- AD, ADF, ADR (Integer): Per-sample read depths for each allele; total (AD), on the forward (ADF) and the reverse (ADR) strand.

- DP (Integer): Read depth at this position for this sample.

- EC (Integer): Comma separated list of expected alternate allele counts for each alternate allele in the same order as listed in the ALT field. Typically used in association analyses.

- LEN (Integer): length of the <*> reference block for this sample.

- FT (String): Sample genotype filter indicating if this genotype was "called" (similar in concept to the FILTER field). Again, use PASS to indicate that all filters have been passed, a semicolon-separated list of codes for filters that fail, or '.' to indicate that filters have not been applied. These values should be described in the meta-information in the same way as FILTERs. No whitespace or semicolons permitted.

- GQ (Integer): Conditional genotype quality, encoded as a phred quality $-10log_{10}$ p(genotype call is wrong, may be conditioned on the site ~~'s being variant~~being polymorphic in the population).

- GP (Float): Genotype posterior probabilities in the range 0 to 1 using the same ordering as the GL field; one use can be to store imputed genotype probabilities.

- GT (String): Genotype, encoded as allele value preceded by either of / or | depending on whether that allele is considered phased. The first phasing indicator may be omitted and is implicitly defined as / if any phasing indicators are / and | otherwise. The allele values are 0 for the reference allele (what is in the REF field), 1 for the first allele listed in ALT, 2 for the second allele list in ALT and so on. For diploid calls examples could be 0/1, 1 | 0, /0/1, or 1/2, etc. Haploid calls, e.g. on Y, male non-pseudoautosomal X, or mitochondria, should be indicated by having only one allele value. A triploid call might look like 0/0/1, and a partially phased triploid call could be |0/1/2 to indicate that the first allele is phased with another variant in the VCF. If a call cannot be made for a sample at a given locus, '.' must be specified for each missing allele in the `GT` field (for example './.' for a diploid genotype and '.' for haploid genotype). The meanings of the phasing indicators are as follows (see the `PS` and `PSL` fields below for more details on incorporating phasing information into the genotypes):

  - / : allele is unphased
  - | : allele is phased (according to the phase-set indicated in `PS` or `PSL`)

  For symbolic structural variant alleles, GT=0 indicates the absence of any of the ALT symbolic structural variants defined in the record. Implementer should note that merging a VCF record containing only symbolic structural variant ALT alleles with a record containing other alleles will result a change of the meaning of the GT=0 haplotypes from the record containing only symbolic SVs.

- GL (Float): Genotype likelihoods comprised of comma separated floating point log_{10}-scaled likelihoods for all possible genotypes given the set of alleles defined in the REF and ALT fields. In presence of the GT field the same ploidy is expected; without GT field, diploidy is assumed.

  GENOTYPE ORDERING. In general case of ploidy P and N alternate alleles (0 is the REF and $1 \ldots N$ the alternate alleles), the ordering of genotypes for the likelihoods can be expressed by the following pseudocode with as many nested loops as ploidy: [‡]

  ```
  for $a_P = 0 \ldots N$
    for $a_{P-1} = 0 \ldots a_P$
        ...
        for $a_1 = 0 \ldots a_2$
            println $a_1 a_2 \ldots a_P$
  ```

  Alternatively, the same can be achieved recursively with the following pseudocode:

  ```
  Ordering($P$, $N$, suffix=""):
      for $a$ in $0 \ldots N$
          if ($P == 1$) println str($a$) + suffix
          if ($P > 1$) Ordering($P$-1, $a$, str($a$) + suffix)
  ```

  Conversely, the index of the value corresponding to the genotype $k_1 \le k_2 \le \ldots \le k_P$ is

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[‡] Note that we use inclusive `for` loop boundaries.