**Supplementary data**

The PCR products were sequenced and contigs of Lem and Lpa *γ-ECS*swere constructed. The genomic sequences of the two *γ-ECS* genes that contain the complete coding sequences are shown in the appendix.

The two genes have the same number of exons (15), where each respective exon pair has approximately the same nucleotide number (Fig. 6). The coding regions of the two genes exhibit a high degree of sequence identity while a high polymorphism is evident in their respective noncoding regions. This polymorphism includes 590 and 160 bp indels in introns IV and IX, respectively.

cDNA fragments of 1.84 kb comprising the full *γ-ECS* cDNA sequences of Lem and Lpa, were obtained by RT-PCR cloning, and sequenced. The resulting sequences of the cDNAs were identical to those of their respective genomic coding sequences, indicating for high fidelity PCR amplification.

**III**

**IV**

**VI**

**VII**

**VIII**

**IX**

**X**

**XII**

**XIII**

**XIV**

**XV**

**TGA**

**XI**

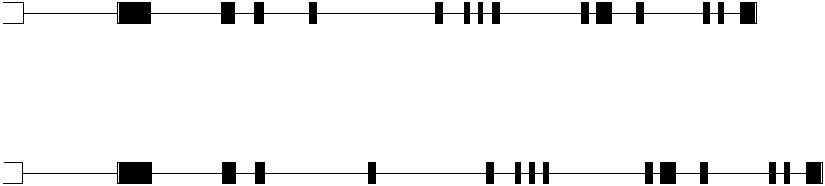
**Lem**

**I**

**II**

**ATG**

**V**

****

**Lpa**

71

93

**XV**

**XIV**

**XIII**

**XII**

**XI**

**X**

**VIII**

**VII**

**IX**

**VI**

**V**

**IV**

**III**

**II**

**I**

192

81

71

92

173

93

71

71

65

87

91

110

151

341

209

**TGA**

**ATG**

189

80

172

93

78

64

65

87

91

110

151

336

219



**1000nt**

**Fig. 6. Schematic representation of the Lem and Lpa *γ-ECS*s.** Empty and black boxes depict the 5`UTR and the coding exons, respectively. The length (bp) of the exons are indicated by numbers, and the lines between the boxes correspond to the introns.

10 20 30 40 50 60

Lem **CATTCAATCTGCTAGCAGTTGTCTCTCTTTATAGCTAAACAAAAATTAAAGAAATGGGAG**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **CATTCAATCTGCTAGCAGTTGTCTCTCTTTATAGCTAAACAAAAATTAAAGAAATGGGAG**

10 20 30 40 50 60

70 80 90 100 110 120

Lem **TGATAAAGCTCTAGCCGCCTCAGCACACCAAAATCCTAATCATTTTGCTGATACCCAATT**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **TGATAAAGCTCTAGCCGCCTCAGCACACCAAAATCCTAATCATTTTGCTGATACCCAATT**

70 80 90 100 110 120

130 140 150 160 170 180

Lem **GTCTCTATATATATATTGGAAGGTTTTCTTTCAATTTTCAGTCAATTCTATAGAACAAAC**

: ::::::::::::::::::::::::::::::: ::::::: ::::::::::::::::::

Lpa **GCCTCTATATATATATTGGAAGGTTTTCTTTCAGTTTTCAGCCAATTCTATAGAACAAAC**

130 140 150 160 170 180

190 200 210 220 230 240

Lem **CCTACAAAGTCTTAATTTTTCCAGTTTACTGAGCCAAGG**TATCACCTTTTTGTCACCTTT

:::::::::::::::::::: :::::::: ::::: ::::::::::::::::::::::::

Lpa **CCTACAAAGTCTTAATTTTTTCAGTTTAC**CGAGCCGAGGTATCACCTTTTTGTCACCTTT

190 200 210 220 230 240

250 260 270 280 290

Lem TATGTTGGTTTCAGTTAGTTTTGTTAATCAAGATT-CAATTTTTCTGACATACCCATGTT

::::::::::::::::::::::::::::::::::: :::::::::::::::::::::: :

Lpa TATGTTGGTTTCAGTTAGTTTTGTTAATCAAGATTACAATTTTTCTGACATACCCATGAT

250 260 270 280 290 300

300 310 320 330 340 350

Lem TCTTTTGTATGCTTTTGTTGCATTTCTGTTTTCTTCATGAAGTTGTTTTGGTTAATCAAG

::::::::::: ::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TCTTTTGTATGTTTTTGTTGCATTTCTGTTTTCTTCATGAAGTTGTTTTGGTTAATCAAG

310 320 330 340 350 360

360 370 380 390 400 410

Lem ATTCAGTTTTTCTGAAGCCCCATGATTTTTTTCTTTTAGTTTTGGTTTGATGGTTTTGTT

::::::::::::::::::::::::::::::: ::::::::::::::::::::::::::::

Lpa ATTCAGTTTTTCTGAAGCCCCATGATTTTTT-CTTTTAGTTTTGGTTTGATGGTTTTGTT

370 380 390 400 410

420 430 440 450 460 470

Lem AGTTGTGTTGTAATTCTTGTTTGTTGCCATATGGGGGTTGATAGTATTGATTAAAGATTC

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa AGTTGTGTTGTAATTCTTGTTTGTTGCCATATGGGGGTTGATAGTATTGATTAAAGATTC

420 430 440 450 460 470

480 490 500 510 520 530

Lem AAAATTTATACATGTGGGTTGTGGTAGTCTGATTGAATGACATGCATAGTAAACTAGAAA

:::::::::::: :::::::: ::::::::::::::::::::::::::::::::::::::

Lpa AAAATTTATACACGTGGGTTGAGGTAGTCTGATTGAATGACATGCATAGTAAACTAGAAA

480 490 500 510 520 530

540 550 560 570 580 590

Lem GAAGAAAGAGATAAATGCTTTAGATAATGTGAACAAGACTTGTATTATAGGTTAGACTGC

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa GAAGAAAGAGATAAATGCTTTAGATAATGTGAACAAGACTTGTATTATAGGTTAGACTGC

540 550 560 570 580 590

600 610 620 630 640 650

Lem TTTACAAGTTTCAGTTTCTCGTGTTCTTCTGAGTAGTTTTAAGTGTTGAATGAAATGGCA

::::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::

Lpa TTTACAAGTTTCAGTTTCTCGTGTTCTTCTGAGTAGTTTTAAGTGTTGAGTGAAATGGCA

600 610 620 630 640 650

660 670 680 690 700 710

Lem TTGTGTAAGATTGCATTTGATGGTCTGGGATTCAGGTATGATTGATGCAGGACAGGAATA

::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::

Lpa TTGTGTAAGATTGCATTTGATGGTCTGGGATTCAGGTATGATTGATGCAGGACAGCAATA

660 670 680 690 700 710

720 730 740 750 760 770

Lem TCAAGCCACATTTTCTTTATTGTAGCTGTGTTTCGATATGGAATGAGATGGGGGTGGGGT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::

Lpa TCAAGCCACATTTTCTTTATTGTAGCTGTGTTTCGATATGGAATGAGATGGGGGTGGCGT

720 730 740 750 760 770

780 790 800 810 820 830

Lem GGGGGAGTTTACAGCATGTAGAA-TTGTAGAGCACTGTAATGAAAA-TTTCTAGATTATT

:::::::::::::: :: ::::: ::::::: :: ::::::::::: :::::::::::::

Lpa GGGGGAGTTTACAGGATCTAGAAATTGTAGATCAATGTAATGAAAAATTTCTAGATTATT

780 790 800 810 820 830

840 850 860 870 880 890

Lem GCAATTCGAATCTTATGTTGCTTATATAGTACATCTTAATTAACTTTAATATTTGTTCGG

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa GCAATTCGAATCTTATGTTGCTTATATAGTACATCTTAATTAACTTTAATATTTGTTCGG

840 850 860 870 880 890

900 910 920 930 940 950

Lem ATTGGTGATTGAGCCTGCTGGGTAGTTGGGTTGGCCCTATCCTATTGGTGTATAACTATG

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa ATTGGTGATTGAGCCTGCTGGGTAGTTGGGTTGGCCCTATCCTATTGGTGTATAACTATG

900 910 920 930 940 950

960 970 980 990 1000 1010

Lem CTCAATGAAGATGCGAGAGGTTCATTTGACGTTTCCCATCAAAAGTACTCTTCAATCATT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa CTCAATGAAGATGCGAGAGGTTCATTTGACGTTTCCCATCAAAAGTACTCTTCAATCATT

960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070

Lem ATTTAGTTATCCTCTTCTGTTACTAAATGTAATACACAAGTTAAACAATAATCTGAATTC

::::::::::::::::::::::::::::: ::::::::::::::::::::::::::::::

Lpa ATTTAGTTATCCTCTTCTGTTACTAAATGCAATACACAAGTTAAACAATAATCTGAATTC

1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130

Lem CTTGTCTACTCAAATGGCAT-ACATTCTAGTTAAAAGTGGTTGACATCAGTTTTTCCTGT

:::::: :::::::::: :: :::::::::::::: ::::: ::::::::::::::::::

Lpa CTTGTCCACTCAAATGGTATGACATTCTAGTTAAA-GTGGTAGACATCAGTTTTTCCTGT

1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180 1190

Lem GATATTC**AGGCACAAAGCATGGCCTTGATGTCTCAGGCAGGTTCTTCACATTGCATTTAC**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa GATATTC**AGGCACAAAGCATGGCCTTGATGTCTCAGGCAGGTTCTTCACATTGCATTTAC**

1140 1150 1160 1170 1180 1190

1200 1210 1220 1230 1240 1250

Lem **TCTGAAAAGGTAAGATGTATCAGTGGACATAGAAGCATCATTAACAATATGGATATGTTC**

::::::::: :::::::::::::::::::::::: :::::: ::::::::::::::::::

Lpa **TCTGAAAAGATAAGATGTATCAGTGGACATAGAAACATCATGAACAATATGGATATGTTC**

1200 1210 1220 1230 1240 1250

1260 1270 1280 1290 1300 1310

Lem **AGAATGCGGGAGATATGCTTTGGCGTGGATATTTCTTCACGCAATGCCTCAAGACGAGTG**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **AGAATGCGGGAGATATGCTTTGGCGTGGATATTTCTTCACGCAATGCCTCAAGACGAGTG**

1260 1270 1280 1290 1300 1310

1320 1330 1340 1350 1360 1370

Lem **CAAGGGAATTATTTGAATCACATAGGAGTGGGAAGTAGACGTGGAGACCTGACAATTGTA**

::::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::

Lpa **CAAGGGAATTATTTGAATCACATTGGAGTGGGAAGTAGACGTGGAGACCTGACAATTGTA**

1320 1330 1340 1350 1360 1370

1380 1390 1400 1410 1420 1430

Lem **GCTGCAAGTCCTCCAACAGAGGATGCTGTTGTTGCAGCAGAGCCGTTAACAAAAGAAGAT**

::::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::

Lpa **GCTGCAAGTCCTCCAACAGAGGATGCTGTTGTTGCAGCAGAGCCGCTAACAAAAGAAGAT**

1380 1390 1400 1410 1420 1430

1440 1450 1460 1470 1480 1490

Lem **CTTGTAGGATATCTTGCTTCTGGATGCAAATCCAAAGAAAAGTGGAGG**TTCGAAGTTAAA

::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::

Lpa **CTTGTAGGATATCTTGCTTCTGGATGCAAATCCAAAGAAAAATGGAGG**TTCGAAGTTAAA

1440 1450 1460 1470 1480 1490

1500 1510 1520 1530 1540 1550

Lem CTTTTCTTAGTGCTCTTAAATTTCAGTTGCATATAGTTAACCAAGAATATGAATATTCAT

:::::::::::::::::::::::::::::::::::::::::::::::::::::::: :::

Lpa CTTTTCTTAGTGCTCTTAAATTTCAGTTGCATATAGTTAACCAAGAATATGAATATACAT

1500 1510 1520 1530 1540 1550

1560 1570 1580 1590 1600 1610

Lem TCTCTCGTTTGGCCTTTATAAGTAGAATAGTCTGCTCATTCACCACATATATGCCTTGAT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TCTCTCGTTTGGCCTTTATAAGTAGAATAGTCTGCTCATTCACCACATATATGCCTTGAT

1560 1570 1580 1590 1600 1610

1620 1630 1640 1650 1660 1670

Lem TGTCTTTCAAGTATGTCGAGTAATTCATGAATCAATTCACATCGCTTGTGTATTTTAATA

:::::::::::::::::::::::::::: ::: :::::: :::::::::::::: ::

Lpa TGTCTTTCAAGTATGTCGAGTAATTCATAAAT----TCACATTGCTTGTGTATTTTATTA

1620 1630 1640 1650 1660 1670

1680 1690 1700 1710 1720 1730

Lem TACGGCTATTTTTTATGTAGTTATTCTTTCTTCAGCTTCTGTTGTAGTGTATGATACGGT

:::: :::: ::::::: ::::::::::::::::::::::::::::::::::::: ::::

Lpa TACGTCTATCTTTTATGCAGTTATTCTTTCTTCAGCTTCTGTTGTAGTGTATGATTCGGT

1680 1690 1700 1710 1720 1730

1740 1750 1760 1770 1780 1790

Lem AGATGTATTATATACTTTTTACATGTCATTATTGTGGTTATTTCTCATTTTCCATTTCTA

:::::::::::::::::::::::::::: :::::::::::::::::::::::::::::::

Lpa AGATGTATTATATACTTTTTACATGTCACTATTGTGGTTATTTCTCATTTTCCATTTCTA

1740 1750 1760 1770 1780 1790

1800 1810 1820 1830 1840 1850

Lem AGAAATATAAATATCATGGGCAAATTCTCACCGTCATGCATTCAAGATGTGGATACTAGG

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa AGAAATATAAATATCATGGGCAAATTCTCACCGTCATGCATTCAAGATGTGGATACTAGG

1800 1810 1820 1830 1840 1850

1860 1870 1880 1890 1900 1910

Lem GAACTAGGACATGATGCAGCTCTTTTCATTGAACTAACAAGTTGTACCATTTGGGCAACT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa GAACTAGGACATGATGCAGCTCTTTTCATTGAACTAACAAGTTGTACCATTTGGGCAACT

1860 1870 1880 1890 1900 1910

1920 1930 1940 1950 1960 1970

Lem TGAACACTGGAAACATTAATCAATTTTTCCTAGGACACTGCTGTCTCTAATTTTGTTGCA

:::::::::::::::::::::::::::::::::::: :::::::::::::::::::::::

Lpa TGAACACTGGAAACATTAATCAATTTTTCCTAGGACGCTGCTGTCTCTAATTTTGTTGCA

1920 1930 1940 1950 1960 1970

1980 1990 2000 2010 2020 2030

Lem AATTTTGAATTGTTGAAAATTCGGTAATACAATTTTTGAACATGGAGTTGGGAGCCATTC

:::::::::::::::::: :::::::::::::::::::::::: ::::::::::::::::

Lpa AATTTTGAATTGTTGAAATTTCGGTAATACAATTTTTGAACATAGAGTTGGGAGCCATTC

1980 1990 2000 2010 2020 2030

2040 2050 2060 2070 2080 2090

Lem CCTGGATCAGGTATTTTTTCATAAATGGGGTAGCTAGGATTCTGCCTCAGTCATTATTTG

:::::::::::::::::: :::::::: ::::::::::::::::::::: :::::::::

Lpa CCTGGATCAGGTATTTTTGCATAAATGTGGTAGCTAGGATTCTGCCTCACACATTATTTG

2040 2050 2060 2070 2080 2090

2100 2110 2120 2130 2140 2150

Lem GAATAGTTTGTTTTACTTAACTGTGCGTCTGGATCTAGACCATAATAATCAGGTTCAACT

:: ::::::::::: :::: :::::::::::::::::::::::::::::::: :::::::

Lpa GA-TAGTTTGTTTTGCTTAGCTGTGCGTCTGGATCTAGACCATAATAATCAG-TTCAACT

2100 2110 2120 2130 2140 2150

2160 2170 2180 2190 2200 2210

Lem TTTCTTGTTCTCTCAAAACTTGATGAGCAGG**ATAGGCACTGAACATGAAAAGTTTGGTTT**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TTTCTTGTTCTCTCAAAACTTGATGAGCAGG**ATAGGCACTGAACATGAAAAGTTTGGTTT**

2160 2170 2180 2190 2200 2210

2220 2230 2240 2250 2260 2270

Lem **CGAGTTTGGAACCCTGCGACCCATGAAGTATGATCAAATAGCTGACTTGCTAAATGGTAT**

:::::::::::: :::::::::::::::::::::::::::::::::::::::::::::::

Lpa **CGAGTTTGGAACTCTGCGACCCATGAAGTATGATCAAATAGCTGACTTGCTAAATGGTAT**

2220 2230 2240 2250 2260 2270

2280 2290 2300 2310 2320 2330

Lem **TGCTGAGCGGTTTGATTGGGAAAAAGTAATGGAGGGTGACAAGATTATTGGCCTGAAACA**

::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **TGCCGAGCGGTTTGATTGGGAAAAAGTAATGGAGGGTGACAAGATTATTGGCCTGAAACA**

2280 2290 2300 2310 2320 2330

2340 2350 2360 2370 2380 2390

Lem **GG**TAACGTGAACTTGGTGCAAACTTTGGTTTAAAATATTCTAGGTTGAATTTGTCATGGC

::::::::::::: :::::::::::::::::::::::::::::: ::::::: :::::::

Lpa **GG**TAACGTGAACTCGGTGCAAACTTTGGTTTAAAATATTCTAGGCTGAATTTTTCATGGC

2340 2350 2360 2370 2380 2390

2400 2410 2420 2430 2440 2450

Lem TCCATACAATGTATTATGCTACTTACCATGAATAGAATCATAATTCCTGATTCATTTTTT

::::::::::::::::::::::::: :::::::::::::::::: :: ::::::::::::

Lpa TCCATACAATGTATTATGCTACTTAGCATGAATAGAATCATAAT-CCCGATTCATTTTTT

2400 2410 2420 2430 2440 2450

2460 2470 2480 2490 2500 2510

Lem TCCTCAAGTGCAAGTCTGTAGTAAGTAGTAATTACTTTAGCATAATTGGTGGATAA-TTT

: ::::::::::::::::::::::: :::::::::::::::::::::::::::::: :::

Lpa TTCTCAAGTGCAAGTCTGTAGTAAGCAGTAATTACTTTAGCATAATTGGTGGATAAATTT

2460 2470 2480 2490 2500 2510

2520 2530 2540 2550 2560 2570

Lem GCACTGTCTTCGCAGG**GAAAGCAAAGCATATCATTAGAACCTGGTGGTCAGTTTGAGCTT**

:::::: :::: :::::::: :::::::::::::: ::::::::::::::::::::::::

Lpa GCACTGCCTTCACAGG**GAAAACAAAGCATATCATTGGAACCTGGTGGTCAGTTTGAGCTT**

2520 2530 2540 2550 2560 2570

2580 2590 2600 2610 2620 2630

Lem **AGTGGTGCACCACTTGAAACACTGCATCAAACTTGTGCAGAGGTTAATTCACATCTTTAC**

::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::

Lpa **AGTGGTGCACCACTTGAAACATTGCATCAAACTTGTGCAGAGGTTAATTCACATCTTTAC**

2580 2590 2600 2610 2620 2630

2640 2650 2660 2670 2680 2690

Lem **CAGGTT**TGTACTTTTGAAACTCCATCAGTTTCCCTTTTAATGAAATAGTGGGCAATTAAG

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **CAGGTT**TGTACTTTTGAAACTCCATCAGTTTCCCTTTTAATGAAATAGTGGGCAATTAAG

2640 2650 2660 2670 2680 2690

2700 2710 2720 2730 2740 2750

Lem ATCTTTCTAACTATACATAGTCTGCACTGGGGAAATGTAAGCGAACTTTAATTATGCGAT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa ATCTTTCTAACTATACATAGTCTGCACTGGGGAAATGTAAGCGAACTTTAATTATGCGAT

2700 2710 2720 2730 2740 2750

2760 2770 2780 2790 2800 2810

Lem AACATGGCTTGGAATAAAAGGGAATCTCATTTTTTTGAGTTTGAGAAATCCTGCAAATGT

::: ::::::::::::::: :::: :::::::::::::::::::::::::::::::::::

Lpa AACTTGGCTTGGAATAAAAAGGAAACTCATTTTTTTGAGTTTGAGAAATCCTGCAAATGT

2760 2770 2780 2790 2800 2810

2820 2830 2840 2850 2860 2870

Lem GTCGGCCATTTTTGCTTCAGGTGGTTGATGACTTATTACACTAGGGATTCTTTACCCAGT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa GTCGGCCATTTTTGCTTCAGGTGGTTGATGACTTATTACACTAGGGATTCTTTACCCAGT

2820 2830 2840 2850 2860 2870

2880 2890 2900 2910 2920 2930

Lem ATTCTGGTTCTTCTGATCAGAGTCTCTAGTTGTATAAGAAAATGTTGCTTCAAAAGAACA

:::::::::::: :::::::::::::::::::::::::::::: ::::: ::::::::::

Lpa ATTCTGGTTCTTTTGATCAGAGTCTCTAGTTGTATAAGAAAATCTTGCTGCAAAAGAACA

2880 2890 2900 2910 2920 2930

2940 2950 2960 2970 2980 2990

Lem TTGTTGGGGTGAAAGTAAAGTTATGACTTCCTGACTGTCTTGTCGATGAACATTTGGAGG

:::::::::::::::: :::::::::::: :: :::::::::: :::::::: :::::::

Lpa TTGTTGGGGTGAAAGTTAAGTTATGACTTTCTAACTGTCTTGTTGATGAACACTTGGAGG

2940 2950 2960 2970 2980 2990

3000 3010

Lem CAAGAAAACCGAAGCTATTC---TCA----------------------------------

::::::::: :::::::::: :::

Lpa CAAGAAAACAGAAGCTATTCATCTCAGCTTTGACATATGTTTTATCTACCTCAACCTCGC

3000 3010 3020 3030 3040 3050

Lem ------------------------------------------------------------

Lpa CCAAGCAACTATCCAAAAGAAGGGTTTCACGTATTCTCTTCTTGTTTTCCTCACTTCGCT

3060 3070 3080 3090 3100 3110

Lem ------------------------------------------------------------

Lpa AAGTGTATGAACACTGTCCTTTAACACATTGATAACAATAACTGTTGTGTTAGTCTAACA

3120 3130 3140 3150 3160 3170

Lem ------------------------------------------------------------

Lpa TTGCTGAAACTGCAAATGAGCTTGGGGTTTACCTTCAGGGAAGTCTAACATTGTGTTCCT

3180 3190 3200 3210 3220 3230

Lem ------------------------------------------------------------

Lpa CTGATCACGAAGGTTCATTTGTTTATTTTTTTTATTAATACATCAAGGTATTATAATACT

3240 3250 3260 3270 3280 3290

Lem ------------------------------------------------------------

Lpa ACTAAGCACCATGCATCTGTACAACGATCATGATTTCAAATATCATATATATACAACAAA

3300 3310 3320 3330 3340 3350

Lem ------------------------------------------------------------

Lpa AAAAATCTTTGCTCCAAAAATCATATACACGACAAAATAGATCTCTTAAGCTTCGAAGAG

3360 3370 3380 3390 3400 3410

Lem ------------------------------------------------------------

Lpa ACTTTTCTTCACATCTGGTTTCTTAGATTGTCTTAACTACCTTTTGAAGTCCTTTAGGAA

3420 3430 3440 3450 3460 3470

Lem ------------------------------------------------------------

Lpa GACAACAAGGAGCATACTCCTGTCCTTTGATCTTCAATTTTTTGAACTTTCTCACAGTAT

3480 3490 3500 3510 3520 3530

Lem ------------------------------------------------------------

Lpa TGTGCCCGTTTAGTATGCTTGCAAAGGACGTAGCTCTTCCCCCCCCCCCCTTCCCCCCCT

3540 3550 3560 3570 3580 3590

3020 3030 3040 3050 3060

Lem ---------CAGGAGAAATATTCACGGATAAA-TTTAAGTTTTGCTGATATGTAATAGTT

::::::::::::::: ::::::: :::::::::::::::::::::::::::

Lpa CCCCAACACCAGGAGAAATATTCATGGATAAAATTTAAGTTTTGCTGATATGTAATAGTT

3600 3610 3620 3630 3640 3650

3070 3080 3090 3100 3110 3120

Lem TTCGTCTAATGGTACAGGTT**AAAGCTGTTGCAGAAGAGATGGGAATTGGATTCTTAGGAA**

:: :::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TTTGTCTAATGGTACAGGTT**AAAGCTGTTGCAGAAGAGATGGGAATTGGATTCTTAGGAA**

3660 3670 3680 3690 3700 3710

3130 3140 3150 3160 3170 3180

Lem **CTGGATTCCAGCCAAAGTGGGGGCTGAAAGATATACCAATAATGCCGAAGG**TAAAAACAA

:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **CTGGATTCCAGCCAAAGTGGGGGCTGAAAGATATACCAATAATGCCGAAGG**TAAAAACAG

3720 3730 3740 3750 3760 3770

3190 3200 3210 3220 3230 3240

Lem TATGCTGATCGATGTTGTAACCAAAAGATTTGTTTGGTGTGTTGGTAACTTAGCATCTTA

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TATGCTGATCGATGTTGTAACCAAAAGATTTGTTTGGTGTGTTGGTAACTTAGCATCTTA

3780 3790 3800 3810 3820 3830

3250 3260 3270 3280 3290 3300

Lem TCTCTTTGAGACTGCTATTTTAACAGTGAAAAGATGTTAATATTTTTGTACACGACCATT

:::: ::::::::::::::::::::::::::::::::::: ::::::::::::::::::

Lpa TCTC--TGAGACTGCTATTTTAACAGTGAAAAGATGTTAATTTTTTTGTACACGACCATT

3840 3850 3860 3870 3880

3310 3320 3330 3340 3350 3360

Lem TCACATATTG-TTCAGCATGTCAAGTGCAGTAGAATCCCAGTTTCTAATATAATTTCATT

:::::::::: ::::::: ::::::::::::::::::: ::::: : ::::::::::::

Lpa TCACATATTGGTTCAGCACCTCAAGTGCAGTAGAATCCC-GTTTCCATTATAATTTCATT

3890 3900 3910 3920 3930 3940

3370 3380 3390 3400 3410 3420

Lem ATTCATTATTATTTGATGAGACTAGTGTAGCTCGAAGCTCATTCTCTCTGATTTCATCAT

::::::::::::::::::: :::::::::::::::::::::::::::::::::::::: :

Lpa ATTCATTATTATTTGATGAAACTAGTGTAGCTCGAAGCTCATTCTCTCTGATTTCATCGT

3950 3960 3970 3980 3990 4000

3430 3440 3450 3460 3470 3480

Lem TTTGCAACACCTCATCTTTTTACCTACAAACCTTACCAGACAATGCCTATTTCGCATAGT

:::::::::::::::::::::::::::::::::::::::::: :::::::::::::::::

Lpa TTTGCAACACCTCATCTTTTTACCTACAAACCTTACCAGACA-TGCCTATTTCGCATAGT

4010 4020 4030 4040 4050 4060

3490 3500 3510 3520 3530 3540

Lem TATTTTTGAAGTGAAATTTTTTTCTAATCCACCTTCGATCATGAAAATCATGAATAAGTT

:: ::: :::

Lpa TACTTTCGAA--------------------------------------------------

4070

3550 3560 3570 3580 3590 3600

Lem AATCATCGTTGATATTTCTAGGAGCCGAAGAGATGACAGATGAGATATTGTTCTAATGAT

::::::::::::::::::::::::::::::::

Lpa ----------------------------AGAGATGACAGATGAGATATTGTTCTAATGAT

4080 4090 4100

3610 3620 3630 3640 3650 3660

Lem TAGTTATTCAGATAAATGGTTCAGATGTAGCTTGTCTCACATCTTATTTCTTCTCTAAAA

::::::::::::: ::::::::::::: :::::::::::::::::::::: ::::::::

Lpa TAGTTATTCAGATTGATGGTTCAGATGTTGCTTGTCTCACATCTTATTTCTCCTCTAAAA

4110 4120 4130 4140 4150 4160

3670 3680 3690 3700 3710 3720

Lem GACACAAGAACAAGTAAATAAAGGTGCAGAACTTCAATTCTTTCCTTTTGAGCTAATCAT

:::::::::::::::::::::::::: ::::::::::::::::::::::: :::::::::

Lpa GACACAAGAACAAGTAAATAAAGGTGTAGAACTTCAATTCTTTCCTTTTGTGCTAATCAT

4170 4180 4190 4200 4210 4220

3730 3740 3750 3760 3770 3780

Lem TCATCTTCTCCATTAGGCTAATCTAGATTAACAATCCCCACTTCTTCGACTCTTCTCTTA

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TCATCTTCTCCATTAGGCTAATCTAGATTAACAATCCCCACTTCTTCGACTCTTCTCTTA

4230 4240 4250 4260 4270 4280

3790 3800 3810 3820 3830 3840

Lem CGGATTTAATAAAAAGGACGAAGGAGAAAGAACAAAAGAAAGCTAAAAAAA-TCTTTTAG

::::::::::::::::::::::::: :::::::: ::::::::::::: ::::::::

Lpa CGGATTTAATAAAAAGGACGAAGGA----GAACAAAATAAAGCTAAAAAAAATCTTTTAG

4290 4300 4310 4320 4330 4340

3850 3860 3870 3880 3890 3900

Lem TTGCTGTACTATTCTCTTACTGTCAACTCGAAGATTAAAAATT-TAGCTTTCTTTTTCTT

::::::::::::::::::::::::::::::::::: ::::: : ::::::::::::::::

Lpa TTGCTGTACTATTCTCTTACTGTCAACTCGAAGATAAAAAAATCTAGCTTTCTTTTTCTT

4350 4360 4370 4380 4390 4400

3910 3920 3930 3940 3950 3960

Lem TTCCTGATCAAAAAGAAAATTACGATTTGACAGTAAGGGAATGCTAAACCTGATCCTTGG

:::::::::::::::: :: ::::::::::::::::::::::::::::::::::::::::

Lpa TTCCTGATCAAAAAGAGAACTACGATTTGACAGTAAGGGAATGCTAAACCTGATCCTTGG

4410 4420 4430 4440 4450 4460

3970 3980 3990 4000 4010 4020

Lem ACCAGATCTAGTAATTATTTCCAATAAATGGAAATTATATATAGATCTTGCCTACCTTTT

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Lpa ACCAGATCTAGTAATTATTTCCAATAAATGGAAATTATAAATAGATCTTGCCTACCTTTT

4470 4480 4490 4500 4510 4520

4030 4040 4050 4060 4070 4080

Lem CCCCCCAGAGTCTTCACAATTTAGAAATGCAAATAGTTTCCCCCCACTTGTTTCTTTTAT

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Lpa TTCCCCAGAGTCTTCACAATTTAGAAATG-AAGTAGTTTCCCCCCACTTGTTTCTTTTAT

4530 4540 4550 4560 4570 4580

4090 4100 4110 4120 4130 4140

Lem GTTCTTTACTTATTTACTTTTAACTAAGCCAGAATTATGGTATGCTATTTTGATTTGCAG

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Lpa GTTCTTTACTTATTTACTTTTAACTAAGCCAGAATTATGGTATGTTATTTTGATTTGCAG

4590 4600 4610 4620 4630 4640

4150 4160 4170 4180 4190 4200

Lem CTGTAATTTAAAAATAATATTTGCACCATCTACCTCTATTCATATTCTGTACTATGTACA

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Lpa CTGTAATTTAAAAATAATATTTGCACCATCTACCTCTATTCATATTCTATACTATATACA

4650 4660 4670 4680 4690 4700

4210 4220 4230 4240 4250 4260

Lem ACATCATGTGCTTCTCAGACCTCAATATTATTTGTGTTGTCATGT--TCTTCTAGCTTTG

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Lpa ACATCATGTGCTTGTCAGACCCCAATATTATTTGTGTTGTCATGTGTTCTTCTAGCTTTG

4710 4720 4730 4740 4750 4760

4270 4280 4290 4300 4310 4320

Lem AAAGATATATCTATTTCTTACTTTTCTCAAGTATGATTTGACCTCTTAGATCTGCGATCA

::::::::::: ::::::::::::: :::::::::::::::::::::::::::::: :::

Lpa AAAGATATATCGATTTCTTACTTTTTTCAAGTATGATTTGACCTCTTAGATCTGCGTTCA

4770 4780 4790 4800 4810 4820

4330 4340 4350 4360 4370 4380

Lem GCTTGTGTTTTCACTGACAAAGTACTTTGACTCAGG**GGAGATATGAGATTATGAGAAATT**

::::::::::::::::::::: ::::::::::::::::::::::::::::::::: ::::

Lpa GCTTGTGTTTTCACTGACAAAATACTTTGACTCAGG**GGAGATATGAGATTATGAGGAATT**

4830 4840 4850 4860 4870 4880

4390 4400 4410 4420 4430 4440

Lem **ACATGCCTAAAGTTGGCTCACTTGGGCTGGATATGATGTTTAGAACATGCACTGTTCAGG**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **ACATGCCTAAAGTTGGCTCACTTGGGCTGGATATGATGTTTAGAACATGCACTGTTCAGG**

4890 4900 4910 4920 4930 4940

4450 4460 4470 4480 4490 4500

Lem **TAA**GCTGAATGGTTTAGCTTTTTTCTTTTCATTTCGTTCCATTTTTTTGATGGGATGCCA

:::::::::::::::: :::::::::::: ::::: :::::: :::::::::::::::::

Lpa **TAA**GCTGAATGGTTTAACTTTTTTCTTTTTATTTCATTCCATCTTTTTGATGGGATGCCA

4950 4960 4970 4980 4990 5000

4510 4520 4530 4540 4550 4560

Lem TTGCCCCTTGACTATTGGAGTGCATACCCCTGTGCAGCATTCAAAGCTATATT-TTTTTT

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Lpa TTGCCCCTTGACTATTGGAGTGCATACCCCTGTGCAGCATTCAAAGCTATATTATTTTTT

5010 5020 5030 5040 5050 5060

4570 4580 4590 4600 4610 4620

Lem TCCTGCCCATTTGTGTCTGGGTTCCCGTCATGCCCTGCATGGTAACATTCATTAGTAAGT

: :::::::::::::::::::::::::::::::::::::::::::::::::: ::::::

Lpa TTTTGCCCATTTGTGTCTGGGTTCCCGTCATGCCCTGCATGGTAACATTCATTGGTAAGT

5070 5080 5090 5100 5110 5120

4630 4640 4650 4660 4670 4680

Lem TGAATCAATATTTACGAATATGTTGTTGACAGGTAA**ATCTGGACTTCAGTTCTGAAGCTG**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TGAATCAATATTTACGAATATGTTGTTGACAGGTAA**ATCTGGACTTCAGTTCTGAAGCTG**

5130 5140 5150 5160 5170 5180

4690 4700 4710 4720 4730 4740

Lem **ACATGATCAGAAAGTTCCGTGCTGGTCTTGCCTTGCAGCCT**GTATGGTACCTTTATCCTT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **ACATGATCAGAAAGTTCCGTGCTGGTCTTGCCTTGCAGCCT**GTATGGTACCTTTATCCTT

5190 5200 5210 5220 5230 5240

4750 4760 4770 4780 4790 4800

Lem TCTGTCCTTTCTATTTCTACATGAAACTTATTTAGTTATCTAACTAATACAATGAAACAG

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Lpa TCTGTCCTTTCTATTTCTACGTGAAACTTGTGTAGTGATCTAACTAATACAATGAAACAG

5250 5260 5270 5280 5290 5300

4810 4820 4830 4840 4850 4860 Lem **ATTGCTACAGCTCTATTTGCAAATTCACCTTTCACTGAAGGAAAACCTAATGGTTATCTC**

::::::::::::::::::::::::::::::::::: ::::::::::::::::::::::::

Lpa **ATTGCTACAGCTCTATTTGCAAATTCACCTTTCACCGAAGGAAAACCTAATGGTTATCTC**

5310 5320 5330 5340 5350 5360

4870 4880 4890 4900 4910 4920

Lem **AGCAAGAGAAG**GTATGTGTTTAAAAAATATAATGCTTGTTTCTTTGAGGACTATAATCGA

:::::::::::::::::::::::::: :::::: ::::::::::::::::::::::: ::

Lpa **AGCAAGAGAAG**GTATGTGTTTAAAAA-TATAATTCTTGTTTCTTTGAGGACTATAATTGA

5370 5380 5390 5400 5410 5420

4930 4940 4950 4960 4970 4980

Lem AGTTGTACATAACAATTTTTTGTTTGTTTCACCAGCGAGAGAAG**CCACATTTGGACCGAT**

:::::::::::::::::::::::::::::::::::: :::::::::::::::

Lpa AGTTGTACATAACAATTTTTTGTTTGTTTCACCAGC**--------CCACATTTGGACCGAT**

5430 5440 5450 5460 5470

4990 5000 5010 5020 5030 5040

Lem **ACAGATAATAACCGCGCTGGGATGCTTCCTTTCGTCTTTGATGACTCTTTTGGGT**AAGTT

::::::::::::::::: ::::::::::::::::::::::::::::::::::::::::::

Lpa A**CAGATAATAACCGCGCCGGGATGCTTCCTTTCGTCTTTGATGACTCTTTTGGGT**AAGTT

5480 5490 5500 5510 5520 5530

5050 5060 5070 5080 5090 5100

Lem CTCCTGTTTTTGCAAATAGTTATAGTTTCTTGAGTCGTGACATATTATTTTCTTTCTTCA

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa CTCCTGTTTTTGCAAATAGTTATAGTTTCTTGAGTCGTGACATATTATTTTCTTTCTTCA

5540 5550 5560 5570 5580 5590

5110 5120 5130 5140 5150 5160

Lem GTCAAGATTACGTTTGTTAAAGTTGGAGGGCAAATGGTAGGGGCAGTAGGAGTCATATTA

:::::::::::::::::::::::::::::::::::::::: :::::::::: ::::::::

Lpa GTCAAGATTACGTTTGTTAAAGTTGGAGGGCAAATGGTAGCGGCAGTAGGAATCATATTA

5600 5610 5620 5630 5640 5650

5170 5180 5190 5200 5210 5220

Lem ACATTTTCTTTTTCTTGTGGTATTTGTAAATGAATTCTTTAAAACTACTCATATGTCTAA

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Lpa ACATTTTCTTTTTCTTGTGGTATTTGTAAATGAATTCCTTAAA-CTACTCATATGTCTAA

5660 5670 5680 5690 5700 5710

5230 5240 5250 5260 5270 5280

Lem CCTGATTGTTTGAAAAAGTGAAGAAACAATTCGACCTATTTACTTGAAACGGAAAGGGTA

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Lpa CCTGATTGTTTGAAAAAGTGAAGAAACAATTCGACCTATTTACTTGAAACGGAAAGGGTA

5720 5730 5740 5750 5760 5770

5290 5300 5310 5320 5330 5340

Lem ATTCAACTTATACTATTTAACCACATATGTTGTGCTGGTTCATAATTATATAGTACATGT

:::::::::::::::::::::::::::::::: :::::::::::::::::::::::::::

Lpa ATTCAACTTATACTATTTAACCACATATGTTGCGCTGGTTCATAATTATATAGTACATGT

5780 5790 5800 5810 5820 5830

5350 5360 5370 5380 5390 5400

Lem GACCACATGAAGGAGACATTATTGTCTACTAGCAATCAATTTCACTTCTTTTGAATGCTG

::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::::

Lpa GACCACATGAAGGAGACATTATTGTCTACTAGCAATCAACTTCACTTCTTTTGAATGCTG

5840 5850 5860 5870 5880 5890

5410 5420 5430 5440 5450 5460

Lem AGTTGAGGTTCATTTCGGGCATTTATGCCTTCACACTATGATTTTCAGCTGGAATTGTGT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa AGTTGAGGTTCATTTCGGGCATTTATGCCTTCACACTATGATTTTCAGCTGGAATTGTGT

5900 5910 5920 5930 5940 5950

5470 5480 5490 5500 5510 5520

Lem ATATATCTTTTTGTTACCTAAGGCTGCTGTGGGATGGTCTTCAAAGCTTCTTGACTTGTC

::::::::::::::::::::::::::::::::::::::: :::::::::: :::::::::

Lpa ATATATCTTTTTGTTACCTAAGGCTGCTGTGGGATGGTCATCAAAGCTTCCTGACTTGTC

5960 5970 5980 5990 6000 6010

5530 5540 5550 5560 5570 5580

Lem AGAAAAAACCGTGCTTCCTTGTACTTTTAAGCGCATGGTCCTTTTGTTTAATGTATCTCA

:::::::::::::::::::::::::::::: :: :::::::::::::::::::::: :::

Lpa AGAAAAAACCGTGCTTCCTTGTACTTTTAATCGTATGGTCCTTTTGTTTAATGTATGTCA

6020 6030 6040 6050 6060 6070

5590 5600 5610 5620 5630 5640

Lem TGGTGAATGCACTTGTCGTACATTATACACGAGCTAGGTTAGGGAAATGGATAAGATTTG

::::::::: ::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TGGTGAATGTACTTGTCGTACATTATACACGAGCTAGGTTAGGGAAATGGATAAGATTTG

6080 6090 6100 6110 6120 6130

5650 5660 5670 5680 5690 5700

Lem TTGGAGTTCGAGATGGGCTGTCCTAACCTGTTTTGATGTTTGTCAACAGAGCTATGTGAT

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TTGGAGTTCGAGATGGGCTGTCCTAACCTGTTTTGATGTTTGTCAACAGAGCTATGTGAT

6140 6150 6160 6170 6180 6190

5710

Lem GGGTTAGG----------------------------------------------------

::::::::

Lpa GGGTTAGGGAAATGGATAAGATTTGTTGGAGTTCGAGATGGGCTGTCCTAACCTGTTTTG

6200 6210 6220 6230 6240 6250

Lem ------------------------------------------------------------

Lpa ATGTTTGTCAACAGAGCTATGTGATGGGTTAGGGAAATGGATAAGATTTGTTGGAGTTCG

6260 6270 6280 6290 6300 6310

Lem ----------------------------------------------------------AA

::

Lpa AGATGGGCTGTCCTAACCTGTTTTGATGTTTGTCAACAGAGCTATGTGATGGGTTAGGAA

6320 6330 6340 6350 6360 6370

5720 5730 5740 5750 5760 5770

Lem TCAAATGAAATTGTGTATTTAGTGTTAGCAAAATTCATCTTTTGTTGTCATCTTCAGAAC

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Lpa TCAAATGAAATTGTGTATTTAGTGTTAACAAAATTCATTCTTTGTTGTCATCTTCAGAAC

6380 6390 6400 6410 6420 6430

5780 5790 5800 5810 5820 5830

Lem TTCCATTG-ATTAATTTCGTTTTCACAGCAAACATTTTCTTTTCTAATGGACGCAGGT**TT**

:::::::: :::::::: ::::::::::::::::::::::::::::::::::::::::::

Lpa TTCCATTGGATTAATTTTGTTTTCACAGCAAACATTTTCTTTTCTAATGGACGCAGGT**TT**

6440 6450 6460 6470 6480 6490

5840 5850 5860 5870 5880 5890

Lem **GAGCAATATGTAGATTATGCACTTGATGTCCCAATGTATTTTGTCTATCGGAAGAAGAAG**

::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **GAGCAGTATGTAGATTATGCACTTGATGTCCCAATGTATTTTGTCTATCGGAAGAAGAAG**

6500 6510 6520 6530 6540 6550

5900 5910 5920 5930 5940 5950

Lem **TATGTTGATTGTACTGGATTGTCTTTCCGGG**TATGTTATTTATAACAATAACAGATTTAT

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Lpa **TATGTTGATTGTACTGGATTGTCTTTCCGGG**TATGTTATTTATAACAATAACAGATTTAT

6560 6570 6580 6590 6600 6610

5960 5970 5980 5990 6000 6010

Lem AAATGTCACTCTCTTGTGCTGATTTAACAACATTGCTGCAGG**ACTTCATGAATGGAAAAC**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa AAATGTCACTCTCTTGTGCTGATTTAACAACATTGCTGCAGG**ACTTCATGAATGGAAAAC**

6620 6630 6640 6650 6660 6670

6020 6030 6040 6050 6060 6070

Lem **TTCCGCCCATTCCCGGCGAATACCCTACTCTTAATGATTGGGAGAATCATCTCACAACAA**

::::::::::::::::::::::::::::::: ::::::::::::::::::::::::::::

Lpa **TTCCGCCCATTCCCGGCGAATACCCTACTCTCAATGATTGGGAGAATCATCTCACAACAA**

6680 6690 6700 6710 6720 6730

6080 6090 6100 6110 6120 6130

Lem **TATTTCCTGAGGTCAGACTCAAAAGATATCTGGAAATGAGAGGTGCTGATGGAGGGCCTT**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **TATTTCCTGAGGTCAGACTCAAAAGATATCTGGAAATGAGAGGTGCTGATGGAGGGCCTT**

6740 6750 6760 6770 6780 6790

6140 6150 6160 6170 6180

Lem **GGAGACGGTTATGCGCATTGCCTGCATTCTGGGT**ACGCAATCTGA--CTCTAGGATTTAT

::::::::::::::::::::::::::::::::::: :::::::: :::::::::::::

Lpa **GGAGACGGTTATGCGCATTGCCTGCATTCTGGGT**ATGCAATCTGTTTCTCTAGGATTTAT

6800 6810 6820 6830 6840 6850

6190 6200 6210 6220 6230 6240

Lem GATGTTGTTTTTTGTAAAAGAAGGAAACAAAAAGCGAGTATTACTCGGTAAAGCACCAGG

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Lpa GATGTTGTTTTTTGTAAAAGAAGGAAACAAAAAGCGAGTATTACTCGGTAAAGCACCAGG

6860 6870 6880 6890 6900 6910

6250 6260 6270 6280 6290 6300

Lem GAAAGGGAGAATAGAATATTGTGCTCACCTCACCTCCCACTGAGAGGAACTTCTTACTCT

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Lpa GAAAGGGAGAATAGAATATTGTGCTCACCTCACCTCCCAGTGAGAGGAACTTCTTACTCT

6920 6930 6940 6950 6960 6970

6310 6320 6330 6340 6350 6360

Lem TTCTCCTGTTTGTTGGGACAATTGCAAAGTTTGTTGTGGCTACTTTGAACCAAACAGCTC

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Lpa TTCTCCTGTTTGTTGGGACAATTCCGAAGTTTGTTGTGGCTACTGTGAACCAAACAGCTC

6980 6990 7000 7010 7020 7030

6370 6380 6390 6400 6410 6420

Lem AGTCATCTTCTTTTTTTCCTTTTCTTTTTTTCAGGT**GGGTATACTCTACGATGAGGGGTC**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa AGTCATCTTCTTTTTTTCCTTTTCTTTTTTTCAGGT**GGGTATACTCTACGATGAGGGGTC**

7040 7050 7060 7070 7080 7090

6430 6440 6450 6460 6470 6480

Lem **TTTGCAAAGCGTTTTGGACATGACATTTGATTGGACTGCAGAAGAAAGAGACATGTTAAG**

:::::::::::::::::::::::::: :::::::::::::::::::::::: ::::::::

Lpa **TTTGCAAAGCGTTTTGGACATGACATCTGATTGGACTGCAGAAGAAAGAGAAATGTTAAG**

7100 7110 7120 7130 7140 7150

6490 6500 6510 6520 6530 6540

Lem **GAATAAGGT**AATATATCCTTGCTCATTAAGGATTATCATGCATTTCCTACCTAATCTGTA

::::::::::::::::::::::::::::: ::::::::::::::::::::::::::::::

Lpa **GAATAAGGT**AATATATCCTTGCTCATTAAAGATTATCATGCATTTCCTACCTAATCTGTA

7160 7170 7180 7190 7200 7210

6550 6560 6570 6580 6590 6600

Lem ATTAGCTAATGTATCCATGGCTGCTGATATATCTGCATTTTGTAA-GCATTTATCTATGT

::::::::::::::::::::::::::::: ::::::::::::: :::::: :::::::

Lpa ATTAGCTAATGTATCCATGGCTGCTGATA-ATCTGCATTTTGTGGTGCATTTCTCTATGT

7220 7230 7240 7250 7260 7270

6610 6620 6630 6640 6650

Lem TTT-ATTGTTATGTAACAATTCGTTCTCCTT---TTTTTCTGTTTTTTTTTG-----GTT

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Lpa TTTTATTGTTATGTAACAATTCCTTCTCCTTCTTTTTTTCTTTTTTTTTTTATTTTTGTT

7280 7290 7300 7310 7320 7330

6660 6670 6680 6690 6700 6710

Lem ATCTTCTCGTGATGTCAAATTTGAACTCTTCAGAAACTGTCGAGAGAAAATAAAAAGCAT

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Lpa ATATTCTCGTGATGTCAAATTTGAACTCATCAGAAATTGTCAAGAGACAATAAAAAGCAT

7340 7350 7360 7370 7380 7390

6720 6730 6740 6750 6760 6770

Lem CCAACTGTCTTATTGTAG--TCTCTAGTCATTTTTCTATTCTTTATCTTCTTGTTGATTT

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Lpa CCAACTGTCTTATTGTAGAGTATCTAGTCATTTTTCTATTCTTTATCTTGTTGATGATTT

7400 7410 7420 7430 7440 7450

6780 6790 6800 6810 6820 6830

Lem CAATATTGTGTATTGAAAATGGTCCATATCCTCATGCTTGGAAAAGAGAAACTGTAAATA

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Lpa CAATATTGTGTATTGGAAATGGTCCATATGTTCATGCTTGGGAAAGAGAAACTGTAAATA

7460 7470 7480 7490 7500 7510

6840 6850 6860 6870 6880 6890

Lem GGCCTTTATTTTTATACACTCTGAAATCCTATCTGTATTAAAATATGCTTGCTTTGCTCT

:::::::::::::::: :::::::::::::::::::::::: ::::::::::::::::::

Lpa GGCCTTTATTTTTATAAACTCTGAAATCCTATCTGTATTAATATATGCTTGCTTTGCTCT

7520 7530 7540 7550 7560 7570

6900 6910 6920 6930 6940 6950

Lem TCTCCTTGTGGAACTTGGACAAACAAAATCATTTAGAAACAAAAAAGGGCAATGTGACCA

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa TCTCCTTGTGGAACTTGGACAAACAAAATCATTTAGAAACAAAAAAGGGCAATGTGACCA

7580 7590 7600 7610 7620 7630

6960 6970 6980 6990 7000 7010

Lem TGAATTCTCTATCTAAGAAAAAAAACAGTTGCTTTTCTTAAACTATAATTTTCAGTTCCT

:::::::::::::::::::::::: ::::::::::: ::: ::::::::::::::::::

Lpa TGAATTCTCTATCTAAGAAAAAAA-CAGTTGCTTTT--TAAGCTATAATTTTCAGTTCCT

7640 7650 7660 7670 7680

7020 7030 7040 7050 7060 7070

Lem CAGATTTGGGGTTAGTAATTTATATTCAATATTGGAGATGACTAATATCACTCCCATTTA

:::::::::::::::::::::::::::::::::::::::::::::::::::::: :::::

Lpa CAGATTTGGGGTTAGTAATTTATATTCAATATTGGAGATGACTAATATCACTCC-ATTTA

7690 7700 7710 7720 7730 7740

7080 7090 7100 7110 7120 7130

Lem GTAGG**TGCCAAAAAGTGGTCTGAAGACACCATTTCGAGATGGATTGCTTATGCATGTTGC**

:::::::::::::::::: ::: ::::::::::::::::::::::::::::::::::::

Lpa ATAGG**TGCCAAAAAGTGGTTTGAGGACACCATTTCGAGATGGATTGCTTATGCATGTTGC**

7750 7760 7770 7780 7790 7800

7140 7150 7160 7170 7180 7190

Lem **TCAAGATGTTGTCAAGTTGGCAAAGG**TGGGTTAAAGCTTCTAATGCTCCATGTCTTGGTA

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **TCAAGATGTTGTCAAGTTGGCAAAGG**TGGGTTAAAGCTTCTAATGCTCCATGTCTTGGTA

7810 7820 7830 7840 7850 7860

7200 7210 7220 7230 7240 7250

Lem TATTTCTACATGCCTACTAACTCATTATTTGCTTTCCGATCTTCAGG**AAGGCTTGGAAAG**

::::: ::::::: ::::::::::::::::::::::::::::::::::::::::::::::

Lpa TATTTGTACATGCTTACTAACTCATTATTTGCTTTCCGATCTTCAGG**AAGGCTTGGAAAG**

7870 7880 7890 7900 7910 7920

7260 7270 7280 7290 7300 7310

Lem **AAGAGGCTTTAAGGAAACAGGATTTCTGAACGAAGTAGCCGAGGTTGTTAAAACAGGT**AA

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Lpa **AAGAGGCTTTAAGGAAACAGGATTTTTGAACGAAGTAACCGAGGTTGTCAAAACAGGT**AA

7930 7940 7950 7960 7970 7980

7320 7330 7340 7350 7360 7370

Lem GTAACGACGTAAATTTTTGGTTTGAGATTGTCTTTTTGGACTTGTGTTAGTATCT-----

:::::::::::::::::::::::::::::::::::::: ::::::::: ::::::

Lpa GTAACGACGTAAATTTTTGGTTTGAGATTGTCTTTTTGAACTTGTGTTGGTATCTCTTTA

7990 8000 8010 8020 8030 8040

7380 7390 7400 7410 7420

Lem -TTGT-CTTTGGATACAACACAAAGTCAAATAATGATA-CATTATTTAAACTGCTAGATC

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Lpa CTTGTTCTTTGGATACAACGCAAAGTCAAATAATGATAACATTTTTTTAACTGCTAGATC

8050 8060 8070 8080 8090 8100

7430 7440 7450 7460 7470 7480

Lem CATTTAGAGTTCCAATTGAACTGTTATTTGTACTTCTGGTAGGT**GTAACACCAGCTGAGA**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa CATTTAGAGTTCCAATTGAACTGTTATTTGTACTTCTGGTAGGT**GTAACACCAGCTGAGA**

8110 8120 8130 8140 8150 8160

7490 7500 7510 7520 7530 7540

Lem **AGCTACTGGAATTGTACCATGGGAAGTGGGGACAAAGTGTGGATCCTATCTTTGAGGAGC**

::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Lpa **AGCTACTGGAATTGTACCATGGGAAGTGGGGACAAAGTGTGGATCCTATCTTTGAGGAGC**

8170 8180 8190 8200 8210 8220

7550 7560 7570 7580 7590 7600

Lem **TTCTCTACTGAAGTTGTTTGAGAGTGCAATTTCAATTCTGTCTTTTT-CCTGTGTTGTAA**

::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::::

Lpa **TTCTCTACTGAAGTTGTTTGAGAGTGCAATTTCAATTCTGTCTTTTTTCCTGTGTTGTAA**

8230 8240 8250 8260 8270 8280

7610 7620 7630 7640 7650 7660

Lem **ATGATTTCTCAATTTCATT--GAGAGTTATATCAGCCGATTTTTCCATCGTTAGAC**

::::::::::::::::::: :::::::::::::::::::::::::::::::::::

Lpa **ATGATTTCTCAATTTCATTTTGAGAGTTATATCAGCCGATTTTTCCATCGTTAGAC**

8290 8300 8310 8320 8330 8340

**Fig. 7. Nucleotide sequences of Lem and Lpa *γ-ECS* ortholog genes.** **Blue**, exons; black, introns, **bold black face**, 5`- and 3`-UTR sequences, **Green** underlined, translation start codon and stop codon; **red**, absence (deletion) of the corresponding nucleotides in the parallel sequence.

**The Complete Deduced *γ-ECS* Amino Acid Sequences of Lem, Lpa, and their Comparison with those of other Plants Species**

**Sequence alignment**

The cDNA of *γ-ECS* was found to be of 1840 bp in length with one open reading frame that encodes a 523-aa protein. As expected, the deduced amino acid sequences of the two tomato orthologs show high sequence identity (98%). When compared to γ-ECS sequences of other plants, both share considerable sequence identity with that of *Zea mays* (84%), *Allium cepa* (87%), *Arabidopsis thaliana* (78%), *Brassica juncea* (79%), *Medicago truncatula* (79%), and *Pisum sativum* (81%) (Fig.8). All the above mentioned species, apart from *Zea* and *Medicago*, contain a putative transit peptide beside the catalytic domain and a conserved cleavage site motif (underlined) (Ala)-X-(Val▼Ala) (Fig. 7).

Lem MALMSQAGSSHCIYSEKVRCISGHRSIINNMDMFRMREICFGVDISSRNASRRVQGNYLN 60

Lpa MALMSQAGSSHCIYSEKIRCISGHRNIMNNMDMFRMREICFGVDISSRNASRRVQGNYLN 60

Zea ------------------------------------------------------------

Allium MASISQLQP-------------------NQSRCWQLERKGFPSSLSS--------SSFLN 33

Arabidopsis MALLSQAGGSYTVVPSGVCSKTGTKAVVSGGVR-NLDVLRMKEAFGSSNSRSLSTKSMLL 59

Brassica MALLSQAGGAYTVPSGHVSSRTGTKTVSG-----CVNVLRMKETYVSSYSRTLSTKSML- 54

Medicago ------------------------------------------------------------

Pisum MATIFRVASSTAPPP---------------------HNFRLRKTPVSN---GFSFSSICF 36

: : . . :. . : : .

Lem HIGVGSRRGDLTIVAASPPTED**AVVA**AEPLTKEDLVGYLASGCKSKEKWRIGTEHEKFGF 120

Lpa HIGVGSRRGDLTIVAASPPTED**AVVA**AEPLTKEDLVGYLASGCKSKEKWRIGTEHEKFGF 120

Zea -------------------------MTEPLTKEDLVAYLVSGCKPKENWRIGTEHEKFGF 35

Allium FEKNAKNLRGKFVVSASPPTED**AVVM**TEPLTKDDLVAYLASGCKTKDKWRIGTEHEKFGF 93

Arabidopsis HSVKRSKRGHQLIVAASPPTEE**AVVA**TEPLTREDLIAYLASGCKTKDKYRIGTEHEKFGF 119

Brassica ---KRSKRGHQLIVAASPPTEE**AVVA**TEPLTREDLIAYLASGCKSKEKWRIGTEHEKFGF 111

Medicago ------------------------VATEPLTKQDLIDYLASGCKTKDKWRIGTEHEKFGF 36

Pisum DRRIVSSGGRRLIVAASPPTED**AVVA**TEPLTKQDLIDYLASGCKPKDKWRIGTEHEKFGF 96

. :::..:..: :\*\*\*\*::\*\*: \*\*.\*\*\*\*.\*:::\*\*\*\*\*\*\*\*\*\*\*

Lem EFGTLRPMKYDQIADLLNGIAERFDWEKVMEGDKIIGLKQGKQSISLEPGGQFELSGAPL 180

Lpa EFGTLRPMKYDQIADLLNGIAERFDWEKVMEGDKIIGLKQGKQSISLEPGGQFELSGAPL 180

Zea EVDTLRPLKYDQIRDILNGLAERFDWDKIMEKNNVIGLKQGKQSISLEPGGQFELSGAPL 95

Allium QINTLRPMTYEQIAYLLNGIAERFDWEKVMEGDYVIGLKQGKQSISLEPGGQFELSGAPL 153

Arabidopsis EVNTLRPMKYDQIAELLNGIAERFEWEKVMEGDKIIGLKQGKQSISLEPGGQFELSGAPL 179

Brassica EVNTLRPMKYDQIAELLNSIAERFEWEKVMEGDKIIGLKQGKQSISLEPGGQFELSGAPL 171

Medicago ELGSLRPMKYEQISELLNGIAERFDWDKVMEGDNIIGLKQGKQSISLEPGGQFELSGAPL 96

Pisum ELGSLRPVKYEQIAELLNAIAERFDWEKIMEGDKIIGLKQGKQSISLEPGGQFELSGAPL 156

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Lem ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGTGFQPKWGLKDIPIMPKGRYEIMRNYMPKV 240

Lpa ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGTGFQPKWGLKDIPIMPKGRYEIMRNYMPKV 240

Zea ETLHQTCAEVNSHLYQVKAVGEEMGIGFLGLGFQPKWALSDIPIMPKGRYEIMRNYMPKV 155

Allium ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGAGFQPKWGLKDIPIMPKGRYEIMRNYMPKV 213

Arabidopsis ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGIGFQPKWRREDIPIMPKGRYDIMRNYMPKV 239

Brassica ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGMGFQPKWRREDIPTMPKGRYDIMRNYMPKV 231

Medicago ETLHQTCAEVNSHLYQVKAVAEEMGIGFLGIGFQPKWERKDIPMMPKGRYEIMKKYMPKV 156

Pisum ETLHQTCAEVNSHLYQVKAVTEEMGIGFLGIGFQPKWERKDIPMMPKGRYEIMKKYMPKV 216

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Lem GSLGLDMMFRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTEGKPNGYLSK 300

Lpa GSLGLDMMFRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTEGKPNGYLSK 300

Zea GTLGLDMMFRTCTVQVNLDFSSEQDMIRKFRAGLALQPIATAIFANSPFKEGKPNGFLSL 215

Allium GSMGLDMMFRTCTVQVNLDFSSESDMVRKFRAGLSLQPIATAIFANSPFTEGKPNGFLSK 273

Arabidopsis GTLGLDMMLRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTEGKPNGFLSM 299

Brassica GSLGLDMMLRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTEGKPNGFLSM 291

Medicago GSLGLDMMFRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTDGKPNGFVSM 216

Pisum GSLGLDMMFRTCTVQVNLDFSSEADMIRKFRAGLALQPIATALFANSPFTEGKPNGFVSM 276

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Lem RSHIWTDTDNNRAGMLPFVFDDSFGFEQYVDYALDVPMYFVYRKKKYVDCTGLSFRDFMN 360

Lpa RSHIWTDTDNNRAGMLPFVFDDSFGFEQYVDYALDVPMYFVYRKKKYVDCTGLSFRDFMN 360

Zea RSHIWTDTDNNRAGMLPFVFDDSFGFEQYVDYALEVPMYFVYRNKKYIDCTGMSFRDFMQ 275

Allium RSHIWTDTDNNRSGMLPFVFKDSFGFEQYVDYALDVPMYFVYRNKKYIDCSGLSFRDFMK 333

Arabidopsis RSHIWTDTDKDRTGMLPFVFDDSFGFEQYVDYALDVPMYFAYRKNKYIDCTGMTFRQFLA 359

Brassica RSHIWTDTDKDRTGMLPFVFDDSFGFEQYVDYALDVPMYFAYRNGKYVDCTGMTFRQFLA 351

Medicago RSHIWTDTDKDRTGMLPFVFDDSFGFEQYVDFALDVPMYFVYRKKKYIDCTGMTFRDFLA 276

Pisum RSHIWTDTDKDRTGMLPFVFDDSFGFEQYVDYALDVPMYFAYRKKKYVDCTGMTFRDFLA 336

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Lem GKLPPIPGEYPTLNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGILYDE 420

Lpa GKLPPIPGEYPTLNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGILYDE 420

Zea GKLPQAPGELPTLTDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGLLYDE 335

Allium GKLSPVPGELPTLNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGLLYDD 393

Arabidopsis GKLPCLPGELPSYNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGLLYDD 419

Brassica GKLPCLPGELPTYNDWENHLTTIFPEVRLKRYMEMRGADGGPWRRLCALPAFWVGLLYDE 411

Medicago GKLPCIPGELPTLNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGILYDE 336

Pisum GKLPCIPGELPTLNDWENHLTTIFPEVRLKRYLEMRGADGGPWRRLCALPAFWVGLLYDE 396

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Lem GSLQSVLDMTFDWTAEERDMLRNKVPKSGLKTPFRDGLLMHVAQDVVKLAKEGLERRGFK 480

Lpa GSLQSVLDMTSDWTAEEREMLRNKVPKSGLRTPFRDGLLMHVAQDVVKLAKEGLERRGFK 480

Zea ESLQSILDMTFDWTKEEREMLRRKVPSTGLKTPFRDGYVRDLAEEVLKLAKNGLERRGYK 395

Allium IALQSVIEITADWTREERDMLRRKVPVTGLKTPFRDGLLKHVAEDVLKLAQGGLERRGYK 453

Arabidopsis DSLQAILDLTADWTPAEREMLRNKVPVTGLKTPFRDGLLKHVAEDVLKLAKDGLERRGYK 479

Brassica DVLQSVLDLTADWTPAEREMLRNKVPVTGLKTPFRDGLLKHVAEDVLKLAKDGLERRGYK 471

Medicago VSLQRVLDMTADWTLEEREMLRNKVTVTGLKTPFRDGLLKHVAEEVLELAKDGLERRGFK 396

Pisum VSLQRVLDMTADWTLEEREMLRNKVTVTGLKTPFRDGLLKHVAEEVLELAKDGLERRGFK 456

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Lem ETGFLNEVAEVVKTGVTPAEKLLELYHGKWGQSVDPIFEELLY 523

Lpa ETGFLNEVTEVVKTGVTPAEKLLELYHGKWGQSVDPIFEELLY 523

Zea EVGFLREVDEVVRTGVTPAERLLSPYETKWQRNVDHVFEHLLY 438

Allium EVGFLREVAEVVNTGVTPAEKLLELYHGKWGCNVDPIFQELLY 496

Arabidopsis EAGFLNAVDEVVRTGVTPAEKLLEMYNGEWGQSVDPVFEELLY 522

Brassica EVGFLNAVTEVVRTGVTPAENLLEMYNGEWGQSVDPVFQELLY 514

Medicago ESGFLNAVAEVVRTGVTPAERLLELYHGKWEQSVDHVFDELLY 439

Pisum ESGFLNAVAEVVRTGVTPAERLLELYHGKWEQSVDHVFEELLY 499

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**Fig. 8. Alignment of known γ-ECS amino acid sequence.** The putative catalytic domains as defined by Lueder and Phillips (1996) are shaded. The underlined residues indicate the putative mitochondrial transit peptide in *Brassica*. Polymorphic Lem and Lpa amino acids are red highlighted. The GenBank accession numbers are as follow: *Zea mays* – CAC83005; *Allium cepa* – AAL61610; *Arabidopsis thaliana* – CAA82626; *Brassica juncea* – CAD91713; *Medicago truncatula* – Q9ZNX6; and *Pisum sativum* – AAF22137.

**Table 2: The primers used for genomic γ-ECS cloning and sequencing**

|  |  |
| --- | --- |
| **Primer** | **Sequence** |
| **fECS12**  **rECS512** | 5’ CAT TCA ATC TGC TAG CAG TTG TCT CT 3’  5’ TTG TTA ACG GCT CTG CTG CAA CAA CA 3’ |
| **fECS467**  **rECS916** | 5' AGT CCT CCA ACA GAG GAT GCT GTT 3'  5' CGG CAT TAT TGG TAT ATC TTT CAG C 3' |
| **fECS893**  **rECS1259** | 5' GCT GAA AGA TAT ACC AAT AAT GCC G 3'  5' CAA AAT ACA TTG GGA CAT CAA GTG C 3' |
| **fECS1235**  **rECS1404** | 5' GCA CTT GAT GTC CCA ATG TAT TTT G 3'  5' GAG TCT GAC CTC AGG AAA TAT TGT 3' |
| **fECS1383**  **rECS1912** | 5' ACA ATA TTT CCT GAG GTC AGA CTC 3'  5’ GTC TAA CGA TGG AAA AAT CGG CTG 3’ |