MapReduce Schema

Phase I

Mapper

```
loading VCF files by parallel mappers
    for each record in each mapper:
        quality check
            if not pass: continue
        total_record++
        if sampled_record/total_record <= sampling_rate:
            sampled_record++
            parse genotype
            send <pos, chr_n> to partitioner
        output <pos, sample_id+chr_n+ref+genotype> to chr_n directory
        on HDFS
```

Partitioner

```
for each record:
    sent to reducer of its chr
```

Reducer

```
for each chr, launch one reducer:
    for each sampled record:
        count++
        if count >= number of input files:
            count = 0
            output <pos, null> to chr_n's partition list file in
            distributed cache
```

Phase II

```
for each chr, launch one MapReduce job:
    for each job:
        Mapper
            loading data from the corresponding chr directory
            for each record:
                output to TotalOrderPartitioner
        Partitioner
            load its chr's partition list from distributed cache:
            if partition list is empty:
                Resample records of its chr with higher rate
            for each record
                find pos_left, pos_right in partition list such that
                pos_record ∈ [pos_left, pos_right]
                output record to reducer of this interval
        Reducer
            for each pos interval in partition list, launch one reducer
                group records by pos
                    join records to TPED format
                    output joined record onto HDFS
```