Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:33:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237307.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_SRR6237307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:33:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,722,167
Mapped reads	2,396,183 / 88.02%
Unmapped reads	325,984 / 11.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,353 / 1.08%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	618,144 / 22.71%
Duplication rate	19.2%
Clipped reads	1,616,077 / 59.37%

2.2. ACGT Content

Number/percentage of A's	37,062,365 / 25.34%
Number/percentage of C's	25,975,373 / 17.76%
Number/percentage of T's	48,126,490 / 32.91%
Number/percentage of G's	35,075,447 / 23.98%
Number/percentage of N's	15,404 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.6826

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

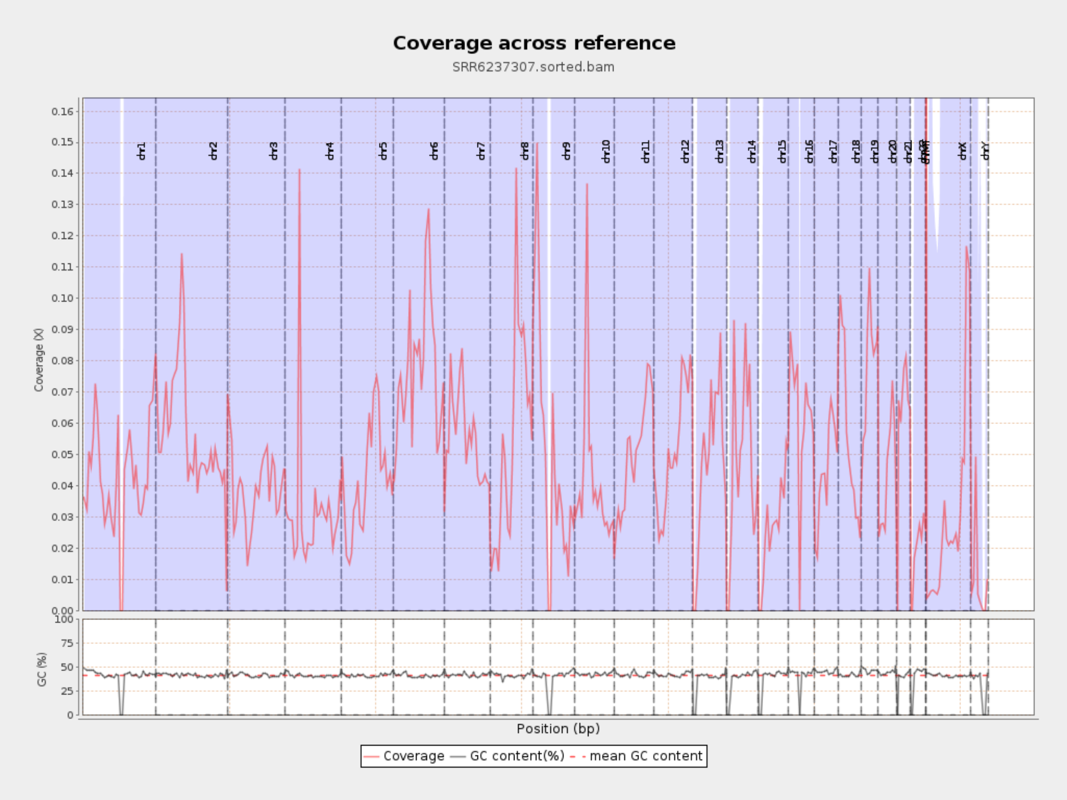
General error rate	0.7%
Mismatches	984,920
Insertions	12,810
Mapped reads with at least one insertion	0.53%
Deletions	49,683
Mapped reads with at least one deletion	2.05%
Homopolymer indels	41.16%

2.6. Chromosome stats

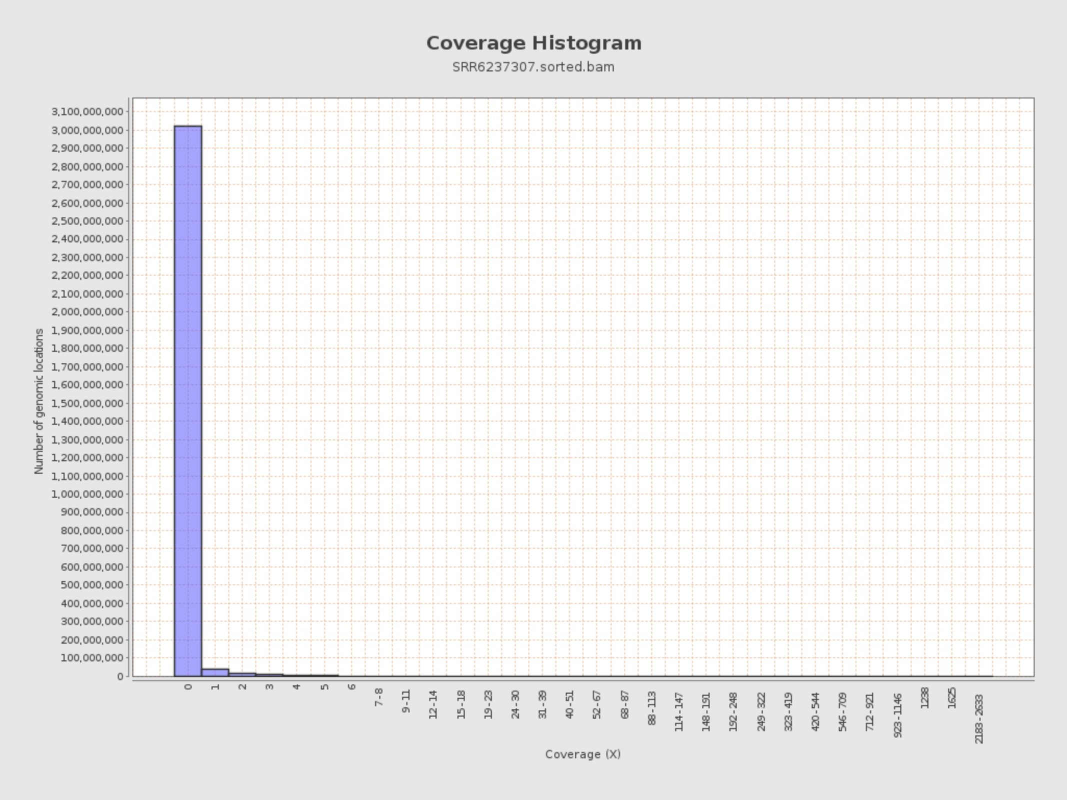
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10693942	0.0429	0.8394
chr2	243199373	13805758	0.0568	1.3766
chr3	198022430	7747759	0.0391	0.3429
chr4	191154276	6103121	0.0319	0.62
chr5	180915260	7687285	0.0425	0.3593
chr6	171115067	13348884	0.078	0.6544
chr7	159138663	8858861	0.0557	0.5547

chr8	146364022	8141964	0.0556	0.7945
chr9	141213431	6889653	0.0488	0.5064
chr10	135534747	5597807	0.0413	0.9285
chr11	135006516	6786876	0.0503	0.4589
chr12	133851895	6955338	0.052	0.4157
chr13	115169878	5424944	0.0471	0.4296
chr14	107349540	5072549	0.0473	0.3896
chr15	102531392	2694160	0.0263	0.3057
chr16	90354753	5602047	0.062	0.4898
chr17	81195210	3639816	0.0448	0.4165
chr18	78077248	4499583	0.0576	1.0882
chr19	59128983	4697518	0.0794	0.7113
chr20	63025520	2773918	0.044	0.3989
chr21	48129895	3056200	0.0635	0.565
chr22	51304566	996366	0.0194	0.2309
chrMT	16571	16337	0.9859	1.53
chrX	155270560	4633818	0.0298	0.3213
chrY	59373566	618603	0.0104	0.5262

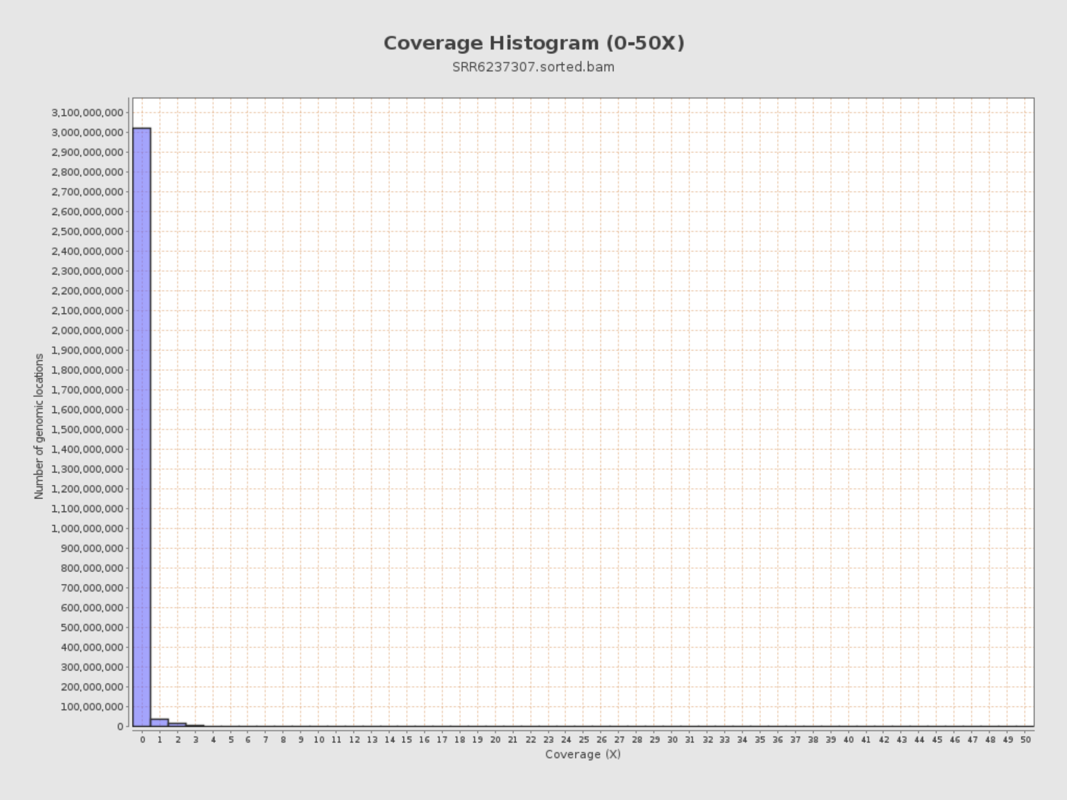
3. Results : Coverage across reference



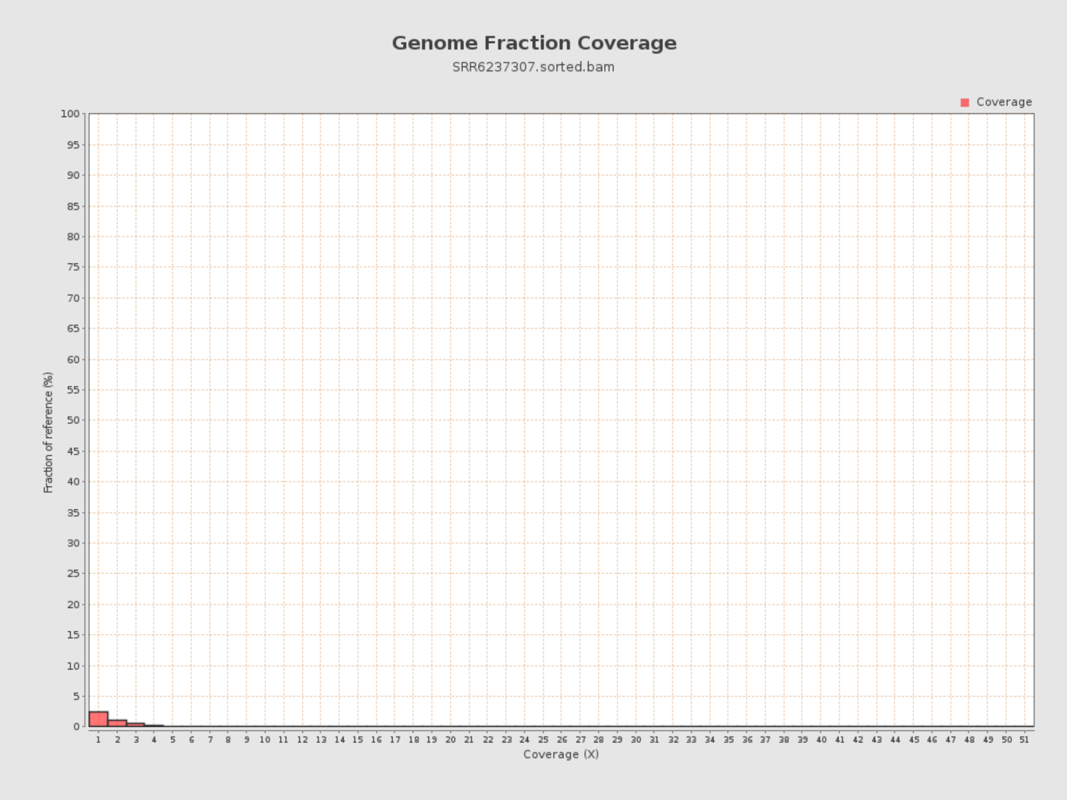
4. Results : Coverage Histogram



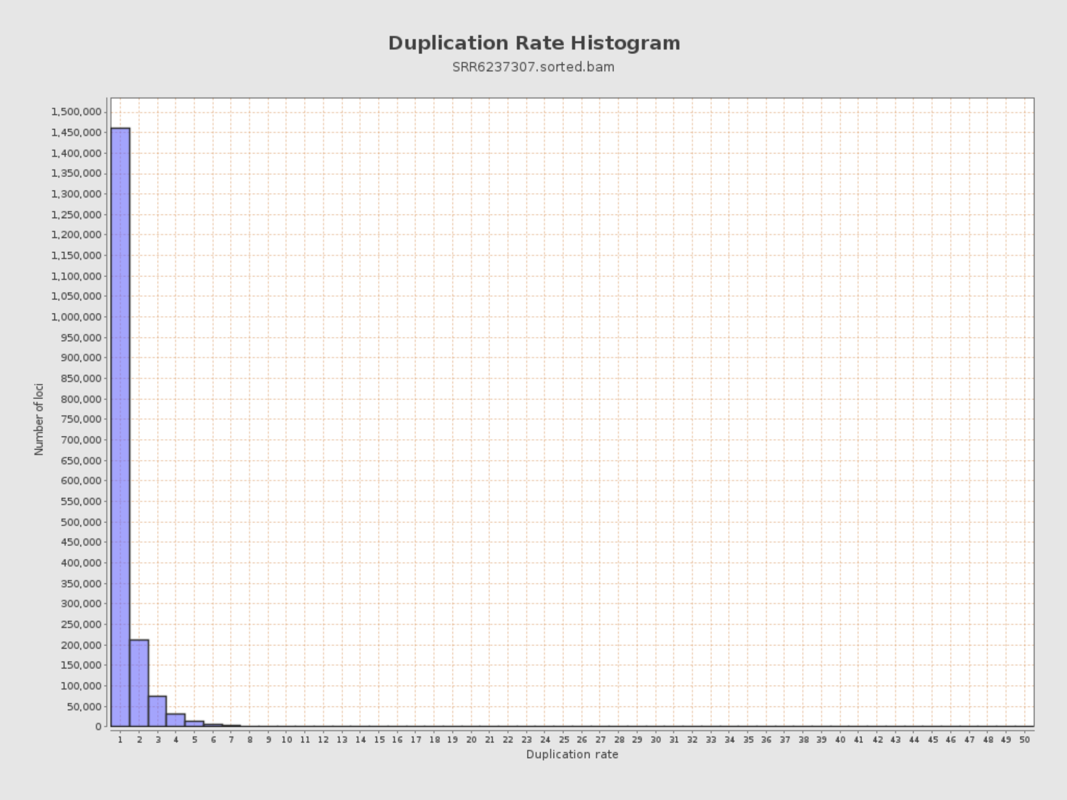
5. Results : Coverage Histogram (0-50X)



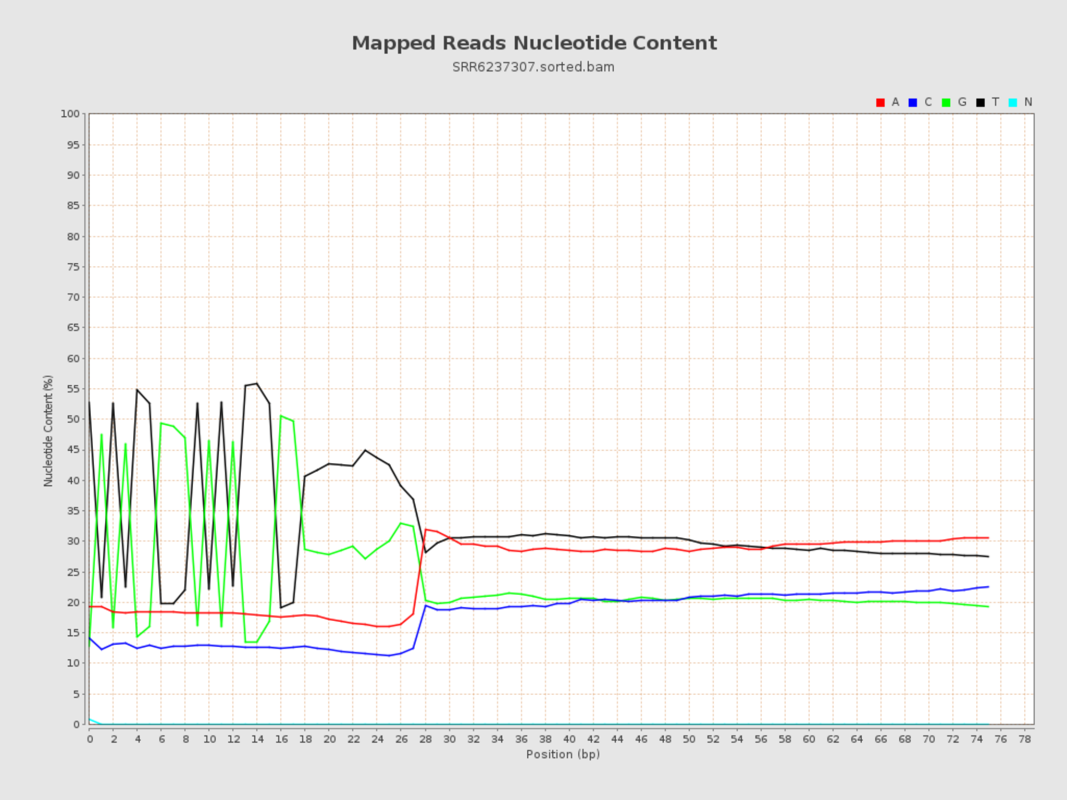
6. Results : Genome Fraction Coverage



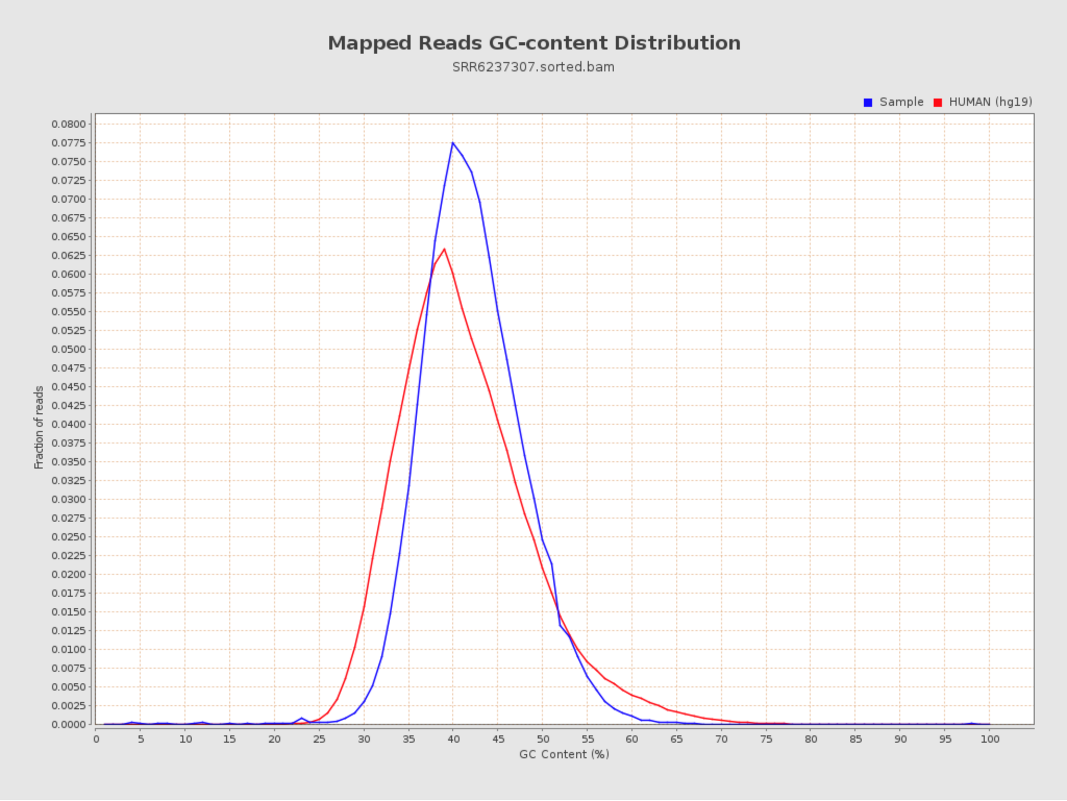
7. Results : Duplication Rate Histogram



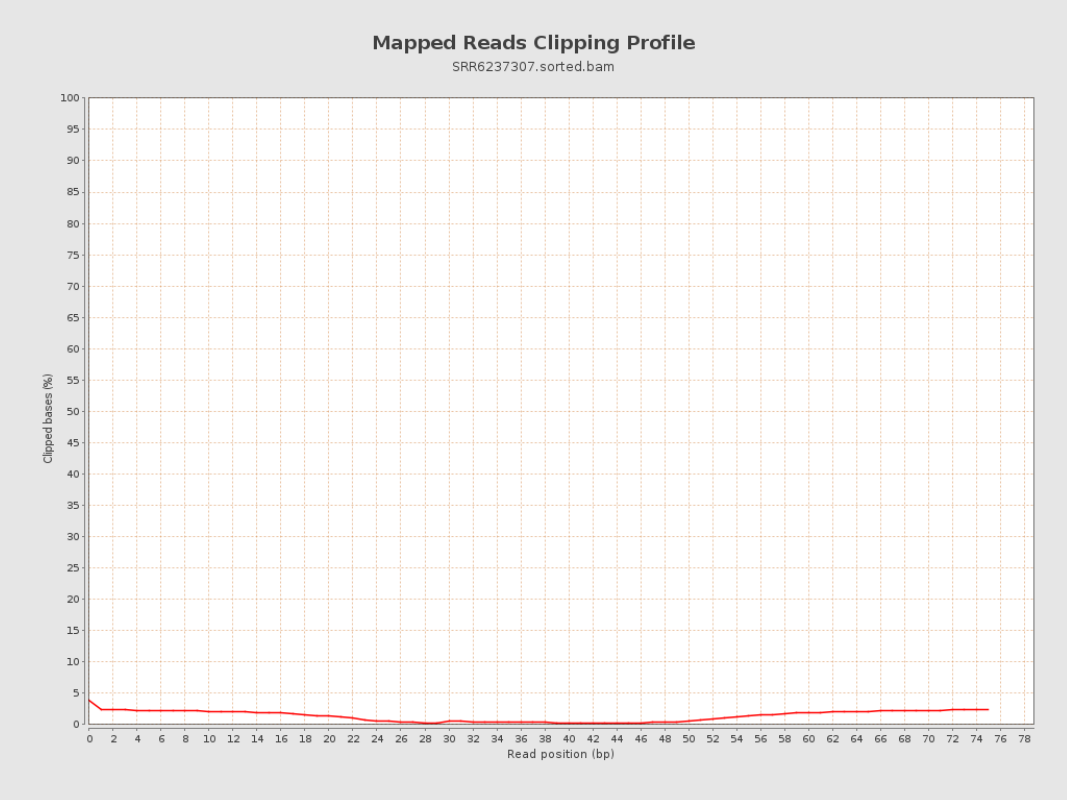
8. Results : Mapped Reads Nucleotide Content



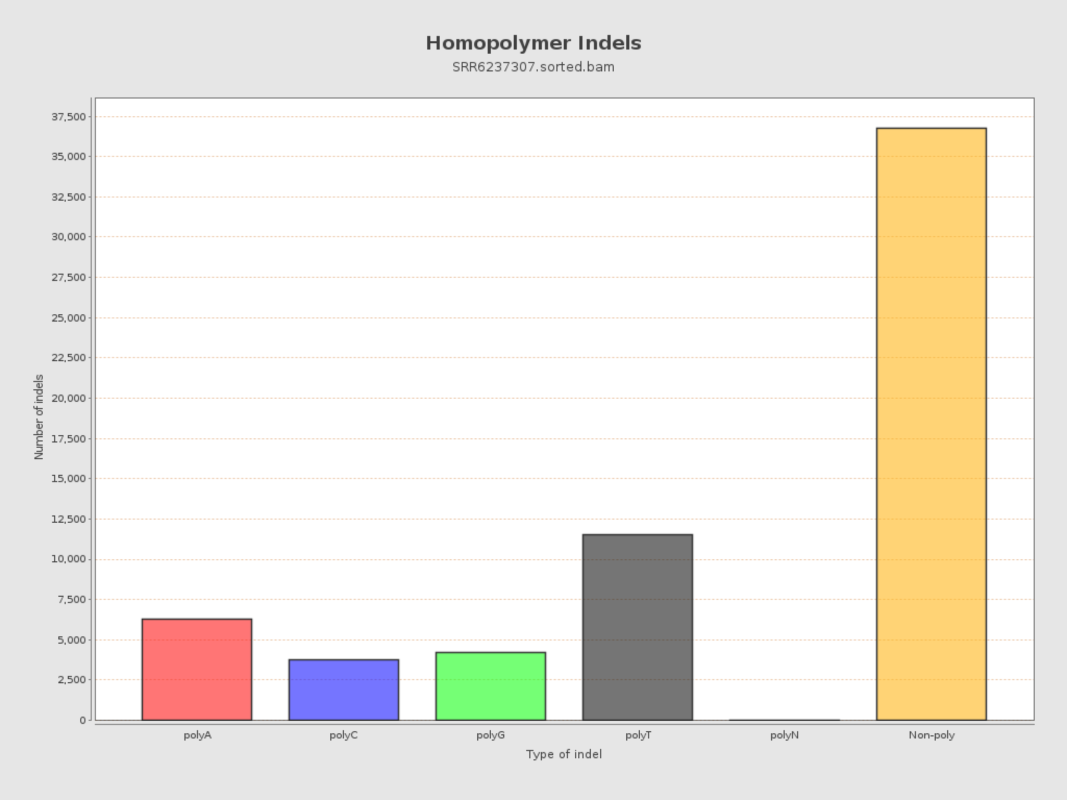
9. Results : Mapped Reads GC-content Distribution



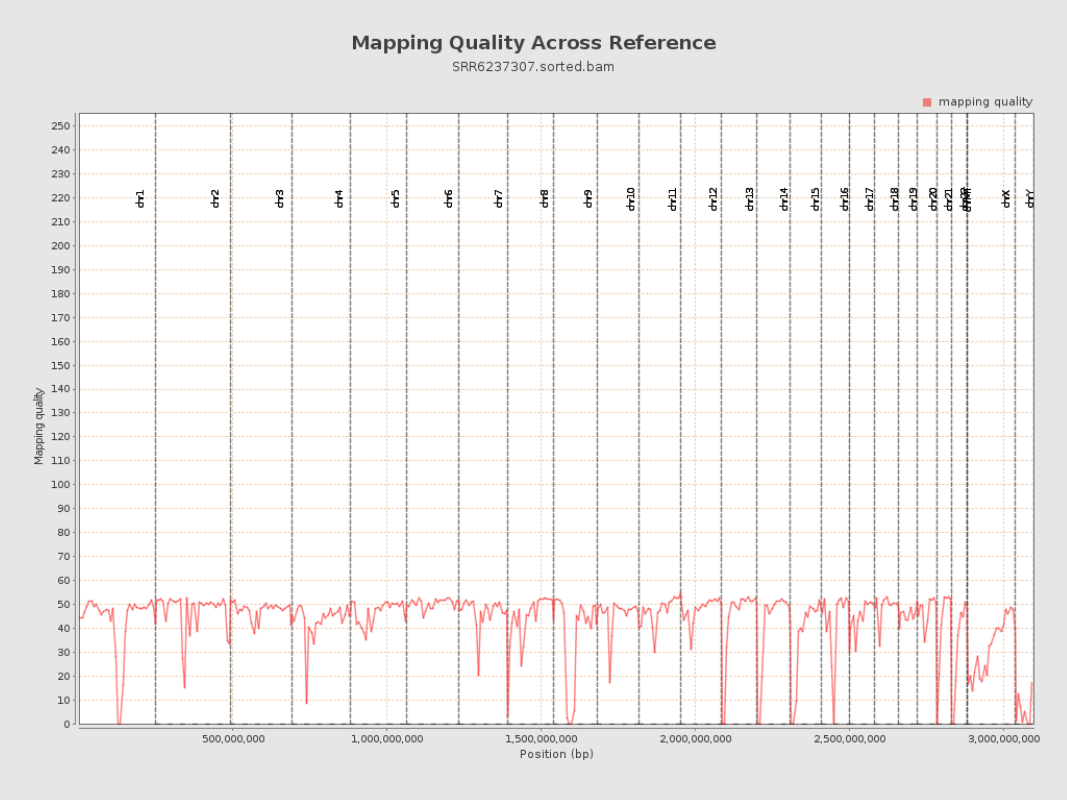
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram