Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:09:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237581.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_SRR6237581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237581.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:09:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,312,683
Mapped reads	1,882,020 / 81.38%
Unmapped reads	430,663 / 18.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,248 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	130,042 / 5.62%
Duplication rate	4.51%
Clipped reads	1,157,046 / 50.03%

2.2. ACGT Content

Number/percentage of A's	29,762,832 / 25.1%
Number/percentage of C's	22,410,619 / 18.9%
Number/percentage of T's	36,029,895 / 30.38%
Number/percentage of G's	30,350,706 / 25.59%
Number/percentage of N's	26,719 / 0.02%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3785

2.4. Mapping Quality

Mean Mapping Quality	38.87

2.5. Mismatches and indels

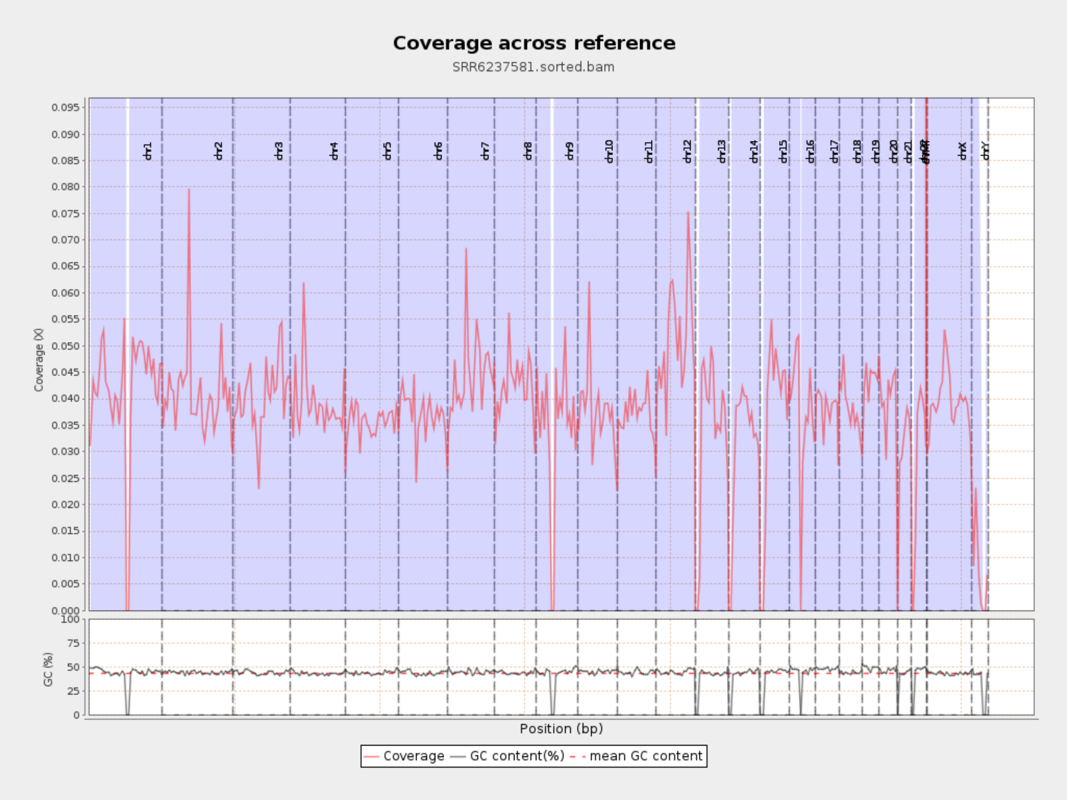
General error rate	0.96%
Mismatches	1,120,998
Insertions	11,300
Mapped reads with at least one insertion	0.59%
Deletions	42,270
Mapped reads with at least one deletion	2.22%
Homopolymer indels	45.93%

2.6. Chromosome stats

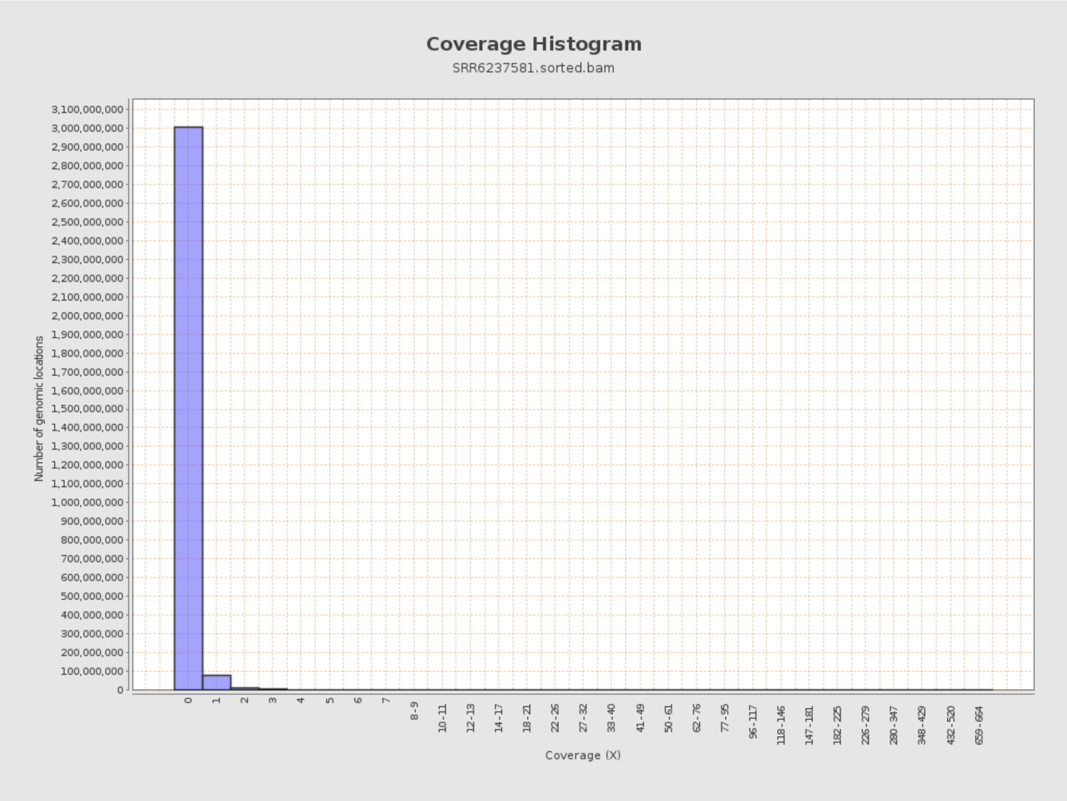
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10359377	0.0416	0.4829
chr2	243199373	10015015	0.0412	0.536
chr3	198022430	7987791	0.0403	0.2875
chr4	191154276	7463117	0.039	0.2997
chr5	180915260	6473692	0.0358	0.2574
chr6	171115067	6342394	0.0371	0.2953
chr7	159138663	7100425	0.0446	0.5636

chr8	146364022	6167060	0.0421	0.3531
chr9	141213431	4787290	0.0339	0.4054
chr10	135534747	5134374	0.0379	0.371
chr11	135006516	4998429	0.037	0.4214
chr12	133851895	6907703	0.0516	0.3422
chr13	115169878	3825095	0.0332	0.2617
chr14	107349540	3338423	0.0311	0.2908
chr15	102531392	3727228	0.0364	0.2845
chr16	90354753	3355477	0.0371	0.313
chr17	81195210	3090382	0.0381	0.3085
chr18	78077248	3015237	0.0386	0.5598
chr19	59128983	2560489	0.0433	0.3929
chr20	63025520	2505123	0.0397	0.2942
chr21	48129895	1426407	0.0296	0.2748
chr22	51304566	1375046	0.0268	0.2354
chrMT	16571	107836	6.5075	5.458
chrX	155270560	6143529	0.0396	0.3018
chrY	59373566	444679	0.0075	0.1815

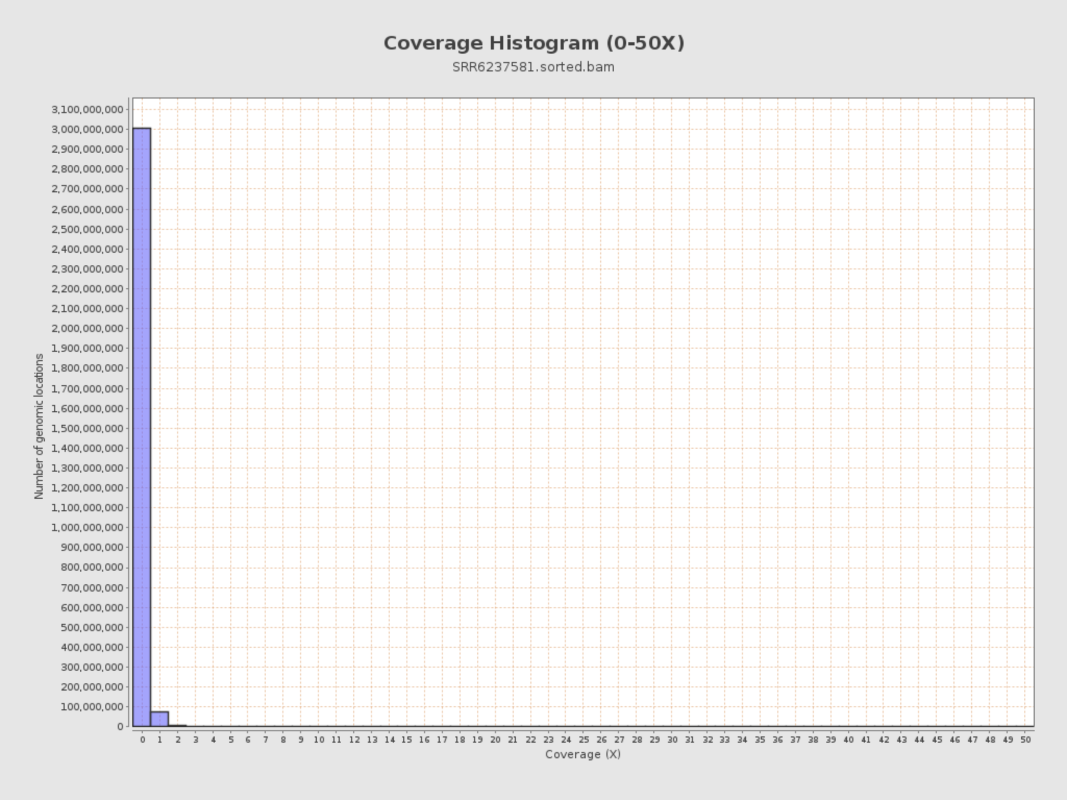
3. Results : Coverage across reference



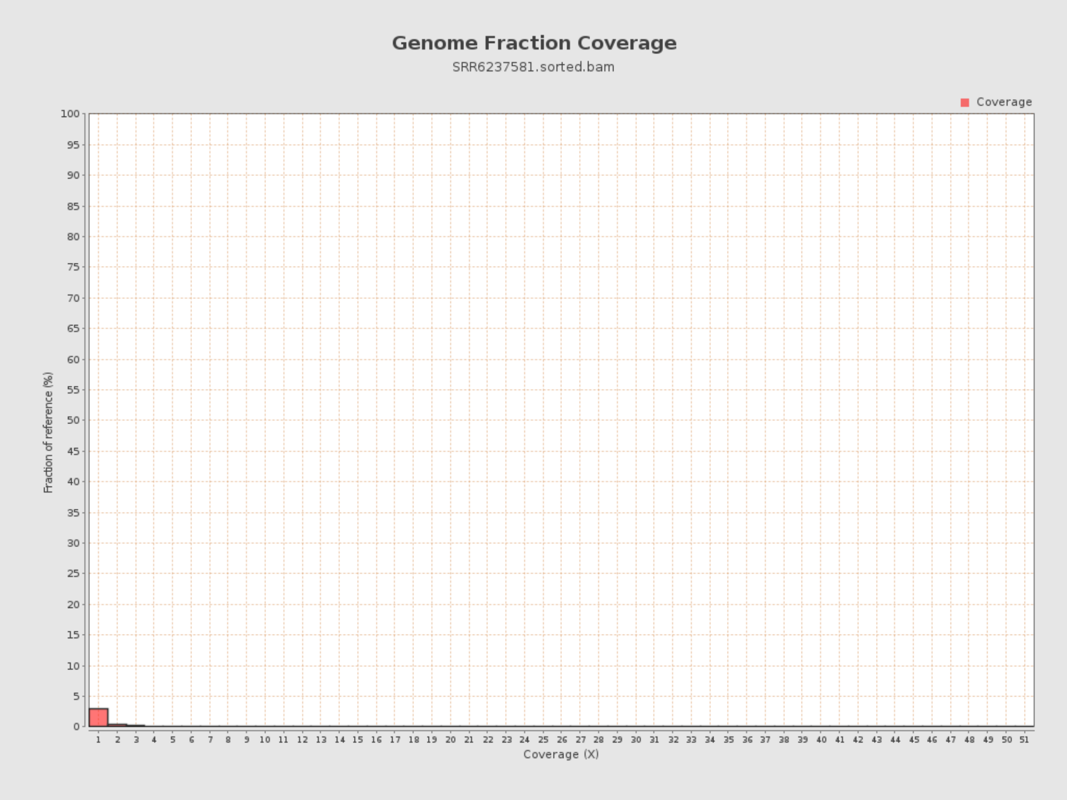
4. Results : Coverage Histogram



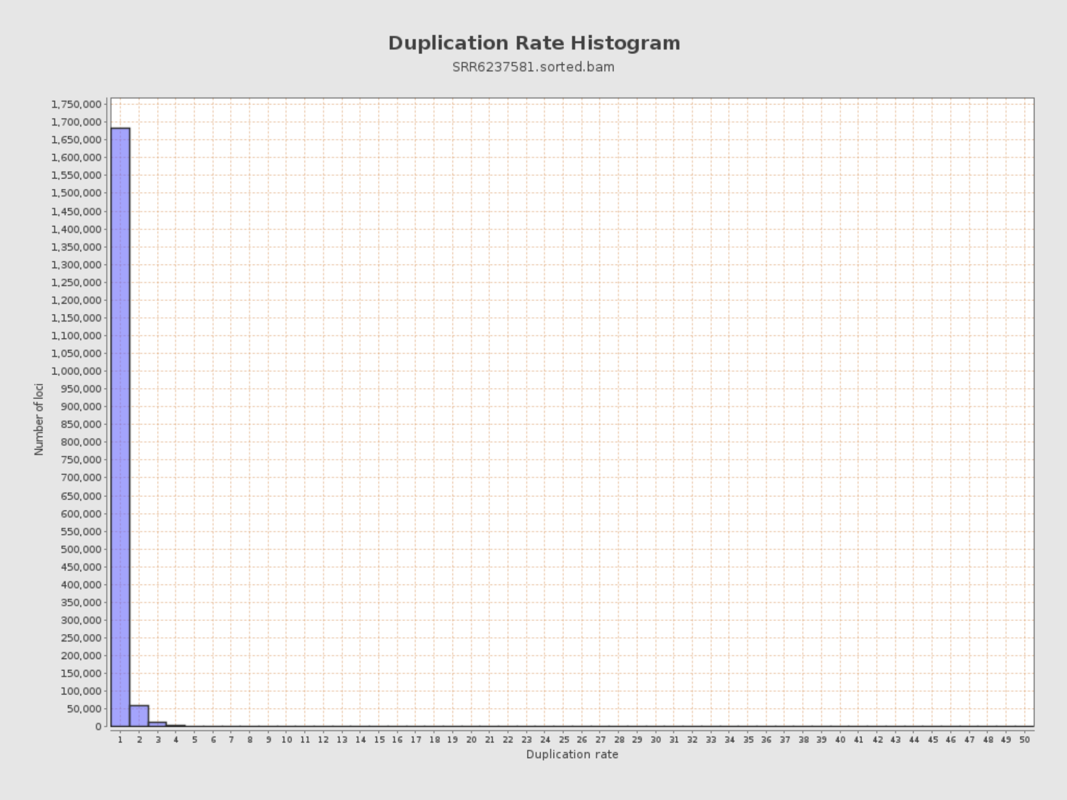
5. Results : Coverage Histogram (0-50X)



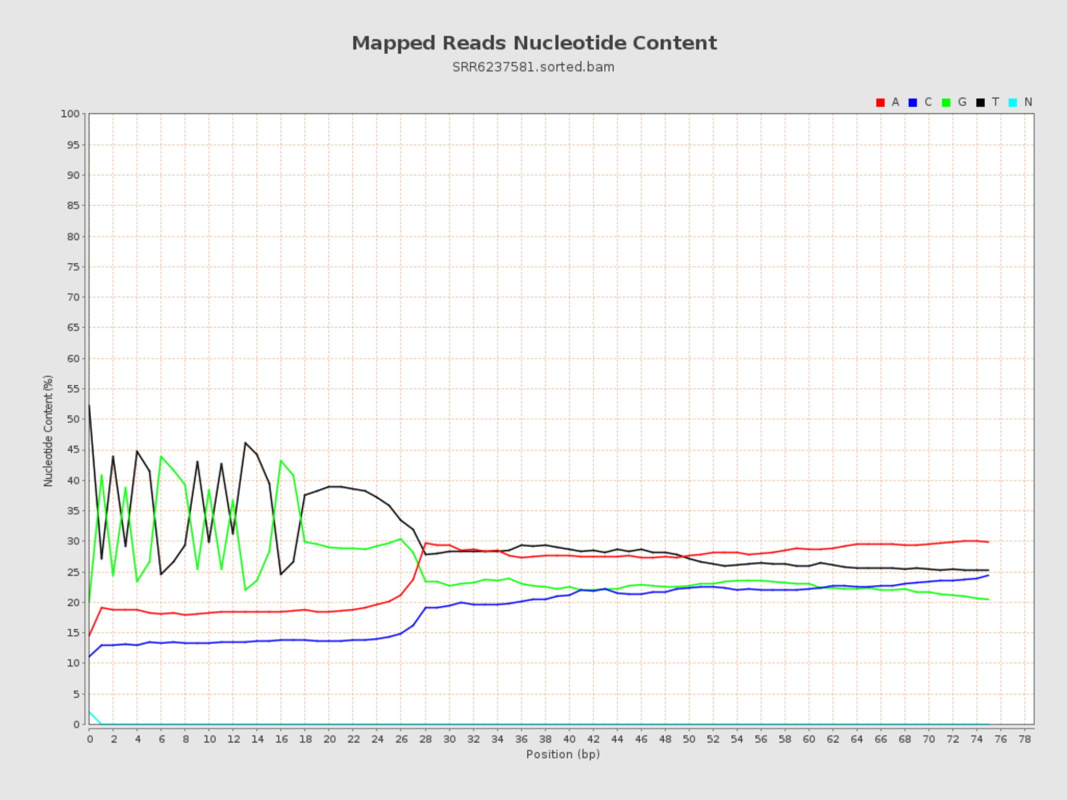
6. Results : Genome Fraction Coverage



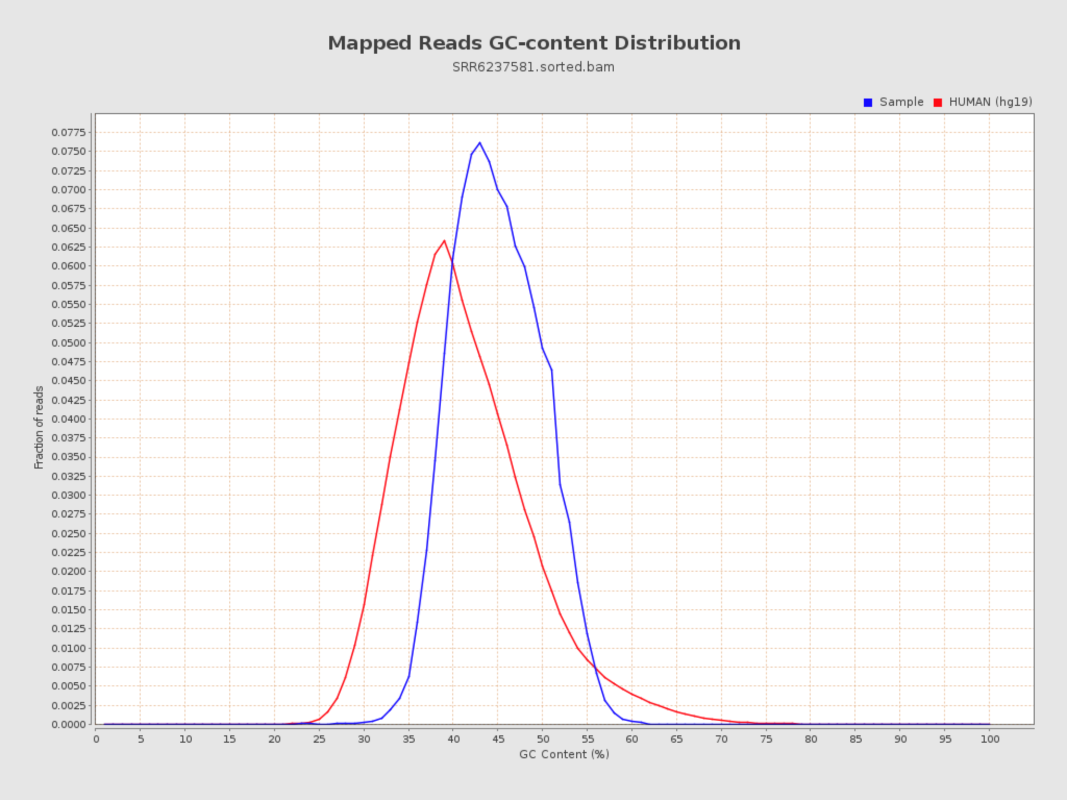
7. Results : Duplication Rate Histogram



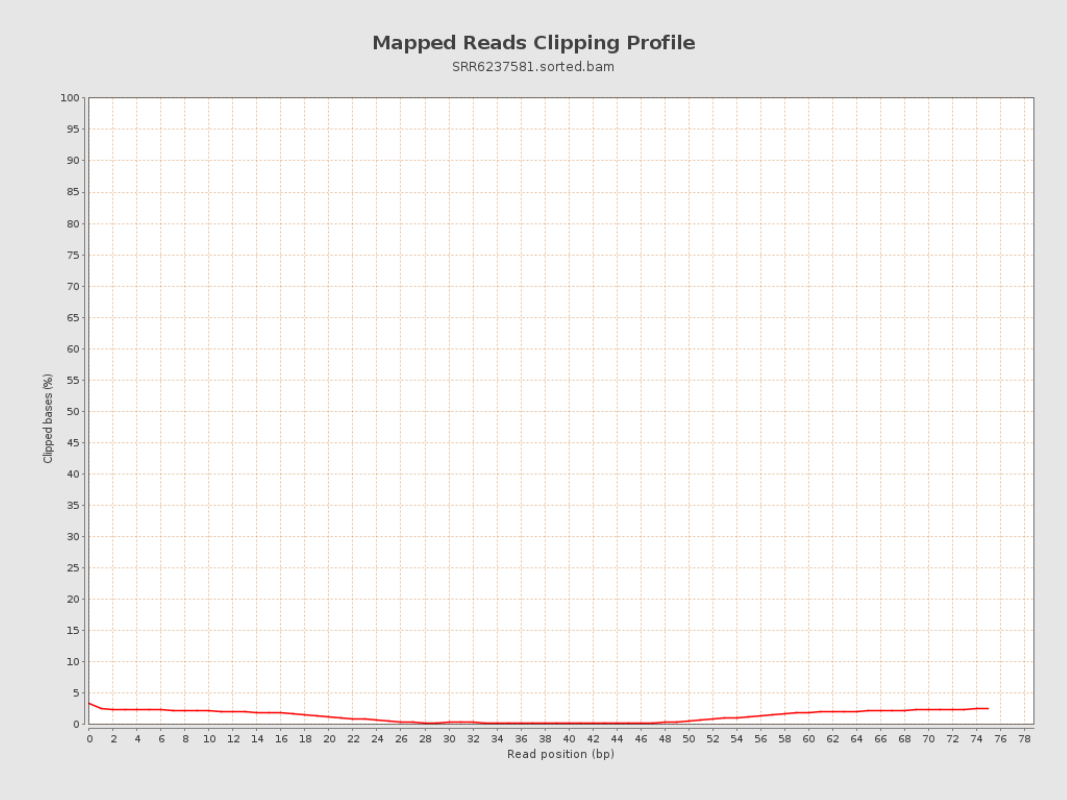
8. Results : Mapped Reads Nucleotide Content



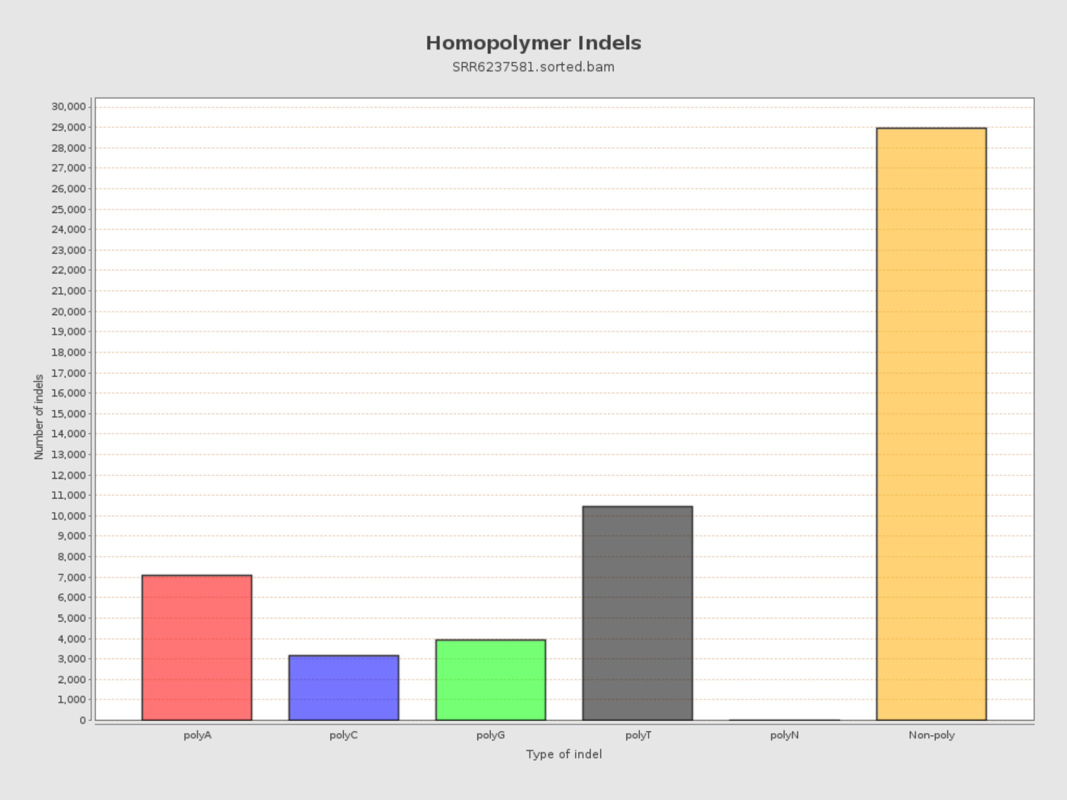
9. Results : Mapped Reads GC-content Distribution



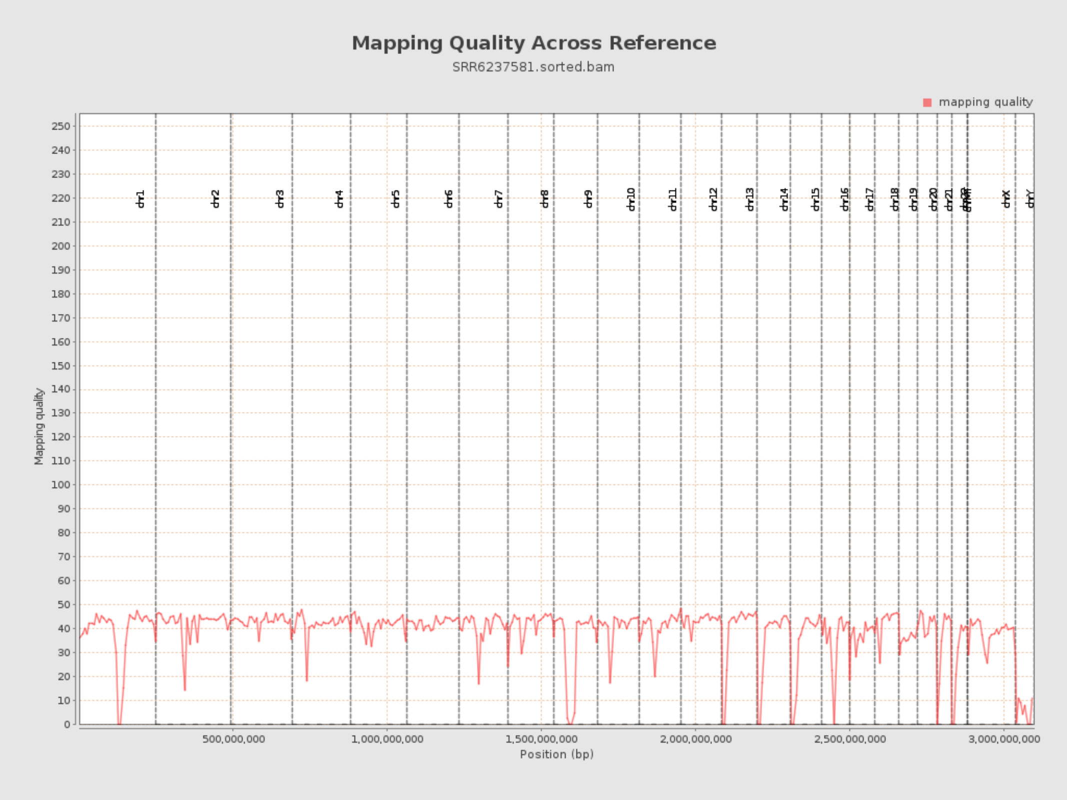
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram