

```

$ cat alignment.maf

s hg18.chrY          57516699 54 + 57772954 CAGGCTGCCGCTGCAAGAGGCACACCAACTGTGTGCAGAAAAGATCTCTTCTG
s panTrol.chrX      159885141 54 + 160174553 CAGGCTGCCGCTGCAAGAGGCACACCAACTGTGTGCAGAAAAGATCTCTTCTG
s rheMac2.chrX      153702647 54 + 153947521 CAGGCTGCCGCTGCAAGAGGCACACCAACTGTGTGCAGAAAAGATCTCTTCTG
s rn4.chr12         29439120 54 - 46782294 CGGGCTGCCGCTGCAAAAATGCACACCAACCCGTGTGCAGAAAAATGTCTTCCG
s mm8.chrUn_random  1510099 54 - 1540053 CAGGCTGCCGCTGTAAGAGGCACACCAACTGTGTGCAGAAAAATCTCTTCTA
s oryCun1.scaffold_202349 11799 51 + 102077 CTGGATGCCGTTGTAAAA---ACTCAAATACAGTTTGTCTGCAAAGTTCCACCG
s bosTau2.scaffold136 707093 54 - 730506 CAGGCTGCCGTTGTAAAGAGGCACACCAACTGTGTGCAGAAAAATCTCTTCTG
s canFam2.chrX      126636680 54 + 126883977 CAGGCTGCCGCTGTAAGAGGCACACCAACTGTGTGCAGAAAAATCTCTTCTG
s dasNov1.scaffold_74633 572 54 + 9076 CAGGCTGCCGCTGTAAGAGGCACACCAACTGTGTGCAGAAAAATCTCTTCTG
s loxAfr1.scaffold_3802 66002 51 - 96620 CCGATGCCGTTGTAAAA---ACTCAAACACAGTTTGTCTGCAAAGTTCCCACTG
s monDom4.chrX      4719891 54 + 60718501 CAGGCTGCCGATGCAAGAGTCACACCAACACCGTCTGCAGAAAAGATCTCCTCTT
s galGal2.chr4      10810201 54 + 90634903 CCGGCTGCCGCTGTCTAGACCCACACCAACACGGTGTGCAGAAAAGATCTCCTCCT
s xenTrol.scaffold_211 277852 54 + 1682130 CTGGCTGTGATGTGAGAATCATACTAACACTGTCTGCAGAAAAATATCCTCAT
s tetNig1.chr20     2379020 39 + 3085572 CCGGCTGCCGCTGCAAGA---ACTCCAACACTGTGTACTGCA-----
s fr1.chrUn         151900182 51 + 349519338 CAGGCTGCAGTGCACCA---ACACCAACACCGTGTGCCGCAAAAATCTCCGCCT
s danRer3.chr21     36356716 51 + 40779743 CTGTTGCCGATGCAGCA---ACACCAACTGTGTGCCGCAAGATCTCTGCCA

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

$ cat perm_001_alignment.maf

s hg18.chrY          57516699 54 + 57772954 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s panTrol.chrX      159885141 54 + 160174553 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s rheMac2.chrX      153702647 54 + 153947521 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGCTTGCTTCTATCGAGT
s rn4.chr12         29439120 54 - 46782294 GCAGCAAACGACAACAATGCTCACCGCCTGACAGTGGCTCGCTTCTATGAAGC
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 GCAGCAAACGAACAACGAGGCTCACCGCCTGCGAGTGGTTTGCTTCTATCAAGT
s dasNov1.scaffold_74633 572 54 + 9076 GCAGCAAACGAACAACGAGGCTCACCGCCTGACAGTGGTTTGCTTCTATCAAGT
s loxAfr1.scaffold_3802 66002 51 - 96620 GTAGAAAACGCACCTTCAA---TCACAGCCTGCCATTGGTTAGCCCCAGTTAAGT
s monDom4.chrX      4719891 54 + 60718501 GAAGCAAACGAACAACGAGTCTCACCGCCTGACACTGGCTCGCCTTATCGATT
s galGal2.chr4      10810201 54 + 90634903 GCAGCAAACGCACAACGACCTCCCCGCTGACAGTGGTTGGCCTTATCGATC
s xenTrol.scaffold_211 277852 54 + 1682130 GAAGCAAACGTACAATGAATCTTGCTGCCTGGCACTGGTTTGCCTCTATAAATA
s tetNig1.chr20     2379020 39 + 3085572 GCAGCAAACGCACCTTCCA---TCACCGCCTGCCAGTAGCTTG-----
s fr1.chrUn         151900182 51 + 349519338 GGAGCAAACGAACCACCA---TCCCGCATGCCAGTGGCTCGCCTCGATCAATC
s danRer3.chr21     36356716 51 + 40779743 GAAGTAAGCGTACCACCA---TCACCGCCTGCCAGTGGCTTGCTTCTGATCGAAC

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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.