Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:50:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525004.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_SRR10525004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525004.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:50:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,528,639
Mapped reads	1,378,057 / 90.15%
Unmapped reads	150,582 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,010 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	36,117 / 2.36%
Duplication rate	1.78%
Clipped reads	1,378,967 / 90.21%

2.2. ACGT Content

Number/percentage of A's	19,626,767 / 24.99%
Number/percentage of C's	14,537,760 / 18.51%
Number/percentage of T's	25,288,940 / 32.2%
Number/percentage of G's	19,086,863 / 24.3%
Number/percentage of N's	875 / 0%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2401

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

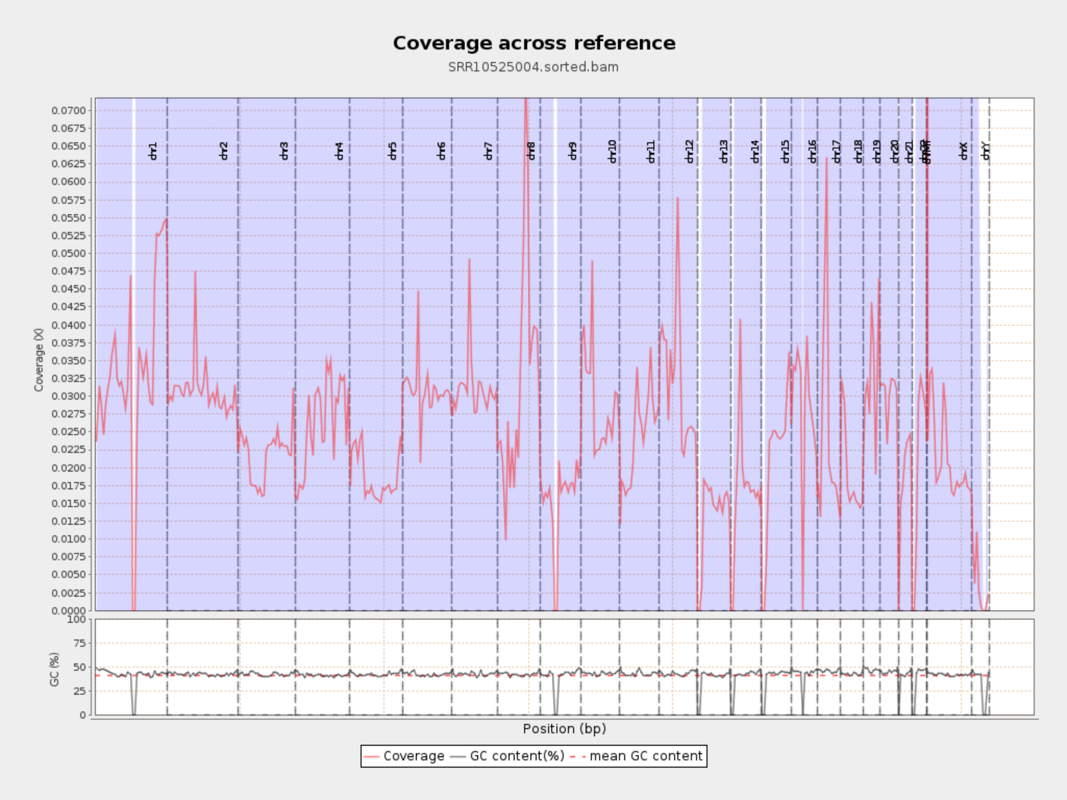
General error rate	0.51%
Mismatches	393,398
Insertions	5,289
Mapped reads with at least one insertion	0.38%
Deletions	14,988
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.7%

2.6. Chromosome stats

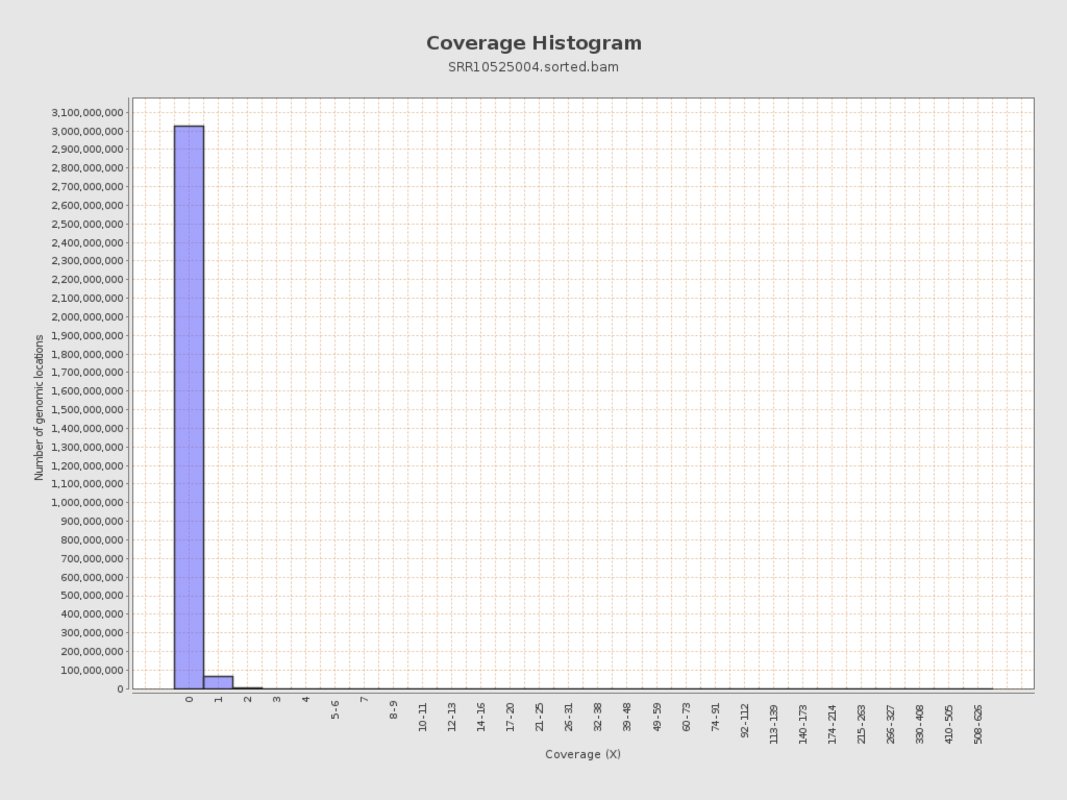
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8415441	0.0338	0.4493
chr2	243199373	7479662	0.0308	0.2728
chr3	198022430	4339013	0.0219	0.1593
chr4	191154276	5058776	0.0265	0.1818
chr5	180915260	3420940	0.0189	0.1494
chr6	171115067	5265788	0.0308	0.2497
chr7	159138663	4981116	0.0313	0.3353

chr8	146364022	4788303	0.0327	0.2305
chr9	141213431	2174399	0.0154	0.1737
chr10	135534747	3983822	0.0294	0.2412
chr11	135006516	3329268	0.0247	0.2193
chr12	133851895	4311140	0.0322	0.1923
chr13	115169878	1522390	0.0132	0.1234
chr14	107349540	1798752	0.0168	0.1418
chr15	102531392	2189750	0.0214	0.1671
chr16	90354753	2543562	0.0282	0.1874
chr17	81195210	2084003	0.0257	0.224
chr18	78077248	1507040	0.0193	0.2652
chr19	59128983	1952034	0.033	0.2903
chr20	63025520	1889191	0.03	0.1854
chr21	48129895	902023	0.0187	0.1503
chr22	51304566	1058326	0.0206	0.1519
chrMT	16571	19248	1.1615	1.1866
chrX	155270560	3346534	0.0216	0.1829
chrY	59373566	205395	0.0035	0.0845

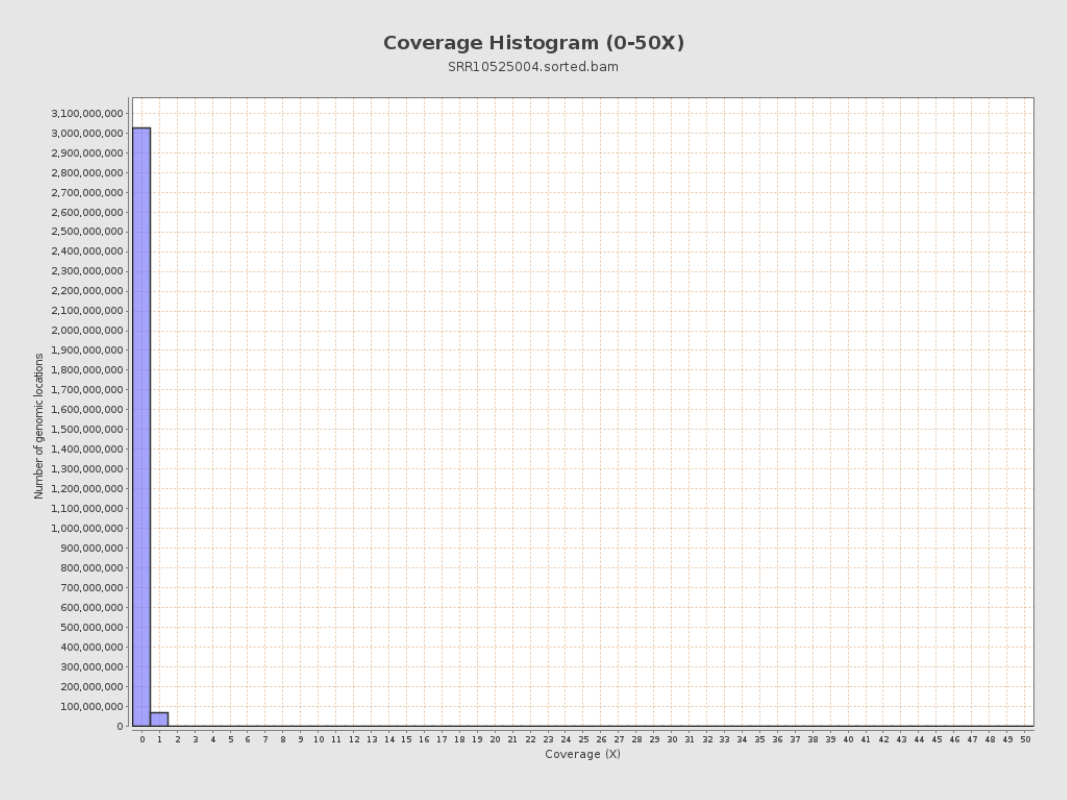
3. Results : Coverage across reference



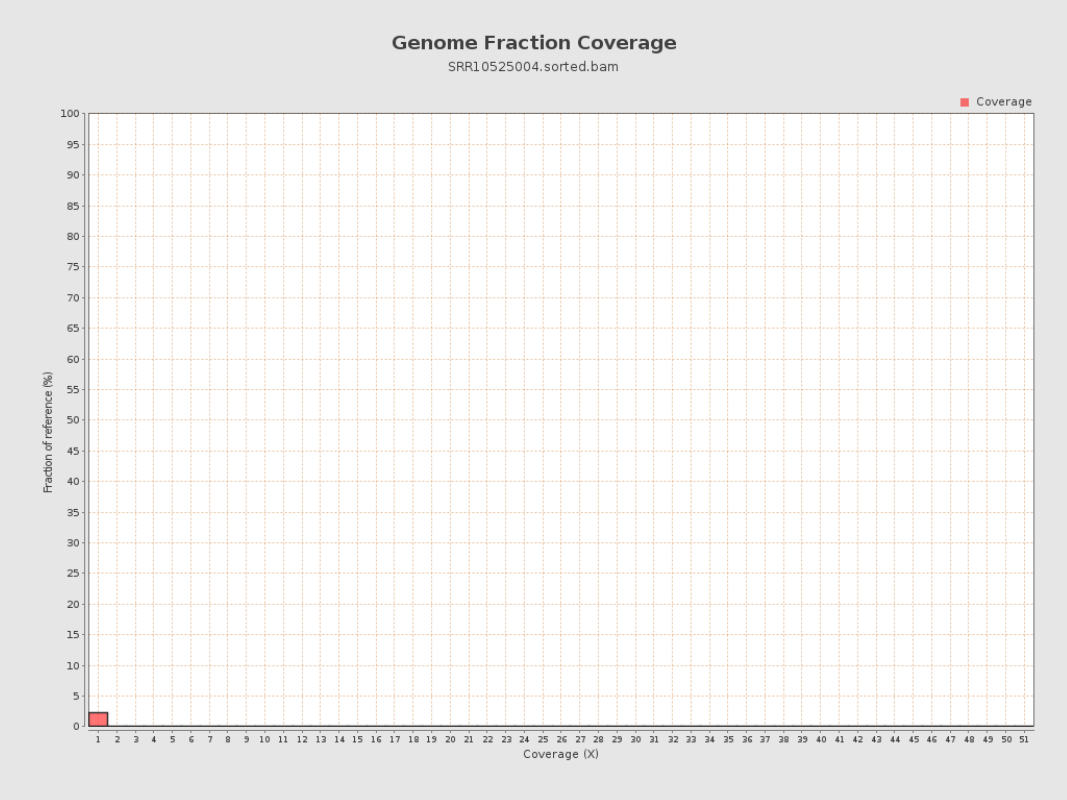
4. Results : Coverage Histogram



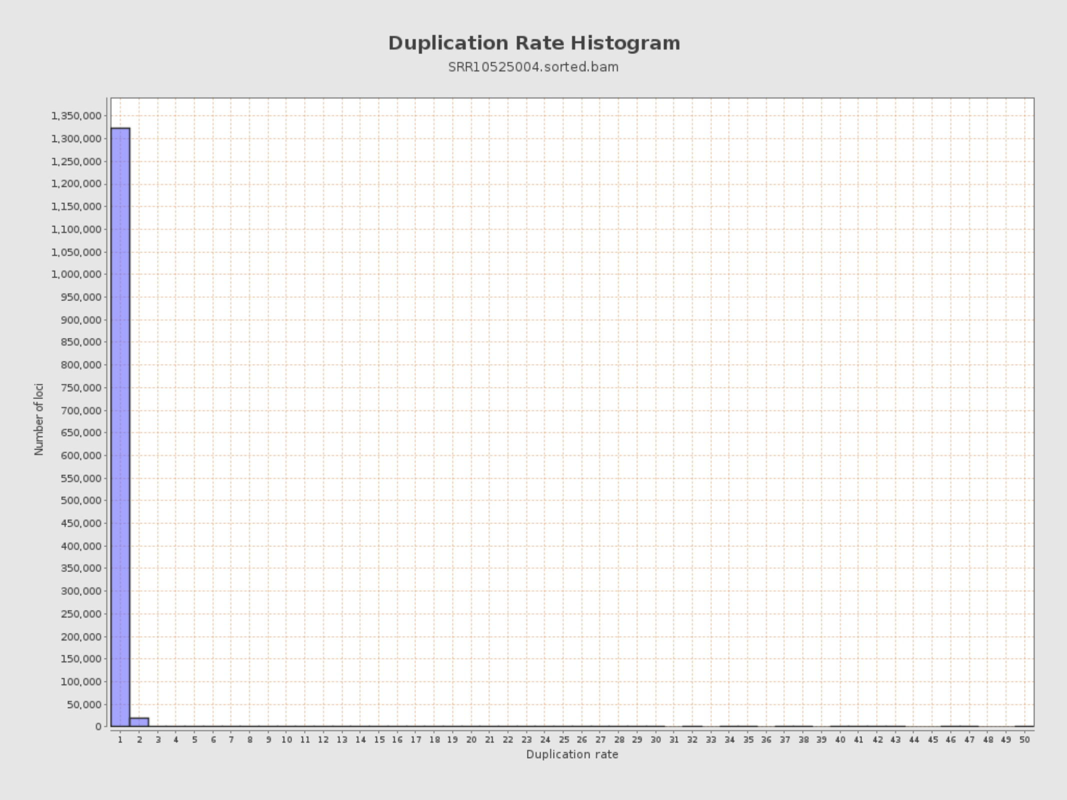
5. Results : Coverage Histogram (0-50X)



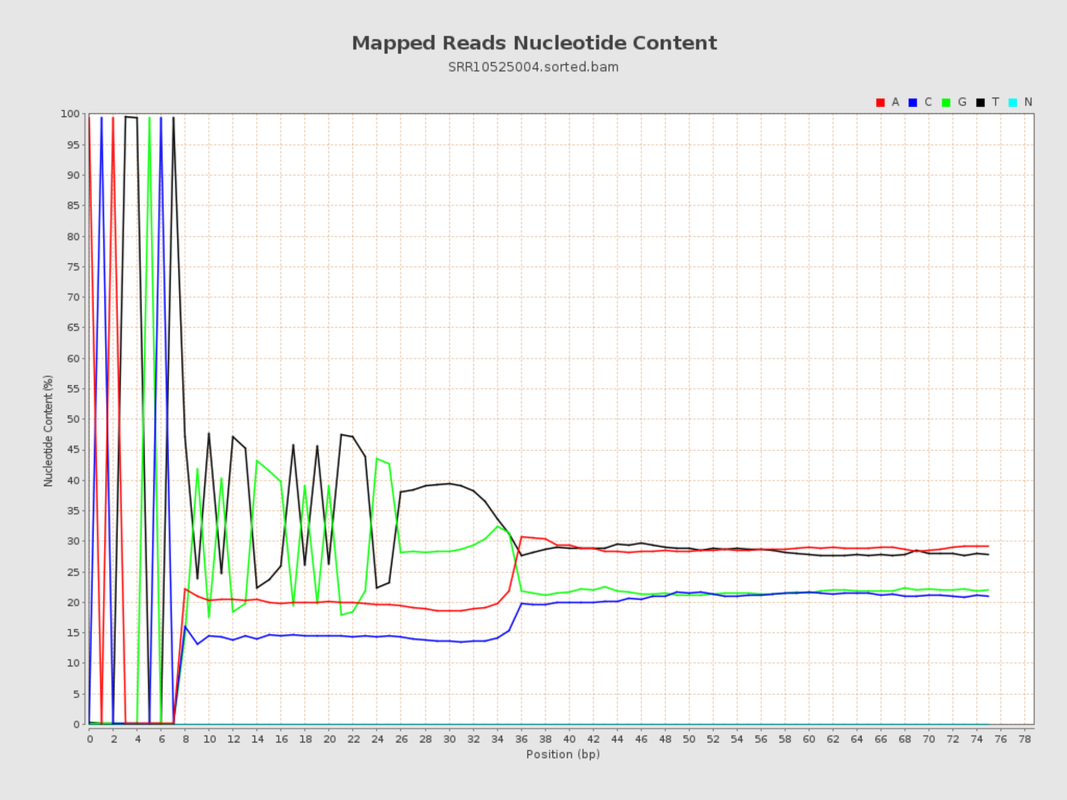
6. Results : Genome Fraction Coverage



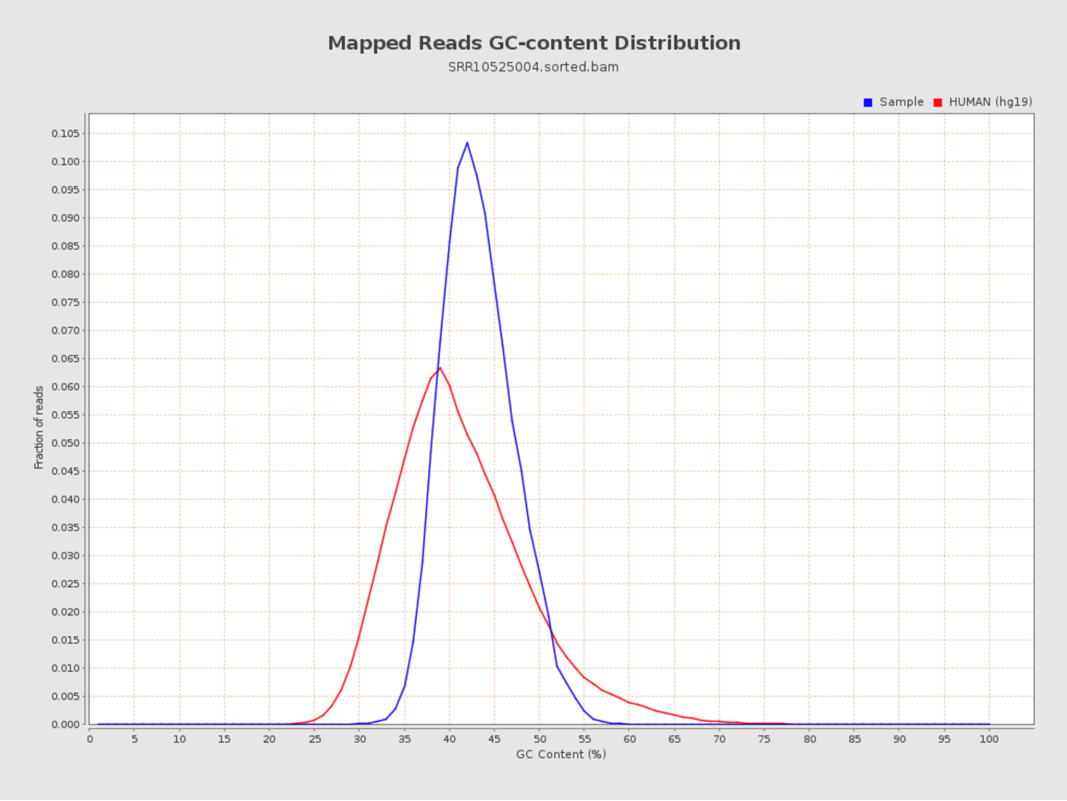
7. Results : Duplication Rate Histogram



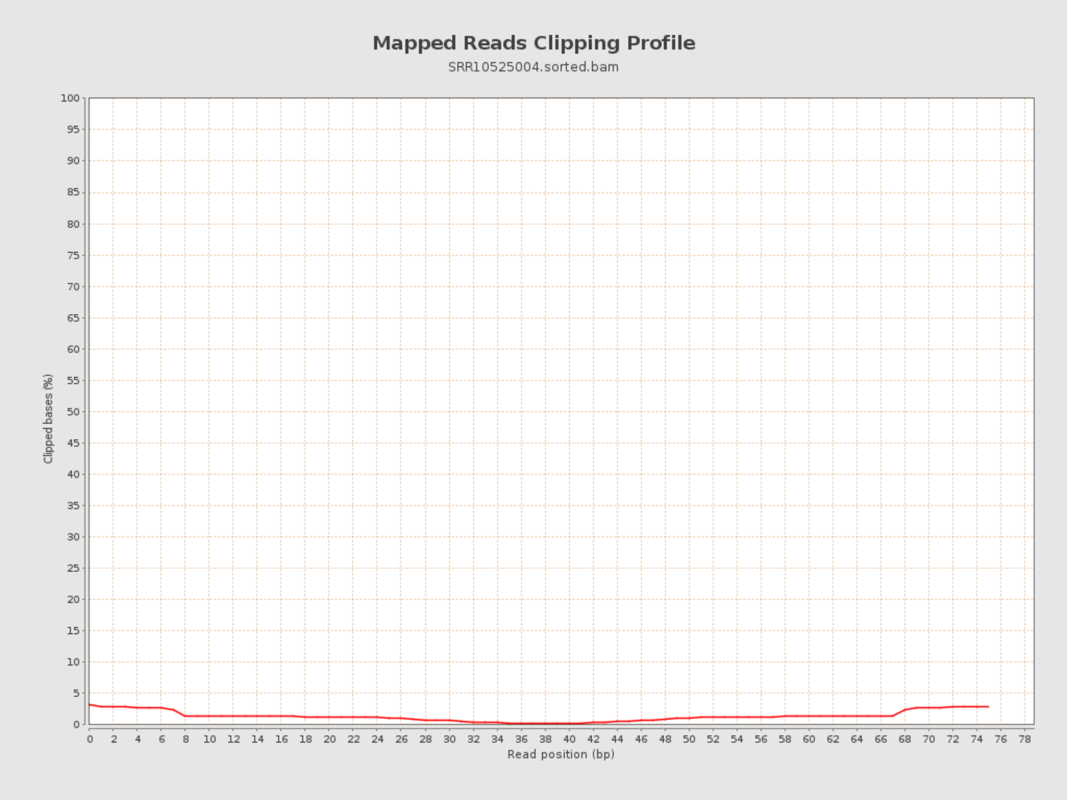
8. Results : Mapped Reads Nucleotide Content



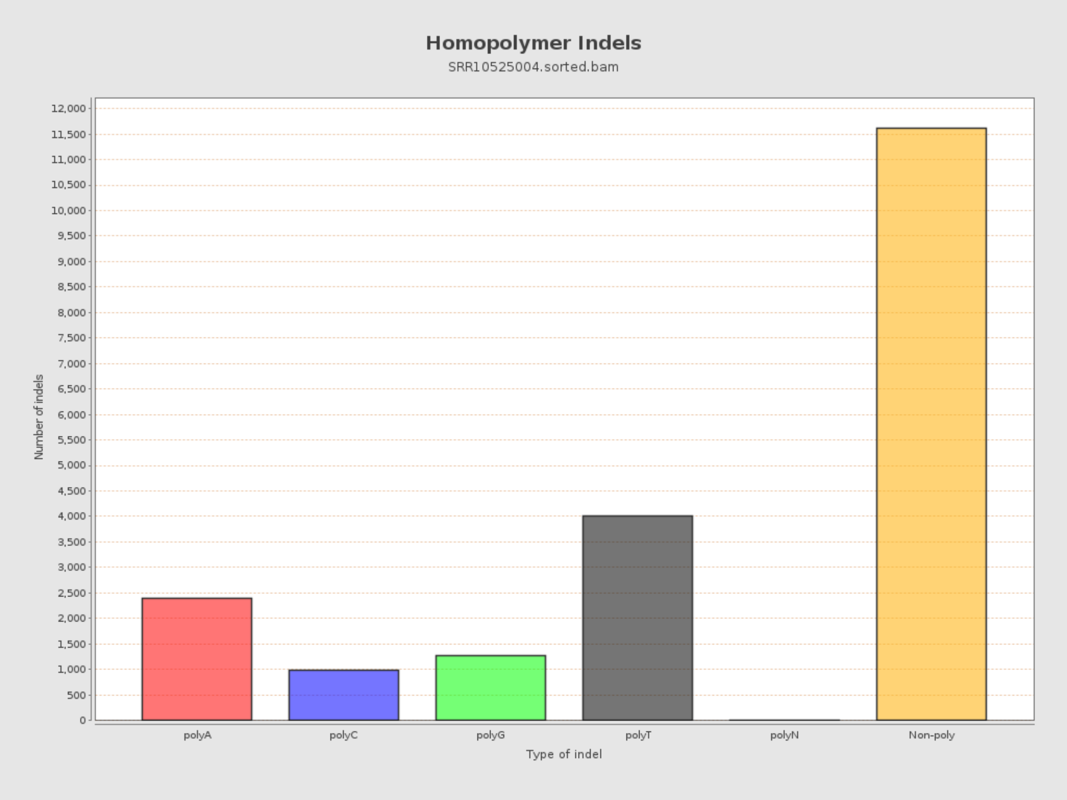
9. Results : Mapped Reads GC-content Distribution



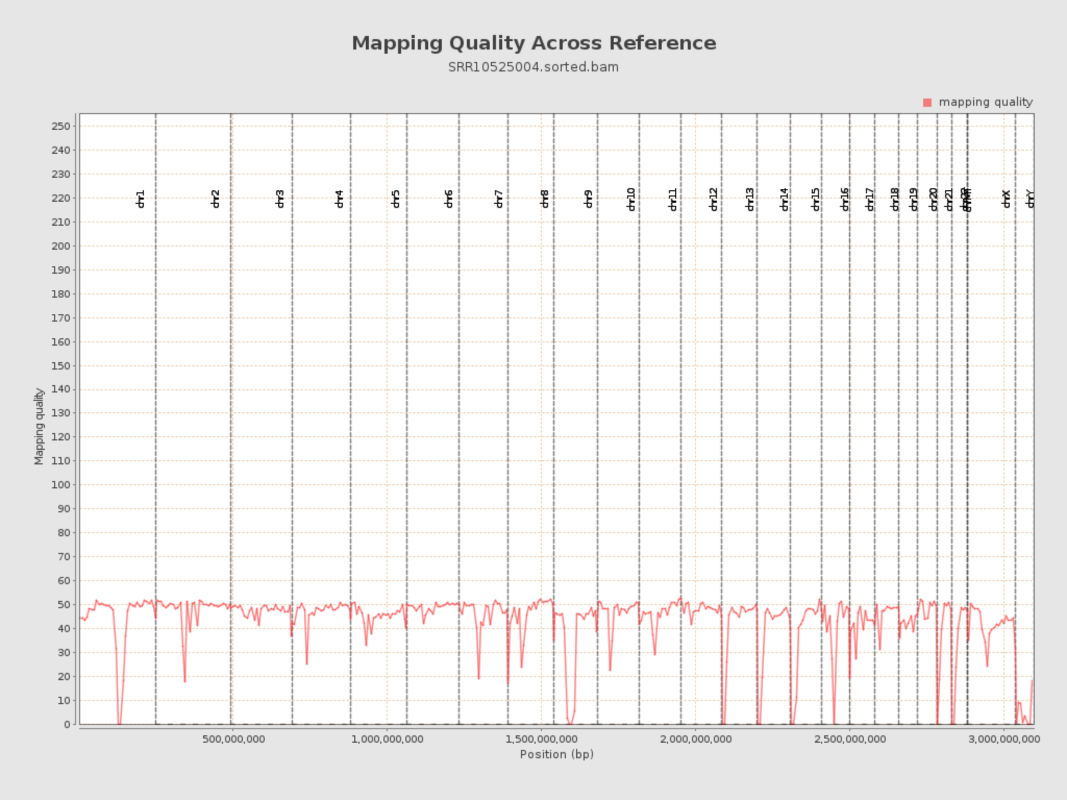
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram