

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:55:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548963.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_SRR1548963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:55:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,524,558
Mapped reads	9,009,882 / 85.61%
Unmapped reads	1,514,676 / 14.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	486,506 / 4.62%
Duplication rate	3.42%
Clipped reads	799,426 / 7.6%

2.2. ACGT Content

Number/percentage of A's	100,175,648 / 28.15%
Number/percentage of C's	76,758,302 / 21.57%
Number/percentage of T's	102,128,894 / 28.69%
Number/percentage of G's	76,859,793 / 21.59%
Number/percentage of N's	515 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.115
Standard Deviation	1.1974

2.4. Mapping Quality

Mean Mapping Quality	36.57
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2.5. Mismatches and indels

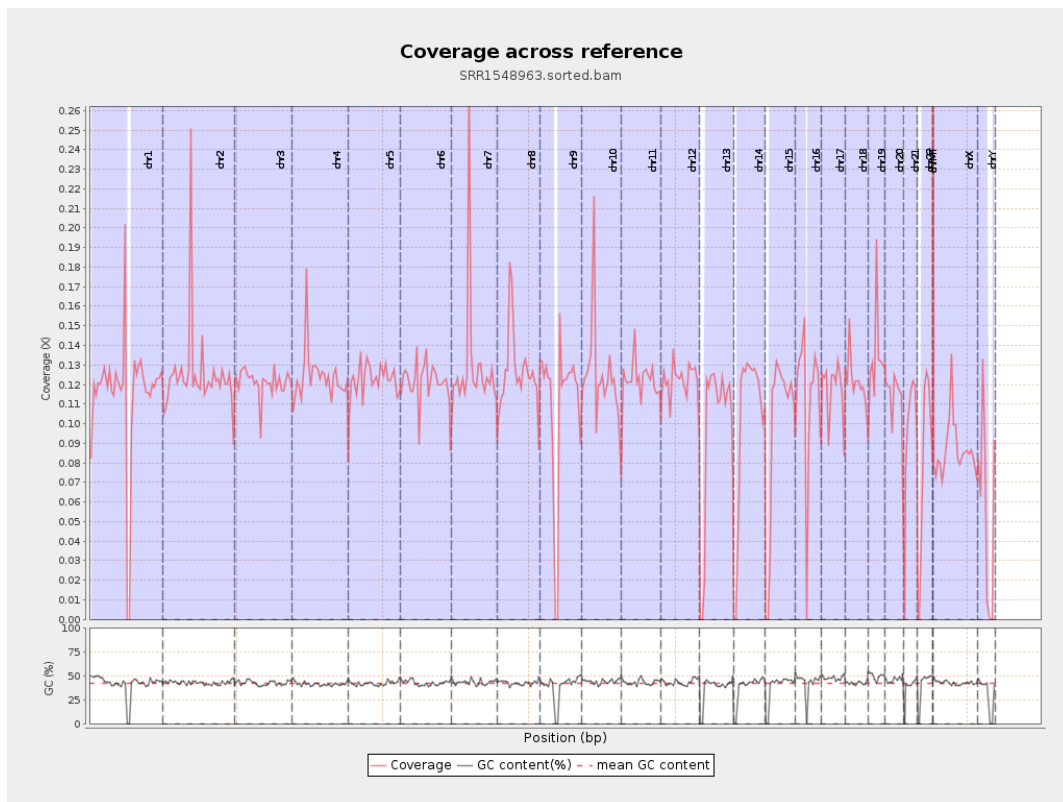
General error rate	0.32%
Mismatches	1,126,822
Insertions	12,807
Mapped reads with at least one insertion	0.14%
Deletions	26,280
Mapped reads with at least one deletion	0.29%
Homopolymer indels	37.99%

2.6. Chromosome stats

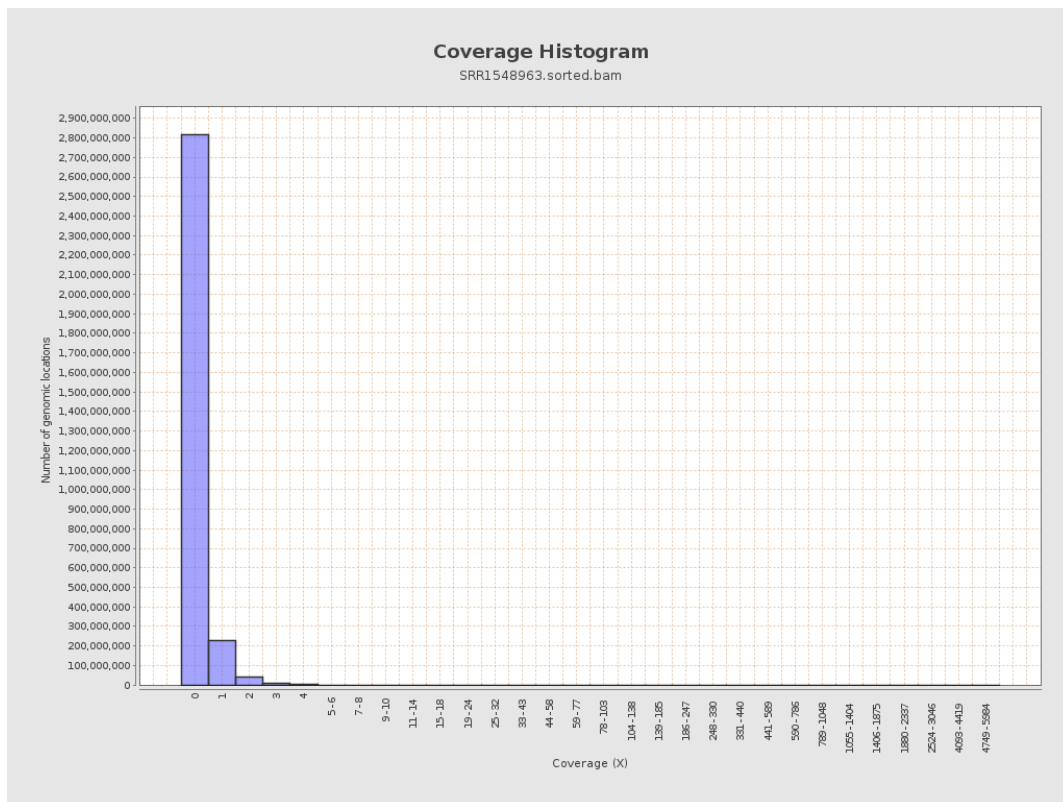
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28636654	0.1149	1.9408
chr2	243199373	30420579	0.1251	1.1196
chr3	198022430	23974154	0.1211	0.4302
chr4	191154276	23730740	0.1241	0.5161
chr5	180915260	22151864	0.1224	0.4573
chr6	171115067	20745425	0.1212	0.4847
chr7	159138663	20495498	0.1288	1.7273
chr8	146364022	18503041	0.1264	2.9788

chr9	141213431	15377965	0.1089	1.1831
chr10	135534747	16878277	0.1245	0.8786
chr11	135006516	16501528	0.1222	0.7619
chr12	133851895	16398990	0.1225	0.495
chr13	115169878	11218554	0.0974	0.3711
chr14	107349540	11044674	0.1029	0.6392
chr15	102531392	9931563	0.0969	0.3919
chr16	90354753	10072097	0.1115	0.5769
chr17	81195210	9651919	0.1189	0.4702
chr18	78077248	9531190	0.1221	2.1677
chr19	59128983	7961662	0.1346	1.9639
chr20	63025520	7170437	0.1138	0.4803
chr21	48129895	4580577	0.0952	0.597
chr22	51304566	4104250	0.08	0.5711
chrMT	16571	11642	0.7026	1.0517
chrX	155270560	13454345	0.0867	0.6098
chrY	59373566	3409388	0.0574	0.5299

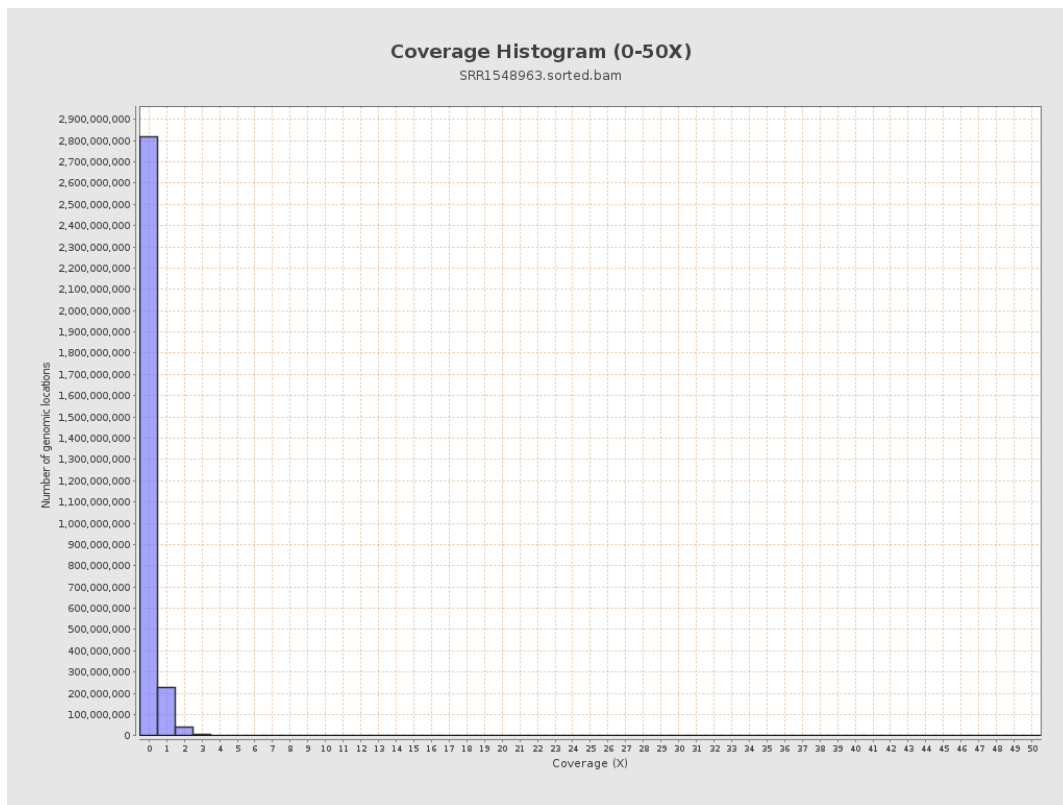
3. Results : Coverage across reference



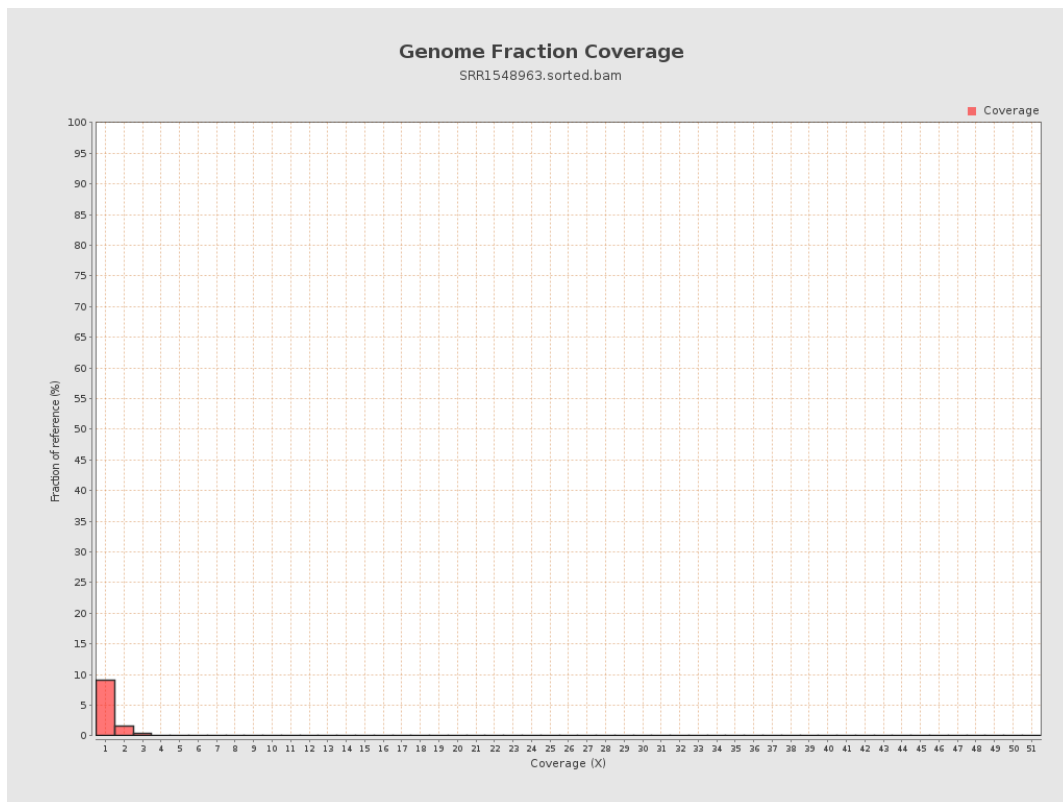
4. Results : Coverage Histogram



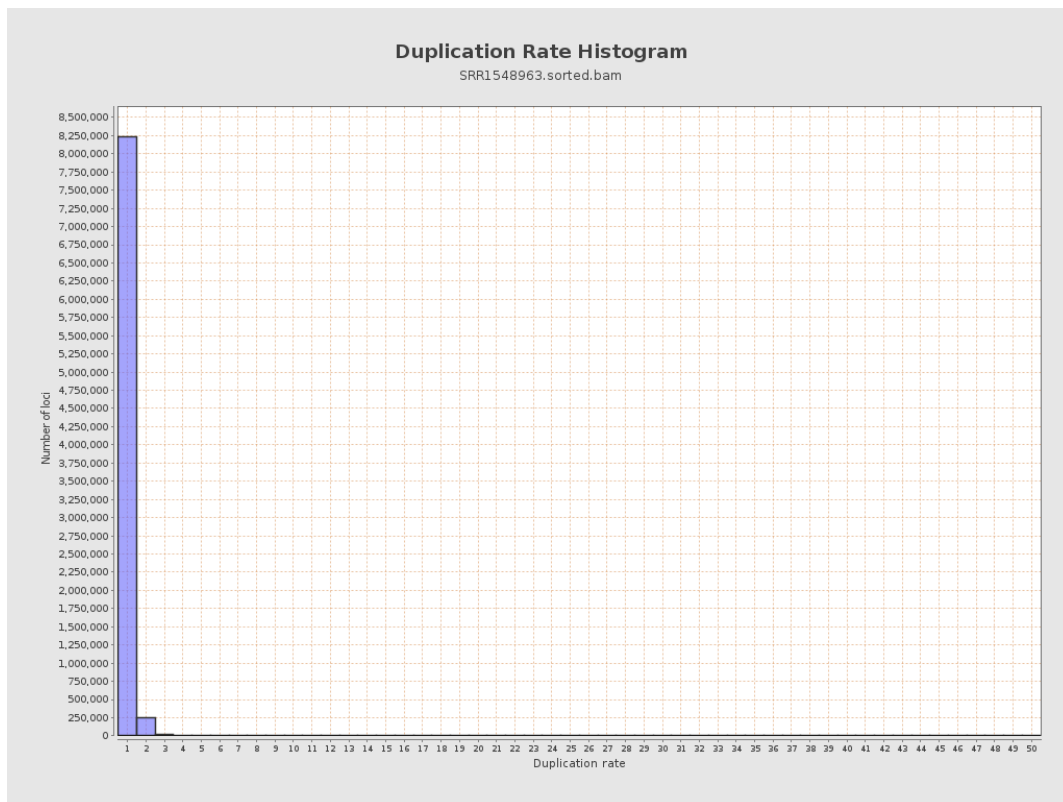
5. Results : Coverage Histogram (0-50X)



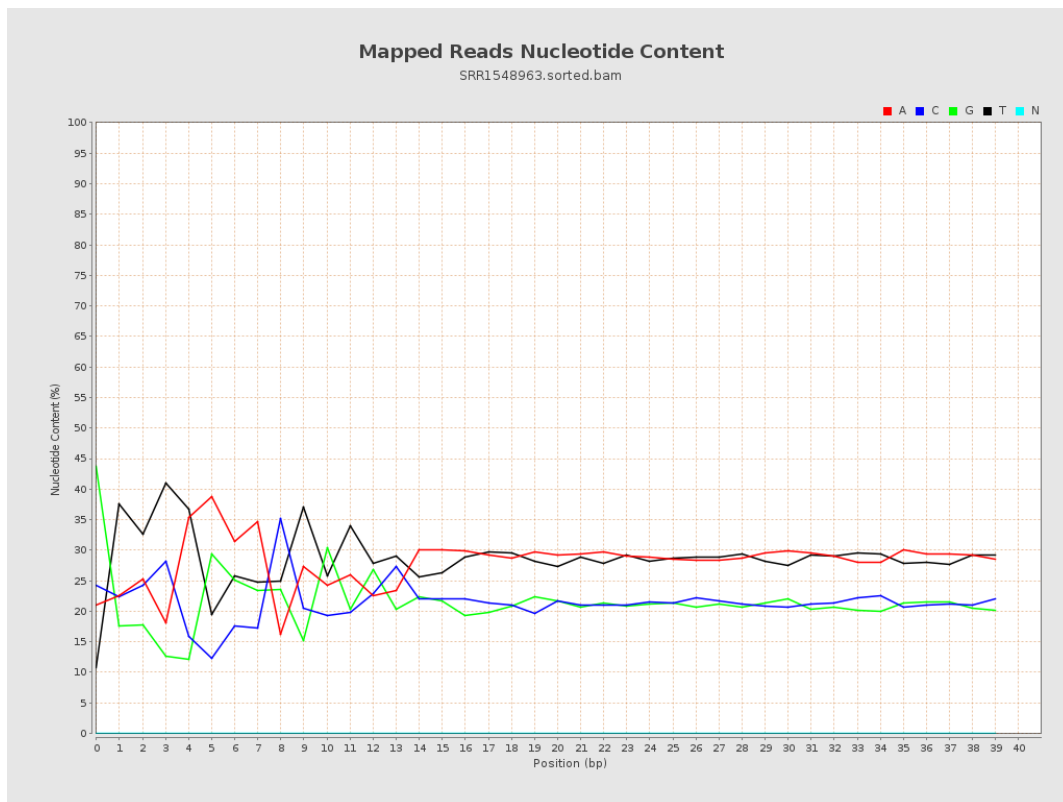
6. Results : Genome Fraction Coverage



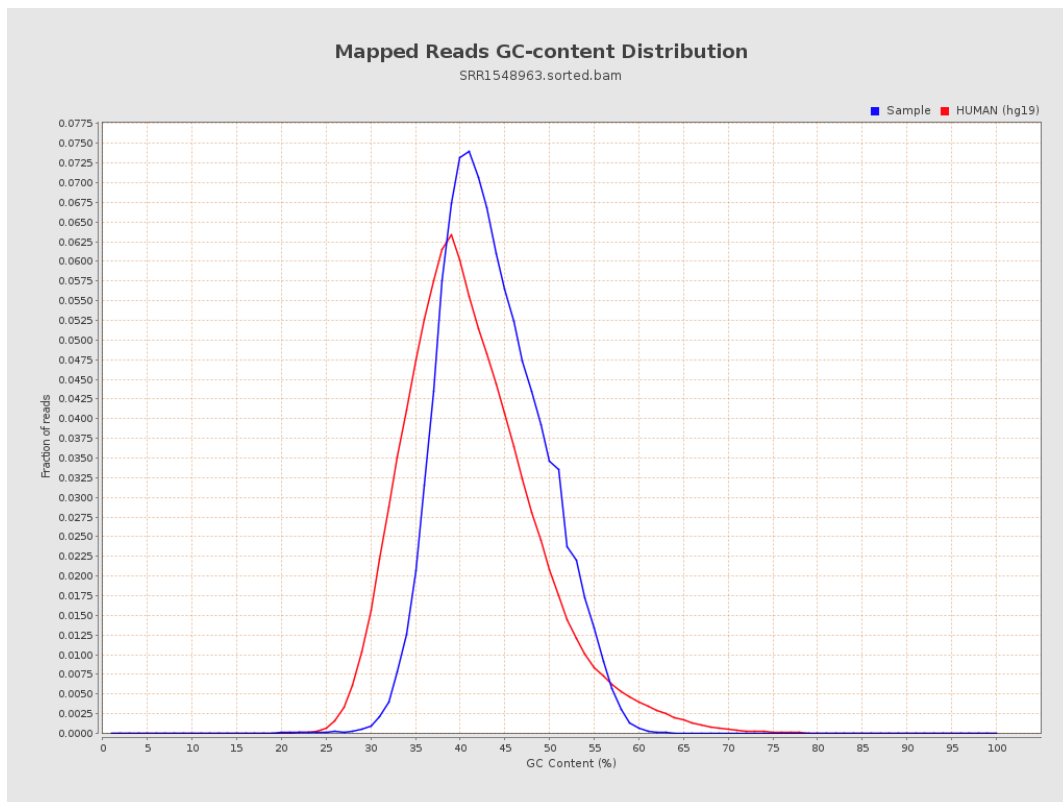
7. Results : Duplication Rate Histogram



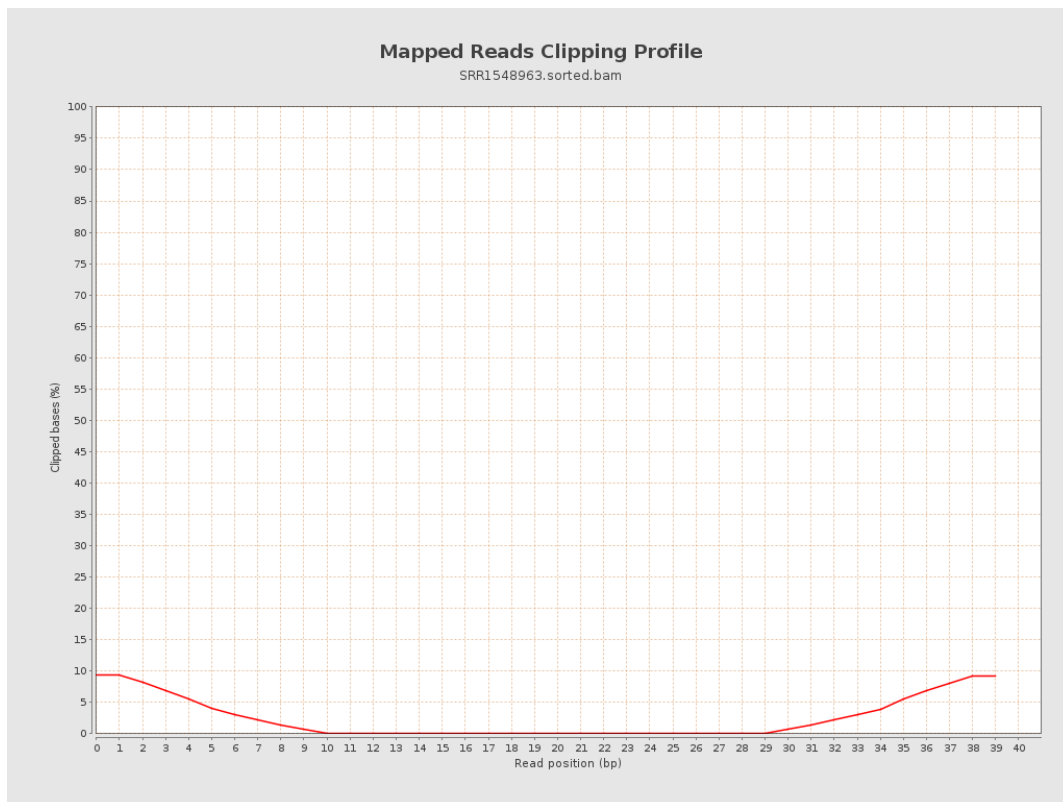
8. Results : Mapped Reads Nucleotide Content



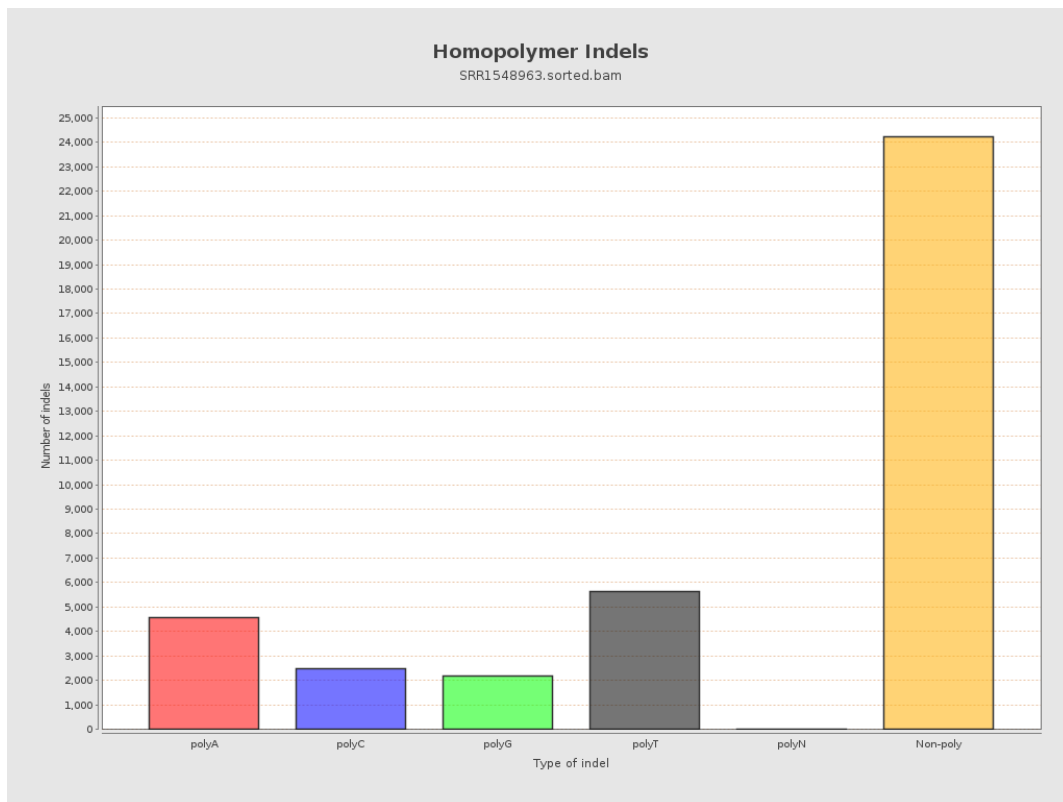
9. Results : Mapped Reads GC-content Distribution



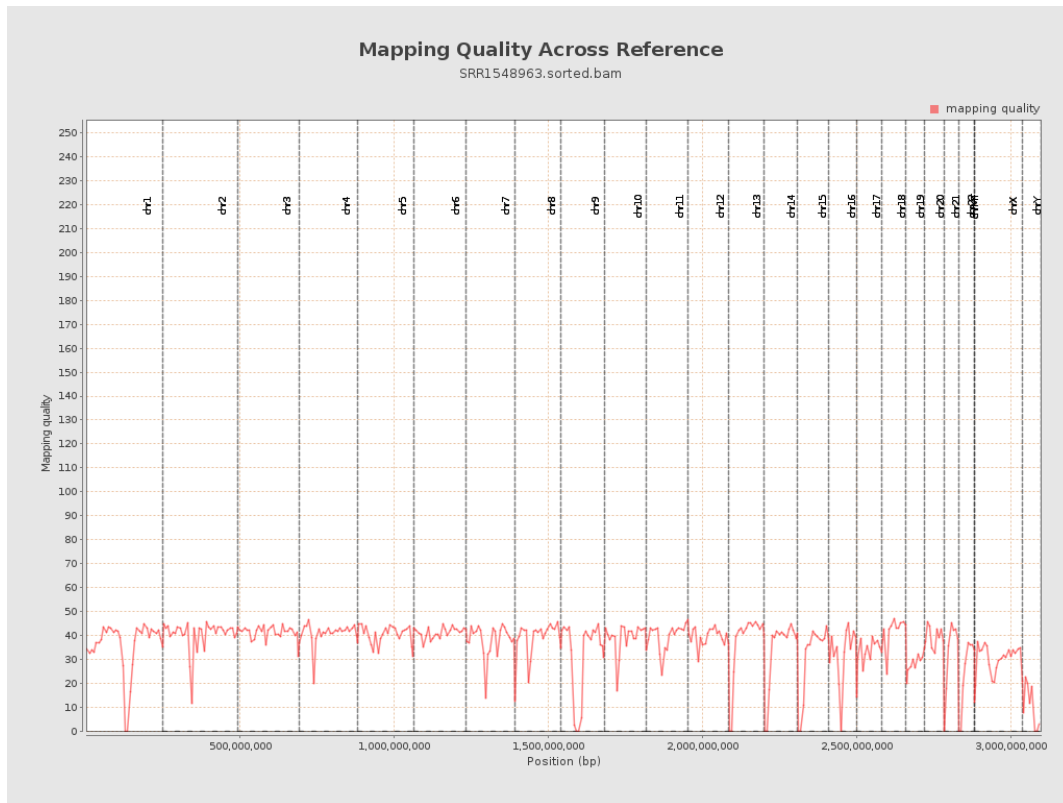
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

