Figure S1. Sequence alignments of promoter regions of acquisition category I pairs. (A) *CTAGE5* and *CTAGE6*. (B) *GK* and *GK2*. (C) *GLUD1* and *GLUD2*. (D) *GSPT1* and *GSPT2*. (E) *GUSB* and *LOC441046*. (F) *H3F3B* and *LOC440093*. (G) *HMGB1* and *HMG1L1*. (H) *MORF4L1* and *MORF4*. (I) *NACA* and *NACA2*. (J) *PABPC1* and *PABPC3*. (K) *PAPOLA* and *PAPOLB*. (L) *PDHA1* and *PDHA2*. (M) *RAB6A* and *RAB6C*. (N) *RPL10* and *RPL10L*. (O) *TAF1* and *TAF1L*. (P) *TRAM1* and *TRAM1L1*. Transcription start sites are often interspersed around a promoter region. Each site is written in red, and protein-coding sequences are indicated by boxes. If splice junctions are included in the sequences, they are indicated by inverted triangles. The frequency of each transcription start site are available in graphical format at the DBTSS Website, http://dbtss.hgc.jp.

A

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CTAGE5    GTGGGGTGGCGAGGACAGGGTACGTCGCAGGCTTGTGCGGGTCGGGCTCGGACCTGCGCT
           |         | |    |   ||  |     ||   ||||| ||||||| |||| |||||
CTAGE6    TTCAAAATATGTGATGTGAAAACTGCCAGAACTAAGGCGGGCCGGGCTCAGACCAGCGCT

CTAGE5    GCCTCGGGATGTAAAGTATAACAAGAGGGTCGGGATGGG----------CAGCGTAGGCC
          ||||| |||||| |||| |||||||||||| | ||   ||           || | | ||||
CTAGE6    GCCTCAGGATGTGAAGTGTAACAAGAGGGCCAGGGGAGGTGGTGGGGGACAACATGGGCC

CTAGE5    TGTGAGGCCTGCGGGTGCCCCTGTCCCCCAGCTCCCCCCGCAGCCGGCTCCGCAGTGGTC
          |||||||||||| ||||||||  || |||||||||||||||||||| ||||| ||||||||
CTAGE6    TGTGAGGCCTGTGGGTGCCCGCGTTCCCCAGCTCCCCCCGCAGCCCGCTCCACAGTGGTC

CTAGE5    CACTCCGGTTG----CCGGGTGCGGATTCGGGTTCCGGACCGAAGGCTGTGTGTTCTCCG
          | |||||||||     |  ||||| |||||||||||| |||| ||||||| |||||||||
CTAGE6    CGCTCCGGTTGGTTGTCACGTGCGCATTCGGGTTCCAGACCCAAGGCTGCGTGTTCTCCA

CTAGE5    CCGTTTATTGTGGCCCCGACAGGCCGGGGTTACTGTGGCGACCACGAGAGCAGCTTTGGC
          ||| || |||||||          | | ||||||| || |||| | |||||||| | | |
CTAGE6    CCGCTTGTTGTGGC----------CAGTGTTACTGCGGTGACCGCCAGAGCAGCCTCGAC

CTAGE5    GCTATGGAGGAGCCCGGGGTTAC
          ||||||||||||||||| | |||
CTAGE6    GCTATGGAGGAGCCCGGTGCTAC
```

B

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GK      AGCGTTCAGCGGACGCGCGCGGCCTCGATCTCTGGACTCGTCACCTGCCCCTCCCCCTCC
        |  | |   |   |||  ||| ||| |  |||  |||| |   |    |||| ||||
GK2     AAAGGTTGCCTTGCGCCTGCG-CCTTGTGCTCCTGACTGGCTGCGC-TCCCTGCCCCCAA

GK      CGCCGCCGTCACCCAGGAAACCGGCC-GCAATCGCCG-GCCGACCTGAAGCTGGTTTCAT
        | |||||||  ||  |||||| | ||   |   || | ||||||||    ||||| |||
GK2     CACCGCCGTGGCCTGGGAAACGGTCCCAGAGCTGCTGAGCCGACCTA---CTGGTGTCAT

GK      GGCAGCCTCAAAGAAGGCAGTTTTGGGGCCATTGGTGGGGGCGGTGGACCAGGGCACCAG
        ||||||| ||||||  |||| | ||||||| |||||||| ||||||| ||||||||||
GK2     GGCAGCCCCAAAGACAGCAGCTGTGGGGCCGTTGGTGGGAGCGGTGGTCCAGGGCACCAA
```

C

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GLUD1     CCGGCGCGC--GCTGCCGCCAGCGAGGCC-CGGGGAGGCCG------CGG-----CGGAG
          |   |  ||  ||     || |||||||| ||| | | |||      |||     ||||
GLUD2     CAAACAGGCCAGCCAGGCCCGGCGAGGCCGCGGCGGGTCCGGCGCCCCGGACCTCCGGAC

GLUD1     GCGGAGGCCCGGCGCCCTGGGCGGCGCCCTGTCCCCGAAGTCCGTCCTCCCCGTTAGGTG
           |||||| |||||||||||  ||||||||| |||| |||||||||||||||||||||||
GLUD2     CCGGAGGTCCGGCGCCCTGGTTGGCGCCCTGCCCCCAAAGTCCGTCCTCCCCGTTAGGTG

GLUD1     GCGAGCGCCCGAGGGGAGGGGACAGCCGGGCAAGCAGGAAGCTGCGGCTTAAAAGGGCAA
          ||    |||| |||||||||||||||||||| |||||||||||||||||||||||||||||
GLUD2     GC----GCCCAAGGGGAGGGGACAGCCGGGCAGGCAGGAAGCTGCGGCTTAAAAGGGCAA

GLUD1     CCCGCGCGGGACCCTTCCTCCCTAGTCGCGGGGAGTCTGAGAAAGCGCGCCTGTTTCGCG
          ||||||| ||||||||||| |||||||||||||||||||||||||||| |||||| ||||
GLUD2     CCCGCGCCGGACCCTTCCTTCCTAGTCGCGGGGAGTCTGAGAAAGCGCACCTGTTCCGCG

GLUD1     ACCATCACGCACCTCCCCTCCGCTTGTGGCCATGTACCGCTACCTGGGCGAAGCGCTGTT
          ||| ||||||||| | ||||||| ||  || |||||||||||||||| | |||||||| |
GLUD2     ACCGTCACGCACCCCTCCTCCGCCTGCCGCGATGTACCGCTACCTGGCCAAAGCGCTGCT
```

D

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GSPT1    CGGGGGTGGGGTTGGCTGTGAGGCCGTCGGAGGTGGTTGGGT-----GGGAGGAGATCCG
         | || || |||| ||  |||  |  |||||| |||||||||      |||||||||||||
GSPT2    CCGGCGTTGGGTCGGGGGTGGAGGAGTCGGAAGTGGTTGGGGTTTGGGGGAGGAGATCCG

GSPT1    CTCACACACACGAGGAGGAGGGTTGAGCTGCCGCCGCCGCCTCTGTCGTCGTCGCGA
         |||||||||| |||||| || ||||||| |||    | || ||  | | ||  || ||||
GSPT2    CTCACACACAAGAGGAG-AGTGTTGAGCCGCCATATCTGCTGCTGCCGCCGCAGTTGCGA

GSPT1    GTGTGGAGTCGGGACTGGAGCTGCTGCCGCGGCGACGCCGGGGATCTTTGTCGCTAGCTC
          ||  |  ||||  ||  ||||||  |||||| |  ||   || || | ||||||| | |
GSPT2    ATGCAGCATCGGCGCTT-AGCTGCCTCCGCGGTGCAGCTAAGGTTCGT-GTCGCTACCCC

GSPT1    CCGGCCCTTCTGCCCCGCCGCCTTCCCTCAGTCAGCGTTGCCCACTCCTCTCCGGCCGGG
           ||||||||   |  || |||||  | | | | |||  |||| ||| |||  |||| |
GSPT2    TTGGCCCTTCGCTCTTGCTGCCTTAACCCCGCCGGCGGAGCCCGCTCTTCT--GGCCTGT

GSPT1    CGCCCCTGCCTCCATTTCCCGCTCTCTGTCCACCACACACACGGCCCCCCCGATCATGGA
          |  |             |||||| ||  |  |||||||  |     ||  || ||||||
GSPT2    TGAGC-------------CCGCTCCCTCACTGCCACACA-GCAAGTTCCGAGACCATGGA
```

E

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GUSB      CAACCAAGATGGCGCGGAT------GGCTTCAGGCGCATCACGACACCGGCGCGTCACG-
          ||    | ||  |  || |         | |   | |    ||  || ||||||||||
LOC441046 CAGTTCAAATCTCTTGGTTTTAAAAAAATACTTTCCCTCTGCGCGACTGGCGCGTCACGT

GUSB      ------CGACCCGCCCTACGGGCACCTCCCGCGCTTTTCTTAGCGCCGCAGACGGTGGCC
                |||||  | ||   |||| |||||||||||  |  |||  |||||||||| ||||
LOC441046 CGCGCGCGACCAGTCCGCAGGGCTCCTCCCGCGCTGCTGATAGGCCCGCAGACGGCGGCC

GUSB      GAGCGGGGGACCGGGAAGCATGGCCCGGGGGTCGGCGGTTGCCTGGGCGGCGCTCGGGCC
           ||| | ||| ||| |||||||| ||||||| ||||||  ||||||  ||||||||||||
LOC441046 CAGCAGAGGAGCGGAAAGCATGGTCCGGGGGGCGGCGGACGCCTGGTAGGCGCTCGGGCC

GUSB      GTTGTTGTGGGGCTGCGCGCTGGGGCTGCAGGGCGGGATGCTGTACCCCCAGGAGAGCCC
          |||||||||||||||||||||||| |||||||||||||||||||||||    ||||| ||
LOC441046 GTTGTTGTGGGGCTGCGCGCTGGCGCTGCAGGGCGGGATGCTGTACCCAAGAGAGAGGCC

GUSB      GTCGCGGGAGTGCAAGGAGCTGGACGGCCTCTGGAGCTTCCGCGCCGACTTCTCTGACAA
          |||||||||| | ||| |||||||| |||||||||||||||||||||||||||  |||||
LOC441046 GTCGCGGGAGCGGAAGAAGCTGGACCGCCTCTGGAGCTTCCGCGCCGACTTCTTCGACAA

GUSB      CCGACGCCGGGGCTTCGAGGAGCAGTGGTACCGGCGGCCGCTGTGGGAGGTGCGATCTCG
           |   |||  |||||| ||||| ||||||| ||||| | |||| | |||  | | ||
LOC441046 ACTGTGCCTTGGCTTCTAGGAGTAGTGGTATCGGCGTCTGCTGCGAGAGTCGGGCTCCAC
```

F

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H3F3B     TGTGTCGGGGGATGTCAGCGCGTCGGCGAAAGCGCCCACCAATAGAAAAAGTCGTTGGTG
            ||| | |    |  | | || |   | |  | ||  ||     || ||  ||    |
LOC440093 GTTGTAGTGAACCGAAATCACGCCACTGCA--CTCCAGCCTGGGCAACAAAGCGAGACTC

H3F3B     TATG-CAAATAAGGGTTCTATGACGCAGAGACGCAGCGT-GAAGCGTGCCTATAAAAACG
            |  |||| ||     | |  ||  | | ||| | |   |||  | || |  || || |
LOC440093 CGTCTCAAAAAACAAAACAACAACA-AAAAACGAAACACCGAAATGGGCTTTGAAGAATG

H3F3B     GAGGCGACGCGG------GGGCTTGGAGCGCAGAGCGGTTTGGTCGTTCGTTGGGC-GGT
          || | || || |      | |    | |||||||||||||||||||||||||| |  ||
LOC440093 GAAGGGATGCAGATAAAAGAGAGGAGGGCGCAGAGCGGTTTGGTCGTTCGTTGGACCAGT

H3F3B     GCTGGTTTTTCGCTCGTCGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGCGGCGGTC
          |  |||| |||||||| |||||||||||||||||||||||||||||| |||||| ||||
LOC440093 GTCGGTTCTTCGCTCG-CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCAGCGCGGAGGTC
                                         ▼
H3F3B     GGAGAAGTGGCCTAAAACTTCGGCGTTGGGTAGGCGTTCGTAGGTTTACCCGCGGCTTCA
          |||||||||||||||||||||||||||||||    |    | |    | ||  |    ||
LOC440093 GGAGAAGTGGCCTAAAACTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAG----CA
```

G

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HMGB1     TGAGTTGGCGGTAGCCAATAGGAGCCG-CGCTGGCTGGAGAGTAATGTTA--CAGAGCGG
          ||  |     |||| ||    |  | |  | ||| |    |  || |||   ||  |
HMG1L1    TGTATCTATCGTAGACATCTTGCACAGATGTTGGATCTGTATCAAAGTTTGTCATGGATT

HMGB1     AGAGAGTGAGGAGGCTGCGTCTGGCTCCCGCTCTCACAGCCATTGCAGTACATTGAGCTC
                || ||||  |||   |      ||  ||   ||||| |||||||||||||||||
HMG1L1    TTCCTTTGGGGAGAGTGCTATTATAAATCGTACTGTTAGCCACTGCAGTACATTGAGCTC

HMGB1     CATAGAGACAGCGCCGGGGCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCG
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
HMG1L1    CATAGAGACAGCGCCGGGGCAAGTGAGAGCCGTACGGGCACTGGGCGACTCTGTGCCTCG

HMGB1     CTGAGGGTGAGT--CTGGGGCAGCGCCGCGGCGGG---GAGAGCGCCTCCGGCAGCTCCC
          |||| |   | |  ||      | ||   || |      |||   |    ||||
HMG1L1    CTGAAGAAAAATAACTAAACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGT
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H

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MORF4L1   GCTGTCGTTGGCTGGAGCAGCGGCTGCGCGGGTCGCGGTGCTGTGAGGTCTGCGGGCGCT
              |    || ||||| |    || |   |     ||        |     || |  | |
MORF4     AAAATAAAGGGATGGAGGAAGATCTACCAAGCAAATGGAAAACAAAAAAAAGCAGAGGTT

MORF4L1   GGCAAATCCGGCCCAGGATGTAG-AGCTGGCAGTGCCTGACGGCGCGTCTGACGCGGAGT
          | |||  |  | |   |||  |  ||     |   |   |  |  |    ||  |  ||
MORF4     G-CAATCCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGAAACAAAGA

MORF4L1   TGGGTGGGGTAGAG-AGTAGGGGGCGGTAGTCGGGGGTGGTGGGAGAAGGAGGAGGCGGC
           ||       | |   |||  |||    | ||          |  |||||||||||| |||
MORF4     AGGCCATTACATAATGGTAAAGGGATCAATTCAACAAGAAGTGCTGAAGGAGGAGGTGGC

MORF4L1   GAATCACTTATAAATGGCGCCGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGTG
           |||||||||||||||| || |||||||||||||||||||||||||||||||||||| |
MORF4     AAATCACTTATAAATGGTGCTGAAGCAGGACCCGAAGCCTAAATTCCAGGAGGGTGAGCG

MORF4L1   TGCGCCTTTGGGAAAAAGGCACCTAACGGCGCAGGAGATAGAGGCGGGCTCGAGGTGATT
           | ||  | |    |  |||  ||   |    | ||   | ||   |  |  ||||
MORF4     AGTGCTGTGGTTTCATGGGCCTCT---GCTTTATGATGCAAAG--TGTGTAAAGGTTGCC
```

I

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NACA      CGTGGGAACGGCCTGACAGTCACTCGTCAAAGGAAGTGGCTGCCGGCAGCTCTTGACCCG
          |     | |     ||   |    | |   |    |   ||   |||||      ||
NACA2     CTCTAAATCCAATAGATCCTTTTCCATTCCAACTTG-ACCTCATGGCAGTGTAGCACTGC

NACA      GAATCGGATCCTAGTCCCACCCCCTCCGCTCCAGGCTTCCTTCTGCAACAGGCGTGGGTC
            |       ||  |   |  | |||   |    ||||||  |||||||| |||||||||
NACA2     TGACAAATGTCTTTTTAAATGCTCTCTTTTT---GCTTCCCGCTGCAACAAGCGTGGGTC

NACA      ACGCTCTCGCTCGG--TCTTTCTGCCGCCATCTTGGTTCCGCGTTCCCTGCACAGTAAGT
          ||||||||||||   |||||||||||||||||| |||||||||||||||||  || |
NACA2     ACGCTCTCGCTCGCGCTCTTTCTGCCGCCATCTTGCTTCCGCGTTCCCTGCACA--AAAT

NACA      ACTTTCTGTGCCGCTACTGTCTATCCGCAGCCATCCGCCTTTCTTTCGGGCTAAGCCGCC
                        ||    |   | || |||  | ||| |  |  | | |   | |
NACA2     ------------GCCGG-GCGAAGCCACAGA-AACCGTCCCTGCTACAGAGCAGGAGTTG
```

J

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PABPC1    AAATCTAAAAAAATCTTTTAAAAAACCCCCAAAAAAATTTACAAAAAATCCGCGTCTCCCC
          ||    |||||||||  ||| |   |            ||  ||   | |     | |
PABPC3    AAGGAGAAAAAAATTCTTTCATTTATTTTT------TTCCCAGGCATTTTAAATTTGGAT

PABPC1    CGCCGGAGACTTTT----ATTTTTTTTCTTCCTCTTTTATAAAATAACCCGGTGAAGCAG
                |  | |||    |   |  ||  | ||||||||| ||||||||||||||||||||
PABPC3    TATAAAAATCATTTTAGAAAAATCATTAATGCTCTTTTACAAAATAACCCGGTGAAGCAG

PABPC1    CCGAGACCGACCCGCCCGCCCGCGGCCCCGCAGCAGCTCCAAGAAGGAACCAAGAGACCG
          | ||| |||| ||||||||| |||||||||||||||||||||||||||||| ||||||||
PABPC3    CTGAGCCCGAGCCGCCCGCCAGCGGCCCCGCAGCAGCTCCAAGAAGGAACTAAGAGACCA

PABPC1    AGGCCTTCCCGCTGCCCGGACCCGACACCGCCACCCTCGCTCCCCGCCGGCAGCCGGCAG
          ||||||||| |||||||||||||||||||| ||||| ||||||||||||||||||||||
PABPC3    AGGCCTTCCTGCTGCCCGGACCCGACACCGCTACCCTGGCTCCCCGCCGGCAGCCGGCAG

PABPC1    CCAGCGGCAGTGGATCGACCCCGTTCTGCGGCCGTTGAGTAGTTTTCAATTCCGGTTGAT
          |||||||||| |||||||||||||||||||||||||||||||||||| ||| ||| ||||
PABPC3    CCAGCGGCAGCGGATCGACCCCGTTCTGCGGCCGTTGAGTAGTTTTCGATTTCGGCTGAT

PABPC1    TTTTGTCCCTCTGCGCTTGCTCCCCGCTCCCCTCCCCCCCGGCTCCGGCCCCCAGCCCCGG
          |||||||||||||||||||| ||||||||||||||| |||||| || ||||| |||||||
PABPC3    TTTTGTCCCTCTGCGCTTGC-CCCCGCTCCCCTCCCTCCGGCTACG-CCCCCGGCCCCGG

PABPC1    CACTCGCTCTCCTCCTCTCACGGAAAGGTCGCGGCCTGTGGCCCTGCGGGCAGCCGTGCC
          ||| |||||| ||||| | |||||||||||||||| ||||  |||||||||||||||||
PABPC3    CACGCGCTCTACTCCTGTAACGGAAAGGTCGCGGCTTGTGTGCCTGCGGGCAGCCGTGCC

PABPC1    GAG-ATGAACCCCAGTGCCCCCAGCTACCCCATGGCCTCGCTCTACGTGGGGGACCTCCA
          ||| |||||||||||  |||||||||||||| | ||||||||||||||||||||||||||
PABPC3    GAGAATGAACCCCAGCACCCCCAGCTACCCAACGGCCTCGCTCTACGTGGGGGACCTCCA
```

K

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PAPOLA    GCTGGTGCGCAGGCGCACGCACGGCGTGCGTGGTGGCGTCAGCAGTTCTAGAACGTTGCT
          ||||| | || || || |   || |  ||| |    ||  ||  ||||| |||||  ||
PAPOLB    GCTGGCG-GCGGGTGCGCAGGCG-CCCGCGCGTGTACGGTAG--GTTCTGGAACGCAGCC

PAPOLA    GTGGTAGCGCTCGGGCGCCATGTTAGGACGAAGGGGAAGGAGGAGAAGCGCTTAAAGCGG
          |  | || | || |||||||||| || |  |||||||||||||||||| | | ||||||
PAPOLB    GCTG-AGGGGTCTGGCGCCATGTTGGGGCTGAGGGGAAGGAGGAGAAGCTCCTGAAGCGG

PAPOLA    CGGGAGCGGTGCGGGAGAGGGGTTGGACCCAGGGCTGAGGCAGGCCCC--CCCCTCCCTC
          |||| |||  ||||||| |||  |||   | || |   |||||       |||  ||||
PAPOLB    CGGGCGCGCAGCGGGAGTGGGAGTGGGGTC-GGACCAGGGCAGCTAGAAGCCCTGCCCTT

PAPOLA    CCGCCTCAGTGGATCATGCCCAGGGCGGCAGCGGCGGCGGTTGCGG----GGGGGAAGTG
          ||||||||| |||||||| || ||||||| || |||  ||| ||||    |||||| |||
PAPOLB    CCGCCTCAGCGGATCATGACCCGGGCGGCGGCCGCGAAGGTCGCGGTGGTGGGGGACGTG

PAPOLA    ACTGGGCGGTGCCGGCGCCGGA-GACGATGCCGTTGTAAGT---AATTTGTATTCTGTTT
           |  ||||| || ||||| | | || |||||||||    ||   ||        |
PAPOLB    CCCTGGCGGGGCGGGCGCTGAAAGATGATGCCGTTTCCGGTGACAACCCAGGGACCACCG
```

L

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PDHA1     GCCTTTAGCGGGGGCGGGGCACCCCCTGGACGCCGTTCTGGTTGGCCCGCGGCCCGGCGC
           |   | || ||  | |  ||   |    |   |   |||  ||||||  | ||| | ||
PDHA2     ACAGCTGGCAGGCACTGTACAAATCAGTCAGCTCAGGCTGCGTGGCCCATGTCCCAGTGC

PDHA1     AGCGCATGACGTTATTACGACTCTGTCACGCCGCGGTGCGACTGAGGCGTGGCGTCTGCT
           | ||| ||| |   |    | |      ||  | |  ||  ||  ||   |||  |  |
PDHA2     TGTGCAGGACCTGCCTCTATCACCCGTGTGC-ACTGCCCGGATGGTGCCAAGCGCAT--T

PDHA1     GGGGCACCTGAAGGAGACTTGGGGGCACCCGCGTCGTGCCTCCTGG--GTTGTGAGGAGT
          || ||||| |||||||||  || |   ||   | |  |||| | ||  || || | | |
PDHA2     GGAGCACCGGAAGGAGACGCGGAG---CCGAGGCCAGGCCTTCCGGCGGTCGTTACGGGA

PDHA1     CGCCGCTGCCGCCACTGCCTGTGCTTCATGAGGAAGATGCTCGCCGCC---GTCTCCCGC
          ||||||||||  |       |  || | ||| ||| ||||| ||||||    ||||||||
PDHA2     CGCCGCTGCCATCTACA---GCACTCCGTGAAGAATATGCTGGCCGCCTTCATCTCCCGC
```

M

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RAB6A    GGGCCGCAGGCTCGCGCCCGGGCTCGCCCCGCGCCGCTCCAGAGGCTCGCGCACTCAGCA
            | |       |||||| ||||||||| |||||     ||||||||||||||||||||
RAB6C    AAACTGTGTTGAGGCGCCCTGGCTCGCCCTGCGCC-----AGAGGCTCGCGCACTCAGCA

RAB6A    GGTTGGGCTGCGGCGGCGGCGGCAGCTGTGGAAGCTCAGGCGCTGCGCGTGAGAGGTCCC
         ||||||||||||||||||||||   |||| ||||||  | |||| ||||||||||| ||||
RAB6C    GGTTGGGCTGCGGCGGCGGCG---GCTGGGGAAGCCGAAGCGCCGCGCGTGAGAGATCCC

RAB6A    AGATACGTCTGCGGTTCCGGCTCCGCCACCCTCAGCTTCTCTTCCCCAGGTCTGGGAGCC
          ||||| |||||||||  |||||||||||||||| |  ||||| || |||||||  |||||
RAB6C    GGATACATCTGCGGTTTGGGCTCCGCCACCCTCCGTCTCTCTCCCGCAGGTCTCTGAGCC

RAB6A    GAGTGCGGAAGGAGGGAACGGCCCTAGCTTTGGGAAGCCAGAGGACACCCCTGGCTCCTG
         | ||||||||||||||||||||||||||| ||||||||||| || ||||||||||||||||
RAB6C    GGGTGCGGAAGGAGGGAACGGCCCTAGCCTTGGGAAGCCAAAGCACACCCCTGGCTCCTG

RAB6A    CCGACACCGCCCTCCTTCCCTTCCCAGCCGCGGGCCTCGCTCGGTGCTAGGCTACTCTGC
         |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||
RAB6C    CCGACACCGCCCTCCTTCCCTTCCCAGCCGCGGGCCTCGCTCCGTGCTCGGCTACTCTGC

RAB6A    CGGGAGGCGGCGGCGGCTGCCAGTCTGTGGAGAGTCCTGCTGCCCTCCAGCCGGGCTCCT
         |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
RAB6C    CGGGAGGCGGCGGCGGCTGCCAGTCTGTGGCGAGCCCTGCTGCCCTCCAGCCGGGCTCCT

RAB6A    CCA--------------CCGGGCCTTGCAGGGGCCGAGAGAGCTCGGTGCCCGCCCTTCC
         |||               |||| |||||||||||  ||||||||||| |||||||||||
RAB6C    CCAGCCGGGCTCCTCCACCGGCCCTTGCAGGGGCGCAGAGAGCTCGGCGCCCGCCCTTCC

RAB6A    GCTCGCCTTTTTCGTCAGCTGGCTGGAGCAGCATCGGTCCGGGAGGTCTCTAGGCTGAGG
         |||||||||||||||||||| |||||||| |||||||||||||||||||||| ||||||||
RAB6C    GCTCGCCTTTTTCGTCAGCCGGCTGGAGGAGCATCGGTCCGGGAGGTCTCTGGGCTGAGG

RAB6A    CGGCGGCCGCTCCTCTAGTTCCACAATGTCCACGGGCGGAGACTTCGGGAATCCGCTGAG
         ||||| | |||||||||||||||| |||||| |||||||||||||||||||||||||||||
RAB6C    CGGCGACAGCTCCTCTAGTTCCACCATGTCCGCGGGCGGAGACTTCGGGAATCCGCTGAG
```

N

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RPL10     TGGGCTACGCCCGGGCGC--AAGCGCCAAGAGCGGCTGCGTCTATGGTCATGACGTC-TG
              ||  || | |||||  | ||||||   |   |||||||| ||||   |||||| ||
RPL10L    GCCACTTGGCGCAGGCGCTGAGGCGCCAGACGTCCCTGCGTCTCTGGTTGGGACGTCCTG

RPL10     ACAGAGCGTC----CACCCGTCTTCGA-----------------CAGGACTCTATGGTT
          | |||| |||    || ||  ||  |                   |||||||||||||||
RPL10L    AAAGAGAGTCGTCACATCCTCCTCAGGACTCTATGGTTCCGGCCTCAGGACTCTATGGTT

RPL10     CTTACGCGCGCAGACAGACCGCCTATATAAGC-----CATGCGCAGGCGGAGGAGCGCCT
          |   || | |  ||  | |  | |||||||       || ||| ||      |||||| |
RPL10L    CCCGCGAGGGACGAGGGGCAACGTATATAAATGCGCGCAGGCGTAGTTAAGAGAGCGCAT

RPL10     CTTTCCCTTCGGTGTGGTGAGTAAGCGCAGTTGTCGTCTCTTGCGGTGCCGTTGCTGGTT
           |||  |||||  |
RPL10L    -TTTGACTTCGAGGCA-----------------------------------------

RPL10     CTCACACCTTTTAGGTCTGTTCTCGTCTTCCGTTCCGACTCTCTCTTTTTCGTTGCAGCC
                                                                    ||
RPL10L    ---------------------------------------------------------CC

RPL10     ACTGAAGATCCTGGTGTCGCCATGGGCCGCCGCCCCGCCCGTTGGTG--AGTCTTG-AAT
           | || | | ||| |||||||||||| ||||| || || || || |    || ||| ||
RPL10L    GCCGACGTTACTG-TGTCGCCATGGGGCGCCGTCCAGCTCGCTGTTACCGGTATTGTAAG
```

O

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TAF1      GCTTTCCACATATCCATCCTCCTGATCCCGTAGCGTCGAATCAAAAGCCGTTAGTAAAGT
          |    |       | ||     |  |   ||   |   | |    |  | |   |  | ||
TAF1L     GAAGGCAGAGCTTGCAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTG--GGCGACGT

TAF1      AGTTACTTCTTTCTCTTAGGATAGCCGGTCTTTCCGGGTTTTCCCCCCTTCCCCCTCCC
           |  |   ||   ||| |  | |               ||||| |     ||     ||||
TAF1L     TGCGAGA-CTCCGTCTCAAAAAAAAAAAAAAAAAAAAGTTTTGCGGGTTTT-----TCCC

TAF1      CTCTCCCCACTTCCCCCTCCCTTTCCCCTCTGTTTTGAGCTTCCGGTAGAGGCTGGTAGG
          | | ||||  | |||||||||   |||  || | || |||||||||||||| |||||||||
TAF1L     CCCGCCCCTTTGCCCCCTCCC---CCCGCCTTTATTCAGCTTCCGGTAGACGCTGGTAGG

TAF1      GTAAGGGAGCTCAGTAAGTCACTTCTGGGCGACTGTTGTTTTATTTCCGGTCTATGGGAC
          |||||||||||| ||||  ||||||| |||||||||||||||||||||||| |||| |||
TAF1L     GTAAGGGAGCTAAGTAGATCACTTCCGGGCGACTGTTGTTTTATTTCCGGTTTATGCGAC

TAF1      CCGGCTGCGATTTGCTGCTGCGGACAGCAGCTACCATCACTGCTGCCGCCATCATGTCAG
          |||||||||||||||||||| || |||||||||||| |||||   |||||||||||||||
TAF1L     CCGGCTGCGATTTGCTGCTGAGGGCAGCAGCTACCGTCACT---GCCGCCATCATGTCAG
```

P

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TRAM1      GCTCGCGGAGG-CGGCCGCGGCACCAGGGAGCGTCGTCTCCCTGGTGCGCATGCTCGCCC
           |  ||||| |  ||    |    || |    || |||| |||||||||||||||||  |
TRAM1L1    GGGCGCGGCGCTCGATTTCCTTCCCTGCCTCCGCCGTCCCCCTGGTGCGCATGCTCAGCT

TRAM1      CCGCTGCGGGCTAGCTGTTGTGTTTTTTTTTTTCCCCCGGGCGGCC-CGGCGGCTGCGTA
           | |||  |  || ||  |||  || |||||||||    |||||||| | ||| |   | |
TRAM1L1    CAGCTCGGCCCTCGCCTTTGATTTATTTTTTTTCT---GGGCGGCCGCTGCGACCCGGGA

TRAM1      CTGGCTGTGGGATGGGAAGTGAAGCCCCAGCGAGCGGCT------GCAGCGGGGCCGTGA
           ||| ||  |||||||||||||| |||||| | |||| |||      || |||| || ||||
TRAM1L1    CTGACTTCGGGATGGGAAGTGGAGCCCCCG-GAGCTGCTACCGTGGCGGCGGCGCTGTGA

TRAM1      GGAGCAGCCAGCGGGAGGCGGCGGCGA---GTCGGTGAGCAGCTGGGAAGAGCAGAACCG
           |||||||||||| ||||||| || |||    | ||||||| | | |||||| ||      |
TRAM1L1    GGAGCAGCCAGGGGGAGGCAGCTGCGGCTCGCCGGTGAGTATCCGGGAAGCGCCACCATG

TRAM1      GGGCGGAGCACCTGCAGGCGCGGGCGGCGGCCCCACCATGGCGATTCGCAAGAAAAGCAC
                | || ||   ||  | |  |   |  ||| ||   |   |  || || ||  ||
TRAM1L1    -----GGGCTCCGTAAGAAGAGCACCAAGAACCCCCCC--GTTCTCAGCCAGGAATTCAT
```