Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:02:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237281.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_SRR6237281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:02:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,559,406
Mapped reads	2,309,266 / 90.23%
Unmapped reads	250,140 / 9.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,580 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	114,336 / 4.47%
Duplication rate	3.56%
Clipped reads	919,433 / 35.92%

2.2. ACGT Content

Number/percentage of A's	44,088,501 / 28.2%
Number/percentage of C's	28,355,928 / 18.14%
Number/percentage of T's	50,071,619 / 32.03%
Number/percentage of G's	33,829,974 / 21.64%
Number/percentage of N's	2,615 / 0%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0505

Standard Deviation	0.5275

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

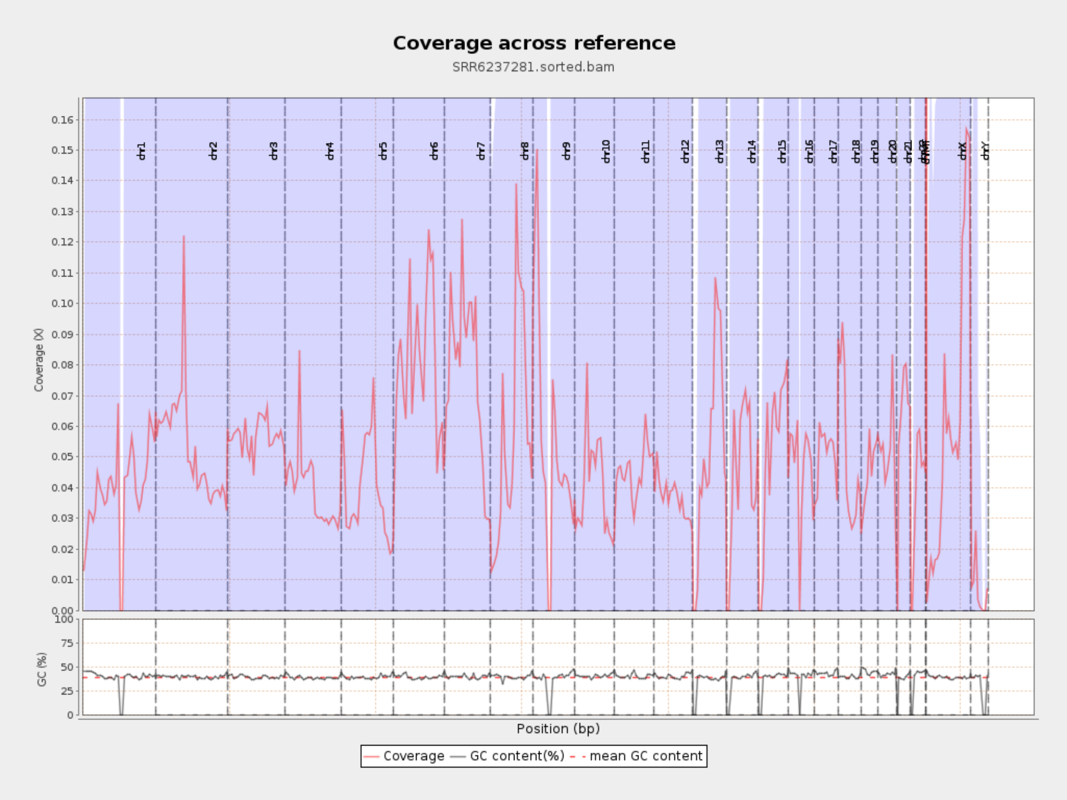
General error rate	0.8%
Mismatches	1,232,200
Insertions	12,612
Mapped reads with at least one insertion	0.54%
Deletions	42,791
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.98%

2.6. Chromosome stats

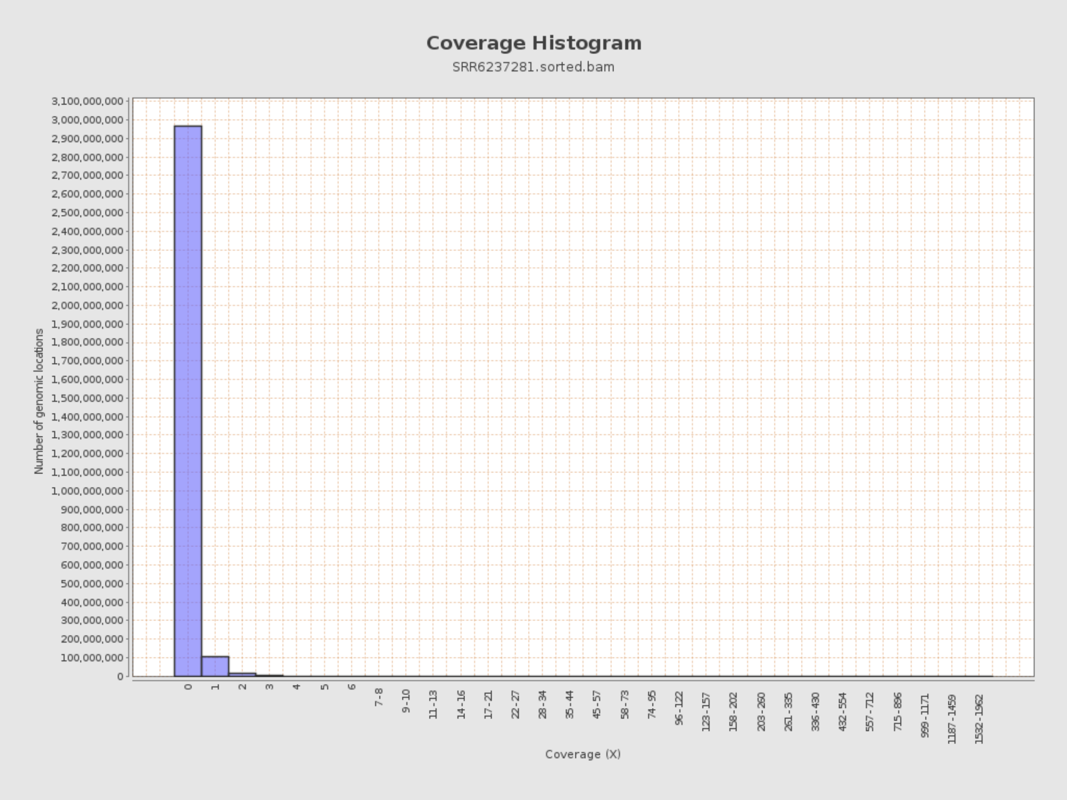
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9772162	0.0392	0.6906
chr2	243199373	12998595	0.0534	0.5756
chr3	198022430	11300666	0.0571	0.2779
chr4	191154276	7504870	0.0393	0.2918
chr5	180915260	7235830	0.04	0.2403
chr6	171115067	13875945	0.0811	0.4572
chr7	159138663	12295293	0.0773	0.7322

chr8	146364022	8366032	0.0572	1.2696
chr9	141213431	7758796	0.0549	0.5321
chr10	135534747	5408486	0.0399	0.4376
chr11	135006516	6107188	0.0452	0.4029
chr12	133851895	4943999	0.0369	0.2419
chr13	115169878	6031229	0.0524	0.2689
chr14	107349540	4801203	0.0447	0.2752
chr15	102531392	5192856	0.0506	0.2702
chr16	90354753	4092921	0.0453	0.3075
chr17	81195210	4106002	0.0506	0.3289
chr18	78077248	4028838	0.0516	1.0049
chr19	59128983	2674548	0.0452	0.4684
chr20	63025520	3322742	0.0527	0.2827
chr21	48129895	2988417	0.0621	0.3378
chr22	51304566	1907671	0.0372	0.2203
chrMT	16571	53332	3.2184	2.8325
chrX	155270560	9250760	0.0596	0.3385
chrY	59373566	404726	0.0068	0.1982

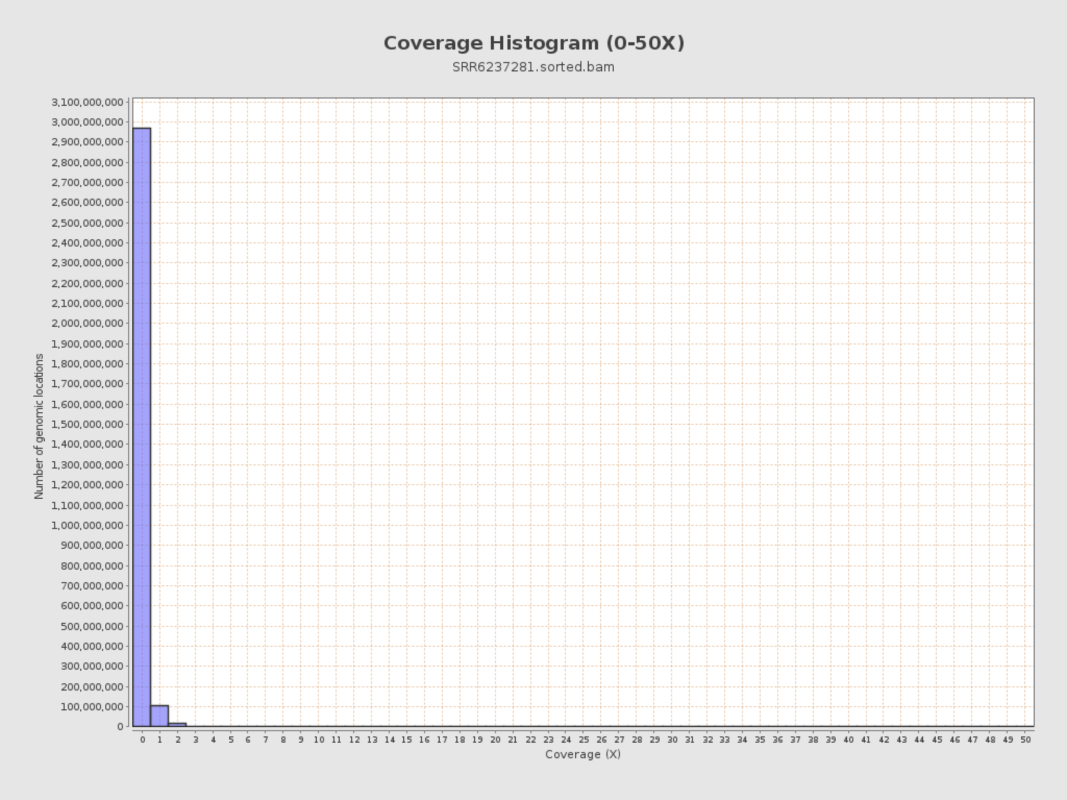
3. Results : Coverage across reference



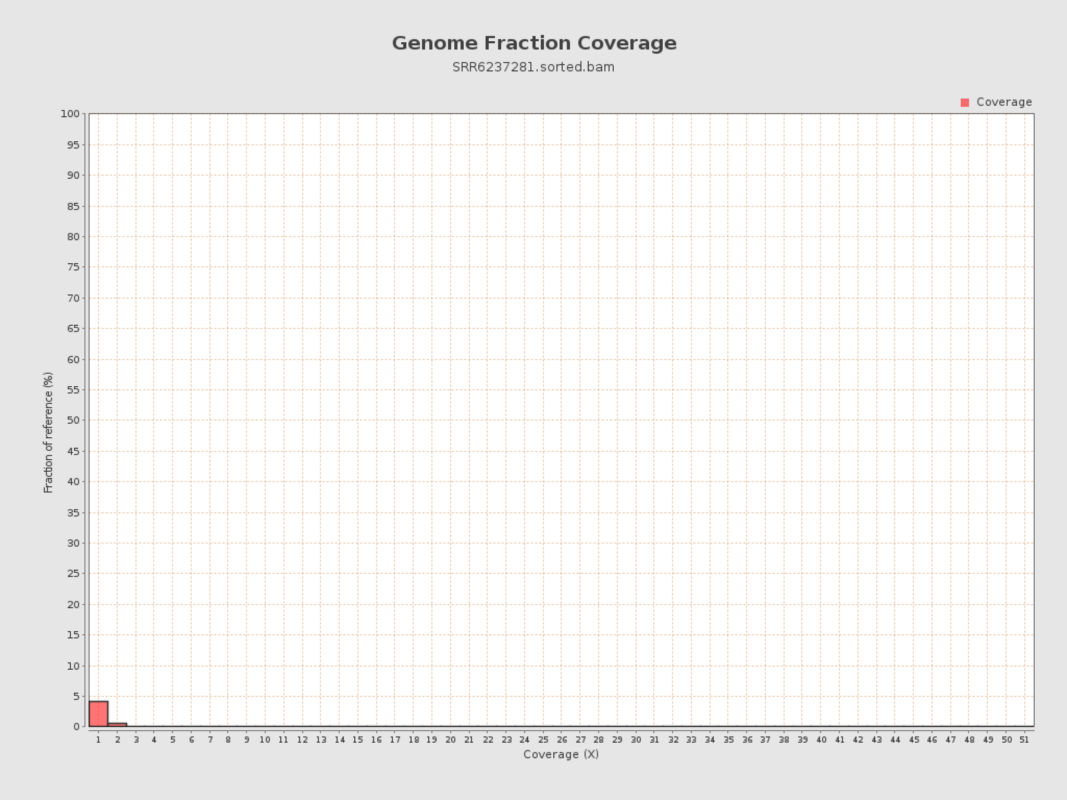
4. Results : Coverage Histogram



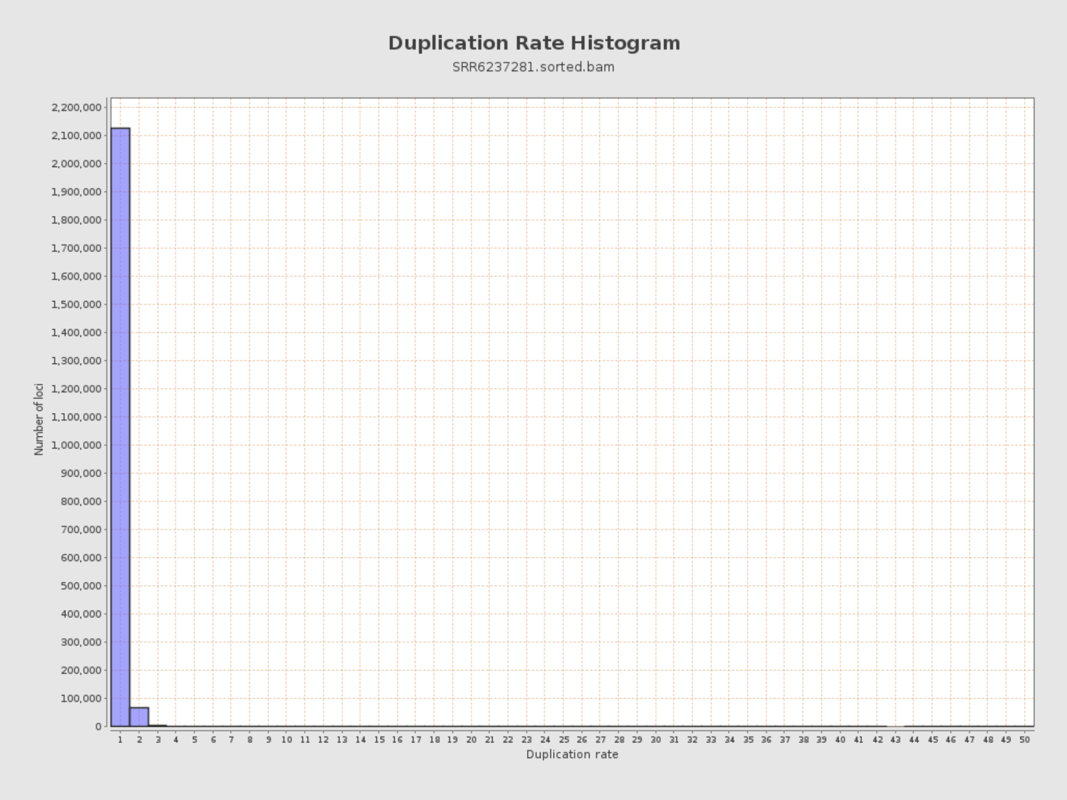
5. Results : Coverage Histogram (0-50X)



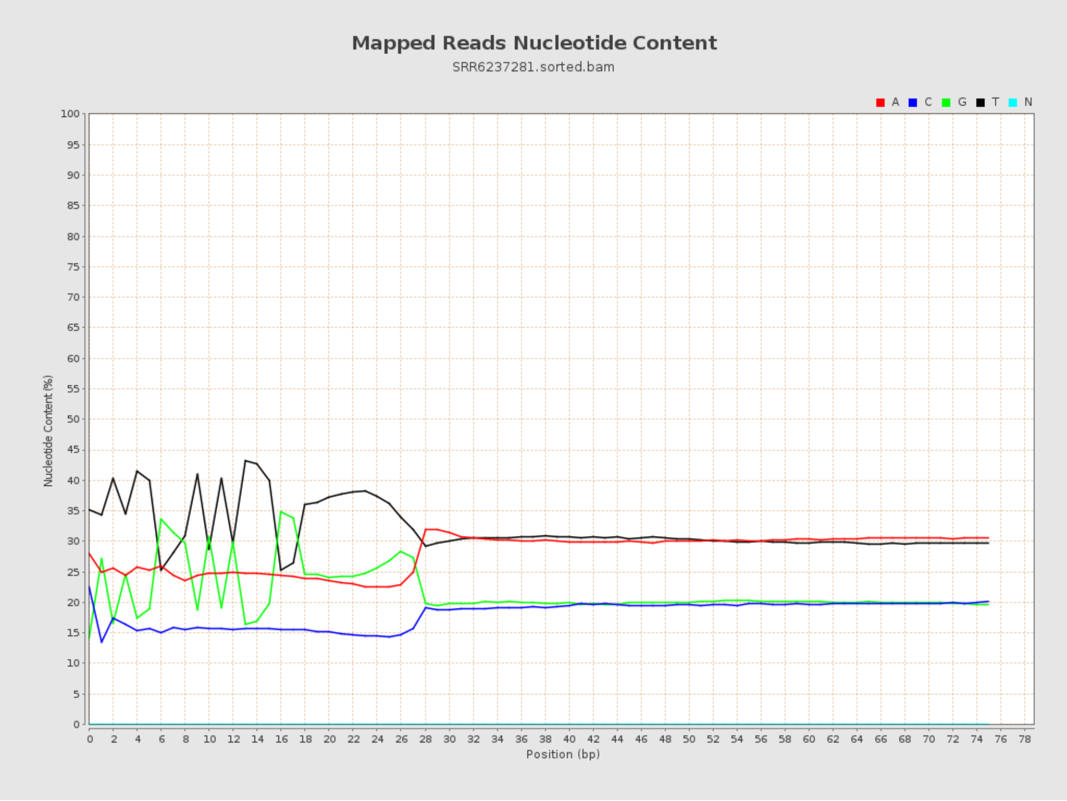
6. Results : Genome Fraction Coverage



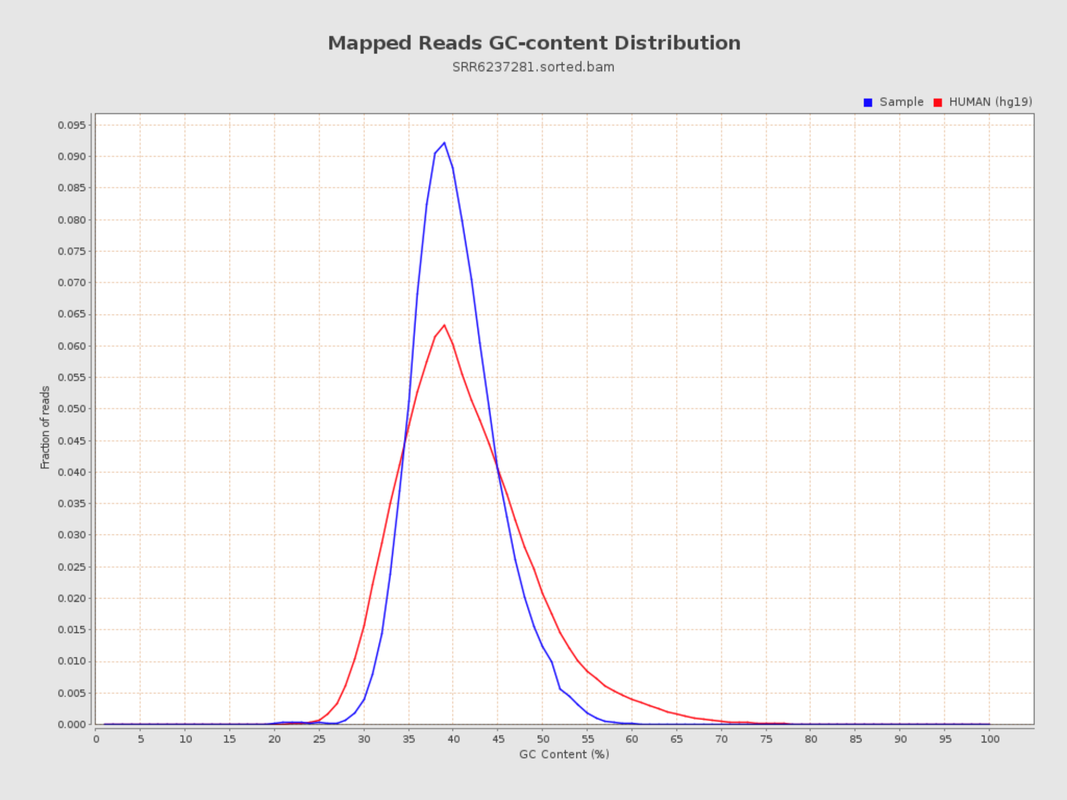
7. Results : Duplication Rate Histogram



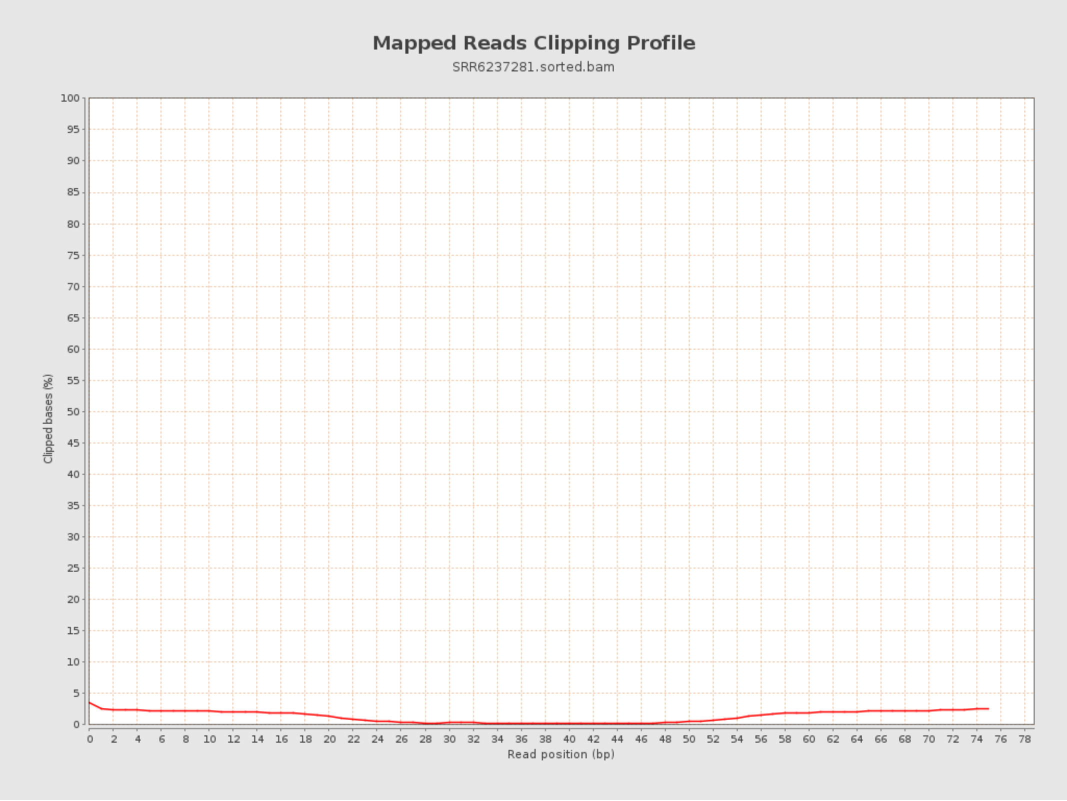
8. Results : Mapped Reads Nucleotide Content



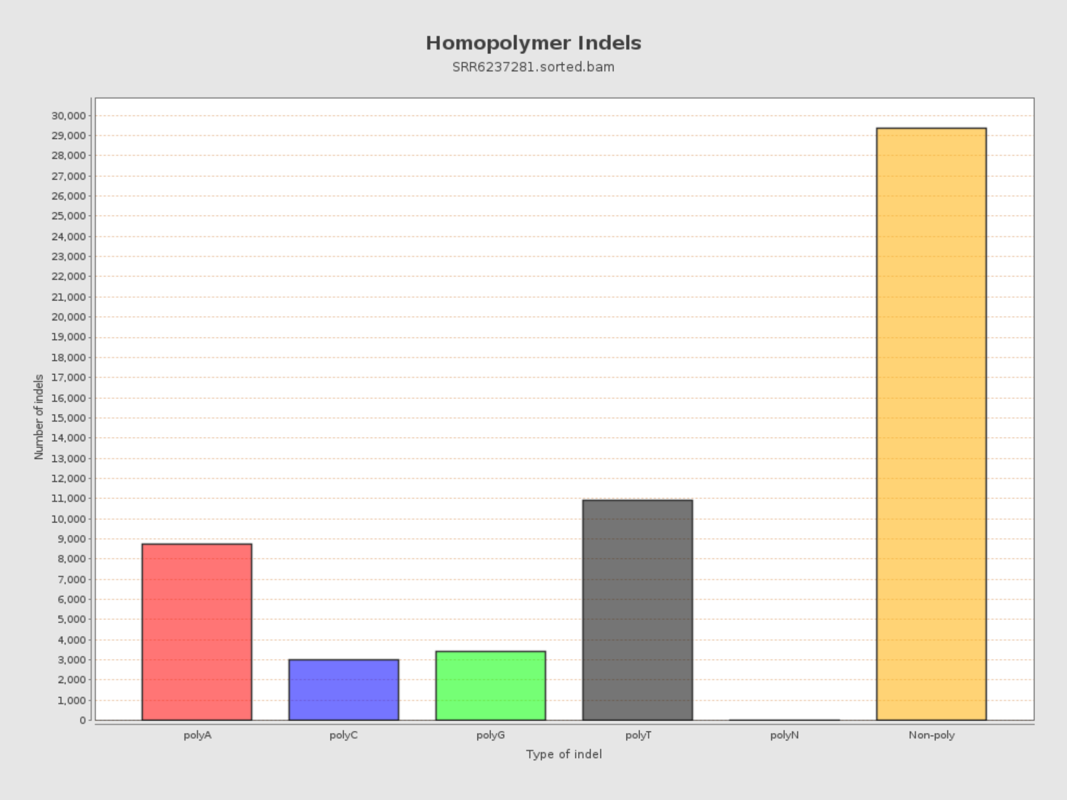
9. Results : Mapped Reads GC-content Distribution



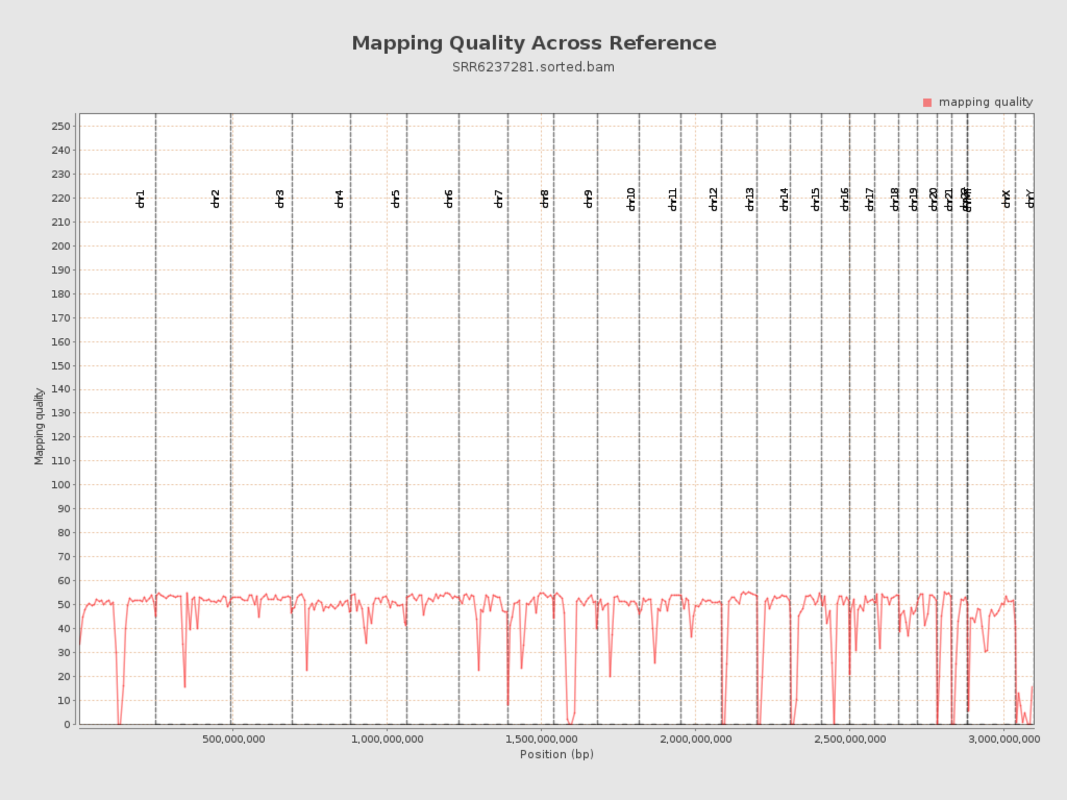
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram