Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:16:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237302.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_SRR6237302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237302.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:16:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,598,730
Mapped reads	3,243,822 / 90.14%
Unmapped reads	354,908 / 9.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,735 / 1.05%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	1,393,264 / 38.72%
Duplication rate	21.95%
Clipped reads	2,146,917 / 59.66%

2.2. ACGT Content

Number/percentage of A's	49,447,752 / 24.86%
Number/percentage of C's	35,101,855 / 17.65%
Number/percentage of T's	65,904,066 / 33.14%
Number/percentage of G's	48,407,459 / 24.34%
Number/percentage of N's	20,640 / 0.01%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0643

Standard Deviation	1.0326

2.4. Mapping Quality

Mean Mapping Quality	32.22

2.5. Mismatches and indels

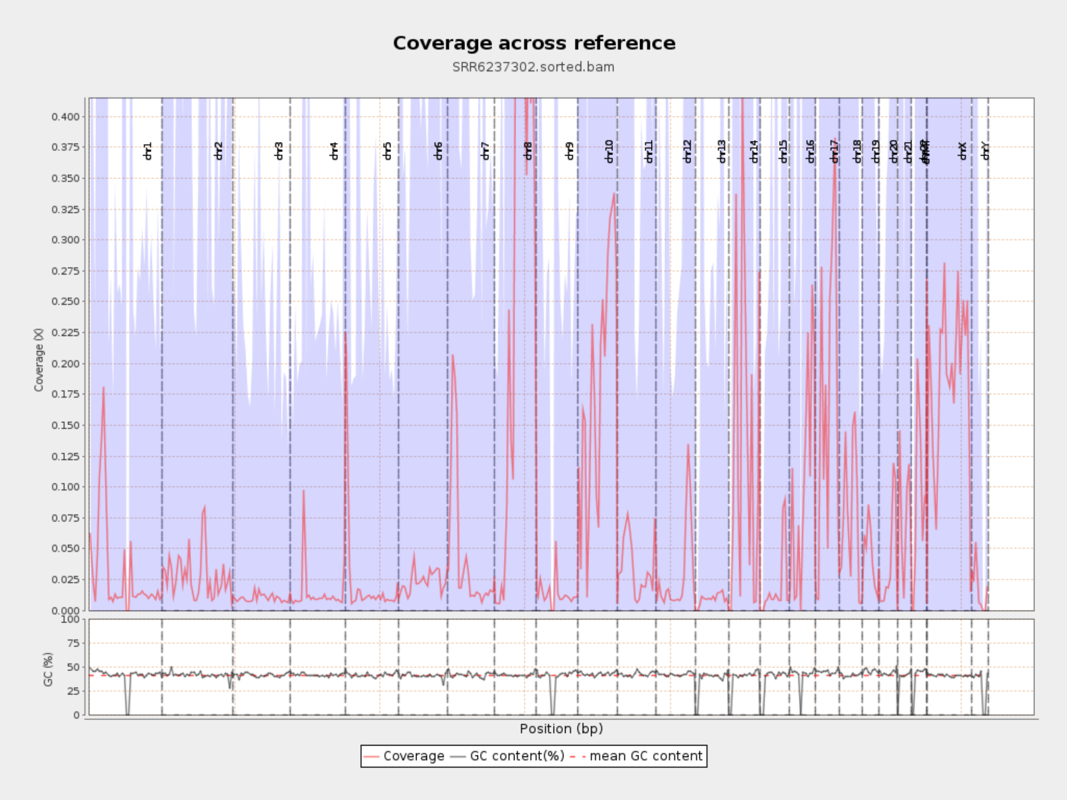
General error rate	0.64%
Mismatches	1,252,518
Insertions	13,466
Mapped reads with at least one insertion	0.41%
Deletions	57,007
Mapped reads with at least one deletion	1.74%
Homopolymer indels	40.52%

2.6. Chromosome stats

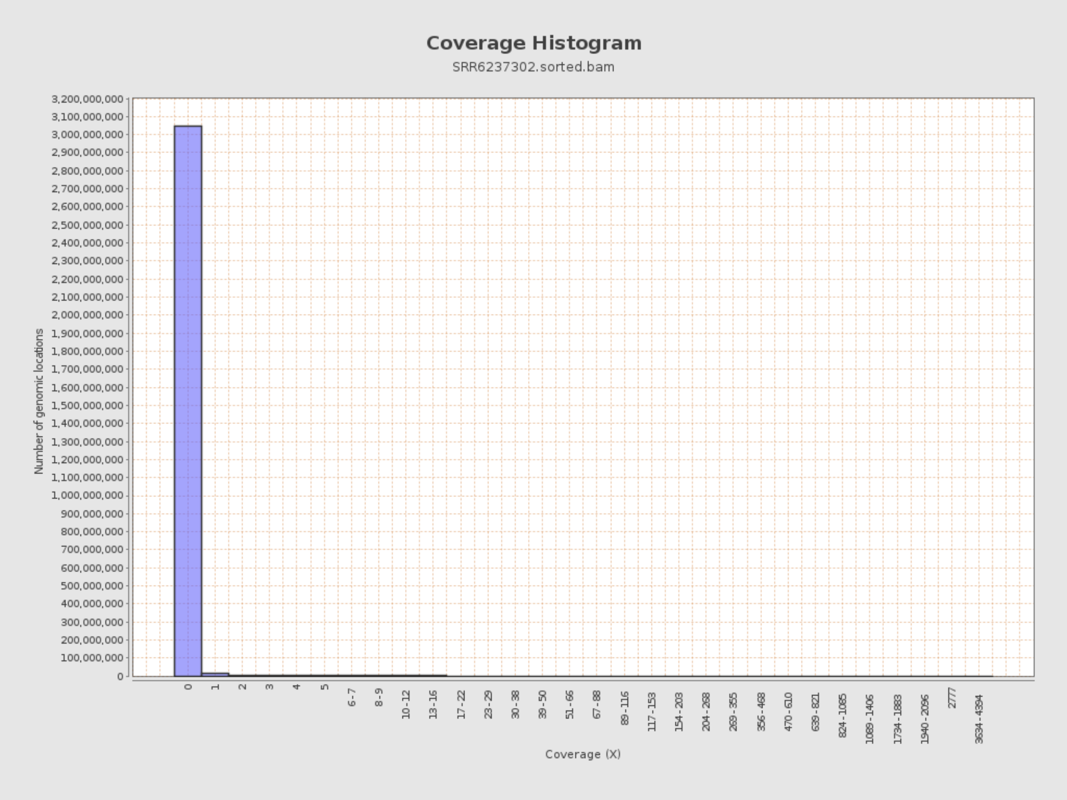
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7821273	0.0314	0.7079
chr2	243199373	6882610	0.0283	2.0457
chr3	198022430	2009061	0.0101	0.2505
chr4	191154276	2673691	0.014	0.3445
chr5	180915260	3720611	0.0206	0.4187
chr6	171115067	4058558	0.0237	0.6983
chr7	159138663	7482252	0.047	0.6863

chr8	146364022	38932688	0.266	1.6387
chr9	141213431	1890322	0.0134	0.4196
chr10	135534747	25103427	0.1852	1.3098
chr11	135006516	4820578	0.0357	0.766
chr12	133851895	3972706	0.0297	0.5037
chr13	115169878	1065006	0.0092	0.3934
chr14	107349540	13785145	0.1284	1.0858
chr15	102531392	2037033	0.0199	0.451
chr16	90354753	9715315	0.1075	1.019
chr17	81195210	13657138	0.1682	1.6511
chr18	78077248	6221560	0.0797	1.8313
chr19	59128983	2688399	0.0455	0.6494
chr20	63025520	2509517	0.0398	0.58
chr21	48129895	3534122	0.0734	0.8241
chr22	51304566	4326286	0.0843	0.8651
chrMT	16571	4454	0.2688	1.0154
chrX	155270560	29057900	0.1871	1.3522
chrY	59373566	1010457	0.017	0.4223

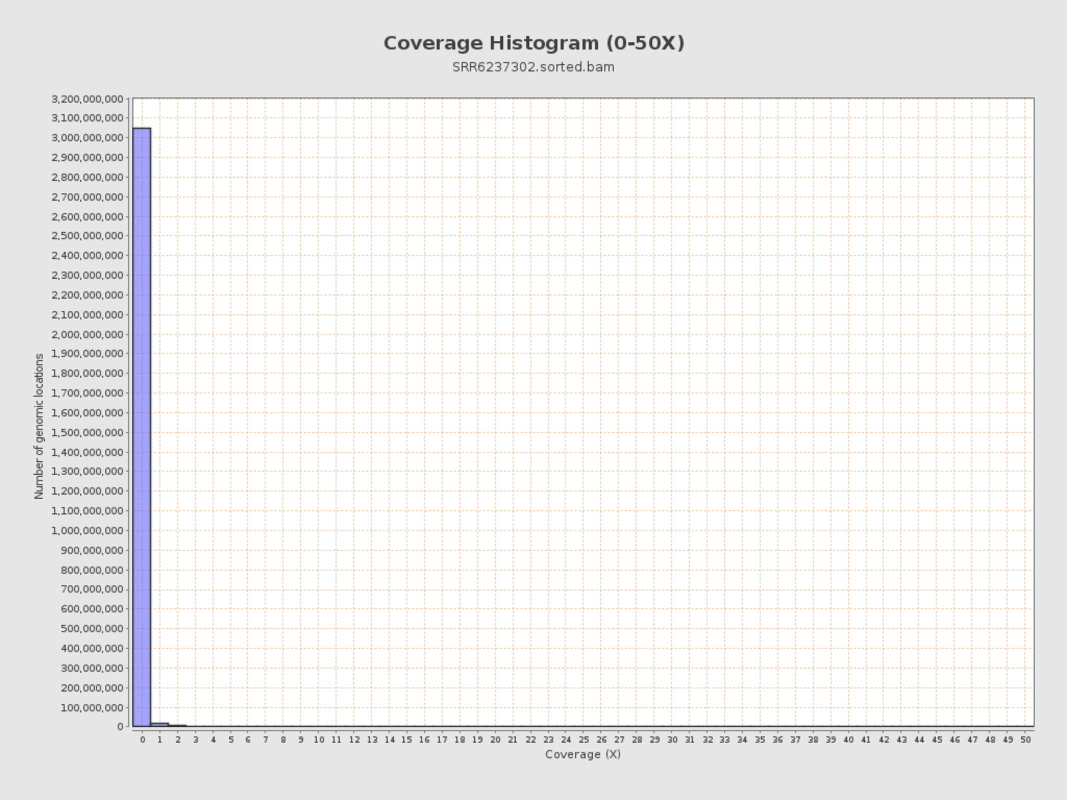
3. Results : Coverage across reference



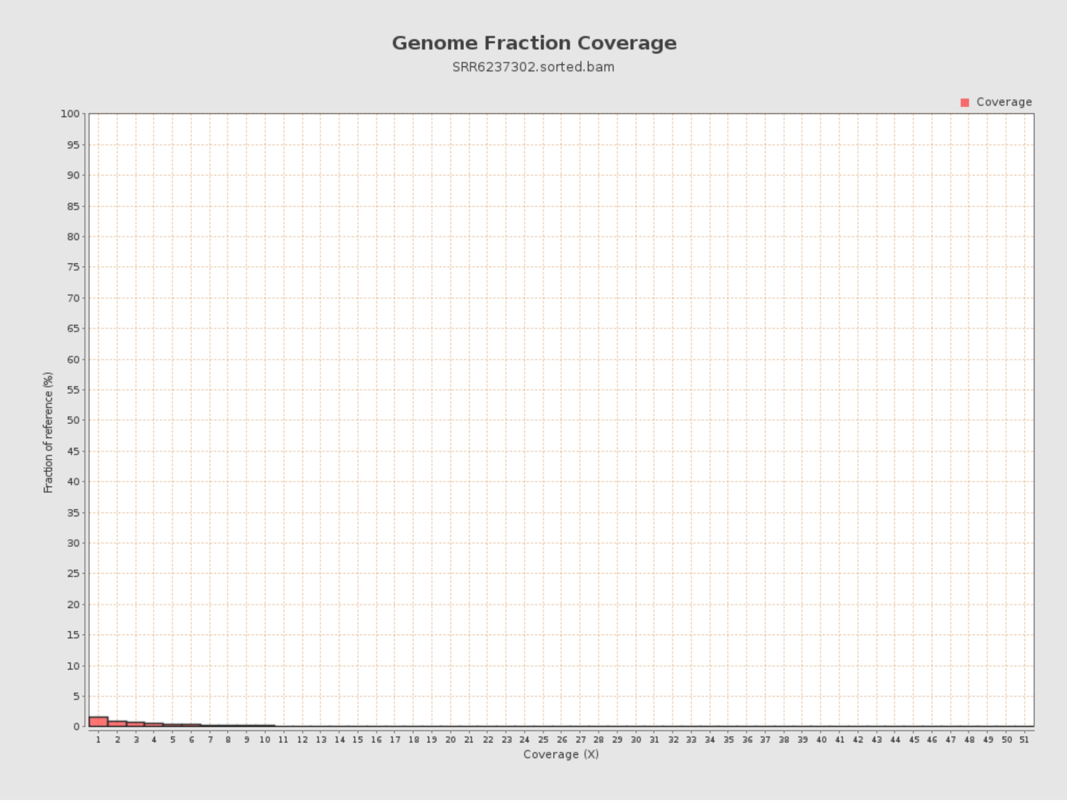
4. Results : Coverage Histogram



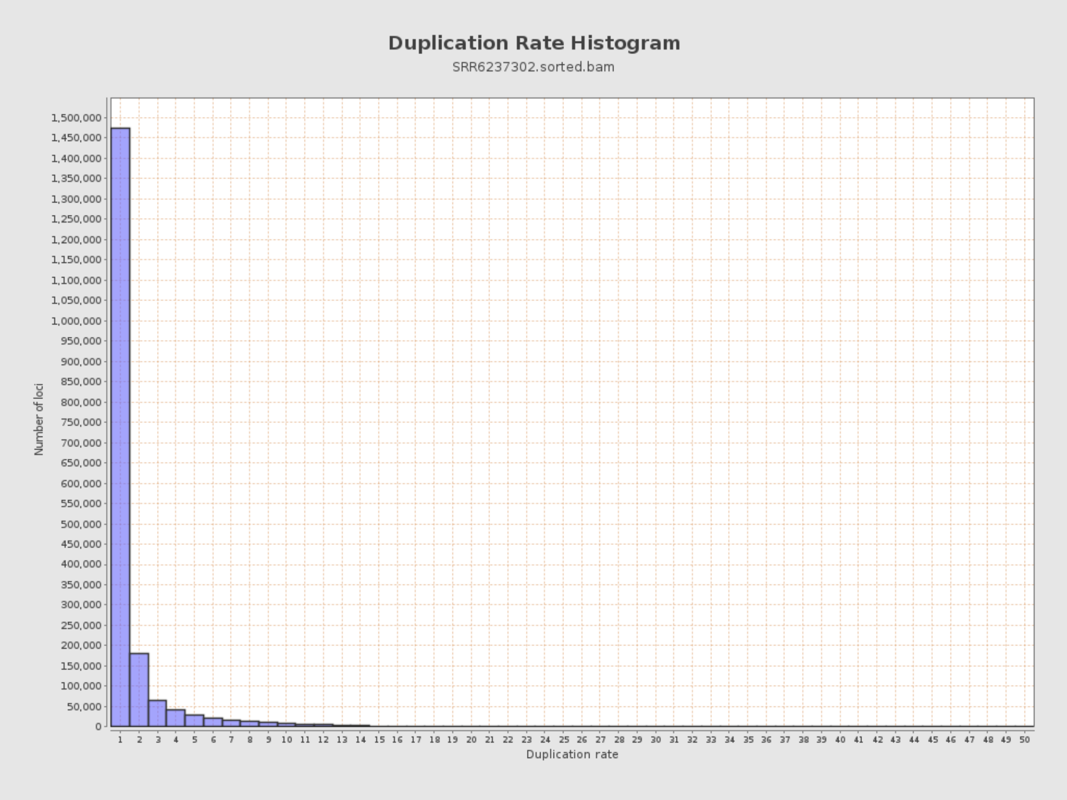
5. Results : Coverage Histogram (0-50X)



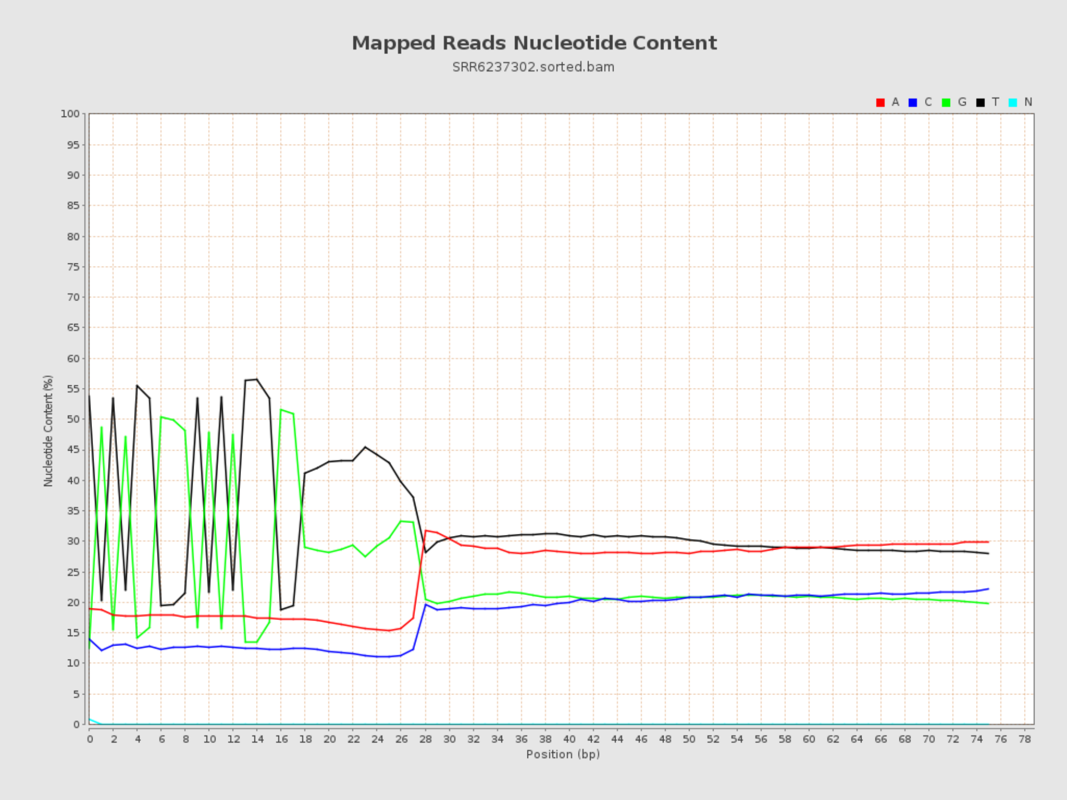
6. Results : Genome Fraction Coverage



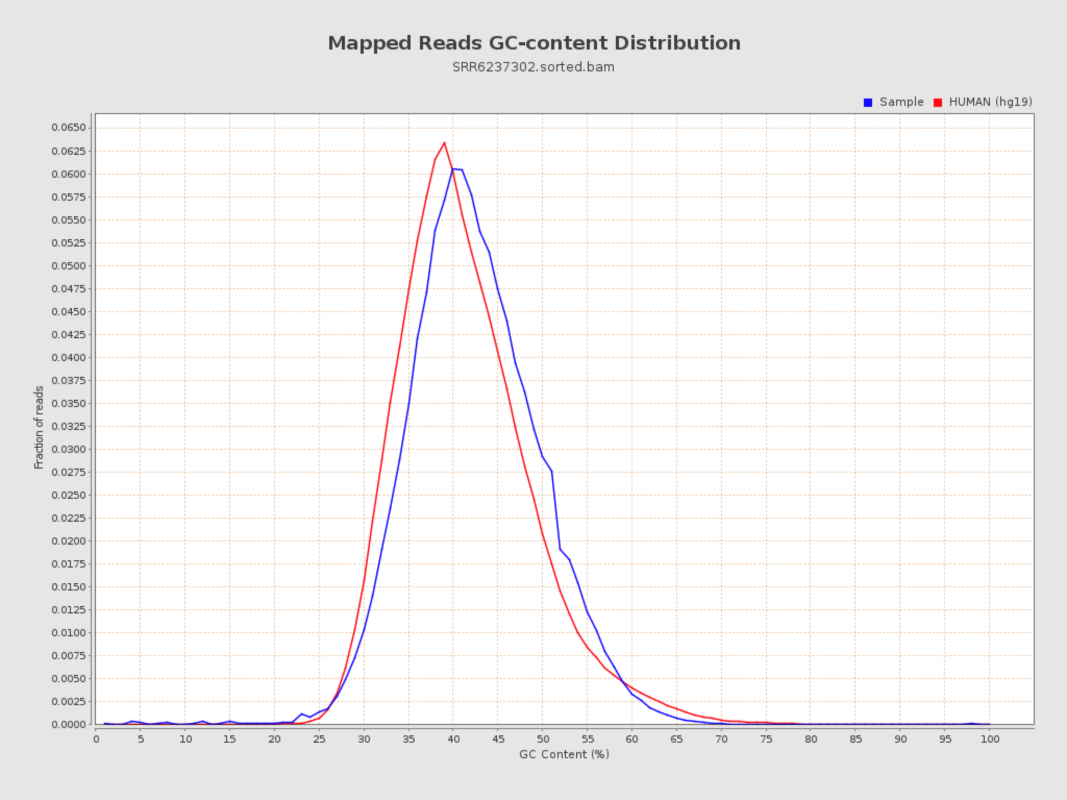
7. Results : Duplication Rate Histogram



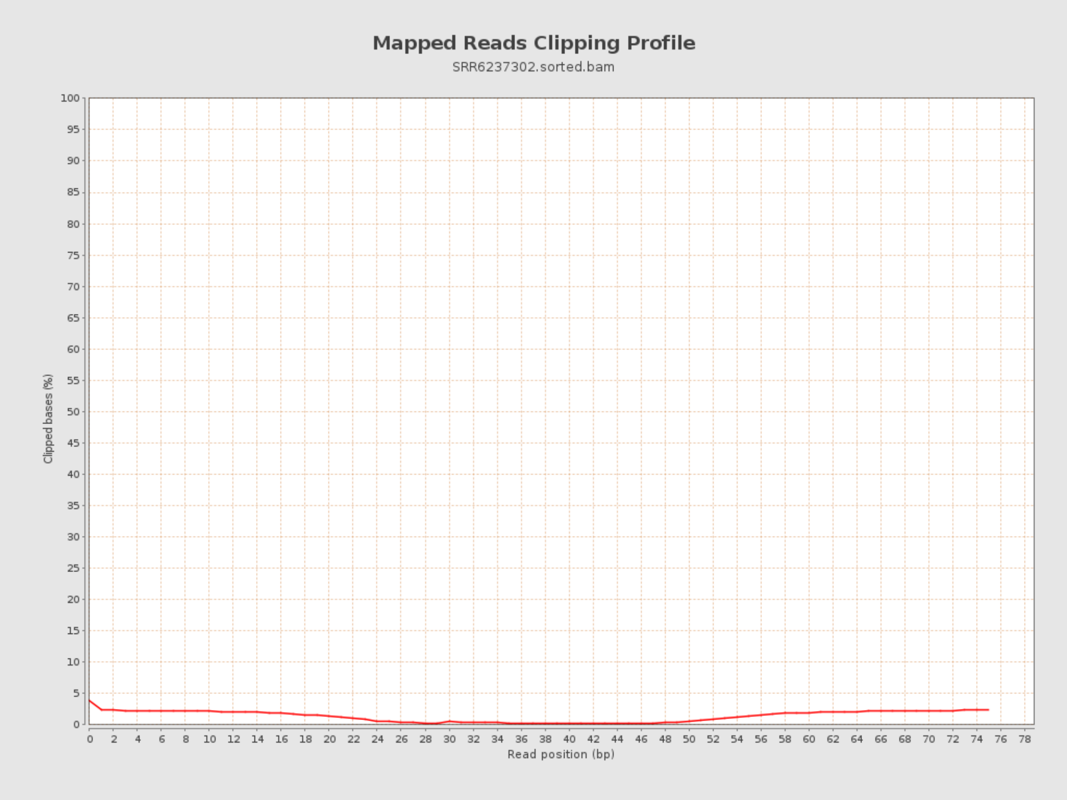
8. Results : Mapped Reads Nucleotide Content



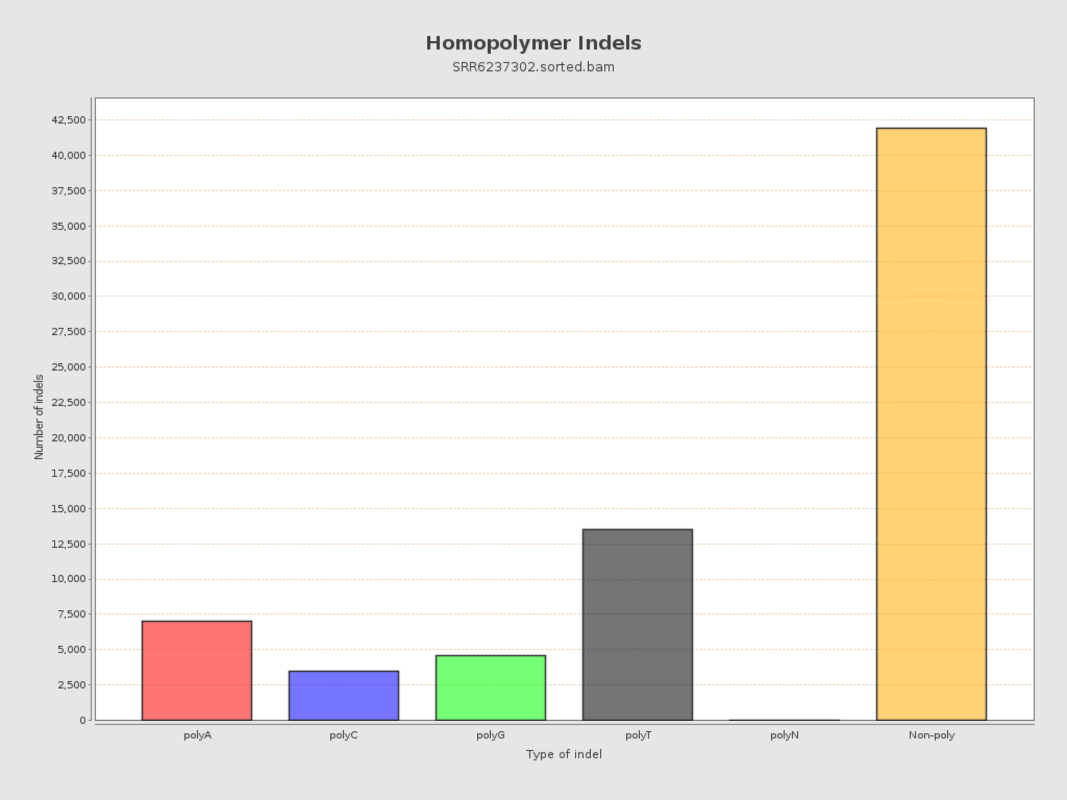
9. Results : Mapped Reads GC-content Distribution



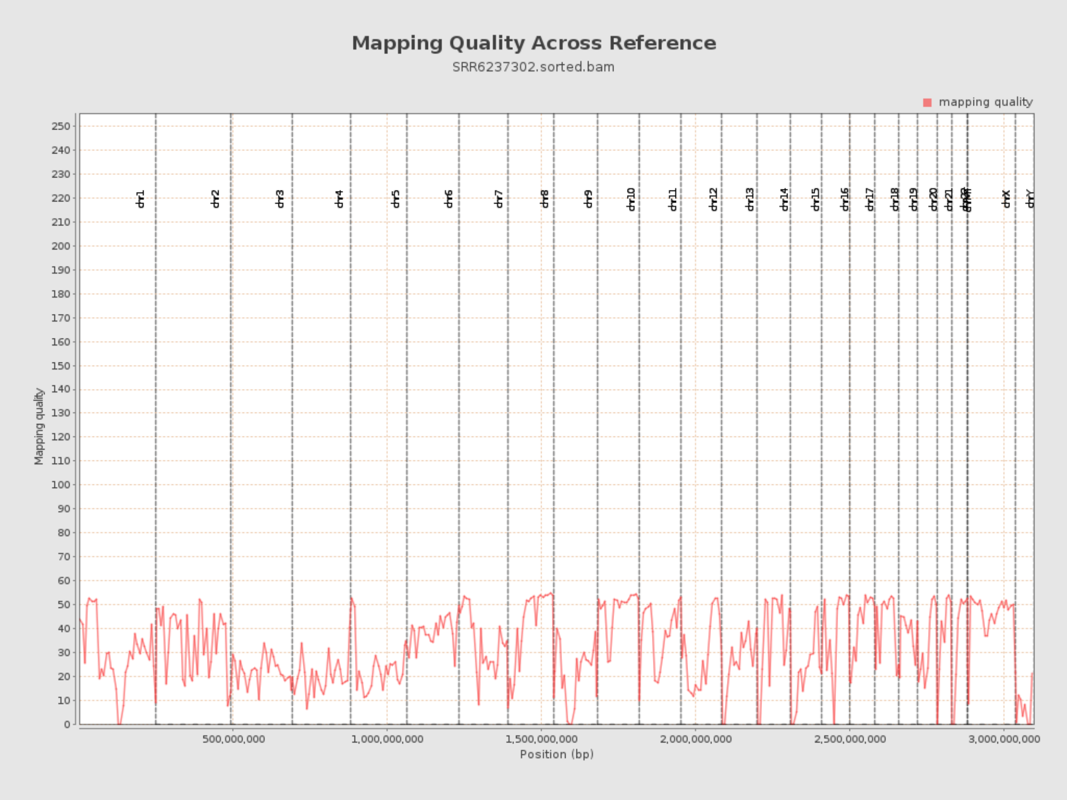
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram