCT
1417	ACCGTATGACTAGCGATGAT	TATCAGGCAGACCTTCTAGC
1418	TTATCACGACTTGAGCAAAA	TCAACCGTTATCTGCCTAAT
1419	TTGATTCAGGACCAGTTCAT	ATGCTTCAGCTTTTATTTGC
1421	CTTCCTATCATGAAGCCAAC	TACCATATTTACGCCGTCTT

*According to NEM316 nomenclature.

Table S5. Single-nucleotide polymorphisms in the three highly conserved regions

			Differences Between Allele 1 and Allele					
Probe	Start position*	Length	2	3	4	5	6	7
0588	599,420	300						
0589	600,280	236	G67A					
0594	603,422	423						
0595	604,139	331						
0596	605,367	417	T284C					
0597	606,219	367	A348T					
0598	606,852	443						
0601	609,932	405	A20G A170C C344T A365T	A20G T31C A170C T323C				
0602	611,128	465	T258C	G437A	C290T			
0605	615,553	483	C198T	A55C T277C A364G				
0608	617,548	367						
0610	620,204	389	C41T C87T C121T T217C C233T C256T	G9A G64A A99G T217C C233T				
0612	622,077	346	T144C A184C	T144C T145C C163A C164A C167T A184C	T144C T145C C163A C164A C167T A184C A221G			
0615	625,231	399						
0628	632,057	412						
0630	634,722	506	C162T					
0636	640,250	396	G163A	C333T				
0641	645,426	465	C111T T344C	C50T G63A C111T T122C C224A C239T G314A A349C C452T	C111T T122C A221C C452T			
0642	646,449	484	A25G C27T G50A G76T T87C T218C T361C					
0645	648,699	412						
0646	649,653	429	A109G	T30C A60G A109G				
0653	655,923	410	G211T A267G	A80G G211T A267G	G128A			
1019	993,041	431	T54C	C252T	G50A			
1020	994,087	410	G343A	C375T	C369T			
1022	997,242	465	C244A T257C	T257C C346T				
1024	998,898	407	T103C	A76G T103C A285G	T103C A285G	A76G T103C G219A A285G A373G	A14G A76G T103C G109A C253T A285G	
1029	1,003,946	372	A68G A92T C131T	A92T C131T T221C C252T	A92T C131T G273A	C131T C131T C272T	A92T C131T C242T	
1032	1,005,559	482	T388C G454A	T34C T79A T235C G454A	T34C A59G C202T C205T A386G G454A	T34C C133T G206A T340C		
1035	1,008,192	391	C103T A192T A349G T373C					
1036	1,009,002	382	C110T	T58C G120A A142C G271A	C298T	A31G T58C G120A A142C G145A T217C G271A		
1038	1,010,717	453	G104A G220A	A26G G84A T298A T325C C400T	A26G T123G T325C C451T	T325C	A26G A76G C218A C307T T325C	T244C C307T T325C
1040	1,051,667	360	G247A					
1416	1,356,675	384	G203A	G100T C179T C258T	C258T G311C			
1417	1,357,674	459	C93T	A69G T190C T265C C289T T292G A295G T436C	C47A C221T A295G	A69G A208G A228C A295G		
1418	1,358,567	356	C162A	C162A G139T	C162A T111C	C162A C114A	C162A G192A	
1419	1,359,632	480	G15A, A333G G374A	G15A C312T	C417T	G15A G271C C432T	G15A C32A G271C C432T	
1421	1,362,672	402	T43G C88T G199A A214G G367A C382T	G199A A214G T247C G286A C382T	C244G	C177G G203A C274A C382T	T43G C88T G199A T247C G367A C382T	

*According to strain 2603 V/R coordinates.

Table S6. Alleles of the 37 sequenced loci among a collection of 22 strains

	Allele for Strain																					
Probe	2603 V/R	18RS21	CJB111	Mad74	Tou26	H36B	A909	CCH268	NEM316	CCH350	515	CCH263	COH1	NEM1575	Ban29	Dak30	411–07	304–36	043–14	501–18	2–22	SS1218
0588	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0*	0	0	0	0
0589	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0
0594	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0
0595	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0
0596	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	0	0	0	0	0
0597	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	0	0	0	0	0
0598	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0
0601	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	2	2
0602	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	4	2	2
0605	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3
0608	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0610	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	2	2
0612	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	3	4	4
0615	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1
0628	1	1	1	1	0	0	1	1	1	1	0	1	1	1	1	0	0	0	0	0	0	0
0630	1	1	1	1	0	0	1	1	2	2	0	2	1	1	1	0	0	0	0	0	0	0
0636	1	1	3	1	0	0	3	1	2	2	0	2	1	1	1	0	0	0	0	0	0	0
0641	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	3	1	4	4
0642	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2
0645	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0646	1	1	1	1	1	2	1	1	2	2	2	2	1	1	1	2	1	1	1	3	0	0
0653	1	1	1	1	4	1	1	1	1	1	1	1	1	1	1	1	2	2	2	3	0	0
1019	1	1	1	4	1	1	1	1	1	1	1	1	1	1	1	1	3	3	3	2	1	1
1020	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	3	4	1	1
1022	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	2	3	3
1024	1	1	1	1	2	1	1	1	2	2	2	2	2	2	2	6	3	5	5	4	3	3
1029	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	5	3	3	6	2	4	4
1032	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	5	1	2	2	3	4	4
1035	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2
1036	1	1	1	1	1	1	1	2	1	4	1	1	1	1	1	1	1	1	1	5	3	3
1038	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	7	5	6	6	3	4	4
1040	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1
1416	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	4	3	3
1417	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	5	5	5	3	4	4
1418	1	1	2	6	2	2	2	2	2	2	2	2	3	3	3	3	3	3	3	4	5	5
1419	1	1	1	1	1	1	1	1	1	4	1	1	1	1	1	1	5	5	6	2	3	3
1421	1	1	1	1	4	1	1	1	1	1	1	1	1	1	1	1	2	3	3	6	5	5

*Denotes the absence of the probe.