

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:35:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549032.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_SRR1549032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:35:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,393,220
Mapped reads	4,571,027 / 84.76%
Unmapped reads	822,193 / 15.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	331,995 / 6.16%
Duplication rate	5.99%
Clipped reads	364,073 / 6.75%

2.2. ACGT Content

Number/percentage of A's	51,557,388 / 28.52%
Number/percentage of C's	38,453,235 / 21.27%
Number/percentage of T's	52,070,553 / 28.81%
Number/percentage of G's	38,669,558 / 21.39%
Number/percentage of N's	1,919 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0584
Standard Deviation	0.9456

2.4. Mapping Quality

Mean Mapping Quality	42.08
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2.5. Mismatches and indels

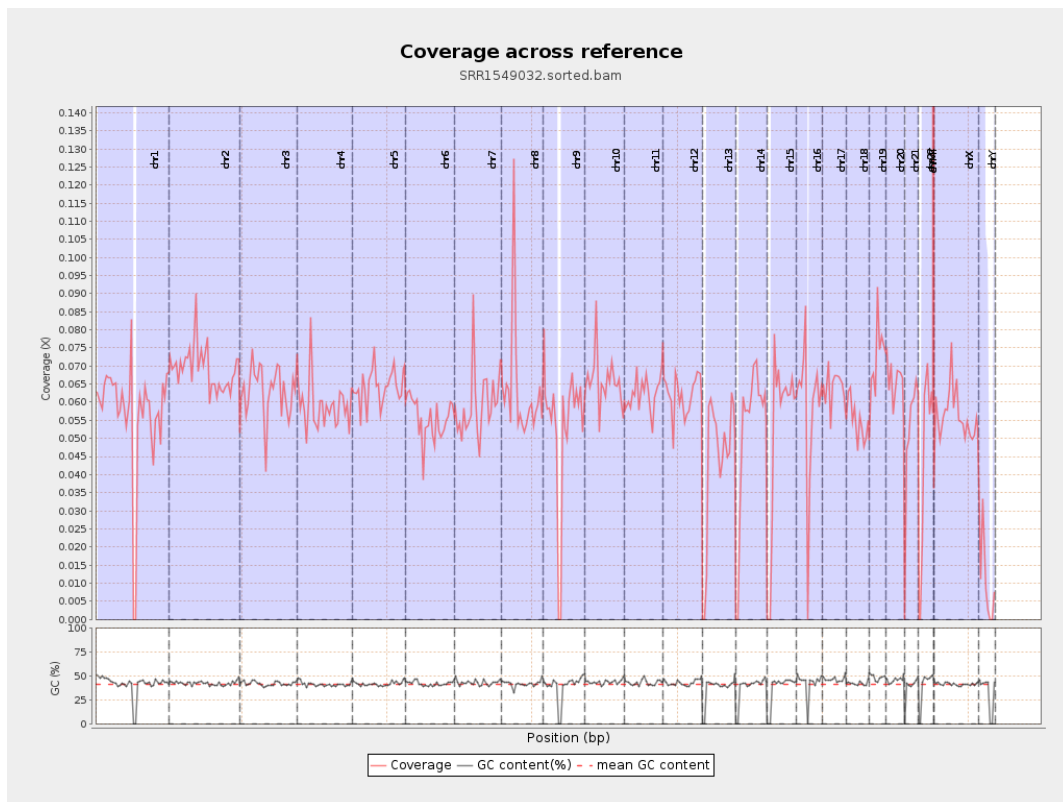
General error rate	0.28%
Mismatches	496,501
Insertions	5,892
Mapped reads with at least one insertion	0.13%
Deletions	14,757
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.86%

2.6. Chromosome stats

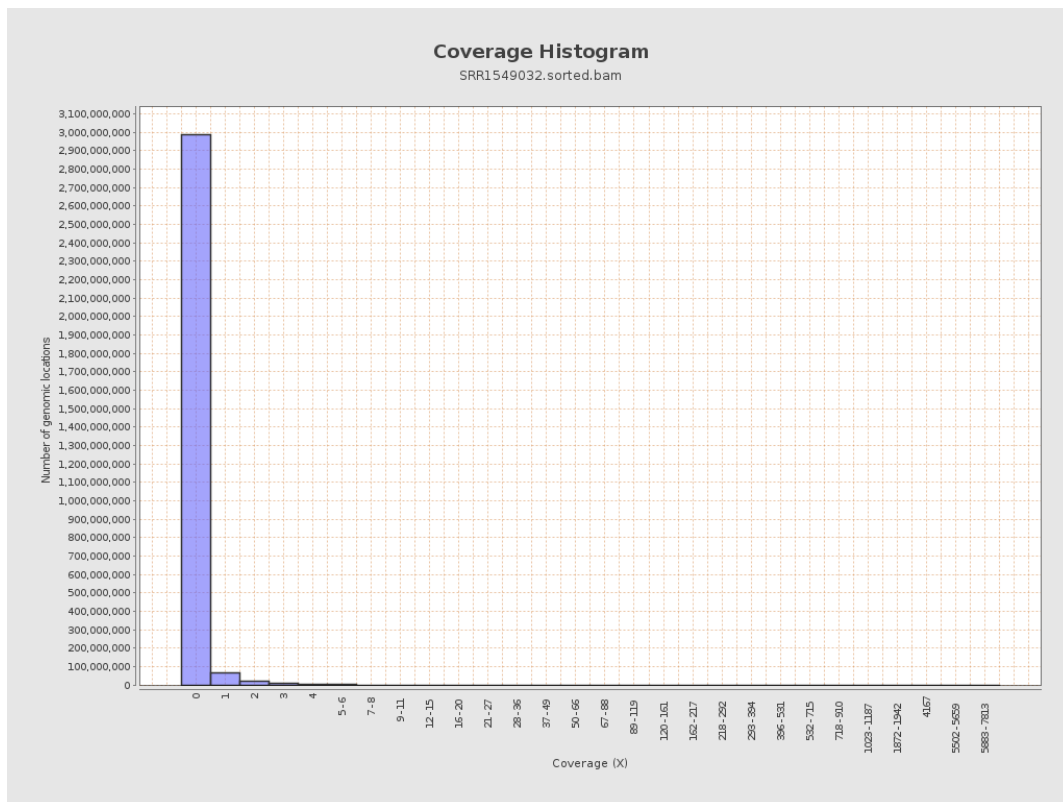
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14154967	0.0568	0.7581
chr2	243199373	16830819	0.0692	0.4903
chr3	198022430	12462419	0.0629	0.3872
chr4	191154276	11222052	0.0587	0.3858
chr5	180915260	11625176	0.0643	0.3947
chr6	171115067	9498326	0.0555	0.3667
chr7	159138663	9408585	0.0591	0.5233
chr8	146364022	9147279	0.0625	3.7992

chr9	141213431	7386338	0.0523	0.4204
chr10	135534747	8914196	0.0658	0.4657
chr11	135006516	8419045	0.0624	0.5347
chr12	133851895	8307029	0.0621	0.3881
chr13	115169878	5027819	0.0437	0.3213
chr14	107349540	5578895	0.052	0.381
chr15	102531392	5434723	0.053	0.351
chr16	90354753	5315517	0.0588	0.3901
chr17	81195210	5195202	0.064	0.4195
chr18	78077248	4287581	0.0549	0.7025
chr19	59128983	4284199	0.0725	0.6927
chr20	63025520	4134928	0.0656	0.4061
chr21	48129895	2499361	0.0519	0.3753
chr22	51304566	2237393	0.0436	0.3549
chrMT	16571	86579	5.2247	6.485
chrX	155270560	8687436	0.056	0.3999
chrY	59373566	626245	0.0105	0.2127

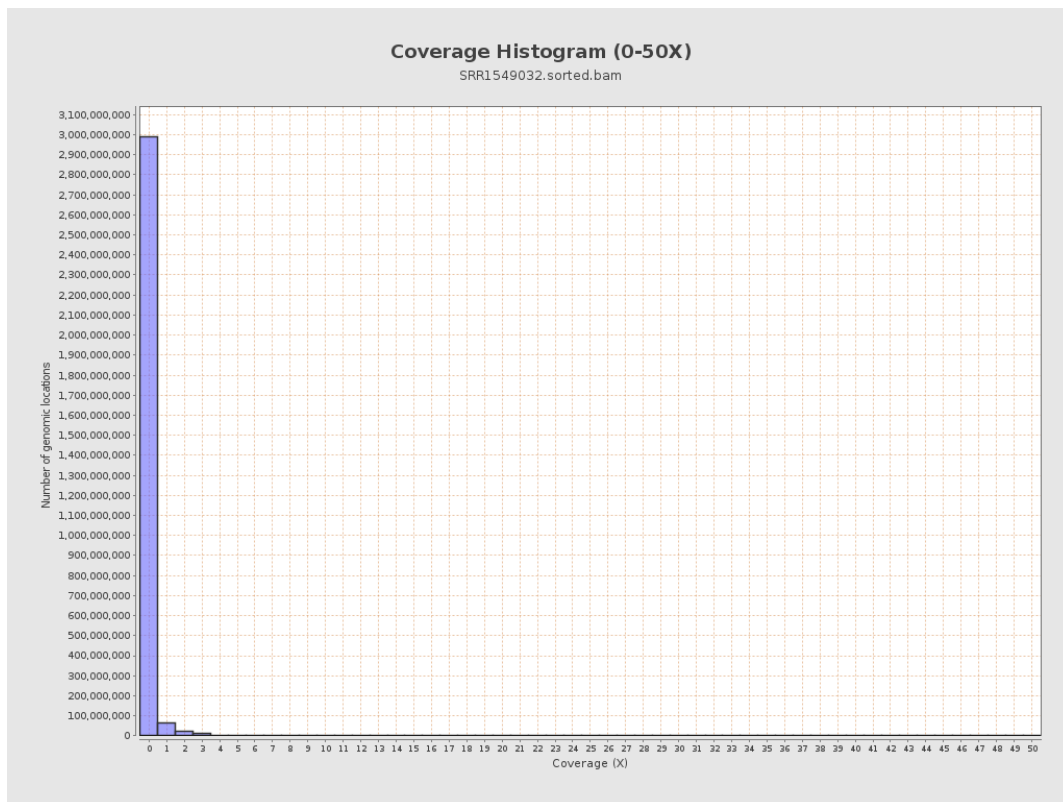
3. Results : Coverage across reference



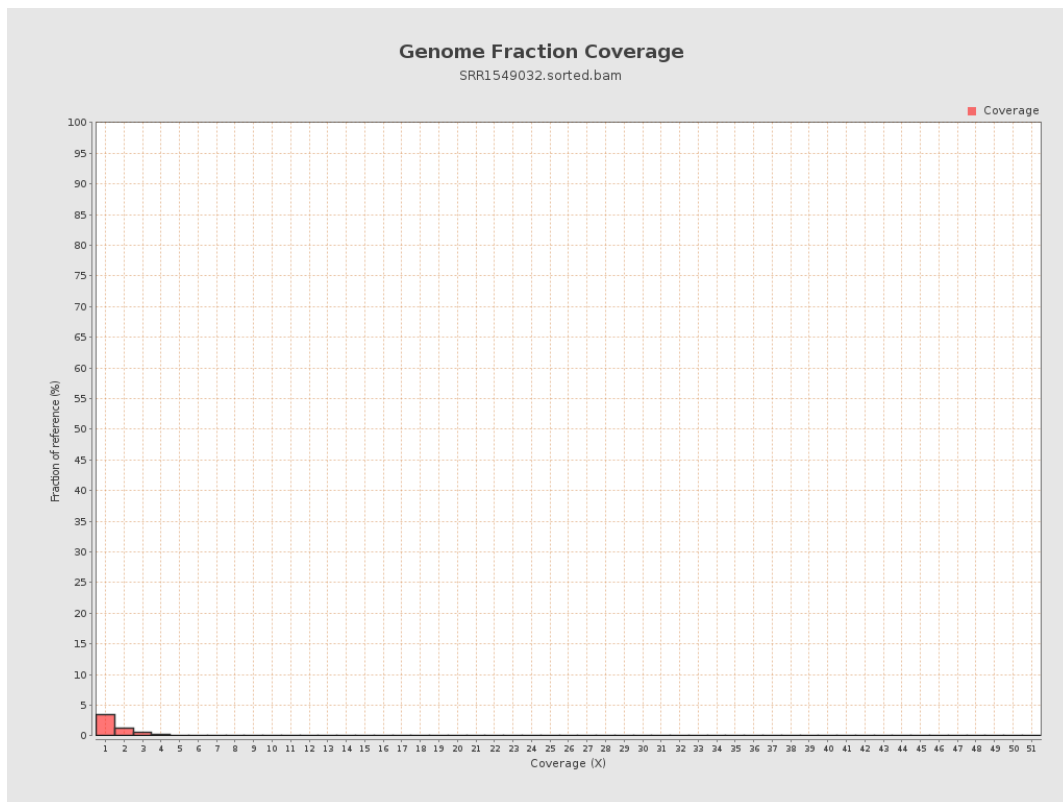
4. Results : Coverage Histogram



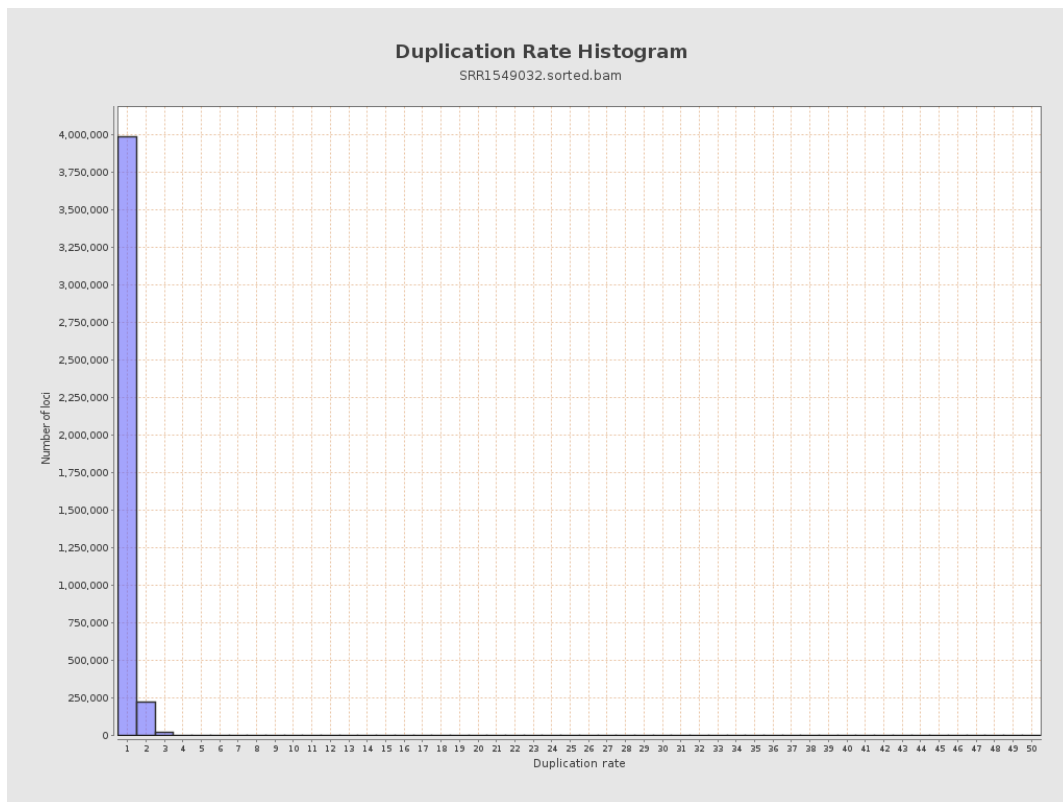
5. Results : Coverage Histogram (0-50X)



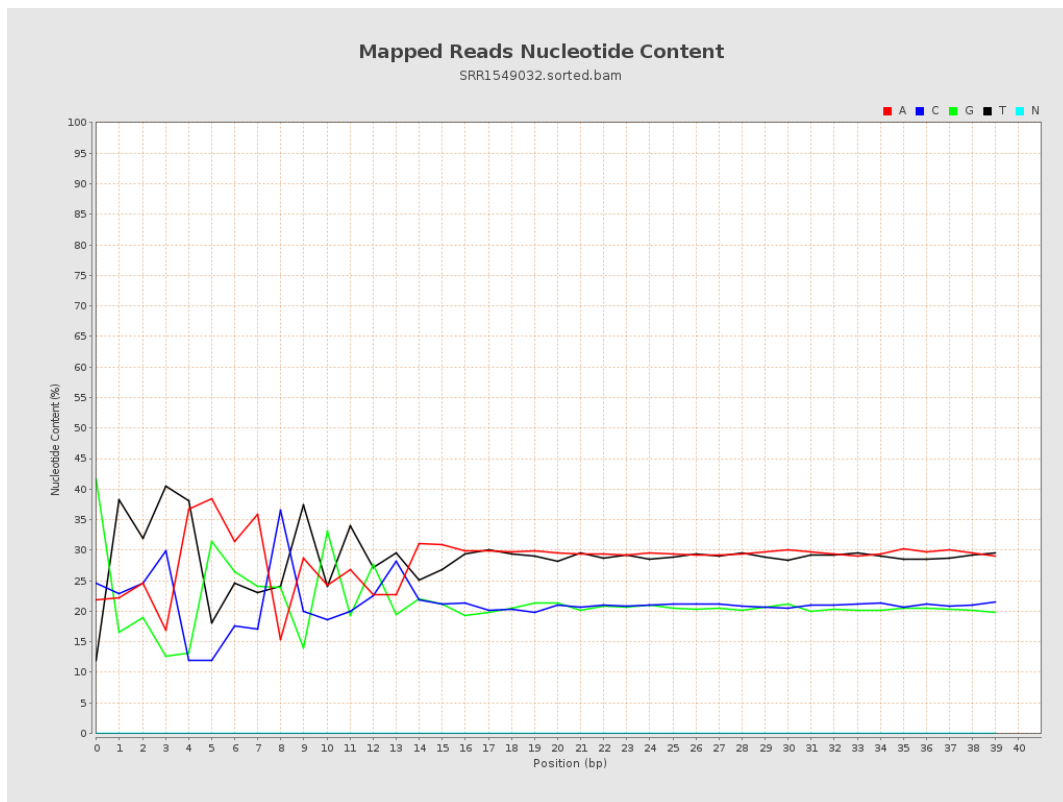
6. Results : Genome Fraction Coverage



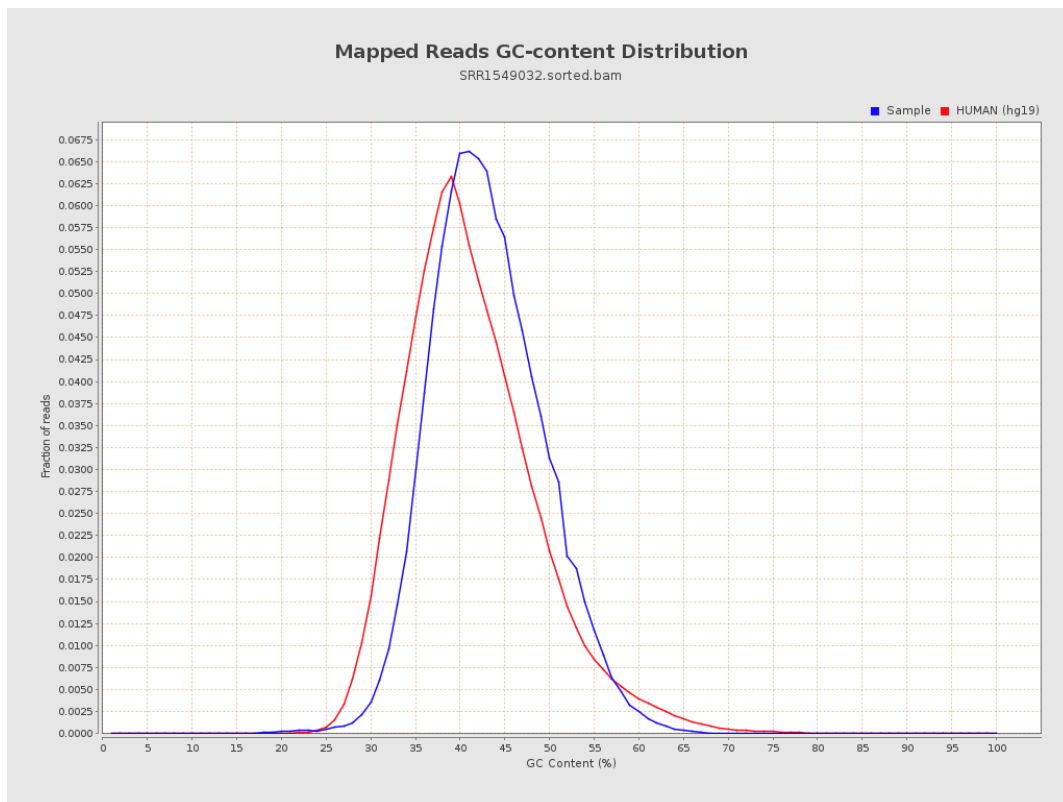
7. Results : Duplication Rate Histogram



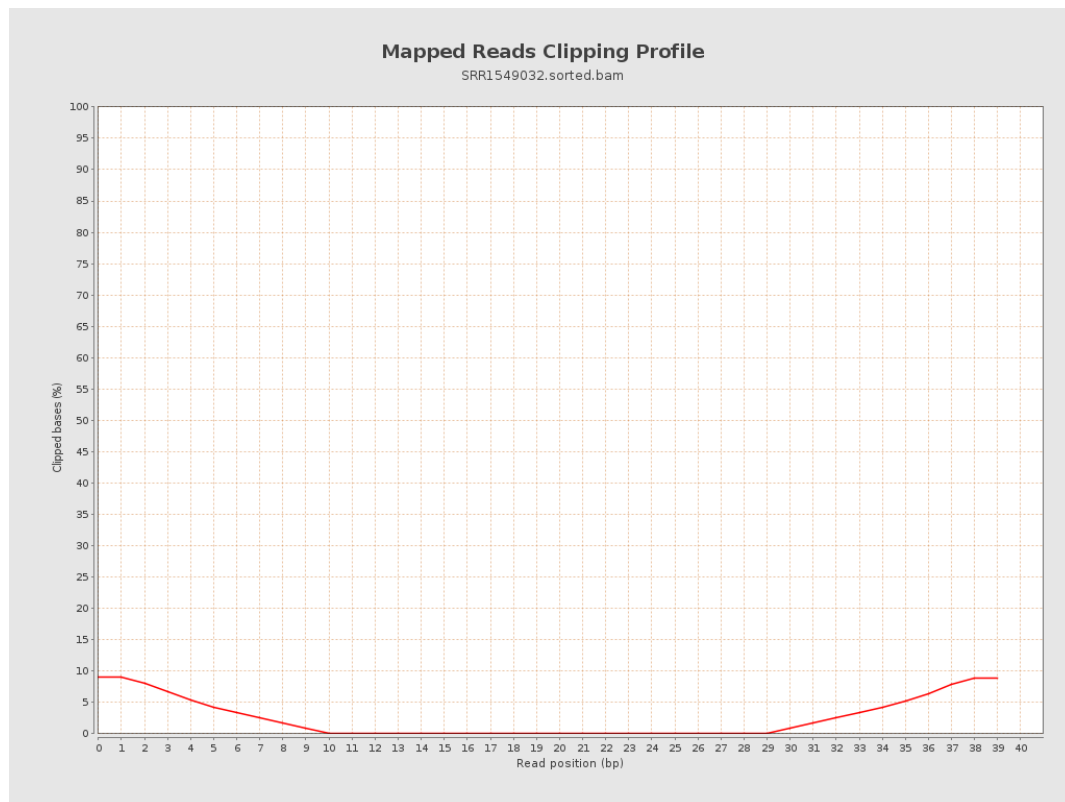
8. Results : Mapped Reads Nucleotide Content



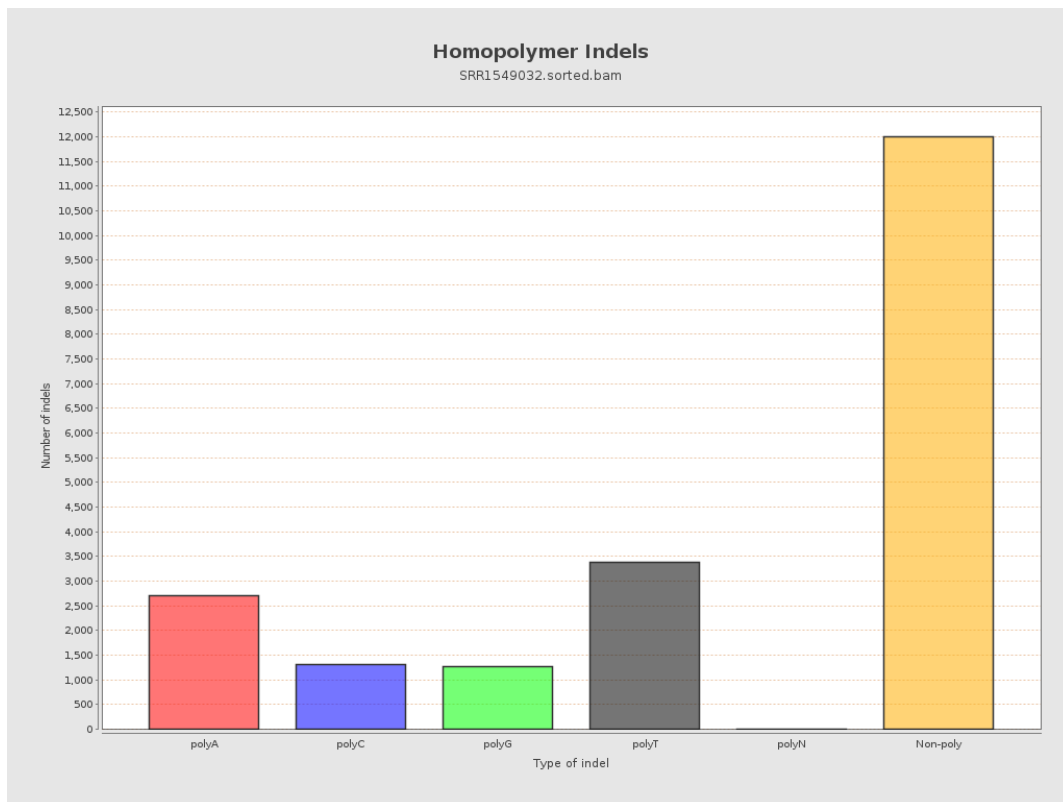
9. Results : Mapped Reads GC-content Distribution



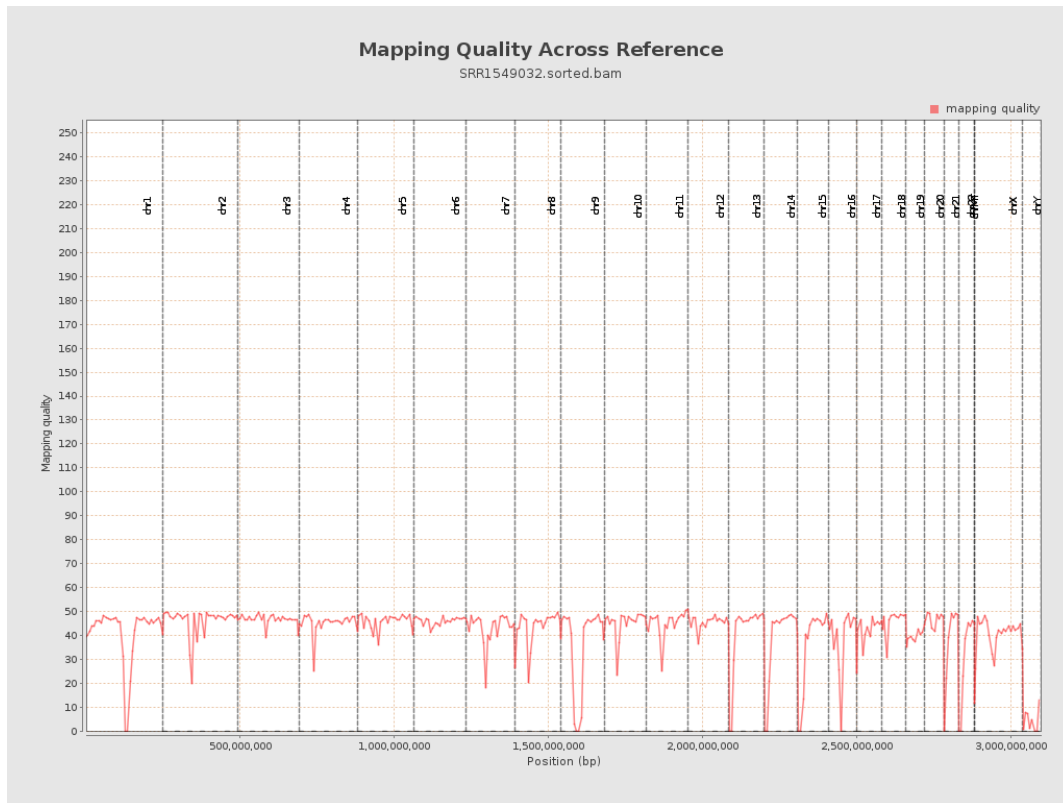
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

