**SNAP file description (v4; 2018-12-06)**

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| **HD (header session)** | | | |
| **Fields** | **Description** | **Type** | **Value** |
| MG | SNAP magic string | String | SNAP |
| VN | Version of SNAP file | String | v4 |
| DT\* | File created date | String |  |
| CD\* | Current working directory where the file is generated | String |  |
| CL\* | Command line | String |  |
| |  |  |  |  | | --- | --- | --- | --- | | **AL (alignment session)** | | | | | PN\* | Program name (i.e. bwa) | String |  | | ID\* | Program ID | String |  | | VN\* | Program Version | String |  | | CL\* | Command Line | String |  |  |  |  |  |  | | --- | --- | --- | --- | | **SQ (Sequence session)** | | | | | ID | Genome identifier | String |  | | SN | Sequence names | String |  | | SL | Sequence lengths | uint32 |  | | | | |

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| **BD (barcode session)** | | | |
| name | Barcode name (i.e. ATTTGGTTT) | String |  |
| TN | Total number of fragments | unit32 |  |
| UM | Uniquely mapped fragments | unit32 |  |
| SE | Single-end fragments | unit32 |  |
| SA | Secondary alignments | unit32 |  |
| PE | Pair-end fragments | unit32 |  |
| PP | Properly paired fragments | unit32 |  |
| PL | Proper fragment length | unit32 |  |
| US | Number of usable Fragments | unit32 |  |
| UQ | Uniq (distinct) fragments | unit32 |  |
| CM | chrM fragments | unit32 |  |

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| **AM (cell x bin accessibility matrix session)** | | | |
| **Fields** | **Description** | **Type** | **Value** |
| nBinSize | Total number of resolutions | uint8 |  |
| binSizeList | A list of bin sizes | unit16 |  |
| |  |  |  |  | | --- | --- | --- | --- | | (*n=nBinSize*) subsession | | | | | binSize/binSize | Bin size | unit16 |  | | binSize/binChrom | Chromosome of bin | String |  | | binSize/binStart | Start position of bin | unit32 |  | | binSize/binEnd | End position of bin | unit32 |  | | binSize/idx | Row / barcode index | uint32 |  | | binSize/idy | Column / bin index | uint32 |  | | binSize/count | Count number | uint8 |  | | | | |

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| **PM (cell x peak accessibility matrix session)** | | | |
| **Fields** | **Description** | **Type** | **Value** |
| peakChrom | Chromosome of peak | String |  |
| peakStart | Start position of peak | unit32 |  |
| peakEnd | End position of peak | unit32 |  |
| idx | Row / barcode index | uint32 |  |
| idy | Column / bin index | uint32 |  |
| count | Count number | uint8 |  |

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| **GM (cell x gene accessibility matrix session)** | | | |
| **Fields** | **Description** | **Type** | **Value** |
| gene | Gene name | String |  |
| geneLen | Gene length | uint32 |  |
| idx | Row / barcode index | uint32 |  |
| idy | Column / bin index | uint32 |  |
| count | Count number | uint8 |  |

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| **FM (fragments session)** | | | |
| **Fields** | **Description** | **Type** | **Value** |
| fragChrom | Fragment chromosome | string |  |
| fragStart | Fragment start position | uint32 |  |
| fragLen | Fragment length | uint16 |  |
| barcodePos | Barcode start position | uint32 |  |
| barcodeLen | Fragments number per barcode | uint32 |  |