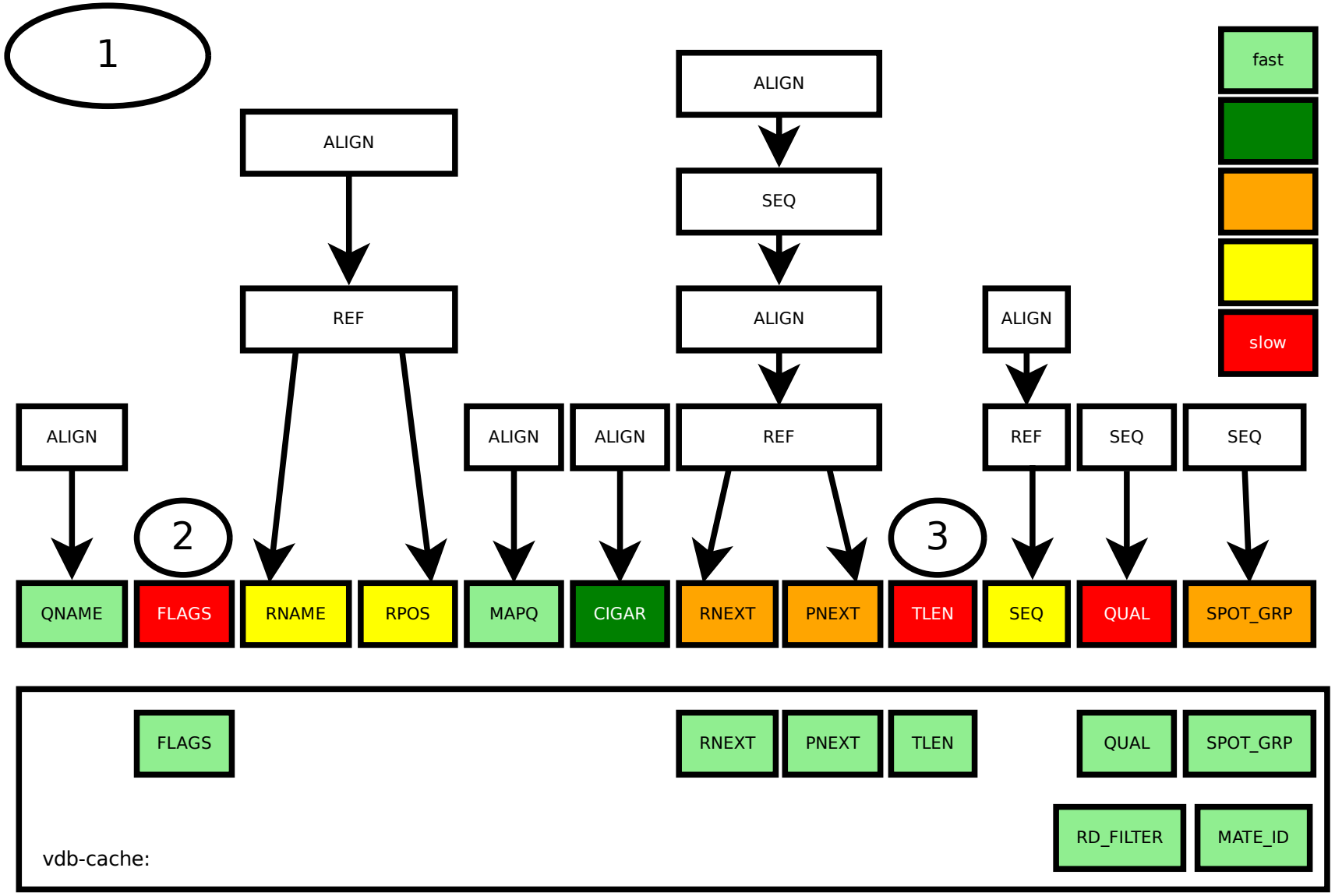
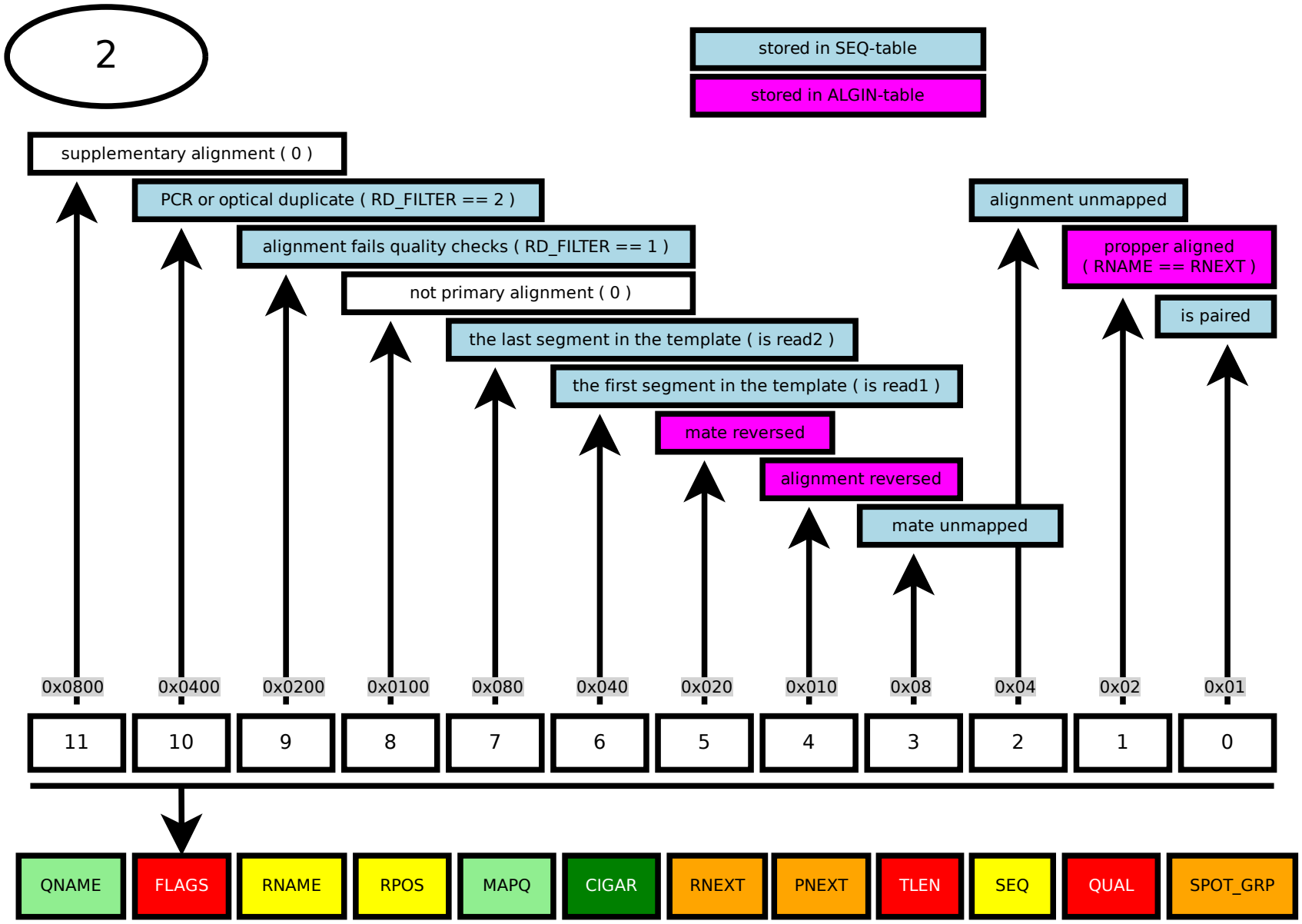
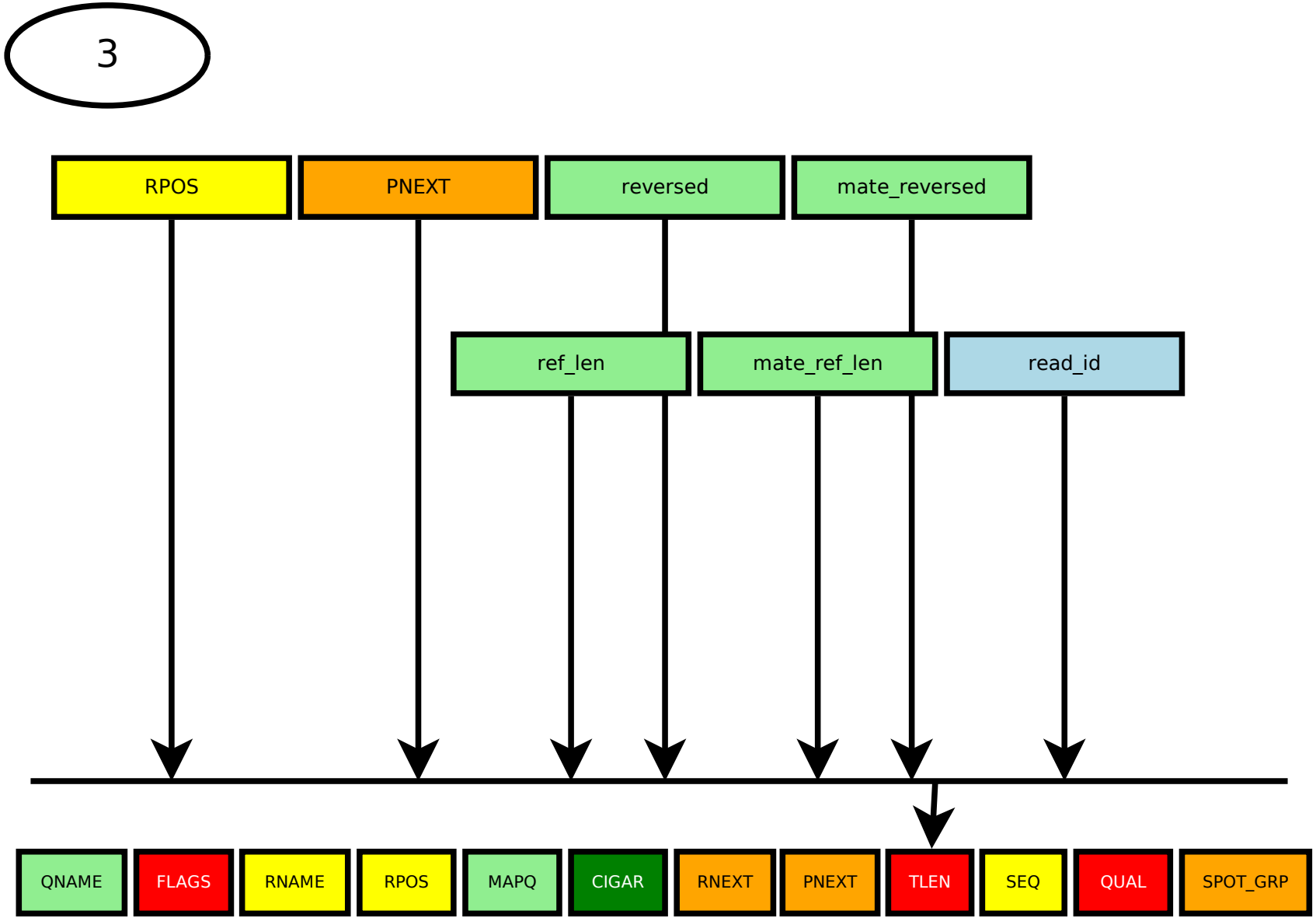
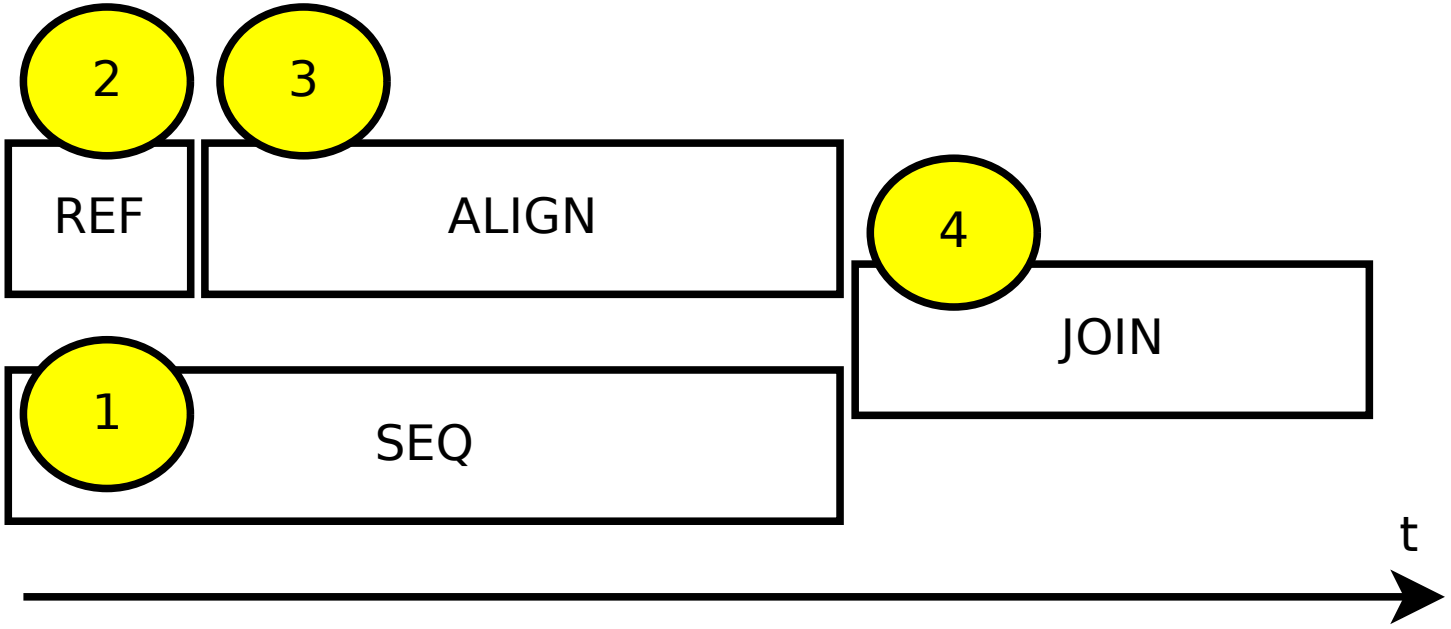
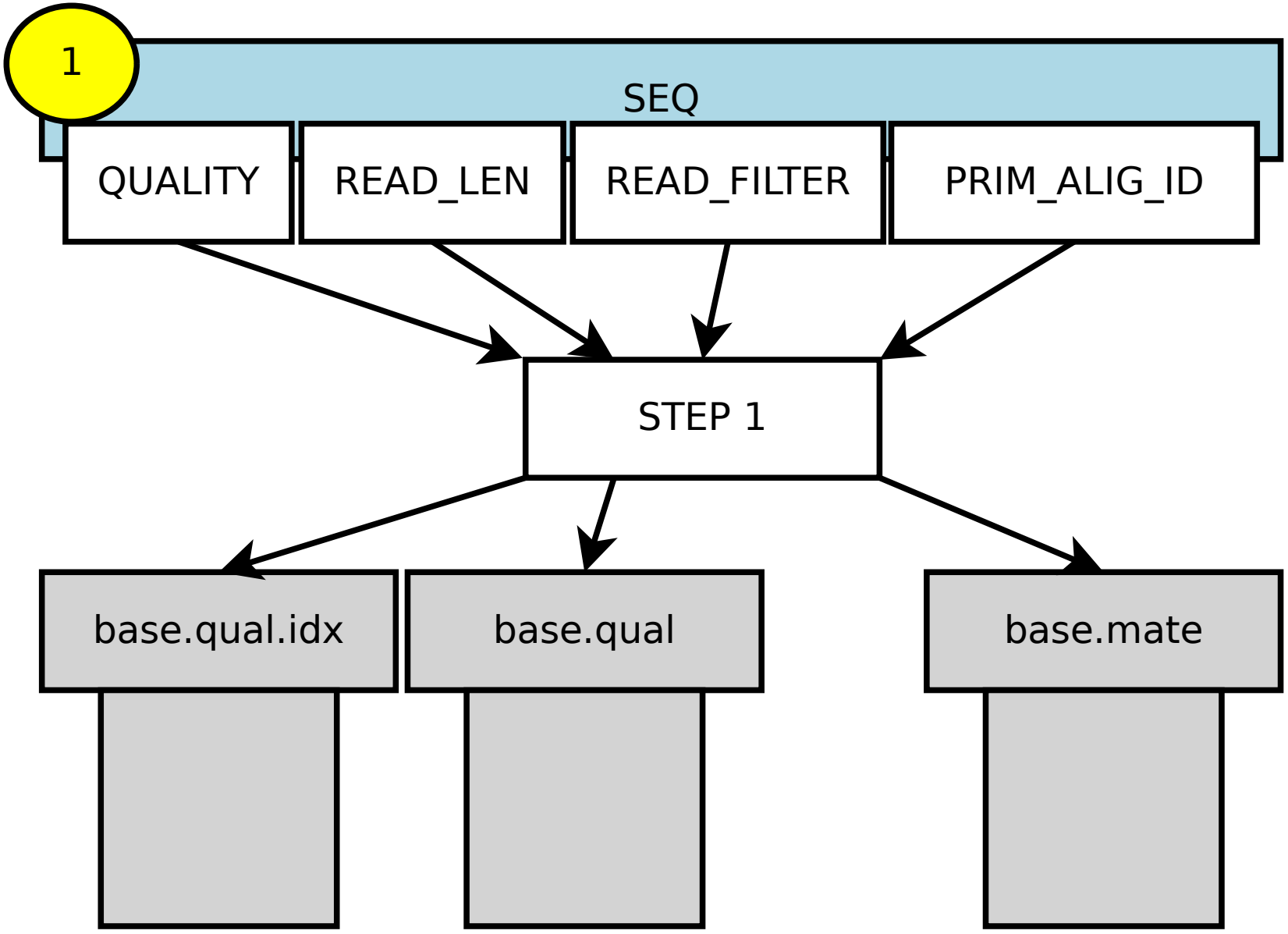
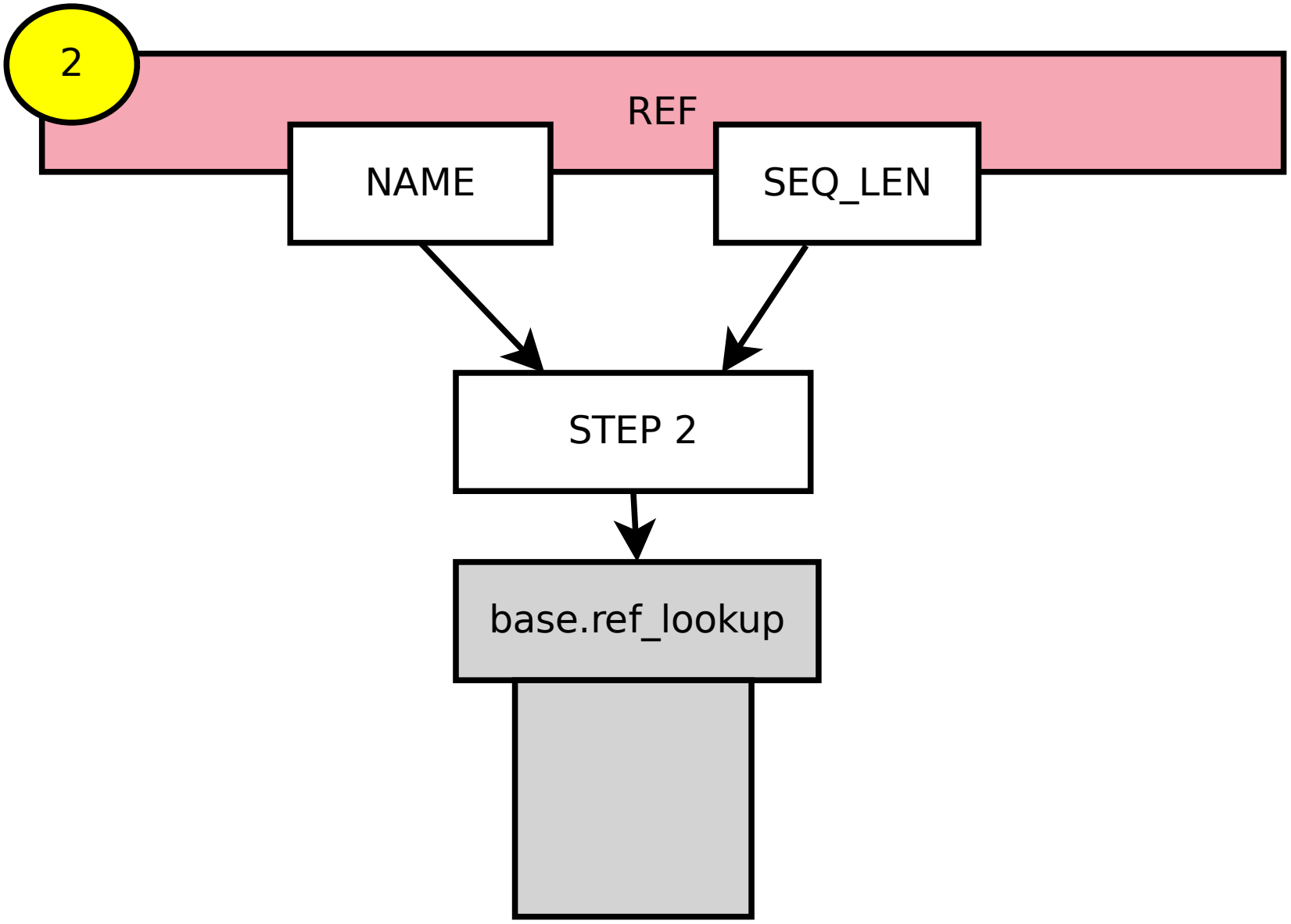

1
ALIGN
REF
ALIGN
SEQ
ALIGN
ALIGN
REF
ALIGN
REF
SEQ
SEQ
fast
slow
ALIGN
2
3
QNAME
FLAGS
RNAME
RPOS
MAPQ
CIGAR
RNEXT
PNEXT
TLEN
SEQ
QUAL
SPOT_GRP
FLAGS
RNEXT
PNEXT
TLEN
QUAL
SPOT_GRP
RD_FILTER
MATE_ID
vdb-cache:

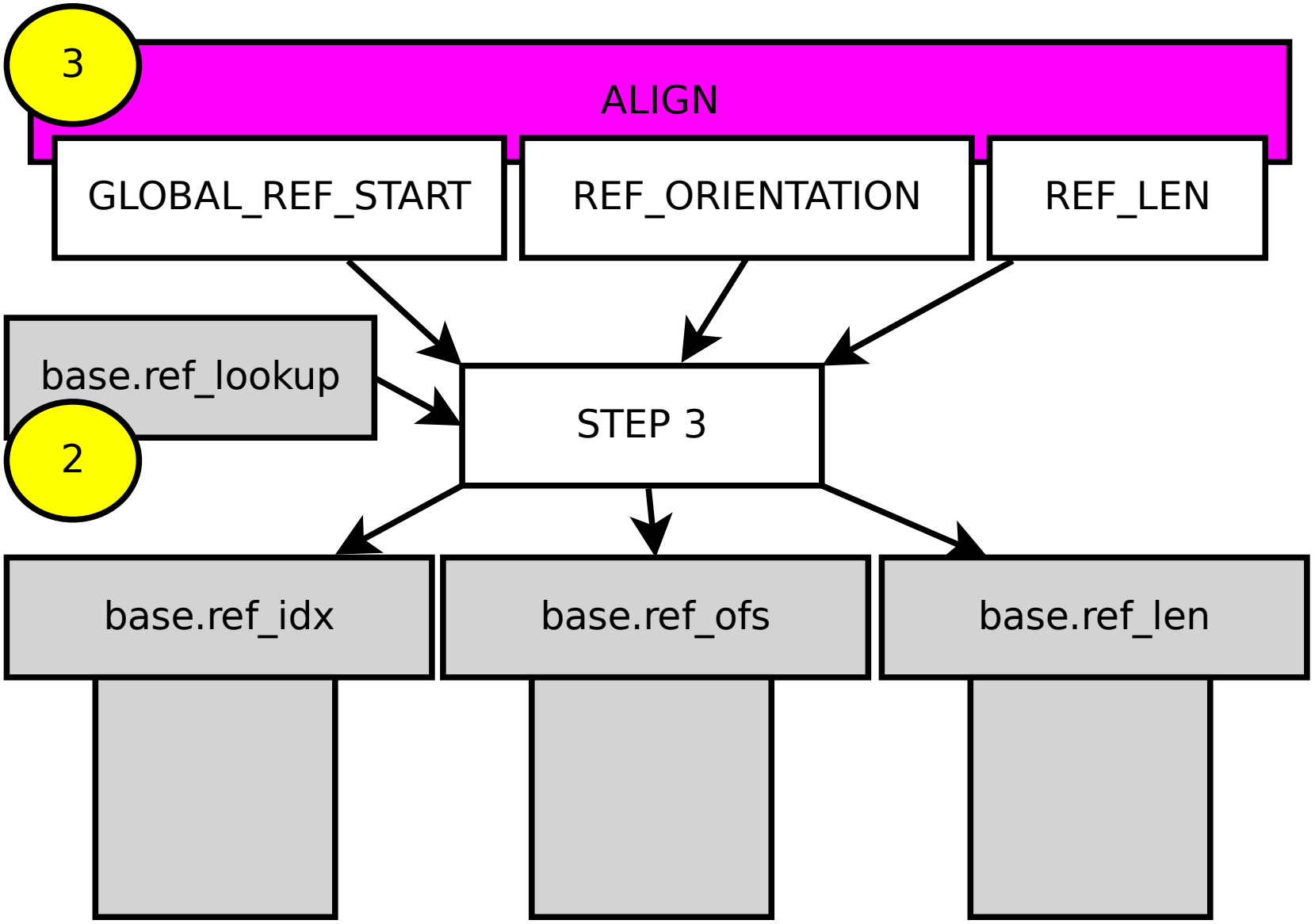

2
stored in SEQ-table
stored in ALGIN-table
supplementary alignment ( 0 )
PCR or optical duplicate ( RD_FILTER == 2 )
alignment fails quality checks ( RD_FILTER == 1 )
not primary alignment ( 0 )
the last segment in the template ( is read2 )
the first segment in the template ( is read1 )
mate reversed
alignment reversed
mate unmapped
alignment unmapped
propper aligned
( RNAME == RNEXT )
is paired
0x0800
0x0400
0x0200
0x0100
0x080
0x040
0x020
0x010
0x08
0x04
0x02
0x01
11
10
9
8
7
6
5
4
3
2
1
0
QNAME
FLAGS
RNAME
RPOS
MAPQ
CIGAR
RNEXT
PNEXT
TLEN
SEQ
QUAL
SPOT_GRP

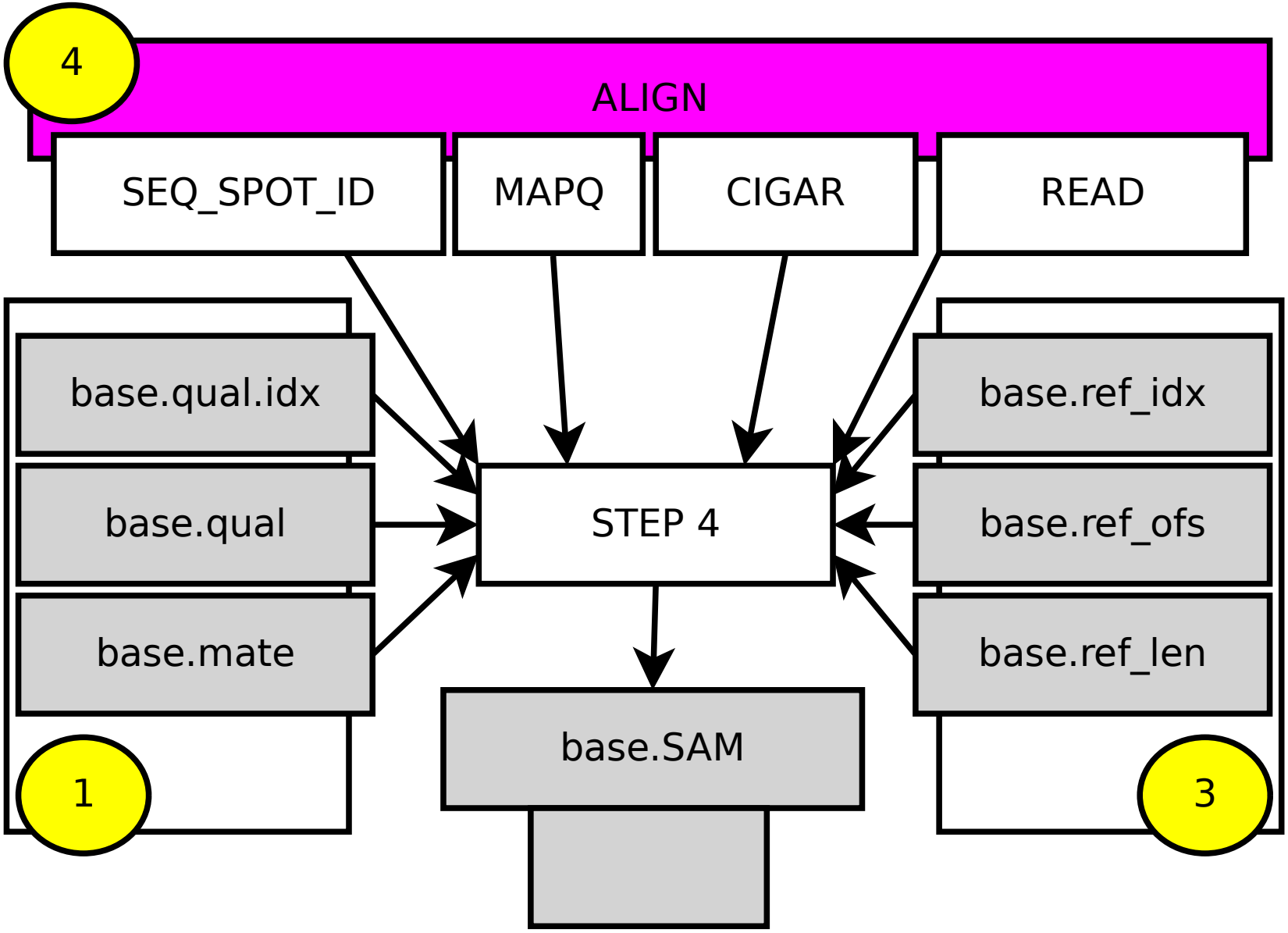

3
RPOS
PNEXT
reversed
mate_reversed
ref_len
mate_ref_len
read_id
QNAME
FLAGS
RNAME
RPOS
MAPQ
CIGAR
RNEXT
PNEXT
TLEN
SEQ
QUAL
SPOT_GRP


2
3
REF
ALIGN
4
JOIN
1
SEQ
t


1
SEQ
QUALITY
READ_LEN
READ_FILTER
PRIM_ALIG_ID
STEP 1
base.qual.idx
base.qual
base.mate


2
REF
NAME
SEQ_LEN
STEP 2
base.ref_lookup


3
ALIGN
GLOBAL_REF_START
REF_ORIENTATION
REF_LEN
base.ref_lookup
2
STEP 3
base.ref_idx
base.ref_ofs
base.ref_len


4
ALIGN
SEQ_SPOT_ID
MAPQ
CIGAR
READ
base.qual.idx
base.qual
base.mate
STEP 4
base.ref_idx
base.ref_ofs
base.ref_len
base.SAM
1
3