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       TGGTCGTACCTGCATCGTCGTCACACATCGCTCATTCTACCTTGCGACACATCTCTTGGCTCGTCACACTCTCATATCGCTCGGGTACTCGACTTTCGTCGACACAA
       TCTCGTACGTCTCGGACCATCTCTAGCGAACAGCTTCGAATTCGCTCGACACCTTATATCGTGCGCCGGTCGA

 181 - ATGGCCACTAACCGGCACGCGACTTCGTTTATAAATCACAACATGTTTATTTGTATTTTCGTCTCGCTCTTGTTGCCGATGGCGAACGAAGGTGCCGCG
   1 - M   A   T   N   R   H   A   T   S   F   I   N   H   N   M   F   I   C   I   F   V   S   L   L   L   P   M   A   N   E   G   A   A

 280 - AATGTGTACGGTGACAGCCGAAGTTTTCCGAACGATGACGGAGGGAAAAGATTGTCGAGGGAATACCACCTGAGACAGGGTGCGCTTAGAGGATTGATA
  34 - N   V   Y   G   D   S   R   S   F   P   N   D   D   G   G   K   R   L   S   R   E   Y   H   L   R   Q   G   A   L   R   G   L   I

 379 - GTGAAACCAAGTCGGCAGTATGATTTTCAGTATGTGGAAATGTTTCTTGGCATACCGTATGCTGCTCCGCCGACGGGGCACCTAAGGTTTATGCCACCA
  67 - V   K   P   S   R   Q   Y   D   F   Q   Y   V   E   M   F   L   G   I   P   Y   A   A   P   P   T   G   H   L   R   F   M   P   P

 478 - GTCAGCGCCCCACCATGGCCTGGAGTGAAGATGGCGACACGTTTCGCCCCTGTCTGTCCCCAGTCACTCCCTCCCATCAAGAAGGGGAACCCTCCATCA
 100 - V   S   A   P   P   W   P   G   V   K   M   A   T   R   F   A   P   V   C   P   Q   S   L   P   P   I   K   K   G   N   P   P   S

 577 - TCAGGTCGGCAGCACTACTTGAACCAGCTGAAGACATTCCTCACTAATGAATCTGAAGACTGCCTGTACTTGAATATTTATGTTCCTTATAGAGAACAA
 133 - S   G   R   Q   H   Y   L   N   Q   L   K   T   F   L   T   N   E   S   E   D   C   L   Y   L   N   I   Y   V   P   Y   R   E   Q

 676 - AAAACAAAGAAGTTTTCCGTCCTGGTGTTCATACACGGTGACTCCTTCGAGTGGAGTTCTGGCAACCCTTATGATGGACGGATGCTGGCCTCGTACGGG
 166 - K   T   K   K   F   S   V   L   V   F   I   H   G   D   S   F   E   W   S   S   G   N   P   Y   D   G   R   M   L   A   S   Y   G

 775 - AATGTCATGGTCATCACTGTCAACTTCAGACTGGGAATTTTGGGTTTCATGAAGCCAAGCCTAACAGAACACGTGTATGGTAACAACGGGTTGCTAGAT
 199 - N   V   M   V   I   T   V   N   F   R   L   G   I   L   G   F   M   K   P   S   L   T   E   H   V   Y   G   N   N   G   L   L   D

 874 - CAGTTGGCAGCACTCCAGTGGATCAAGGATAATATTGAGGATCTAAACGGAGATCCATCATCAGTTACCTTGATGGGACATGGCACTGGAGCAGCCTGT
 232 - Q   L   A   A   L   Q   W   I   K   D   N   I   E   D   L   N   G   D   P   S   S   V   T   L   M   G   H   G   T   G   A   A   C

 973 - GTTAATTTCTTGATGCTTTCTCCTATATCAAATGGGTTATTCCATCGAGCAATACTGATGTCGGGTTCTGCGCTATCAGACTGGGCAATGACAAAGGAC
 265 - V   N   F   L   M   L   S   P   I   S   N   G   L   F   H   R   A   I   L   M   S   G   S   A   L   S   D   W   A   M   T   K   D

1072 - CCAACGCCGTATACACTACAAGTGGCCCAGAGTTTGGGCTGCAATCCTAGCTCTAAGAATATGATGGCTTGCTTGCAGAAGAAACCATTATCAGAAATC
 298 - P   T   P   Y   T   L   Q   V   A   Q   S   L   G   C   N   P   S   S   K   N   M   M   A   C   L   Q   K   K   P   L   S   E   I

1171 - AAAAAAGTCCAGATCTTAGCCCGAGAGTTTGAGACACCACTGGGTCCTGTTGTAGCTGGCTCGTTCATACCGAATGAGCCAGCCAAGACTATGGAGTCT
 331 - K   K   V   Q   I   L   A   R   E   F   E   T   P   L   G   P   V   V   A   G   S   F   I   P   N   E   P   A   K   T   M   E   S

1270 - TATCCGAATCTGTTGAGCAAATATCAACTTCTAAGCGGTGTGACAGAAATGGAAAGGTATCACGACTTCGGCGTAATTGAGTTAGAGCATGGAGTGCTA
 364 - Y   P   N   L   L   S   K   Y   Q   L   L   S   G   V   T   E   M   E   R   Y   H   D   F   G   V   I   E   L   E   H   G   V   L

1369 - GAGAACCAAAGAGATGACTTTATCAAGAAGTATGCTAAGATCATCTTTGAAGGTGCAGAGGATGAAACGCTGAAGTCTATTTTGAAAGAATATGCACCA
 397 - E   N   Q   R   D   D   F   I   K   K   Y   A   K   I   I   F   E   G   A   E   D   E   T   L   K   S   I   L   K   E   Y   A   P

1468 - TCGAAGTTAGACCCCCAGCGCTGGAACGTGGAGGCCAACCGAGACGTTATTCTGAACATGTTCAGTGACGCTCGCACTTTGGCCCCCGTCATCCGCTTC
 430 - S   K   L   D   P   Q   R   W   N   V   E   A   N   R   D   V   I   L   N   M   F   S   D   A   R   T   L   A   P   V   I   R   F

1567 - GCCAACTATCAGTCGAAGGCCAACCGTCATTCCTACTTCTATGTCTTTGGACATAATTCTATCAGCTCGGATTACGCTGCGCTCAACAAAAGCGTACAA
 463 - A   N   Y   Q   S   K   A   N   R   H   S   Y   F   Y   V   F   G   H   N   S   I   S   S   D   Y   A   A   L   N   K   S   V   Q

1666 - GGTCAGGAATTGCCCTATGTATTCGGTGTTCCACTTGGAGCTACGAACACGCACTTCAGTCCTGACTACACCCAGCAGGAGAAGTTACTCAGTGAAGTC
 496 - G   Q   E   L   P   Y   V   F   G   V   P   L   G   A   T   N   T   H   F   S   P   D   Y   T   Q   Q   E   K   L   L   S   E   V

1765 - CTCATGAGGATGTGGACCAACTTCGTCAAATATGGGTCTCCCAACTCACAGGCTCCAGTCAAGTTCTACAATTTGGATAGAAGACATTGGAGCCTCTAT
 529 - L   M   R   M   W   T   N   F   V   K   Y   G   S   P   N   S   Q   A   P   V   K   F   Y   N   L   D   R   R   H   W   S   L   Y

1864 - GATCTTGACTGGCCAGAATACGACAGTACTGGACAGTCATACTTAAGGTTCGACATTCCACCTGAAGTAGATACGTCATACCGGTCAAACTATACCAAG
 562 - D   L   D   W   P   E   Y   D   S   T   G   Q   S   Y   L   R   F   D   I   P   P   E   V   D   T   S   Y   R   S   N   Y   T   K

1963 - TTTTGGATGGACACATTACCAAACAAGATGAGCAAATACGTAGTGGATCCTCTATTTGAGTACACACCACCTCCTTCCTCGCCGAGGCCCAAAATCACT
 595 - F   W   M   D   T   L   P   N   K   M   S   K   Y   V   V   D   P   L   F   E   Y   T   P   P   P   S   S   P   R   P   K   I   T

2062 - CACAGAAATACTGCAGGAAATACGGGTGGGAGTGCAGGAGGAAATTCAGACCCAGGCCGTAGAATTTGGACACCGCATGTGCCAGAAACGCCACACTAT
 628 - H   R   N   T   A   G   N   T   G   G   S   A   G   G   N   S   D   P   G   R   R   I   W   T   P   H   V   P   E   T   P   H   Y

2161 - TCCTCATCATCAATATATGGGAGAATGCGTCCGTATTCGCAGCCAGTACATAAGCCAGACACCAATGTTATATACAAGGAGATTATGTCTATCGAGAAG
 661 - S   S   S   S   I   Y   G   R   M   R   P   Y   S   Q   P   V   H   K   P   D   T   N   V   I   Y   K   E   I   M   S   I   E   K

2260 - CCTTCGCGACCTGTTCCATCAGGATTAATTGAAAAAACCTTCCTATATACTACTACACCCAAACCTAAAGCCAACATGTCCGTAAAAACGTCCAGCGCG
 694 - P   S   R   P   V   P   S   G   L   I   E   K   T   F   L   Y   T   T   T   P   K   P   K   A   N   M   S   V   K   T   S   S   A

2359 - ACCATTACATTGATAGTCTCGTTAGCTATTCTCTTTCTCGCCGTCAACGTTGGAATTTGCTCTATATTGTATTTCAAAAAACGGAAGCTCAGACTACGG
 727 - T   I   T   L   I   V   S   L   A   I   L   F   L   A   V   N   V   G   I   C   S   I   L   Y   F   K   K   R   K   L   R   L   R

2458 - GAACAAACACTCGAGAGTTCTCATCAGCCGCGCGCTGAAATAGGCGAAGTGGATGTAATCGGTCAAAAGAGCTCGAAGGACGACAAAAGCGCTTTGCAA
 760 - E   Q   T   L   E   S   S   H   Q   P   R   A   E   I   G   E   V   D   V   I   G   Q   K   S   S   K   D   D   K   S   A   L   Q

2557 - ACTCTAAAAAACGGCTGCAGCGTCATCAAGTCGATGAGTTTTAATAAAAAGAAAAATAATTCTAAGAAACATAAAAAGAAATCGGATGTCTGTAAAACG
 793 - T   L   K   N   G   C   S   V   I   K   S   M   S   F   N   K   K   K   N   N   S   K   K   H   K   K   K   S   D   V   C   K   T

2656 - CCGAAGTCTGATGACTCAGGTGGATTCAGAGAGAGATTTAAGCTAAGACGGCACTTATCAACGAGTACTCTGGACGCTCATACTAAAGTTAGGGACTGG
 826 - P   K   S   D   D   S   G   G   F   R   E   R   F   K   L   R   R   H   L   S   T   S   T   L   D   A   H   T   K   V   R   D   W

2755 - ATTGCCAATGAAATGATGCATCGATGTTCCCCAGGTATACTAAGAAAATCAAACTCTGATTTAAACGAAAAGCATTCGACTGTGACAAAGCCTTTCACT
 859 - I   A   N   E   M   M   H   R   C   S   P   G   I   L   R   K   S   N   S   D   L   N   E   K   H   S   T   V   T   K   P   F   T

2854 - AGATCGGAAGAACTACTTTCAGACACAAAGAAAAACAAAAAAGATACCATACTGATGAATGACAGCGTAAATTCGAAGAGTTTTGCGTCAAAAACATAC
 892 - R   S   E   E   L   L   S   D   T   K   K   N   K   K   D   T   I   L   M   N   D   S   V   N   S   K   S   F   A   S   K   T   Y
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2953 - AGTAAAACTAGAACTTCTGAGAAAACTACATCCACGTCGGCATTAGGCTCGCATTCATCCATAGAAAGTCATAAGCAATCACTCAACAGTATTAAACAA
 925 -  S  K  T  R  T  S  E  K  T  T  S  T  S  A  L  G  S  H  S  S  I  E  S  H  K  Q  S  L  N  S  I  K  Q

3052 - ACAAGTAAATCAAATGAATCCATAAAAAGTAAAGCTACTGAAAGTATTAAGTCTAAAAAAGTGTCAGTAGCTATCGATGCTACACCTGCAGCTCGAACT
 958 -  T  S  K  S  N  E  S  I  K  S  K  A  T  E  S  I  K  S  K  K  V  S  V  A  I  D  A  T  P  A  A  R  T

3151 - CACTCCATATTAAATCAAGAACCAATCGAAATATCGAAATCATTCGACGCTGGTGACCAAATACATTCCAATAAAGTCGAAAAATCAACGGAAGTTGAA
 991 -  H  S  I  L  N  Q  E  P  I  E  I  S  K  S  F  D  A  G  D  Q  I  H  S  N  K  V  E  K  S  T  E  V  E

3250 - TTTAAAGCTCCAAGTACTATCGATCCAATGAAGAATGAACAAACGTTCACAAATGTTGTAACTCTATCAGTTCAAGATAAACCTTTGGTAATTACTCAC
1024 -  F  K  A  P  S  T  I  D  P  M  K  N  E  Q  T  F  T  N  V  V  T  L  S  V  Q  D  K  P  L  V  I  T  H

3349 - AAGCATTCCTCATCTGATCCAGTTACTGATGTGAATTATGATAAATTACTAGAAAAGATGGAGTCTGCTAATCTTGCAAACATCTTACCACCTGTCACT
1057 -  K  H  S  S  S  D  P  V  T  D  V  N  Y  D  K  L  L  E  K  M  E  S  A  N  L  A  N  I  L  P  P  V  T

3448 - TTCAGAAATGATATAAATGTGACTTCTCGTGAAGAAGTTCACAAGTTAATCCAATGACAGCTGAAGAAGCCTTATTGACTATCAAAAAGAGGAATTTT
1090 -  F  R  N  D  I  N  V  T  S  R  E  E  S  S  Q  V  N  P  M  T  A  E  E  A  L  L  T  I  K  K  R  N  F

3547 - CCTAAAGTATTACCTGATTTGCCAAAGGCGCAAAAGCGTTTATCACTTCAACCGGCGTCGTTGCAAACTTTTCGTGGATATTCGTCCATGGATGATCGT
1123 -  P  K  V  L  P  D  L  P  K  A  Q  K  R  L  S  L  Q  P  A  S  L  Q  T  F  R  G  Y  S  S  M  D  D  R

3646 - CCTAAGGTCCCACCGCAGCCCCCGCCGAGAACTACGACTTTAGAGAGACGTCTTGCATACAAAAACACGAACCATTATCTTCGTTTGATGCTTCCGGT
1156 -  P  K  V  P  P  Q  P  P  P  R  T  T  T  L  E  R  R  L  A  Y  K  N  T  K  P  L  S  S  F  D  A  S  G

3745 - GTTAAAAGAATAAATGAAGACACTGTTAAAAATTATGAAAACATCGATAGTTTGTCACCTTACACGTATTCTGCAGCGACATCGCGTAATGCTTCCTTC
1189 -  V  K  R  I  N  E  D  T  V  K  N  Y  E  N  I  D  S  L  S  P  Y  T  Y  S  A  A  T  S  R  N  A  S  F

3844 - GACAGTAGTAAAGCGGAAACGTCTATTATATTGACAAAAGACAGAGAGATTCCTCGAGTCATAATAGCATCTAGTGACTTGCCTTCCGCGCAAGAACCC
1222 -  D  S  S  K  A  E  T  S  I  I  L  T  K  D  R  E  I  P  R  V  I  I  A  S  S  D  L  P  S  A  Q  E  P

3943 - AGAATAGTAATCACACCATCGCCCAGCCAGGTCGAGATACCTACAAATGCGCCCAGGGTTCGTCTACCTGCTGATTTCCACGTCCAAGCTGGATCACTC
1255 -  R  I  V  I  T  P  S  P  S  Q  V  E  I  P  T  N  A  P  R  V  R  L  P  A  D  F  H  V  Q  A  G  S  L

4042 - ACGTCTTTCTCATCGTTTTGCTCTGATGAAGATGACGATGACGACATTGATATTGATGAAGAATTTGAAGATAAACTCATACAAGAATTGGTTGGTGGC
1288 -  T  S  F  S  S  F  C  S  D  E  D  D  D  D  D  I  D  I  D  E  E  F  E  D  K  L  I  Q  E  L  V  G  G

4141 - GTTGATTCACCAACAAACATGGATGACGTATTAGATTCTAAGGGCCCGGACTCAATTTTTGAGAAGAAATTGGAAATTGTACCTGTAAAAATTAATCCC
1321 -  V  D  S  P  T  N  M  D  D  V  L  D  S  K  G  P  D  S  I  F  E  K  K  L  E  I  V  P  V  K  I  N  P

4240 - GGTATAGTAGTTCCTAAAAAGAAAGAAGATTACGTATGTGTTAGTGATTTATTTTTACCAGACGCTGGTGATTTAGAAAAAACTGCCCAAATAAAACCA
1354 -  G  I  V  V  P  K  K  K  E  D  Y  V  C  V  S  D  L  F  L  P  D  A  G  D  L  E  K  T  A  Q  I  K  P

4339 - AATTTTGGTTTAAACAAACTGCAGCATAGGACAGATAGCATAAATAGGCCACCAGAAAAAGCAGTTAAAATGAAACAAAGGAAGAGCATAAGAACGCCT
1387 -  N  F  G  L  N  K  L  Q  H  R  T  D  S  I  N  R  P  P  E  K  A  V  K  M  K  Q  R  K  S  I  R  T  P

4438 - TCTATTTTGAACCGTAGTGCTAAAGGTAGAGGTAGTGATAAAAGTAGAGATGATTCAGTGAAACTGGAACATTCTAATTCAGGTTCTTCCAATGATACT
1420 -  S  I  L  N  R  S  A  K  G  R  G  S  D  K  S  R  D  D  S  V  K  L  E  H  S  N  S  G  S  S  N  D  T

4537 - GAAACAAGCACAGGGACTGTGAAAAAGGTAGAATTCAAGAAAGGT
1453 -  E  T  S  T  G  T  V  K  K  V  E  F  K  K  G
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TAAATCTCGTCGACACATGCCGTCTGAACAATGCTCGTGCAACATGCGTCAACGTCTGCTCTCGTCGAACATGCTCGACAATGCTCATCGTCGAACTTGCTGCCTGA
ACACACTCGTCGTCAACTACACTGCTCATGCTACTCGTCAACCGTCTCGGCGAGACATCGTCGTCGAACACTCTCGAGACAACTGCTCAACACACTCTCGTCACATC
TCTCAACTCTGCGAGAGACATACAACTCGAACTGCACACTGCTCAGTCGTCAACACAGAGAGTCGTCGATAGCACTGC**AATAA**GCTCGTCTTACACTCGAGTCGACA
ATGCTCGATCGCTCACACTGCTCGAGAGTCTGCGTACGTCGCACATGGTCACATCTCATCTAACAATTGCACATTCGAGCATCGTCTGCCACATGTCGTCAAGTCGA
CATGCACACTGCTGCTCACTCGAAAAAAAAAAAAAAAA
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Fig. S1. Nucleotide and deduced amino acid sequences of *A. ipsilon* NLG1. Nucleotide (upper line) and amino acid (lower line) numbers are given on the left. The *AiNLG1* cDNA of 5047 bp contains a 180-bp 5'-untranslated region, an open reading frame of 4401 bp and a 466-bp 3'-untranslated region with a polyadenylation signal upstream of the poly(A) tail. The *AiNLG1* ORF was translated into a 1467 amino acid sequence.

Table S1. List of the primers used in the study.

Primer name	Sequence
NLG1dir	5'-TACGGGTGGGAGTGCAGGAGG-3'
NLG1rev	5'-GCCTAATGCCGACGTGGATGT-3'
NLG15'-RACE1	5'-GCGAATACGGGACGCATTCTCC-3'
NLG15'-RACE2	5'-CCAGTCTGATAGCGCAGAACCC-3'
NLG13'-RACE1	5'-CCATACTGATGAATGACAGCG-3'
NLG13'-RACE2	5'-GCGCCCAGGGTTCGTCTACCTG-3'
qNLG1dir	5'-CCTCCTTCCTCGCCGAGGCCC-3'
qNLG1rev	5'-GGAACAGGTCGCGAAGGCTTC-3'
RpL8dir	5'-CCAGTTTGTCTACTGCGGCAA-3'
RpL8rev	5'-GCTTAACCCTAGTACGCTTGGCA-3'