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VCF Format Quick Reference

Decode the Variant Call Format and recognize the fields used in genomic variant analysis.

Core VCF columns

Column	Meaning
CHROM	Chromosome or contig
POS	1-based variant position
ID	Variant identifier if known
REF	Reference allele
ALT	Alternate allele(s)
QUAL	Variant quality score
FILTER	Filter status
INFO	Annotation fields
FORMAT	Per-sample field definitions
Sample columns	Genotype and sample-level data

Example record

```
chr7  140453136  .  A  T  99  PASS  DP=42  GT:DP  0/1:42
```

Common genotype codes

GT	Interpretation
0/0	Homozygous reference
0/1	Heterozygous
1/1	Homozygous alternate
./.	Missing genotype

Important: A variant in a VCF is not automatically pathogenic or biologically important. Quality control, annotation, population frequency, inheritance and phenotype context are separate interpretation steps.