A

```
CHR  START     END       ID            REF, ALT(s)

chr1 248458100 248458100 rs1294550520  A,  C
chr1 248458100 248458126 rs1553320400  AGTGGTTTAACTATTTTAAAATTGGAG,  AG
chr1 248458101 248458101 rs945532251   G,  C
chr1 248458102 248458101 rs370077035   -,  C,  CTCCAATTTTAAAA
chr1 248458102 248458104 rs1558344009  TGG,  CTCCAA
chr1 248458102 248458109 rs774785163   TGGTTTAA,  -
chr1 248458102 248458126 rs766858754   TGGTTTAACTATTTTAAAATTGGAG,  CTCCAATTTTAAAATAGTTAAATCA
chr1 248458103 248458103 rs55778336    G,  C,  T
chr1 248458103 248458108 rs1312056438  GGTTTA,  -
chr1 248458104 248458104 rs11488140    G,  A,  C
chr1 248458105 248458104 rs75431795    -,  AA
chr1 248458108 248458108 rs61834525    A,  T
chr1 248458108 248458111 rs1558344025  AACT,  TAAA
chr1 248458109 248458109 rs1325281402  A,  C
chr1 248458110 248458110 rs78430540    C,  A
chr1 248458110 248458110 rs1283571306  C,  -
chr1 248458111 248458111 rs79278902    T,  A
chr1 248458112 248458111 rs759219409   -,  CCA,  TCA
chr1 248458112 248458112 rs1217534201  A,  C,  T
chr1 248458112 248458112 rs1408812771  A,  -
chr1 248458114 248458114 rs77716920    T,  A
chr1 248458114 248458117 rs1558344038  TTTA,  AGTT
chr1 248458115 248458115 rs78627666    T,  G
chr1 248458117 248458117 rs61834526    A,  T
chr1 248458119 248458119 rs1259249878  A,  C
chr1 248458120 248458120 rs1442840868  A,  G
chr1 248458122 248458122 rs56040868    T,  C
chr1 248458122 248458124 rs752225071   TGG,  -
chr1 248458122 248458126 rs386642020   TGGAG,  AGTTAAATCA,  CA
chr1 248458123 248458124 rs58657081    GG,  -
chr1 248458124 248458124 rs1042592330  G,  A,  C
chr1 248458126 248458126 rs866296781   G,  A
chr1 248458126 248458126 rs58743262    G,  -
chr1 248458127 248458126 rs373041964   -,  TTAAACCA,  TTAAATCA
chr1 248458127 248458128 rs1553320408  CT,  CTCCAATTTTAAAATAGTTAAATCACT
chr1 248458129 248458129 rs1003776664  T,  C
chr1 248458130 248458130 rs1208388863  A,  G
```

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Alignment:

REF GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTGATAAGTGGTTTAACTATTTTAAAATTGGAGCTTATGTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC
ALT GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTGATAAGCTCCAATTTTAAAATAGTTAAATCACTTATGTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC

Switch process:

                                                  ①                                                  ④
F1: GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTG                                                   GTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC
F3:
RF: GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTGATAAGCTCCAATTTTAAAATAGTTAAATCACTTATGTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC
F2:                                                   TATTCGAGGTTAAAATTTTATCAATTTGGTGAATA
                                                      ③                                              ②

Template-switch alignment:

REF GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTG|ATAAGTGgTTTAACTATTTTAAAATTGGAGCTTAT|GTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC
ALT GAAGCAAAAAAACACCAAAAAACTAAAATTATTTCCAGCTTCACTG|ATAAGTGATTTAACTATTTTAAAATTGGAGCTTAT|GTAAAAAAGTCATTGGCTTTTGCTAGATTCTTCATATATTCCTTC
```

B

```
CHR  START     END       ID            REF, ALT(s)

chr1 248437366 248437371 rs1282560120  TTACTT,  TT
chr1 248437373 248437383 rs1362375318  AGTTGTGGAAG,  AG
chr1 248437375 248437375 rs1403073841  T,  A,  C
chr1 248437376 248437376 rs1282373520  T,  G
chr1 248437378 248437378 rs1451470978  T,  C
chr1 248437381 248437382 rs1379895247  AA,  A
chr1 248437388 248437387 rs879403957   -,  TG
chr1 248437389 248437390 rs1234910043  CC,  -
chr1 248437390 248437391 rs879504096   CA,  -
chr1 248437396 248437397 rs369794123   CT,  CTTCCACAACT
chr1 248437398 248437397 rs1205190376  -,  TCC
chr1 248437399 248437398 rs1287619838  -,  CAACTG
```

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Alignment:

REF AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTTTAGTTGTGGAAGAAAA--GCCATTTTCT---------AGAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA
ALT AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTTTAG---------AAAATGGC--TTTTCTTCCACAACTAGAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA

Switch process:

                                                  ①                                                  ④
F1: AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTT                                                   GAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA
F3:
RF: AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTTTAGAAAATGGCTTTTCTTCCACAACTAGAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA
F2:                                                   ATCTTTTACCGAAAAGAAGGTGTTGAT
                                                      ③                                              ②

Template-switch alignment:
REF AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTT|TAGTTGTGGAAGAAAAGCCATTTTCTA|GAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA
ALT AATCAAAACTTCTCTATCGTTCTAAAGATTCCCCAAGTGATTTTACTT|TAGTTGTGGAAGAAAAGCCATTTTCTA|GAAGTGACACTTCATGTGAAAATACTGCTGGGGAGGAAACATAATGA
```

Fig S11. Description of TSM variants in the dbSNP database. (**A**) The TSM locus is described in full with a 25 bp MNV (cyan), but the same changes are also given as multiple SNVs and indels. (**B**) TSM haplotypes can be reconstructed from four different variants (cyan, magenta) but the region has also additional variants annotated.