Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:35:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237325.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_SRR6237325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:35:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,614,810
Mapped reads	3,190,028 / 88.25%
Unmapped reads	424,782 / 11.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,099 / 0.97%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	1,271,752 / 35.18%
Duplication rate	22.54%
Clipped reads	2,087,399 / 57.75%

2.2. ACGT Content

Number/percentage of A's	49,365,304 / 25.11%
Number/percentage of C's	34,917,348 / 17.76%
Number/percentage of T's	64,747,603 / 32.94%
Number/percentage of G's	47,530,491 / 24.18%
Number/percentage of N's	20,656 / 0.01%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0635

Standard Deviation	0.9209

2.4. Mapping Quality

Mean Mapping Quality	43.35

2.5. Mismatches and indels

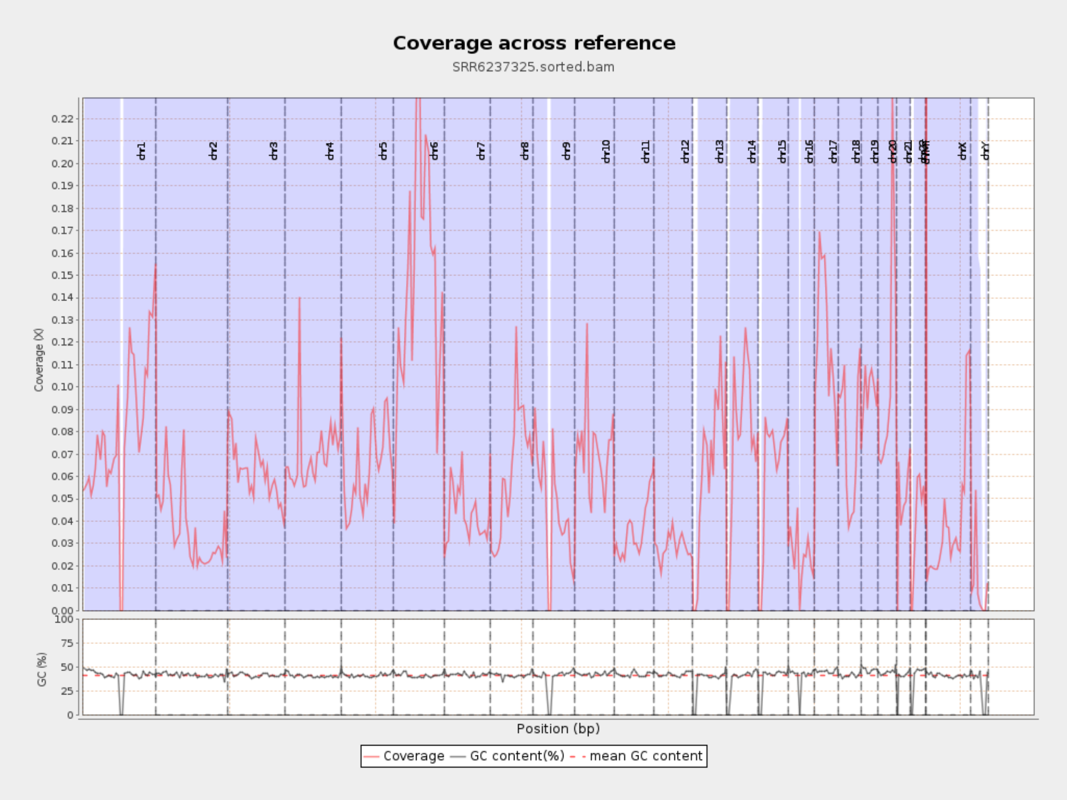
General error rate	0.65%
Mismatches	1,250,709
Insertions	15,330
Mapped reads with at least one insertion	0.48%
Deletions	55,257
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.84%

2.6. Chromosome stats

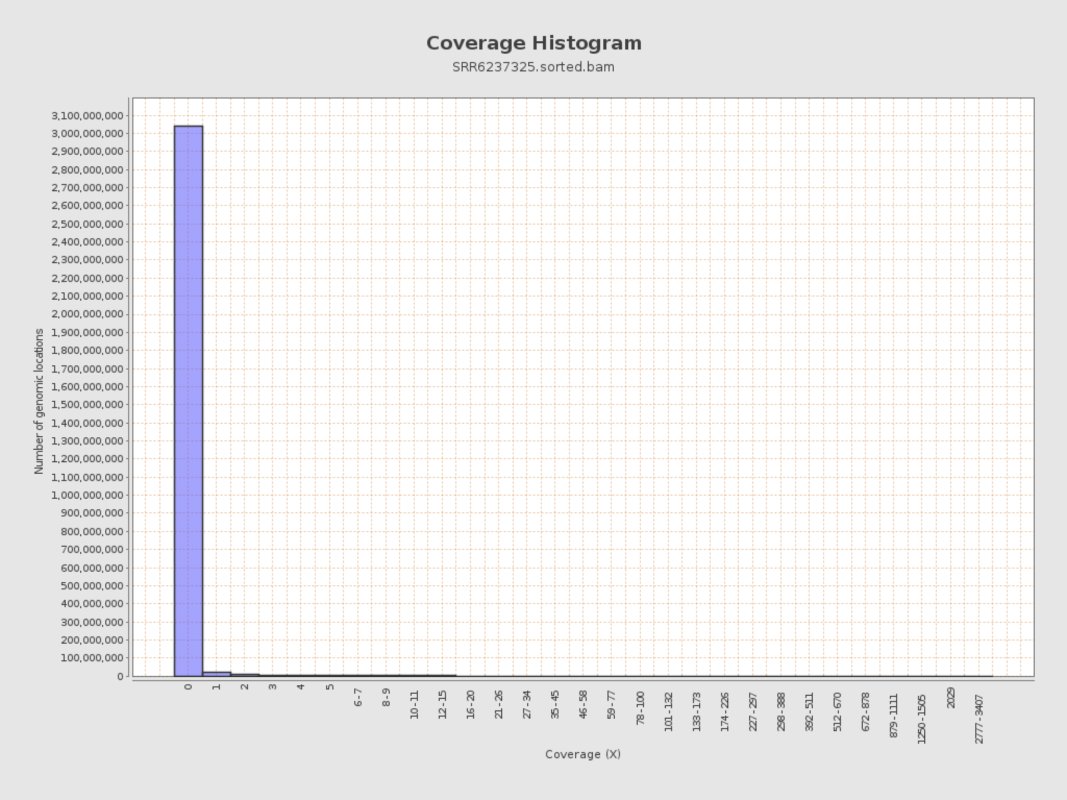
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19966440	0.0801	1.0477
chr2	243199373	9005664	0.037	1.6646
chr3	198022430	12215728	0.0617	0.6456
chr4	191154276	13348573	0.0698	0.7756
chr5	180915260	11737420	0.0649	0.6711
chr6	171115067	25636830	0.1498	1.1916
chr7	159138663	6842037	0.043	0.6476

chr8	146364022	9150191	0.0625	1.0683
chr9	141213431	6478204	0.0459	0.667
chr10	135534747	9612756	0.0709	0.9084
chr11	135006516	4833797	0.0358	0.5545
chr12	133851895	3847459	0.0287	0.4772
chr13	115169878	7280815	0.0632	0.7099
chr14	107349540	8379603	0.0781	0.7418
chr15	102531392	6320298	0.0616	0.662
chr16	90354753	2177336	0.0241	0.4555
chr17	81195210	9907736	0.122	0.967
chr18	78077248	5967286	0.0764	1.6927
chr19	59128983	5806126	0.0982	0.905
chr20	63025520	6901927	0.1095	0.8817
chr21	48129895	2391683	0.0497	0.6548
chr22	51304566	2008673	0.0392	0.5184
chrMT	16571	17966	1.0842	2.961
chrX	155270560	6122507	0.0394	0.5512
chrY	59373566	721897	0.0122	0.4698

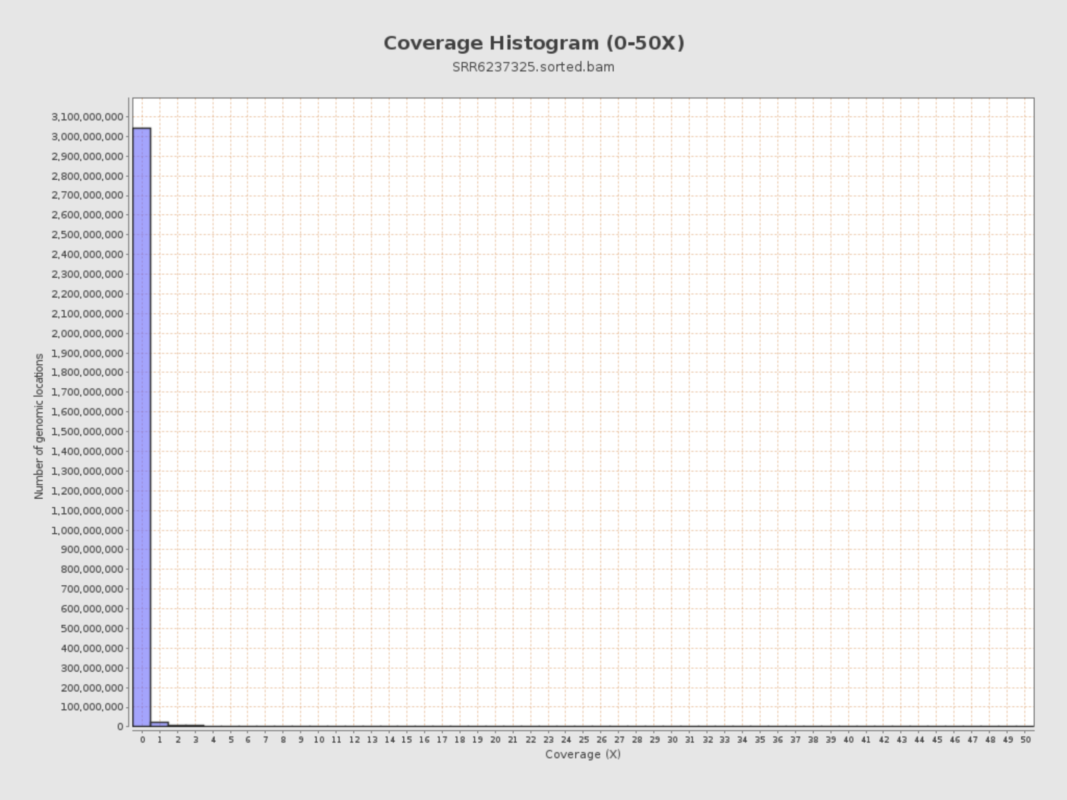
3. Results : Coverage across reference



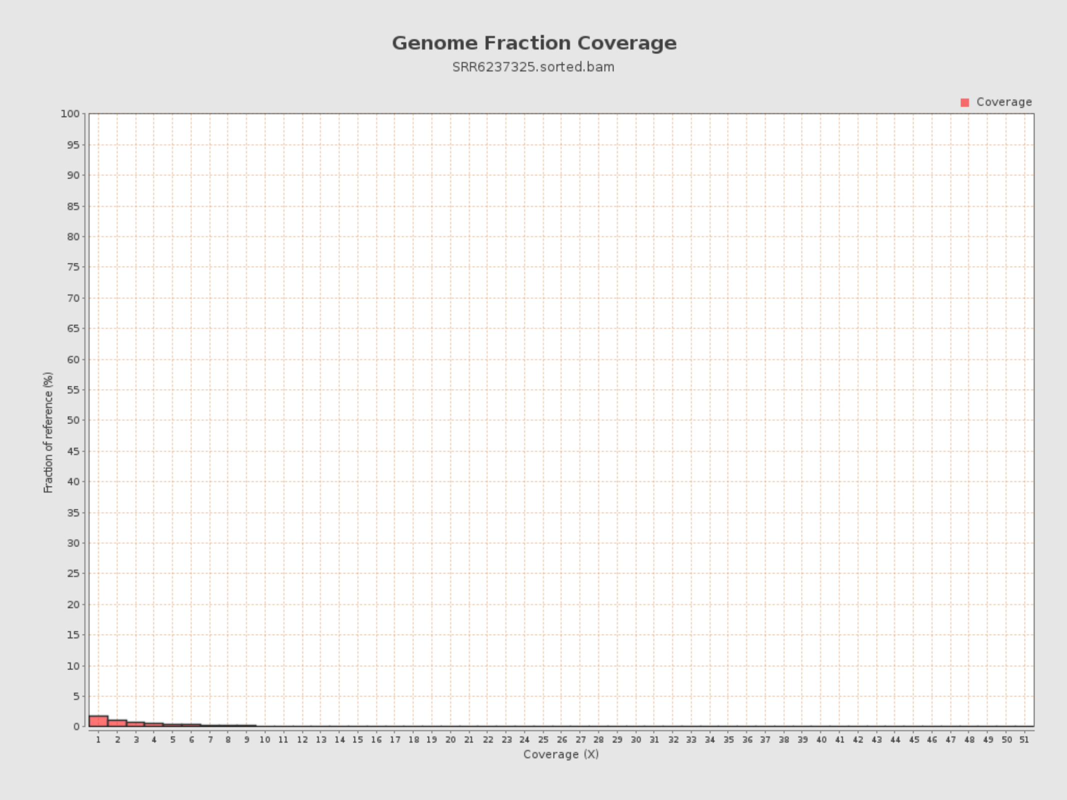
4. Results : Coverage Histogram



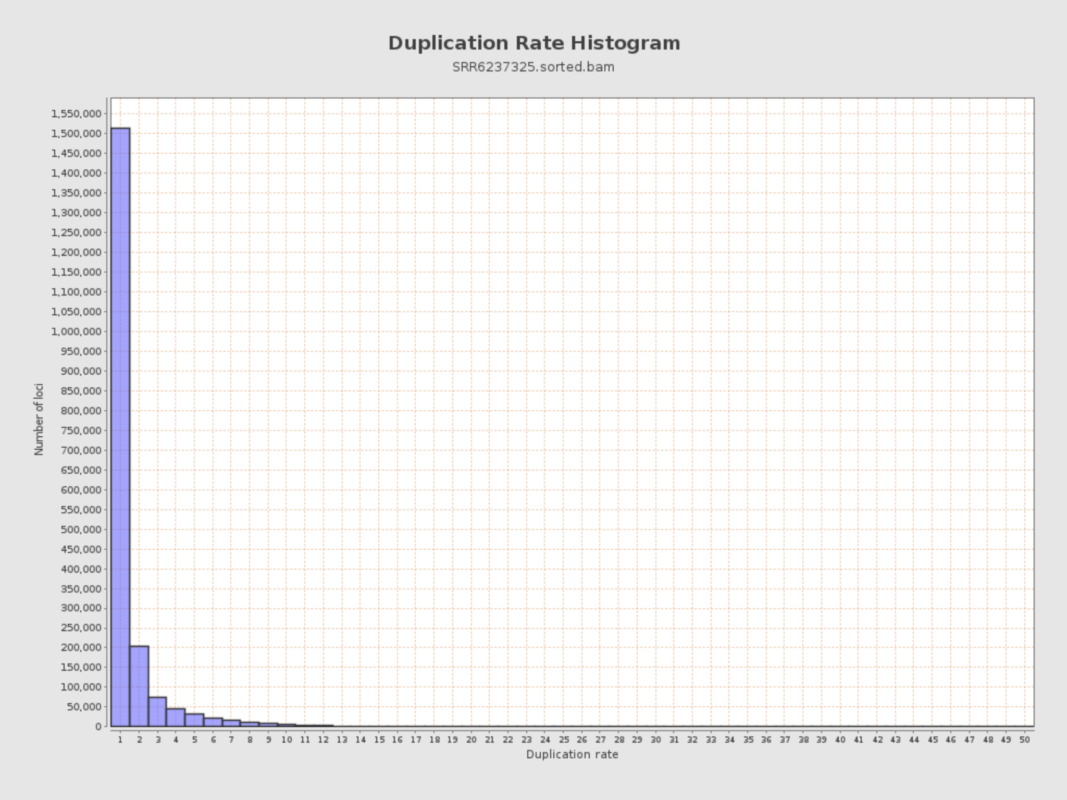
5. Results : Coverage Histogram (0-50X)



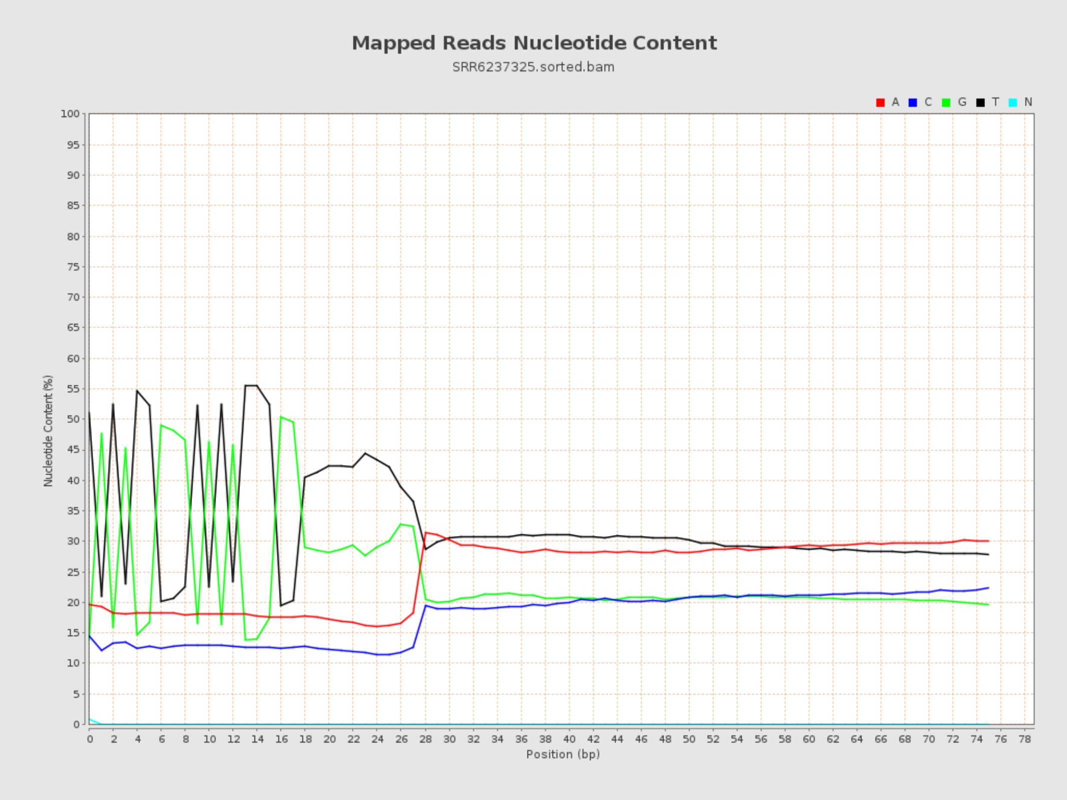
6. Results : Genome Fraction Coverage



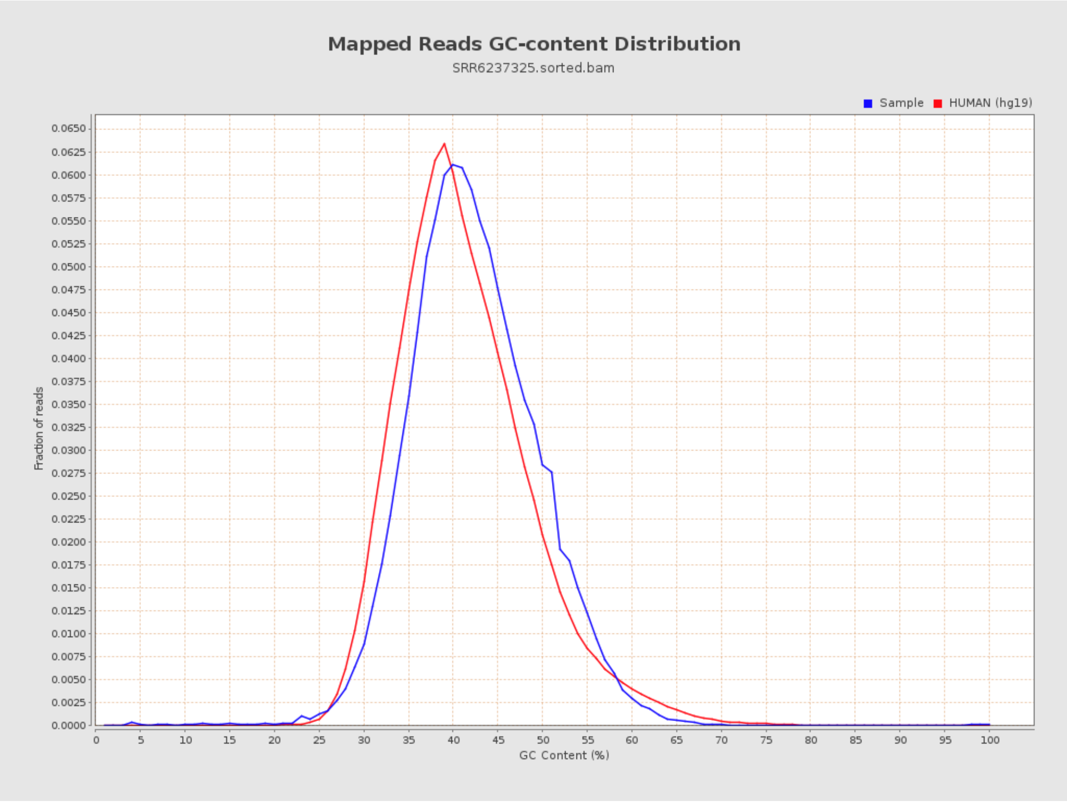
7. Results : Duplication Rate Histogram



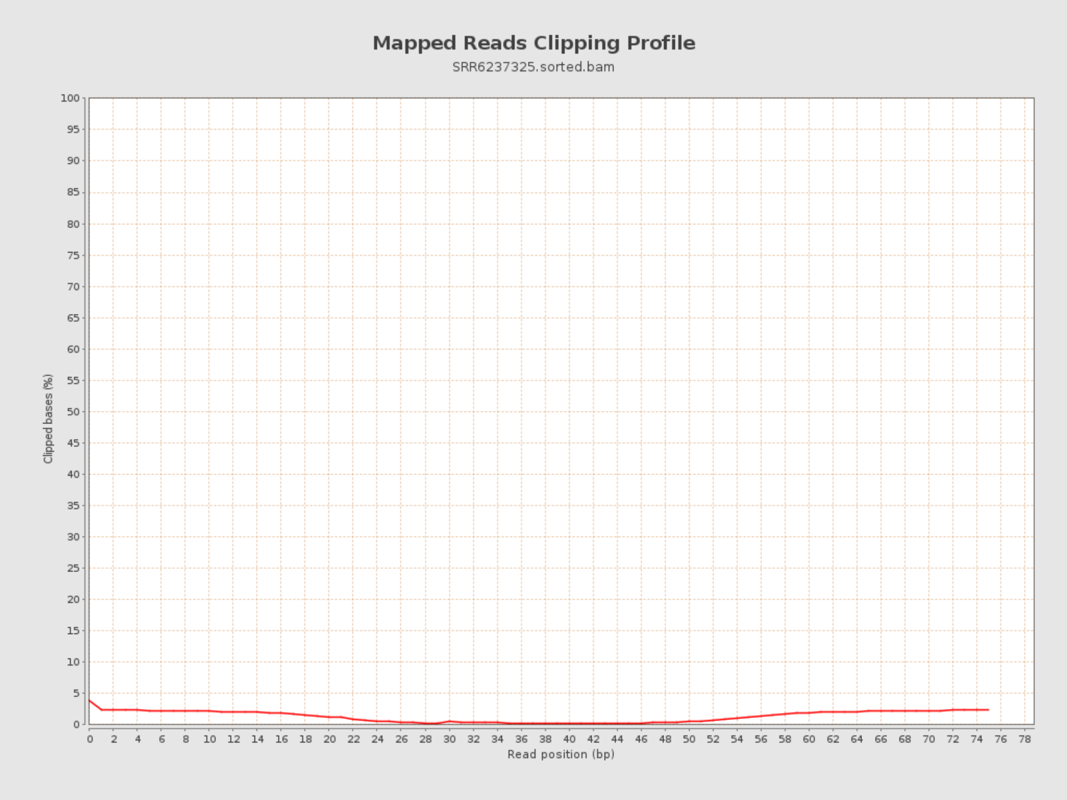
8. Results : Mapped Reads Nucleotide Content



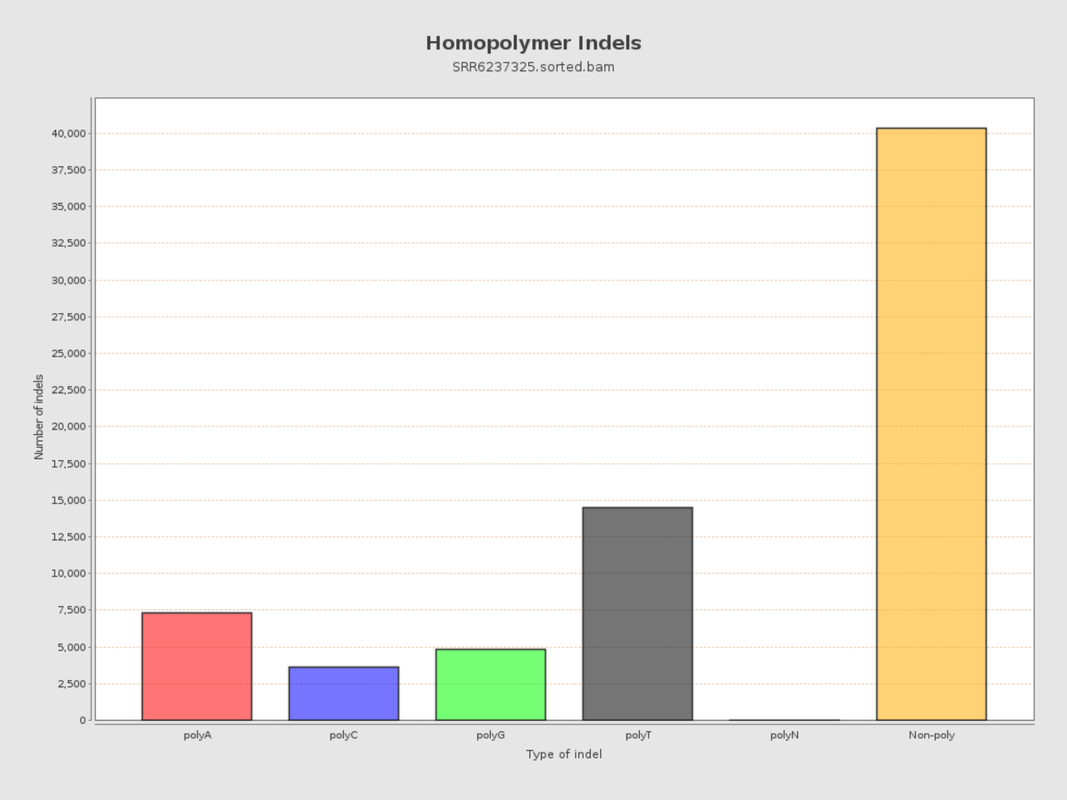
9. Results : Mapped Reads GC-content Distribution



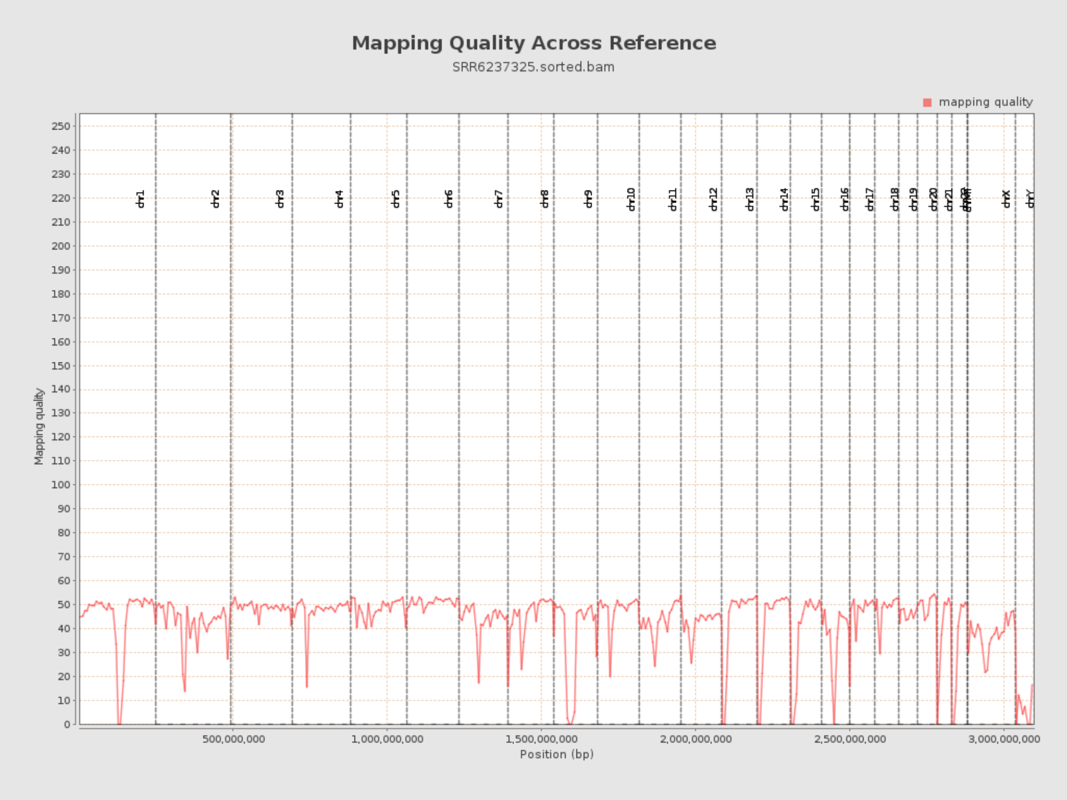
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram