Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:12:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231885.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_SRR6231885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231885.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:12:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,105,879
Mapped reads	4,126,717 / 40.83%
Unmapped reads	5,979,162 / 59.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,933 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	300,319 / 2.97%
Duplication rate	2.87%
Clipped reads	2,396,780 / 23.72%

2.2. ACGT Content

Number/percentage of A's	74,579,711 / 28.37%
Number/percentage of C's	53,320,838 / 20.28%
Number/percentage of T's	69,826,615 / 26.56%
Number/percentage of G's	65,128,191 / 24.78%
Number/percentage of N's	20,121 / 0.01%
GC Percentage	45.06%

2.3. Coverage

Mean	0.0849

Standard Deviation	15.9864

2.4. Mapping Quality

Mean Mapping Quality	41.2

2.5. Mismatches and indels

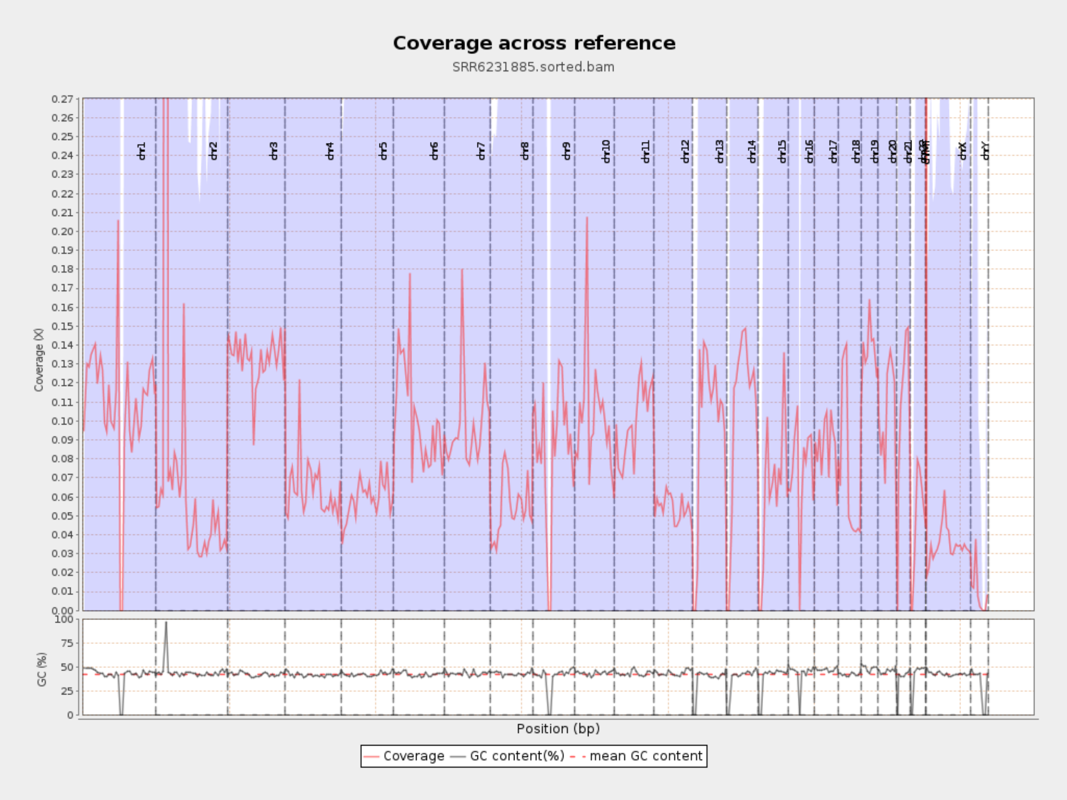
General error rate	0.76%
Mismatches	1,939,831
Insertions	24,090
Mapped reads with at least one insertion	0.57%
Deletions	62,711
Mapped reads with at least one deletion	1.5%
Homopolymer indels	42.38%

2.6. Chromosome stats

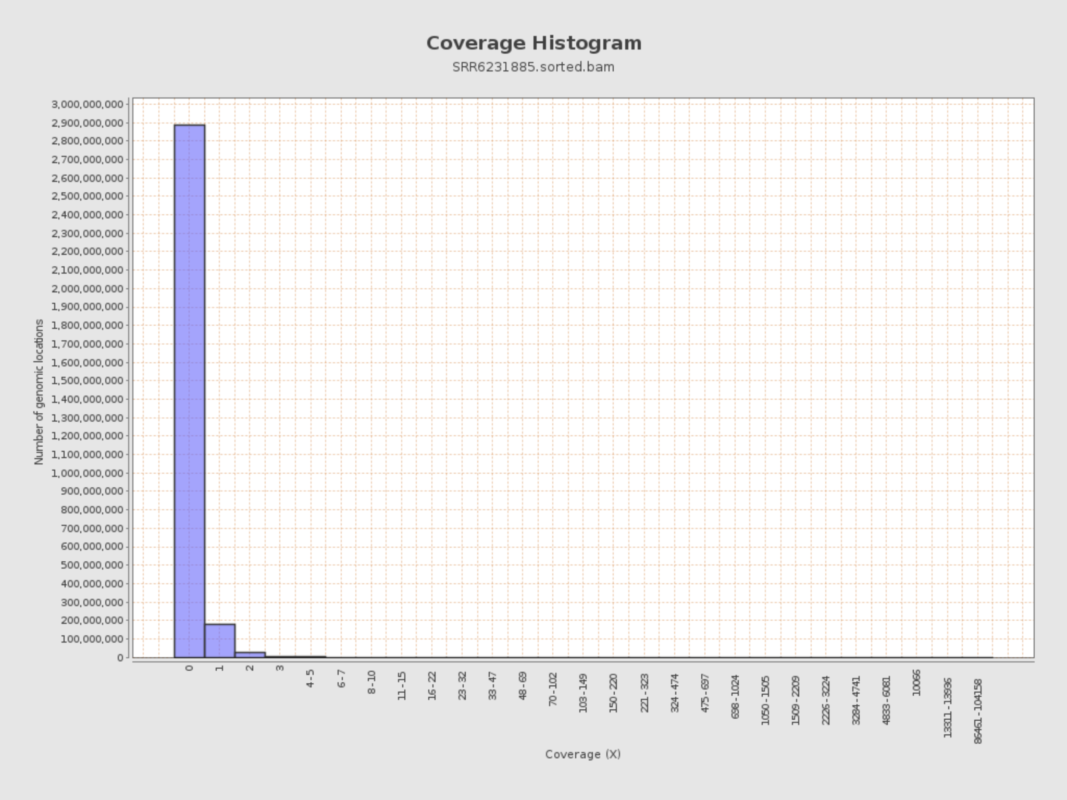
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27254513	0.1093	2.301
chr2	243199373	21645801	0.089	56.9452
chr3	198022430	26312143	0.1329	0.4404
chr4	191154276	12252047	0.0641	0.3764
chr5	180915260	10686554	0.0591	0.2956
chr6	171115067	17488310	0.1022	0.6761
chr7	159138663	15749774	0.099	1.1606

chr8	146364022	7901059	0.054	0.7019
chr9	141213431	11974992	0.0848	0.669
chr10	135534747	13889689	0.1025	1.0363
chr11	135006516	13302737	0.0985	0.7791
chr12	133851895	7275669	0.0544	0.2892
chr13	115169878	11234592	0.0975	0.3587
chr14	107349540	11381330	0.106	0.643
chr15	102531392	6528623	0.0637	0.2949
chr16	90354753	6513220	0.0721	0.4606
chr17	81195210	7159561	0.0882	0.4432
chr18	78077248	5873490	0.0752	1.5875
chr19	59128983	8159815	0.138	1.245
chr20	63025520	6665871	0.1058	0.4149
chr21	48129895	5089821	0.1058	0.4373
chr22	51304566	2422086	0.0472	0.2485
chrMT	16571	233653	14.1001	9.4222
chrX	155270560	5395825	0.0348	0.3541
chrY	59373566	584822	0.0098	0.2463

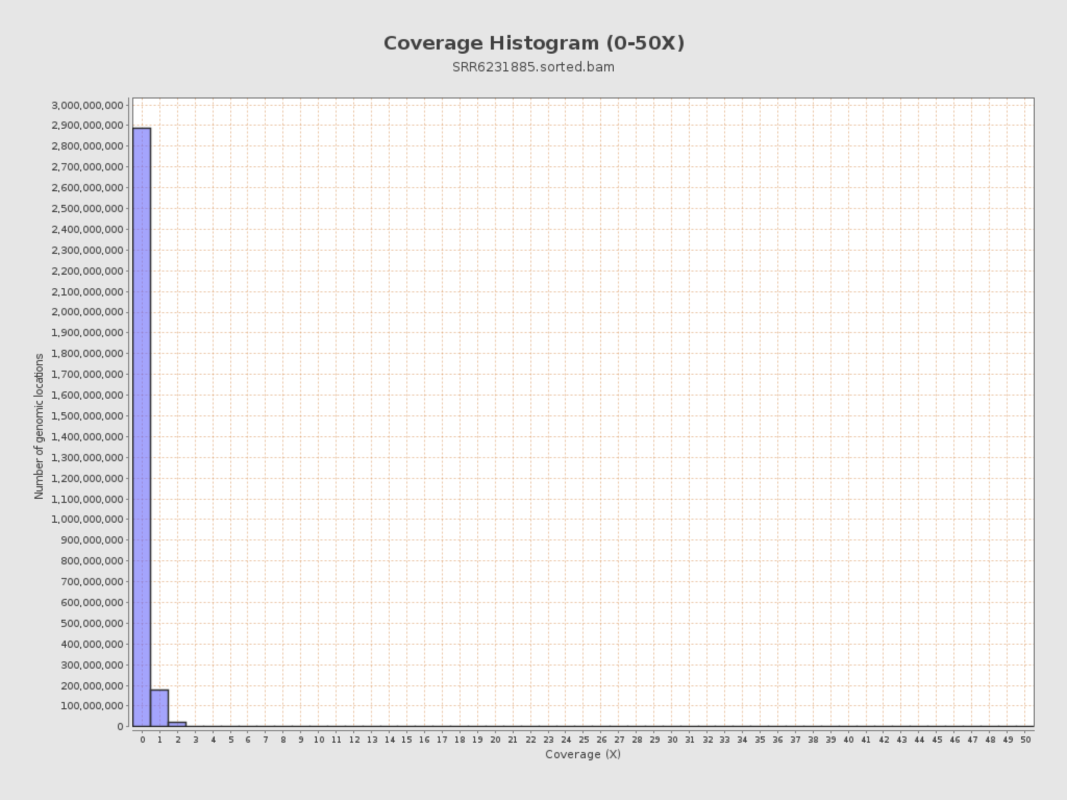
3. Results : Coverage across reference



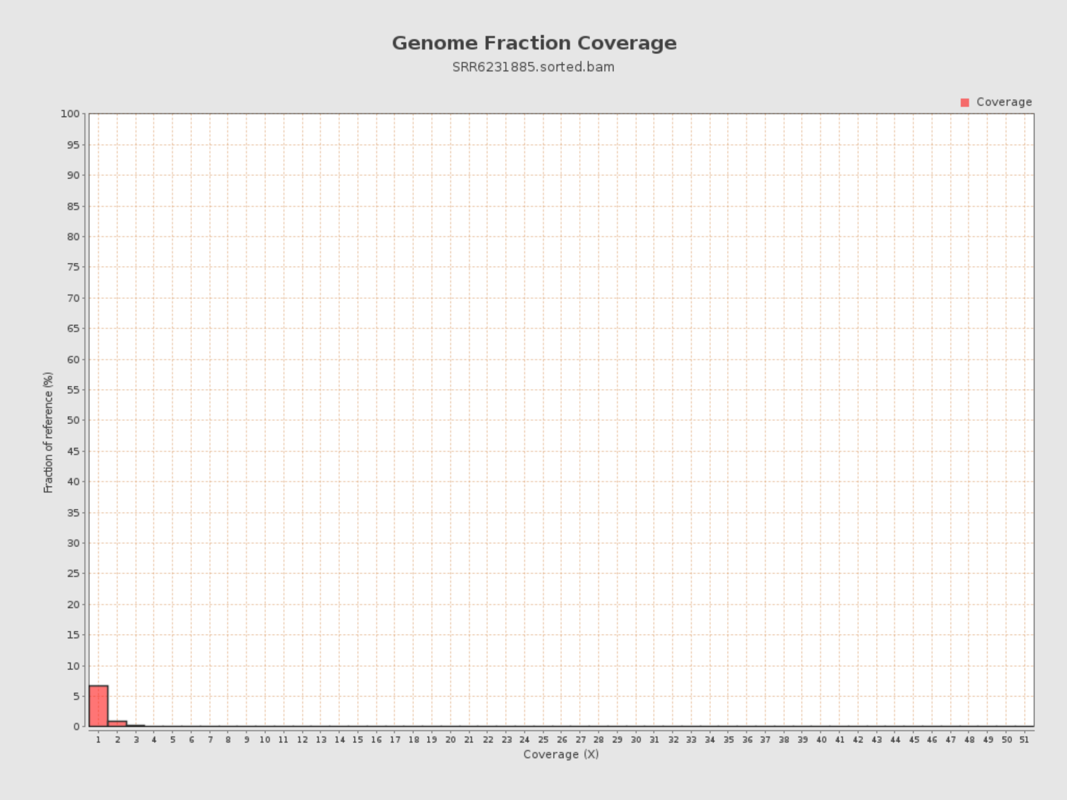
4. Results : Coverage Histogram



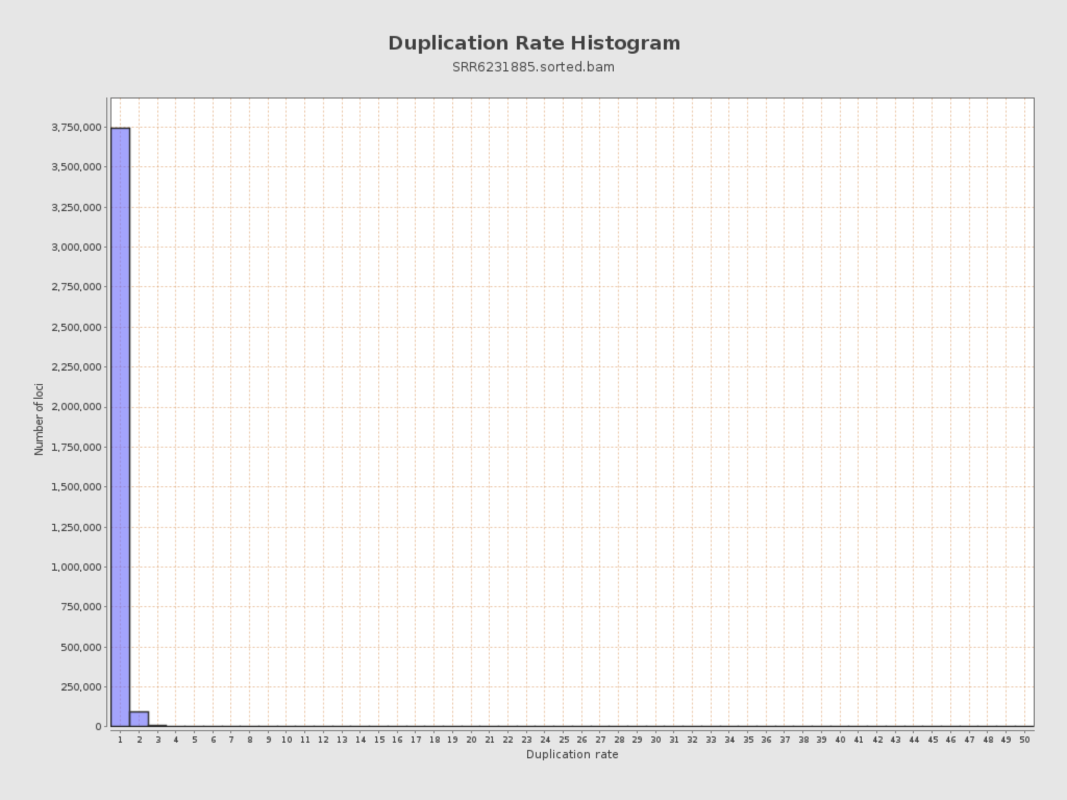
5. Results : Coverage Histogram (0-50X)



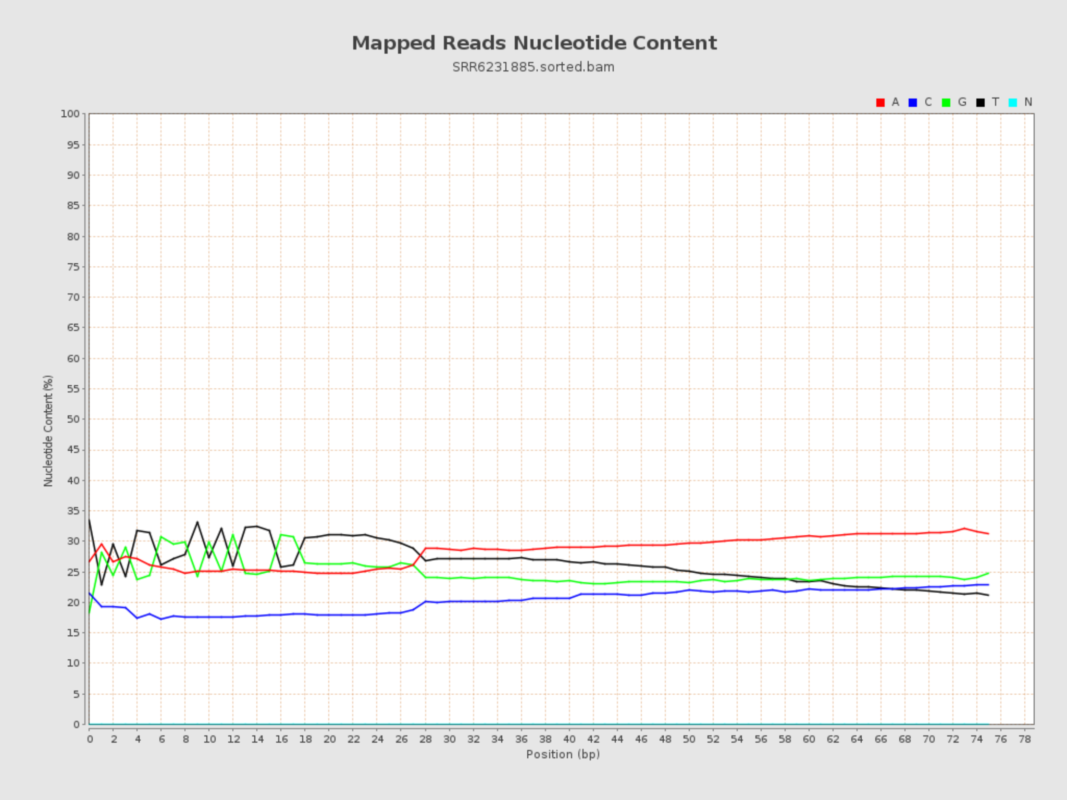
6. Results : Genome Fraction Coverage



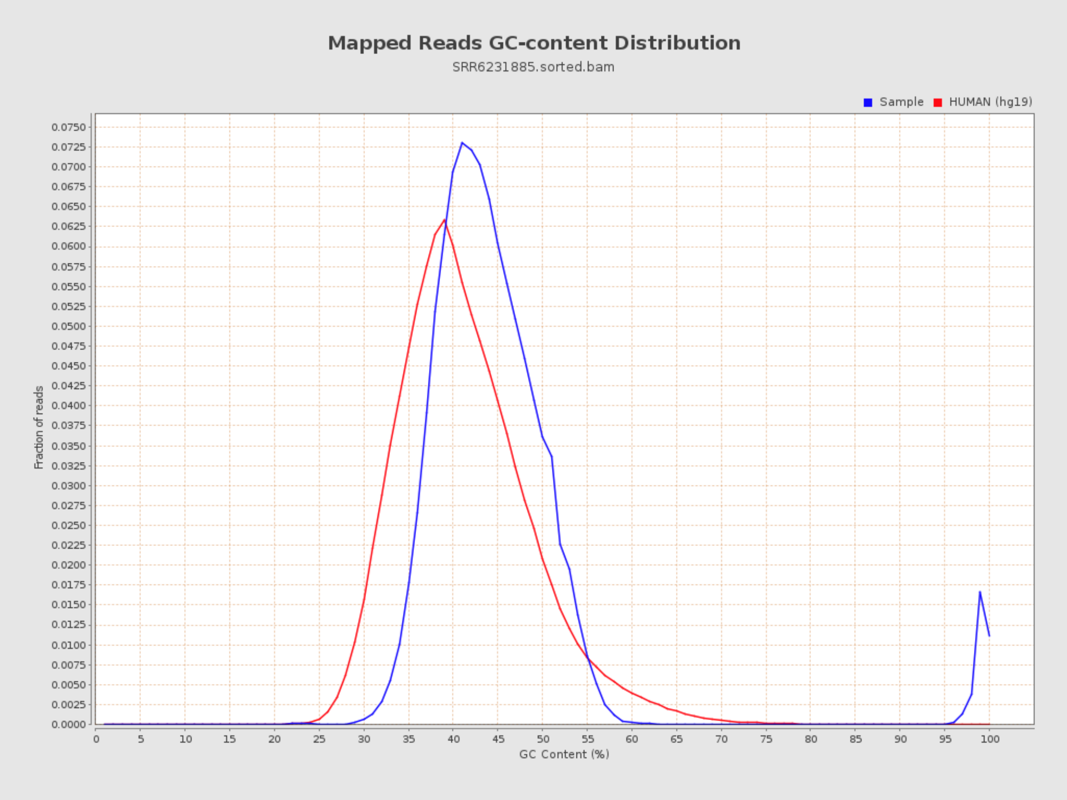
7. Results : Duplication Rate Histogram



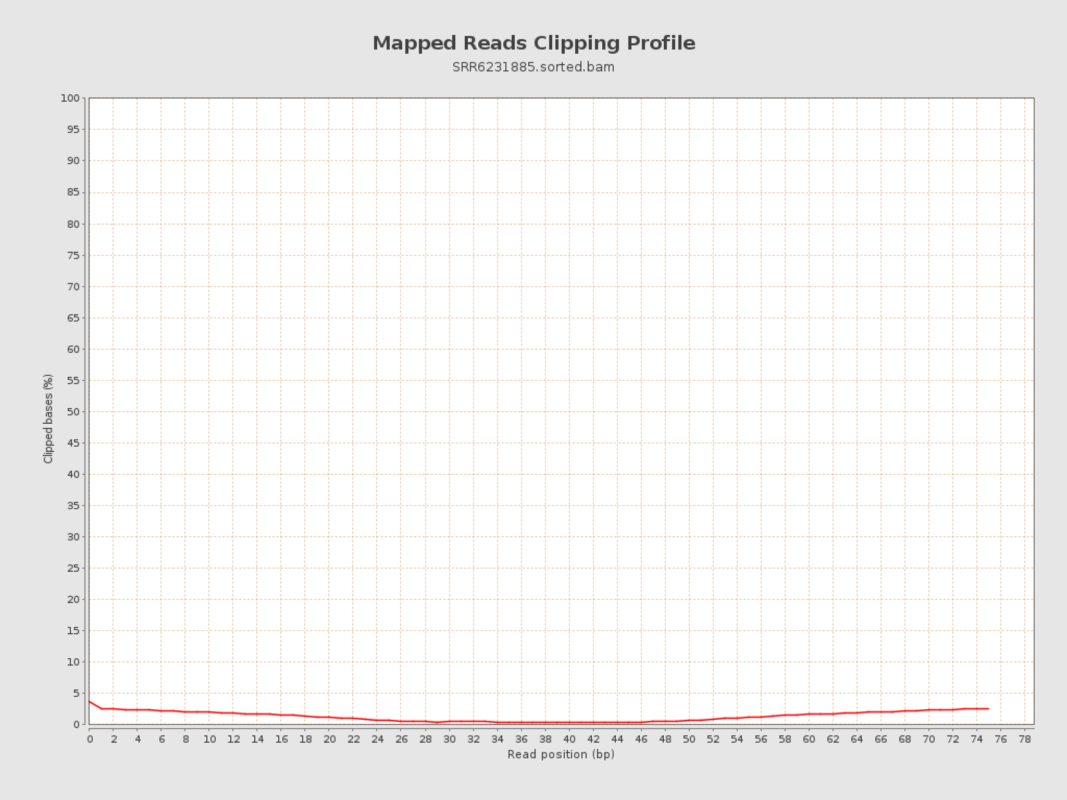
8. Results : Mapped Reads Nucleotide Content



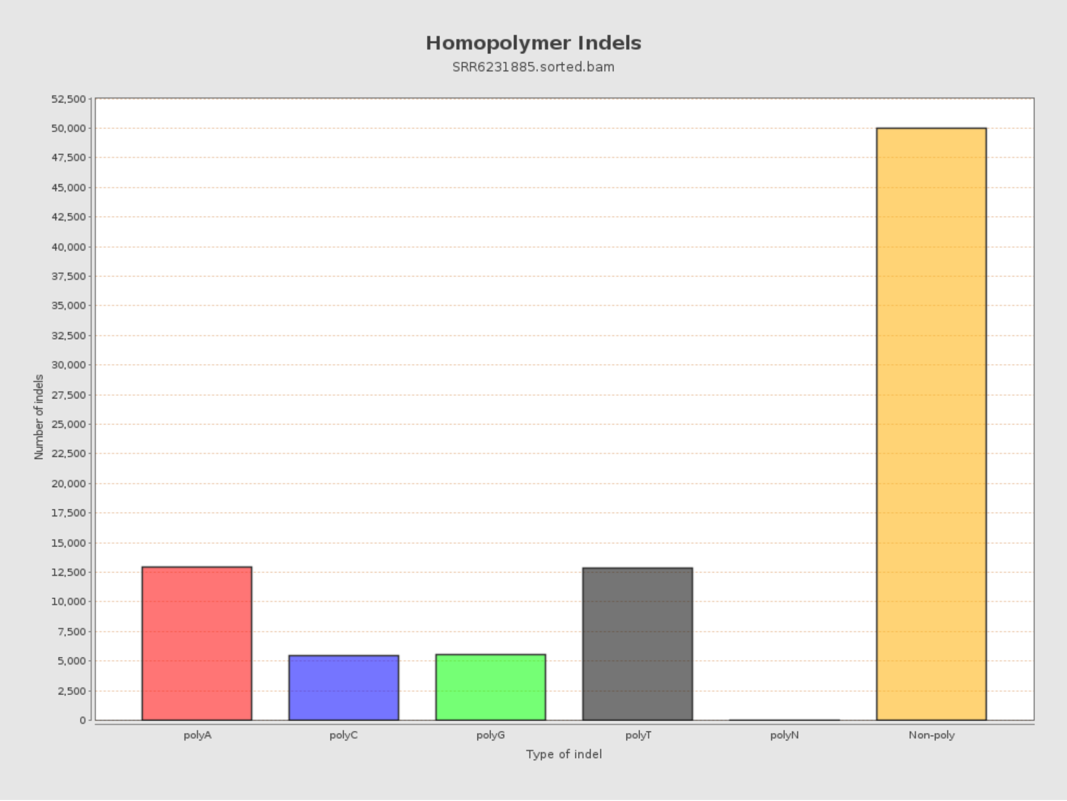
9. Results : Mapped Reads GC-content Distribution



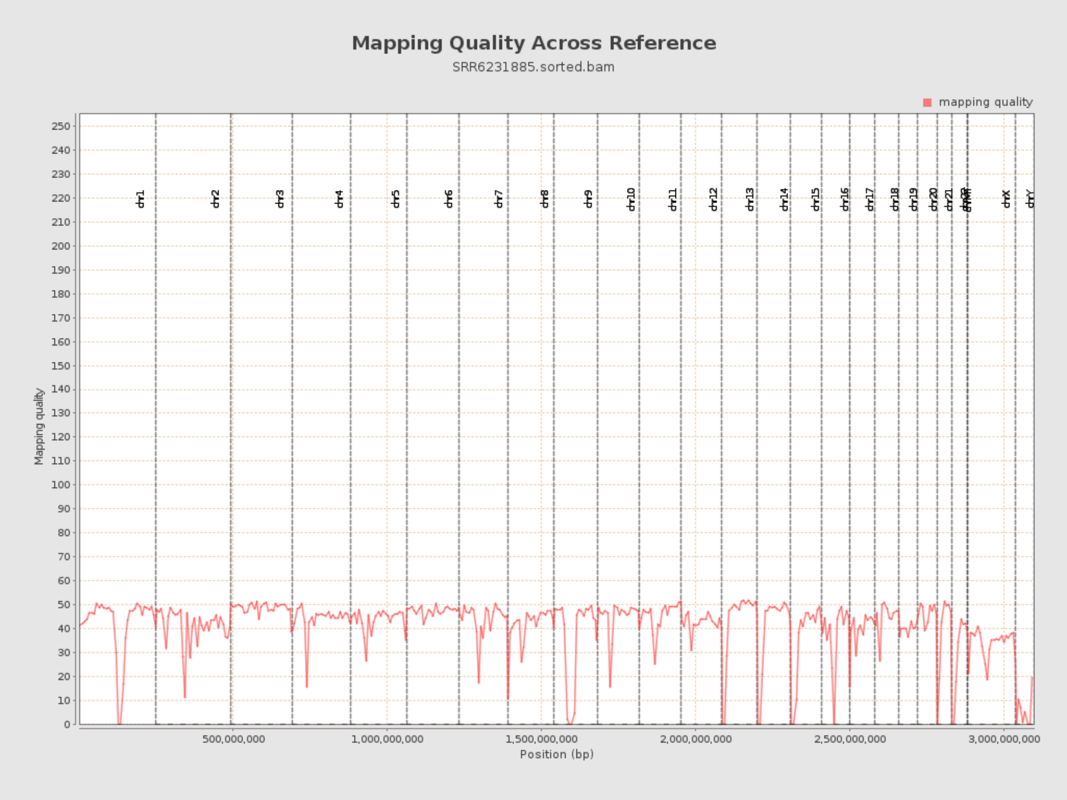
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram