Sequence Alignment/Map Optional Fields Specification

The SAM/BAM Format Specification Working Group

30 Jan 2019

The master version of this document can be found at https://github.com/samtools/hts-specs. This printing is version 6eb3cd6 from that repository, last modified on the date shown above.

This document is a companion to the Sequence Alignment/Map Format Specification that defines the SAM and BAM formats, and to the CRAM Format Specification that defines the CRAM format. Alignment records in each of these formats may contain a number of optional fields, each labelled with a tag identifying that field’s data. This document describes each of the predefined standard tags, and discusses conventions around creating new tags.

1 Standard tags

Predefined standard tags are listed in the following table and described in greater detail in later subsections. Optional fields are usually displayed as TAG:TYPE:VALUE; the type may be one of A (character), B (general array), f (real number), H (hexadecimal array), i (integer), or Z (string).

<table>
<thead>
<tr>
<th>Tag</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AM</td>
<td>i</td>
<td>The smallest template-independent mapping quality in the template</td>
</tr>
<tr>
<td>AS</td>
<td>i</td>
<td>Alignment score generated by aligner</td>
</tr>
<tr>
<td>BC</td>
<td>Z</td>
<td>Barcode sequence identifying the sample</td>
</tr>
<tr>
<td>BQ</td>
<td>Z</td>
<td>Offset to base alignment quality (BAQ)</td>
</tr>
<tr>
<td>BZ</td>
<td>Z</td>
<td>Phred quality of the unique molecular barcode bases in the OX tag</td>
</tr>
<tr>
<td>CB</td>
<td>Z</td>
<td>Cell identifier</td>
</tr>
<tr>
<td>CC</td>
<td>Z</td>
<td>Reference name of the next hit</td>
</tr>
<tr>
<td>CG</td>
<td>B,I</td>
<td>BAM only: CIGAR in BAM’s binary encoding if (and only if) it consists of &gt;65535 operators</td>
</tr>
<tr>
<td>CM</td>
<td>i</td>
<td>Edit distance between the color sequence and the color reference (see also NM)</td>
</tr>
<tr>
<td>CQ</td>
<td>Z</td>
<td>Color read base qualities</td>
</tr>
<tr>
<td>CR</td>
<td>Z</td>
<td>Cellular barcode sequence bases (uncorrected)</td>
</tr>
<tr>
<td>CS</td>
<td>Z</td>
<td>Color read sequence</td>
</tr>
<tr>
<td>CT</td>
<td>Z</td>
<td>Complete read annotation tag, used for consensus annotation dummy features</td>
</tr>
<tr>
<td>CY</td>
<td>Z</td>
<td>Phred quality of the cellular barcode sequence in the CR tag</td>
</tr>
<tr>
<td>E2</td>
<td>Z</td>
<td>The 2nd most likely base calls</td>
</tr>
<tr>
<td>FI</td>
<td>i</td>
<td>The index of segment in the template</td>
</tr>
<tr>
<td>FS</td>
<td>Z</td>
<td>Segment suffix</td>
</tr>
<tr>
<td>FZ</td>
<td>B,S</td>
<td>Flow signal intensities</td>
</tr>
<tr>
<td>GC</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>GQ</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>GS</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>H0</td>
<td>i</td>
<td>Number of perfect hits</td>
</tr>
<tr>
<td>H1</td>
<td>i</td>
<td>Number of 1-difference hits (see also NM)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Tag</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>H2</td>
<td>i</td>
<td>Number of 2-difference hits</td>
</tr>
<tr>
<td>HI</td>
<td>i</td>
<td>Query hit index</td>
</tr>
<tr>
<td>IH</td>
<td>i</td>
<td>Query hit total count</td>
</tr>
<tr>
<td>LB</td>
<td>Z</td>
<td>Library</td>
</tr>
<tr>
<td>MC</td>
<td>Z</td>
<td>CIGAR string for mate/next segment</td>
</tr>
<tr>
<td>MD</td>
<td>Z</td>
<td>String for mismatching positions</td>
</tr>
<tr>
<td>MF</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>MI</td>
<td>Z</td>
<td>Molecular identifier; a string that uniquely identifies the molecule from which the record was derived</td>
</tr>
<tr>
<td>MQ</td>
<td>i</td>
<td>Mapping quality of the mate/next segment</td>
</tr>
<tr>
<td>NH</td>
<td>i</td>
<td>Number of reported alignments that contain the query in the current record</td>
</tr>
<tr>
<td>NM</td>
<td>i</td>
<td>Edit distance to the reference</td>
</tr>
<tr>
<td>OA</td>
<td>Z</td>
<td>Original alignment</td>
</tr>
<tr>
<td>OC</td>
<td>Z</td>
<td>Original CIGAR (deprecated; use OA instead)</td>
</tr>
<tr>
<td>OP</td>
<td>i</td>
<td>Original mapping position (deprecated; use OA instead)</td>
</tr>
<tr>
<td>OQ</td>
<td>Z</td>
<td>Original base quality</td>
</tr>
<tr>
<td>OX</td>
<td>Z</td>
<td>Original unique molecular barcode bases</td>
</tr>
<tr>
<td>PG</td>
<td>Z</td>
<td>Program</td>
</tr>
<tr>
<td>PQ</td>
<td>i</td>
<td>Phred likelihood of the template</td>
</tr>
<tr>
<td>PT</td>
<td>Z</td>
<td>Read annotations for parts of the padded read sequence</td>
</tr>
<tr>
<td>PU</td>
<td>Z</td>
<td>Platform unit</td>
</tr>
<tr>
<td>Q2</td>
<td>Z</td>
<td>Phred quality of the mate/next segment sequence in the R2 tag</td>
</tr>
<tr>
<td>QT</td>
<td>Z</td>
<td>Phred quality of the sample barcode sequence in the BC tag</td>
</tr>
<tr>
<td>QX</td>
<td>Z</td>
<td>Quality score of the unique molecular identifier in the RX tag</td>
</tr>
<tr>
<td>R2</td>
<td>Z</td>
<td>Sequence of the mate/next segment in the template</td>
</tr>
<tr>
<td>RG</td>
<td>Z</td>
<td>Read group</td>
</tr>
<tr>
<td>RT</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>RX</td>
<td>Z</td>
<td>Sequence bases of the (possibly corrected) unique molecular identifier</td>
</tr>
<tr>
<td>S2</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>SA</td>
<td>Z</td>
<td>Other canonical alignments in a chimeric alignment</td>
</tr>
<tr>
<td>SM</td>
<td>i</td>
<td>Template-independent mapping quality</td>
</tr>
<tr>
<td>SQ</td>
<td>?</td>
<td>Reserved for backwards compatibility reasons</td>
</tr>
<tr>
<td>TC</td>
<td>i</td>
<td>The number of segments in the template</td>
</tr>
<tr>
<td>U2</td>
<td>Z</td>
<td>Phred probability of the 2nd call being wrong conditional on the best being wrong</td>
</tr>
<tr>
<td>UQ</td>
<td>i</td>
<td>Phred likelihood of the segment, conditional on the mapping being correct</td>
</tr>
<tr>
<td>X?</td>
<td>?</td>
<td>Reserved for end users</td>
</tr>
<tr>
<td>Y?</td>
<td>?</td>
<td>Reserved for end users</td>
</tr>
<tr>
<td>Z?</td>
<td>?</td>
<td>Reserved for end users</td>
</tr>
</tbody>
</table>

### 1.1 Additional Template and Mapping data

**AM:i:score** The smallest template-independent mapping quality of any segment in the same template as this read. (See also SM.)

**AS:i:score** Alignment score generated by aligner.

**BQ:Z:qualities** Offset to base alignment quality (BAQ), of the same length as the read sequence. At the $i$-th read base, $BAQ_i = Q_i - (BQ_i - 64)$ where $Q_i$ is the $i$-th base quality.

**CC:Z:raane** Reference name of the next hit; ‘*’ for the same chromosome.

**CG:B:I:encodedCigar** Real CIGAR in its binary form if (and only if) it contains >65535 operations. This is a BAM file only tag as a workaround of BAM's incapability to store long CIGARs in the standard way. SAM and CRAM files created with updated tools aware of the workaround are not expected to contain this tag. See also the footnote in Section 4.2 of the SAM spec for details.
CP:i:pos Leftmost coordinate of the next hit.

E2:Z:bases The 2nd most likely base calls. Same encoding and same length as SEQ. See also U2 for associated quality values.

FI:i:int The index of segment in the template.

FS:Z:str Segment suffix.

H0:i:count Number of perfect hits.

H1:i:count Number of 1-difference hits (see also NM).

H2:i:count Number of 2-difference hits.

HI:i:i Query hit index, indicating the alignment record is the i-th one stored in SAM.

IH:i:count Number of alignments stored in the file that contain the query in the current record.

MC:Z:cigar CIGAR string for mate/next segment.


The MD field aims to achieve SNP/indel calling without looking at the reference. For example, a string '10A5^AC6' means from the leftmost reference base in the alignment, there are 10 matches followed by an A on the reference which is different from the aligned read base; the next 5 reference bases are matches followed by a 2bp deletion from the reference; the deleted sequence is AC; the last 6 bases are matches. The MD field ought to match the CIGAR string.

MQ:i:score Mapping quality of the mate/next segment.

NH:i:count Number of reported alignments that contain the query in the current record.

NM:i:count Number of differences (mismatches plus inserted and deleted bases) between the sequence and reference, counting only (case-insensitive) A, C, G and T bases in sequence and reference as potential matches, with everything else being a mismatch. Note this means that ambiguity codes in both sequence and reference that match each other, such as 'N' in both, or compatible codes such as 'A' and 'R', are still counted as mismatches. The special sequence base '=' will always be considered to be a match, even if the reference is ambiguous at that point. Alignment reference skips, padding, soft and hard clipping ('N', 'P', 'S' and 'H' CIGAR operations) do not count as mismatches, but insertions and deletions count as one mismatch per base.

Note that historically this has been ill-defined and both data and tools exist that disagree with this definition.

PQ:i:score Phred likelihood of the template, conditional on the mapping locations of both/all segments being correct.

Q2:Z:qualities Phred quality of the mate/next segment sequence in the R2 tag. Same encoding as QUAL.

R2:Z:bases Sequence of the mate/next segment in the template. See also Q2 for any associated quality values.

SA:Z:(rname,pos,strand,CIGAR,mapQ,NM;)+ Other canonical alignments in a chimeric alignment, formatted as a semicolon-delimited list. Each element in the list represents a part of the chimeric alignment. Conventionally, at a supplementary line, the first element points to the primary line. Strand is either '+' or '-', indicating forward/reverse strand, corresponding to FLAG bit 0x10. Pos is a 1-based coordinate.

SM:i:score Template-independent mapping quality, i.e., the mapping quality if the read were mapped as a single read rather than as part of a read pair or template.
TC:i: The number of segments in the template.

U2:Z: Phred probability of the 2nd call being wrong conditional on the best being wrong. The same encoding
and length as QUAL. See also E2 for associated base calls.

UQ:i: Phred likelihood of the segment, conditional on the mapping being correct.

1.2 Metadata

RG:Z:readgroup The read group to which the read belongs. If @RG headers are present, then readgroup
must match the RG-ID field of one of the headers.

LB:Z:library The library from which the read has been sequenced. If @RG headers are present, then library
must match the RG-LB field of one of the headers.

PG:Z:program_id Program. Value matches the header PG-ID tag if @PG is present.

PU:Z:platformunit The platform unit in which the read was sequenced. If @RG headers are present, then
platformunit must match the RG-PU field of one of the headers.

CO:Z:text Free-text comments.

1.3 Barcodes

DNA barcodes can be used to identify the provenance of the underlying reads. There are currently three
varieties of barcodes that may co-exist: Sample Barcode, Cell Barcode, and Unique Molecular Identifier
(UMI).

• Despite its name, the Sample Barcode identifies the Library and allows multiple libraries to be combined
and sequenced together. After sequencing, the reads can be separated according to this barcode and
placed in different “read groups” each corresponding to a library. Since the library was generated from
a sample, knowing the library should inform of the sample. The barcode itself can be included in the
PU field in the RG header line. Since the PU field should be globally unique, it is advisable to include
specific information such as flowcell barcode and lane. It is not recommended to use the barcode as
the ID field of the RG header line, as some tools modify this field (e.g., when merging files).

• The Cell Barcode is similar to the sample barcode but there is (normally) no control over the assignment
of cells to barcodes (whose sequence could be random or predetermined). The Cell Barcode can help
identify when reads come from different cells in a “single-cell” sequencing experiment.

• The UMI is intended to identify the (single- or double-stranded) molecule at the time that the barcode
was introduced. This can be used to inform duplicate marking and make consensus calling in ultra-
deep sequencing. Additionally, the UMI can be used to (informatically) link reads that were generated
from the same long molecule, enabling long-range phasing and better informed mapping. In some
experimental setups opposite strands of the same double-stranded DNA molecule get related barcodes.
These templates can also be considered duplicates even though technically they may have different
UMIs. Multiple UMIs can be added by a protocol, possibly at different time-points, which means that
specific knowledge of the protocol may be needed in order to analyze the resulting data correctly.

BC:Z:sequence Barcode sequence (Identifying the sample/library), with any quality scores (optionally)
stored in the QT tag. The BC tag should match the QT tag in length. In the case of multiple unique
molecular identifiers (e.g., one on each end of the template) the recommended implementation con-
catenates all the barcodes and places a hyphen (‘-’) between the barcodes from the same template.

QT:Z:qualities Phred quality of the sample barcode sequence in the BC tag. Same encoding as QUAL,
i.e., Phred score + 33. In the case of multiple unique molecular identifiers (e.g., one on each end of
the template) the recommended implementation concatenates all the quality strings with spaces (‘ ’)
between the different strings from the same template.
CB:Z:str Cell identifier, consisting of the optionally-corrected cellular barcode sequence and an optional suffix. The sequence part is similar to the CR tag, but may have had sequencing errors etc corrected. This may be followed by a suffix consisting of a hyphen (‘-’) and one or more alphanumerical characters to form an identifier. In the case of the cellular barcode (CR) being based on multiple barcode sequences the recommended implementation concatenates all the (corrected or uncorrected) barcodes with a hyphen (‘-’) between the different barcodes. Sequencing errors etc aside, all reads from a single cell are expected to have the same CB tag.

CR:Z:sequence+ Cellular barcode. The uncorrected sequence bases of the cellular barcode as reported by the sequencing machine, with the corresponding base quality scores (optionally) stored in CY. Sequencing errors etc aside, all reads with the same CR tag likely derive from the same cell. In the case of the cellular barcode being based on multiple barcode sequences the recommended implementation concatenates all the barcodes with a hyphen (‘-’) between the different barcodes.

CY:Z:qualities+ Phred quality of the cellular barcode sequence in the CR tag. Same encoding as QUAL, i.e., Phred score + 33. The lengths of the CY and CR tags must match. In the case of the cellular barcode being based on multiple barcode sequences the recommended implementation concatenates all the quality strings with spaces (‘ ’) between the different strings.

MI:Z:str Molecular Identifier. A unique ID within the SAM file for the source molecule from which this read is derived. All reads with the same MI tag represent the group of reads derived from the same source molecule.

OX:Z:sequence+ Raw (uncorrected) unique molecular identifier bases, with any quality scores (optionally) stored in the BZ tag. In the case of multiple unique molecular identifiers (e.g., one on each end of the template) the recommended implementation concatenates all the barcodes with a hyphen (‘-’) between the different barcodes.

BZ:Z:qualities+ Phred quality of the (uncorrected) unique molecular identifier sequence in the OX tag. Same encoding as QUAL, i.e., Phred score + 33. The OX tags should match the BZ tag in length. In the case of multiple unique molecular identifiers (e.g., one on each end of the template) the recommended implementation concatenates all the quality strings with a space (‘ ’) between the different strings.

RX:Z:sequence+ Sequence bases from the unique molecular identifier. These could be either corrected or uncorrected. Unlike MI, the value may be non-unique in the file. Should be comprised of a sequence of bases. In the case of multiple unique molecular identifiers (e.g., one on each end of the template) the recommended implementation concatenates all the barcodes with a hyphen (‘-’) between the different barcodes.

If the bases represent corrected bases, the original sequence can be stored in OX (similar to OQ storing the original qualities of bases.)

QX:Z:qualities+ Phred quality of the unique molecular identifier sequence in the RX tag. Same encoding as QUAL, i.e., Phred score + 33. The qualities here may have been corrected (Raw bases and qualities can be stored in OX and BZ respectively.) The lengths of the QX and the RX tags must match. In the case of multiple unique molecular identifiers (e.g., one on each end of the template) the recommended implementation concatenates all the quality strings with a space (‘ ’) between the different strings.

1.4 Original data

OA:Z:(RNAME, POS, strand, CIGAR, MAPQ, NM;)+ The original alignment information of the record prior to realignment or unalignment by a subsequent tool. Each original alignment entry contains the following six field values from the original record, generally in their textual SAM representations, separated by commas (‘,’) and terminated by a semicolon (‘;’): RNAME, which must be explicit (unlike RNEXT, ‘=’ may not be used here); 1-based POS; ‘+’ or ‘-’, indicating forward/reverse strand respectively (as per bit 0x10 of FLAG); CIGAR; MAPQ; NM tag value, which may be omitted (though the preceding comma must be retained).
In the presence of an existing OA tag, a subsequent tool may append another original alignment entry after the semicolon, adding to—rather than replacing—the existing OA information.

The OA field is designed to provide record-level information that can be useful for understanding the provenance of the information in a record. It is not designed to provide a complete history of the template alignment information. In particular, realignments resulting in the removal of Secondary or Supplementary records will cause the loss of all tags associated with those records, and may also leave the SA tag in an invalid state.

OC:Z:cigar Original CIGAR, usually before realignment. Deprecated in favour of the more general OA.

OP:i:pos Original 1-based POS, usually before realignment. Deprecated in favour of the more general OA.

OQ:Z:qualities Original base quality, usually before recalibration. Same encoding as QUAL.

1.5 Annotation and Padding

The SAM format can be used to represent de novo assemblies, generally by using padded reference sequences and the annotation tags described here. See the Guide for Describing Assembly Sequences in the SAM Format Specification for full details of this representation.

CT:Z:strand;type(;key(=value)?)*

Complete read annotation tag, used for consensus annotation dummy features.

The CT tag is intended primarily for annotation dummy reads, and consists of a strand, type and zero or more key=value pairs, each separated with semicolons. The strand field has four values as in GFF3, and supplements FLAG bit 0x10 to allow unstranded (’.’), and stranded but unknown strand (’?’) annotation. For these and annotation on the forward strand (strand set to ‘+’), do not set FLAG bit 0x10. For annotation on the reverse strand, set the strand to ‘-’ and set FLAG bit 0x10.

The type and any keys and their optional values are all percent encoded according to RFC3986 to escape meta-characters ‘=’, ‘%’, ‘;’, ‘|’ or non-printable characters not matched by the isprint() macro (with the C locale). For example a percent sign becomes ‘%25’.

PT:Z:annotag(\|annotag)* where each annotag matches start;end;strand;type(;key(=value)?)*

Read annotations for parts of the padded read sequence.

The PT tag value has the format of a series of annotation tags separated by ‘|’, each annotating a sub-region of the read. Each tag consists of start, end, strand, type and zero or more key=value pairs, each separated with semicolons. Start and end are 1-based positions between one and the sum of the M/I/D/P/S/=/X CIGAR operators, i.e. SEQ length plus any pads. Note any editing of the CIGAR string may require updating the PT tag coordinates, or even invalidate them. As in GFF3, strand is one of ‘+’ for forward strand tags, ‘-’ for reverse strand, ‘.’ for unstranded or ‘?’ for stranded but unknown strand.

The type and any keys and their optional values are all percent encoded as in the CT tag.

1.6 Technology-specific data

FZ:B:S:intensities Flow signal intensities on the original strand of the read, stored as (uint16_t) round(value * 100.0).

1.6.1 Color space

CM:i:distance Edit distance between the color sequence and the color reference (see also NM).

CS:Z:sequence Color read sequence on the original strand of the read. The primer base must be included.

CQ:Z:qualities Color read quality on the original strand of the read. Same encoding as QUAL; same length as CS.

2The Generic Feature Format version 3 (GFF3) specification can be found at http://sequenceontology.org.
2 Locally-defined tags

You can freely add new tags. Note that tags starting with ‘X’, ‘Y’, or ‘Z’ and tags containing lowercase letters in either position are reserved for local use and will not be formally defined in any future version of this specification.

If a new tag may be of general interest, it may be useful to have it added to this specification. Additions can be proposed by opening a new issue at https://github.com/samtools/hts-specs/issues and/or by sending email to samtools-devel@lists.sourceforge.net.

Appendix A Tag History

This appendix lists when standard tags were initially defined or significantly changed, and other historical events that affect how tags are interpreted or what files they may appear in.

January 2019
Added the OA tag for recording original/previous alignment information.
Deprecated the OC and OP tags.

July 2018
Clarified the calculation of NM score.

May 2018
Cellular barcode tags CB, CR, and CY added.
Removed the RT:Z tag, which was a long-deprecated synonym for BC.

November 2017
SAM version number VN: 1.6 introduced, indicating the addition of the CG tag representation of very long CIGAR strings. Files that contain records with more than 65,535 CIGAR operators should not declare a version number lower than 1.6 in their @HD headers.

August 2017
Unique molecular identifier tags BZ, MI, OX, QX, and RX added.
Usage of sample barcode tag BC clarified.

June 2017
Corrected the description of the E2 (second-most-likely bases) tag, which was previously unclear as to whether it contains bases or base qualities.

September 2016
Predefined tags, previously listed as a brief table within the main SAM specification, have been split out into this new document. There is now space for clearer and more complete tag descriptions.

February 2014
MC tag added.
May 2013
SAM version number \textsc{VN:1.5} introduced, with limited impact for tags other than indicating that the CT/PT annotation tag definitions are considered finalised.

SA tag added.

March 2012
Descriptions of CT and PT annotation tags significantly clarified.

October 2011
Sample barcode tags QT and RT added, with RT being identified as a deprecated alternative to BC. Read annotation tags CT and PT added.

September 2011
FZ tag’s type changed from $H$ to $B,S$-array.
BC and CO tags added.

April 2011
SAM version number \textsc{VN:1.4} introduced, indicating the addition of the $B$-array tag type. Files that contain records with $B$-array fields should not declare a version number lower than 1.4 in their \texttt{@HD} headers.

FZ tag added, with type $H$.
MD tag description changed to allow IUPAC ambiguity codes in addition to ACGTN.

March 2011
CC and CP tags reinstated with their original meanings.

November 2010
BQ tag added.

July 2010
The specification was rewritten as a \LaTeX{} document specifying SAM version number \textsc{VN:1.3}.

Tags FI, FS, OC, OP, OQ, and TC added.
Tags GC:Z, GQ:Z, and GS:Z, briefly proposed for representing repeatedly-sequenced reads, noted as reserved for backwards compatibility. Existing tags MF:i (MAQ pair flag), SQ:H (suboptimal bases), and S2:H (mate’s suboptimal bases) removed and noted as reserved for backwards compatibility.
CC and CP tags temporarily removed.

July 2009
The original SAM “0.1.2-draft” specification specified version number \textsc{VN:1.0} and defined a total of thirty standard tags (though SQ and S2 were already deprecated in favour of E2 and U2):

<table>
<thead>
<tr>
<th>AM</th>
<th>CM</th>
<th>CS</th>
<th>H1</th>
<th>IH</th>
<th>MF</th>
<th>NM</th>
<th>PU</th>
<th>RG</th>
<th>SQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>AS</td>
<td>CP</td>
<td>E2</td>
<td>H2</td>
<td>LB</td>
<td>MQ</td>
<td>PG</td>
<td>Q2</td>
<td>S2</td>
<td>U2</td>
</tr>
<tr>
<td>CC</td>
<td>CQ</td>
<td>H0</td>
<td>H1</td>
<td>MD</td>
<td>NH</td>
<td>PQ</td>
<td>R2</td>
<td>SM</td>
<td>UQ</td>
</tr>
</tbody>
</table>