Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:44:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237791.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_SRR6237791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:44:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,135,607
Mapped reads	1,410,676 / 66.06%
Unmapped reads	724,931 / 33.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,726 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	65,738 / 3.08%
Duplication rate	3.82%
Clipped reads	1,145,102 / 53.62%

2.2. ACGT Content

Number/percentage of A's	23,090,541 / 29.34%
Number/percentage of C's	14,659,222 / 18.63%
Number/percentage of T's	23,499,721 / 29.86%
Number/percentage of G's	17,372,789 / 22.08%
Number/percentage of N's	64,422 / 0.08%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.243

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Mismatches and indels

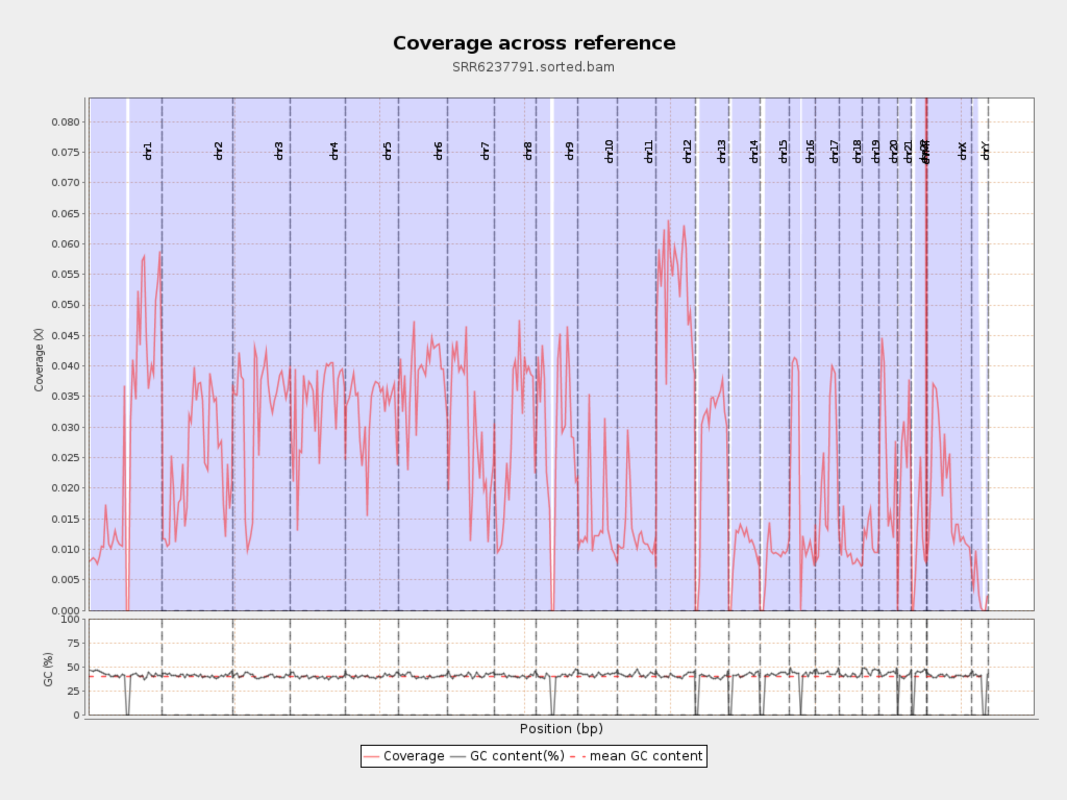
General error rate	0.83%
Mismatches	643,301
Insertions	5,166
Mapped reads with at least one insertion	0.36%
Deletions	20,018
Mapped reads with at least one deletion	1.41%
Homopolymer indels	46.5%

2.6. Chromosome stats

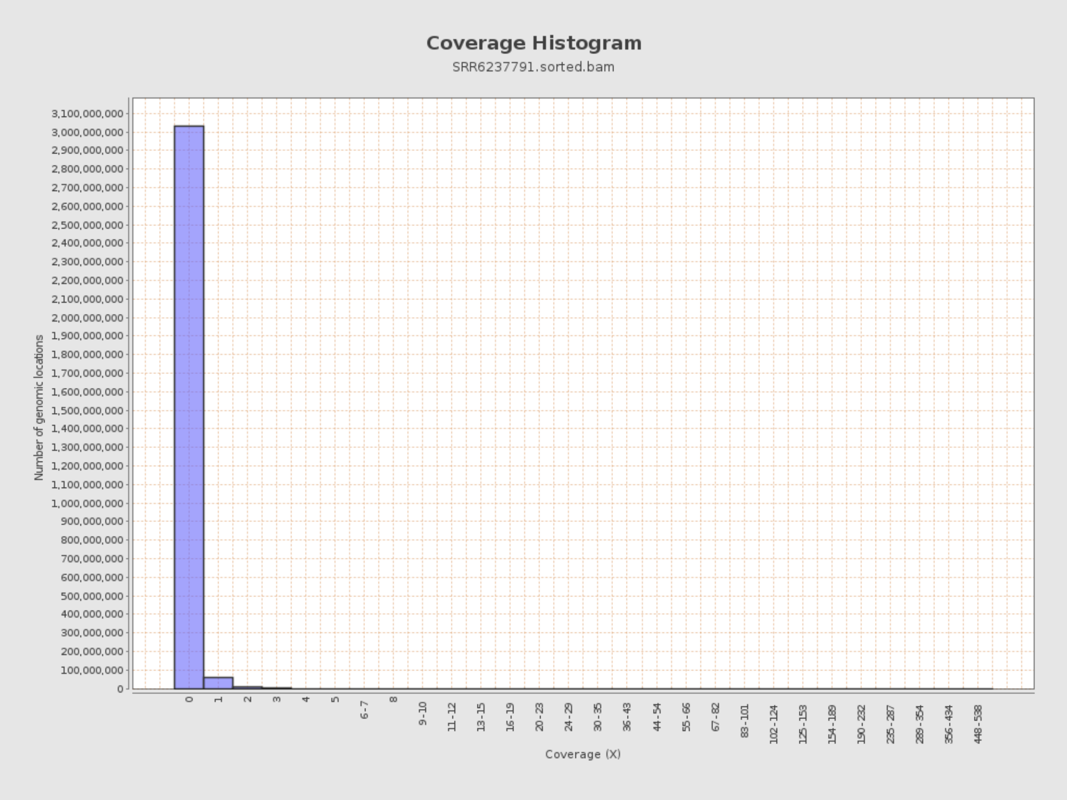
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6530789	0.0262	0.2962
chr2	243199373	5916855	0.0243	0.2253
chr3	198022430	6591999	0.0333	0.2147
chr4	191154276	6498019	0.034	0.2186
chr5	180915260	5980547	0.0331	0.3293
chr6	171115067	6626461	0.0387	0.2524
chr7	159138663	4692719	0.0295	0.2949

chr8	146364022	4226610	0.0289	0.2463
chr9	141213431	4163449	0.0295	0.2268
chr10	135534747	1888003	0.0139	0.2183
chr11	135006516	1745926	0.0129	0.1503
chr12	133851895	7201629	0.0538	0.4383
chr13	115169878	3177872	0.0276	0.1946
chr14	107349540	1063194	0.0099	0.1977
chr15	102531392	843599	0.0082	0.1072
chr16	90354753	1830818	0.0203	0.1756
chr17	81195210	1841071	0.0227	0.22
chr18	78077248	744562	0.0095	0.2621
chr19	59128983	714284	0.0121	0.2009
chr20	63025520	1635763	0.026	0.1902
chr21	48129895	1142087	0.0237	0.1843
chr22	51304566	514935	0.01	0.1134
chrMT	16571	49133	2.965	3.469
chrX	155270560	2925389	0.0188	0.1767
chrY	59373566	171014	0.0029	0.0761

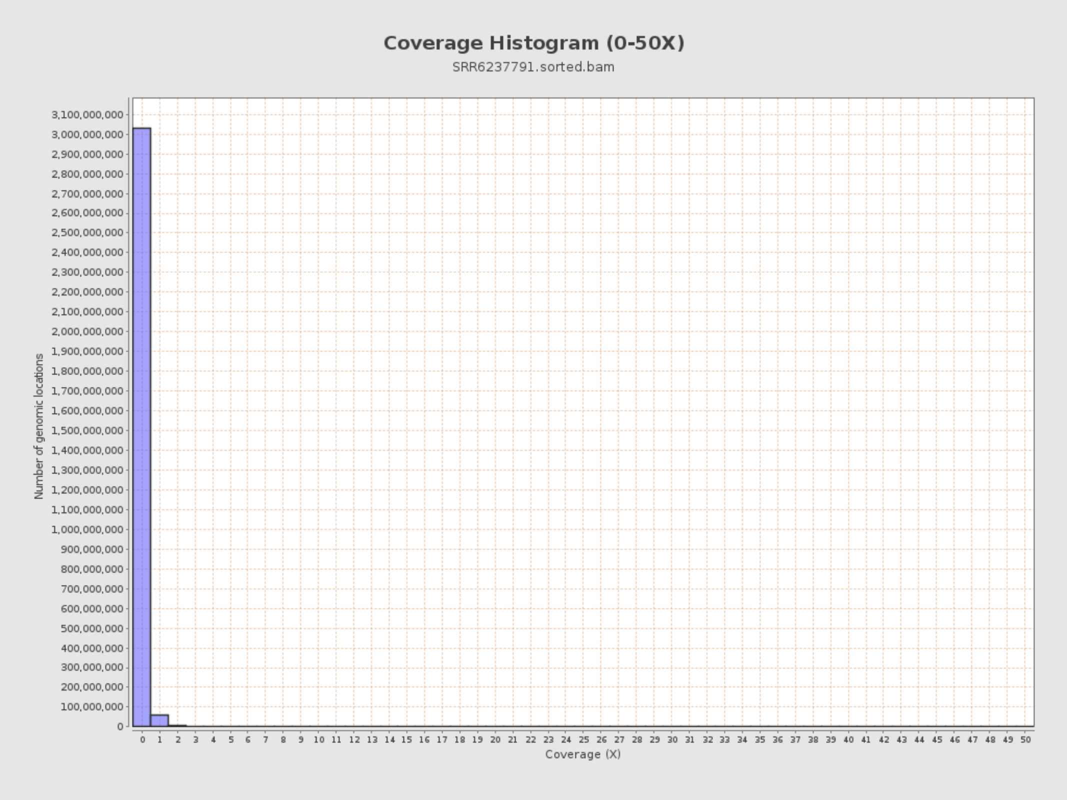
3. Results : Coverage across reference



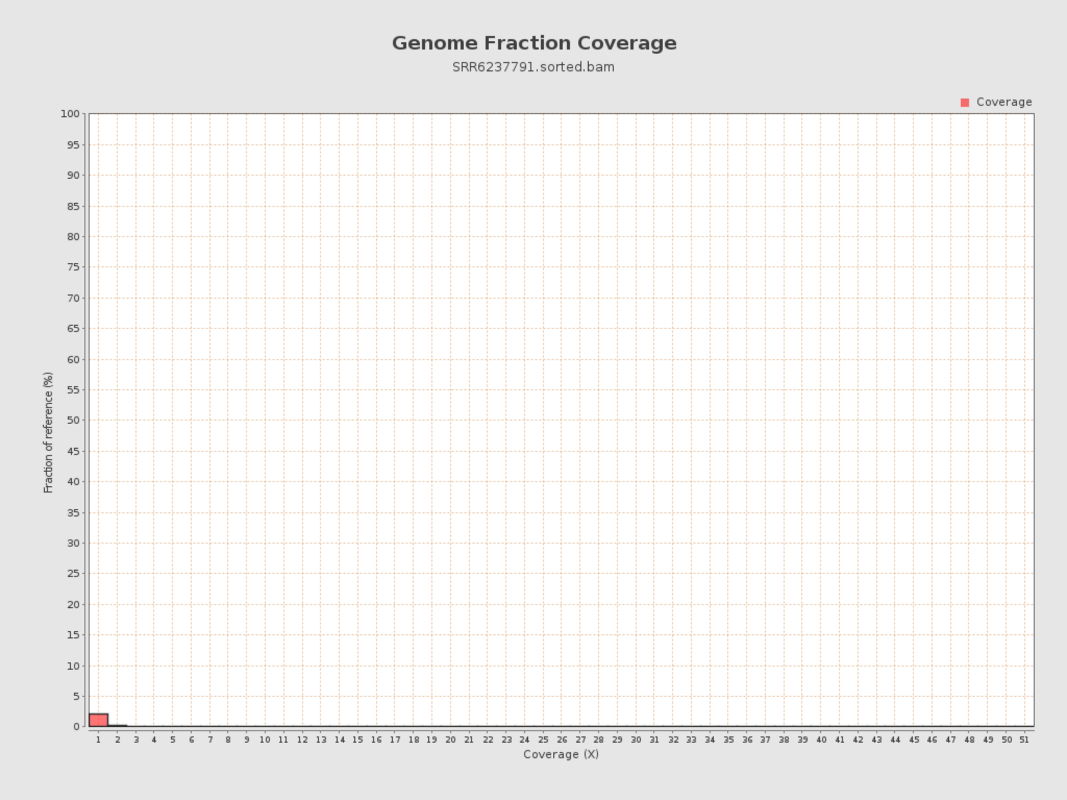
4. Results : Coverage Histogram



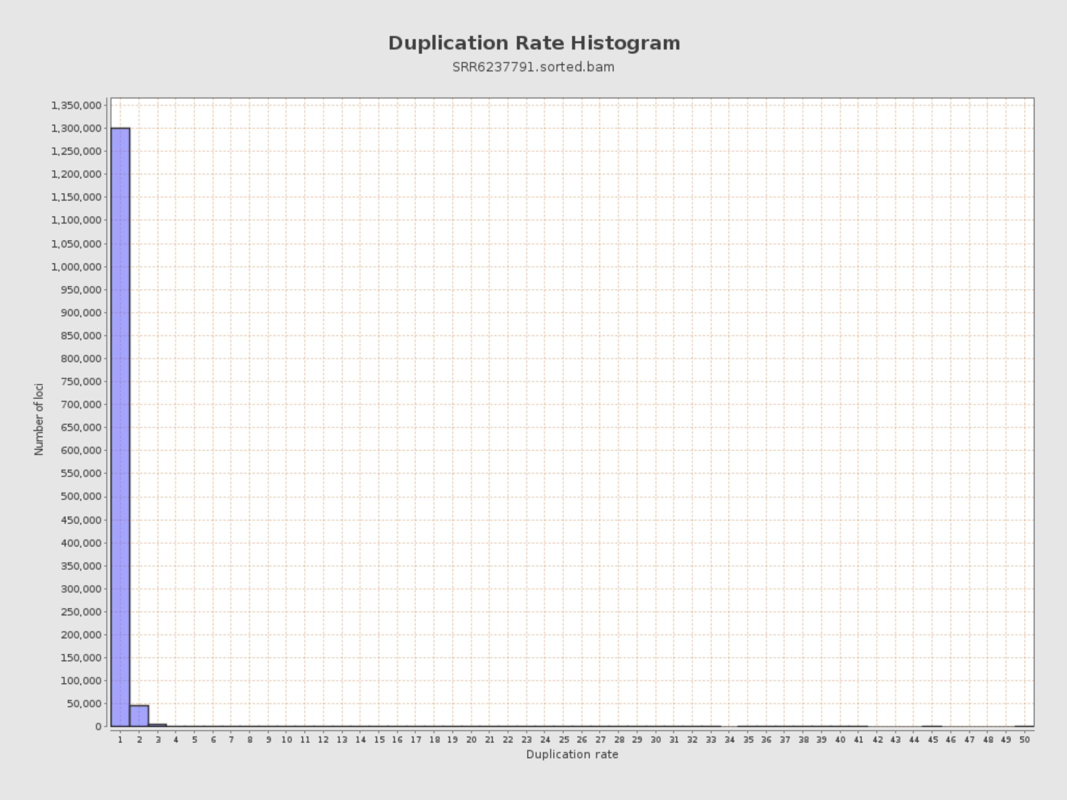
5. Results : Coverage Histogram (0-50X)



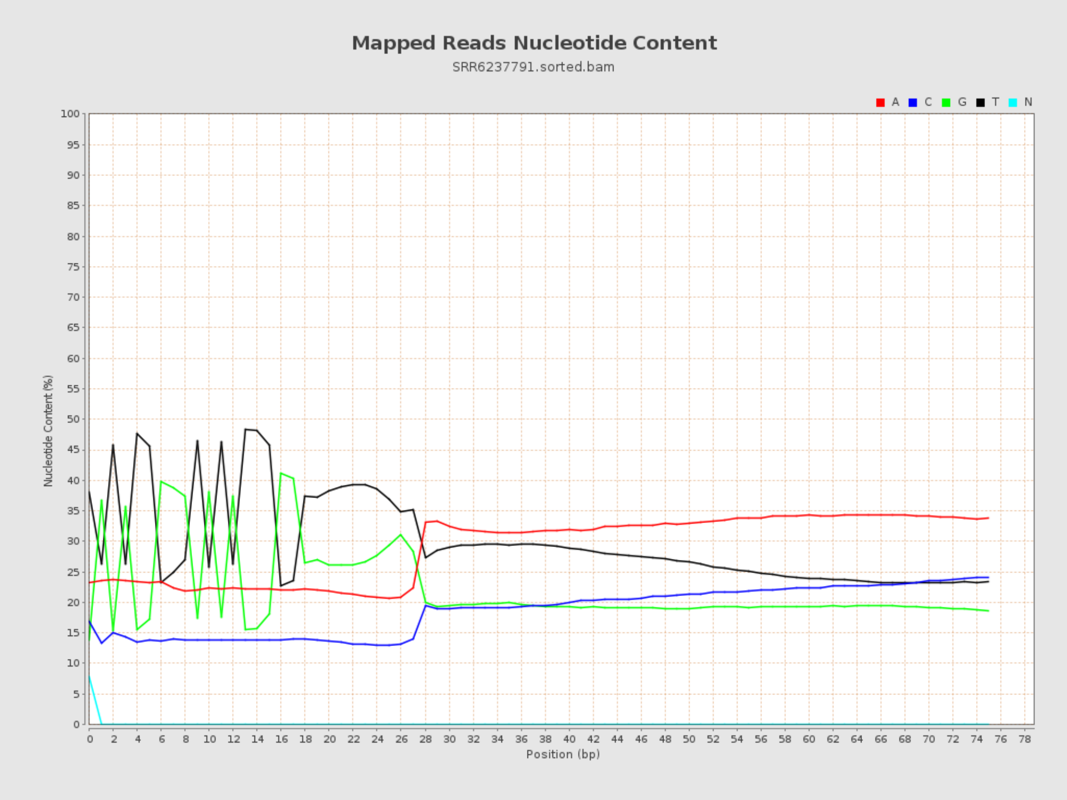
6. Results : Genome Fraction Coverage



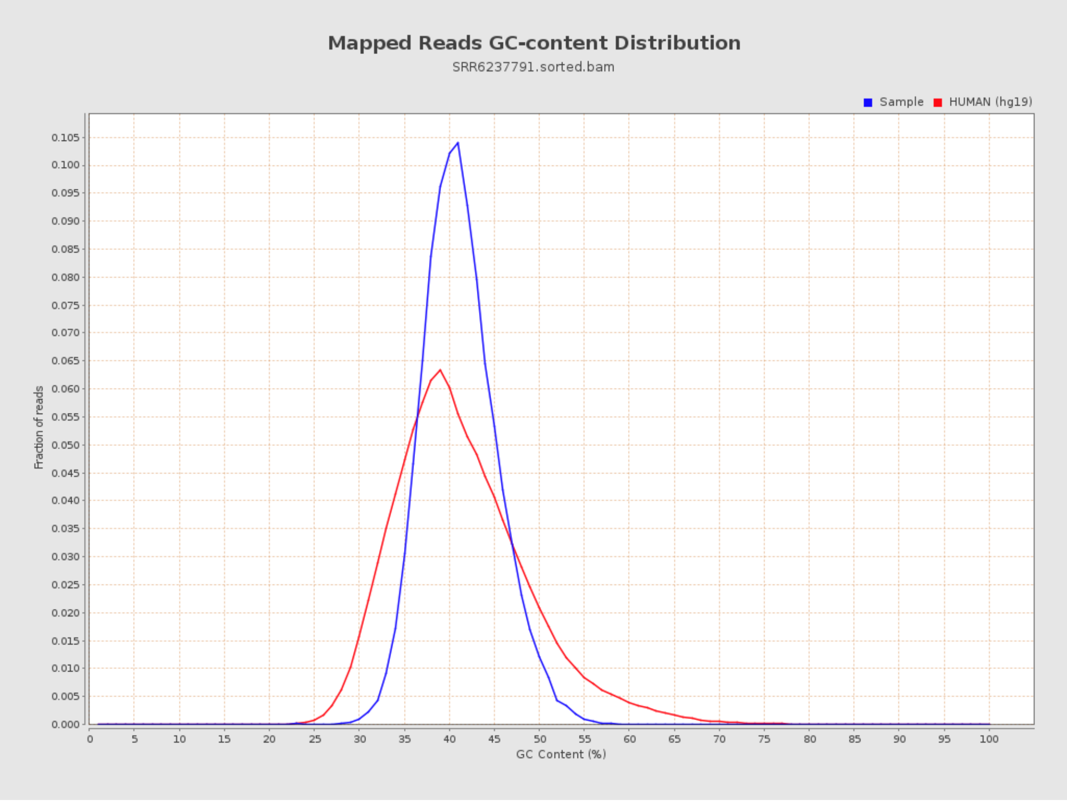
7. Results : Duplication Rate Histogram



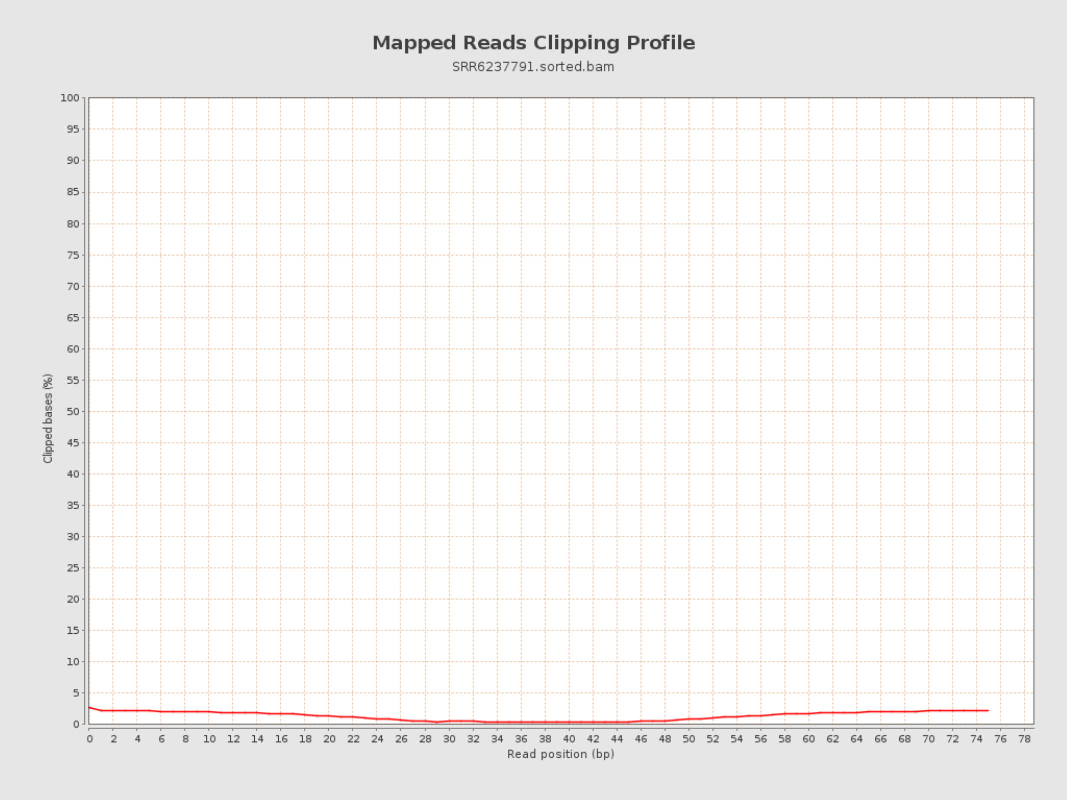
8. Results : Mapped Reads Nucleotide Content



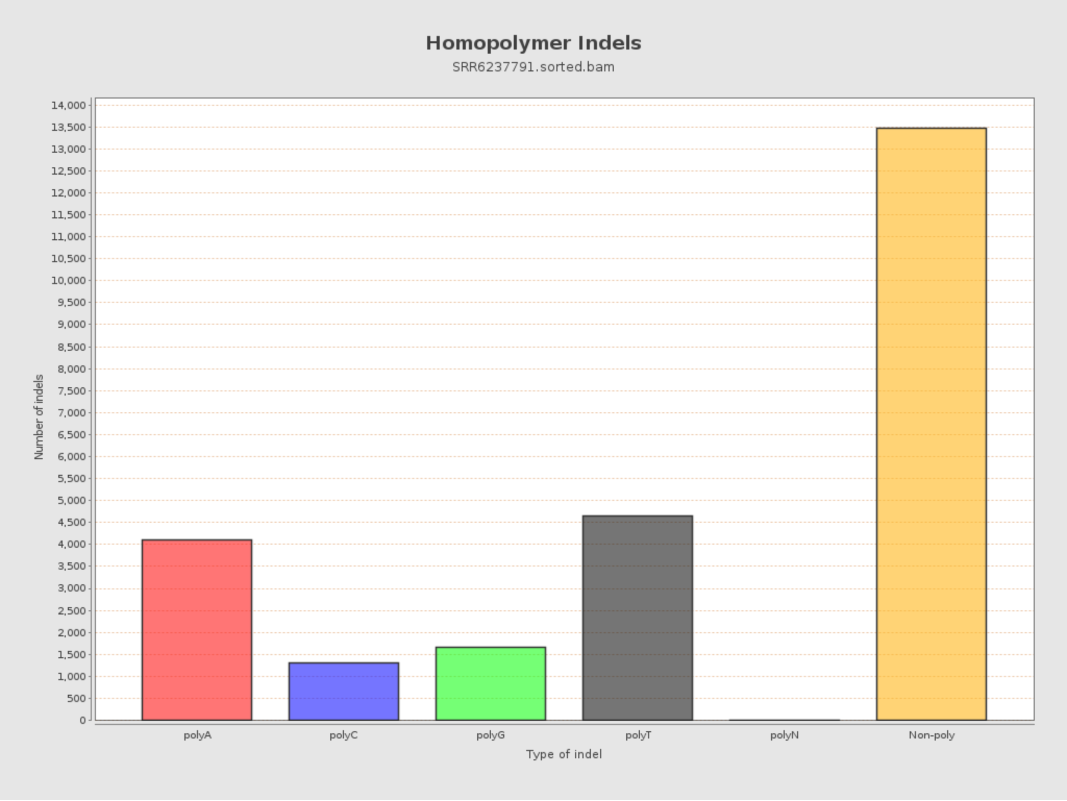
9. Results : Mapped Reads GC-content Distribution



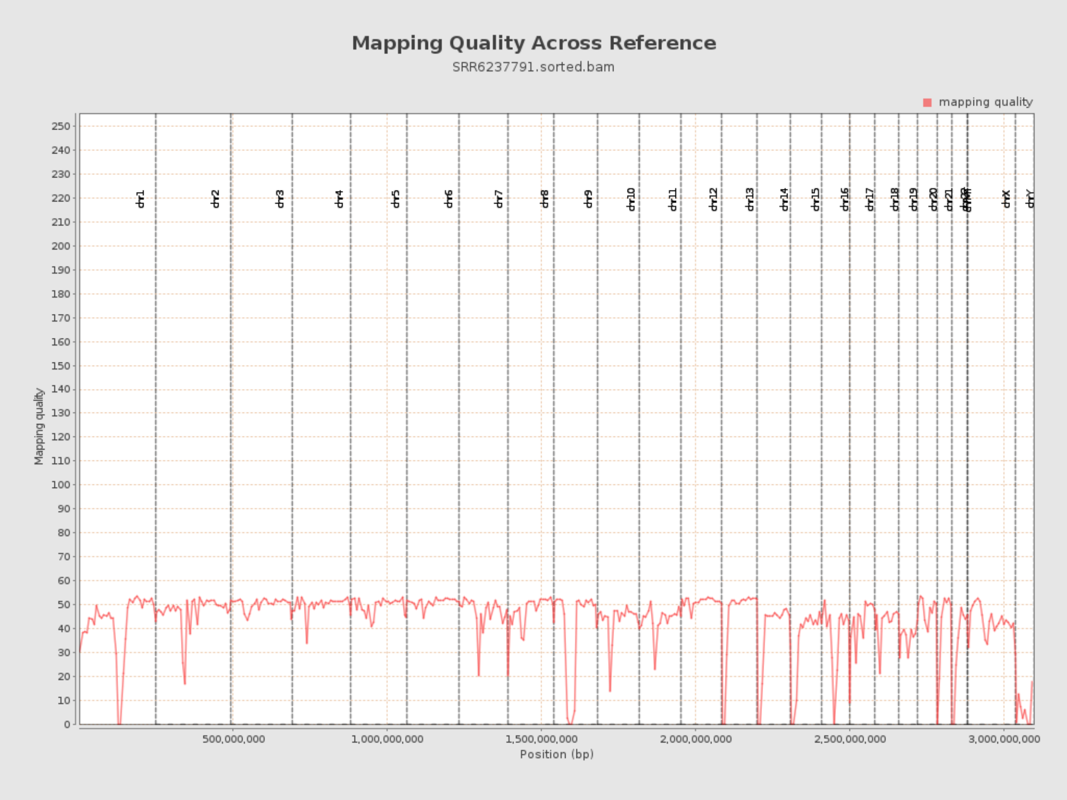
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram