Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:38:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231787.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_SRR6231787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:38:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,560,220
Mapped reads	5,875,834 / 55.64%
Unmapped reads	4,684,386 / 44.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,110 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	300,140 / 2.84%
Duplication rate	2.38%
Clipped reads	2,579,583 / 24.43%

2.2. ACGT Content

Number/percentage of A's	112,754,233 / 28.33%
Number/percentage of C's	84,123,950 / 21.13%
Number/percentage of T's	106,160,771 / 26.67%
Number/percentage of G's	94,964,182 / 23.86%
Number/percentage of N's	31,606 / 0.01%
GC Percentage	44.99%

2.3. Coverage

Mean	0.1286

Standard Deviation	11.2901

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

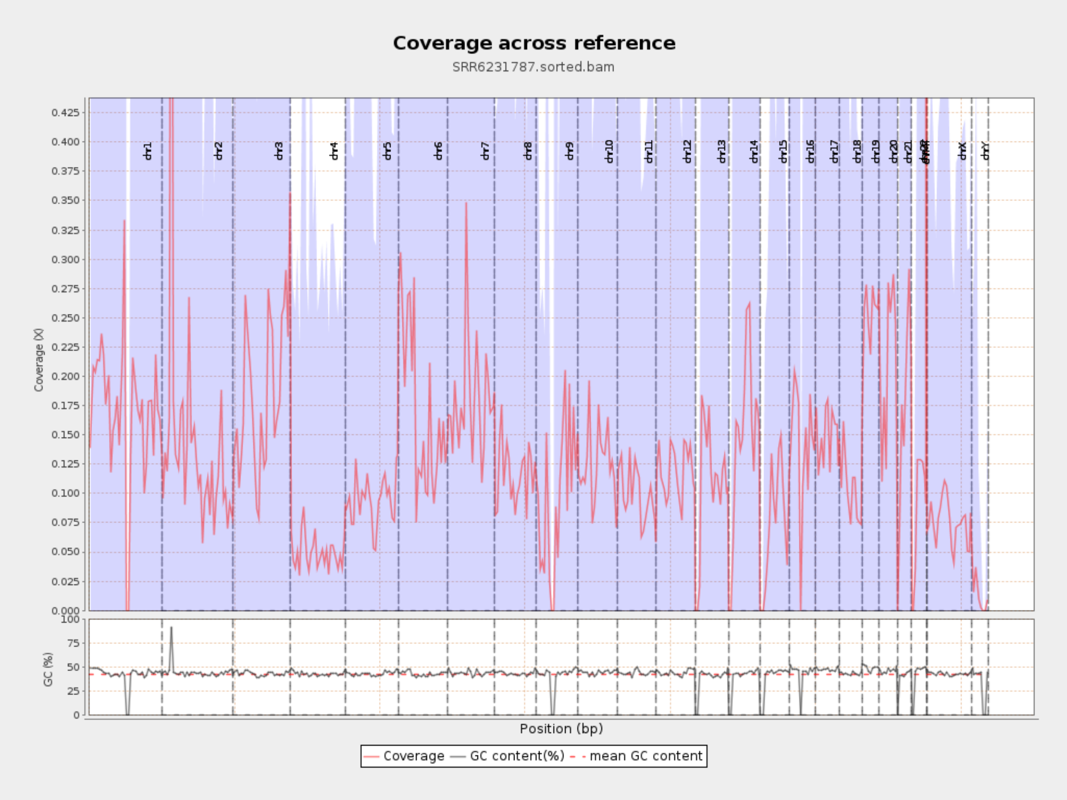
General error rate	0.62%
Mismatches	2,402,526
Insertions	31,087
Mapped reads with at least one insertion	0.52%
Deletions	89,831
Mapped reads with at least one deletion	1.51%
Homopolymer indels	43.8%

2.6. Chromosome stats

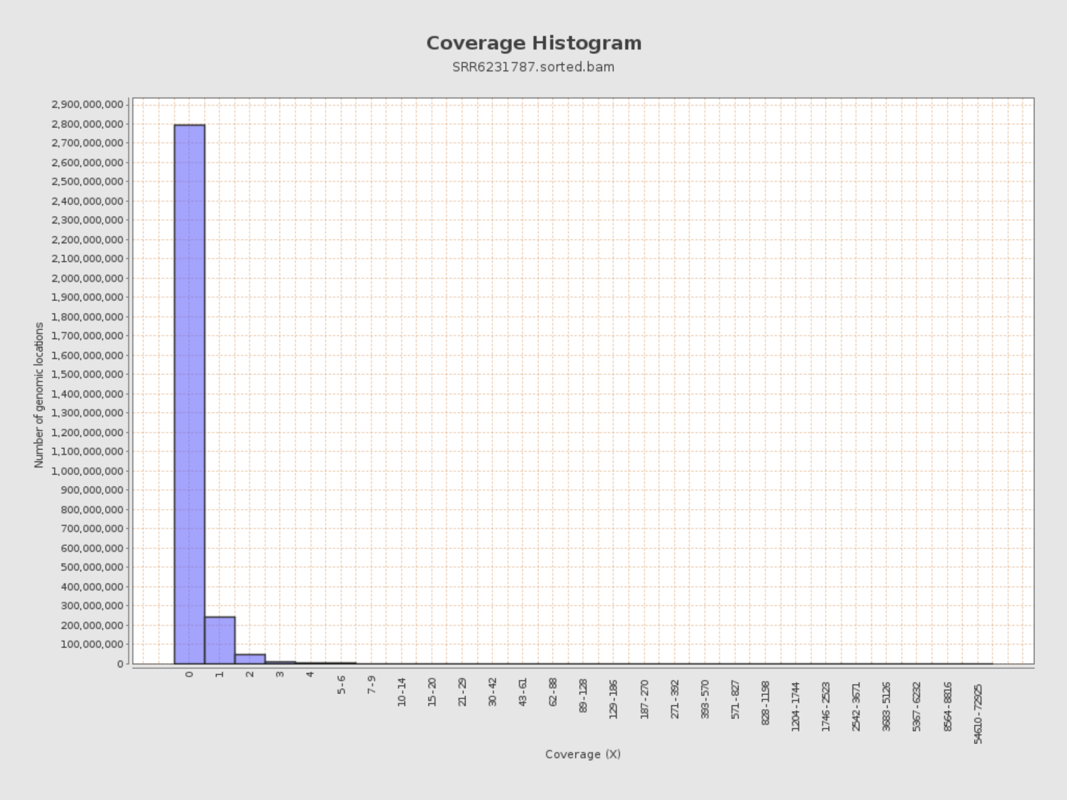
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42324550	0.1698	3.4033
chr2	243199373	36414239	0.1497	40.0243
chr3	198022430	36188574	0.1827	0.5326
chr4	191154276	9366384	0.049	0.3112
chr5	180915260	17094677	0.0945	0.3912
chr6	171115067	29494688	0.1724	0.8846
chr7	159138663	28659245	0.1801	2.2766

chr8	146364022	16972936	0.116	0.7819
chr9	141213431	13045877	0.0924	0.7034
chr10	135534747	17001172	0.1254	1.0581
chr11	135006516	13371665	0.099	0.7887
chr12	133851895	15997098	0.1195	0.4255
chr13	115169878	12399701	0.1077	0.3868
chr14	107349540	15577580	0.1451	0.5549
chr15	102531392	7626488	0.0744	0.3272
chr16	90354753	12943571	0.1433	0.5791
chr17	81195210	12231538	0.1506	0.5704
chr18	78077248	8239862	0.1055	1.7203
chr19	59128983	14962403	0.253	1.8521
chr20	63025520	13130218	0.2083	0.6042
chr21	48129895	8182359	0.17	0.5386
chr22	51304566	4331437	0.0844	0.3512
chrMT	16571	196634	11.8662	7.4
chrX	155270560	11679053	0.0752	0.4312
chrY	59373566	757022	0.0128	0.2074

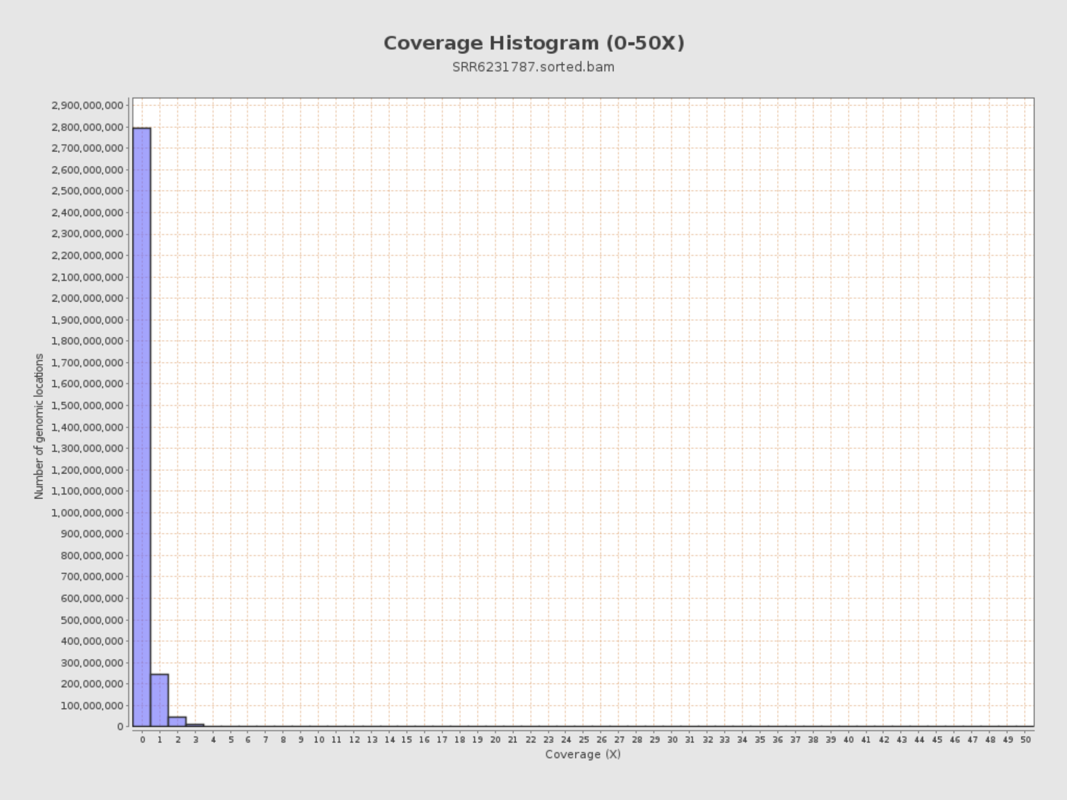
3. Results : Coverage across reference



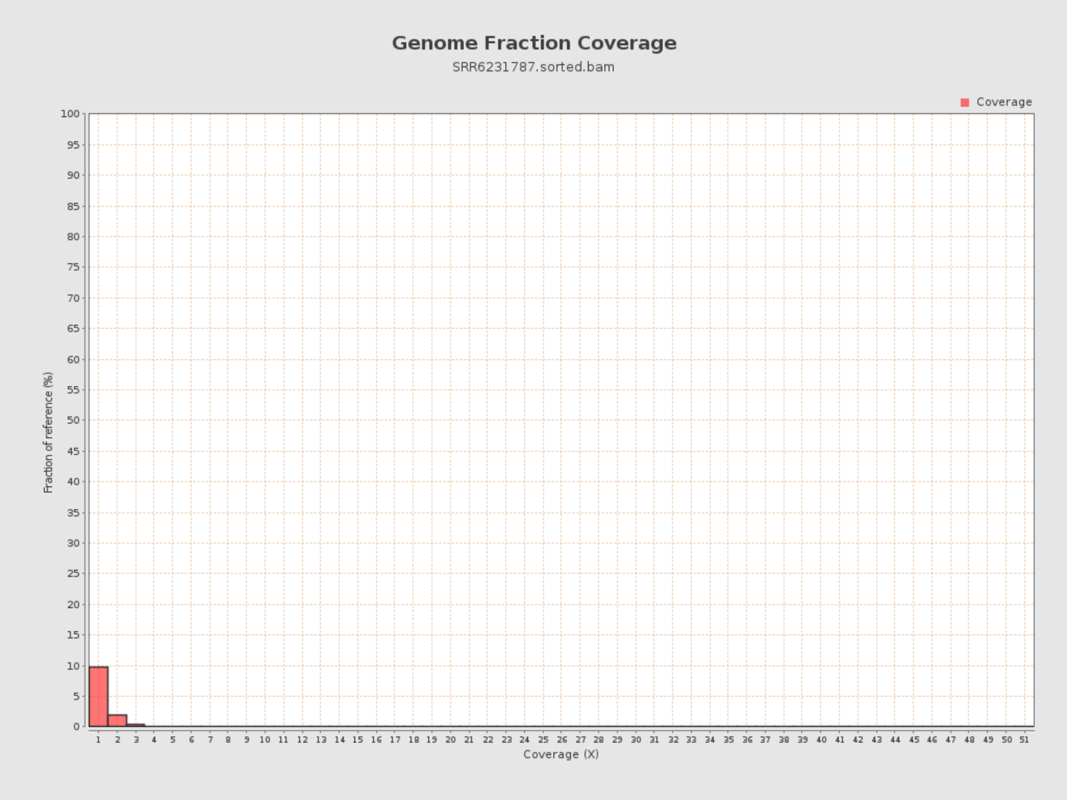
4. Results : Coverage Histogram



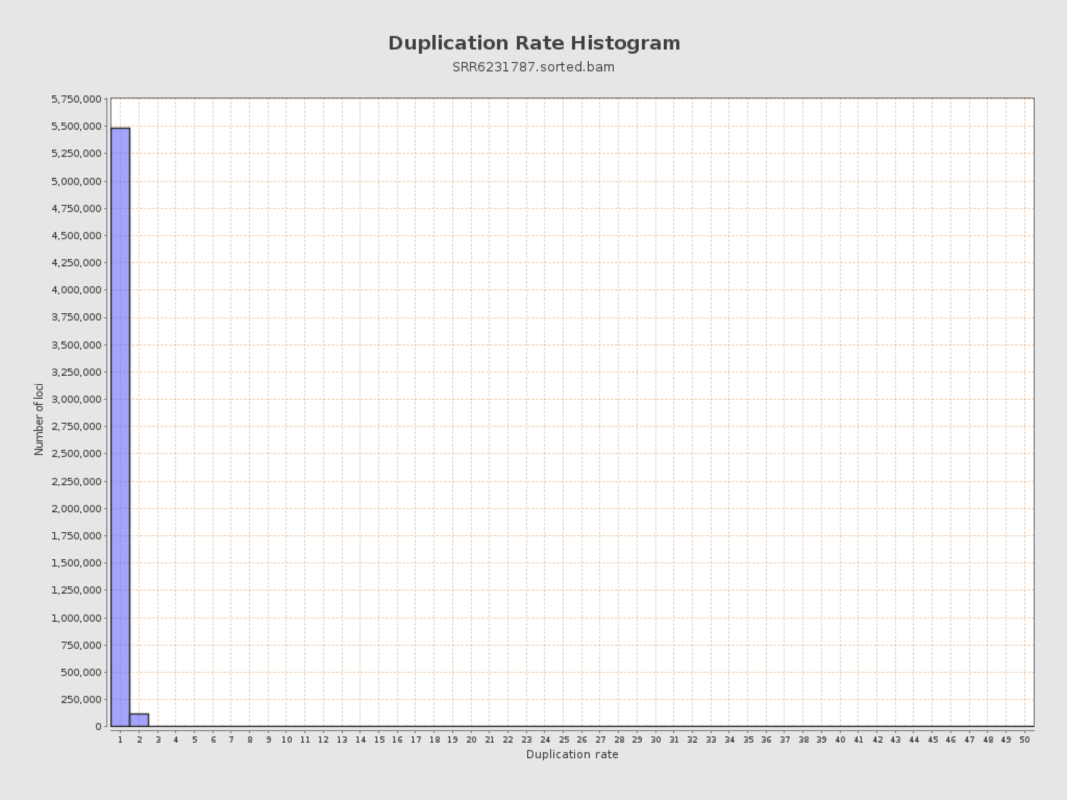
5. Results : Coverage Histogram (0-50X)



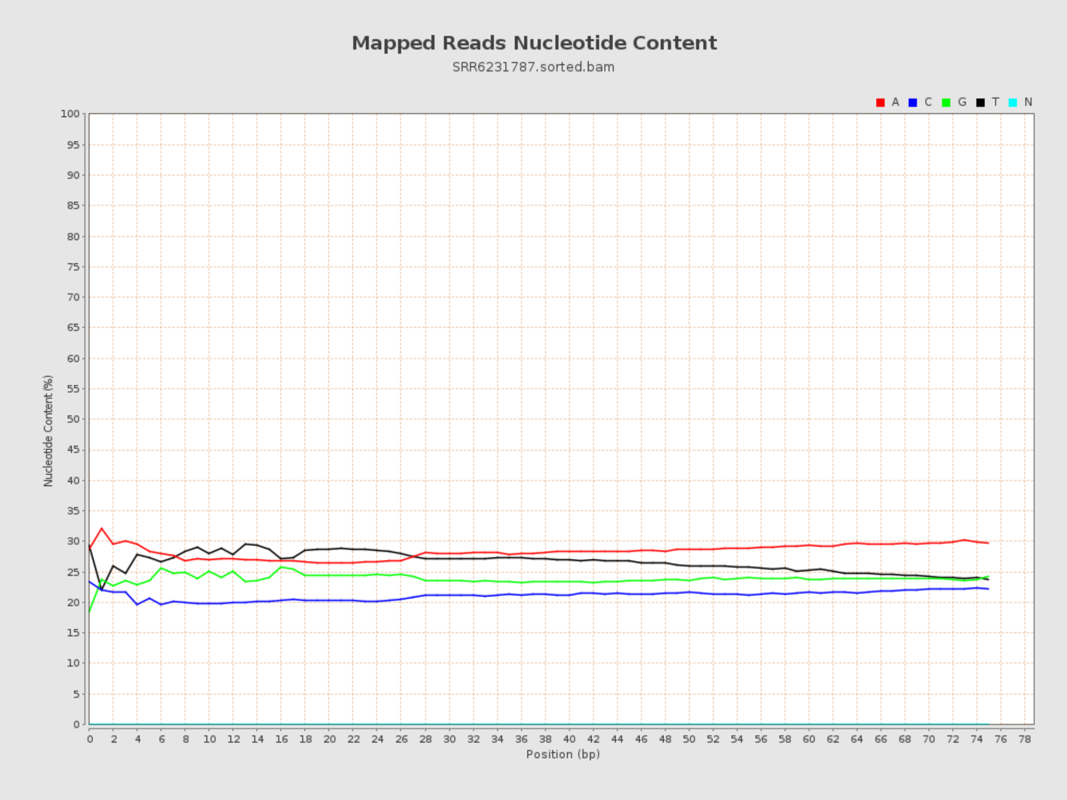
6. Results : Genome Fraction Coverage



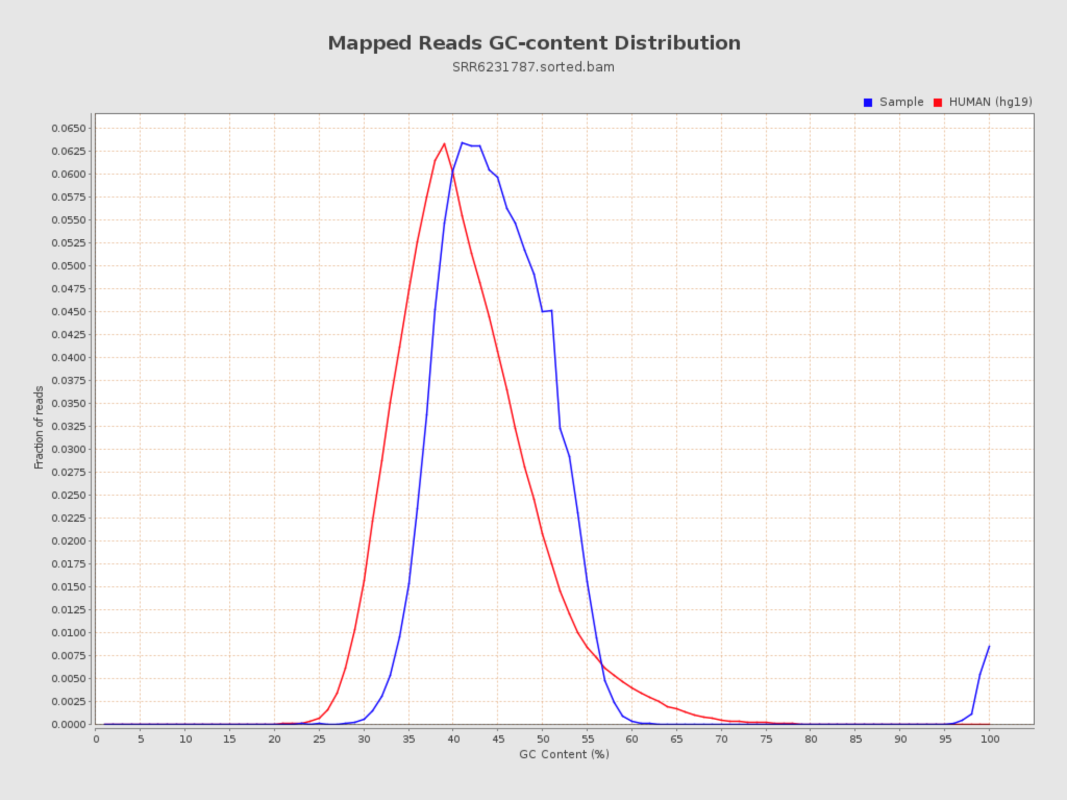
7. Results : Duplication Rate Histogram



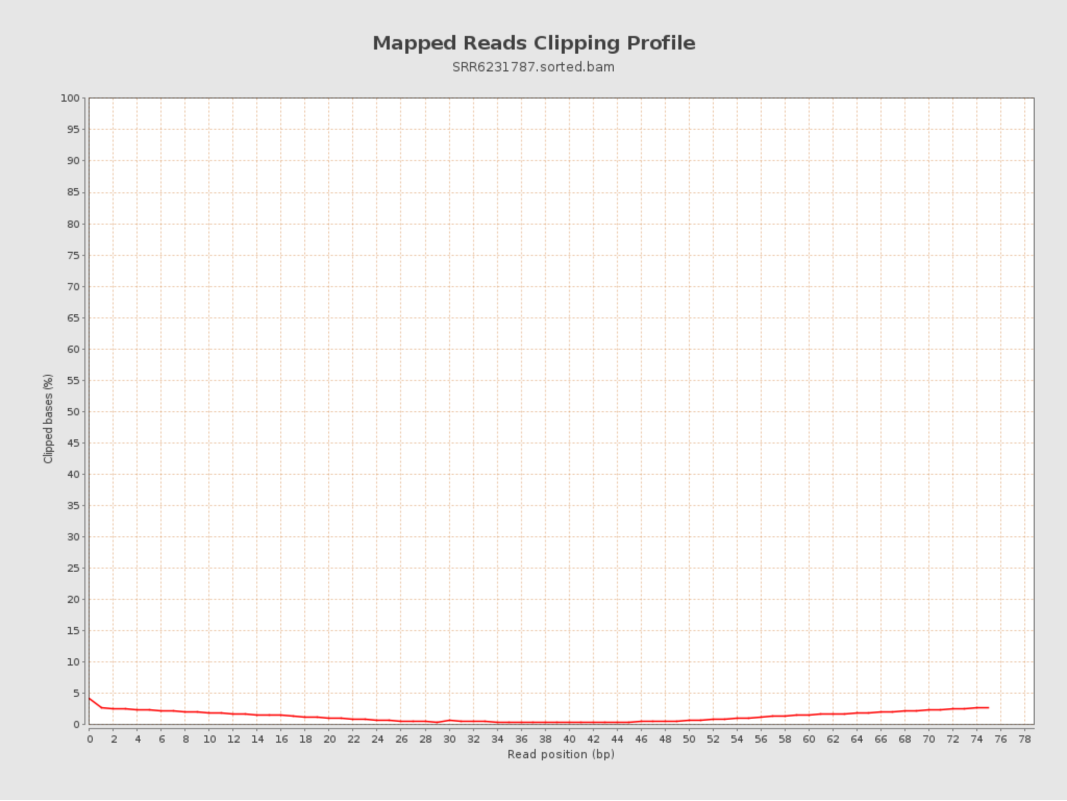
8. Results : Mapped Reads Nucleotide Content



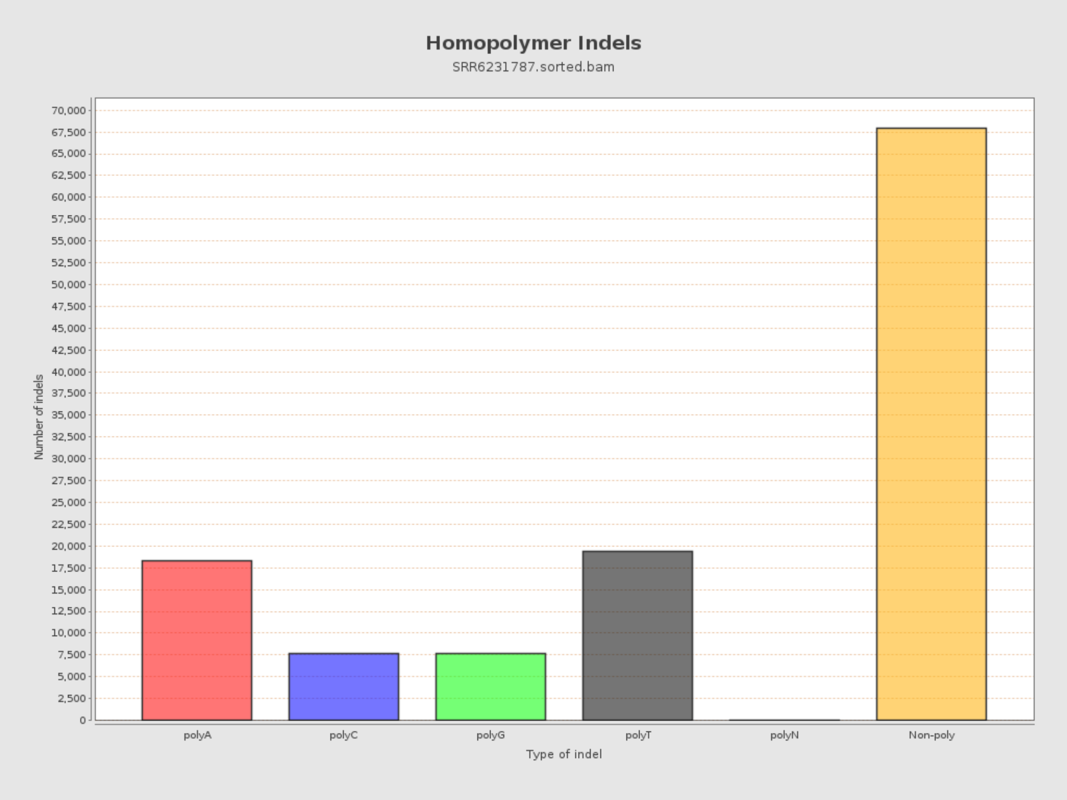
9. Results : Mapped Reads GC-content Distribution



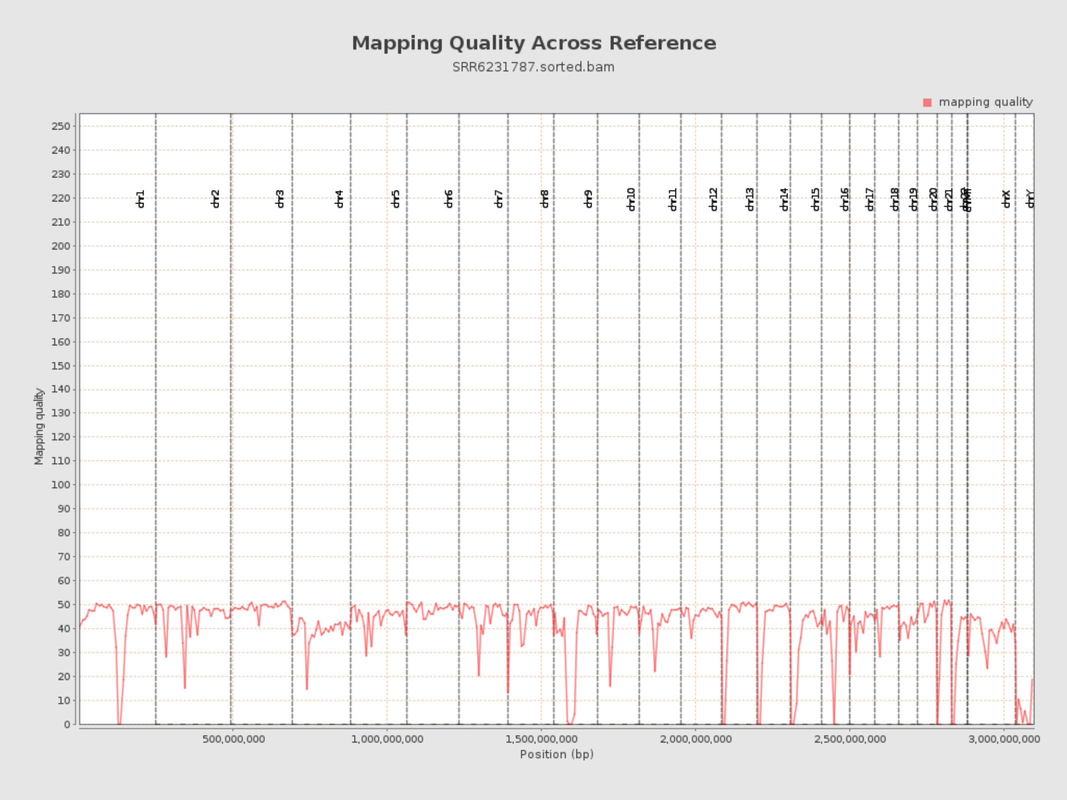
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram