

Table 4: Fields included in the *motifs.gff* file (generated only when motif analysis is active).

Column	Description
Seqid	Reference tag (e.g. ref00001). Same as refid in the .csv file.
Source	Name of tool -- "kinModCall".
Type	Modification type – a generic tag "modified_base" is used for unidentified bases. For identified bases, m6A, m4C, and m5C are used. A '.' indicates a site where methylation was expected, but was below the significance threshold during the initial kinetics analysis. This suggests a site that is possibly being demethylated in the genome.
Start	Location of modification.
End	Location of modification.
Score	-10 log (p-value) score for the detection of this event. Analogous to a Phred quality score. A value of 20 is the minimum default threshold for this file, and corresponds to a p-value of 0.01. A score of 30 corresponds to a p-value of 0.001. This is the Modification QV for the statistical event detection at this position only, not for the identification. In the case of a multi-site kinetic variation event, such as with Tet-converted 5-mC, it is likely that this score will be very low and the identificationQv (in the Attributes field, below) will contain a higher score that incorporates the full multi-site signal.
Strand	Native sample strand where kinetics were generated. "+" is the strand of the original FASTA and "-" is the reverse complement of the strand. Note that in the .csv file these are marked "0" and "1" respectively.
Phase	Not applicable.
Attributes	<p>Contains extra fields. IPDRatio is traditional IPD Ratio, context is the reference sequence -20bp to +20bp around the modification plus the base at this location as the 21st character, and sequencing coverage of that position. Context is always written in 5' -> 3' orientation of the template strand. The id attribute is added with the complete double-strand methyltransferase motif. The motif attribute is added with the single-strand methyltransferase motif for the modification described in this row of the file. If the motif is palindromic, then the id and motif attributes will be the same. identificationQv is the score for the identification call, if applicable. This is a separate statistical test from the Score field above. Example:</p> <p>context=ATACGCCGGCCATAATGGCGATCGACATTTCTCGCCACGG;motif=GATC;coverage=99;IPDRatio=3.71;id=GATC;identificationQv=174</p>