Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:22:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237287.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_SRR6237287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:22:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,658,791
Mapped reads	2,422,277 / 91.1%
Unmapped reads	236,514 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,052 / 1.06%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	1,116,617 / 42%
Duplication rate	24.42%
Clipped reads	1,677,120 / 63.08%

2.2. ACGT Content

Number/percentage of A's	37,100,733 / 25.12%
Number/percentage of C's	25,119,337 / 17.01%
Number/percentage of T's	49,758,451 / 33.69%
Number/percentage of G's	35,705,588 / 24.17%
Number/percentage of N's	14,615 / 0.01%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.7882

2.4. Mapping Quality

Mean Mapping Quality	41.51

2.5. Mismatches and indels

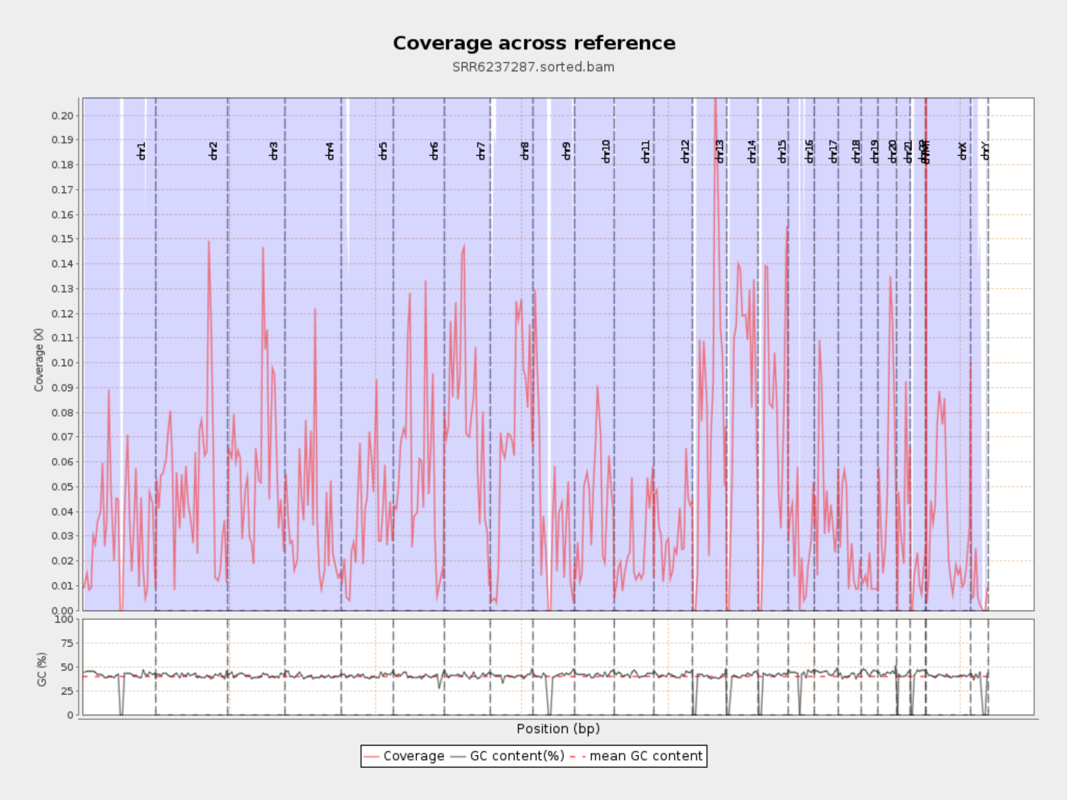
General error rate	0.66%
Mismatches	950,715
Insertions	9,893
Mapped reads with at least one insertion	0.4%
Deletions	51,992
Mapped reads with at least one deletion	2.12%
Homopolymer indels	42.2%

2.6. Chromosome stats

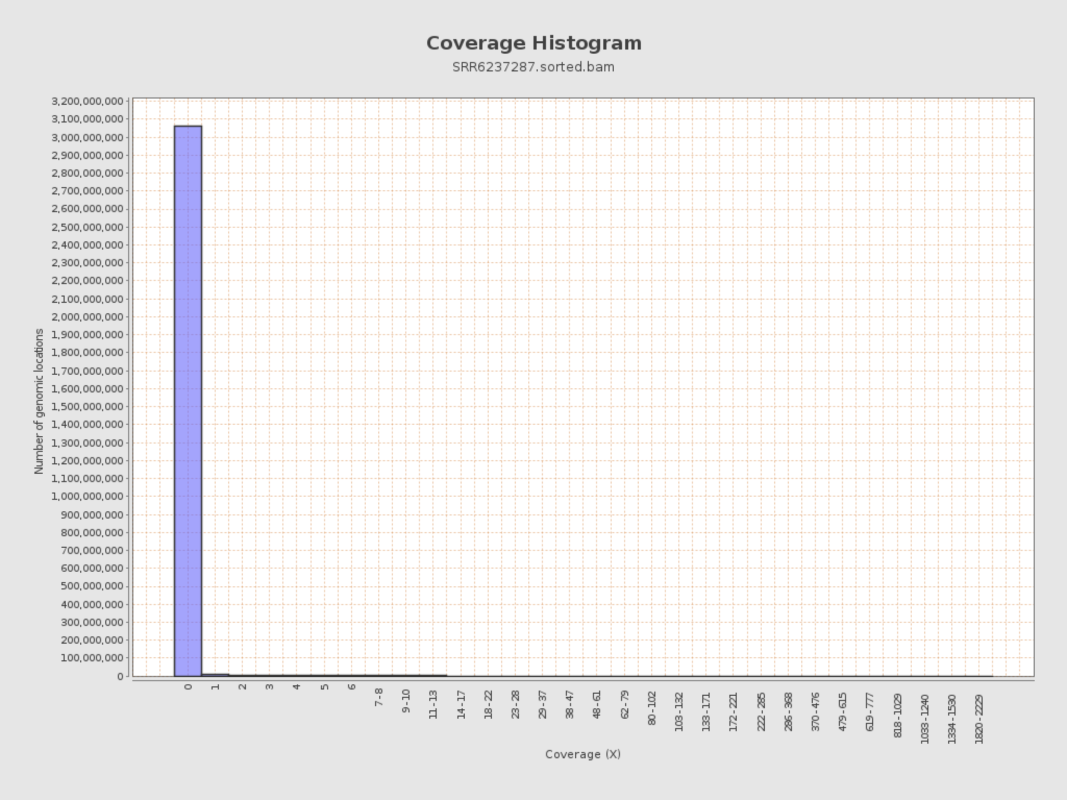
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7675244	0.0308	0.541
chr2	243199373	12745126	0.0524	1.2371
chr3	198022430	12096762	0.0611	0.7379
chr4	191154276	7218406	0.0378	0.5808
chr5	180915260	6763302	0.0374	0.5742
chr6	171115067	9648310	0.0564	0.7941
chr7	159138663	12787957	0.0804	1.0948

chr8	146364022	10212950	0.0698	1.2546
chr9	141213431	5486228	0.0389	0.5898
chr10	135534747	5784021	0.0427	0.6399
chr11	135006516	3310660	0.0245	0.488
chr12	133851895	4357564	0.0326	0.5336
chr13	115169878	9624064	0.0836	0.8998
chr14	107349540	10376335	0.0967	0.9456
chr15	102531392	7968236	0.0777	0.8415
chr16	90354753	2332728	0.0258	0.4862
chr17	81195210	3806528	0.0469	0.7119
chr18	78077248	2240078	0.0287	1.0395
chr19	59128983	715664	0.0121	0.459
chr20	63025520	4014934	0.0637	0.7765
chr21	48129895	2134687	0.0444	0.6405
chr22	51304566	608510	0.0119	0.3074
chrMT	16571	12733	0.7684	2.8539
chrX	155270560	5466978	0.0352	0.586
chrY	59373566	398420	0.0067	0.2525

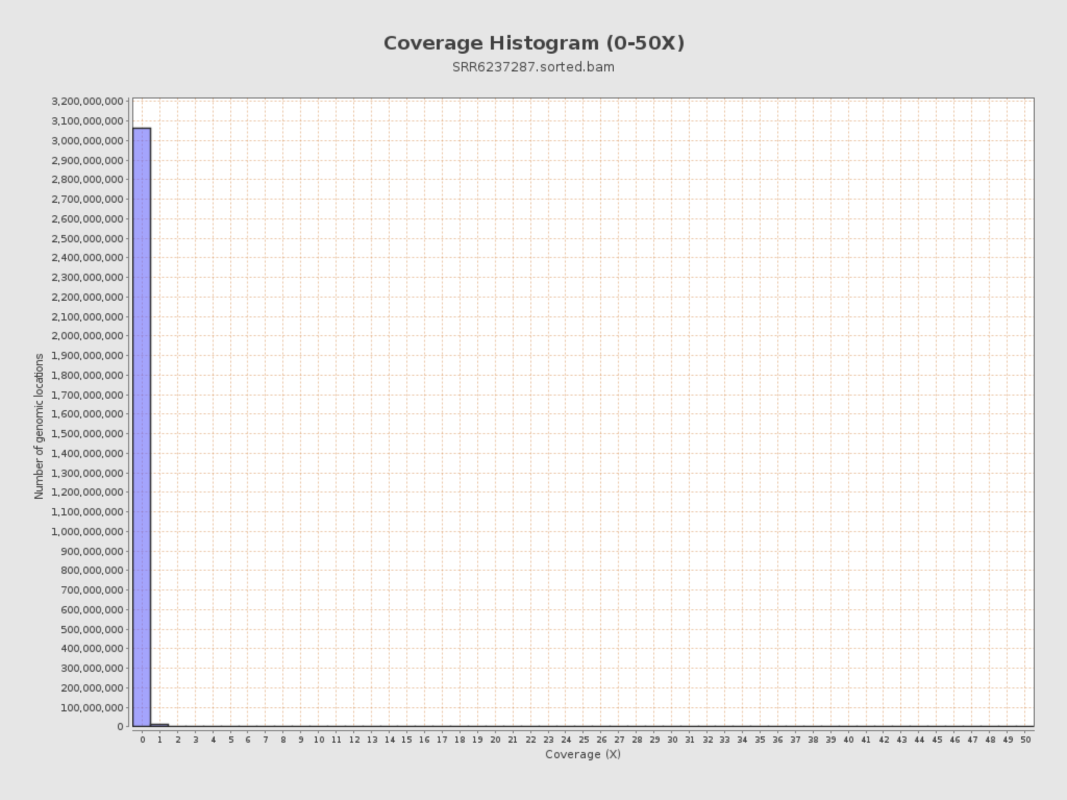
3. Results : Coverage across reference



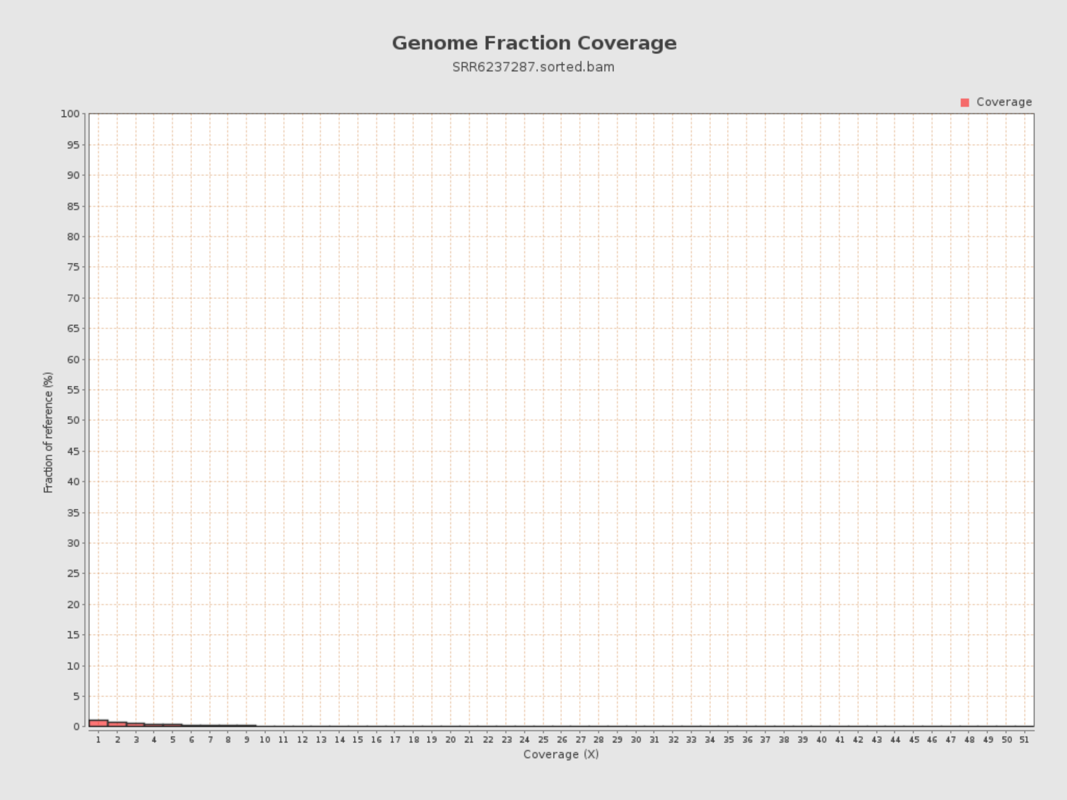
4. Results : Coverage Histogram



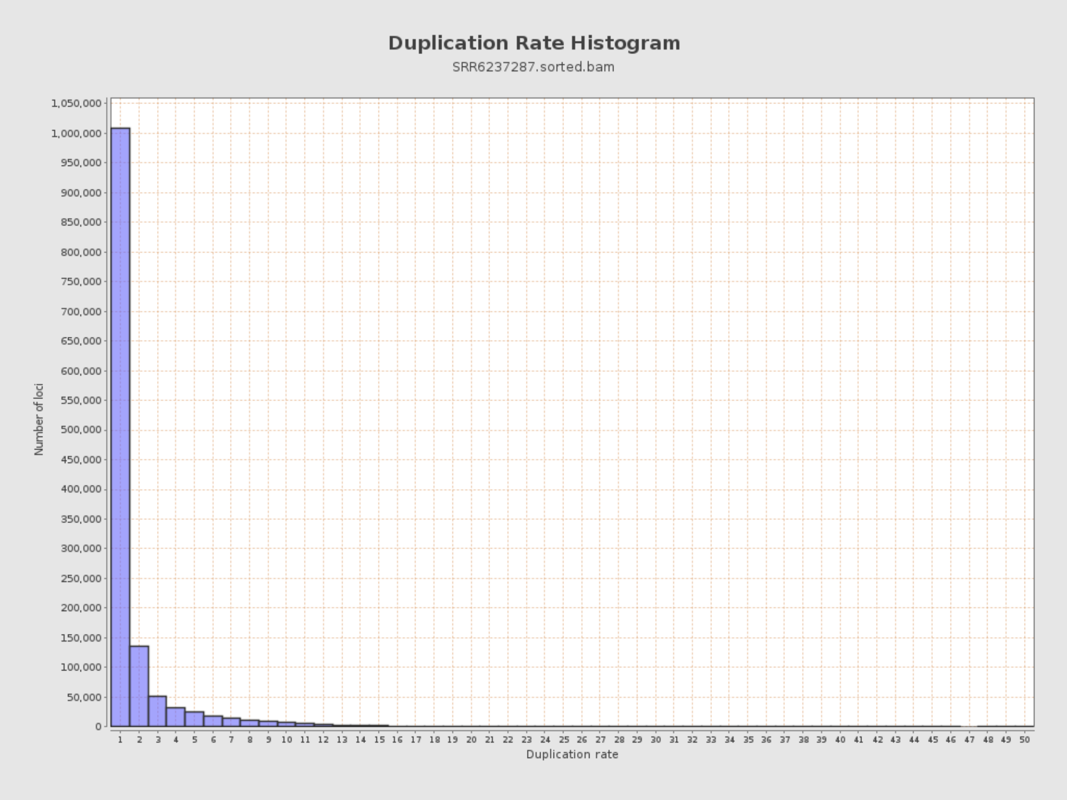
5. Results : Coverage Histogram (0-50X)



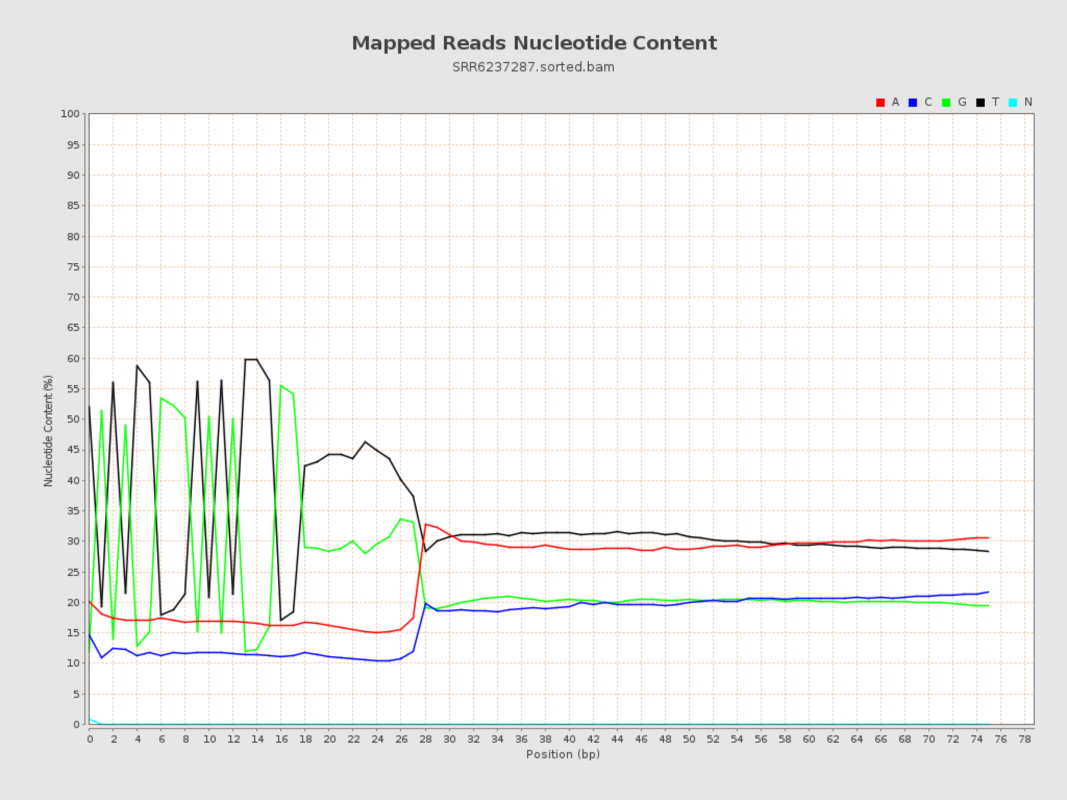
6. Results : Genome Fraction Coverage



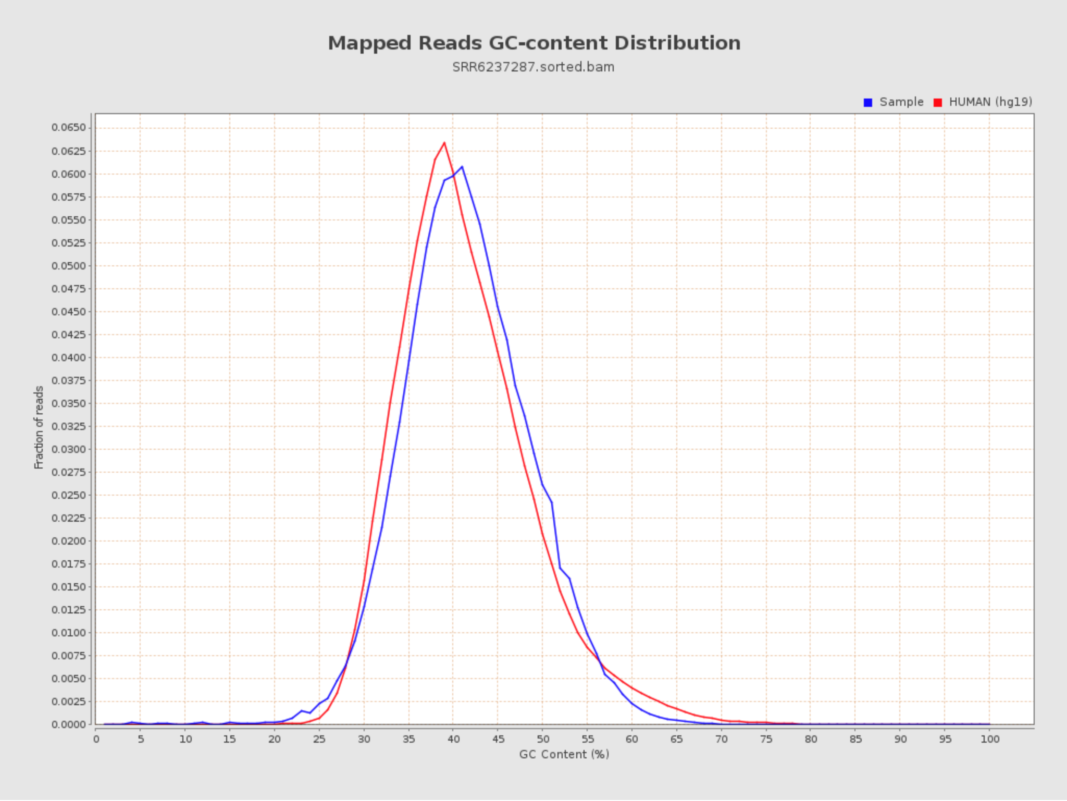
7. Results : Duplication Rate Histogram



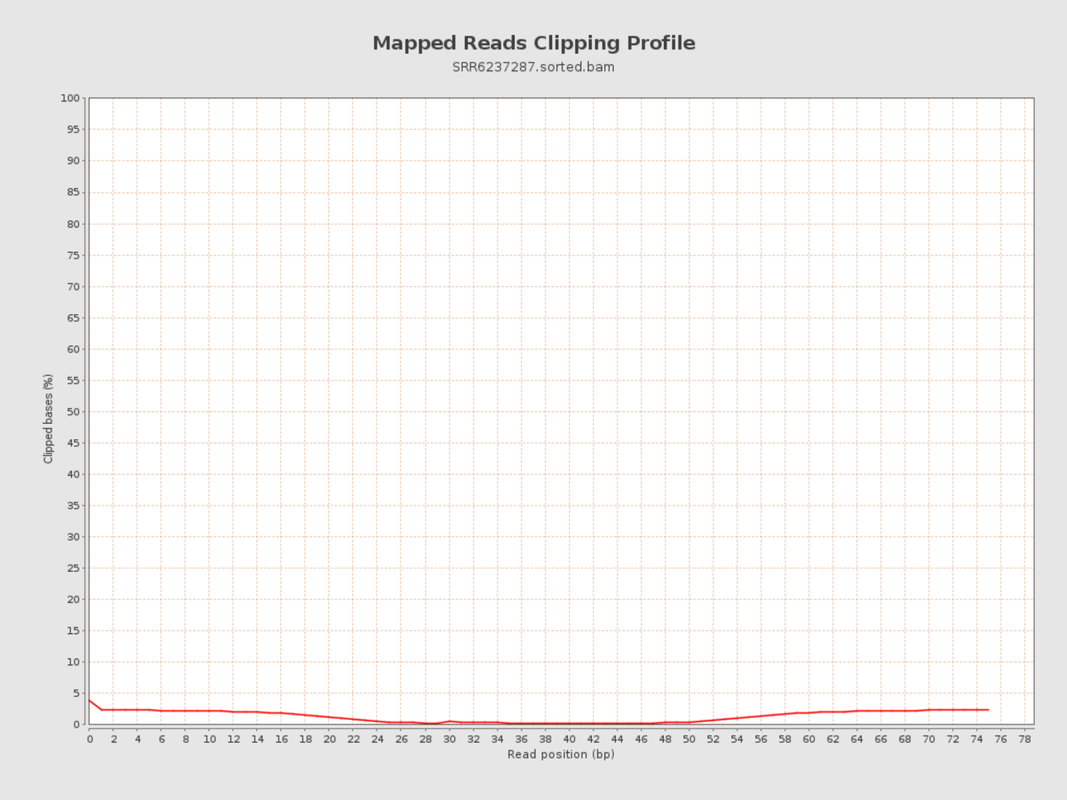
8. Results : Mapped Reads Nucleotide Content



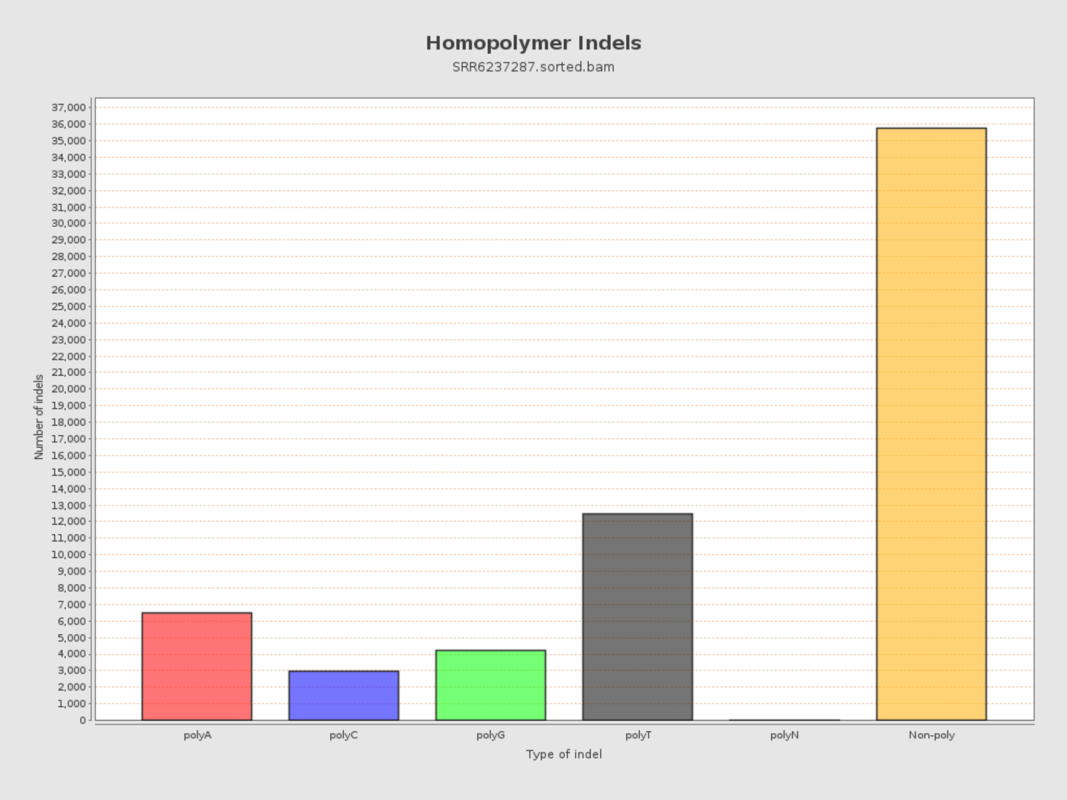
9. Results : Mapped Reads GC-content Distribution



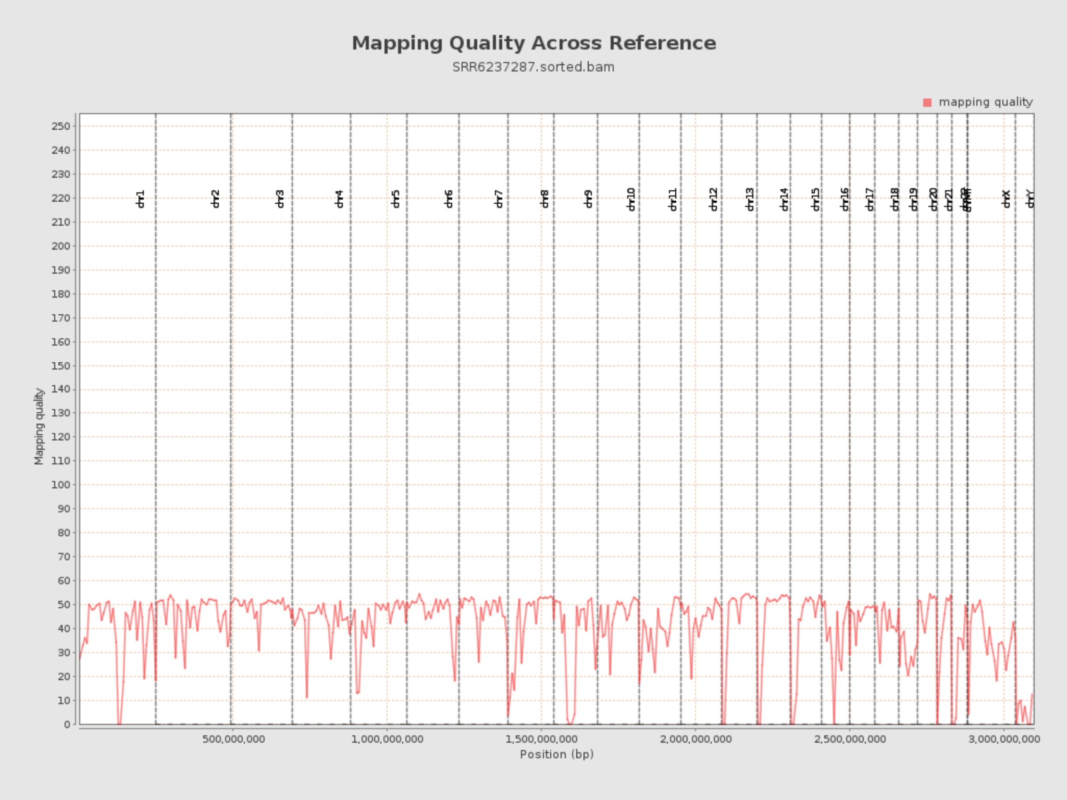
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram