

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082917.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3082917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,152,816
Mapped reads	1,942,916 / 90.25%
Unmapped reads	209,900 / 9.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,117 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	95,226 / 4.42%
Duplication rate	3.94%
Clipped reads	896,158 / 41.63%

2.2. ACGT Content

Number/percentage of A's	34,417,289 / 26.73%
Number/percentage of C's	24,327,394 / 18.89%
Number/percentage of T's	40,181,887 / 31.21%
Number/percentage of G's	29,830,328 / 23.17%
Number/percentage of N's	6,116 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.3557
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2.4. Mapping Quality

Mean Mapping Quality	44.96
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2.5. Mismatches and indels

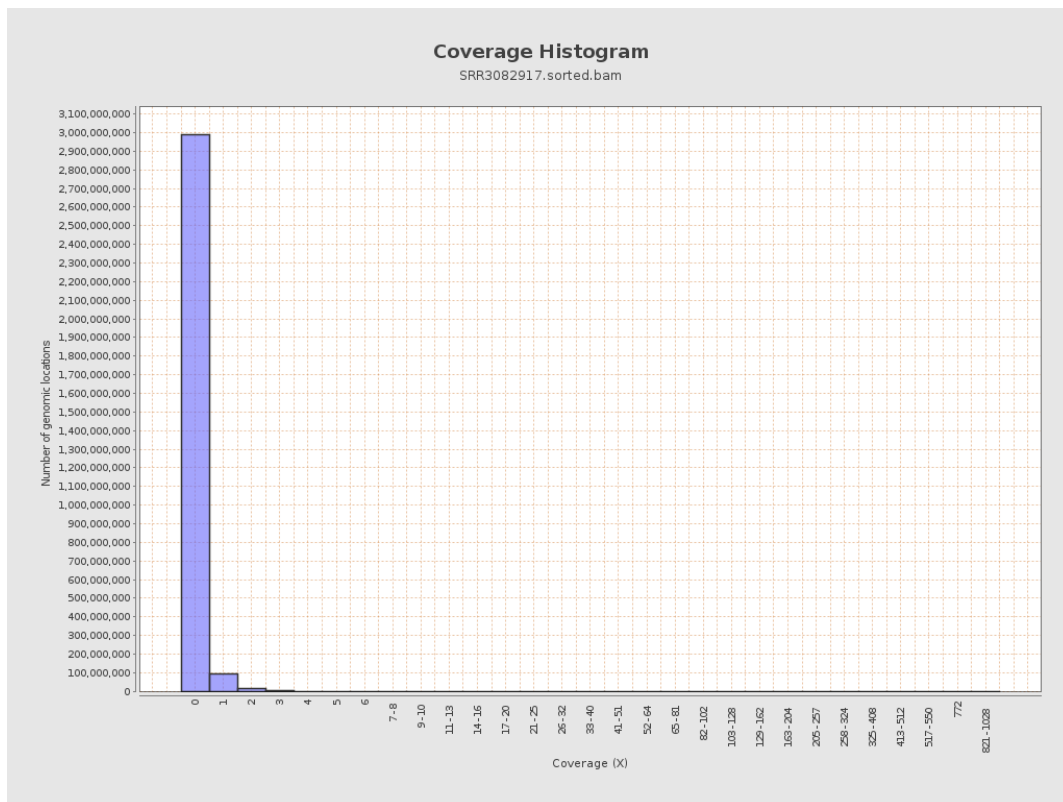
General error rate	0.76%
Mismatches	961,499
Insertions	10,477
Mapped reads with at least one insertion	0.53%
Deletions	30,474
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.98%

2.6. Chromosome stats

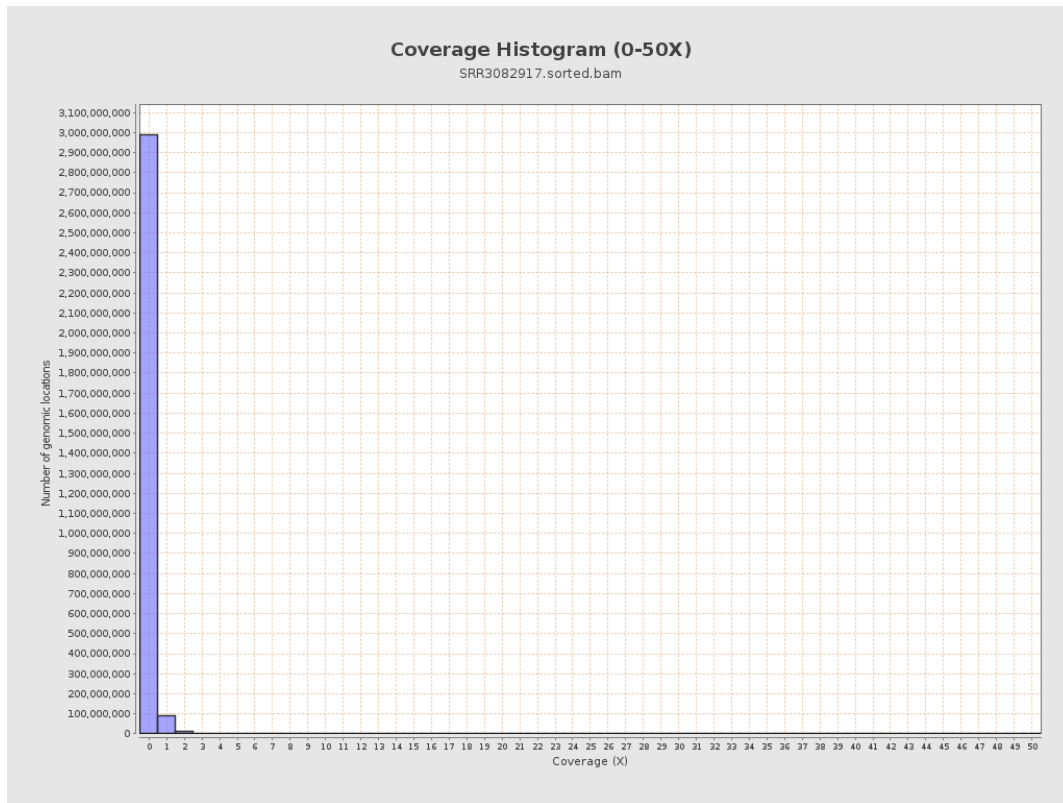
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12688384	0.0509	0.5171
chr2	243199373	12318048	0.0506	0.5535
chr3	198022430	8457951	0.0427	0.2384
chr4	191154276	9266833	0.0485	0.2617
chr5	180915260	6892646	0.0381	0.227
chr6	171115067	8814380	0.0515	0.3571
chr7	159138663	7468969	0.0469	0.4462

chr8	146364022	10184100	0.0696	0.3918
chr9	141213431	4317024	0.0306	0.3467
chr10	135534747	4794123	0.0354	0.2533
chr11	135006516	5245969	0.0389	0.3049
chr12	133851895	3465871	0.0259	0.1925
chr13	115169878	2620988	0.0228	0.1769
chr14	107349540	3027712	0.0282	0.231
chr15	102531392	2853729	0.0278	0.202
chr16	90354753	5055087	0.0559	0.2947
chr17	81195210	3559638	0.0438	0.2839
chr18	78077248	3401575	0.0436	0.7218
chr19	59128983	1899348	0.0321	0.3723
chr20	63025520	3069050	0.0487	0.2667
chr21	48129895	2911130	0.0605	0.2933
chr22	51304566	1955957	0.0381	0.2265
chrMT	16571	105784	6.3837	4.3154
chrX	155270560	4219719	0.0272	0.2247
chrY	59373566	218979	0.0037	0.0839

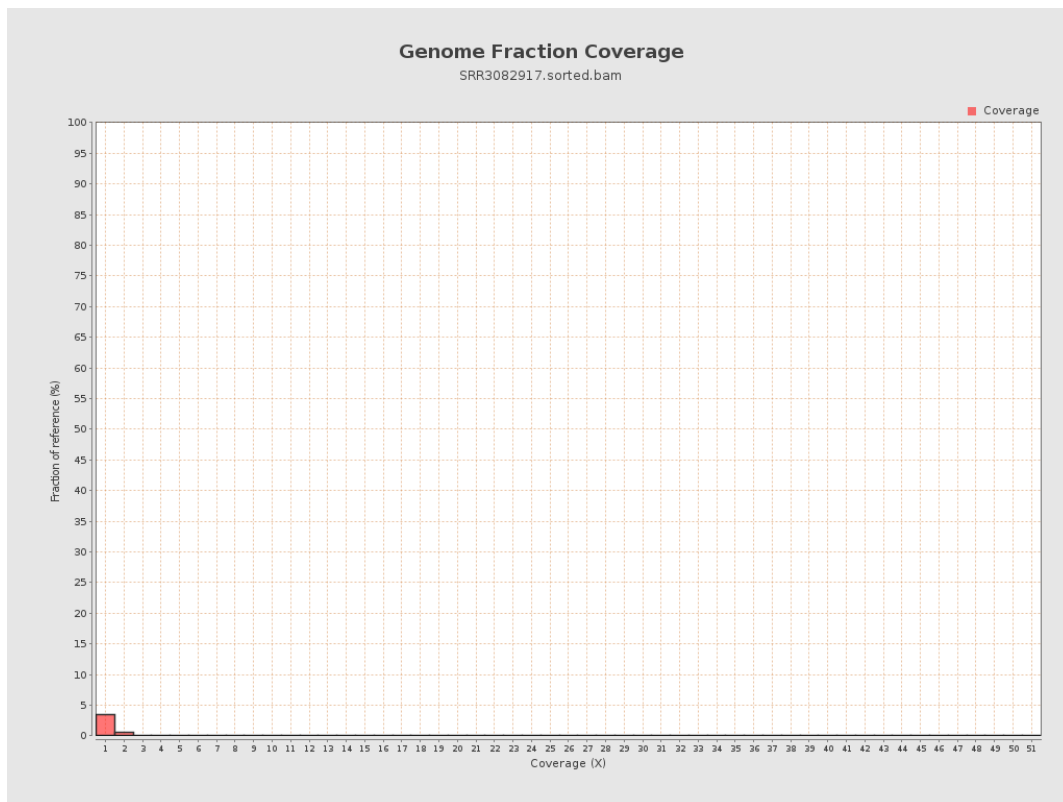
4. Results : Coverage Histogram



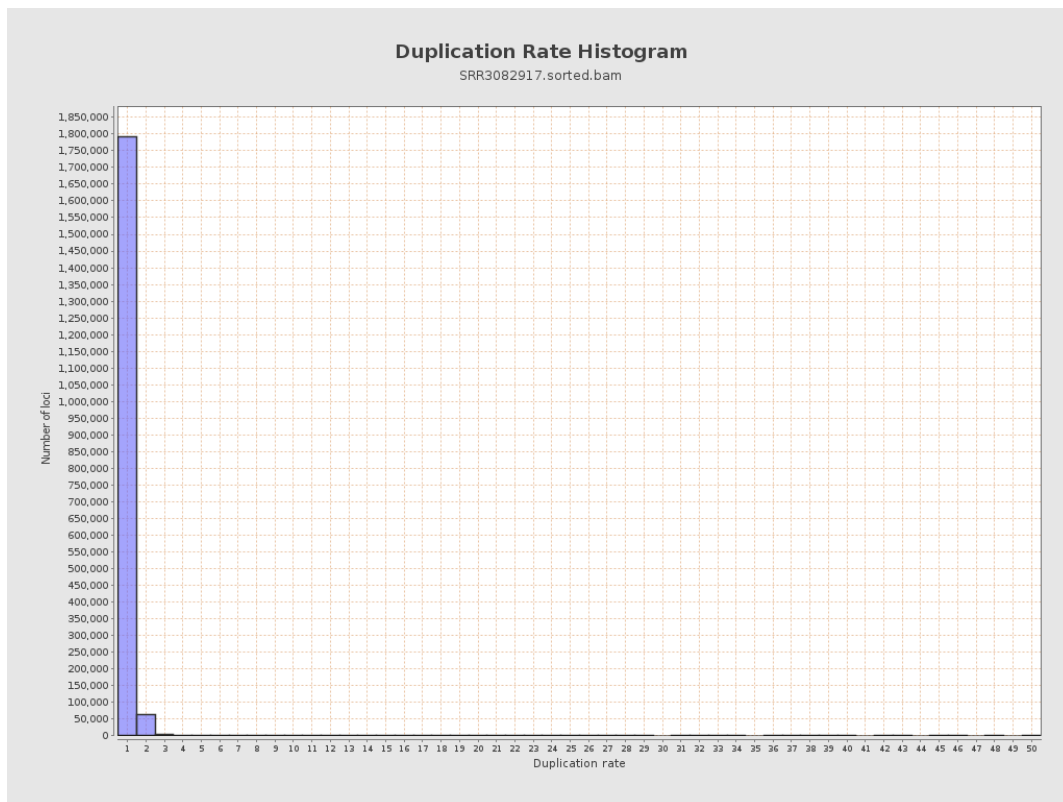
5. Results : Coverage Histogram (0-50X)



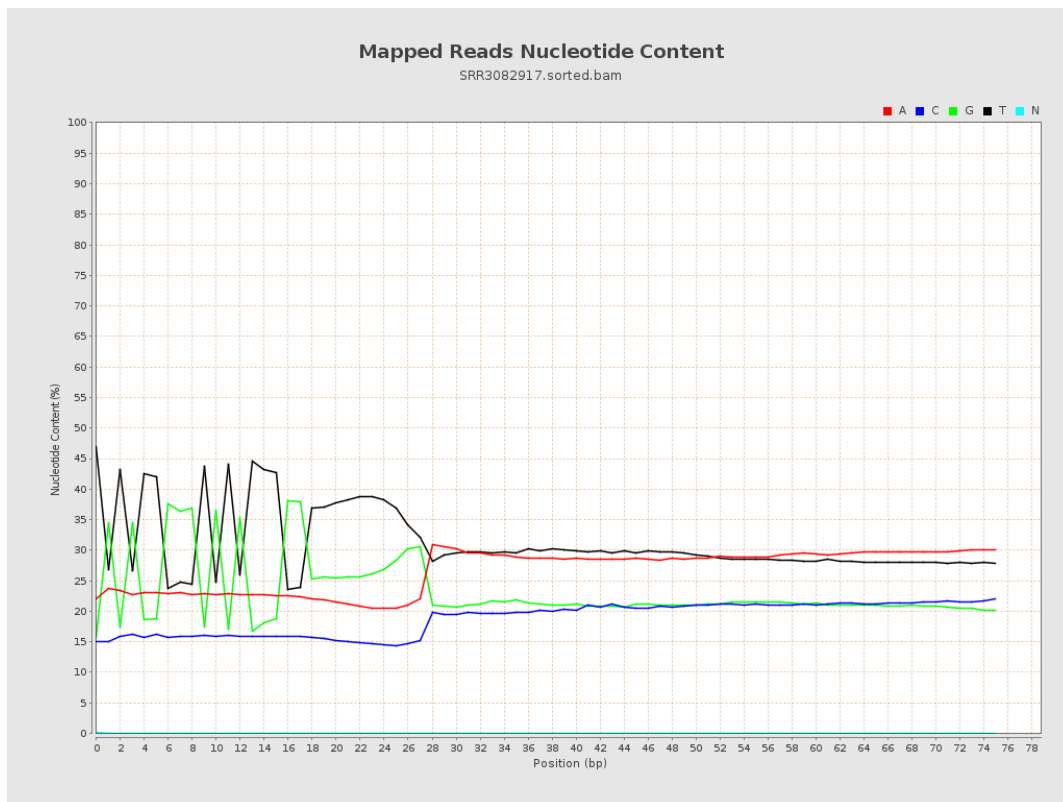
6. Results : Genome Fraction Coverage



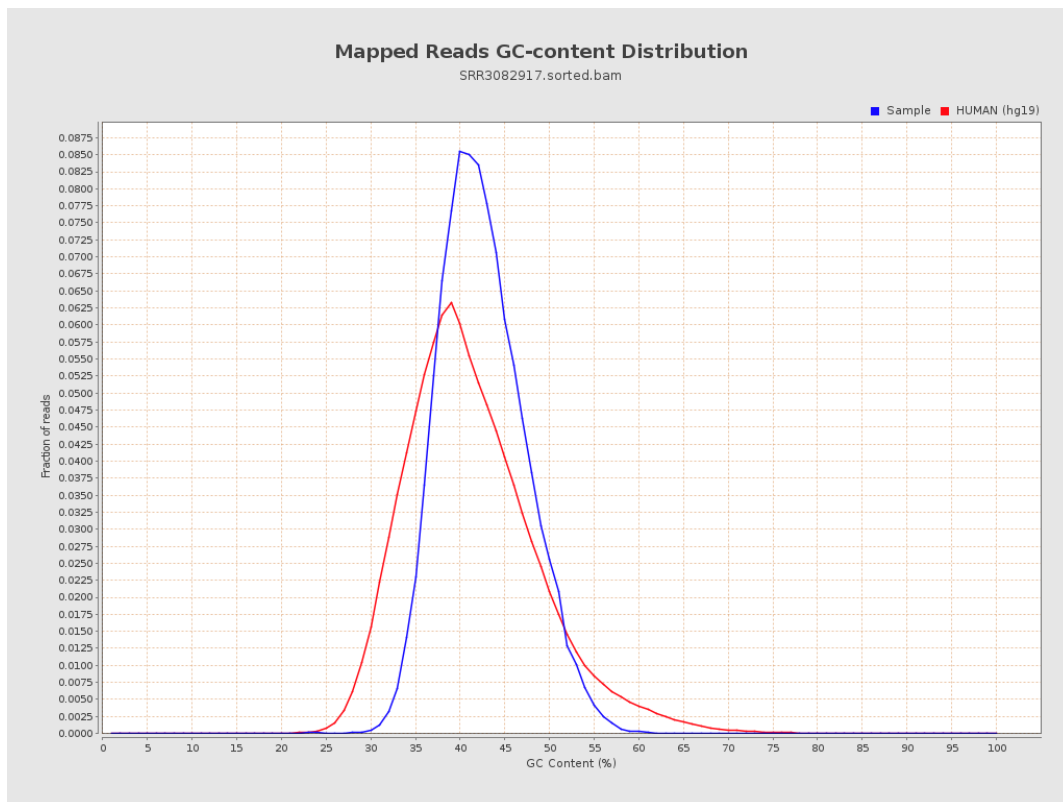
7. Results : Duplication Rate Histogram



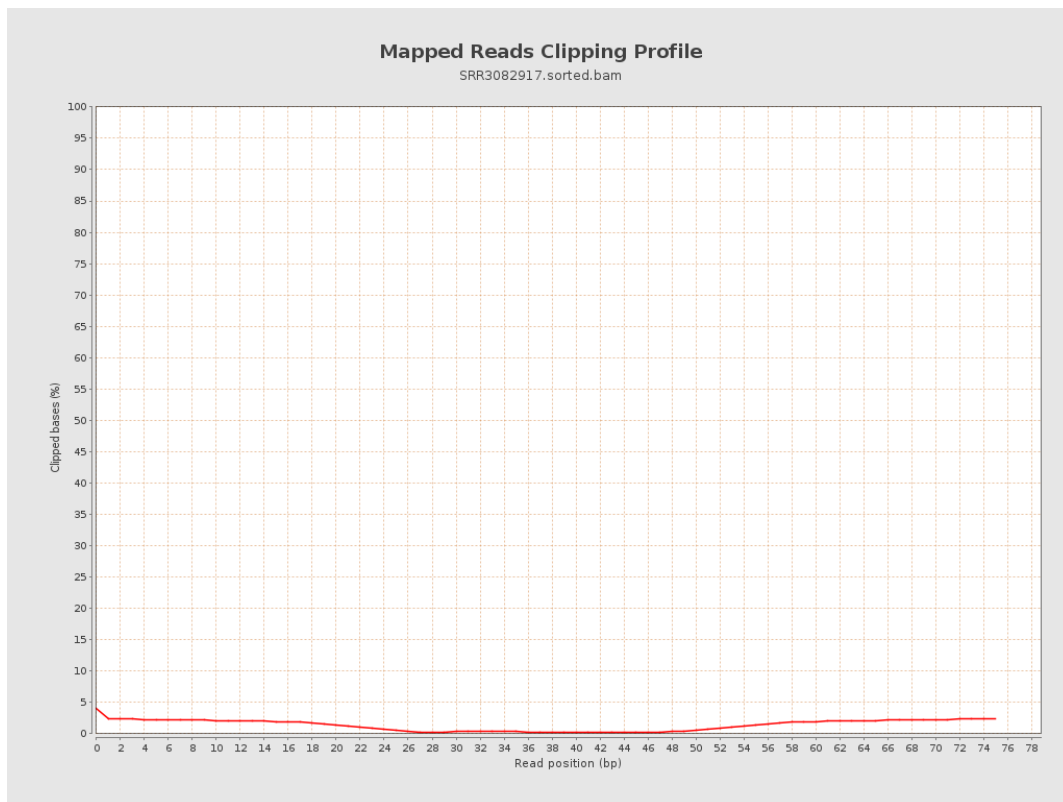
8. Results : Mapped Reads Nucleotide Content



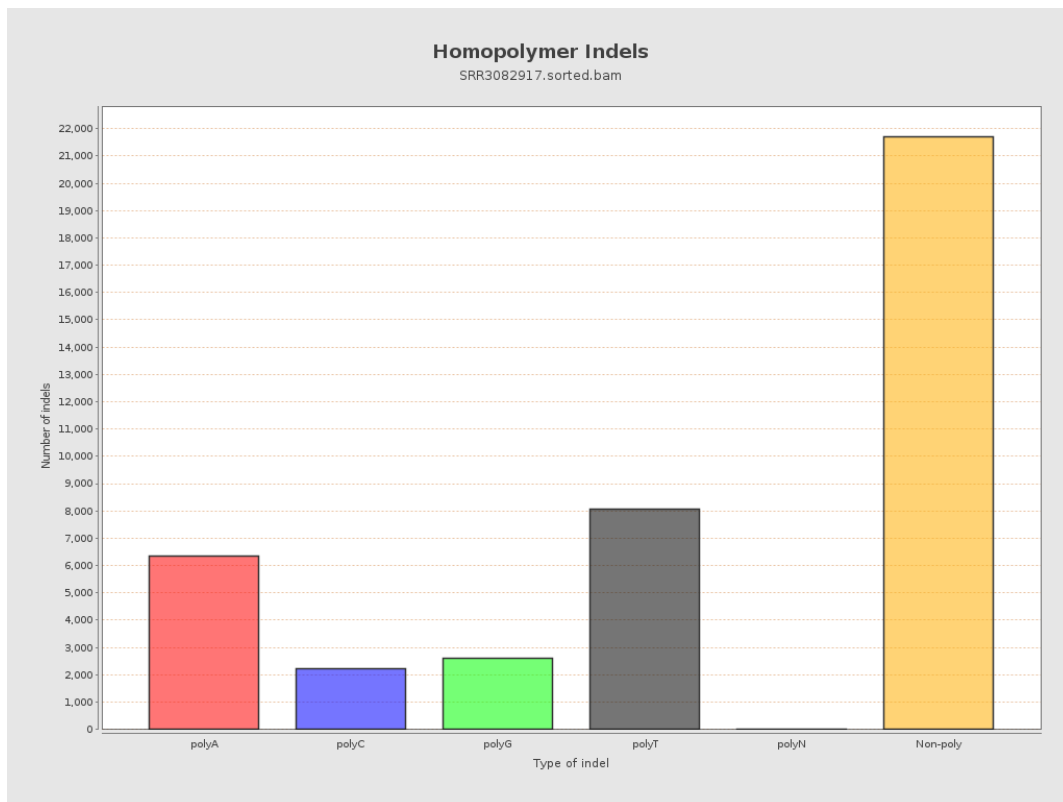
9. Results : Mapped Reads GC-content Distribution



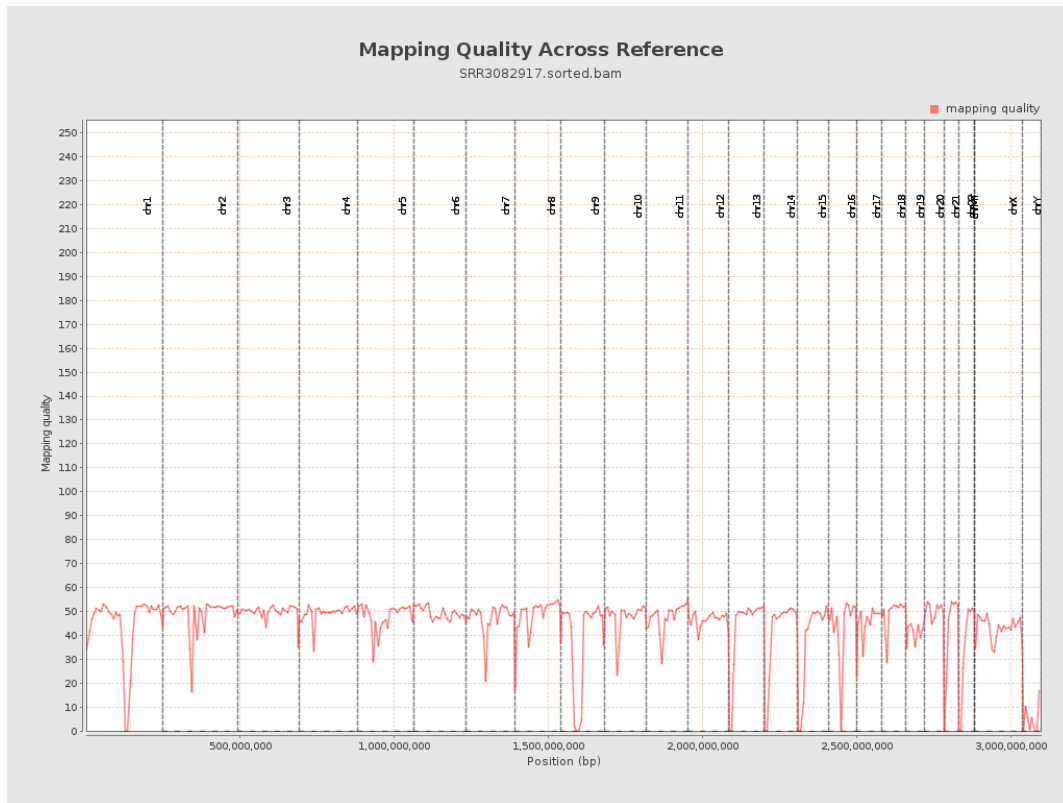
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

