Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:59:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237297.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_SRR6237297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237297.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:59:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,155,294
Mapped reads	1,978,526 / 91.8%
Unmapped reads	176,768 / 8.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,109 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	172,445 / 8%
Duplication rate	6.87%
Clipped reads	724,164 / 33.6%

2.2. ACGT Content

Number/percentage of A's	39,540,858 / 29.04%
Number/percentage of C's	25,178,673 / 18.49%
Number/percentage of T's	43,050,593 / 31.62%
Number/percentage of G's	28,374,671 / 20.84%
Number/percentage of N's	2,239 / 0%
GC Percentage	39.33%

2.3. Coverage

Mean	0.044

Standard Deviation	0.5494

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

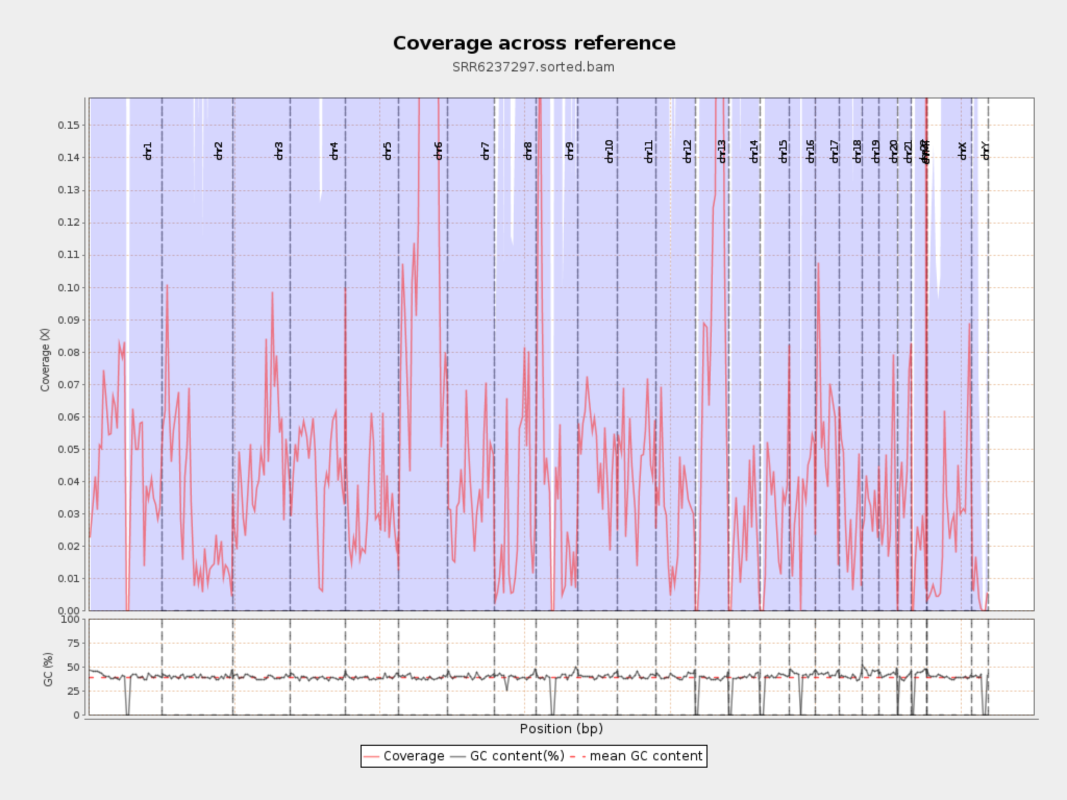
General error rate	0.76%
Mismatches	1,014,861
Insertions	10,264
Mapped reads with at least one insertion	0.51%
Deletions	34,958
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.1%

2.6. Chromosome stats

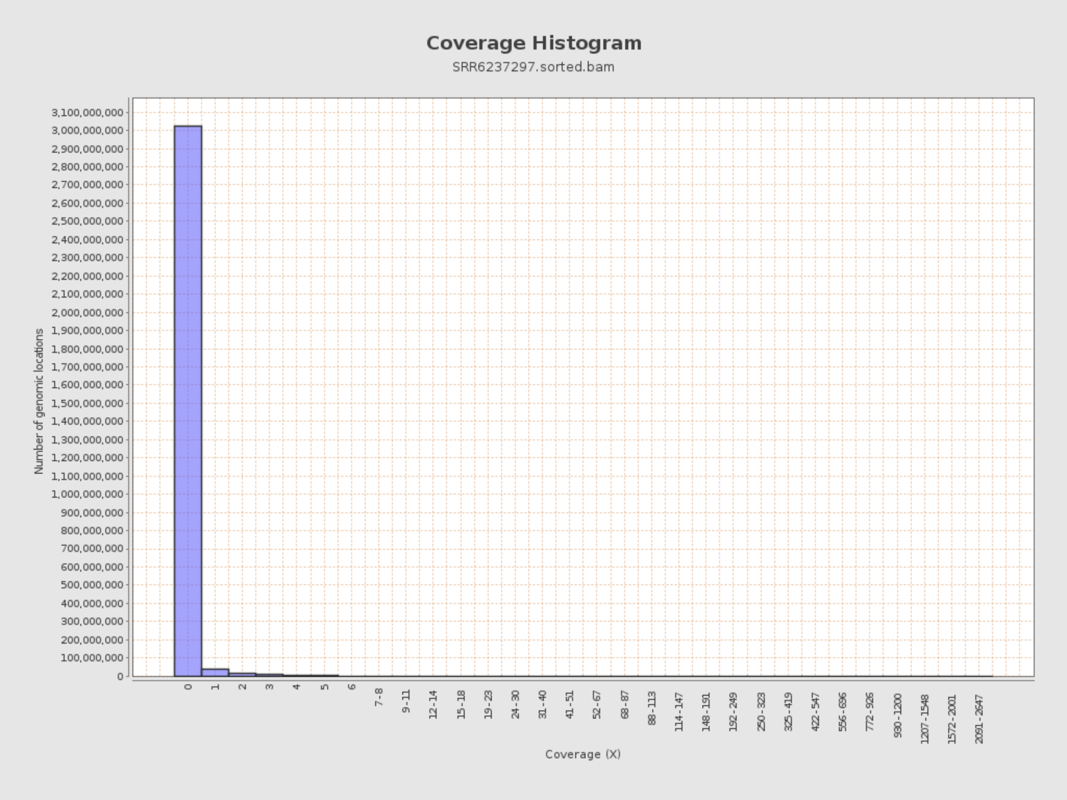
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11543684	0.0463	0.505
chr2	243199373	7460766	0.0307	0.3893
chr3	198022430	9331813	0.0471	0.3623
chr4	191154276	8383821	0.0439	0.3621
chr5	180915260	5652330	0.0312	0.2914
chr6	171115067	22041608	0.1288	0.6694
chr7	159138663	6042815	0.038	0.4259

chr8	146364022	4248481	0.029	1.7461
chr9	141213431	5936852	0.042	0.3928
chr10	135534747	6783003	0.05	0.4266
chr11	135006516	6183446	0.0458	0.4227
chr12	133851895	4061787	0.0303	0.2914
chr13	115169878	11341907	0.0985	0.5465
chr14	107349540	2490875	0.0232	0.2728
chr15	102531392	2972714	0.029	0.2836
chr16	90354753	3118348	0.0345	0.3162
chr17	81195210	4630580	0.057	0.4133
chr18	78077248	2362333	0.0303	0.5056
chr19	59128983	1873974	0.0317	0.3982
chr20	63025520	2151790	0.0341	0.3082
chr21	48129895	2184213	0.0454	0.3651
chr22	51304566	848252	0.0165	0.2005
chrMT	16571	20107	1.2134	1.867
chrX	155270560	4253926	0.0274	0.2921
chrY	59373566	288656	0.0049	0.1401

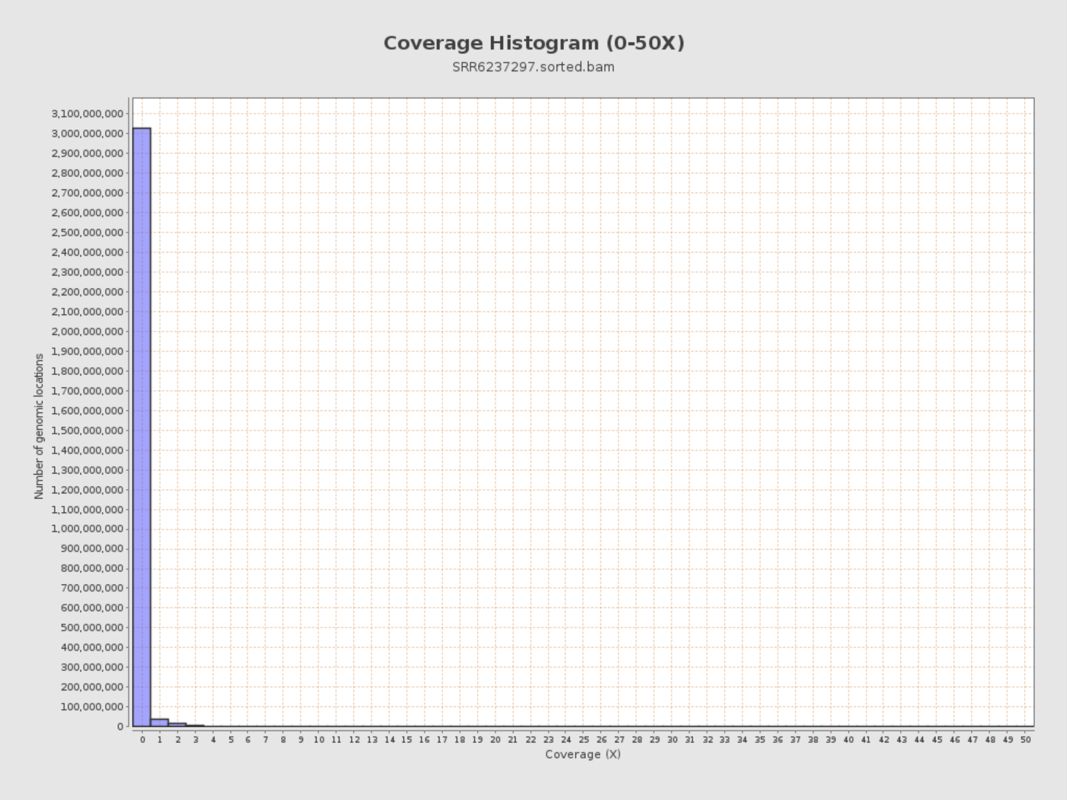
3. Results : Coverage across reference



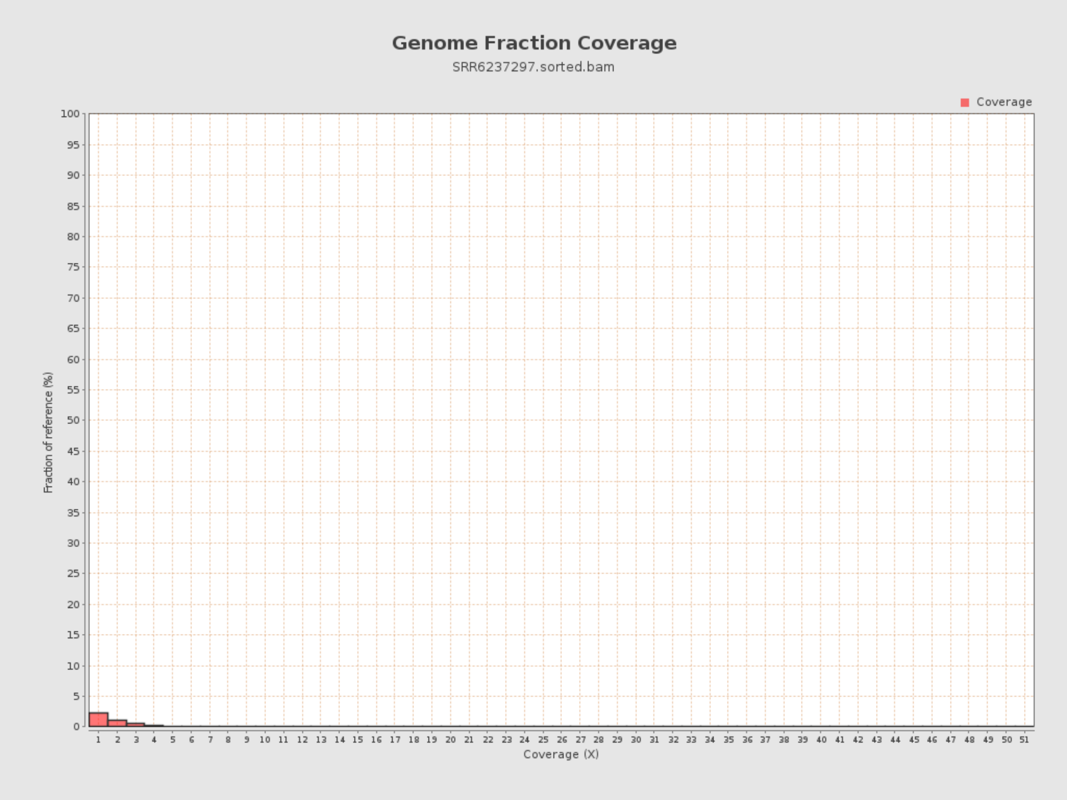
4. Results : Coverage Histogram



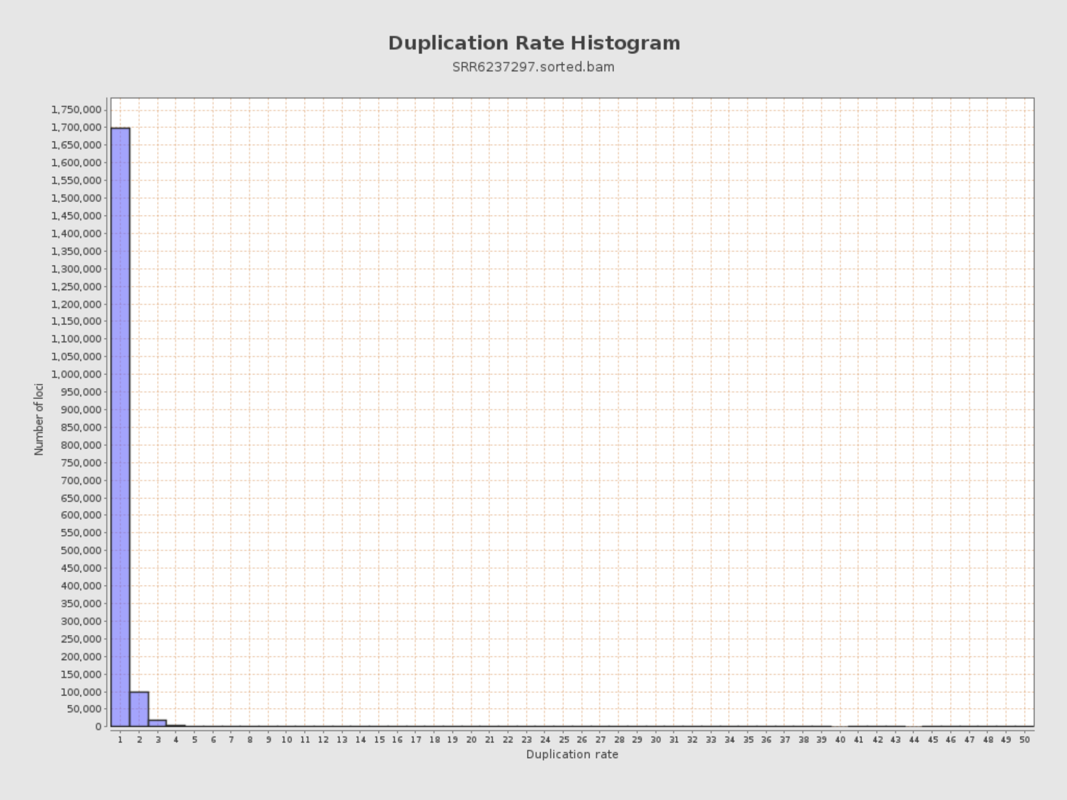
5. Results : Coverage Histogram (0-50X)



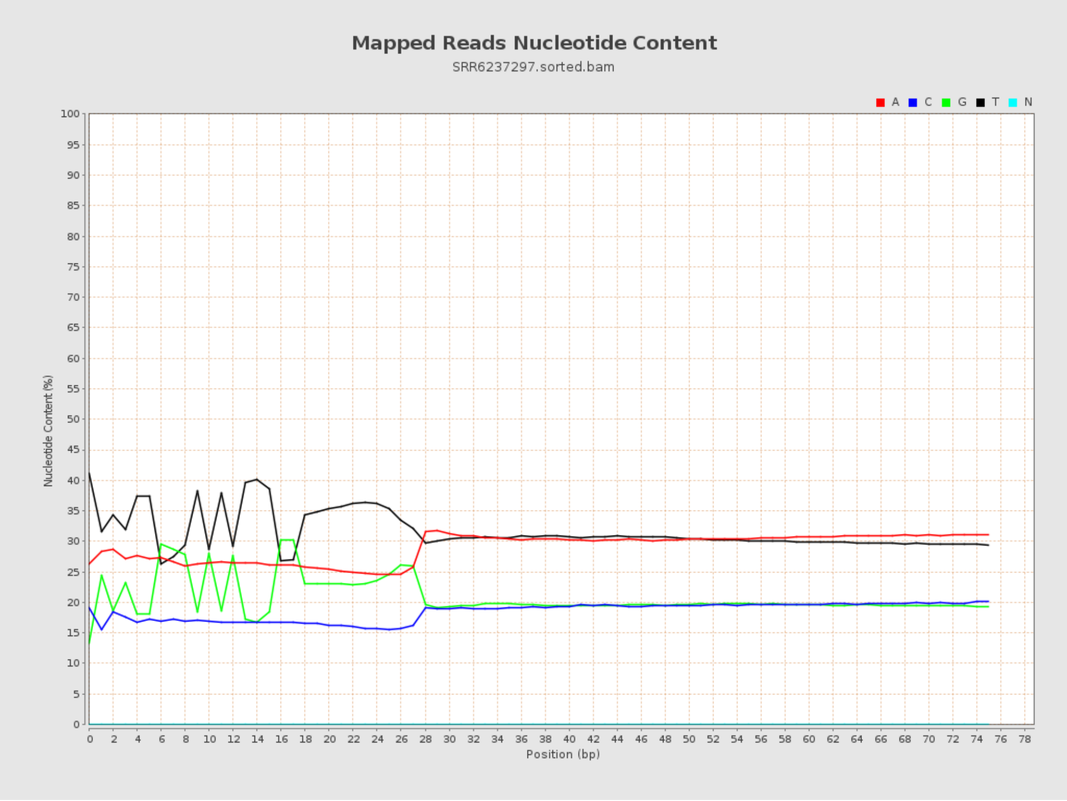
6. Results : Genome Fraction Coverage



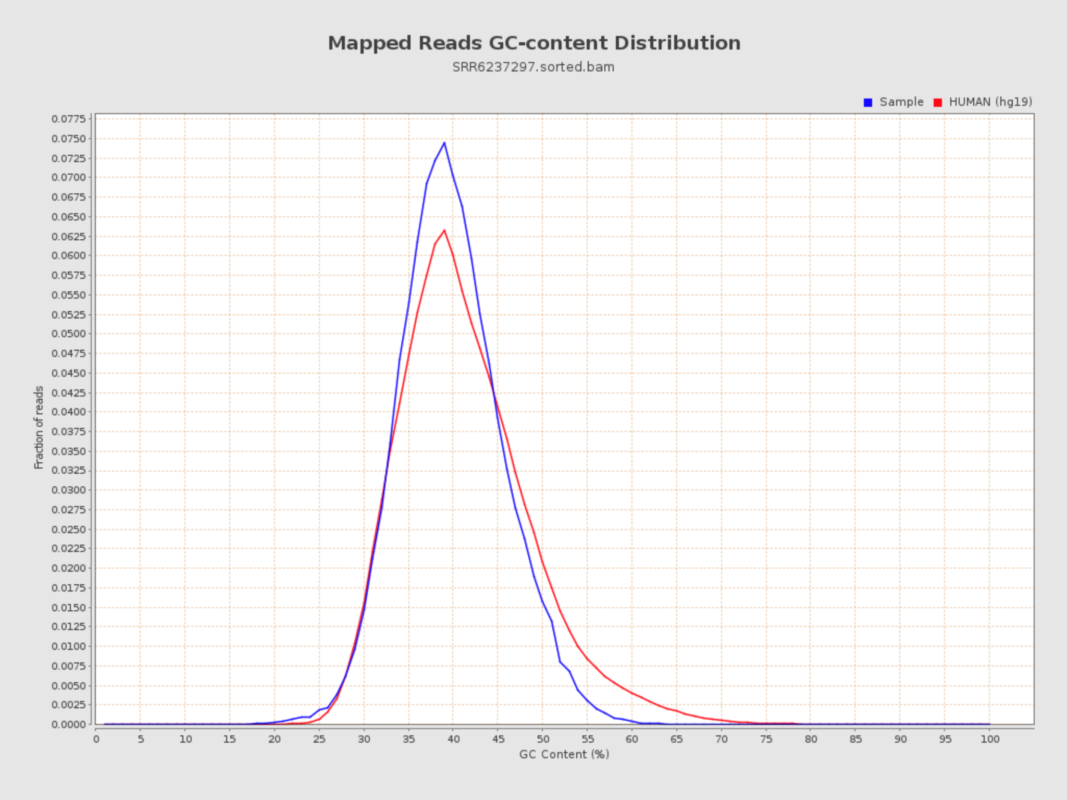
7. Results : Duplication Rate Histogram



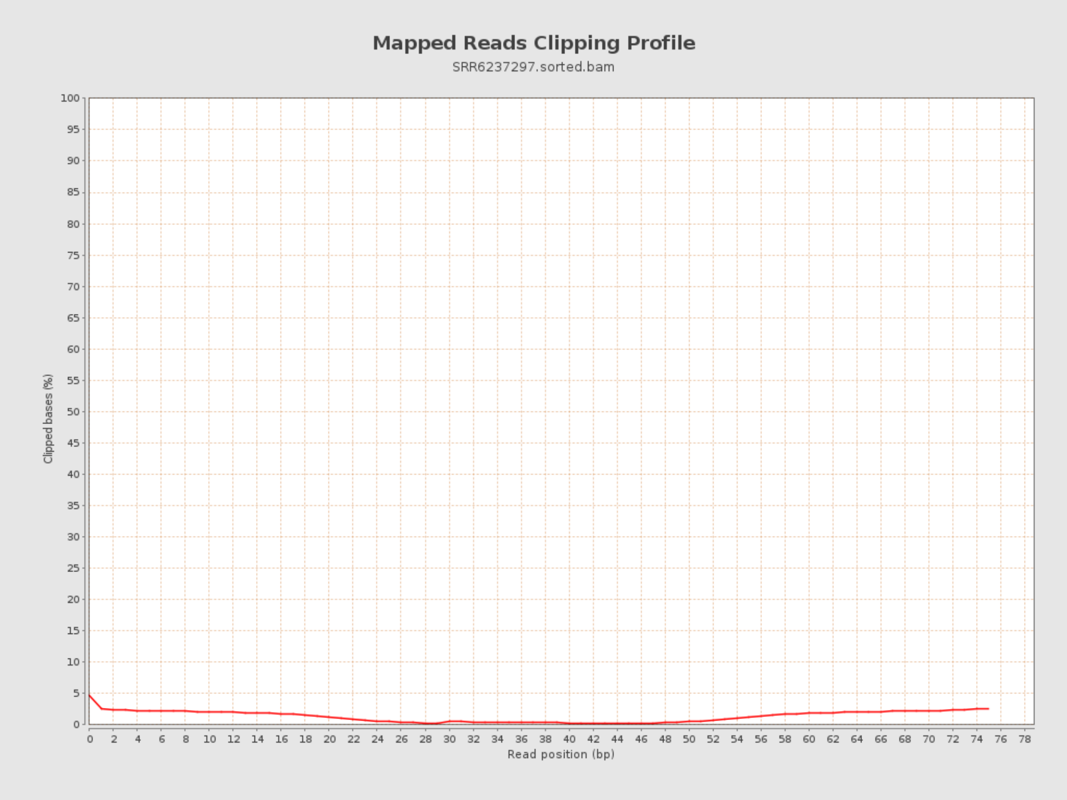
8. Results : Mapped Reads Nucleotide Content



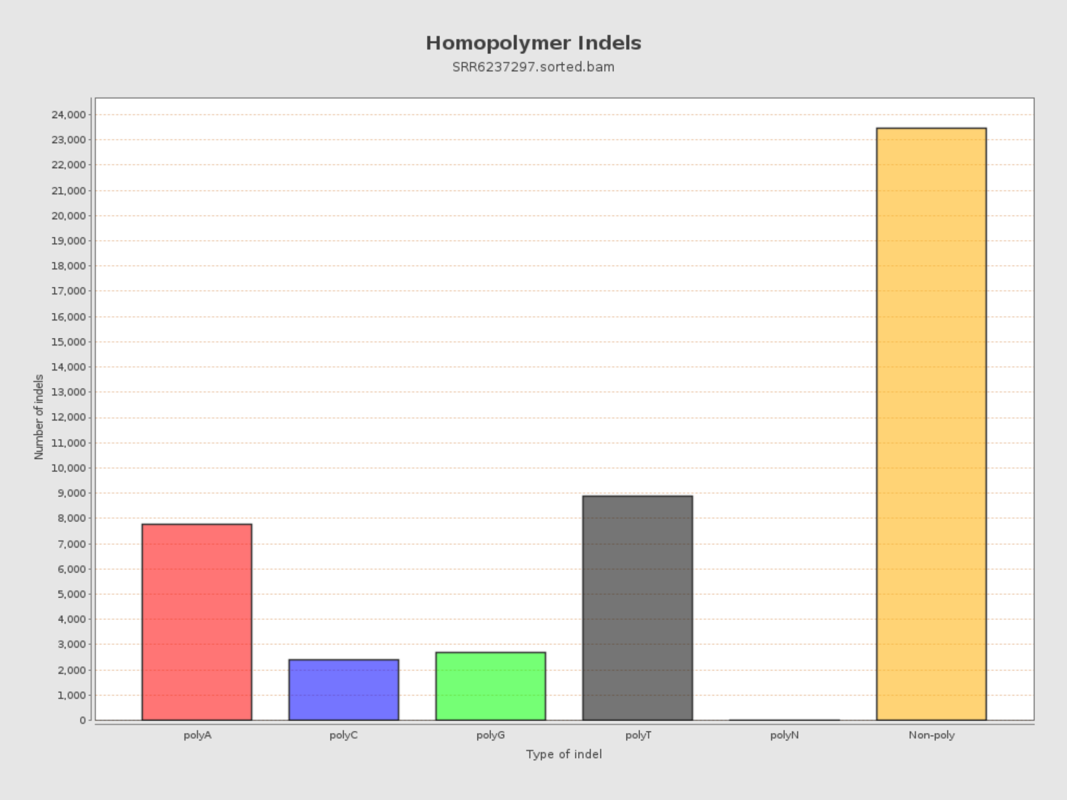
9. Results : Mapped Reads GC-content Distribution



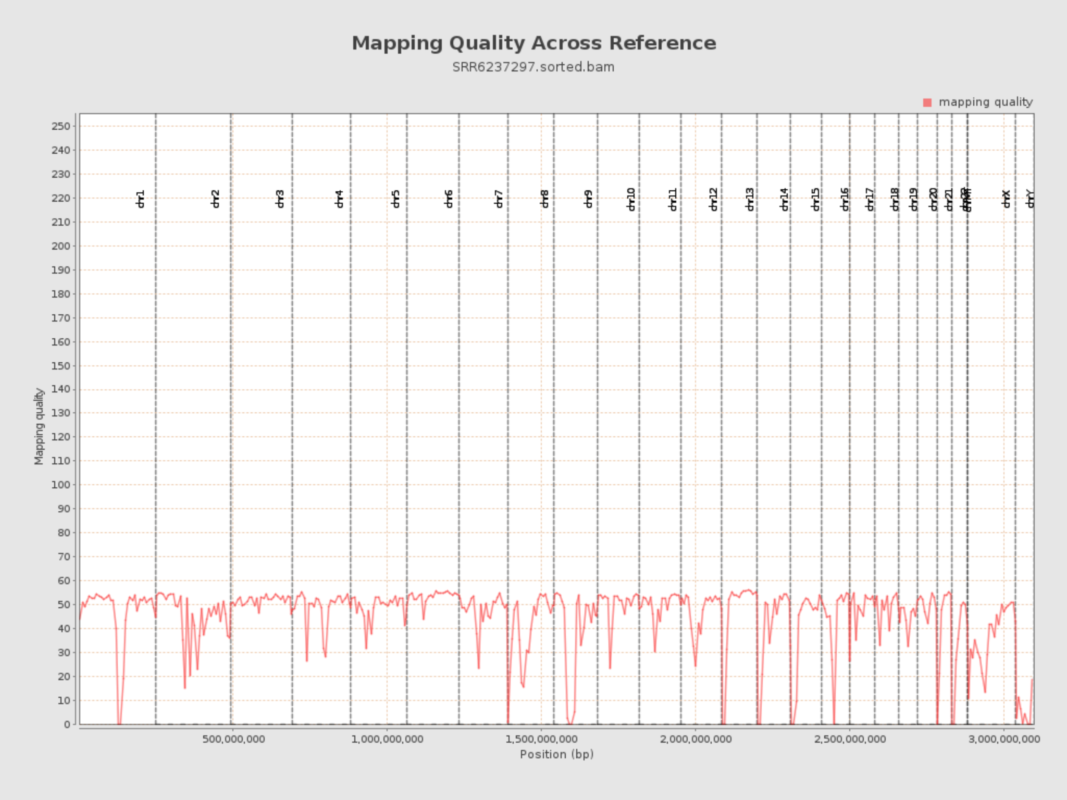
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram