spalt is functionally conserved in *Locusta* and *Drosophila* to promote wing growth

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Supplementary Information

Sup Fig. 1 Lmsal cDNA and putative translation

Lmsal411 (1-2087 bases)

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1      TGAGGTTTCGTTCTAGCTGATATTTTTAGAGGACGTATTTTAAATGACTGTTTTAACGATACCCGTGTTCTGAACCTAATTTTCGTTTTC
1       *  G  F  V  L  A  D  I  F  R  G  R  I  L  N  D  C  F  N  D  T  R  V  L  N  L  I  F  V  F

91     TTCTGTTCCAGGTGAGTACCCAGTGTTGAATGCCTCTGCACCATGCAAGTCTTACCTGGTAAGTCGGAGCAAGCTTCGCCGTGTTCTGAA
31      F  C  S  R  *  V  P  S  V  E  C  L  C  T  M  Q  V  L  P  G  K  S  E  Q  A  S  P  C  S  E

181    GTGGCCTGTTACCAGTTCAGTATTCGCTCTCGAAATCACGATAAAGCGGACTTTCGACTGCAGCGGCGCCTGCAATGCATCGCATCACCA
61      V  A  C  Y  Q  F  S  I  R  S  R  N  H  D  K  A  D  F  R  L  Q  R  R  L  Q  C  I  A  S  P

271    AAGACTTCGGCGCTGGCCTTCGCCACGACACTGTCCGCGTGCGCCGACGAGGACGAGGCCAGCTCGTGCTCGGAGGCGGCAGTCTGTGAA
91      K  T  S  A  L  A  F  A  T  T  L  S  A  C  A  D  E  D  E  A  S  S  C  S  E  A  A  V  C  E

361    GAAGCCGCCGACGTCGACGCCGATGCGGACGGAGACGTGGACGCGGACGGCGAACCAGACGCCGACTGCGACATGATGCTGCTCGACGAG
121     E  A  A  D  V  D  A  D  A  D  G  D  V  D  A  D  G  E  P  D  A  D  C  D  M  M  L  L  D  E

451    CGCAACAACAACGAGGACGACGTAGAGCCCGAGGACGCCGTCTGCGCCGACGTGGCCGACGGAGTCGTCGGCTCCGGCGACGGAGACGCA
151     R  N  N  N  E  D  D  V  E  P  E  D  A  V  C  A  D  V  A  D  G  V  V  G  S  G  D  G  D  A

541    GACACCGACGAGCCCGAGCCGGACGCCGAGCCCGAGGCGCTGACGTCCCCGGCGGCGGGCGTGGTGTCGGCGTTCGGGGCTGCGGTGGCG
181     D  T  D  E  P  E  P  D  A  E  P  E  A  L  T  S  P  A  A  G  V  V  S  A  F  G  A  A  V  A

631    CCGTTCCCGCTGGCAGGGCACGTGACGCTGGAGGCGCTGCAGAACACCAAGGTGGCCGTGGCGCAGTTCGCCGCCACCGCCATGGCCGGC
211     P  F  P  L  A  G  H  V  T  L  E  A  L  Q  N  T  K  V  A  V  A  Q  F  A  A  T  A  M  A  G

721    AACGCCGACAACGCCGCCGCGCTGCAGGAGCTCGCCGTGCTGCAGTCCACGCTCTTCACGCTGCAGCACCAACAGGTGATGCAACTATCG
241     N  A  D  N  A  A  A  L  Q  E  L  A  V  L  Q  S  T  L  F  T  L  Q  H  Q  Q  V  M  Q  L  S

811    TTGATCCAGCAGCTGCAGCAGCAGCTACAGATCACACGCTGCCCCAAGGAGGCAGTGGCGCTCGCGAGTCCACCCCCGGTGCCTGCACCA
271     L  I  Q  Q  L  Q  Q  Q  L  Q  I  T  R  C  P  K  E  A  V  A  L  A  S  P  P  P  V  P  A  P

901    GCAGCAGGACCTGCCTCCGCCCCCGATGCCAGCCCTCCGCCCCCACTGGCACTGCCCCTACCAGCCCAGCAGCAGCACCCATCGCTAGCG
301     A  A  G  P  A  S  A  P  D  A  S  P  P  P  P  L  A  L  P  L  P  A  Q  Q  Q  H  P  S  L  A
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991 CAGGTGCAGCAGTCGACACCTCCGAGCACGCAGTCACTACCCGCCTCTCCGCCTGCTGCCAAGCAGCAGCTTAAGGTGGCGGGGCCATCT
331 Q V Q Q S T P P S T Q S L P A S P P A A K Q Q L K V A G P S

1081 CCTCCACCACCACCTCCGCCCCCACAGGCAGTTCCACAGCAGCAGCAGCTCCACTCGCAGCTCCAGCCACAGCAGCAGCCAGCCCAGGTG
361 P P P P P P P P Q A V P Q Q Q Q L H S Q L Q P Q Q Q P A Q V

1171 CCCCAGCAGCTGCTGCCATGCTCCATCTCGTCATCACTGGCGGCATCTATCATTACCAACCCAGAGCCCCCACCACTCAATGAGCCCAAC
391 P Q Q L L P C S I S S S L A A S I I T N P E P P P L N E P N

1261 ACGTTGGAGATGTTGCAGCGGCGTGCACAAGAGGTACTAGAGAATGCCAGCCAGGGTCTGCTGGCCAACAACCTGGCCGATGAGCTGGCC
421 T L E M L Q R R A Q E V L E N A S Q G L L A N N L A D E L A

1351 TTCCGCAAGGGCGGTGCCGGCGGCAAGTCCAGCTCGCTCTCCCCATACGACTCCAAGTCGGGCCGGAACGAACCCTTCTTCAAGCACCGG
451 F R K G G A G G K S S S L S P Y D S K S G R N E P F F K H R

1441 TGTCGCTACTGTGGAAAGGTCTTCGGAAGTGACTCGGCACTGCAGATACACATCAGGTCGCACACGGGAGAGCGACCGTTCAAGTGCAAC
481 C R Y C G K V F G S D S A L Q I H I R S H T G E R P F K C N

1531 GTATGTGGTAGTCGATTCACCACCAAGGGCAATCTGAAGGTCCATTTCCAGAGGCACTCGGCCAAATTCCCACACATCAAAATGAACCCG
511 V C G S R F T T K G N L K V H F Q R H S A K F P H I K M N P

1621 AACCCAGTGCCAGAACACCTGGACAAGTATCACCCTCCACTGCTGGCACAACTGGGACAAAGCCTGTCACCGCACGGACAGCAGCCGACA
541 N P V P E H L D K Y H P P L L A Q L G Q S L S P H G Q Q P T

1711 CCACCTGTGCCACCAGTCCCACCCCCTCAGAGCCCATTCAGCTTCCCACTGTACAGACCTCCGCAGCCACCGCCTCCACCCCCACAGCAA
571 P P V P P V P P P Q S P F S F P L Y R P P Q P P P P P P Q Q

1801 CAGCAAGCGCAGCATCAGCAACAGCAGCAGCCGTCACAGCAACAGCAGCAAAAACCACAGCCACCACAGCTGCACTCACAGCCCCAGAGA
601 Q Q A Q H Q Q Q Q Q P S Q Q Q Q Q K P Q P P Q L H S Q P Q R

1891 CCGCAACTGCCTGGAACCGCTAATGGGAGCCTACCTCACAACTCACCTGGCTCAGATATACGACACGGTCCTCGTCCGAGGCAGGGACAC
631 P Q L P G T A N G S L P H N S P G S D I R H G P R P R Q G H

1981 GACATCGGACCGAGGATGCCTCACGGTGGCGGAAGCAGCTACGGTCCGCCCCGACCGATGGCTGCGGCCCCACCCCCTCCGCCCCCACCT
661 D I G P R M P H G G G S S Y G P P R P M A A A P P P P P P P

2071 GGCCAGCCCGGGGTCGG
691 G Q P G V

Lmsal468 (1-1073 bases)

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1      GCAGCAACAACAACAACAACAACCGCGACCTCATGAACAGCAGCAGCAGCAGCAGGATGCCAATGAGGAGACACCGTTTGTCAAACA
1        Q  Q  Q  Q  Q  Q  Q  P  R  P  H  E  Q  Q  Q  Q  Q  Q  Q  D  A  N  E  E  T  P  F  V  K  Q

91     GGAAGAGATGGATGACATTGGGTCAACGCAGAGGCGGCAAGATGATGACGAGTGTGAAGGTCACCTTAGTCCGAAGCGTGAACCACCAGA
31       E  E  M  D  D  I  G  S  T  Q  R  R  Q  D  D  D  E  C  E  G  H  L  S  P  K  R  E  P  P  E

181    GGAACCGGAGGATGTCGATATGTCTGCAAGGTTCCCATCATCTTCACCATATGATGACAGTCTGGACAGTAAATACAACAGCCAAGATGA
61       E  P  E  D  V  D  M  S  A  R  F  P  S  S  S  P  Y  D  D  S  L  D  S  K  Y  N  S  Q  D  E

271    GGAGAACAGCCTACAAGACCAGCCAGAGAATCTGTCCAGTAAAGGTGCGGGTGCCTCTAGTAGGCTCTCGCCACCAAGTTCAACGTCTTC
91       E  N  S  L  Q  D  Q  P  E  N  L  S  S  K  G  A  G  A  S  S  R  L  S  P  P  S  S  T  S  S

361    TGGCAGTGCAGTCGCCATAGACCCTGCTAAGGACCCAGCCATCTACACCAGTCTCCTACCACGCCCGGGAAGTAATGACAACTCGTGGGA
121      G  S  A  V  A  I  D  P  A  K  D  P  A  I  Y  T  S  L  L  P  R  P  G  S  N  D  N  S  W  E

451    GTCCCTCATTGAGATCACCAAAACATCGGAGACATCCAAGCTGCAGCAGCTTGTCGACAATATTGAGCACAAATTGACCGACCCAAACCA
151      S  L  I  E  I  T  K  T  S  E  T  S  K  L  Q  Q  L  V  D  N  I  E  H  K  L  T  D  P  N  Q

541    GTGTGTTATCTGCCACCGTGTCCTATCGTGCAAGAGTGCCCTGCAAATGCACTACCGTACGCATACTGGTGAACGGCCCTTCAAGTGCAA
181      C  V  I  C  H  R  V  L  S  C  K  S  A  L  Q  M  H  Y  R  T  H  T  G  E  R  P  F  K  C  K

631    GATATGTGGTCGTGCATTCACAACTAAGGGGAACCTCAAGACACACATGGGCGTGCACCGTGCCAAGCCGCCTGCACGAGTGCTGCACCA
211      I  C  G  R  A  F  T  T  K  G  N  L  K  T  H  M  G  V  H  R  A  K  P  P  A  R  V  L  H  Q

721    GTGCCCCGTATGCCATAAGAAGTTCACCAATGCACTGGTACTGCAGCAGCACATCAGGTTGCACACAGGAGAACCCACCGACCTGACCCC
241      C  P  V  C  H  K  K  F  T  N  A  L  V  L  Q  Q  H  I  R  L  H  T  G  E  P  T  D  L  T  P

811    AGAGCAGATACAAGCTGCAGAGGTGAAGGACTTTCCTGCAGCAGCCTCAGCTCCAGGGCCTGCCTTTCCTGGTCCAGTTTCGTTTCTGCA
271      E  Q  I  Q  A  A  E  V  K  D  F  P  A  A  A  S  A  P  G  P  A  F  P  G  P  V  S  F  L  Q

901    GGCATTCCCACCATTGCCACCACCTGGCATTCACCTTCCACCTGCACAGCACCACACAAAGCTATCAGCAGGATCCACACATGGGGATTT
301      A  F  P  P  L  P  P  P  G  I  H  L  P  P  A  Q  H  H  T  K  L  S  A  G  S  T  H  G  D  F

991    TAAGGAAGAAAAGCCTGACTATCCTGACGATGATAATTCAAGTAGCAGTGGGGGTGGAGGGCAGCAGCAGCAGCAACAACAGC
331      K  E  E  K  P  D  Y  P  D  D  D  N  S  S  S  S  G  G  G  G  Q  Q  Q  Q  Q  Q
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