Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 21:36:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514769.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_SRR5514769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 21:36:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,683,915
Mapped reads	2,443,564 / 52.17%
Unmapped reads	2,240,351 / 47.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	393,760 / 8.41%
Read min/max/mean length	30 / 100 / 102.34
Duplicated reads (estimated)	923,245 / 19.71%
Duplication rate	21.52%
Clipped reads	1,354,794 / 28.92%

2.2. ACGT Content

Number/percentage of A's	71,971,625 / 31.33%
Number/percentage of C's	42,404,346 / 18.46%
Number/percentage of T's	70,984,617 / 30.9%
Number/percentage of G's	44,351,413 / 19.31%
Number/percentage of N's	15,005 / 0.01%
GC Percentage	37.76%

2.3. Coverage

Mean	0.0743

Standard Deviation	3.3351

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

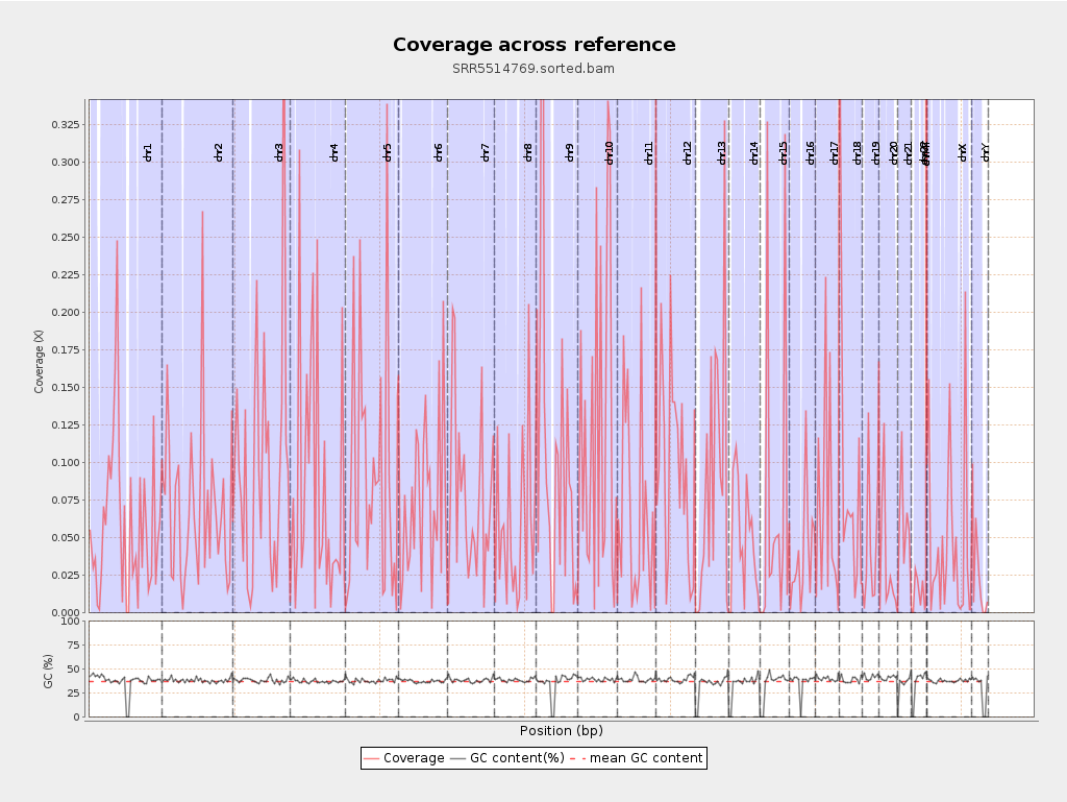
General error rate	0.62%
Mismatches	1,232,248
Insertions	110,915
Mapped reads with at least one insertion	4.36%
Deletions	52,047
Mapped reads with at least one deletion	2%
Homopolymer indels	50.06%

2.6. Chromosome stats

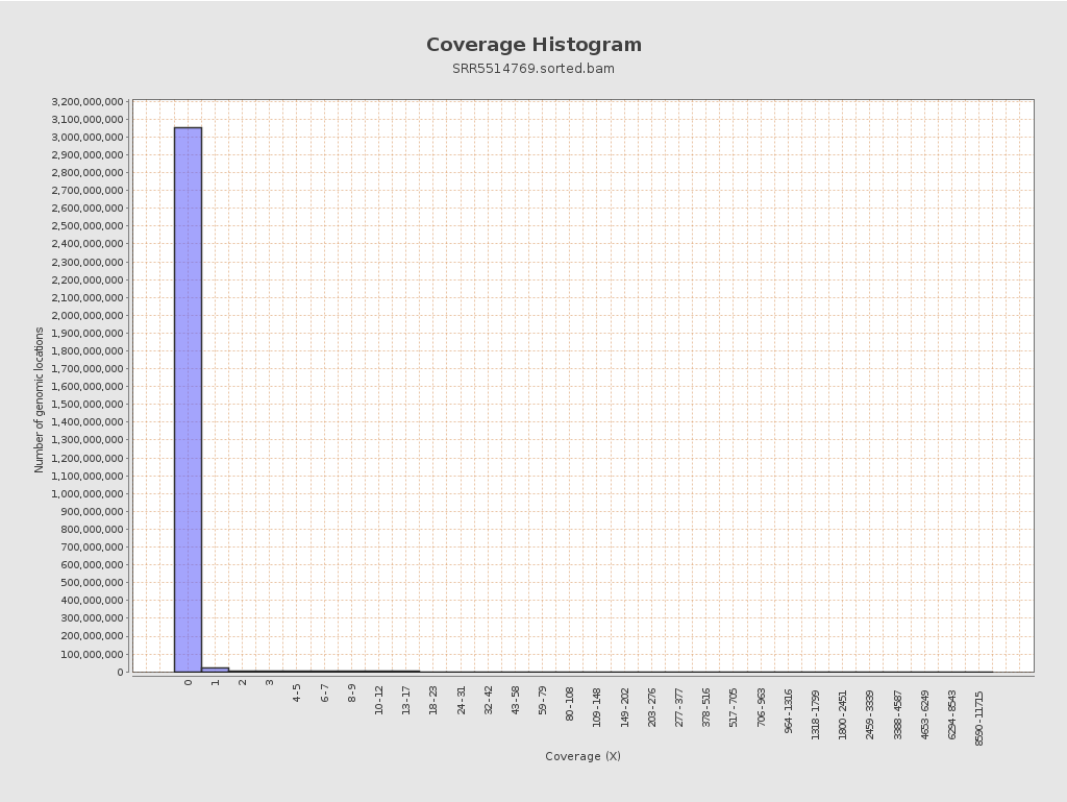
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14774922	0.0593	1.4017
chr2	243199373	16674495	0.0686	2.1739
chr3	198022430	19847957	0.1002	2.0013
chr4	191154276	15940217	0.0834	1.5278
chr5	180915260	16396414	0.0906	2.2662
chr6	171115067	13048941	0.0763	1.6891
chr7	159138663	12359026	0.0777	1.7508

chr8	146364022	8163082	0.0558	1.6253
chr9	141213431	15071034	0.1067	2.7457
chr10	135534747	15850813	0.117	2.7245
chr11	135006516	9239555	0.0684	1.8357
chr12	133851895	12750210	0.0953	2.7043
chr13	115169878	9816866	0.0852	12.1033
chr14	107349540	5129196	0.0478	1.3334
chr15	102531392	7159882	0.0698	5.5133
chr16	90354753	3478870	0.0385	1.0863
chr17	81195210	5529787	0.0681	1.7443
chr18	78077248	7043752	0.0902	4.2411
chr19	59128983	2782385	0.0471	1.6416
chr20	63025520	2078850	0.033	1.1065
chr21	48129895	2685907	0.0558	1.6584
chr22	51304566	629477	0.0123	0.4182
chrMT	16571	4623264	278.9973	328.6036
chrX	155270560	7424168	0.0478	1.3658
chrY	59373566	1375160	0.0232	1.1156

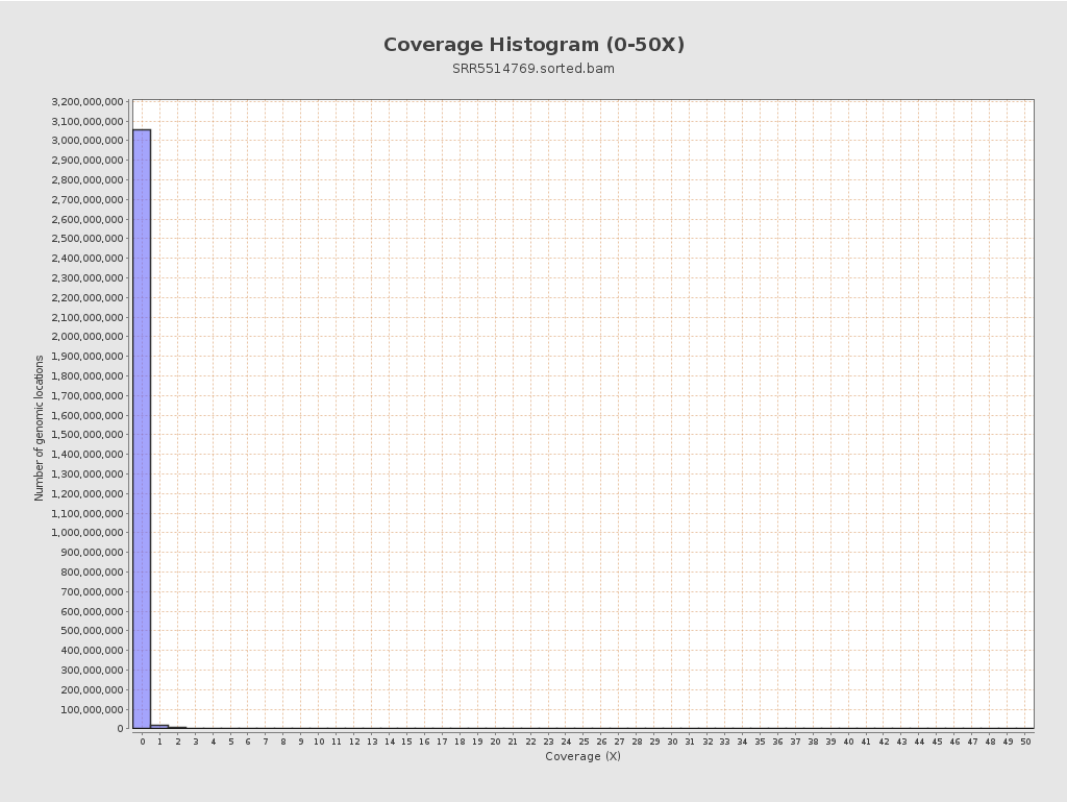
3. Results : Coverage across reference



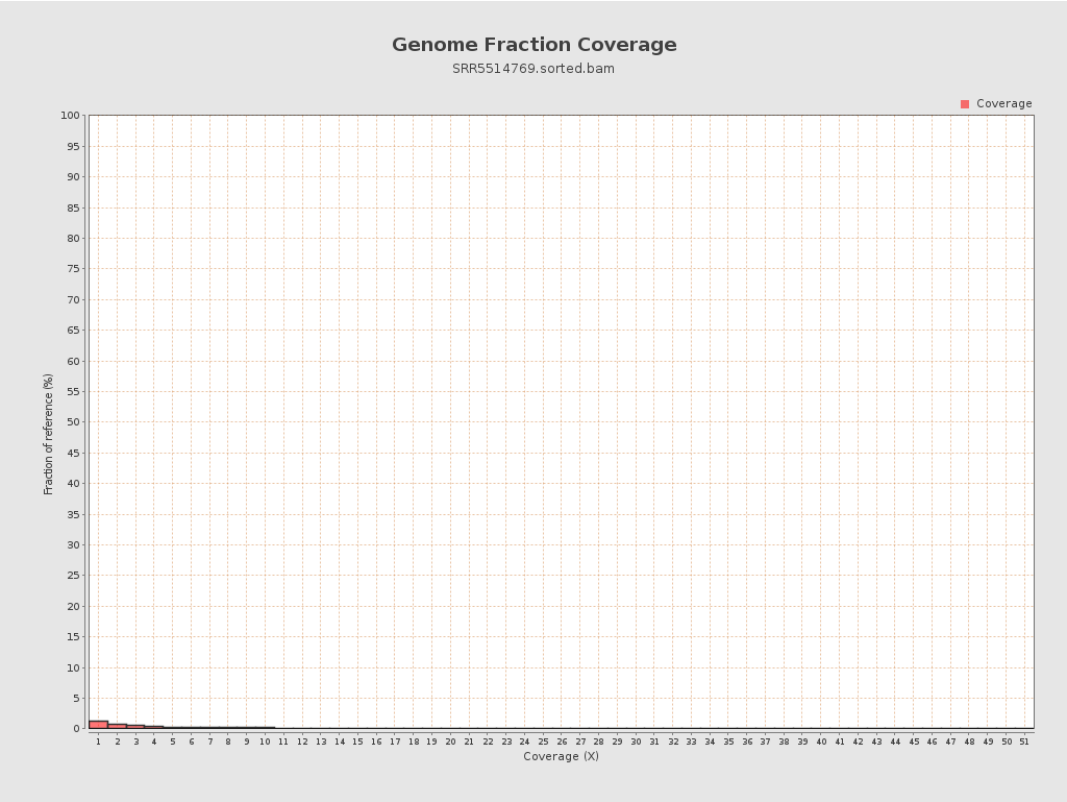
4. Results : Coverage Histogram



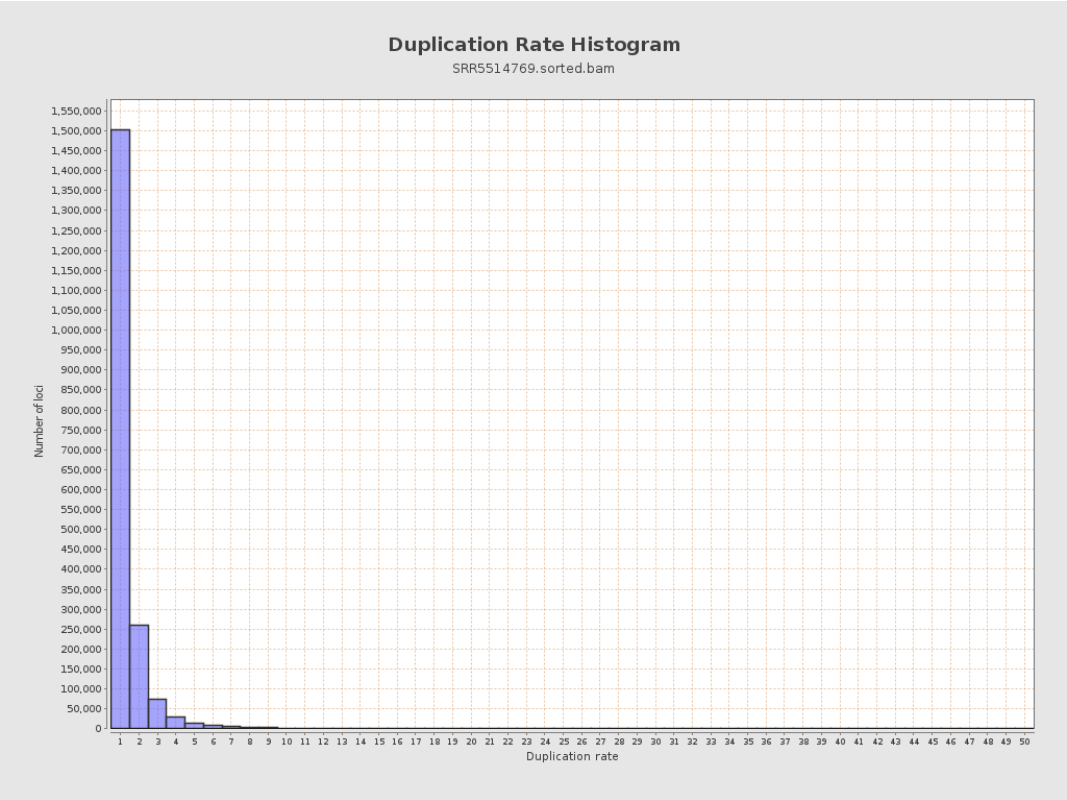
5. Results : Coverage Histogram (0-50X)



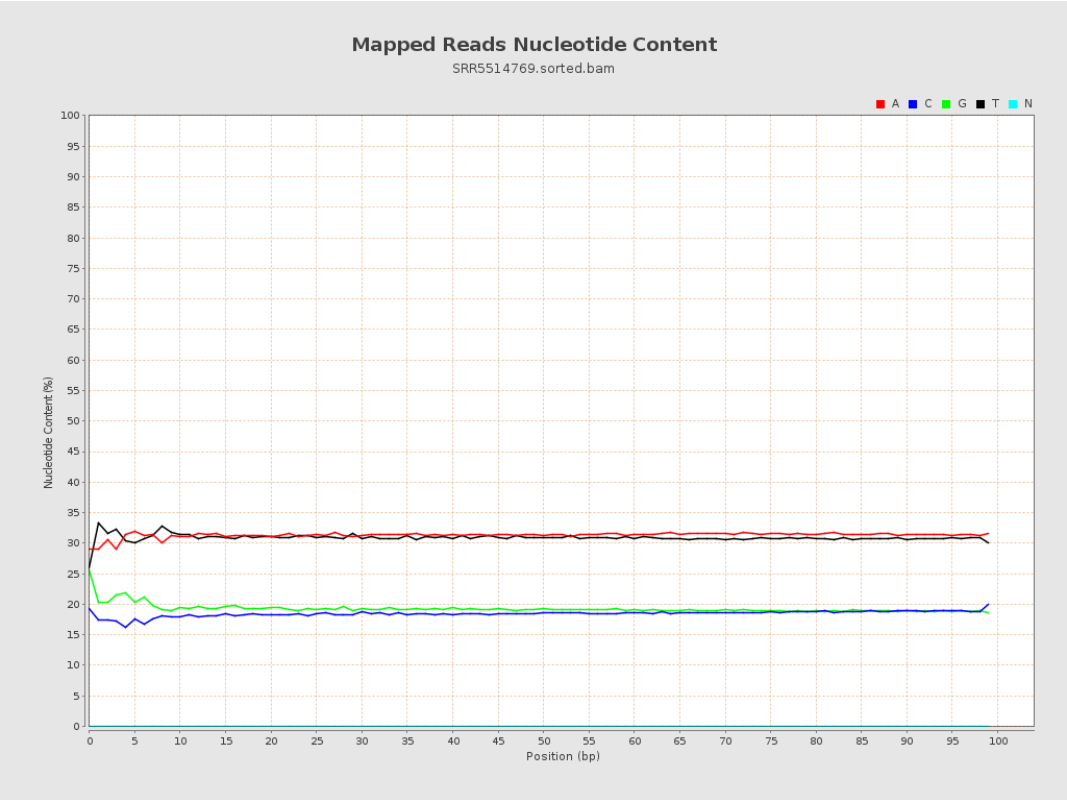
6. Results : Genome Fraction Coverage



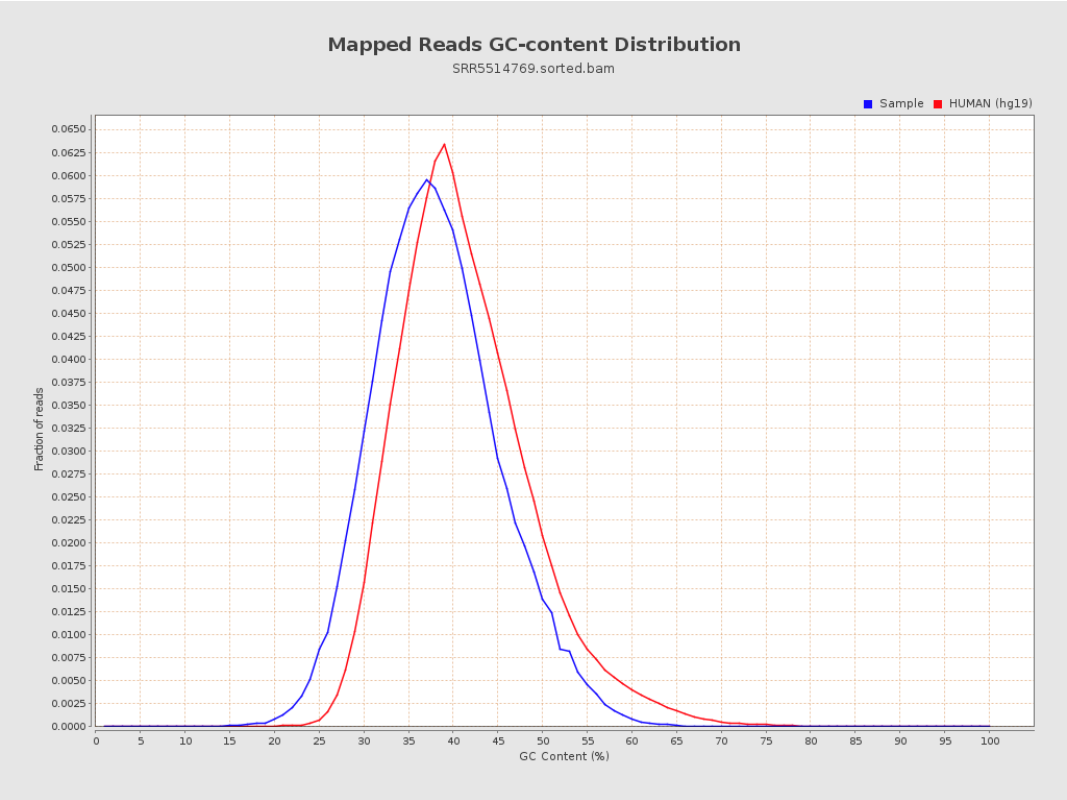
7. Results : Duplication Rate Histogram



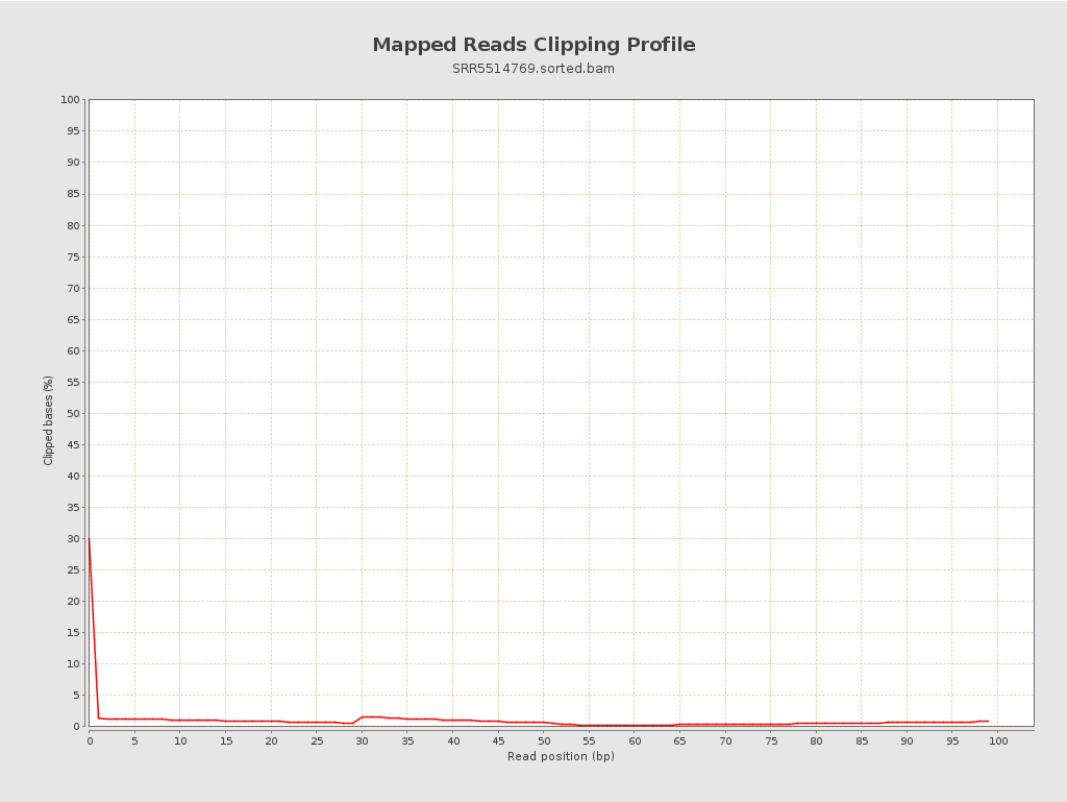
8. Results : Mapped Reads Nucleotide Content



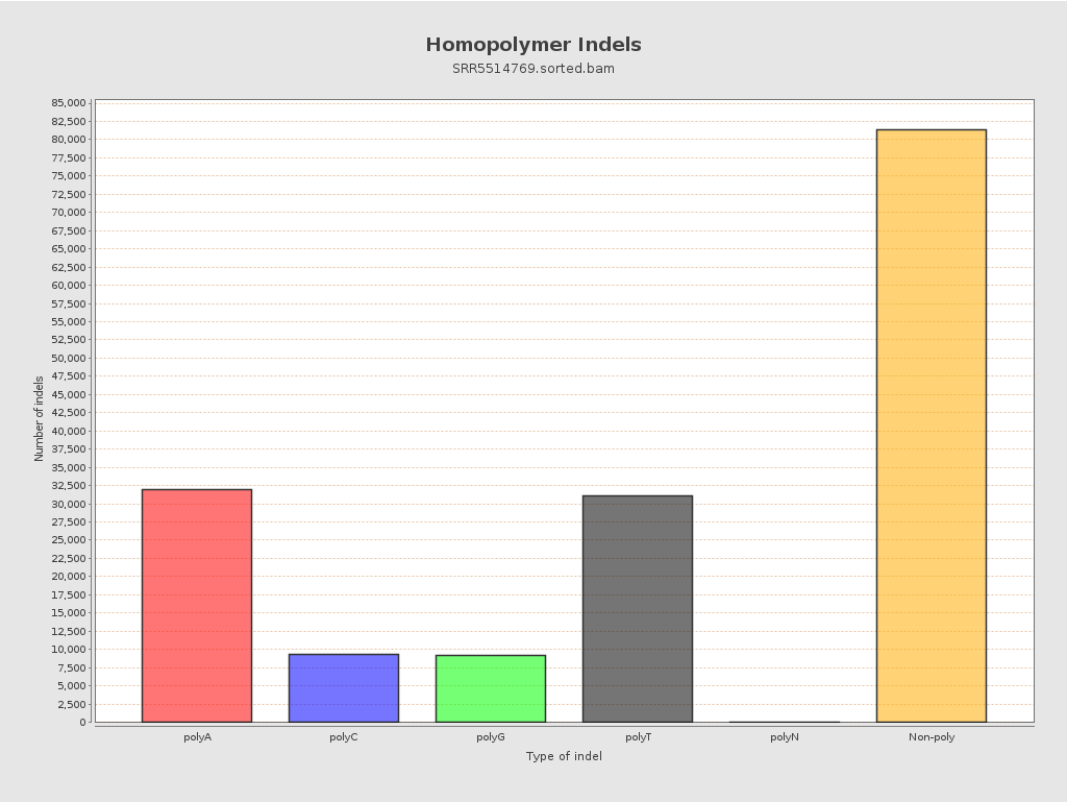
9. Results : Mapped Reads GC-content Distribution



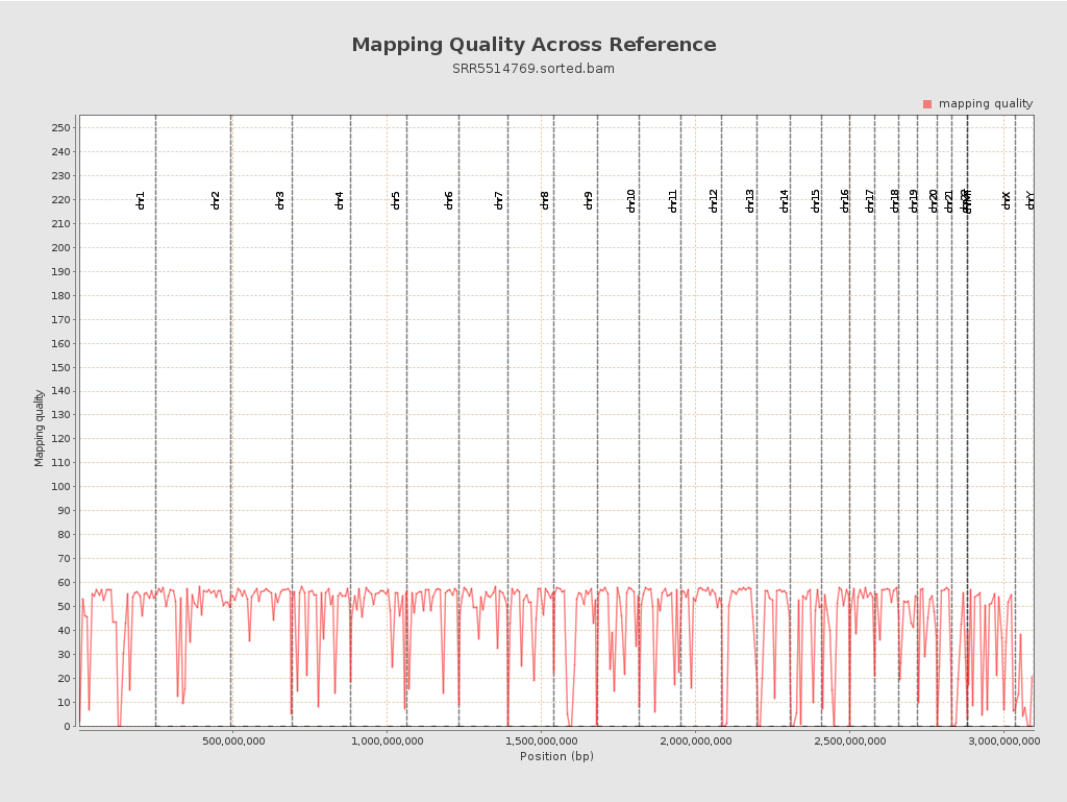
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram