Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525027.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_SRR10525027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:07:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,443,460
Mapped reads	1,329,650 / 92.12%
Unmapped reads	113,810 / 7.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,854 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	57,887 / 4.01%
Duplication rate	3.36%
Clipped reads	1,331,394 / 92.24%

2.2. ACGT Content

Number/percentage of A's	19,962,790 / 25.68%
Number/percentage of C's	14,542,014 / 18.71%
Number/percentage of T's	24,946,443 / 32.09%
Number/percentage of G's	18,277,449 / 23.51%
Number/percentage of N's	915 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.237

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

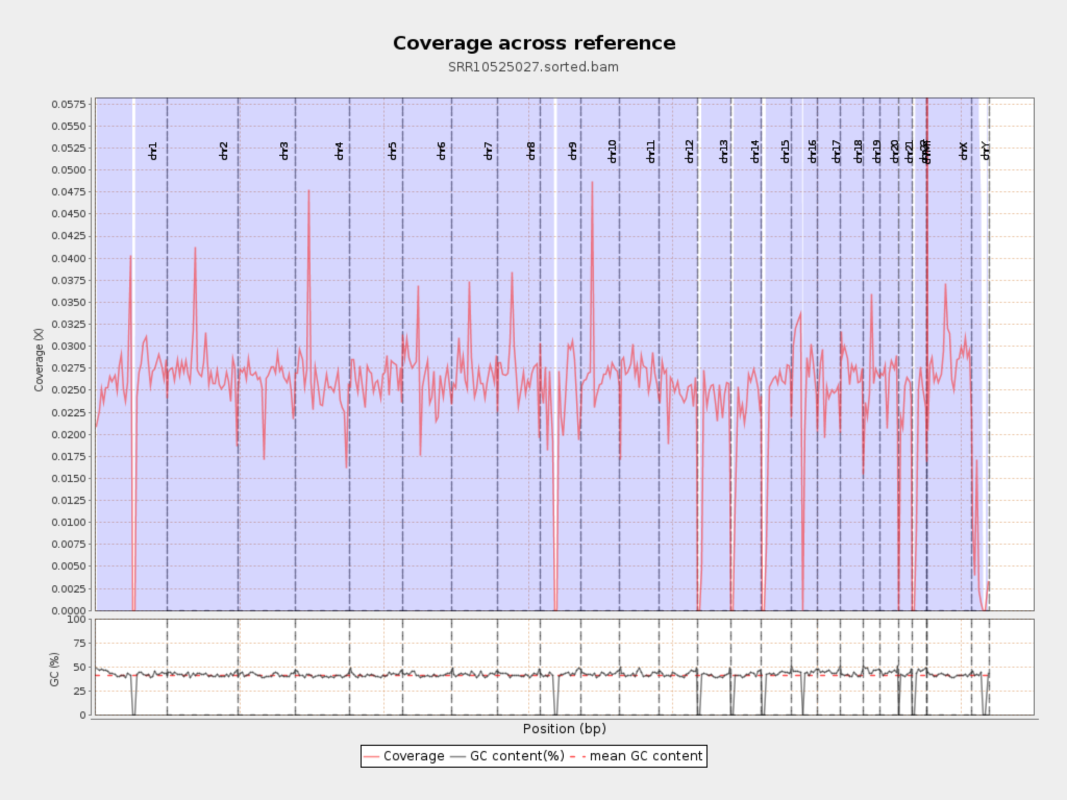
General error rate	0.51%
Mismatches	387,094
Insertions	5,389
Mapped reads with at least one insertion	0.4%
Deletions	14,767
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.41%

2.6. Chromosome stats

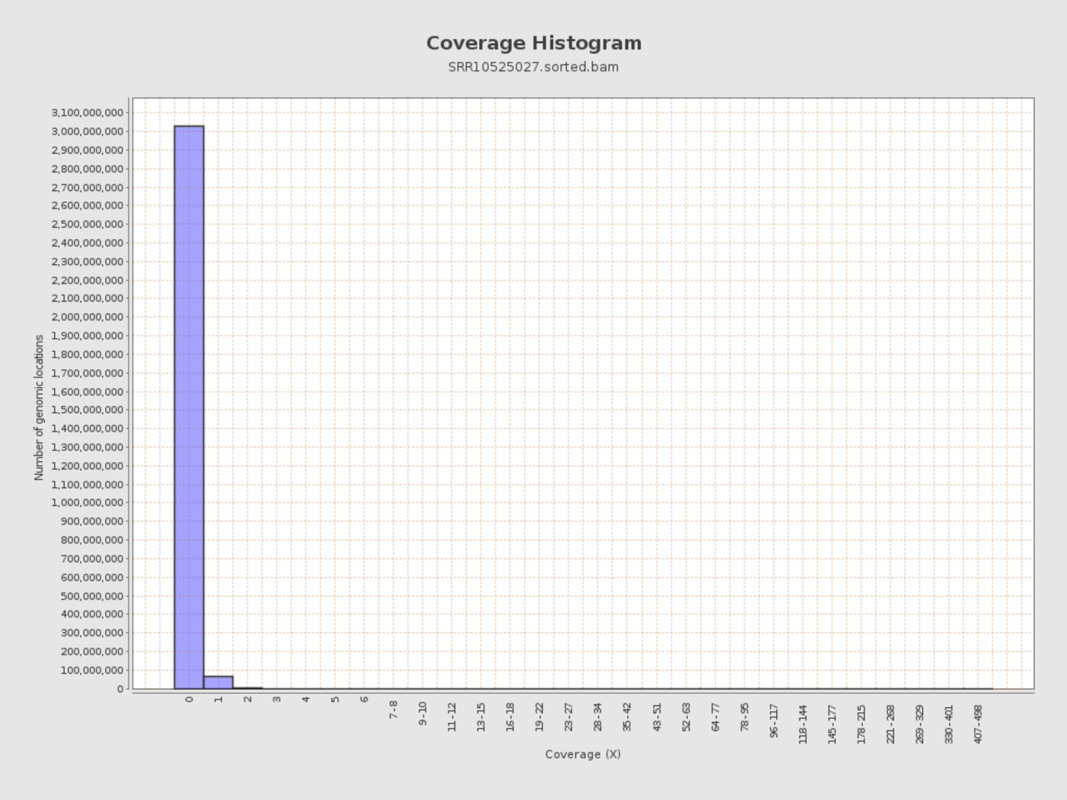
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6292005	0.0252	0.3951
chr2	243199373	6658826	0.0274	0.2714
chr3	198022430	5199889	0.0263	0.1777
chr4	191154276	4991302	0.0261	0.2099
chr5	180915260	4801642	0.0265	0.1804
chr6	171115067	4543691	0.0266	0.2136
chr7	159138663	4313210	0.0271	0.2571

chr8	146364022	3981626	0.0272	0.2797
chr9	141213431	3116816	0.0221	0.203
chr10	135534747	3738825	0.0276	0.2606
chr11	135006516	3670835	0.0272	0.2328
chr12	133851895	3349206	0.025	0.1773
chr13	115169878	2359927	0.0205	0.1576
chr14	107349540	2203556	0.0205	0.1631
chr15	102531392	2180747	0.0213	0.1623
chr16	90354753	2338571	0.0259	0.1861
chr17	81195210	2024591	0.0249	0.1912
chr18	78077248	2164894	0.0277	0.3354
chr19	59128983	1537415	0.026	0.271
chr20	63025520	1662940	0.0264	0.1851
chr21	48129895	1051029	0.0218	0.1878
chr22	51304566	887991	0.0173	0.1438
chrMT	16571	1977	0.1193	0.354
chrX	155270560	4419065	0.0285	0.2019
chrY	59373566	263861	0.0044	0.1463

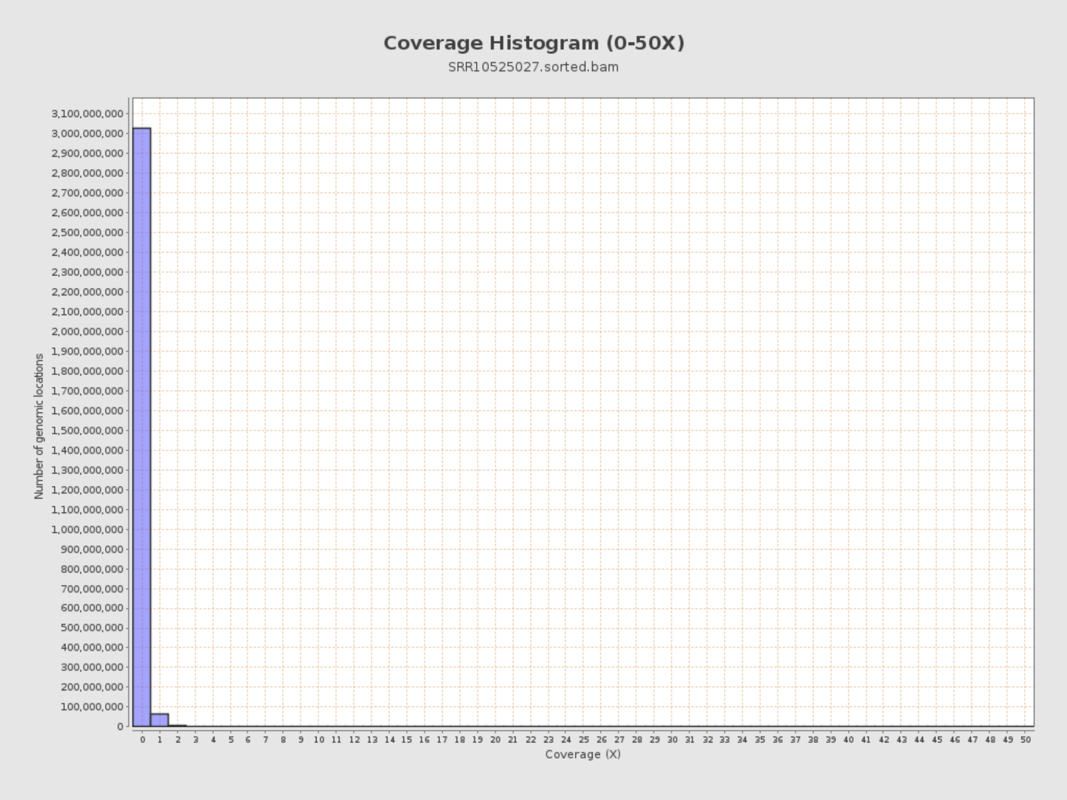
3. Results : Coverage across reference



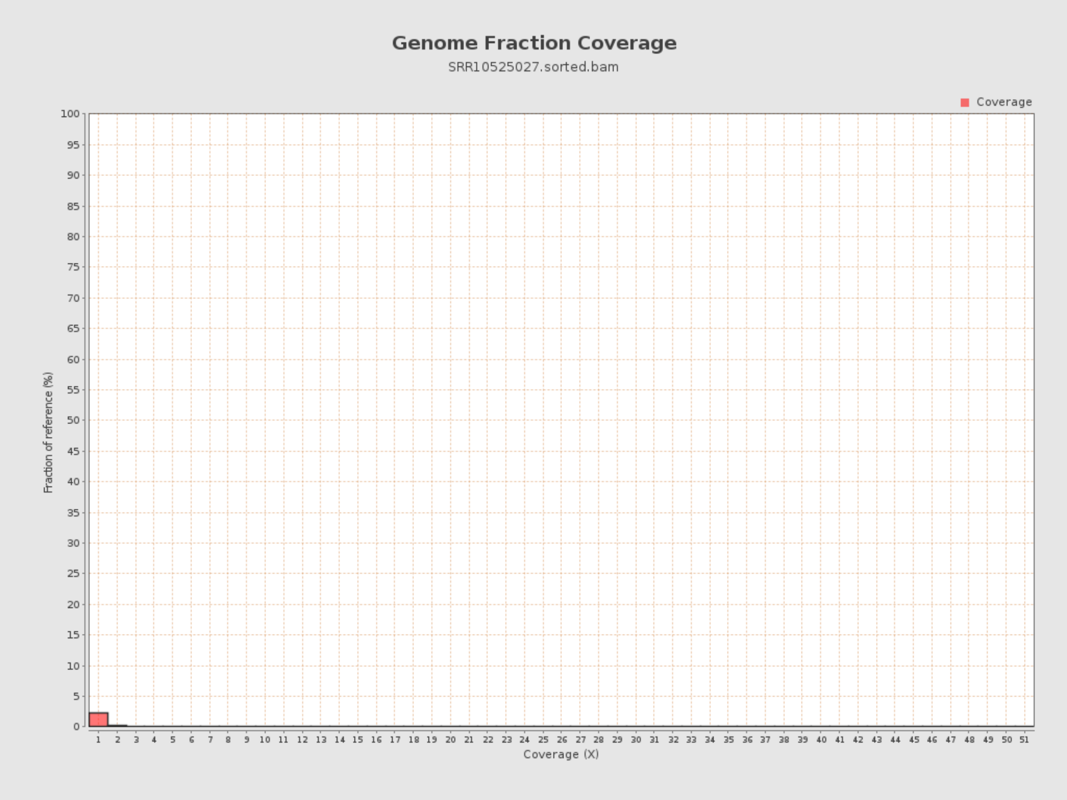
4. Results : Coverage Histogram



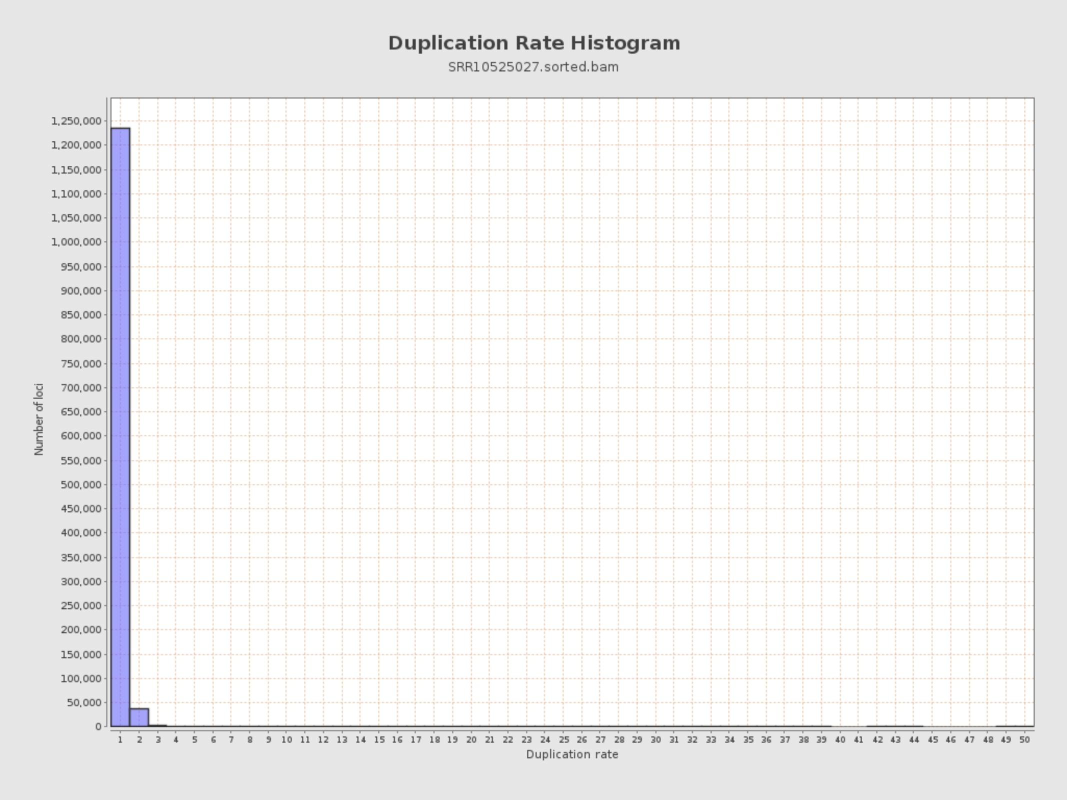
5. Results : Coverage Histogram (0-50X)



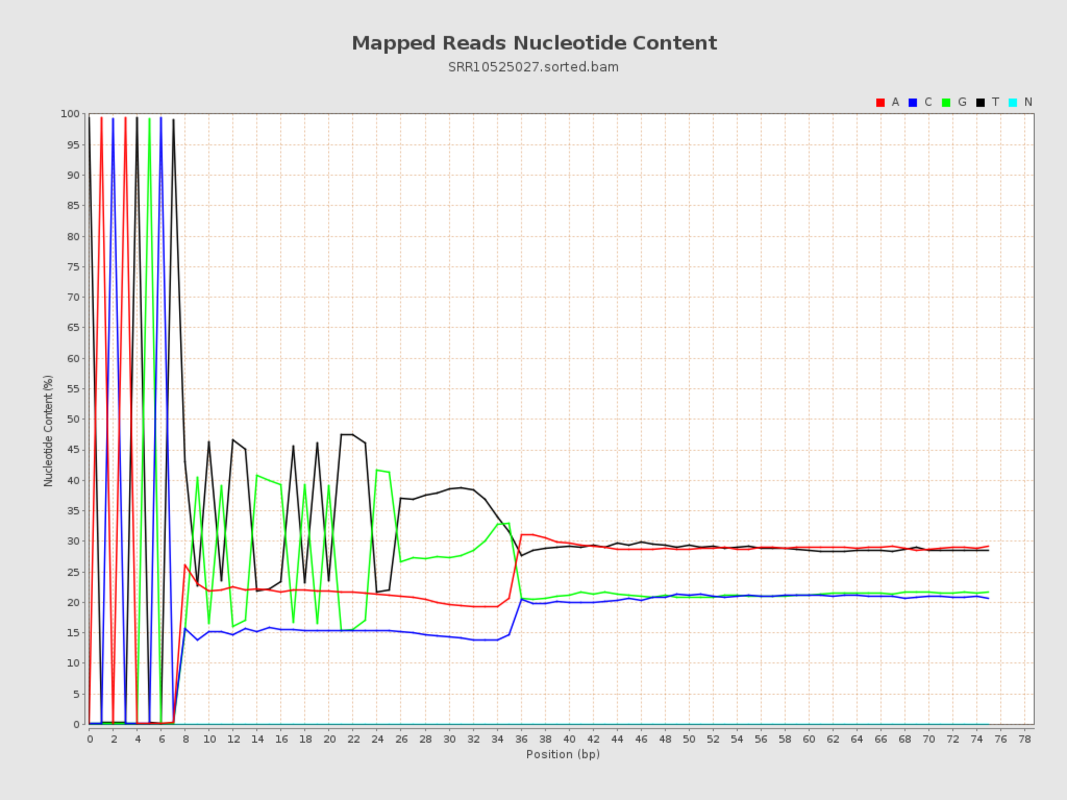
6. Results : Genome Fraction Coverage



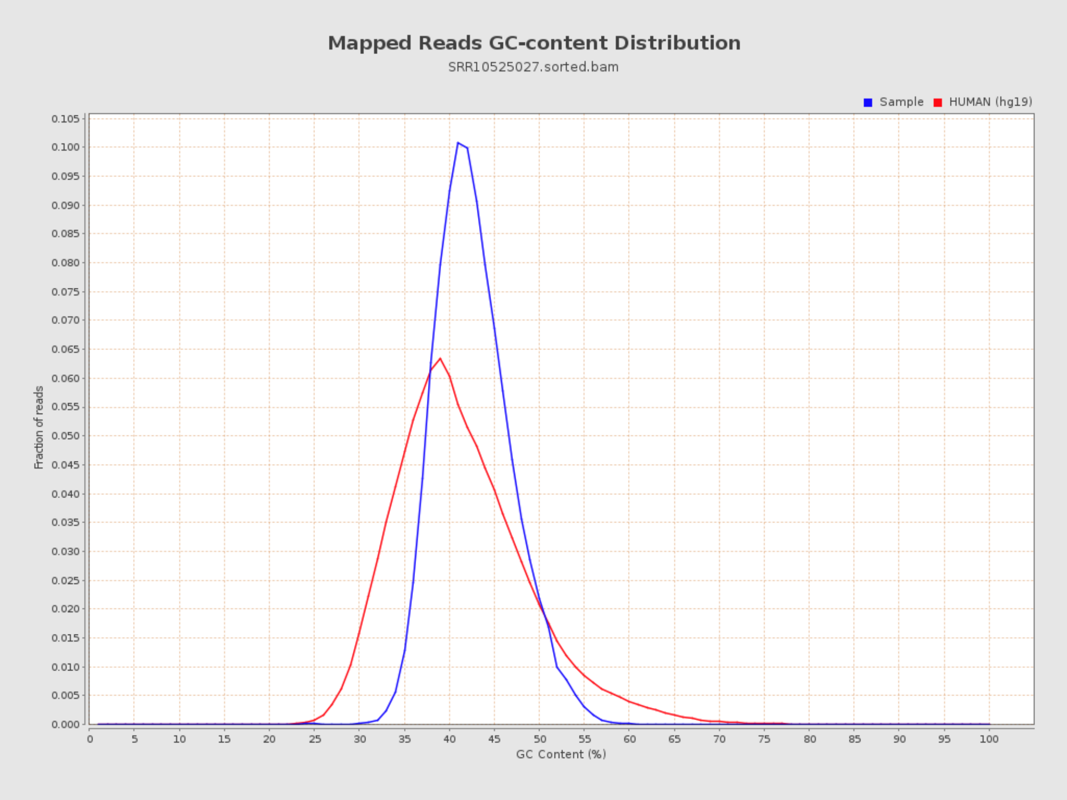
7. Results : Duplication Rate Histogram



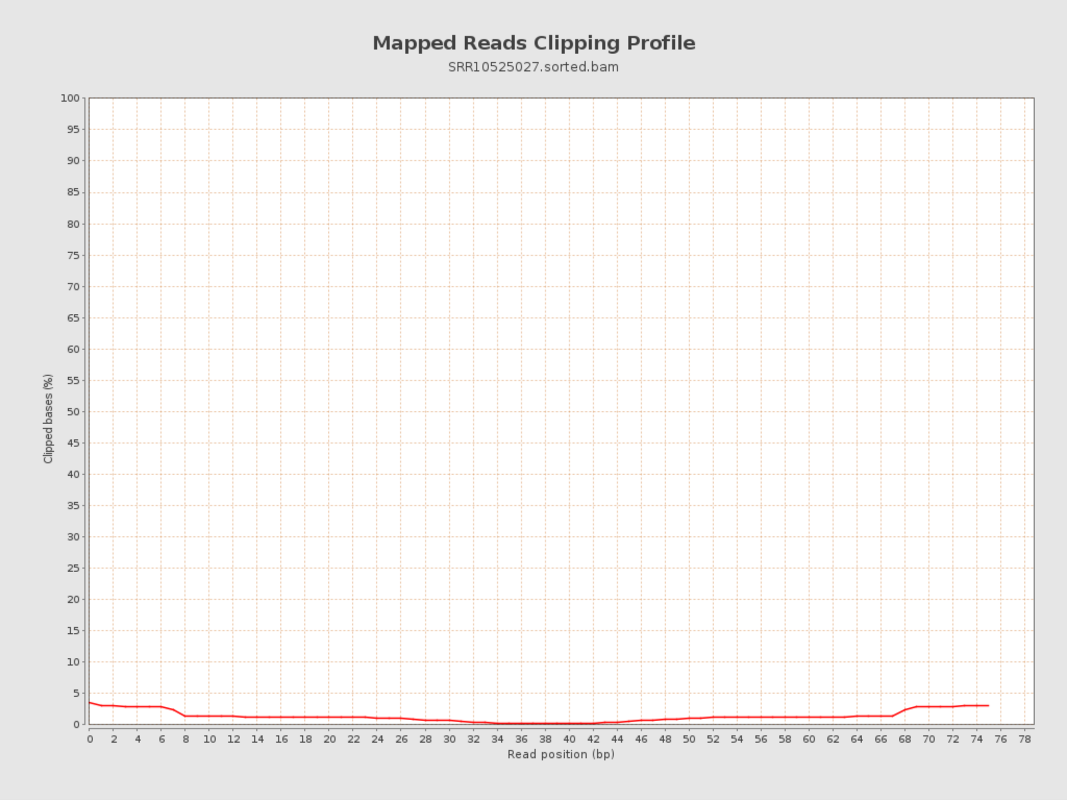
8. Results : Mapped Reads Nucleotide Content



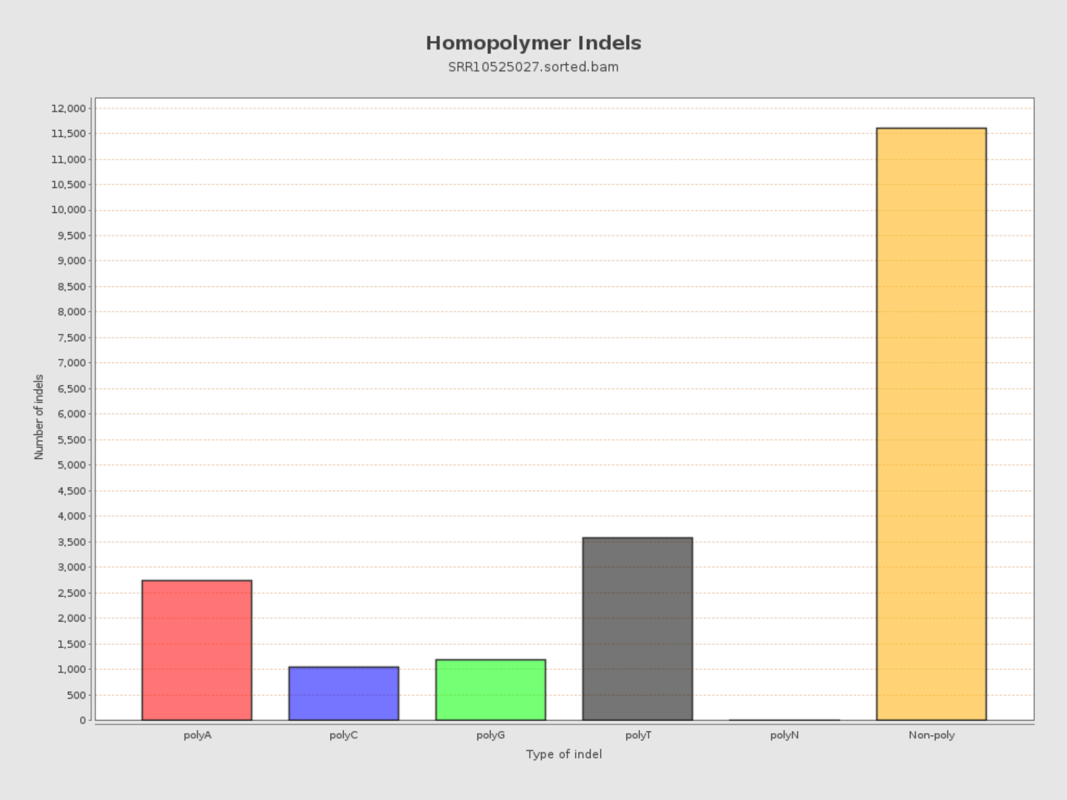
9. Results : Mapped Reads GC-content Distribution



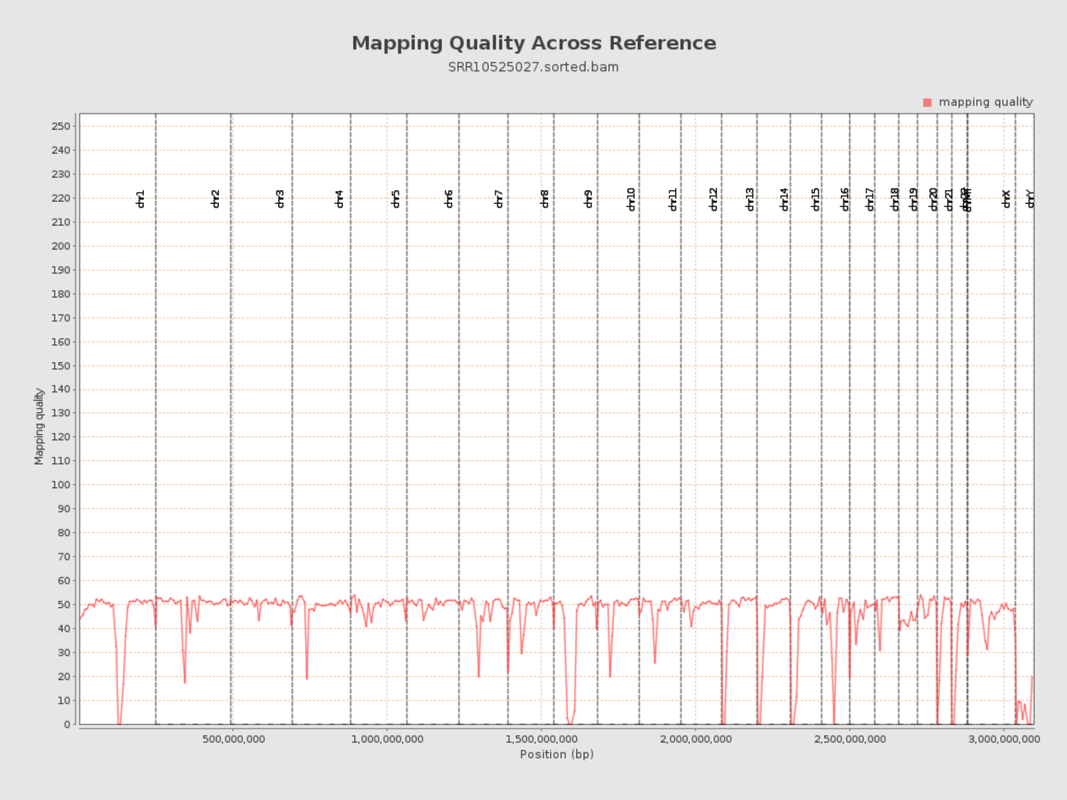
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram