BCF2 Quick Reference (r198)

In BCF2, each key in the FILTER, INFO and FORMAT fields is required to be defined in the VCF header. For each record, a key is stored as an integer which is the index of its first appearance in the header. 'PASS' is always indexed at 0, which is special cased as VCF does not require the presence of this word.

In BCF2, a typed value consists of a typing byte and the actual value with type mandated by the typing byte. In the typing byte, the lowest four bits give the atomic type. If the number represented by the higher 4 bits is smaller than 15, it is the size of the following vector; if the number equals 15, the following typed integer is the array size. The highest 4 bits of a Flag type equals 0 and in this case, no assumptions can be made about the lower 4 bits. The table below gives the atomic types and their missing values:

Bit 0-3	C type	Missing value	Description
1	int8_t	0x80	signed 8-bit integer
2	$\mathtt{int}16_\mathtt{t}$	0008x0	signed 16-bit integer
3	$\mathtt{int} 32_\mathtt{t}$	0x80000000	signed 32-bit integer
5	float	0x7F800001	IEEE 32-bit floating pointer number
7	char	'\0'	character

A genotype (GT) is encoded as an integer vector with each integer describing an allele and its phase w.r.t. the previous allele. The first allele does not carry the phase information. In the vector, each integer is organized as '(allele+1)<<1|phased' where allele is set to -1 if the allele in GT is a dot '.' (thus the higher bits are all 0). The vector is padded with missing values if the GT having fewer ploidy.

A BCF2 file is BGZF compressed and all multi-byte value are little endian.

Field	Description	Type	Value		
magic	BCF2 magic string	char[5]	BCF\2\1		
I_text	Length of the header text, including any NULL padding	uint32_t			
text	NULL-terminated plain VCF header text	char[l_text]			
List of VCF records (until the end of the BGZF section)					
I_shared	hared Data length from CHROM to the end of INFO				
I_indiv	div Data length of FORMAT and individual genotype fields				
CHROM	ROM Reference sequence ID				
POS	0-based leftmost coordinate				
rlen	0				
QUAL	QUAL Variant quality; 0x7F800001 for a missing value				
n_allele_info	n_allele_info n_allele<<16 n_info				
n_fmt_sample	n_fmt_sample n_fmt<<24 n_sample				
ID	Variant identifier	typed str			
List of alleles in the REF and ALT fields (n=n_allele)					
allele	A reference or alternate allele	typed str			
FILTER	List of filters; filters are defined in the dictionary	typed vec			
List of key-value pairs in the INFO field (n=n_info)					
info_key	Info key, defined in the dictionary	typed int			
info_value	Value	typed val			
List of FORMATs and sample information $(n=n_fmt)$					
fmt_key	Format key, defined in the dectionary	typed int			
fmt_type	Typing byte of each individual value, possibly followed by	uint8_t+			
	a typed int for the vector length				
fmt_value	Array of values. The information of each individual is	(by fmt_type)			
	concatenated in the vector. Every value is of the same				
	fmt_type. Variable-length vectors are padded with missing				
	values; a string is stored as a vector of char.				