Supporting Information

Brochet et al. 10.1073/pnas.0803654105

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

PNAS PNAS

Coordinates of the Erm ^R Insertion on the			
Insertion	NEM316 Chromosome (bp)	Transfer Frequency ($ imes$ 10 ⁻⁸)	Standard Deviation
I-1	144,753	ND*	_
I-2	297,448	0.11	0.10
I-3	332,423	ND	_
1-4	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

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 2: 150–411
Region 4: 698 5–1019
Region 5: 13/8 5–1369
Region 6: 1/22 5-1/35
Region 7: 1/83_1/87 5
Region 8: 16/0_1728 5
NEM216
Region 1: 1798 5-16 5
Region 2: 44–53
Region 2: 297-328 5
Region 4: 236 5-411
Region 4: 550.5-411
Region 6: 717-795
Region 7: 987 5-1065 5
Region 9: 1229 1241
Region 0: 1249 E 1260
Region 10: 1422 1405
Region 10. 1422-1495
Region 12: 1507.5-1522
Region 12: 1541–1572.5
Region 13: 1678–1688
Region 1: 1798.5–44
Region 1: 1798.5–44 Region 2: 512–529.5
Region 1: 1798.5–44 Region 2: 512–529.5 Region 3: 534.5–547.5
Region 1: 1798.5–44 Region 2: 512–529.5 Region 3: 534.5–547.5 Region 5: 599.5–674.5
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 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 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 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
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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 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
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: 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 10: 1507.5–1522 Region 11: 1547–1572.5 Region 12: 1678.5–1688 COH1 Region 1: 433–438.5
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 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 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 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 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 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 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

18RS21

	Gei
Region	8: 1499.5–1679.5
Region	9: 1702.5–1798.5
Region	10: 2100–2114
Region	11: 2119–2128.5
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 Decise	1. 154 5 172 5
Region	1: 154.5-1/3.5
Region	2: 180-411
Region	3:4/0-0/4.5
Region	4: 098.5-1019
Region	5: 1124-1132.5 6: 1157 1167 5
Region	0. 113/-110/.3
Region	7. 1542-1509 9. 1404 1729 E
нзев	0. 1494-1720.9
Region	1.15/15_1735
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
NEM31	6
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	b: 1069.5-1081
Region	7: 1124-1132.5
Region	o: 115/-116/.5
Region	9: 1232.5-1241
Region	10: 1342-1384.5
Region	11. 1422-1495
Region	12: 1507.5-1522
region	15. 154/-15/2.5

Reference

CJ	В	1	1	1

	Gen
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	0: 1232.5-1309 7: 1424 1449
Region	7. 1424-1440 8: 1/100 5-1670 5
Region	9· 1702 5-1798 5
Region	10· 2100_2114
Region	11: 2119–2128.5
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	/: 1608.5-1688
Region	8: 1/28.5-18/8.5
Region	9:2019-2115.5
Rogion	1.15/15/11
Region	7: 480-494 5
Region	2.400-404.0
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
NEM31	6
Region	1: 44–53
Region	2: 297–328.5
Region	3: 336.5-411
Region	4: 512-795
Region	5: 987.5-1029
Region	0. 1005.5-1124 7: 1232 5-12/13 5
Region	7. 1232.3-1243.3 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	1.0.0
Region	1:0-9
Region	2: 599.5-6/4.5
Region	3: 946.5-1019
Region	4. 1103.3-1124
Region	5. 1255-1241 6: 13/8 5-1260
negion	0. 1340.3-1303

Reference

	Region 7: 1608.5–1679.5
A909	
	H36B
	Region 1: 1640–459
	Region 2: 476-1103.5
	Region J: 1124-1152.5
	Region 5: 1/87 5-1/95
	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 7: 1311 5-1369
	Region 8: 1507 5-1522
	Region 9: 1547–1522
	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: /1/-/95
	Region 5: 987.5-1019
	Region 6: 1103.5-1132.5
	Region 7: 1311.3-1333
	Region 9: 1/22_1/35
	Region 10: 1/83_1/87 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

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	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	Region 7. 1702.5-1720.5
	515
	Bagion 1: 15/7 16 5
	Region 7: 219 E 229
	Region 2: 218.3-228
	Region 5. 445–447
	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: 2110-2128 5
	Ney1011 12. 2113-2120.3

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

SANG SAL

Strains	
NEM316	ST23; III; Isolated from neonate ⁺
A909RF	ST7; Ia; Isolated from neonate [‡] , spontaneous mutant for Rif and Fus
A909RF <i>recA</i> ⁻	<i>recA</i> ⁻ ; 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; lb; Fish; Israël**, ^{††}
043–14	ST340; NT; Bovine mastitis; Great Britain
SS1218	ST260; lb; 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 ^{§§}

*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.

⁺Tettelin H, et al. (2005) Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: Implications for the microbial "pan-genome". Proc Natl Acad Sci U S A 102:13950–13955.

[§]Stalhammar-Carlemalm M, Stenberg L, Lindahl G. (1993) Protein rib: A novel group B streptococcal cell surface protein that confers protective immunity and is expressed by most strains causing invasive infections. *J Exp Med* 177:1593–1603.

¹Horodniceanu T, Bougueleret L, El-Solh N, Bouanchaud DH, Chabbert YA. (1979) Conjugative R plasmids in *Streptococcus agalactiae* (group B). *Plasmid* 2:197–206.

Brochet M, et al. (2006) Genomic diversity and evolution within the species Streptococcus agalactiae. Microbes Infect 8:1227–1243.

**Eldar A, et al. (1997) Restriction fragment length polymorphisms of 16S rDNA and of whole rRNA genes (ribotyping) of Streptococcus 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 lb *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

Determination of the Ern® marker insertion Himar AcAACATCRAGAGCTTAGTACGTG AACACATCTAAGGTTGCTAAGTACGTG AACACATCTAAGGTTGCTAAGTAGGTT Rec4 inactivation gbs1121 inactivation gbs121 inactivation gbs122 inactivation gbs123 GGATCCATGGCAATCTAGCAGAT GGATTCCGTGGTGGTGCGTGT TAGGACGAGGGGCCATTGGCAAAGGGTG CGTAAGAGTGGCCAATGAGGAGGT TAGGACGAGGGGCCATTGGCAAGGGGG TTAGGCAAGAGGGCCAATGAG 232 GGAACAGGGGCGCAATGAG CGTAAGAGTGGCCAATGAG 235 GGATCAAGTGGCGCAATGAG CGTAAGAGTGGCCAATGAG 235 GGATCAAGTGGCGCAATGAG 235 GGATCAAGTGGCGCAATGAG 236 GGATCCACGGCGGGCGATTGGA 236 GGAACCACGTAGGCGCAATGAG 237 GGAAGAGGGCGCAATGAG 238 GGAACGAGGGCGCAATGAG 238 GGAACGAGGGCGCGCGCG 238 GGAACGAGGGCGCGCGGGCG 238 GGAACGAGGGGCGCGCGGCGG 238 GGAACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Name	Forward Probe	Reverse Probe
ImmarCAAACATGGGGGCTTGGTAGTGGGAACACATCTTAGGTTGCTCRecA inctivationsGAATTCGGTGATGGAACGTGGAAAGGATCCATGGCAGTTGGAACGTGGAACGTGGAACGTGGAACGTTGGCAGGGCTTGCCGAGgb1121 inctivationsGGATCCATGGGCAATGTAGCGAGTGAATTCCCTGGCAGGCTTGGCAGAgb121 cinctivationsTIGGCTTATGTCAAAGGTTTATGACCAGGGGCTCGCAGTgb122 inctivationsGGATCCATGGCAGTGGCGAGTGGCCAGGAACGAGTGGCAGTGGGGTGCCAGTAGGgb123 CinctivationsGGCTACCTGTGTGGAGGTGTTATGACCAGGGGCTTCCCAGTAGGgb124 CinctivationsGGCTACCTGTGTGGGGGTGCGGGGTGCGGCGAGGGGGCGGGGGGGGGGGCGGGGGGGGGCGGGGGGG	Determination of the Erm ^R marker insertion		
Rec4 inactivation Rec4 GATTCGGTGATGGACGTGGAAA GGATTCCGTGCGATGGAAACGTCGAAA GGATTCCGTGCGATGGCAATGGACAGT GGATCCATGGGATGGTGGTGCAGA GGATCCATGGGCAATGAAGGGT CATGCGGATGGTGGTGGCGAGA GGATCCATGGGCAATGAAGGGT CAGAGGGGCCCATGGA GGATCCATGGCGAATGAA GGATCCATGGGCAATGAAGGGT TATGCACCAGAGGGCCCATGA GGATCCATGGGCAATGAAGGGT TATGCACCAGAGGGCCCATGA GGATCCATGGGGATGCA GGATCCATGGGGATGC GGATGGGGTGCAGGGA GGATCCATGGGGATGC TATGCGCAGAGGGGG TATGCCCAGGAGTGGGGATGC TGCCTGCAGGATGGGGGATGC TGCCTGCAGGATGGGGGATGC GGATCGAGGGGGGGGG GGACAGCAGGGGGGGGGG	Himar	CAAACATGAGAGCTTAGTACGTG	AACACACTCTTAAGTTTGCTTC
Reck GAATTCGGTGATGAACGTCGAAA GGATCCATAGGAGCTTGGAACG ght171 GGATCCATGGGCAATTGAGCGAGAT GATTCCCTGGCGATGTGTGCCAACG ght171 GGATCCATGGCGATGTGCCAATGAGCGAGAT GATTCCCTGGCGGTGTGTGCCAACGAGGTGC Characterization of transconjugants* TTGGCTTATGTCAAAAGGTT TATGACCAGAGGTGCTTC 0225 GGATCCACTGTGCGGATGGG TATGACCAGAGGTGCTTC 0268 GATCACGTTGGGGAGAGAGCGTTT ACGAACCACCGTAGGGAGGG 0276 GAGTCGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RecA inactivation		
gbr121 GATTCATGGCATCTAGCAGAT GATTCCTGCCATGCTAGCTGCCA Characterization of transconjugants" TGGCTTATGTCAAAAGGT TATGACCAGAGGTCCCTAGA 023 CGCTACCCTAGGAGATGTC CAGAAACAGAGGTCCCTAGA 0236 GATTCATGTCAAATGGA AACACCAAATTGAGCAGATGAG 0236 GATTCATGTCAATTGAG AACACCAAATTGAGCAAACTGGCCCAATGA 0236 GATTCATGTCAATTGAGAGAGCGGTT CAGAAACGACCAATTA 0237 CACAAACGGCTAACTGAGAACCATT ACCAAACCACCAATGAGAACGAGGT 0238 TATGGCTTAGGTGTCAGGGATACC TTGCTCCAGAGGTGGGTCGA 0239 TATGGCTTGGGTGTCAGTGGG TTTGCTCCAGAGGTGGCGTCAACGGGATACC 0241 GCCAAGGTGGGTGCCTGA AAAGCCCCCCAT 0232 CTGGTTTGGAGTGGGTGCCTGA AAAGCCCCCCAT 0242 CGGGTTAGAAGGCGCACAGGAATA TGGCTTATAGGGGGTCCGCAAGGAACAATT 0322 CGGAAACCAAATGAAGCACAGTGA TGACAACACCCAACGAGGAACACCATT 0324 TGGCTTTGCAAGAAGGCAACGCGT TCACAAACCTCCCAAGGAAGGAACACCATT 0325 GGAAACCAAACGAACACAGCACCATT TCACAAACCTCCCAAGGAAGGAACACCATT 0326 CGAAACCAAACGAACACACGCGTCC TCACAAACCTCCCAAGACGAGTACCATT 0327 TATGGCGTC	RecA	GAATTCGGTGATGAACGTCGAAA	GGATCCCATACGAGCTTGCAAAC
gbr!121 GGATECATEGCANTECATAGCAGAT GCATECCTEGCATECTTECGA 0183 TTGGCTTATGTCAAAAGGTT TATGACCAGAGGTCCCTAGA 0235 CGCTANCGTCAGATTGTC CAGAAACCAGGTCCCTAGA 0245 ATAAAAGGCTGCAGTTGTC CAGAAACCAGCTGGTATTGC 0246 GATCAACTTAGCAAAAGGCT TATCACCAGAGGTATTCAGCAGAATG 0318 CAGAAAGAAGACGCT TATCACCAGAGGCTATTCAGCAGAATG 0319 AATGAGCTTAGGGTAACAA TTGGTCTGAGAACGAGAAGCGT 0319 AATGAGCTTAGGGTAACAATT TTGGTCTGAGAAGAAGCCGT 0319 AATGAGCTTAGGGTAACAATT TTGGTCTGAGAAGAAGCCGT 0314 CGTCGGTAGTCAGGAGAACAATT TTGGTCTGGAAGACAACTTGCAGGGAAGACAATTGCAGACGCCGT 0442 CGTCGGTAGTCAGGAAGACAATT TTGGTCTGAAAGACAATTGCGGTC 0443 CGTCGGTAGTCAGAAGACAATT TTGGACTGGAGACAGAT 0444 CGTCGGTAGTCAGGAAGACAGT TTGGACTGGAGACAGAT 0514 TTGGGCTTGACAAGGACAATT TTGGACTGGAGACAGAGA 0514 TGGACTGGAGAGACGGAAGAATTGGGGA TTGCGTAAGGGAAGACAGAT 0522 TGGACTGGAGGACAGAGAGAGGAGAGATGGGA TTGCGTAAGCTGTAGGGAAGACAGGGA 0534 TGGGGTTGGAGGACACAGGAGAGAGGGAGGAGAGAGGGA <	gbs1121 inactivations		
Characterization of transconjugants* UTGGCTTATGTCAAAAGGTT ATGTCAAAGGGTCCCTAG 223 GCGTACCCTAGTGAGTATGTC CAGAAGGACGTCAATTGGA AAACAGCCAAGTGCGTTTTC ACAACCCAAGTGCGCGATTGGA 228 GATCAACGTAGTATGGCAGAGCG TTACCCAAGGGCTATTGC ACACACCCAATGCAGAGCG TTCCAAGGGCTAGTGG 235 ATGTGGAGAGGCAGGGGCG ATTGAGGCGCAAGGCG TTGCCAAGGCGCAAGGCG TTGCCAAGGCGCAAGGCG TTGCCAAGGCGCAAGGCG TTGCCAAGGCGCAAGGCG TTGCCAAGGCGCAAGGCG TTGCGCCAAGGGCG CTGCCCAAGGGCG CTGCCCAAGGGCG CTGCCCAAGGCG CTGCCCAGGCG CTGCCCAAGGCG CTGCCCAGGCG CTGCCCCAGGCG CTGCCCCCCCCCC	gbs1121	GGATCCATGGCAATCTAGCAGAT	GAATTCCCTGCATGCTTGTCCGA
0183 TTGGCTTATGTCAAAAGGTT TATAAAGGTGCTCAGAT 0235 CGCTACCTAGTGGAGTTGTC CAGAAACAAGTCGGTTATGC 0266 GATTCAACTTAGCAGAGG TTACTCCAAGGGGTATTCA 0318 CAGAATGGACTAGCAGGT ATCACTACTAGGGGTATTCA 0319 CAGAATGGACTAGCAGAACCATTT ACCAAGCACTAGCAGAAAGTG 0319 CAGAATGGACAGAACCAGT TTCGTCCAGAAGTAGCAGAACCAAGTGG 0319 CAGAATGGACTAGGGATAC TTGGTCCAGAAGTAGCAGAACCAGCT 0420 CCTGGTAGTCAGGAGCATT CTCAAAAAGCACTCCCT 0421 CCTGGTAGTCAGGAGCAGT CTCAAATAGCACAACCACCT 0422 CCTGGTAGTCAGGACGACT CTGCAAAAGAATGGGC 0422 CCTGGTAGTCAGGACAGCT CTGCAAAAGAAGTGGC 0423 TGGGTTTGAATGAGGCAGCT CTGCAAACGAATGGA 0424 CCTGGTAGTCAGGACAATT TGGGTCAGAAGGAAGGAAGGAA 0525 GGAAACCAACTTGGTCTGTAG TACCAAAGTCAGACGAAGGAA 0526 TGGAAACAAAGGGCAGTGGA TCACAAAGTCAGACGAGGAGGA 0527 TGGGTTTGAATGGCGCTAC TTTACCAAATGGACGGAGGAGGA 0528 GGAAAACAAGTGGCTGTCGTGTCA TTACCAAAGTCGACGGAGGAGGAATGAC 0494 GACATTACAGGTCGGGCT CTAAATAAGGGCGAAGGAAT 0529 TGGTAAGGGGAATGGAC TTACCAAAGTCGAAGGCGAATCG 0494 GACATTAGGGGAATGGGGCT CTAAATTGAGGGGAATTACGGGGTAACCT	Characterization of transconjugants*		
2235 CGCHACCCTAGTAGTAGT CAAAACAAGTCGTTTT 2622 ATAAAAGGCTGCAATTAGA AAACACAATTAGCCAATAGGAATGGAATAGGAATGGAAGGAATGGAATAGGAATAGGAATGGAATAGGAAGGAATAGGAATAGGAATGGAATAGGAAGGAATAGCAATAGGAAGGA	0183	TTGGCTTATGTCAAAAGGTT	TATGACCAGAGGTCCCTAGA
2622 ATAAAAGGCCTGCAATTAGA AACACCAATTAGACGCAATTAGA 2786 GATTCAACTTTAGACAGGCG TTACTCCAAGGCCTAATTAGA 2787 CAGAATGGAACGAAACCATT ACCACACATAGAGGCTAATGACGCT 2788 AATGCATTATGCGGGATAC TTCGTTGATTTTCACAGGCAT 2789 AATGCATGCGGATAC TTCGTTGATTTCCCCCAACTTCTCLAT 2789 AATGCGTTACTGCGGGATAC TTCGTTGATTTACCAGCCT 2782 TTAGGTTTGTACTGCGGATAC TTCGTTCACACCTTCTCA 2829 GACATGTGTGTCTTGA AAAGTCTCTTAAGGACGTTCGA 2820 CTTCTCAAAAGAAGGACGTC CTCACAAAGCAACTTCCA 2820 CTTCTCCAAAAGGACAGTTGA TCGCGACACAACCTCCC 2821 TAGGGTTTGAATGAGCACTTGA TCGCACAGGACAACTAC 2822 TGGGTTTGAATGAGCACGTC CTAGACCACATACCAGTACA 2823 GGAAAACAAGCACTTGGCT CTAGACCACATACCAGTACA 2824 TGGGTTTGAATGCGTCA TTAGCCCAGGAAGCAGA 2824 TGGGTTTGAATGCGTCA TTGCCTGCGAGAAGCAGA 2824 TGGGTTGCGCCCCCCCCCC TTGCCTGCTGACCATTTGGCGGACAGACGA 2829 CAAAGGCGTCGACACAT TTTCGTGCGAAGGCAACAAT 2820 CAAGGCGAGGAAGACGAT CTGCCAGCGGAAGCGGA 2821 CAAGGCGAGGAAGACGAT CTGCCAGCGGAGGACAA 2822 CAAGGCGAGGAAGACGAT CTGCCAGCAGGCGGACAAGCCGTCACA 2829	0235	CGCTACCCTAGTGAGTTGTC	CAGAAACAAGTCGGTCTTTC
0286 GATTCAACTTTACAGGACGA TATCCAAGGACTATTTC 0318 CAGAATGGACAGAACCATTTT ACCAAACCCATAGGACAATG 0355 TATTGAAGAACAAAACGCGT TICATGACGCATATGCTAGAATG 0411 GCTCAACAATGGTTAGATGGC TICATGACGCATACGGACAATG 0412 CCTGGTACTCATGAACGGCT TTCATTGCCGAAACTCCATA 0423 TTAGGTTTTGAACGGCATT TCTTCATTAACCATCCCCCAA 0424 CCTGGTACTCATGAACGACT TCACATACACGGACAACTCCAA 0429 GACATGTGTGCTCAG AAACTACCTTAAGCAAACTCCAAT 0520 CTTCTCCAAAATGATCCGGTC GAAACAACTTTCAAACCGACT 0521 TGGGATTGCAAATGACGACTG TGCAAACGACATCGACGGTC 0522 TGGGATTGCGGTCACT TTGCACAACGCATTGCG 0524 TGGGATTGCGGTCACT TTGCACAACGCATTGCG 0524 TGGAATGCAACAAGGCCAACTC TCACAACCTCAACCATTGC 0524 TGGAAGTCAGGCGCACAC TTGCACAACGCATTGC 0524 TGGAAGTCAGGCGCACAC TTGCACAACGCTTGCGCGCACGAGACGACGC 0525 TCAAAACGACGCGCACACAGTCGT TTGCTGAACACATTGCGCAAAGACGCGC 0526 CCTTTGGCACAGGCGGCAGGAGGGACGGCACGCGCGCCATATGCCGCAAAGGCCCAAAGGCCCAAAGGCCCAAAGGCCCCAAAGGCGCCAAAGGCCCCAAAGGCGCCAAAGGCCCCATA	0262	ATAAAAGGCGTGCAATTAGA	AACACCAAATTAGCCAAATAA
0218 CAGAARIGBAACGAARCATT AICCARGCACACACT 0255 TATGGAAGAACAAACCAGT TICGTTGGATTTCCACACGT 0256 AATAGGTTACTGCGGATAC TICGTTGGATTTCCACACTTTCCAC 0257 TTAGGTTTGTACTGCGGATAC TICGTTGGATTTACCTTCCACA 0422 CCTGGTACTCATGACGGCAT TICGTTCACACATTTCCACT 0422 CCTGGTACTCATGACAGCAT TTGCTCACACACTTTCCACT 0422 CCTGGTACTCATGACAGCAT TCGACACATTTCCACGTC 0525 GGAAACACAATGAGTTGA TGGGTCACAGAGCATT 0526 CTTCTCAAAAAGCACATTGA TGGGTCACAGAGCAATA 0527 TGGGTTTGAATGAGCGTC GAAACTACACACTCACAGCATC 0528 GGAAACACACTGTGTCTTTG TACCAACGCTGACGTACCACATTTG 0524 TGGAGTTTGCACTGTGTCAC TTACCACACTGAGGAAGCAGA 0535 GGAAACACAGGCTGGTCAC TTACCACATCCAAGCGTGAGCAC 0544 CTTTGGCACACGGCAC TTACCACATCCAAGCGTGAGCACACAT 0545 TTGAACGCGGCACACACAT TTCGTTGCGTGACCACTTTGCGGCAC 0747 GCACTTGGGTGCACCCCTGTGTGT TTGCGTCGACAGCAGCATTGGG 0747 CCACATTGAGCGGAATTGGGA ATGCCACCTAGGCGGAATTGGGGA 0748 TACAAAGGCAGTGCGAACACAAT TTCGCTGCAAGCGGCATAGGACAGGTT 0748 TACAAAGGCAGTGCGAGGAATTGGGG CATTGCTGAAGCGCGGATTAGGCGCACTAGGACGGATTGT 0749 GAAAAAGGCAGTCGAGGAATTGGTT	0286	GATICAACITIAGCAGGACG	
2335IAI TAGAGNAAACUMAGUCGIITICATIGAGUAGUAGUAGU2339AATAGCTATAGTAGCAGUTTICATIGAGUAGUAGUAGU2411GCITAAATGATAGATAGTTTGATIGAGUAGUAGUAGU2423TTAGGTTIFAACGGACTTCATITTACTIFICTA2424CCIGGTAGTCAXGAACGATTCATITTACGTGATCTGA2429GGACATGTGACGACGATTGAGTAGAACAACTCAT2520CTICICAAAAGAGTCCATATGAGAACAACTICAAAACGGAC2522GGAAAAAAGAGTCCAAGACAATATGAGAACAACTICAAACGGACA2523GGAAAAAAGAGTCCAAGACAATATGAGAACAACTACAACGGACA2524TGAGATGAACAAGGTCCAAGCACTCTACCAACACTITAGCGAGAGCA2525GGAAAACAACTICGAACGGTCATTGACAACGGAGAGCAGTAC2526GGAAAGAACGCAGGTCAGTCCTACCAACGCATTAGC2527GGAATGCAAGGTCCAGCGGCACTTGCTAAGGGCAGAGCAGTAC2538TTATAGTGGTGCAGGGCATTGCTAAGGGCAGGGAGT2542TGGAGTGGCGGCACTTGCTAAGGGCAGGGCAG2543TCTTTAACTGAGTGGGCACTTGCTAAGGGCAGGGCAGGCAGCATC2544GGAATGCGGCACACGGCGCACTTGCTAAGGGCCAGGGCAGGCAGCAGTGGT2545TCTTTAACTGGCGCCACTTTGCTTGCGAACCATTTG2646CCTATGGCGGCACACGGCGCACATTAGCCTATCCTATACCGGCAAAGCGCAC2747CCAAATGCGGCAGGCGGCAGGAGGCGCACTTATGCGCCAAATGCGCCACATGGCGCAAAGCGCC2748CTAAATGCGGCAATGAGCGTTCATGCGCCAAAGTGGCCAATGGGCACATGCGGCAATGATGCGCACATGGCGCAAAGTGCGCCAATGGCGCAAAGTGCGCCAATGGCGCAAAGTGCGCCAATGGCGCAATGATGGCACATGGGCAATGATGCGACAATGCGGCAATGATGCGCAACTGCGGCAATGATGCGCAATGGGCAATGATGCGCAACTGCGGCAATGATGCGCAACTGCGCCAATGGGCGCAATGATGCGCCAAGTGCGCCAAAGTGCGCCAAAGTGCGCCAACTGCGCGCAATGATGCCCAAAGTGCGCGCAAAGTGCGCGCAAAGTCCGCGCGAATGATGCGCCAAAGTGCGCGCAAATGCGCGCG	0318		ACCAAACCACCATAAGAATG
D33ALAQUED INCLOSINGITEGLIGATIOND411GCTCAAGAATGGTGATGGGTTIGCTCCAGACTTICCATD422TTAGGTTTGTAACGGCATCTCATTICTTAGGAACTCCATD423GACATGTGGGTCCTCAGAACGGCTCTCACAAACTTICCAAACTCCAAACCGGCD424CCTGGTGATCCTAGAAGCGCTGAAAACCGCCATD502CTTCTCAAAAGGAGTCCGTCGAAAACCGCCATD523GGAAAACAAACAAAGCAAGTTGATCACACACTCCAAACCGAACGAAD524TGGGTTTTGAATTAGGAGAGCACTTATTGTACCACACTCCAAACGGAACCAAATD525GGAAAACCACCTCATTTGTACACACTCCAAACGGAACGAATAD526CTTAGGAGACCCCGTCGTCACATTTGTACCAAAGCGAGCGAATAD527GGAATTACAGGTCCCACCTCTCTTACGAATGGCGAGGAGCGAD528TGAACGCACCCCGTCGTCACTTIGCTTAAGTGCGAGGAGGAD747GCACTTGAGTGAGAACAAATTTICTTAATGGCCGTGGTD747GCACTTGCGGAGACGACAATTTICTTGTCGATACGGCGAGGAGD748TCAAAATGGCGGAATGGGAGGACAATGGGAATGCCCTCTAAACCGCGCTAAATD748TCAAAATGGCGGCAATGGGAATGCCCACTAAGCGCGAAD749GCACTTGGGTGCGTGATTTAGCATAAGCGGAGCAATD749GGACAAGGAGCATCGATCGTGCGAGATTTICTTATGGCGCACTTATD749GGACAAGGAGCATCGATCGTGCGAGATTTATTTGCGGAGCGAAD749GGACAAGGAGCATCGATCGTGCGAGATTATTTATGGCGCACTTATD749GGACAAGGACTCGGTGCATATTAGCATAGGCGCCCTTATD749GGACAAGGACTCGTGGCGCATTATTGGGGCCCATTTGGGCGAGCACTAGGCD749GGACAAGGACTCGTGCGCATTATTGCAGAGCCCACGGAGGACCACCACTTGGGCGCACTTATGGCGCGACCACTAGGCD740GGACAAGGCCCCTGTGCGCCATTATTCCAAGGCCCATTAATGGCGAGCCD741GGGACAAGGCCCTTGTGCGCCACTAGGC	0355		
0411 GL CARDAD ALGOS ITAGGITTAGALGOS 0422 CTGGITTAGALGOSCATT CLARLADALGOS 0442 CCTGGITACTAGAACGACT CTCAATAACCATCCATCACAGCAACT 0442 CCTGGITACTAGAACGACT CATACTATAGCAAACTCAAT 0502 CTTCTCAAAAGAAGTCGAT GGAAAACACAAAGTCGAT 0514 TATGGCGTCACAAGACAATA TGAGACAAATACCGAGAGAACTCAAT 0523 GGAAAACAAAAGCGAAGTGA TCACAACATCACAAGACGAGAGTGA 0542 TGGTTTTGAATTAGAGGACAATG TTAGACTACAGAGACAATACGGGAGAGAGAGAG 0543 TGAACGCACTCGTGTTCTATTG TTACCAAAATACGGGAGAGAGAGAGGA 0544 CTTTAGGAGTTCGGTCAC TTTACCTAAATTGCGAGACTGGT 0747 GCACTTGAGTCGAGCAACTGGAT TTTCGTTGCGGTAC 0748 TTAAAGGCAGAGAAGAAGTGGA ATTGCCTTGAATCACCGCCAAATGGA 0747 GCACTTGAGTGAAGCAGAGAAGTGGA ATGCCATCTGACGCTAAAGCT 0748 AAAGGCACTCAAGTGGAATGGA ATTGCATGTGAGCAAA 0749 GGACAAGACTTCAGTGTGTAGAG TATATGCATGGACCAATAGGC 0749 GCACATGAGCTGATGTGAGAGT CTAAATTGCAGCGCAA 0749 GCACTTGAGTGTATAGAGCC TACGTTGATAGGCAGAA 0747 GCACTTGAGCTGAATGGAATGGAC TTAGTGTAGGCACAAAGCC 0748 AAAGGCACTCAAGTGTGAAGCC TTACGTGTTGAGCGAAA 0749 GCACATGGAGATATGGTT AGGCAGCACAAAGCCTCTGAGGTT	0358	ATAGEGHACIGEGGATAC	
DashTradian modulationDefinition of the constructionD422CCTGGTACTCATGAACGCTTCTTCCAATGACCTTD449GACATGTGGTACTCATGAACGCTCTTCCAATGACATTD449GACATGTGGTACTCAAGACACTTCTACACACTTCCAAAGCCAATCD502CTTCTCAAAATGAGTCCGTCGAAAACCACTTCCAAACGCCAATCGACGATAD514TATGGCGTCACAAGACAATTATGACTCAGAGACATTAGCAACCTGCAD535GGAAAACACAAAGCCAAGTTGATCACAACATTCCAAACGGAACGAATAD542TGGGTTTTCAATTAGAGGACTTAGAAATAACCGGCACAATAD543GGAATTACAGGTCCACCTTTTGTTCCAAAGCTGAGCCAACTAD654GAAATTACAGGTCCAGCATCCTTAGCGATGCGAGCATTTGD747GCACTTGAGTCGACACTTTTTCCTAAGTGTCCAGGTGTD748TAAAAGGAGCAAGACATGGATTGCTAAGTGTCCAACGTTTD748TAAAAGGAGCAGTCGTGGTGAGTATTATTGATGCGCGATAGCGTD747CCAGATTAGCGGAATTAGGCGCTAAATTACGCGCGTAATTD788TAAAAGGAGCAGTCGTGAGAGTATTATTGATGCGGCACATAGCD789TAAAAGGAGCAGTCGTGTGAGGTATTATTGATGGGCGCACATAGCD780GGACAAGACATGCGAATTAGGCCTACGTATTAGCGAGCATAGCD822AAAGGCACTCAGTCGTAGAGCTATCATTAGCGCACATAGCD820GGACAAGACATCGGATTCTCTCCCATACGAGCGACATAGCD820GGACAAGACATCGGACTATTAGCATAGCCGCATAGAGCD820GGACAAGACATCGGACAGACGTACCGTATTTAGCGAGCAGCAGCD820GCTCAACTGAGCACGACGGATTCTCACCATGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	0477		
CHAPCALATCREGTGTCCTTGAAAAGTCTCTAGCAMACTICAT2502CTTCCAAAATGAGTCCTGCGAAACAACTTTCAAACCTGC2514TATGGGCTACAAGACAATGATGAGTTCCAAAGCAGCGACTGC2533GGAAAACAAAAGCAAGCAGTGATCACAACATCCAAGGAGCGA2542TGGGTTTCAATGAGGGAATCACAAACATCCAAAGCAGGAGCGA2644GAAATACAGGGAACCACTGCCTACCAAAGCAGGAGCGA2654TGAACGCATCGTTCTATTGTTACCAAAGCAGGAGCGA2654GAAATACAGGGAAGGAGCGACTTACCAAAGCTGAGCAGTCC26674GAAATACAGGGAAGGAGGAGGAGGAGAGGAGTTCCTTAAGTGTCCAAGGCAGGGGT26784CTTTAGGAGTCTGCGTCACTTTACCTAAGTGCGAGGGGT27895TCAAAAGGGCAAGAGGAGGGGAGGGGATTCCTTAAGTGTCCAAGGGCAAAGCC2789TCAAAAGGCGAGAGGAGGGGAGTGGATTCCTCTCTAACGCCGCAAATG2789TCAAAAGGCGACGAGGAGGGGATGGATTCTTAGCTGGCGCCA2890GGAAAAGAGCTCAGTCGTAGGGATATAGTGTCACAGTGTAGGCGGAA2890GGAAAAGAGCTTCGGGTATTCCCCATAGGCGGAGAAGAGC2890GGACAAGACTCAGTCGTGGACAAGCCTACCGTGTTGTCGGGAGA2990GGAAAAGGCGTCCAGGATTCTCCCATAGGCGAGGAGAGAGGC2983CAAAATGGGACATAGTCGTTCACCGTGTTGTGCGGAGA2984CAAAATGGGACTCAGTCGTGGTATAGAACGACGCGAGTTAGGGGAGGC2985CAAAATGGGAAGAAGCCTTGCGAAAAGCCACGGGAT2986CAAAATGGGAAAGCCACGGGATTTTCCGAAAGTCGCGCACTTGAGG2987CAGAGTAACCTTCCAAGTGGCTTGCGTGAAAGCCACGGTAT2988CAAAATGGAAACCCACAGGGCTTTCGCAAAGACCCGCATTAGGGGT2989GGAAAAACCCAAGGAAGCCCCCTTGTTTGCGAAAAGCCACGCATTGG2989GGAAAAACCCGAAAGCCCCT	0425	CCTGGTACTCATGAACGACT	
S92 CITCICAMAATIGAGICCGTC GAAACAACTITUAAACCIGUC 2514 TATGGCGTACAAAGACAATA TGAGTCAGAACCAATATGCG 2535 GGAAAACAAAGCAATA TCACAACTITCAAACGAATA 2542 TGGGTTITGAATACGGGAA TCACAACGACAACGAAGCAA 2543 TGGACGCAITCGTTCATTG TACCAAACGCAAGCGAGTAG 2544 GAAATACAGGTCCAGCATC CTAGCCATACAACCATTTG 2547 GAAATACAGGTCCAGCATC CTAGCCATACAACCATTTTG 2684 CITTAGCATCATGCTGGTAC TTACTAAGTGCCAGGAT 2747 GCACTTCGATCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	0449	GACATGTGGTGTCCTTGA	ΔΑΔΑΤΟΤΟΤΑΤΑΓΟΔΑΔΑΓΤΟΓΑΤ
614 TATGCCGTCACAGACAATA TGAGTGAGACAATA 6355 GGAAAACAAAGCAAGTGA TGAGTGAGACAATATTGCG 6355 GGAAAACAAAGCAAGTGA TAGAATAATCGGAACAATA 0542 TGGACGCTCATCAGAGGAA TAGAATAATCGGAGGAAGACAAT 0554 TGAACGCATCTGTCTATTG TAGCAAAGCTGAGGAAGACAAT 0554 GAAATAACGGTCCACACACT CTGACCCTCAACACCACTTTG 0674 GAAATAACGGTCCAGCACT CTGACCCTCAAACCACTTTTG 0684 CTTTAGGAGTCTGCGTGAC TTTACCTAAGTCCAAGGGTG 0747 GCACTTGAGTCGAGAACAAT TTTCTGTGTGCAATGACTCCAAGGC 0748 TACAAAAGGGCGGACATGGGA ATGCCATCGAGCCCAAGCGCGAGAGGGAGATGGGA 0788 TAAAAGGACGTGGAGTGGGGGATTAGGC CTACATACGGGCGCAAAGC 0807 TCAAAAGGACGTGGAGTATGTGGG CATAGTTAGCGGGCGCCATAGGC 0832 AAAGGACGTGGAGTGTGGGGGGGGGGGGGGGGGGGGGGG	0502	CTTCTCAAAATGAGTCCGTC	GAAACAACTTTCAAACCTGC
0735GGAAAACAAAAGCAAGTTGATCACAACATCCAAACGCAATA07642TGGATTTTAAATGAGGGAATAGAAATAACGGAGCAGACAC07644GAAATTACAGGTCAGCTCACTTAGCCTACAACCAATTG07674GAACTTACAGGTCAGCTCACCTTAGCCTACAACGCAGTACA0747GCACTTGAGCTGACACGTCACTTGCTTAAAGTGTCCAGGGT0747GCACTTGAGTCGGTACATTGCTTAAAGTGTCCAGGGT0748TAAAAGGAGCAAGAGAGTGGTACCTTAGCCTGTAACTCATACC0747GCACTTGAGTCGAGAGAGAGAGTGGGAATGCCATCGAGCGTAACTT0788TAAAAGGAGCAAGAGAGTGGTAAGGGCTATTTATTGACTGGAGCGAA0790GGACAAGCGAGCAGGGGGCCAGGGGCATATTTATTGACTGGAGCCAA0864AACCGGAGGTGCATATTGTGGCTATTTATTGACTGGAGCCAA0890GGAAAAAGAGCGTGCAGTATTAGCATAAGGAACCTAGAGC0890GGACAAGAAGCGTGCAGTTTAAAGGAGCATCAATAGC0890GGCACAAGCGTGCAGTTTAAAGGAGCGTTCAATGGAAC0890GGCAAAAGGCGTGCAGTTTAAAGGAGCGTTCAATGGAAC0890GGCAAAAAGGGCGTGCAGTTTAAAGGAGCGTTCAATGGAAC0890GGCAAAAAGGGCGTCAGTTGTAAAGGAGCGTTCAATGGAAC0990GGCAAAAAGGGCGTCAGTTTAAAGGAGCGTACATGGAAC0990GGCAAAAAGGGCGCTGATTCTCCCTATGGAGGCTCAATGGAAC0990GGCAAAAAGGGCCCGTTTAAAGGAGCGTACATGGAAC0990GGCAAAAAGGGCCCAATGGCCTCCCCTATGGAGGCTAATGGAAC0990GGCAAAAAGGGCCCCGTTTAAAGGAGCCTACATGGAAC0990GGCAAAAAGGGCCCGTATTCCCCTATGTGGGGTAGCTCGAC0990GGCAAAAAGGGCCCCGTATTAAGGAGGCTACAATGGACCCATGGCT0991GGCAAAACGGCCCCGTATTTAAAGGAGCCACCAGTGGGCCCTTT	0514	TATGGCGTCACAAGACAATA	TGAGTCAGAGACATATTGCG
0542TGGGTTTGAATTAGAGGAATAGAAATAACGGGAAGACGA0654GAAATTACAGGTCAGCATCTGTTCTATTGTACCAAAGCTGAGCAGTACA0654CTTTAGGAGTTCTGCGTCAGCATTTACCTAATTGCGAGCAGTGGT0743CTTTTAATCGATGCCGGTTTGCTTAAGTGCTGCAACGATT0747GCACTTGAGTCGAGGAGCAGCAGCATTGCTTAAGTGCATCGACT0788TAAAAGGGCAAGAGTGGACACAATTTGCTTGAGTGCAACGACTTACC0890GCACTGAGTCGAGGGAGCAGCAGGAGGAGCAGCAGTGGGAATAGCCACTCAGTCGAATCACTACC0891GAAAAGGAGCCAGAGCTGTGAGGGCATAGTTAGGCACCAATGGC0892CAAAAAGGGGGAGAGTGGACGGCACTAGGCTACCGATAGTGGACGGAG0894GAAAAAGGGGGGGAGTTGATATGTGGCAGATAAGCTGCGAGGGG0890GGCAAAGACTACGGGGGGATATGGTTAAGGAGGCACCAATGGGAG0900GGCACAGGGGGGGATATGGTTCACCGGATGTGTAGGGG0927CCAGGATAAGGGGGGGATATCGTTAAAGGAGCACAATGGAG0928CAAAATGGGACTTCATGGCACGGTTTCACCGGATGCTAAG0929GTCTAAATAGGCACCAGTTGGTATAGGAGGACATCAATGGAC0930GTCTAAATAGGACTGGGGCTTCCCCCAGGATGCTAAG0948CAAAATGGACCCGGGTTTAGAGGCAATTAATGACACGAGTGA1044ACTGAGCGAAATGGAGCCTTGCTAAAGGCCAGGTGA1044ACTGAGCGCAAATGGACCCGGGCCTTGCTTAAGGGCTCAACGTGGGGT1045CAGAGTTACTCCCAGTGCCCTGTGTAGACAATGGGGT1046TGCACAATAGCTGCGCCCCTTGGTTAGGCCTGTGTAGACAATGGGGT1047CGCGCTTGCCGGAATGCGCCCCCCGGGGCCCCCGGCGCCATTGACGGGGCTTTGGCTAAGGCGCATTGCCAAAGGCCCGGGCCATTGACGGGGCT1046TGCACACGTTGCCGGGCCCCCCCCGGGGCCCCCGGGCCGCGCGCG	0535	GGAAAACAAAAGCAAGTTGA	TCACAACATCCAAACGAATA
0654TGAAGCATICTGTTCTATTGTACAAAGCTGAGCAGTACA0674GAAATTACAGGTCGAGCATCTAGCCCTACAACCATTTG0674CTTTAGGAGTCGGTCACTTTACCTAATTGGATGGT0743TCTTTTACGATGCTGGTTTGCTTAAGTGTCCAAGGAT0747CGACTTGAGTGAGACAATTTGCTGATGGATAGCTTT0788TAAAAGGAGCAAGAGATGGAATGCCATCTGAATCATACC0807TCAAAAAGGGCAATAGAGATAGGACATGCCATCTGAACTCATACC0822AAAGGGAGTCAGTCGTGGAGTATTATGACTGGACGCAA0864AACGGGGTGGTGGTGATATAGCATAGGGCACCAATGGC0869GAAAAAGGGGGTGGGTGGTGATTAGCATAGGGGAGCACAAGGC0869GGACAAGACTACGACGGTGCAGTATAGCATAGGGCAGCAATAGGC0890GGACAAGACTACGACCAGTCGTCCCGTATTGGGAGG0927CCAGGTAATAGGGAGAGATTGCTAAAGGGAGCTCAATGGC0930GTCTAACTGAGCACGGTTCCTCCATACGGAGAGCACATGAGGAAGAGCC0948CAAAAAGGACTCGTGCTATAGACGACCAATGAGTAAGGAGAGACCCATTGGGC0948CAAAATGGACTTCGTGCTATAAAGGGACATTAGTGACAA0959TGCTAACTGAGCAAGTTGGCCTCGTGTAGTAAGGAGAGCACCTTTGGGT104ACTGACGCAATGAGCGTTGTCAAAGACGACGCATTATGTACA105CAGAATAACCTTCCAAGTGCCTGTGAGACATTGGGGT106TGCACAGATTAGTGCACCTTCCCAAGGGCGCATTATGGGGTTAAGAGGAGCCATACGGTG1163CAGAATACGTTAGTGGGCCTTGGTGAGAAAGCCAGGTGT1164GGGAAAACGCGCTTACGGGCACCTTACCTTGGGGTATTGGGGTTAGTGAGAAAAGCCAGGTTCCCAAGGGCGTATACGGGT1178GGACACGACTTCTCCCAAGGGCCCTTACACGGGTATTTAGTGAGAAAAGCCAGGTACTCTCCG1180TGACCGCTTACCAAGGGGGCGTTACACCGGGTATTTGCACGGAAAAGCGCGTTACCGGGTAGT </td <td>0542</td> <td>TGGGTTTTGAATTAGAGGAA</td> <td>TAGAAATAACGGGAAGACGA</td>	0542	TGGGTTTTGAATTAGAGGAA	TAGAAATAACGGGAAGACGA
0674GAAATTACAGGTCCAGCATCCTAGCCCTACAACCATTTG0684CTITTAGGATGTCTGCGTCAGCTITTACCTAATTGGGATGGT0743TCITTTAATGATGCTGGGTTITGCTTAAGTGCAGGATTGGAT0747GCACTTGAGTCGAGAACAATTITGCTTAGTGCAATGCTTACC0788TAAAAGGAGCGAGAGGATGGAATGCCATTGAGTGAACTCATCC0807TCAAAATGGGGGATTAGACTCTAATTACGGGCTAAATC08082AAAGGACCTAGGTGTGAGAGTATTATGTGGACGGCAA0809GGACAACAGTCGGTGAGAGCATAGTTAGGGACCACATGGC0900GGACAAGCATCGAGCGTTCAAAGGAGCATCAGTGCG0900GGACAAGCATCGAGCGTTCCTCCCATACGGAGGGG0927CCCAGATAAGGGGGCAGCATCCGTTAAAGGAGCATCAATCGAAC0928CAAAATGAGCATCGACGGTTCCTCCCATACGAGACTGAGG0929GTCTAACTGAGCAGCGGTCCGTTAAAGGAGCAATCGAAC0930GTCTAACTGAGCAGCGGTTCCTCCCATACGAGATCGAGG0948CAAAATGGGCAATATCGTTAAAGGGCCAATTATGAA0968CCAGATAATGGACCGGGCTATAAAGGGCCAATTATGACA0968CCAGAATGGCATCAAGGACATTCGTTAGGGCTAACTTTAGTGA1075CGAGAATACCTTCCCCACGGCCCTTGTGTAGGGGT108TTAATCAAGGCATTAATGGACACTCGTGTAGGGGT1091GAAGCTTTTCCGGATTTATAGAGGGCATTCCCA1092CTGCTGAAAAGGGGCCATACAAGGGGCTCGGTGAAGCACTCCCA1093TGACAACCGTTACCAAGGGCACTCGGTGAAGCACTCCCA1094CTGCGCGAAAAGCTCCCCCAAGGGGCCTCGGTGAAGCACTCCCCCATGGGGGGGGGGGGGGGGGG	0654	TGAACGCATCTGTTCTATTG	TACCAAAGCTGAGCAGTACA
0684CTTTAGGAGTTCIGGTCACTTTACCTAATTIGGATGGT0743TCTTTTAATGGATGGTGGTTTIGGTCAAGGGAT0747GCACTTGAGTGCAGACAATTTTCIGTTGGGGTAGGCTTT0788TAAAAGGAGCAATGGAATGCCATTGAAGTCAAACTCATACC0807TCAAAATGGGGAATTAGACTCTAAATGCGGAACAAAT0822AAAGGCACTCAGTGTAGAGTATTTATTGACTGGGCCACAATGGG0854AACCAGGAGTTGATATGTGGCATAGTTGGGCACAATGGG0864AACCAGGAGTTGATATGTGGCATAGTTGGCACCATAGGC0864GCACAGACTCAGTGCAGAGACAAGCTATCGGCATGGTAATAG0900GGACAAGACTCAGGAACAAGCTACCGATTTGGGCAGGAGA0900GGACAAGACTCAGGAACAAGCTACCGATGGGGG0927CCASATAAGGGGGAGATATCGTTAAGAGAGGCATCAGAACAGG0930GTCTAACTGAGCGCAGTGCGTTTCAGCGCAATGGAAGAGCGTTTC0948CAAAAAGGACTTCGTGCTATAGATGGGCCAATTGAGACA0958TCGGTGATATCATTAATTCCGGCATTTCATCAAAGTTGGGCCAATTTGATGACAA1076ATGCCCTTGATTAGGACCTTTGTTATGAAGACCAGGTGA1082TGTCAAAATAGGAATGGAGCTTTGGTAGACATTGTGGGT1183CAAGATTTTCCCGGATTTTATAGGTGAGACATGGTGC1189TGACAACCGTTACTTCGGGTCCTTGGTGAGACATTGTGGGT1180TGACAACCGTTACTTCCAAGGGCCACCTTACTTGGGATTT1181GAAGATTCCGGATTTTTCTGTGAGAGATGGAGGATT1182CAAGCTTATTTCTCCAAGGGCCTACACACGTTGG1183GAAAACCGCAGGACACTACGAGAAACCCCAAGGCACA1180TTGCGTAGACATTGGGGGTATTCTGTGGAGACATGGGA1183GAACACCGCTTTTCCCAAGGGCCTACCAAAGTGCGCATTG1184GGGGAAAACCCGCAGGTTTCCCCGGGGTA	0674	GAAATTACAGGTCCAGCATC	CTAGCCCTACAACCATTTTG
0743TCTTTAACGATGCTGGTTTTGCTAAGGTCCAAGGAT0747GCACTTGAGTCGAGAACAATTTGCTGTGCGATAGCTTT0748TAAAAGGACGAGAGAGAGAGGAATGCCATTGAACTCGTACCC0807TCAAAATGCGGAATTAGACTCTAAATCACGCGCGCAAATGC0832AAAGGACCTCGTGAGAGTTTTTTATGACTGGACGCCAA0864AACCAGGAGTTGATATGTGACGCATACGACCATAGGC0890GGACAAAAGAGCGTCGCAGTATTACGCATAAGCTCCATGATAA0900GGACAAGACTACGAACAAGCTACCGTATTTGTTAGCGGAGGG0927CCAGATAAGGGAGATTAGGTAAGCAGGAGCCACTAAGGC0930GTCTAACTGAGCACGGTTTCTCCCATACGAGACTAAGGAGATTAGTT0948CCAAAATGGACTCCTGCTATAGAACGACCACATTGGAGAA0968TCGGGATATCATTAATTCAAAAGTGGGCCAACTTTGAGAGA0976ATGCGCCCTGATTATATTCAAAAGTGGACCACATTTGAGAGA1076ACTGACGCAATGAGATTAGTCCAAGGCTTCTATTAAAGAGCAGGTGA1076CAGAATAACTTCCCAAGTGCCTGATAAAGCACCAGGTTT108TTAATCAAGCATTAGGAAATCTGAAAAAGTCACTTCCCA1091GAAGCTTTTCCGAGTTACTGACATGGAGAAAAGTCAGCATTTGGGT1163CAAGATTACGTCCAAGGCCTGGTAAAGTTGGGT1164TGAAAAAGCAGTAGTTCCAAGGTCTGCGAAAAGTCCAAGTTCGG1165CAAGCTTTATTCCCAAGGTCTGCGAAAAGTCACAAATTCGGA1167TGGAAAAACCGCTTATTCGAGGTTGGAGAAAACTCGACAATTGGG1168GAACCATTGGGGAAAGTCTGTTTTGGAGAAAACTCGAGTATTCGAGG1169GAACCCGTTATCTCCAAGGGCTTTTGCAAGGAGCAATTGGG1161GAACCCGTTATCTCCAAGGGCTTTGCTAATGGCGAGAAACTCCGAATAGGGAAACCCCAAGGATGCC1163GAATCGTTTATCTCCAAGGGCTTGTGATAAAAG	0684	CTTTAGGAGTTCTGCGTCAC	TTTACCTAATTTGCGATGGT
0747CCACTTGAGTCGAGAACAATTTTCTGTTGCGATAGTTTT0788TAAAAGGAGCAGCAGAGAGTGGAATGCCATTGGAACTCTATACC0807TCAAAATGCGGAATTAGACTCTAAATCACGGGCTAAATCT0832AAAGGCACTCAGTCGTAGAGTATTTATTGACTGGACGCAA0864AACCAGGAGTTGGATTGTGGCATAGTTAGGCACCTAAGC0890GAAAAAGGAGCGTGCAGTATTAGCATAAGCTCGATGATAA0900GGACAAGGACTACGACACAGCTACCGTATTTGTTACGGAGG0927CCAGATAAGGGAGATATCGTTAAGGAGGCTCAATGGAG0930GTCTAACTGAGCAGCACTCGTGCTATAGCAGAGAGCTCAATGGAGC0948CCAAATGGACTTCGTGCTATAGAGCACACGCAGTTTGAGAAA0958TCGGTGATATCATTAATTCAAAAGTGGGCGAATTAGGAGA0968TGGCGCATGGATTAGTAATTGAACATTTGTGAAGACAAGC0976ATGCCCTTGGTTATAAAGGCCAAGTTAGGAGAA0968TGGCAAAATGGACTCGGGTTATAAAGGCCAAGTTAGGCAAATTAGGAATTAGGACTTCCCA1044ACTGGCCGCTGGATTTAGTACATTTGTAAAGGCCAGTGTG105CAGAAATAACCTTCCGGATTTATAGCGCAATAAGCCTCCCA1091GAACCTTCTGCGGATTTATAGCGAAATGACCTCCCA1092TGCAAAATGCCGGATTTTATAGCGACATCATGGGGT1105CAAGCTTATTTCCCGGATTTATAGCGACAACGCCGATT1106TTAATCAAGCATGCTTACTTGAGTTTGGAGAAAAACTCAGGGT11180TGAAACAGCTAGTTACTTAGGGTCTCGTAGGCACAATGTGG1181TGGAGCAAAACGCTAATACTTTCCTGCAAGGGTCAACACTCGGA111111111111111111111111111111111	0743	TCTTTTAATCGATGCTGGTT	TTGCTTAAGTGTCCAAGGAT
0788TAAAAGGAGCAAGAGATGGAATGCCATTGAACTCATACC0807TCAAAATGGGAGCAATTAGACTCTAACTACGGCGCAAATCA0832AAAGGACCTCAGTCGTAGAGTATTTATTGACTGGACGCAA0864AACCAGGAGTTGATATGTGGCATAGTTAGGCACCATAGGC0890GAAAAAGAGGCGTGCAGTATTAGCGATAAGCTCCGACAGGGG0900GGACAAAGACTACGAACAAGCTACCCGTAATTGATGCGAGGG0927CCAGATAAGGGCGGAGATATGCTAAGAGGACCATACTGAAC0930GTCTAACTGAGCAGGGTTCCTCCCATACGAGAGTGCTAAG0938CGACAATGGACTCGTGCTGTAGAAGGACCACATGAGAA0948CGAAAATGGACTCATTAATTCAAAAGTGGGCTAACTTGAGAAA1044ACTGACGCCAATGAATTTTAAAGGCCAATTTAATGACAAA1076ATCGCCTGGATTACTACAATTGTCAAAGACAGGTGCA1082TGTCAAAATAGGAATGGAGCTTTGCTTACAAGACAGGTGA1083TAAACAGCCCTTCTCCAAGTGCCTTGGTAAAGTCAGCATCT1105CCAGATTACGGACAATTAAAAGTCACTCCCGCATC1167TGGAAAAAGCGAGCAATTACGGACAATGAAAGCCACACTTACGGATT1168TTAATCAAGCATTACGGACAATGGAGAAAACTCCAAGTGGC1178CGAAAACGCTACTCCAAGTGGCTTACTACAGACACTCGGACT1167TGGAAAAAGCTGAGTTCCCAAAGTGGAGAAAACTCCAGGTGCA1168TGACAACCGTTATCTCCAAGGACATGCAAGAGGCGCCACATA1169GGAAAACGCTGCTTCCAAGTGGCTTACCAAGGGGCTAATA1160TGACAACCGTTACTTCCCTCCTACTAGCGCACACTCGG1178GGAAACCGCTTCCAAGGTGGGCTACCCAAGGGCCCACATA1180TGACAACCGTTACTTCCCTCCTACTGCGAAGACCACCACTACTA1180GGAAACCGCTCTACACGGGGGGGGGGGGCGGCCCCCCCTACTAGGGGGTGCACACGGTTATTCCCCAAGGGG	0747	GCACTTGAGTCGAGAACAAT	TTTCTGTTGCGATAGCTTTT
0807TCAAAATGCGGAATTAGACTCTAAAATCACGCGCTAAATCT0832AAAGGCACTCACACTGGTGAGATATTTGACTGCGCGCAA0864AACCAGGAGTGATATGTGGCATAGTTAGGCACCATAGGC0890GAAAAAGGCGTGCAGTATTAGCATAAGCTCGATGATAA0900GGACAAGACTACACAGCAAAGCTCCGCTATTTGTTAGGAAGA0927CCAGATAAGGCAGGGTCACTGTAAAGAGAGCATCAATGGAAC0930GTCTAACTGAGCAGGGTTCCTCCACTACGAAGAGC0934CAAAATGGACAGGATTACGTACAGAAAAGGAGCAGCATCAATGGAAC0936GTCTAACTGAGCACGGTTTCCTGCACATAGGAGAGTGCTAAG0948CAAAATGGACATGATATGATAATTCAAAAGTTGGGCTAACTTTTGAGAAA0968TCGGTGATATCATTAATTCAAAAGTTGGGCTAACTTTTGGCAGA1076ATCGCCCTGATTAGTGACATTCATTCAAAGACCAGGTGGA1082TGCAAAATGAGGAATGGAGCTTTCGTTATGGACAAGCAGGTGGA1082TGCAAAATAGGAATGGGACTTTGGTATAGGCACTCCCA1091GAAGCTTTTCCCGGATTTATAGGACAACATGTGGGGG1163CAGAATTACCTTCCAAGTGCCTGGTAGACATTGTGGGGT1164CGGAAAACGTACTTACTGGACATGGAGAAAAACTCAGGATA1178GGAAAAACGTGCTACTTTCTTGGAGAAAAACTCAGGATA1180TGAAGAATACGTTACTGGACCTACCTAAGGAGCCACGATA1181GGAAAAACGCTACAGTTGTATTGCAAAGAGCCACGATA1182GGAAAACGGCTACAGTTGTATTGCAAAGGAGCACACATCTGA1183GGAAAACGCTACAGTTGTATTGCAAGGGGTACACTCTGA1184GGAAAAACGCTACAAGTTGGGCTACCTGAAGGAGCACATCT1185CTGCGGAAAACGCTACAAGTTGGGCTACCTGCAAAGAGGGGTAGT1184CGGCTATACCACAAGATGGGTGGATTGCAAGGAGCACATCGGT1184<	0788	TAAAAGGAGCAAGAGATGGA	ATGCCATCTGAACTCATACC
0832AAAGGCACTCAGTCGTAGAGTATTIATTGACTGGACGCAA0864AACCAGGAGTGCATATGGCATAGTTAGGCACCATAGGC0890GAAAAAGAGCGTGCAGTATTAGCATAAGCCCCGATGATAA0900GGACAAGACTACGAACAAGCTACCGTATTTGTTACGGAGG0927CCAGATAAGGGAGATATCGTTAAAGAGAGCACCAATCGAAC0930GTCTAACTGAGCACGGGTTCCTCCCATAGGAGATGCTAAG0948CAAAATGGACTTCGTGCTATAGGACGACCAATTGAGAA0948CAAAATGGACTTCGTGCTATAGGACGACCAGTTGAGGAA1044ACTGACGCAAATGAATTTCAAAAGTGGGCTAACTTTAGTG1044ACTGACGCAAATGAGACCATTCATAACGAGCAGGGA1076ATGCGCCTTGATTACATTAATTCAAAAGTGGGCTAACTTTAGGGGA1071GAAGCTTTCCGGAGTTTACATTAATAGGACCCAGGTGA1082TGCAAAATAGGAACCTTCCAGAGCCTTGGTAGACATTGTGGGGT1105CAGACTAACCTTCCAGAGCAATAAAAGTCACCTCCGCATC1108TTAATCAAGCATTACGGACAATGAAAAGTCAGCCAGTGT1167TGCGAAAACGCTATCTGAGGCCTTGGTAGACATTCGGGGT1168GAAACCGCTTACTTTGCAAGGAGAAACTCCAAGGTGG1180TGACAAACGGCTATACTGAGGGTTGCAAACCGATTACTGAGGG1181GAATCGTTTATCCTCCAAAGCTTGCTAAGCCAAGATGC1182GGAAAACAGCTACAAGTGGGTTGCAAGAAGCCCAGGAT1183GGAAAACGCTACAAGTTGGGGTTGCAAGAAGCCCAGGATAATA1184GGAAAACGCTACAAGTTTGCGGACTACCAAAGAAGCCAGGATAATA1189GGAAACAGCTAACAGTTTGCGCACTTGCCAAGAGAGCCACTGG1180TTGCACCGTTAACTTATCCTCCAAGGCTTCCAAAGAGCCACTGG1180TGCAGACAACGCTTATCTTGCGGATTGCCAAAGAGCCACGTGC1180GGAAACAGCTAA	0807	TCAAAATGCGGAATTAGACT	CTAAATCACGCGCTAAATCT
0864AACCAGGAGTTGATTATGTGGCATAGTTAGGCACCATAGGC0890GAAAAAGAGGGTCAGTATTAGCATAAGCTCGATGATAA0900GGACAAGACTACGAACAAGCTACCGTATTGTTACGGAGG0927CCAGATAAGGCAGCATCGTTCACCGTATTGGTACGAAGAGCACGGTTC0930GTCTAACTGAGCACGGTTTCCTCCCATACGAGAGTCAAAG0948CAAAATGGACTTCGTGCTATAGGAGGCAACTTTGATG0948CCAGGTAATCATTAATTCAAAAGTTGGGCTAACTTTGATG1044ACTGACGCAAATGAATTTTTAAAGGCCAATTAATGACAAA1076ATCGCCCTTGATTAGGAGCTTTCGTATAGGCATGGTTT1082TGTCAAATAGGAATGCATTTTTAGCATGAGTCCCCA1091GAAGCTTTTCCGGATTTTATAGCATGAGTCCCCA1093CAGAATTAGCACGGTCACTTGGTAGACATTGGTTGGTT1105CAGAATTAGCCACGGTCACTTGGTAGACATTGGTTGGGT1108TTAATCCAAGCATTACGGACAATGAAGCTCCCCAATTGGTGGGT1109TGACAACGCTTACTGAGCACTACCATACTTCGGCATATT1167TGGAAAAAGCCGTTACTTGAGCACTACCAAGAGTCCAAGATGCG1180TGACAACGCTTACTTGAGTTGGAGAAAAACCCACGATA1180TGACAACGCTTACTGAGTTGTCAAAATCCAAGGTCCAAG1180TGACAACGCTACAAGTTGCCCTCCATACCAAGGTCCAAGTCCG1180TGACAACGCTACAAGTTCCGGCCATTTGCCAAGGCGCATATA1180TGACAACGTTACTGAGTTGTCAAACATCCAGGATCT1181TGACAACGTTACTGAGAAGTCCCGGACACTCCAAGCAAGCTCCGGATAATA1182GGAAAACAGCCCTTACTTTTGCAACTGCAGCATCT1184CACCTTTTAGGTTAACGGAACGTACAACTCAGCGCAATACTAG1184CACCTTTTAGGTAAGACGTACGTTGTCAACGCGAGGTCCTTGAGCCAAGTTCT1184CA	0832	AAAGGCACTCAGTCGTAGAG	TATTTATTGACTGGACGCAA
0890GAAAAAGACGTGCAGTATTAGCATAAGCTCCAGATAATAA0900GGACAAGACTACGAACAAGCTACCGTATTITGTACGGAGG0927CCAGATAAGGGAGATATCGTTAAAGAGAGCATCAATCGAAC0930GTCTAACTGAGCACGGTTTCCTCCCATACGAAGACCAATGAAA0948CAAAATGGACTTCGTGCTATAGAACGACCAGTTTGAGAAA0958TCGGTGATATCATTAATTCAAAAGTTGGGCTAATGAATGAAA1076ACTGACCCTTGATTAGATTTATAAAGGCACAGTTGAAGAAAA1076ACTGACCCTTGATTAGATATCATAAAGTTGGGCTAACTGAAAA1076ACTGACCCTTGATTAGATTTAAAGAGCAGCACAGGTGA1082TGTCAAAATAGGAATGGGACTTCTATTGAAGTCTCCCAA1091GAAGCTTTCCGAGATGCGCCTTGGTAAGACATTGGGT1105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTCCCGATG1167TCGAAAAAGCTAGGTTCCCAAATGGAGAAAACTCAGGTGC1183GAAACCGTTTATCTGTCACACCTACTTTGGGGTATTTCGAGT1180TGACAACCGTTTATCTGTGTCACTACCAAAGAGTCCAAGTGG1198GGAAAAACCTCCAAGTTGGCCTTCGTGACACTTCGA1231GAATCGTTTATCTCCCAAGACTACCAAAGAGCCCACGATA1379TGAAGAATATCAGTTTCCTTGTAACTAGCAAGAGTCACGGT1445ATGGAGCAAAAGTCCTGTATTGTAACTAGCAAAGAGTCACGGT1451TCAGACAACTTTTCTTGTAACTAGCAAAGAGTCCTGTA1452ATGGAGCAAAAGTCCTGTATTGCCTTGCAAAGAGAGCCACGGAT1453ATGGAGCAAAAGTCCTGTATTCTTGTAACTAGCAAAGATGCGTGT1454ATGGAGCAAAAGTCCTGTATTCTTGTGAAAATAGCAGTCT1555TTCTTCCTTACTTGCGGAACGACAAATCGAGCAAAGAGTGCTT1569GC	0864	AACCAGGAGTTGATATGTGG	CATAGTTAGGCACCATAGGC
0900GGACAAGACTACGAACAAGCTACCGTATTTGTTACGGAAG09277CCAGATAAGGGAGATTACGTTAAGAGGAGCATCAATCGAAC0930GTCTAACTGAGCACGGTTTCCTCCCATACGAGAGTGCTAAG0948CAAAATGGACTTCGTGCTATAGACGACCAGTTTGATGAAA1044ACTGACGCAAATGAATTCATAATTATTAATTCAAAAGTTGGGCTAACTTTTGATG1044ACTGACGCCATTAATGACAACTCTATTCAAAAGGACCAGGTGA1075ATCGCCCTTGATTTAGTACATTTGTTAAGGTCTTCCCA1082TGTCAAAATAGGAATGGAGCTTTGGTTAAGACATCCGAGCAT1083TTAATCAAGCATTACGGACCAATAGAAGTCAGCATCTT1105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGTGGGT1163CAAGCTTATTTTCCAGTGTCACACCTTACTTTGGCGTATT1167TGGAAAAACGTAGTGCGACATGAGAAAAACCCAGGTGC1180TGACAACCGTTACTTGAGTTTGAGGAAAAACTCAGGTCCATTGGAGT1180GGAAAACAGCTACAGTTGGGGCTTCGTAGTCAACATTCGGA1180GGAAAACAGCTACAGGTGGCTACCCAAGAGAGCCCAGGATT1180GGAAAACAGCTACAGGTGGGCTTCGTAGTCAACACTCTGA1180GGAAAACAGCTACAGTTGGGCTTCGTAGTCAACACTCTGA1180TGCAGACACGTACCAGGTTACTCGGCCATTGGCCAAGGACCCAGGATA1181TGAGGACACAGTACCAGGTTACTCTTGTAAACTAGCCAGGGT1182ATGGAGCACAAATCCGTCTCTTTGTAAACTAGCGAGCTCATCG1184TGCAGGACACAGTTCCGGACAACTCAGCCAAAGTAGCGGT1185TGCAGGACACAGTCCTTGTTTGTACAAGAGAGCCCAGGATCACG1186GGATACCTCTAGGTTACCCGGACAACTCAGCCAAAGTAGCGGGT1187TGAGGACAAAGCTCCTCTATTTGTAAACTAGCAGGATCACGGGT1188GGAGAAACGCTACAGTCGCGAACAGCCCGGACATTGTG	0890	GAAAAAGAGCGTGCAGTATT	AGCATAAGCTCCGATGATAA
0927CCAGATAAGGGAGATATACGTTAAAGAGAGCATCATCGAACA0930GTCTAACTGAGACAGGTTCCTCCACTACGAGATGCTAAC0948CAAAATGGACTTCGTGCTATAGAACGACCAGTTTGAGAAA0968TCGGTGATATCATTAATTCAAAAGTTGGGCTAACTTTGATG1044ACTGACGCAAATGAATTTTTAAAGGCCAATTAATGAAAA1076ATGGCCTTGATTAGTACAAATCTATTCAAAGGCCAATTGATGACAAA1076ATGGCCTTGATTAGTACAATCTATTCAAAGGCCCATTTATGACCAA1082TGTCAAAATAGGAATGGAGCTTTGTTATGGACAACAGGTGA1091GAAGCTTTTCCGGATTTTATAGCATGAAAGTCAGCCACTT105CAGAATTACCTTCCAAGTGCCTGGAGAACATGTGTGGGT1163CAAGCTTATTTCTCATGTTCACACCTTACTTGGGGTATT1167TGGAAAAACGCTACAAGTGGGGTCTGATGCAGAGTGC1180TTAATCAAGCGTTTACTGAGTTTAGGAGGCGTATTTGGGGT1180GGAAAACAGCTACAAGTGGGCTTCGTAGTGCAACACTGAG1180GGAAAACAGCTTACAGAGTGGGCTCCAAAGGACACAGGTAC1198GGAAAACAGCTTACAGAGTGGGCTCCAAAGGACCAGATA1199GGAAAACAGCTTACTTGAGTTAGTGCAAGGCATAATA1199TGAAGCATATCCTCCAAGACTACCAAAGAAGCCCAGGATA1379TGAAGCAAAATGCCTGTATTTGCAAAGGAGCACAGGT1410TTTTGGACACCGTTACTTCTTGTAAACTAGCAGCATGGT1521TCAGGCAAAAGGCCCTGTTATTGCAAGGAGAGGGGT1445ATGGAGCAAAAGTCCTGTATTTGCTCAAAGGAGGGT1450GGTATCATCACACAGAAGGCCCTGTTATTGCATGTAAACTAGGAGGT1581TCAGGACAAATTGGGGAAGGAACATTTGCTGCAAGGGATTAGCTG1582GCTATGCGGAAAGGGCCTCTTATTGCAGCAGGATTAGCTG1583TCTGCGGAAA	0900	GGACAAGACTACGAACAAGC	TACCGTATTTGTTACGGAGG
0930GICLAACIGACACGGITLCICCATAGGACAGGATIC0948CAAAATGGACTCGTCATAGCAACAGACGATGAAA0968TCGGTGATATCATTAATTCAAAAGTTGGGCTAACTTTTGATG1044ACTGACGCAAATGAATGGACTTTAAAGGCCCAATTAATGACAAA1076ATCGCCCTTGATTTAGTACATCTATCAAAAGCCAGGTGA1082TGTCAAAATAGGAATGGAGCTTTGGTTATAGGTCTTCCCA1091GAAGCTTTTCCCGATTTTATAGCACTAAAGTCACCAGTGGT1105CAGAATAACCTTCCCAAGTGCCTTGGTAGACATTGTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTTGCGATT1167TGAAAAAGCTAGTTCCAAGTGCCTGGTAGACATTGGGGT1180TGACAAACGTTACTGAGTTTAGTTAGGGTGCTATTTCGAG1180TGACAACCGTTTACTGAGTTTAGTGAGAGAACCCCGATA1231GAATCGTTACTCCAAGGGCTCGTAGTCAACACTCGGG1410TTTGGACACCGTTACTTGGCTACCAAAGACGCCACGATA1410TTTGGACACCGTACTTTCTGTAAACTAGCAGCATCACG1445ATGGACAAAAGTCACTGTTATTGTAAACTAGCAGGATCACGGT1581TCAGACAAATTCGGAACGAAACACTCAAGCAAAGACTACGGT1581TCAGACAAATTGGAGTAGCAAGAGCACTCAAGCAAAGTACGGGT1589TGATGGAAAAGGCCTCTTTAGACCTCAATGGATACGGGT1589TGATGGAAAAGGCCTCTTATTCAACAGGATACGGT1589TGATGGAAAAGGCCTCTTATTCAAAGGAAGGCCTTACACAA1589TGATGGAAAAGGCCTCTTATTCAACAGGATACCGCA1589TGATGGAAAAGGCCTCTTATTCAACAGGATACCCA1589TGATGGAAAAGGCTCCTTATTCAAAGGAAGGCCATTACACA1589TGATGGAAAGAGGCATTACACAATTGAAATGAAAGGAGCCATTACACC1589TGATGGAAAGAGGCATTACTACACAA	0927		AAAGAGAGCATCAATCGAAC
0948CAAAA IGAACITICS IGCTATAGAACGACCAGITISAGAAA1044ACTGACGCAAATGAACTTCAAAAAGTGGGCTAACTTTTGATG1044ACTGACGCAAATGAAGATGGACTCTATTCAAAAGCCAAGTGA1076ATCGCCCTTGATTTAGTACATCTATTCAAAAGCCAGGTGA1082TGTCAAAAATAGGAATGGAGCTTTCGTTATAGGCATCA1091GAAGCTTTTCCGGATTTATAGCATGAACGAGCATTGCTGGGT1105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGCTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTCCCGACT1163CAAGCTTATTTTCCTATGTCACACCTTACTTTGCGGTT1164TGGACAACGCTTACTGAGGGGTATACATTGCGCAAA1165GGAAAAACGCTACACAGTTCCAAAATGGAGAAAAACTCCAAGATGC1166TGGACAACCGTTTACTTGAGTTTAGTTGAGGTGCTATTTGCGC1167TGGAAAAACGCTACACAGTTGGGCTTACTACAACATCTGA1180TGGACAACCGTTACTTGAGTTTAGTTGAGGGCCATTTGCGC1180TGGACAACCGATTACTGAGTTTAGTTGAGGGCCACGATA1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCCACGATA1379TGAAGAATACCGTTACTTCCTTGTAAACTAGCAGCATCACG1445ATGGAGCAAAAGCTCCTGTTATTTCTAAAGCAGCACGCAACGAT1445ATGGAGCAAAAGCCCTGTTATTTCTAAAGCAGAGTCACG1444CACCTTTTAGCGGGTAGCGGACAACTCAAGCCGAAGTGGT1581TCCAGCACAATTGGGGGTATTGCACGCGAATAGCGGT1582GGTATTCGTCTAAACAAGTCGGAAGATTGCAGCGATACCGCA1589TGATGGAAAAGGCCTCTTATTTCCAACGGCTATCCAACCA0588CTTCGTCTAAACAAATGGAATGAAGAGAGCCATTACCAC0595TCCTTACTCTCAGGGGTTCTAAACAAGGCGAGGAAA0596ACCAAAGAT	0930	GICIAACIGAGCACGGIIIC	
0500TCGGGGAATAGATTAGAATAAAGGGCGAACTAGCAACAAA1044ACTGGGCAACTAATGGAATTTTAAAGGCCAACTAATGGACAAAA1076ATCGCCCTGGATTTAGAACATCTATTCAAAGACCAGGGGA1082TGTCAAAATAGGAATGGAACTTTCGTTATAGGTCTTCCCA1091GAAGCTTTCCCGGATTTATAAGCATGAAAAGTCAGCATCTT1105CAGAGCTTACTGGAGCAATAAAAGTCAGCATCGGGT1108TTAATCAAGCATTACGGACAATAAAAAGTCACGCATCTT1167TCGAAAAAGCTAGTTCCAAGTGCCTTGGTAGACATTGTGGGT1168TTAATCAAGCATTACTGGACAATAAAAAGTCACTCCGCATC1169CAAGCTTATTTCCATGTTCCAAATGGAGAAAAACTCCAAGATGC1160TGACAACCGTTACTTCCATGTCAAATGGAGAAAAAACTCCAAGATGC1180TGACAACCGTTACTTCCCGAAGGCTTCGTAGTCAACACTCGA1198GGAAAACAGCTACCAAGGTGGGCTTCGTAGTCAACACTCGA1199TGAAGATATACGGTTTCCTCTGTGAAGCACCGAATATCGAGT110TTTTGGACGTCTAGGGCCTTCGTAGCCAAGGACCACGATA1110TTTGGACCCGTATCTCCTGTAAACTAGCAAGCACCGATA1110TTTGGACACCGTACCTTTCTTGTAAACTAGCATACGGTT1140TTTGGACACCGAACGATTGACCTCAAAGTAGGGT1144CACCTTTTAGGCGAACACCAACTCAGCCCAAGGACGGGT1151TCAGGCAAAAGTCCTGTTATTGTAACTGGCAGCAGCACGGT1152GCATTTGGGGTTAGTGGAACGATTGCTCTGCTGACGAGACGGCACA1153TCAGGCAAAAGGCCTCTTATTGTAAATGGATAGCGGTT1164CACCTTTAGGGGTTAGTGGAACAGATTGGGTATTGCTGTAAACGAGTGCCTT1175TGAGGAAAAGGCCTCTTAATTTGCACGCTGAACACTGGGT1184TCAGGCAAAAGGCCTCTTAATTTGCACGCTAACACCGGTT1194	0948		AGTIGGGCTAACTITIGAGAAA
DefiACCOCCUTTANTACCOCCUTTANT1076ATCGCCCUTTGATTAGTACATCTATTCAAAGACCGGTGA1082TGTCAAAATAGGAATGGAGCTITTCGTTATAGGTCTCCCA1091GAAGCTITTCCGAATTATAGCATGAAAGTCAGCATCTT1105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACCATCTGGC1163CAAGCTTATTTTCTCATGTTCACACCTTACTTTTGGCGTATT1167TGGACAAACGTTACTGAGATGAGAGAAAACTCAAGATGC1180TGACAACCGTTTACTTGAGTTTAGTGAGGTGCTATTTCGAG1180GGAAAACAGCTACAAGTTGCGACTACCAAAGAAACTCAGAGTGC1180GGAAAACAGCTACAGGTGCGCTTCGTAGTCAACATCTGA1180GGAAAACAGCTACAGGTTGCCGACCACTTGCAAGGACTAACAGCTAGA1180GGAAAACAGCTACAGGTTTCCCGCCATTTGCGCAAGGACTAATA1198GGAAAACAGCTACCAGATTGCGCCATTTGCAGGACTAATA1199TGAAGAATATCAGTTTCCCGCCATTTGCCAAGGACTAATA1100TTTTGGACACCGTACTTTCTGTAAACTAGCAGGACTAACG1180TTTGGACACCGTACTTTCTGTAAACTAGCAGGACTAACG1181TCAGCACAAATTGCGGACCAACGAACTCAGCCAAAGTAGGGT1182CACCTTTTAGACGAACGACCGAACGAACTCAGCCAAAGTAGGGT1183CACCATTTGGGGTACTGGTATTTCTAAATGCAAGAGAGGGT1184GGAGAAACGCTACCGAACGAACGAACTCAGCGAAAAGCCCGGTT1184CACCTTTTAGGGGTTAGCAGGACAGGTAACTCAGGATAACGCGGT1184CACCATTGGGGTTAGTGGGTATTTGCAACGAGTATACCGGGT1184CACCATGGGGTTACTACCAACGGATGACCTCAAATGGAACGGGT1184CACCATGGGGTTAGCACGGGGAAATTTGCAACGACGAGGAACGGTTACAACGCTGCCGAAA	1044	ΔΟΤΘΑΓΑΓΟΑΤΑΤΟΑΑΑ	
1075ATGCCAAAATAGGAATGGAAGCTTTCGTTATAGGCTCTCCCA1082TGTCAAAATAGGAATGGAAGCTTTCGTTATAGGCTCTCCCA1091GAAGCTTTTCCGGATTTATAGCATGAAAGTCAGCACTTT1105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTCCCGATC1163CAAGCTTATTTCTCATGTTCACACCTTACTTTGGGGTATT1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGATGC1180TGACAACCGTTACTTGAGTTTAGTGAGGTGCTATTTCGAG1198GGAAAACAGCTACACAGTTGGGCTTCGTAGTCAACATCTGA1198GGAAAACAGCTACAAGTTGGCTTCCAAAGAAGACCCACGATA1379TGAAGAATATCAGTTTCCCCCCATTTGCCAAGGACCCACGATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGGCACCACGGT1445ATGGAGCAAAAGCTCAGTATATTTCTAAATGCAAGGATCACGG1581TCAGACACCATTTTGGTGGTATTGTAACTAGCAGGATCACGG1606GGGTTATCATCACACGGATGCCTCTGTCAGCGAAGAGGCGT1627GCTATTGGGGTTAGTGACCGAACCTCAGCCAAAGTAGCGGT1627GCGTATTCATCACACGGATGCTCGTGCAGGAACGGAC0588CTTCGCTGAAAGGCTCTCTTATTTCACACGGTATACCTG0589TGATGGGAAAAGGCTCCTTATTTCACACGGTATACCAACA0594GCTTGCCTTAAACAAATTGAAATGAAAAGGCCATTCACCA0595TTCTTCCTTACTTGCAAGAGGCATAAGGGACTTCCTC0598CATATTGGAACAGAGGAGAAGGCATAAGGGAACCTTCCGCTA0598CATATTGGAACGAGGAGAAATTGCTGTTACGCAAGATTACTCGCAAGATTACTCCA0598CATATTGGAACGAGGTGTTTAAAATGCCAAGATTACCCA0598CATATTGGAAGCGAGGAAAATTGCTGTTACGCAAGATTACCCA0	1076	ΑΤΓΑΟΟΟΑΑΤΤΑΑΤΤΤΑ	TCTATTCAAAGACCAGGTGA
InstructureInstructure1091GAAGCITTICCGGATITIATAGCATGAAAGTCAGCACTTT1105CAGAATAACCITCCAAGTGCCITIGGTAGACATTGTGGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTTCCGCATC1163CAAGCITATITTCCATGTTCACACCITACTTTGGCGTATT1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGAGG1180TGACAACCGTTACTTGAGTTTAGTGAGGAGCACACTCAGG1180TGACAACCGTTACTTGAGTTTAGTGAGGTGCACTTGCGAG1180GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAAAATCGAGT1180GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACACTCGAG1180TGACAACCGTTACTCCCAAGACTACCAAAGAAGCCACGGATA1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGGATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCACAGGTGT1445ATGGAGCAAAAGTCGTGTTATTTCTAAAGCAGCACAGGTGT1494CACCTTTGGAGCAAACGCTGTTATTGTATCATTGCAGGATAGGGT1494CACCTTTTGGGGTAACTGACCTCAAAGTAGCTGGT1581TCAGACACAATTGGTGGGTATTGTATCATTGCAGGATAGCTG1606GGGTTATCATCACAACGATTGACCTCAAATGATAGCTG1627GCTATTGGGGTAAGTTTAGGGTTATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTAGGGTTATTGCATGTAAATAGCGGGTT0589TGATGGAAAAGGCCTCTTACTTTGTAAAGAGGGCCATTACAAC0594ACCAAGATGCAACAATTGAATGGAAGGGCATTACCAACGAA0595TCTTCCTTACTTGCAGGACTTCAAGGGATCTCTCGCGAGAA0596ACCAAGATGCAACAATTGTTTTGTGGATACCTCCAGGTT0597TCAGGCTAAACGGAGGGAGAATTTGCGTTTTAGTTGTCCA0598CATATTGGGACACAGGGGAAATTT	1082	TGTCAAAATAGGAATGGAGC	TTTCGTTATAGGTCTTCCCA
105CAGAATAACCTTCCAAGTGCCTTGGTAGACATTGTTGGT1108TTAATCAAGCATTACGGACAATAAAAGTCACTTCCGCATC1163CAAGCTTATTTTCTCATGTTCACACCTTACTTTGGGTATT1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGATGC1180TGACAACCGTTACTTGAGTTTAGTGAGGTGCTATTTCGAG1180TGACAACCGTTACTTGAGTTTAGTGAGGTGCTATTCGAG1198GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACATCTGA1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGATA1379TGAAGAATATCAGTTCCCGCCATTTGCCAAGGAGCACACAGTGG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1581TCAGACACAATTGGTGGTGATATTGTATCATTTGCAGCGATGGGT1627GCTATTGGGGTTACCACCAAGTTGACCTCAAATGGATAGCTG5NP mapping in a collection of 14 additional strainsCTTCGCTGAATGGAACGAGTATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTAGGTTATTGCATGTAAATAGCGGTT0594GCTGCCTTAAACAAAGTGCTCTTTATTTCCAAATGGATAACCACA0595TTCTTTCCTTACTTGCAGGAACTAAAAGGGCCCATTACAACA0596ACCAAGATGCAACATTTGGAAGTTGTAGAAGAGTCCTTCGCAGAA0597TCAGGGCTAAAGAGGCAGAGAAATTGCTGCTGCAGCGTA0598CATATTGGAGACGAGGAGAAATTGCTTGCTGCAGCGTAC0598CATATTGGAGGACGAGGAAAATTGCTTGCTGCAGCAGAA0596ACCAAGATGCAACAGAGGAGGAAATTGCTTGCTGCAAGCAGACCACACCACA0597TCAGGCTAAAAGGAGGCAGAGGAAAATTGCGTTTAGCTCAACAGAATTGCCA0601GATGTTCACACGAGGAGGAAAAACCGAGGGGAAAATTGCGTTTAGCTCAACAAATTGCAAAATTCCAACAAATTGCAAAT	1091	GAAGCTTTTCCGGATTTTAT	AGCATGAAAGTCAGCATCTT
1108TTAATCAAGCATTACGGACAATAAAAGTCACTTCCGCATC1163CAAGCTTATTTTCCATGTTCACACCTTACTTTGGGGTATT1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGATGC1180TGACAACCGTTTACTTGAGTTTAGTIGAGGTGCTATTCGAGG1180GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACACTCTGAG1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGATA1379TGAAGAATATCAGTTCCCGCCATTTGCCAAGGAGCCACGGT1410TTTGGACGCGACACGTACTAGTTGTAAACTAGCAGCATCGGGT1494CACCTTTTAGACGAACCGTACTGTTATTTCTAAATGCAAGATGGGGT1581TCAGACACAGTTAGTAGCAGCATAGGCTCCTAAGTGAGTAGGGT1627GGCTTACTACACAAGAGTGGGGTATTGTATCATTTGCAGGATGAGG1627GCGTTATCATCACAACGATTGACCCTAATGGAGTAGGGT1627GCTATCGGGGTTAGTGGACAGATTGCATGTAAATAGCGGTT588CTTCGCTGAAGGTTAGTGGACAGATTGCATGTAAATAGCGGTT0588CTTGCTGAAAGGCTCTTTATTTCACAGCGTATCAACCA0594GCTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAACCA0595TCCTTCCTTACTTGCAGGATCTAAAATGAATACCGCGTT0596ACCAAGATGCAAATGGAAAGGCCATAAGGGACTCTCTA0597TCAGGCTAAAGGAAGGAAGGATTGCTGTAAGTGCTA0598CATATTGGAGACGAGGAGAATTGCGTGTTTAGGTGTCCA0601GATGTTCAGCAGGTCTTAAAATTGCCAAGATTACCAA0601GATGTTCAGCAGGTCTTAAAATGGAATGCCAAGATTACCAA	1105	CAGAATAACCTTCCAAGTGC	CTTGGTAGACATTGTTGGGT
1163CAAGCTTATTTTCTCATGTTCACACCTTACTTTGGCGTATT1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGATGC1180TGACAACCGTTTACTTGAGTTTAGTTGAGGTGCTATTTGGAG1198GGAAAACGCTACACAGTTGGGCTTCGTAGTCAACACTCTGA1231GAATGCTTTATCCTCCAAGACTACCAAAGAAGCACCACGATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCAGCACGGA1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGAGTACGGGT1494CACCTTTAGACGAACGAACAATCCAGCCAAAGTGGGT1581TCAGACACAATTTGGTGGTATTGTATCATTGCAGGATGAGTG1606GGTTATCATCACCACGATTGACCTCAAATGGGTT1627GCTATTGGGGTTAGTGACAGATCCTTGCAGGGTTAGCGTGSNP mapping in a collection of 14 additional straimsCTTCGCTGAATGTTAGGTGTATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTTAGGTGTATTTGCACGGTATACACCA0595TCTTCCTTACTTGCAGGAATTGCATGTAAATAGCGGTT0595TCTTCCTTACTTACTGCAGGAAATGAAGAGGCCATTACACA0596ACCAAGATGCAAACAGATTGTTTGTGTGAAATGCGCTAT0597TCAGGCTAAAGGAGGACAAAGGGCATAAAGGAGTCTCTTGCAGCTA0598CATATTTGGAAGAGGAGGAAAATTGCTGTTAGGTATATCCGCA0598CATATTTGGAAGAGGGCAACAATTGTATTGCTGTTTAGGTAGTACCA0598CATATTTGGAAGAGGAGGAAAACATAATGGCAATATCCGCAA0598CATATTTGGAAGCGAGGAAAATTGCTGTTTAGGTTGTCCA0598CATATTTGGAAGCGGGTGTCTTAAAATGGCAAGATTATCCA0598CATATTTGGAAGCGGGGTGTCTAAAATGGCAAGATTATCCA0598CATATTTGGAAGCGGGGGGTGTCTAAAATGGCAAGATTATCCA0598CATATTGGAAGCGGGGTGTCT <td>1108</td> <td>TTAATCAAGCATTACGGACA</td> <td>ATAAAAGTCACTTCCGCATC</td>	1108	TTAATCAAGCATTACGGACA	ATAAAAGTCACTTCCGCATC
1167TCGAAAAAGCTAGTTCCAAATGGAGAAAAACTCAAGATGC1180TGACAACCGTTTACTTGAGTTTAGTTGAGGTGCTATTTCGAG1198GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACATCTGA1231GAATCGTTTACTCCCAAGACTACCAAAGAAGACCCACGATA1379TGAAGAATATCAGTTTCCTCTGTAAACTAGCAGCATCACG1410TTTGGAGCACCGTACTTTCTTGTAAACTAGCAGCATCACG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGT1606GGGTTATCATCACACAGATTGACCCTCAAATGGATTAGCTG1627GCTATTGGGTTAGTGACAGGATTGCATGTAACTAGCGGTT5NP mapping in a collection of 14 additional strainsCTTCGCTGAATGGTTATTGCATGTAAATAGCGGGTT0589CTTCGCTGAAAAGGCCTCTCTTATTTCCACAGGTCAATACACAA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCCATTACAAC0595TTCTTTCCTTACTTGCAGGAATCTAAAATGATATCCGCAGAAA0596ACCAAGATGCAAACATTCTTTTGTGAAGATATCCTCAGCAGAA0597TCAGGCTAAAGAGGGGAAAATTTGTGTAATCTTCGCTG0598CATATTTGGAGAGAGAGAAATTGCTGTTTAGTTGCCA0601GATGTTCCAGCAGGTGTCTTAAATTGGCAAGATTCTCA	1163	CAAGCTTATTTCTCATGTTCA	CACCTTACTTTTGGCGTATT
1180TGACAACCGTTTACTTGAGTTTAGTTGAGGTGCTATTTCGAG1198GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACATCTGA1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGATA1379TGAAGAATATCAGTTTCCCGCCATTTGCCAAGGACTAATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCACGGT1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGTG1606GGGTTATCATCACAAGGACCAAGTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCGCTGAATGGTATCATCAGCGATCCTGSNP mapping in a collection of 14 additional straimUTCGCTGAATGTTAAGCTGTTTCCACACGTCTATCAACCA0588CTTCGCTGAAAGGTTCTCTTATTTCACACGGTATACAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCCATTACAACCA0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAAA0596ACCAAGATGCACAATTTGTTGTGAATCCTTCAGCTT0597TCAGGCTAAAGAGGGACAAGGGCATAATGGCAACTTCTGCTA0598CATATTTGGAGACGAGGAAAATTTGCTTTAGCTTCAGCTA0598CATATTTGGAGACGAGGAAAAGTTTGCTTTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTTTCTTCGCTAGGAAATGGCAACATTCTT0598CATATTTGGAACGAGGAAAAGGCCTTAAAATTGGCAAGATTACCCA0598CATATTTGGAACGAGGAAAAGGCCTTAAAATTGCCAAGATTGCCAA0598CATATTTGGAACGAGGAAAAGGGTCTTTAAAATTGCCAAGATTACCACA0598CATATTTGGAACGAGGACAAGGTGTCTTAAAATTGGCAAGATTATCCA0599GATGTTCAGCGTACGAGGACAAGGTGTCTTAAAATTGGCAAGATTATCCA0598CATATTTGGAACGAGGACGAGGAAATTTGCTTTAGCTTCACGCAAGATTA	1167	TCGAAAAAGCTAGTTCCAAA	TGGAGAAAAACTCAAGATGC
1198GGAAAACAGCTACAAGTTGGGCTTCGTAGTCAACATCTGA1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGATA1379TGAAGAATATCAGTTTCCCGCCATTTGCCAAGGACTAATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCAGCAGCG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTAGCGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTGCACGATGTGGT1606GGGTTATCATCACAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional straimsTCAGGAAAAGCCTCTCTTATTTCACACGGTATCCTT0588CTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCCATTACAAC0595TTCTTTCCTTACTTGCAGGAGTCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACAATTCTTTTGTGAATCCTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGAATCCTTCAGCTT0598CATATTIGGAGACGAGGAAAATTTGCTGTTTATGTGCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1180	TGACAACCGTTTACTTGAGTT	TAGTTGAGGTGCTATTTCGAG
1231GAATCGTTTATCCTCCAAGACTACCAAAGAAGCCACGATA1379TGAAGAATATCAGTTTCCCGCCATTTGCCAAGGACTAATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCATCACG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGCGGT1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTACGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGAT1606GGGTTATCATCACAAAGTGCACAGGATCCTTGCAGCGTAACGGATG1627GCTATTGGGGTTAGTGACAGGATCCTTGCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsCTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTTAGGTTTTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTCCTTACTTGCAGGATCTAAAATGATATCGCAGAAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAATGGGATCTCTCGCTA0598CATATTTGGAGAGAGGAAAATTTGCTGTTTAGTTGTCCA0601GATGTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1198	GGAAAACAGCTACAAGTTGG	GCTTCGTAGTCAACATCTGA
1379TGAAGAATATCAGTTTCCCGCCATTTGCCAAGGACTAATA1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCATCACG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTACGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGT1606GGGTTATCATCACAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsCTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0588CTTGCGTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0599GGCTTGCCTTAAACAAATTGATTTCACACGTCTATCAACCA0595TTCTTTCCTTACTTGCAGGAATGAAGAGGCCATTACAAC0596ACCAAGATGCAACATTCTTTTGTGAATCCTGCGCGAA0597TCAGGCTAAAGATGGAAGGCATAAAGGATCCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1231	GAATCGTTTATCCTCCAAGA	CTACCAAAGAAGCCACGATA
1410TTTTGGACACCGTACTTTCTTGTAAACTAGCAGCATCACG1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTACGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATTAGCTG1606GGGTTATCATCACAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsTCTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTAAGGATTTTCACACGTCTATCAACCA0599TGATGGAAAAGGCTCTCTTATTTCACACGGTCATCAACCA0594GCTTGCCTTAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACAATTGTTTGTAAATAGCGTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGAGGTGTCTTAAAATTGGCAAGATTATCCA	1379	TGAAGAATATCAGTTTCCCG	CCATTTGCCAAGGACTAATA
1445ATGGAGCAAAAGTCCTGTTATTTCTAAATGCAAGATGGGT1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTACGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGT1606GGGTTATCATCACAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsTTGATGGAAAAGGCTCTCTTAATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0599TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1410	TTTTGGACACCGTACTTTCT	TGTAAACTAGCAGCATCACG
1494CACCTTTTAGACGAACGAACAACTCAGCCAAAGTACGTGT1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGT1606GGGTTATCATCACCAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsTGATGGAAAAGGCTCTCTTAATTGCATGTAAATAGCGGTT0588CTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0599TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1445	ATGGAGCAAAAGTCCTGTTA	TTTCTAAATGCAAGATGGGT
1581TCAGACACAATTTGGTGGTATTGTATCATTTGCACGATGT1606GGGTTATCATCACCAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strains0588CTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0589TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1494	CACCTTTTAGACGAACGAAC	AACTCAGCCAAAGTACGTGT
1606GGGTTATCATCACAACGATTGACCTCAAATGGATTAGCTG1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strains0588CTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0589TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1581	TCAGACACAATTTGGTGGTA	TTGTATCATTTGCACGATGT
1627GCTATTGGGGTTAGTGACAGATCCTTGTCAGCGTATCCTTSNP mapping in a collection of 14 additional strainsCTTCGCTGAATGTTTAGGTTATTGCATGTAAATAGCGGTT0588CTTCGCTGAAAGGCTCTCTTATTTCACACGTCTATCAACCA0599TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAACC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	1606	GGGTTATCATCACAACGATT	GACCTCAAATGGATTAGCTG
SNP mapping in a collection of 14 additional strains0588CTTCGCTGAATGTTAGGTTATTGCATGTAAATAGCGGTT0589TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAACC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA		GCTATTGGGGTTAGTGACAG	ATCCTTGTCAGCGTATCCTT
0588CITEGETGAATGTTAGGTTATTGEATGTAAATAGEGGTT0589TGATGGAAAAGGCTCTCTTATTTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	SNP mapping in a collection of 14 additional stra		
0535IGATGGAAAAGGCTCTTTAITTCACACGTCTATCAACCA0594GCTTGCCTTAAACAAATTGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	0500		
0534GCTGCCTTAAACAAATIGAAATGAAGAGGCCATTACAAC0595TTCTTTCCTTACTTGCAGGATCTAAAATGATATCCGCAGAA0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	0509 0504		
0535Interfective receivedInterfective received0596ACCAAGATGCAACATTCTTTTTGTTGAATCCTTCAGCTTC0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	0595		
0597TCAGGCTAAAGATGGAAGGCATAAGGGATCTCTTCGCTA0598CATATTTGGAGACGAGGAAATTTGCTGTTTTAGTTGTCCA0601GATGTTTCAGCAGGTGTCTTAAAATTGGCAAGATTATCCA	0596	ΔΓΓΔΔΓΑΤΓΓΛΛΓΑΤΤΓΤΤΤ	TIGTIGAAATOATATCCGCAGAA
0598 CATATTTGGAGACGAGGAAA TTTGCTGTTTTAGTTGTCCA 0601 GATGTTTCAGCAGGTGTCTT AAAATTGGCAAGATTATCCA	0597	ΤΓΔGGCTΔΔΔGΔTGGΔΔGG	CATAAGGGATCTCTTCGCTA
0601 GATGTTTCAGCAGGTGTCTT AAAATTGGCAAGATTATCCA	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.

	Start				Differences Between	Allele 1 and Allele		
Probe	position*	Length	2	m	4	5	9	7
0588	599,420	300						
0589	600,280	236	G67A					
0594 0595	603,422 604 139	423						
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 0605	615,553	483	C198T	A55C T277C A364G				
0608	617,548	367						
0610	620,204	389	C41T C87T C121T T217C ריזיד ריזהניד	G9A G64A A99G T217C С233T				
0612	220 023	376			T144C T145C C163A C164A			
7100	110'770	040		C167T A184C	C167T A184C A221G			
0615	625,231	399						
0628	632,057	412						
0€30	634,722	506	C162T					
0636	640,250	396	G163A	C333T				
0641	645,426	465	C111T T344C	C50T G63A C111T T122C	C111T T122C A221C C452T			
				C224A C239T G314A A349C C452T				
0647	646 440	101	VJEC CJTT GEON GJET	- - 				
7400	0+0	t 0	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	GEDA			
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	A14G A76G T103C G109A	
						A373G	C253T A285G	
1029 1032	1,003,946 1,005,559	372 482	A68G A92T C131T T388C G454A	A92T C131T T221C C252T T34C T79A T235C G454A	A92T C131T G273A T34C A59G C202T C205T Δ386G G454Δ	C131T C131T C272T T34C C133T G206A T340C	A92T C131T C242T	
1035	1.008.192	391	С103Т А192Т А349G					
			T373C					
1036	1,009,002	382	C110T	T58C G120A A142C G271A	С298Т	A31G T58C G120A A142C		
1038	1,010,717	453	G104A G220A	A26G G84A T298A T325C C400T	A26G T123G T325C C451T		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	С93Т	A69G T190C T265C C289T T2026 A 2056 TA36C	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	G199A A214G T247C G286A	C244G	C177G G203A C274A C382T	T43G C88T G199A T247C	
			G367A C382T	C382T			G367A C382T	
*Accordir	ng to strain 2605	3 V/R coord	linates.					

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										A	llele fc	or 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	3 2-22	SS1218
0588	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	*0	0	0	0	0
0589	٢	1	2	-	1	-	1	٢	-	٢	٦	-	٦	-	-	1	1	0	0	0	0	0
0594	-	-	-	-	1	-	1	-	1	-	٦	-	1	1	-	1	1	0	0	0	0	0
0595	-	1	-	-	1	-	1	-	-	-	٦	-	1	1	-	1	1	0	0	0	0	0
0596	٢	1	٢	-	1	-	1	٢	-	٢	٦	-	٦	-	-	2	1	0	0	0	0	0
0597	٢	-	٢	-	-	-	٦	٢	-	٢	2	2	٢	-	-	٦	-	0	0	0	0	0
0598	-	1	-	-	1	-	1	-	-	-	٦	-	1	1	-	1	1	0	0	0	0	0
0601	٢	1	-	-	1	-	1	-	1	-	1	-	1	1	-	1	1	1	٢	Μ	2	2
0602	٢	-	٢	-	-	m	٦	٢	-	٢	٦	-	٢	-	-	٦	-	-	٢	4	2	2
0605	-	1	-	-	2	-	1	-	-	-	٦	-	1	1	-	1	1	1	٢	-	m	m
0608	٢	1	٢	-	1	-	1	٢	-	٢	٦	-	٦	-	-	1	1	1	٢	-	-	-
0610	1	1	٢	-	1	-	٦	٢	-	٢	٦	-	٦	-	-	1	1	1	٢	m	2	2
0612	-	1	-	-	1	-	1	-	-	-	٦	-	1	1	-	1	1	2	٢	m	4	4
0615	-	-	-	-	0	-	-	-	1	-	٦	-	1	1	1	1	0	0	0	0	-	-
0628	-	-	-	-	0	0	1	-	1	-	0	-	1	1	-	0	0	0	0	0	0	0
0630	-	1	-	-	0	0	1	-	2	2	0	2	1	1	-	0	0	0	0	0	0	0
0636	-	-	m	-	0	0	m	-	2	2	0	2	1	1	1	0	0	0	0	0	0	0
0641	-	-	-	-	-	2	-	-	1	-	-	-	-	1	-	-	-	-	m	-	4	4
0642	-	1	-	-	1	-	1	-	-	-	٦	-	1	1	-	1	1	1	٢	-	2	2
0645	-	-	-	-	-	-	-	-	1	-	٦	-	1	1	1	1	-	-	-	-	-	-
0646	-	-	-	-	1	2	1	-	2	2	2	2	1	1	-	2	1	1	-	m	0	0
0653	٢	-	٢	٢	4	-	-	1	-	٢	٢	-	٢	-	-	1	2	2	2	m	0	0
1019	٢	-	1	4	-	-	1	1	-	1	٢	-	٢	-	-	1	m	m	m	2	-	٢
1020	1	1	٢	-	1	-	٦	٢	-	٢	٦	-	٦	2	-	1	-	1	m	4	-	٦
1022	-	-	-	-	-	-	1	-	1	-	1	-	1	1	-	-	2	2	2	2	Μ	m
1024	٢	-	1	-	2	-	1	1	2	2	2	2	2	2	2	9	m	ß	2	4	m	m
1029	٢	-	٢	-	-	-	٦	٢	-	٢	٦	-	٢	-	-	2	m	m	9	2	4	4
1032	1	-	٦	1	-	٢	-	1	-	٦	٦	-	-	-	٢	2	-	2	2	m	4	4
1035	٢	-	1	-	-	-	1	1	-	1	٢	-	٢	-	-	1	-	-	-	-	2	2
1036	٢	-	٢	-	-	-	-	2	-	4	٢	-	٢	-	-	-	-	-	-	S	m	m
1038	-	1	-	-	1	-	1	-	2	2	٦	-	1	1	-	7	S	9	9	m	4	4
1040	٢	-	٢	٢	-	٢	٦	٢	-	٢	٢	-	٢	-	-	2	-	-	-	-	-	٢
1416	٢	-	٢	-	-	-	-	-	-	٢	٢	-	٢	-	-	-	2	2	2	4	m	m
1417	2	-	-	٢	-	-	-	٢	1	-	-	1	-	1	1	-	S	S	5	m	4	4
1418	-	-	2	9	2	2	2	2	2	2	2	2	m	m	m	m	m	m	m	4	S	ß
1419	-	-	-	-	-	-	-	-	1	4	-	-	-	-	-	-	S	S	9	2	m	m
1421	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	2	m	m	9	S	ß
*Denc	otes the ak	sence of .	the probe																			