```
$ cat alignment.maf

s hg18.chrY                   57516699 54 +  57772954 CAGGCTGCCGCTGCAAGAGGCACACCAACACTGTGTGCAGAAAGATCTCTTCTG
s panTro1.chrX               159885141 54 + 160174553 CAGGCTGCCGCTGCAAGAGGCACACCAACACTGTGTGCAGAAAGATCTCTTCTG
s rheMac2.chrX               153702647 54 + 153947521 CAGGCTGCCGCTGCAAGAGGCACACCAACACTGTGTGCAGAAAGATCTCTTCTG
s rn4.chr12                   29439120 54 -  46782294 CGGGCTGCCGCTGCAAAATGCACACCAACACCGTGTGCAGAAAAATGTCTTCCG
s mm8.chrUn_random            1510099 54 -   1540053 CAGGCTGCCGCTGTAAGAGGCACACCAACACTGTGTGCAGAAAAATCTCTTCTA
s oryCun1.scaffold_202349       11799 51 +    102077 CTGGATGCCGTTGTAAAA---ACTCAAATACAGTTTGCTGCAAAGTTCCCACCG
s bosTau2.scaffold136          707093 54 -    730506 CAGGCTGCCGTTGTAAGAGGCACACCAACACTGTGTGCAGAAAAATCTCTTCTG
s canFam2.chrX               126636680 54 + 126883977 CAGGCTGCCGCTGTAAGAGGCACACCAACACTGTGTGCAGGAAAATCTCTTCTG
s dasNov1.scaffold_74633          572 54 +      9076 CAGGCTGCCGCTGTAAGAGGCACACCAACACTGTGTGCAGAAAAATCTCTTCTG
s loxAfr1.scaffold_3802         66002 51 -     96620 CCGGATGCCGTTGTAAAA---ACTCAAACACAGTTTGCTGCAAAGTTCCCACTG
s monDom4.chrX                4719891 54 +  60718501 CAGGCTGCCGATGCAAGAGTCACACCAACACCGTCTGCAGAAAGATCTCCTCTT
s galGal2.chr4               10810201 54 +  90634903 CCGGCTGCCGCTGTCAGACCCACACCAACACGGTGTGCAGAAAGATCTCCTCCT
s xenTro1.scaffold_211         277852 54 +   1682130 CTGGCTGTCGATGTGAGAATCATACTAACACTGTCTGCAGGAAAATATCCTCAT
s tetNig1.chr20              2379020 39 +   3085572 CCGGCTGCCGCTGCAAGA---ACTCCAACACTGTGTACTGCA-----------
s fr1.chrUn                 151900182 51 + 349519338 CAGGCTGCAGGTGCCACA---ACACCAACACCGTGTGCCGCAAAATCTCCGCCT
s danRer3.chr21             36356716 51 +  40779743 CTGGTTGCCGATGCAGCA---ACACCAACACTGTGTGCCGCAAGATCTCTGCCA

$ ./multiperm --num=1 --conservation=level1 alignment.maf

$ cat perm_001_alignment.maf

s hg18.chrY                   57516699 54 +  57772954 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s panTro1.chrX               159885141 54 + 160174553 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s rheMac2.chrX               153702647 54 + 153947521 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s rn4.chr12                   29439120 54 -  46782294 GCAGCAAACGGACAACAATGCTCACCGCCTGACAGTGGCTCGCTTCTATGAAGC
s mm8.chrUn_random            1510099 54 -   1540053 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGTTTGCTTCTATCAAAT
s oryCun1.scaffold_202349       11799 51 +    102077 GTAGAAAATGTACTTCAA---TCACAGCCTGCCATTGGTTAGCCCCAGTTAAGC
s bosTau2.scaffold136          707093 54 -    730506 GTAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGTTTGCTTCTATCAAGT
s canFam2.chrX               126636680 54 + 126883977 GCAGCAAACGAACAACGAGGCTCACCGCCTGGCAGTGGTTTGCTTCTATCAAGT
s dasNov1.scaffold_74633          572 54 +      9076 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGTTTGCTTCTATCAAGT
s loxAfr1.scaffold_3802         66002 51 -     96620 GTAGAAAACGCACTTCAA---TCACAGCCTGCCATTGGTTAGCCCCAGTTAAGT
s monDom4.chrX                4719891 54 +  60718501 GAAGCAAACGAACAACGAGTCTCACCGCCTGACACTGGCTCGCCTCTATCGATT
s galGal2.chr4               10810201 54 +  90634903 GCAGCAAACGCACAACGACCCTCCCCGCCTGACAGTGGTTGGCCTCTATCGATC
s xenTro1.scaffold_211         277852 54 +   1682130 GAAGCAAACGTACAATGAATCTTGCTGCCTGGCACTGGTTTGCCTCTATAAATA
s tetNig1.chr20              2379020 39 +   3085572 GCAGCAAACGCACTTCGA---TCACCGCCTGCCAGTAGCTTG-----------
s fr1.chrUn                 151900182 51 + 349519338 GGAGCAAACGAACCACCA---TCCCCGCATGCCAGTGGCTCGCCTCGATCAATC
s danRer3.chr21             36356716 51 +  40779743 GAAGTAAGCGTACCACCA---TCACCGCCTGCCAGTGGCTTGCTTCGATCGAAC
```

Fig. S2. Sample run of the multiperm program. The input file is in MAF format. The command line parameter num specifies how many permutations to output; there is just one output file perm_001_alignment.maf in this example. The parameter conservation specifies which of several conservation patterns to use; level 1, as described in the paper, is used here.