Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:19:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237286.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_SRR6237286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237286.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:19:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,591,722
Mapped reads	2,106,423 / 81.28%
Unmapped reads	485,299 / 18.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,508 / 0.91%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	800,549 / 30.89%
Duplication rate	22.36%
Clipped reads	1,434,192 / 55.34%

2.2. ACGT Content

Number/percentage of A's	32,240,066 / 25.14%
Number/percentage of C's	22,198,780 / 17.31%
Number/percentage of T's	42,912,463 / 33.46%
Number/percentage of G's	30,898,410 / 24.09%
Number/percentage of N's	12,646 / 0.01%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.756

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

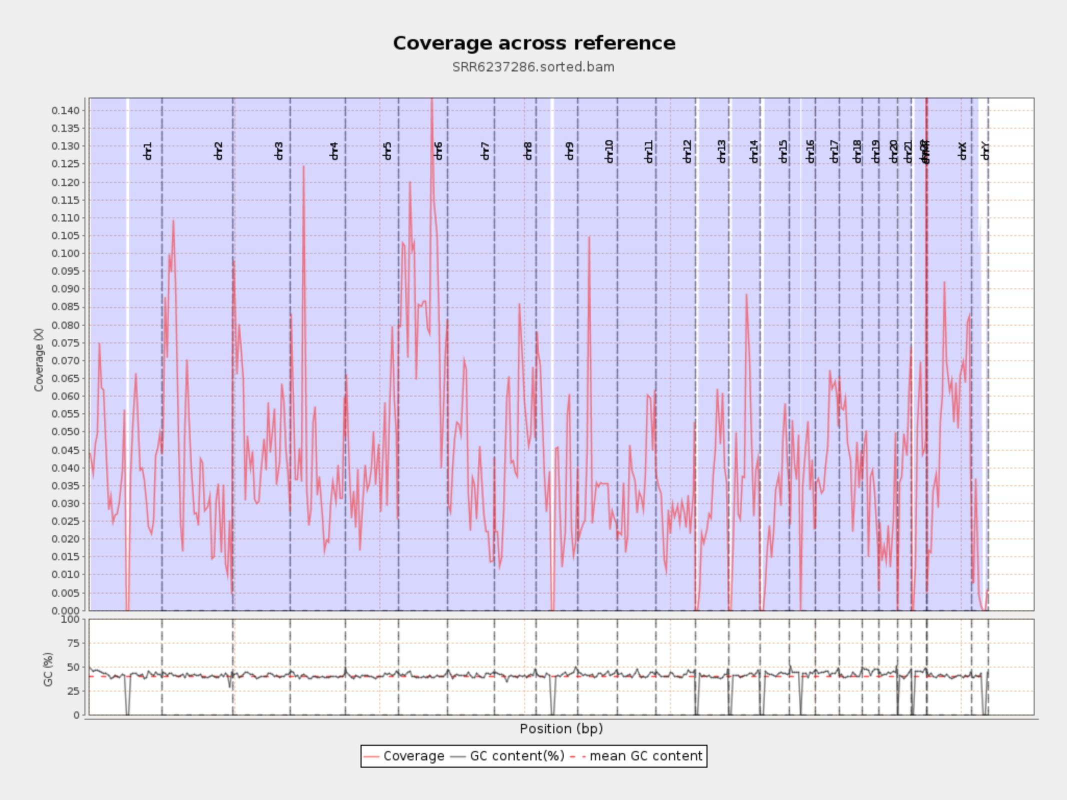
General error rate	0.72%
Mismatches	892,916
Insertions	10,876
Mapped reads with at least one insertion	0.51%
Deletions	49,559
Mapped reads with at least one deletion	2.32%
Homopolymer indels	40.92%

2.6. Chromosome stats

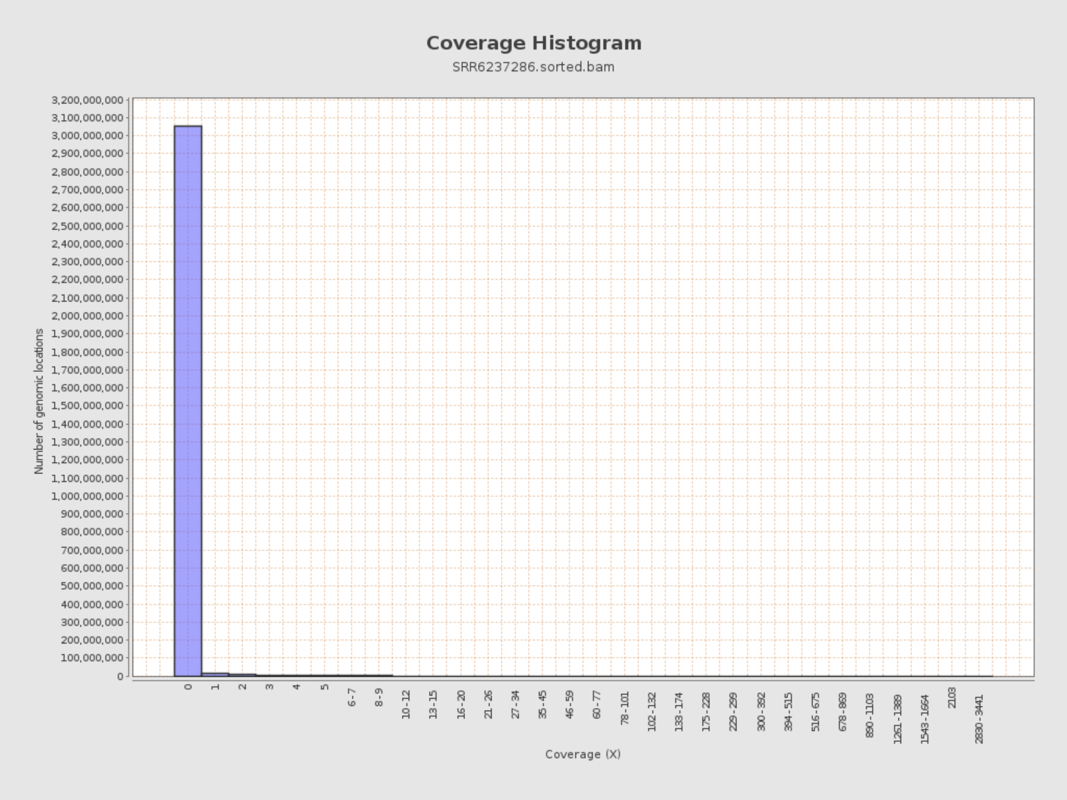
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9779287	0.0392	0.6681
chr2	243199373	10434488	0.0429	1.6798
chr3	198022430	10002577	0.0505	0.5385
chr4	191154276	7793800	0.0408	0.6602
chr5	180915260	7443539	0.0411	0.4815
chr6	171115067	15078436	0.0881	0.8478
chr7	159138663	5868605	0.0369	0.5991

chr8	146364022	6644215	0.0454	0.9501
chr9	141213431	4948185	0.035	0.4604
chr10	135534747	4635538	0.0342	0.8009
chr11	135006516	4905740	0.0363	0.4908
chr12	133851895	3670013	0.0274	0.3932
chr13	115169878	3519888	0.0306	0.4786
chr14	107349540	3958579	0.0369	0.4566
chr15	102531392	2691371	0.0262	0.407
chr16	90354753	3329733	0.0369	0.4812
chr17	81195210	3908742	0.0481	0.5452
chr18	78077248	3536533	0.0453	0.9923
chr19	59128983	1972775	0.0334	0.5752
chr20	63025520	1426294	0.0226	0.3718
chr21	48129895	2129802	0.0443	0.5795
chr22	51304566	1814432	0.0354	0.4535
chrMT	16571	5609	0.3385	0.8698
chrX	155270560	8372760	0.0539	0.5744
chrY	59373566	477204	0.008	0.4531

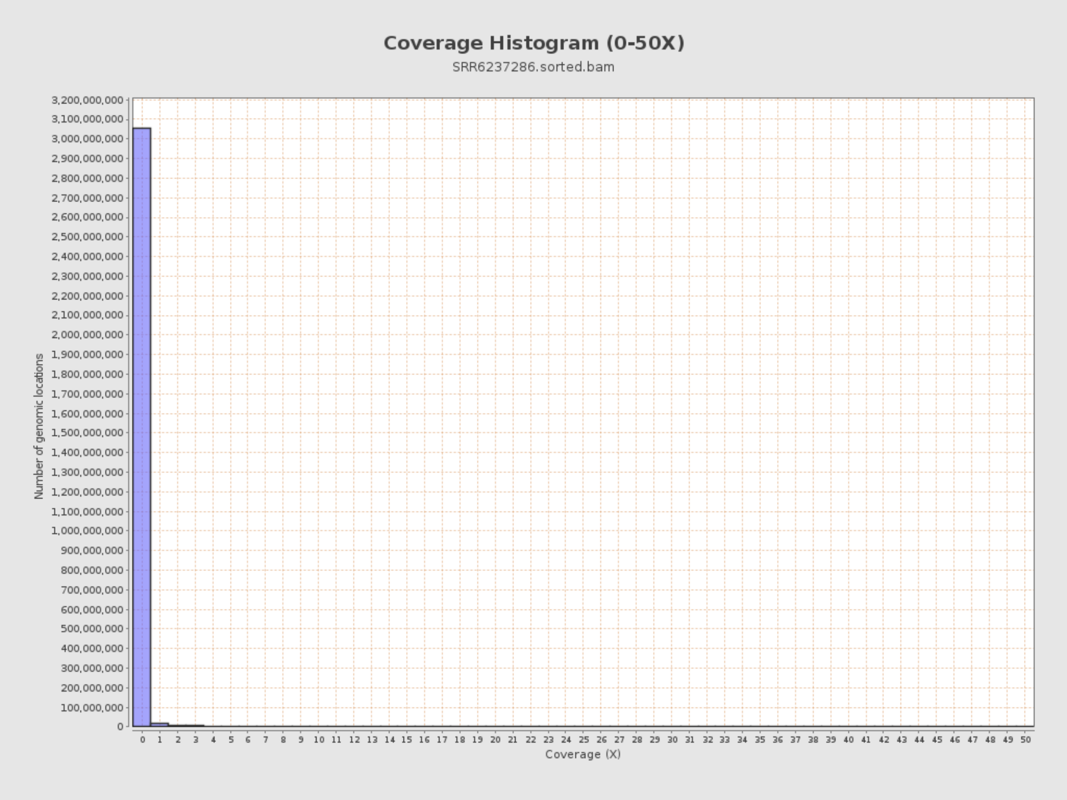
3. Results : Coverage across reference



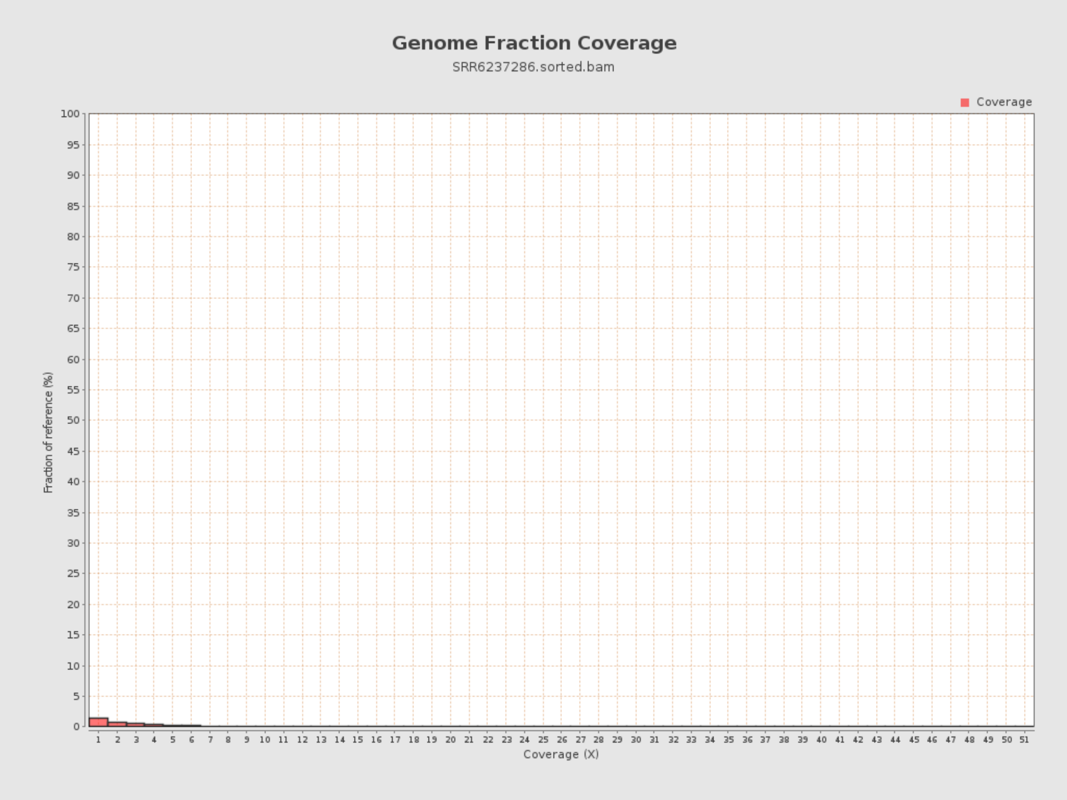
4. Results : Coverage Histogram



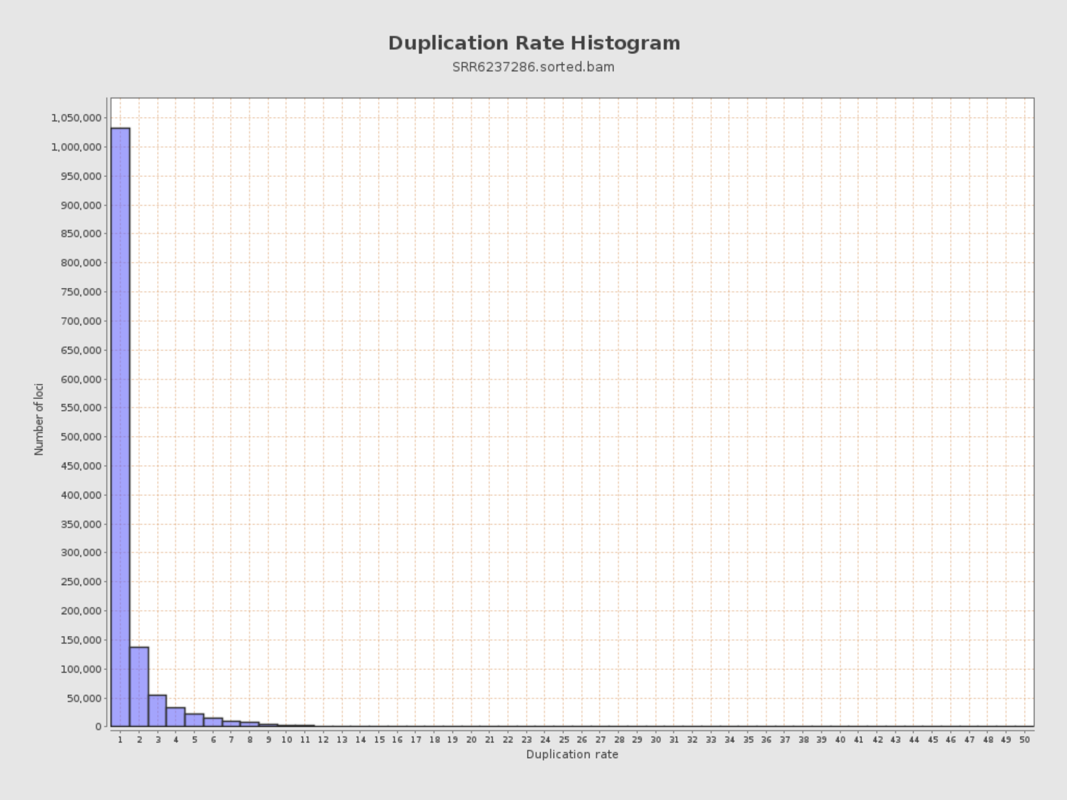
5. Results : Coverage Histogram (0-50X)



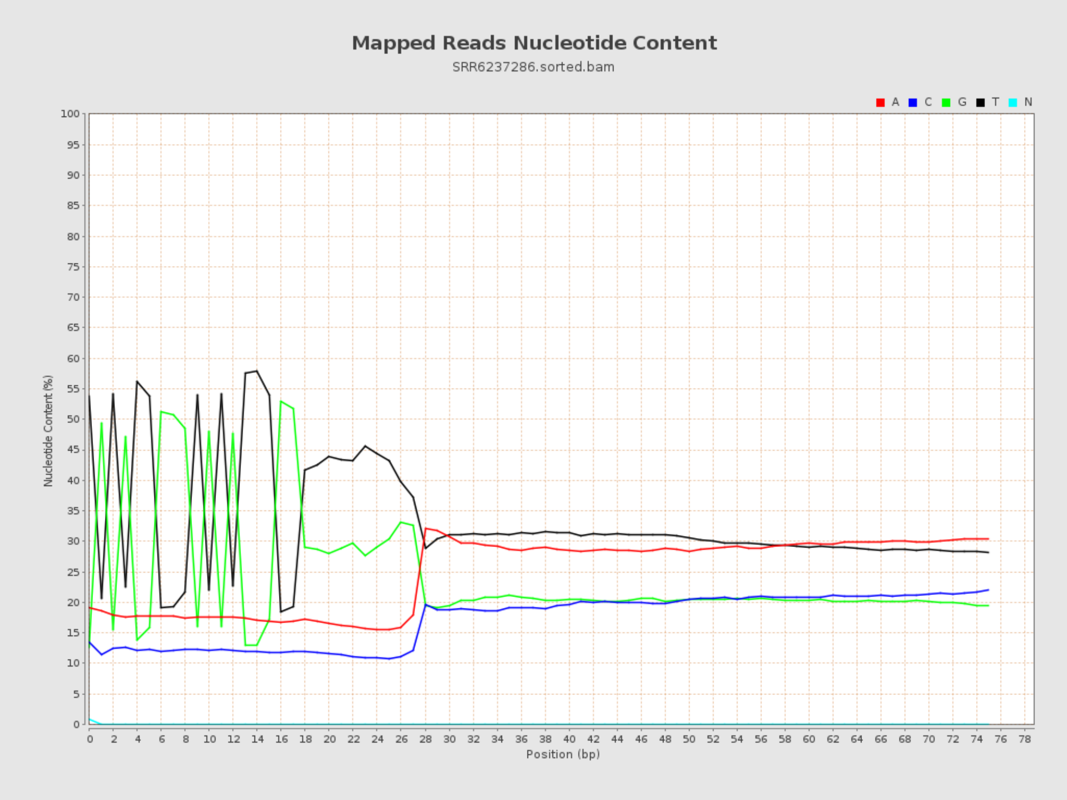
6. Results : Genome Fraction Coverage



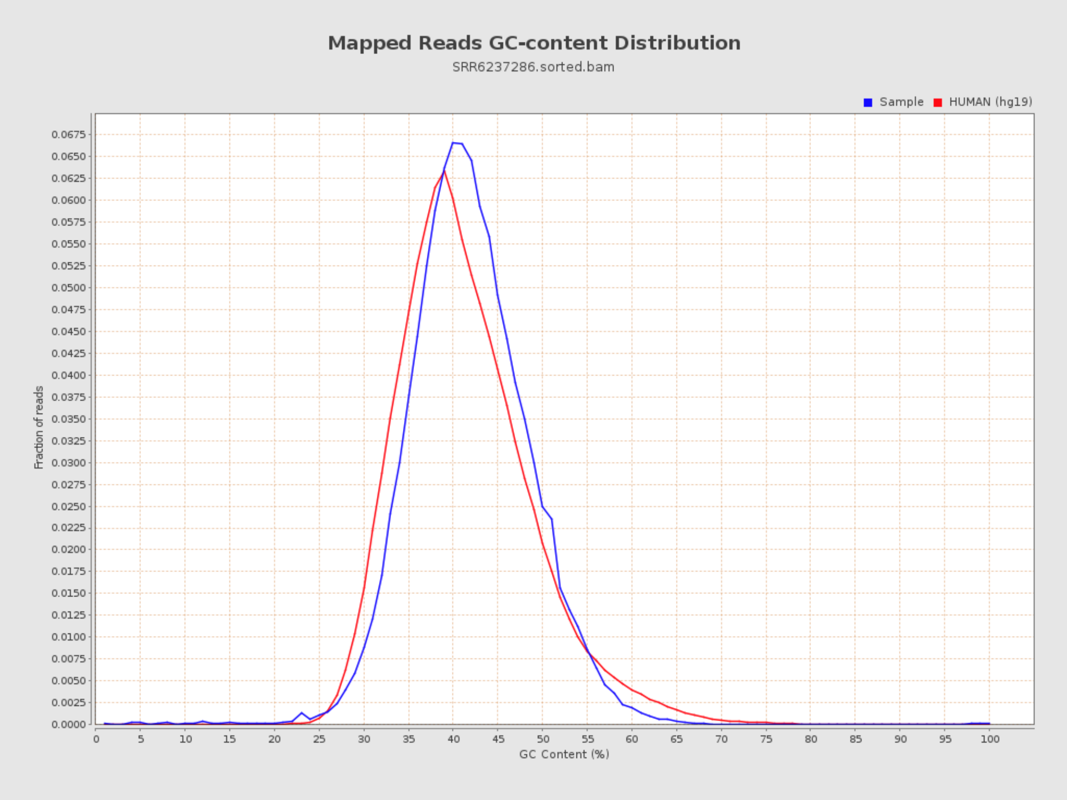
7. Results : Duplication Rate Histogram



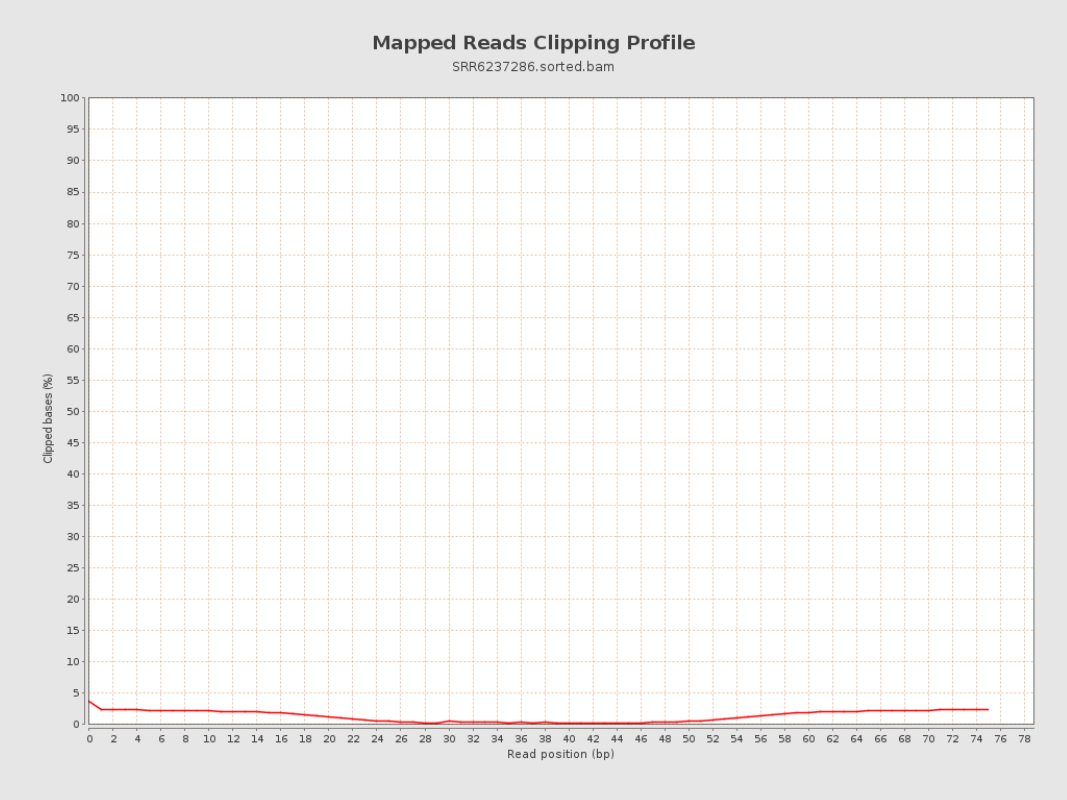
8. Results : Mapped Reads Nucleotide Content



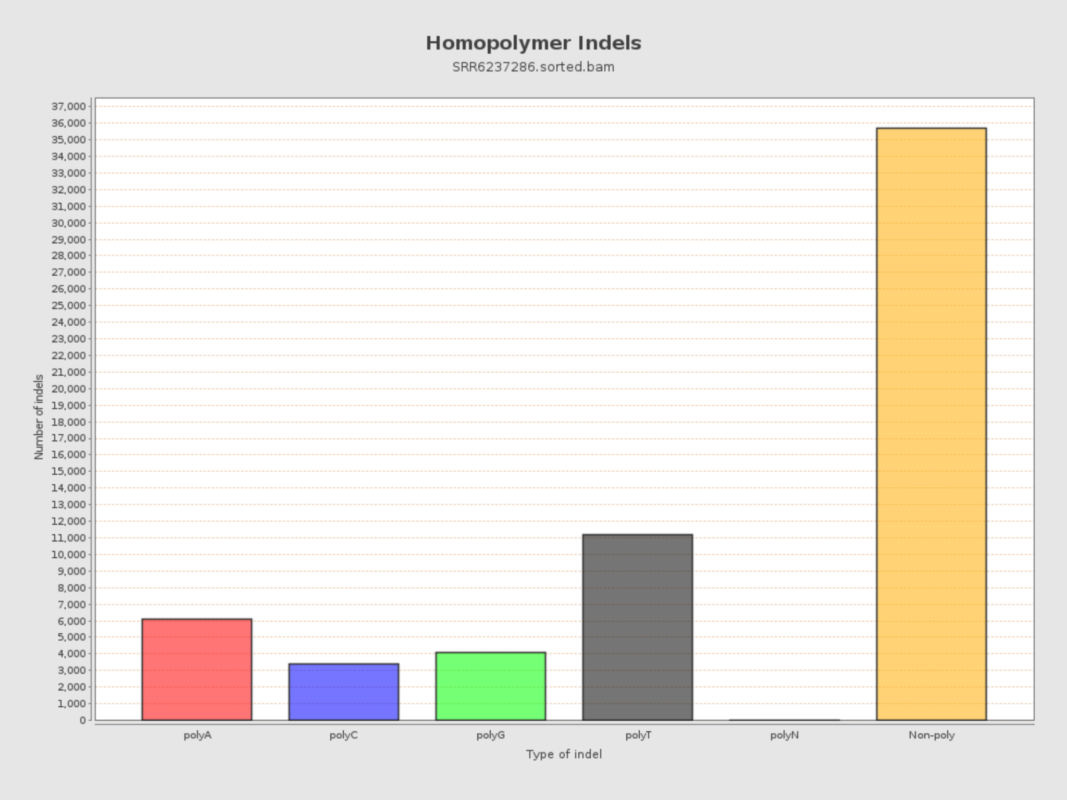
9. Results : Mapped Reads GC-content Distribution



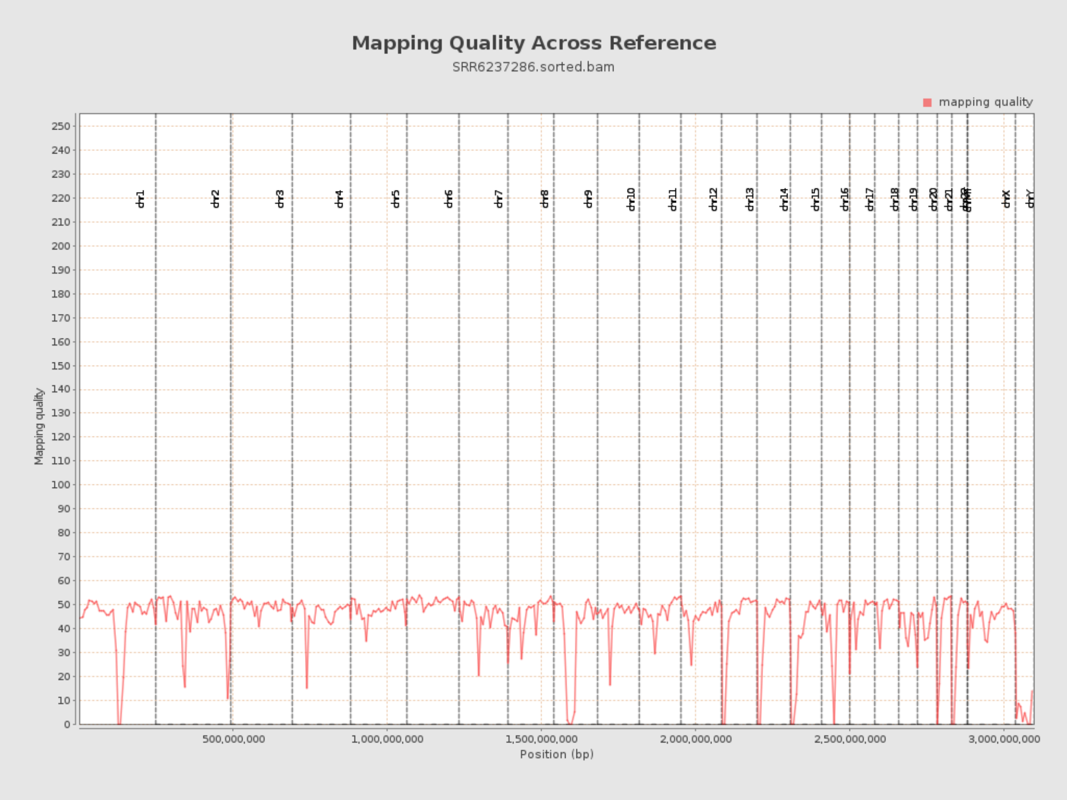
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram