

Supplementary Materials: Patterns of Spontaneous Nucleotide Substitutions in Grape Processed Pseudogenes

Andrea Porceddu and Salvatore Camiolo

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1 genewise output Score 386.00 bits over entire alignment
2 Hits merged in pseudogene model:
3 query VIT_09s0054g00930.t01 6 subject: chr1 16287427 16287552
4 query VIT_09s0054g00930.t01 7 subject: chr1 16287550 16287651
5 Blastn e-value 2e-11 blastn score 117.8
6
7      21 LTLCPPFVILLWYTMVHADGSVLQTDYDKQHGVQGFIDIWPRPTAIW
8          LTLCPPFVILLWY MVHADGSVLQTDYDKQHGVQGFIDIWPT IA
9          LTLCPPFVILLWYIMVHADGSVLQTDYDKQHGVQGFIDIWPTVIA-
10     558 cactcctgaccttaagcgggtgtcatgtcaccggcgtagatc4cagag
11          tctgcctttttgatttacagcttacgaataaagtagttatgc ccttc
12          ctctccctaagtagtctttagatgccaggtagaacaccgc ctgta
13
14      70 KLIACYAAFEALQLFLPGKTVEGPISPCGNRPVYKANGMQAYAVTLIT
15          FEA LQLFLPGKTVEGPIS GNR VYKAN MQ Y VTLIT
16          -----FEAVLQLFLPGKTVEGPISSSGNRSVYKANNMQTYVTLIT
17     703 tgggccctccgaaggcatttgactgtagaacaatggataa
18          tacttatttcgactagctcccagagctaacaatacattcttc
19          tatatgttattggtgcgatttggtttgaccgaataaggtt
20
21     119 YLSLWWFGIFNPAIVYDHLGEIYSALIFGSLIFCIFYIKGHVAPSSTD
22          YLSLWWFGI+NPAIVYDHLGEIYS L+FGS IFCIFYIKGHVAPSSTD
23          YLSLWWFGILNPAIVYDHLGEIYSTLLFGSFIFCIFYIKGHVAPSSTD
24     826 tcattttgacacgagtgccggtattacctgatattatttaagcggcttag
25          atgtggtgttaccttaaatgatacctttggtttgtttatagatcccca
26          tggggtcacctatttttaaaataatttatcctccacaattgaatgtc
27
28     168 SGSSGNIIIDFYWGMELYPRIGKNFDIKVFTNCRFGMMSWAVLAVTYCI
29          S SS NIIIDFY GMELY RIGKNFDIKVFTN F +MS AVLA+TYCI
30          SSSSNIIIDFYXGMELYLRIGKNFDIKVFTNYXFRVMSRAVLALTYCI
31     973 tattaaaaagtttgagttccagaatgaagtaatttagatcggtgtatta
32          cgccaatttataggtatatgtgaatatattcaagtgttcgcttctcagt
33          ttaccaattctatgggtcattgctccgtcactatgggtgatgtgctta
34
35     217 KQYEENGKVADSMVLNTILMLVYVTKFFWWEAGYW
36          KQYEENGK+A+SM+VNTILML YV KFFWW + W
37          KQYEENGKIANSMIVNTILMLEYVIKFFWWASLLW
38     1120 actggagaagataagaaatcgtgaattttgattt
39          aaaaaagatcactttacttttaattattggcgttg
40          gatagtgaattgtattagggatgagctggatgag
41
42 Dup:      DUP_amb:      AMB:      RET: 30 105 123 158 180 218
43 Disablements 63 180 201 Introns_blastn: none
```

Figure S1. Pseudogene-pater locus alignment.

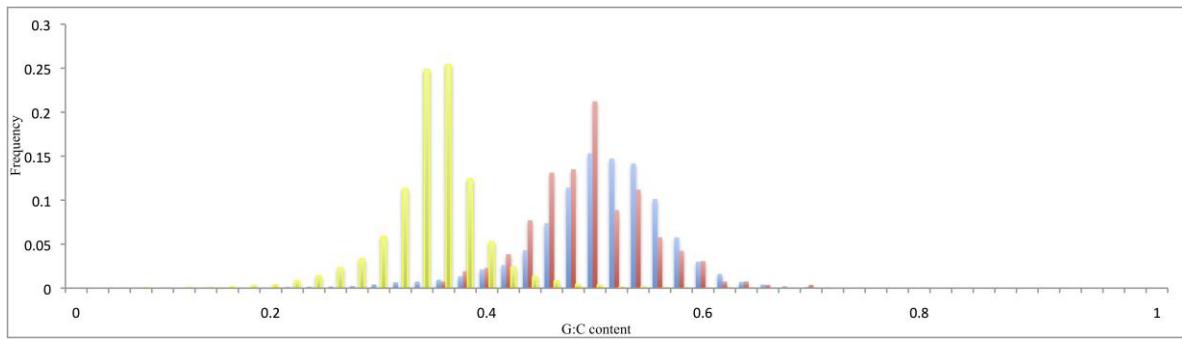
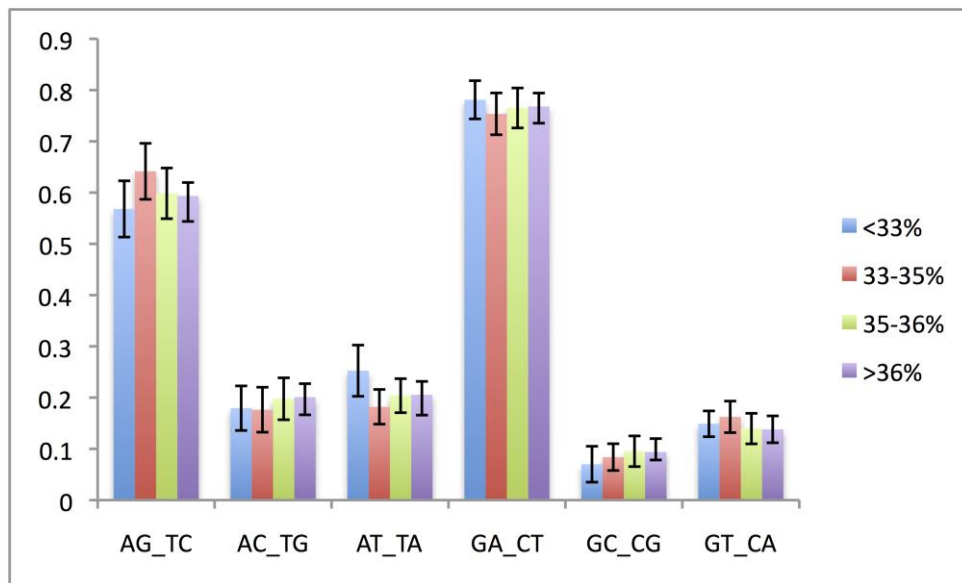
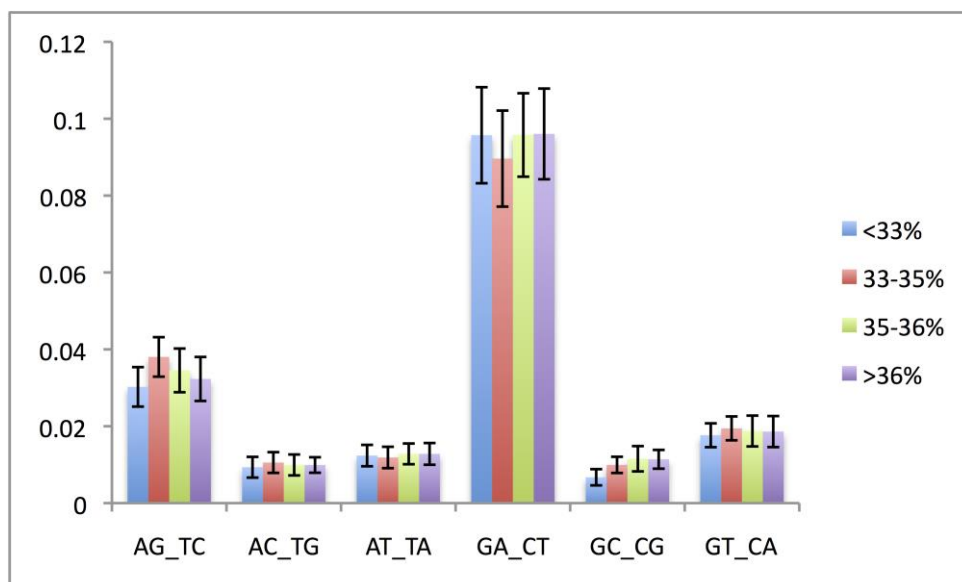


Figure S2. GC3 content of pseudogenes and functional genes.



(a)



(b)

Figure S3. Substitution patterns between nucleotide pairs (non-synonymous dataset).