Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525191.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_SRR10525191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,974,421
Mapped reads	2,703,677 / 90.9%
Unmapped reads	270,744 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,374 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	150,533 / 5.06%
Duplication rate	4.06%
Clipped reads	2,705,849 / 90.97%

2.2. ACGT Content

Number/percentage of A's	38,796,660 / 24.69%
Number/percentage of C's	28,940,675 / 18.42%
Number/percentage of T's	51,025,707 / 32.48%
Number/percentage of G's	38,353,465 / 24.41%
Number/percentage of N's	3,713 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.4696

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

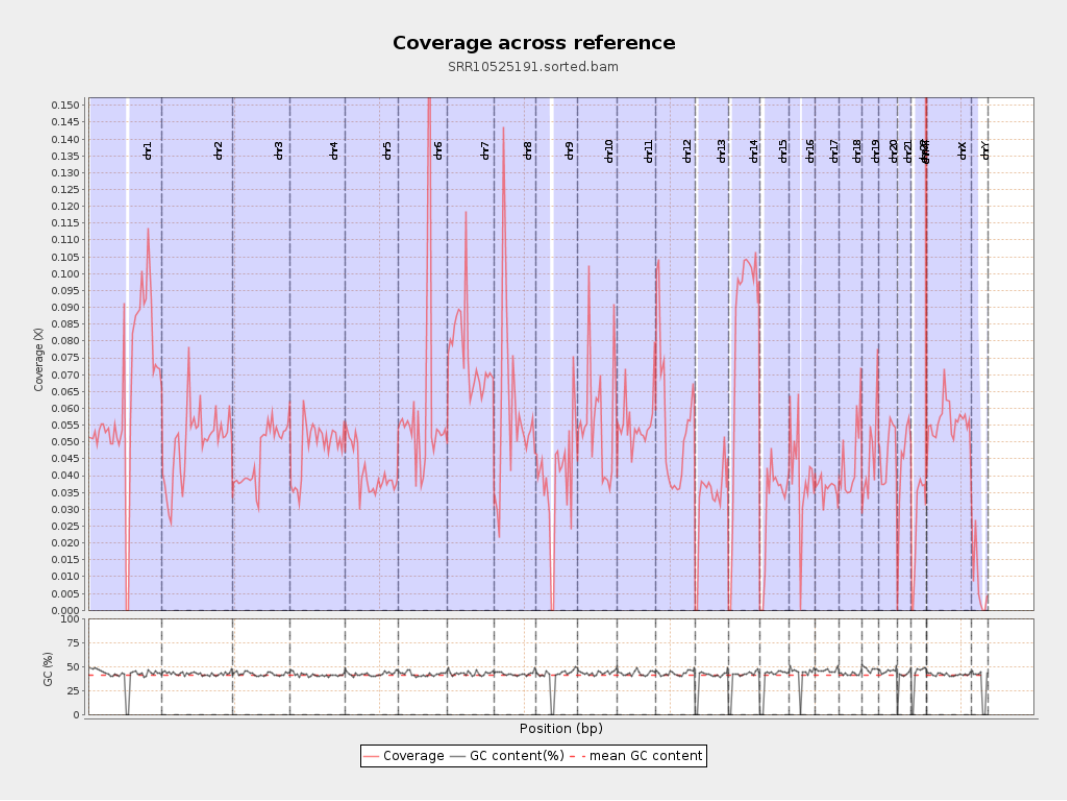
General error rate	0.53%
Mismatches	807,467
Insertions	10,675
Mapped reads with at least one insertion	0.39%
Deletions	33,396
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.11%

2.6. Chromosome stats

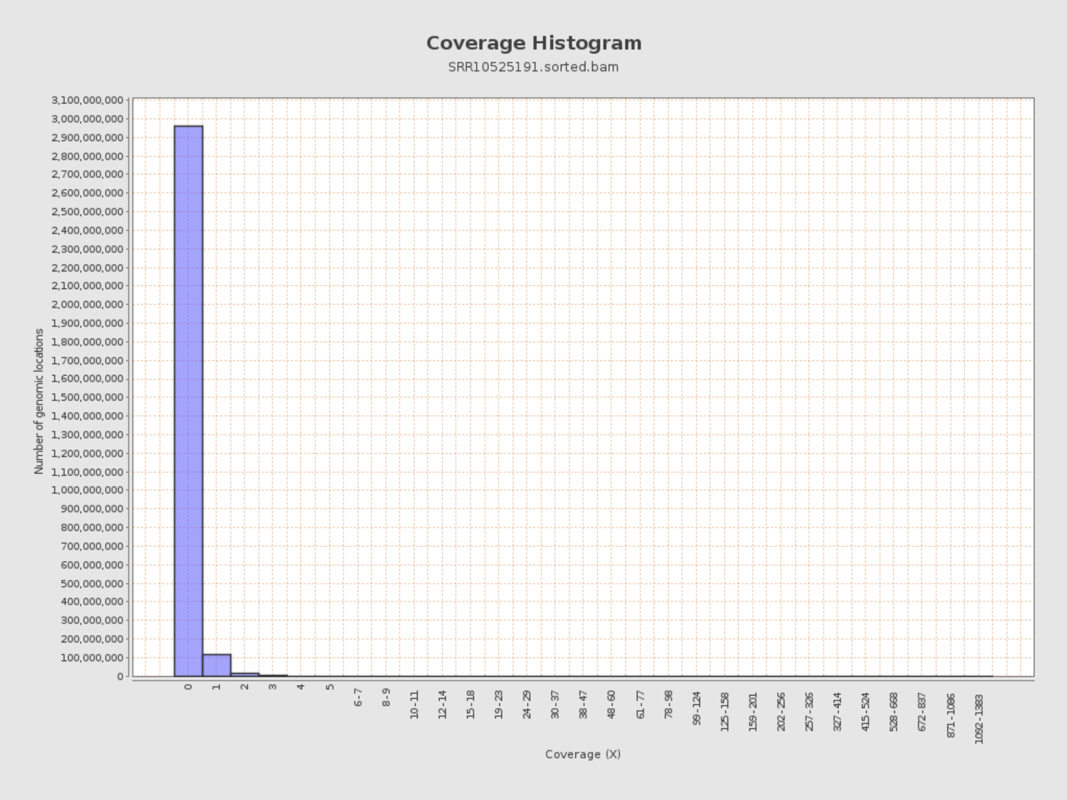
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16019431	0.0643	0.8658
chr2	243199373	12084831	0.0497	0.6222
chr3	198022430	9079433	0.0459	0.2518
chr4	191154276	9230666	0.0483	0.2785
chr5	180915260	7411563	0.041	0.2327
chr6	171115067	10377968	0.0606	0.3337
chr7	159138663	12070428	0.0758	0.861

chr8	146364022	8486308	0.058	0.4442
chr9	141213431	5477402	0.0388	0.3072
chr10	135534747	7657895	0.0565	0.473
chr11	135006516	7514111	0.0557	0.3717
chr12	133851895	7381894	0.0551	0.274
chr13	115169878	3815684	0.0331	0.2155
chr14	107349540	8749515	0.0815	0.3352
chr15	102531392	3171180	0.0309	0.2082
chr16	90354753	3568236	0.0395	0.2635
chr17	81195210	2928444	0.0361	0.2323
chr18	78077248	3456904	0.0443	0.6108
chr19	59128983	2732301	0.0462	0.5994
chr20	63025520	2942919	0.0467	0.2542
chr21	48129895	2076107	0.0431	0.2667
chr22	51304566	1328201	0.0259	0.1843
chrMT	16571	447991	27.0346	14.9015
chrX	155270560	8698576	0.056	0.308
chrY	59373566	465902	0.0078	0.2271

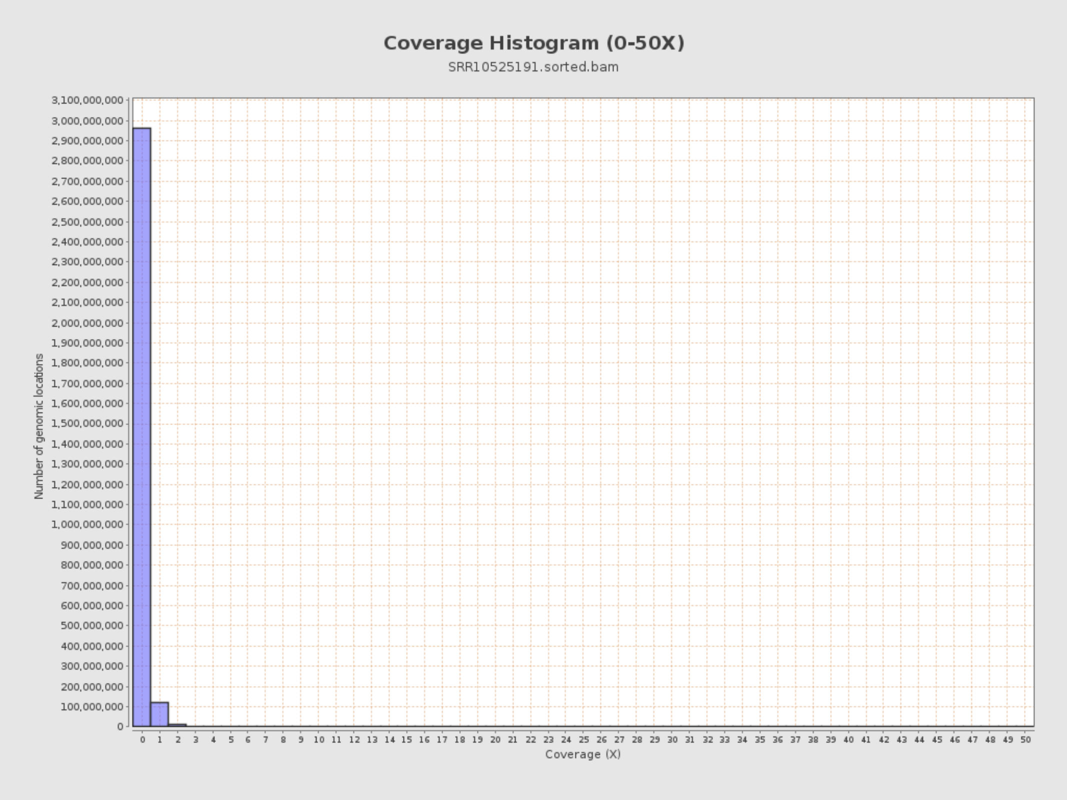
3. Results : Coverage across reference



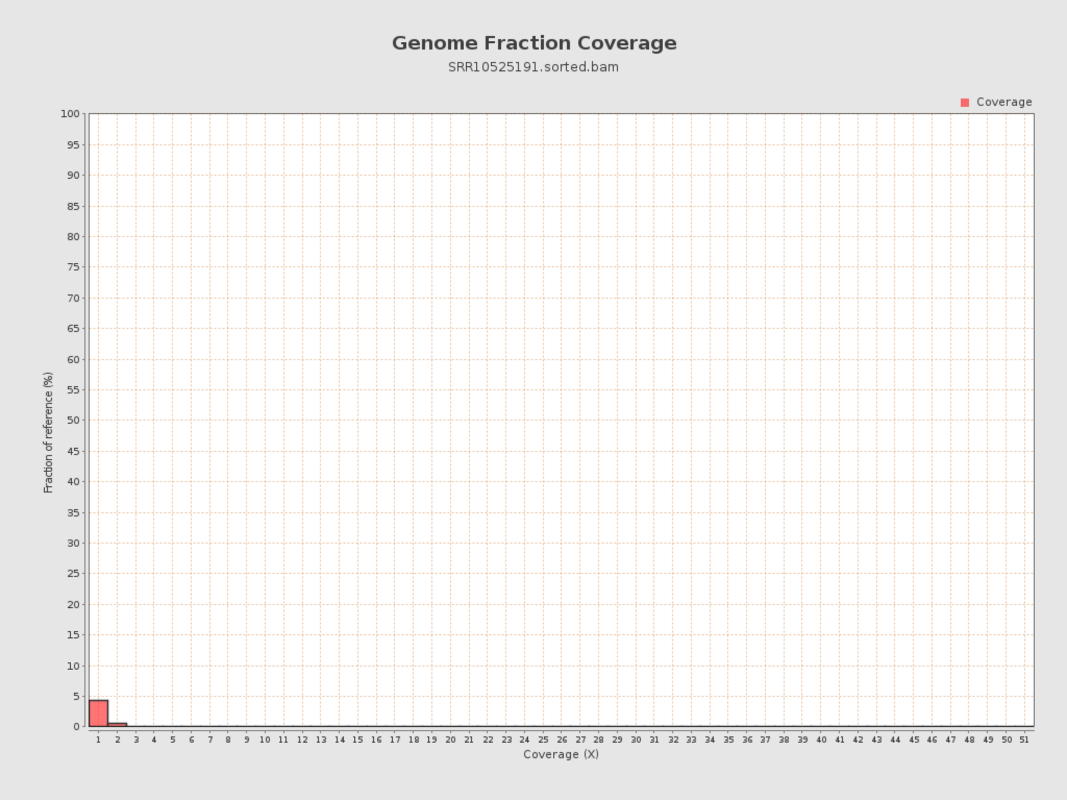
4. Results : Coverage Histogram



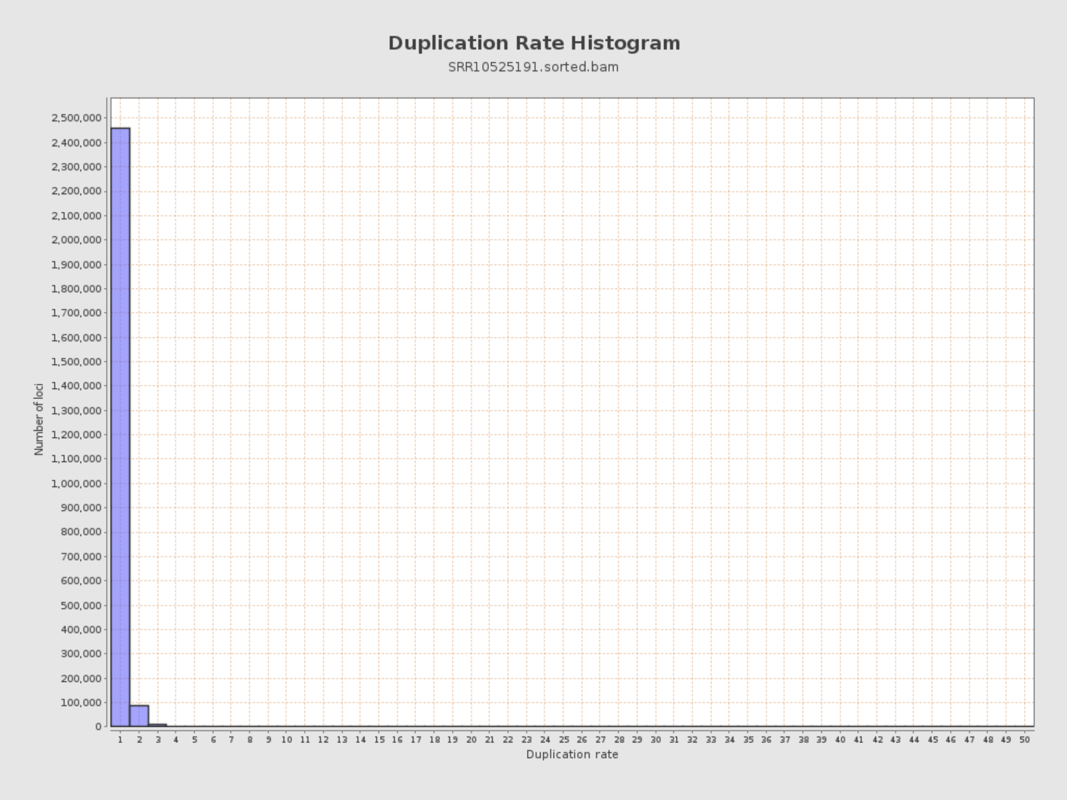
5. Results : Coverage Histogram (0-50X)



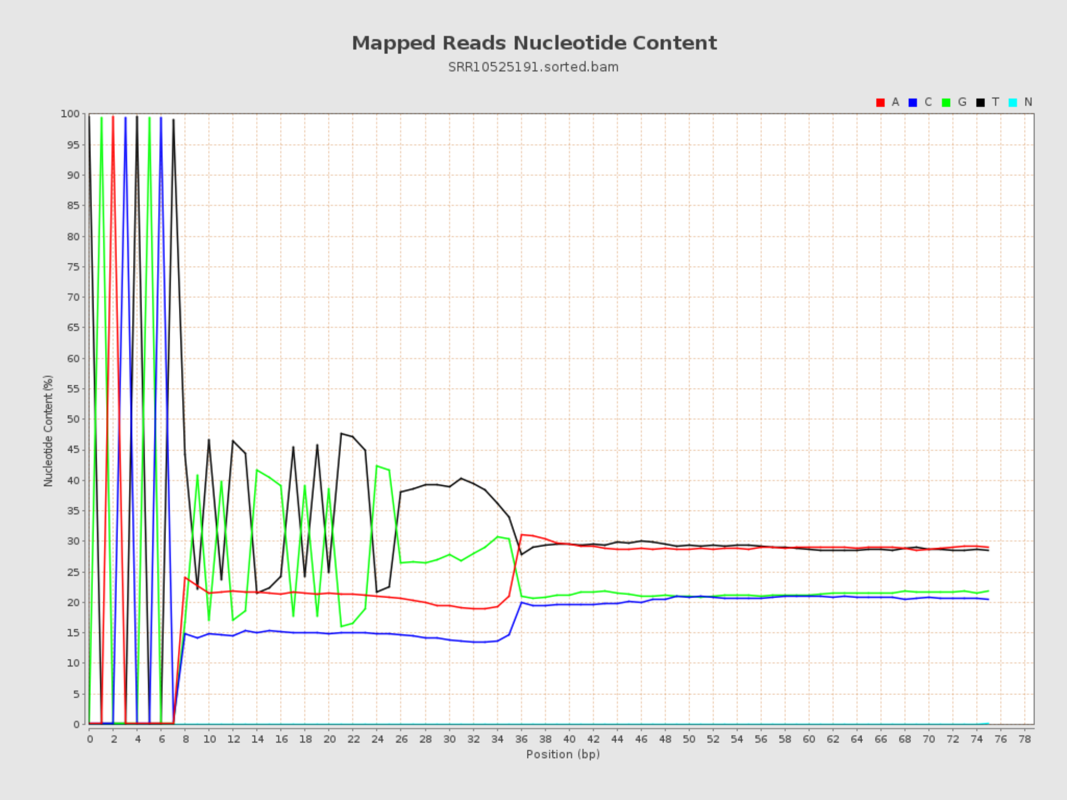
6. Results : Genome Fraction Coverage



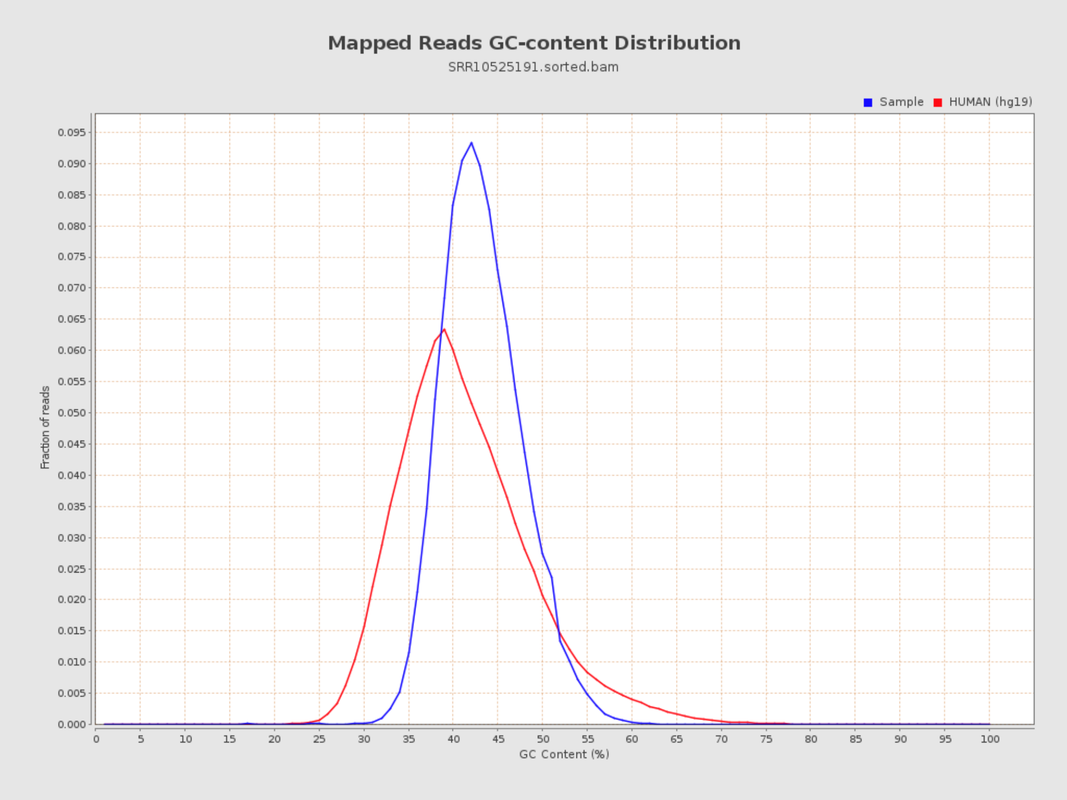
7. Results : Duplication Rate Histogram



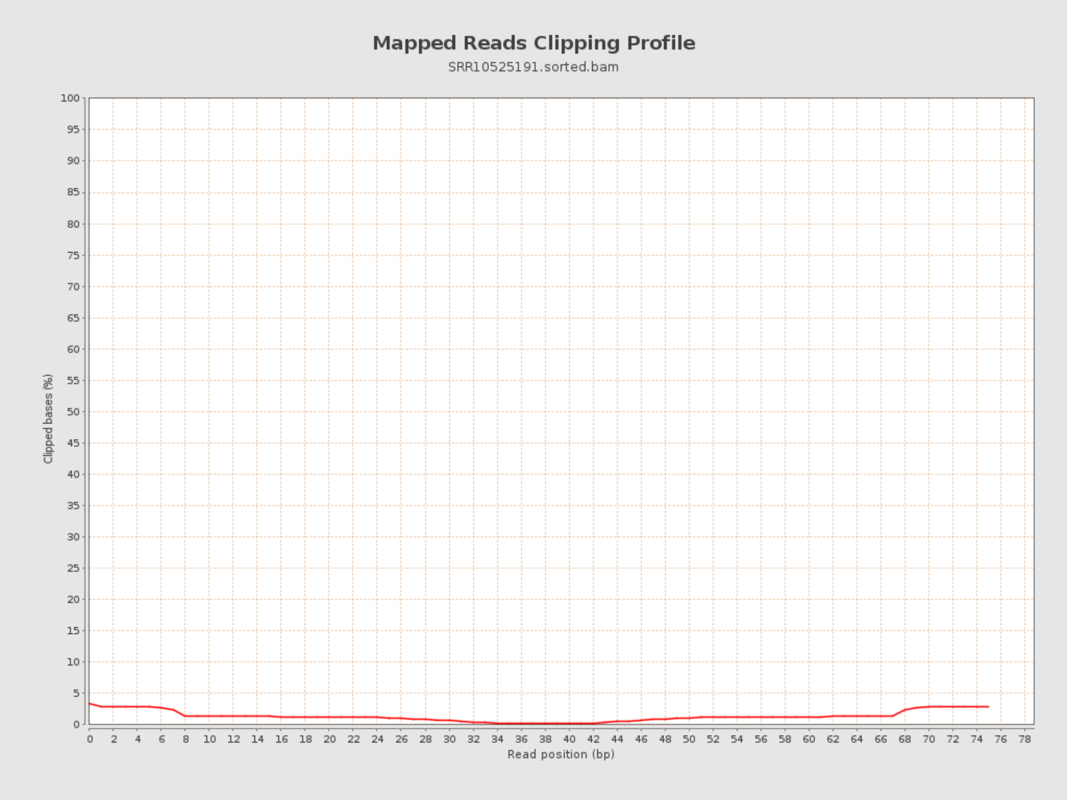
8. Results : Mapped Reads Nucleotide Content



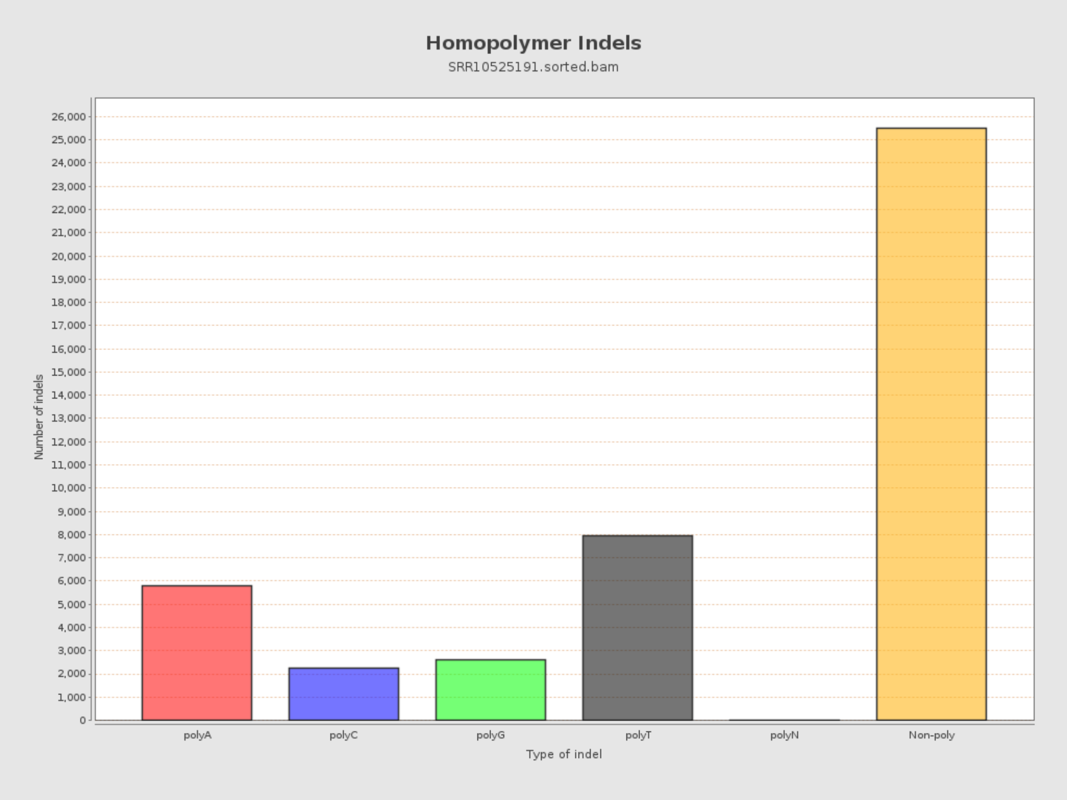
9. Results : Mapped Reads GC-content Distribution



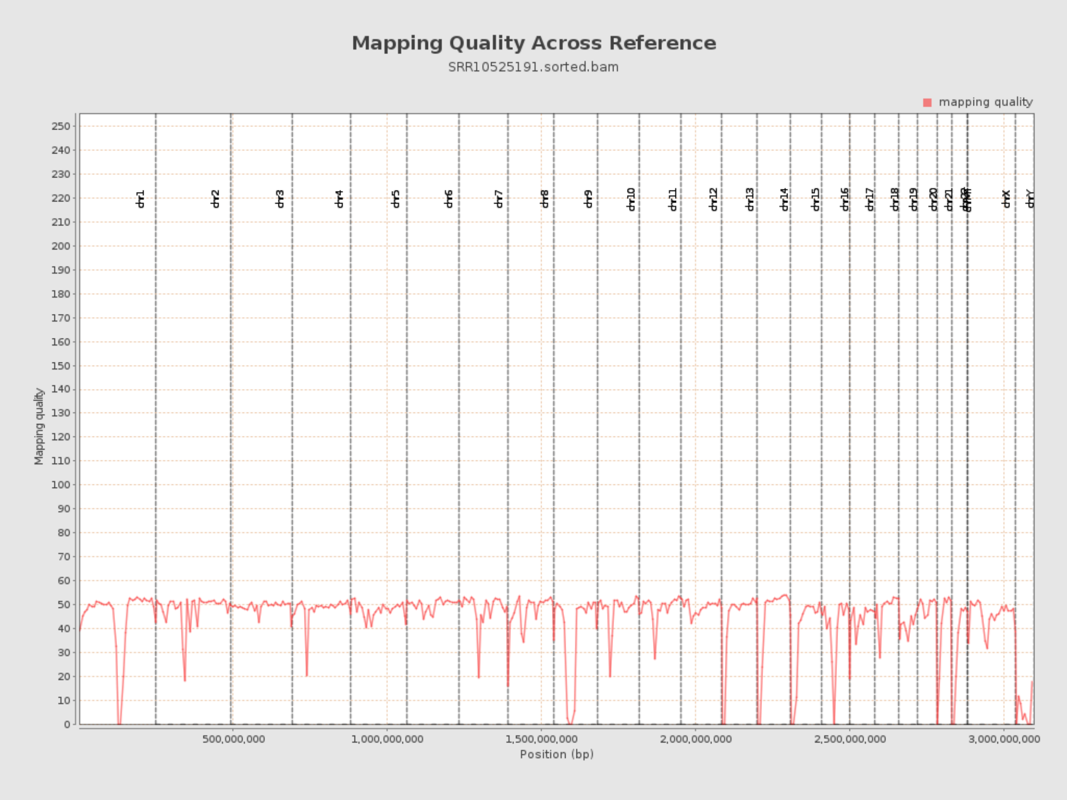
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram