Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:51:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081203.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_SRR3081203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:51:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,672,424
Mapped reads	6,647,895 / 86.65%
Unmapped reads	1,024,529 / 13.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,661 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	494,335 / 6.44%
Duplication rate	5.14%
Clipped reads	2,406,848 / 31.37%

2.2. ACGT Content

Number/percentage of A's	135,469,149 / 29.56%
Number/percentage of C's	88,770,859 / 19.37%
Number/percentage of T's	140,516,850 / 30.66%
Number/percentage of G's	93,312,340 / 20.36%
Number/percentage of N's	260,033 / 0.06%
GC Percentage	39.73%

2.3. Coverage

Mean	0.1481

Standard Deviation	1.6806

2.4. Mapping Quality

Mean Mapping Quality	47.95

2.5. Mismatches and indels

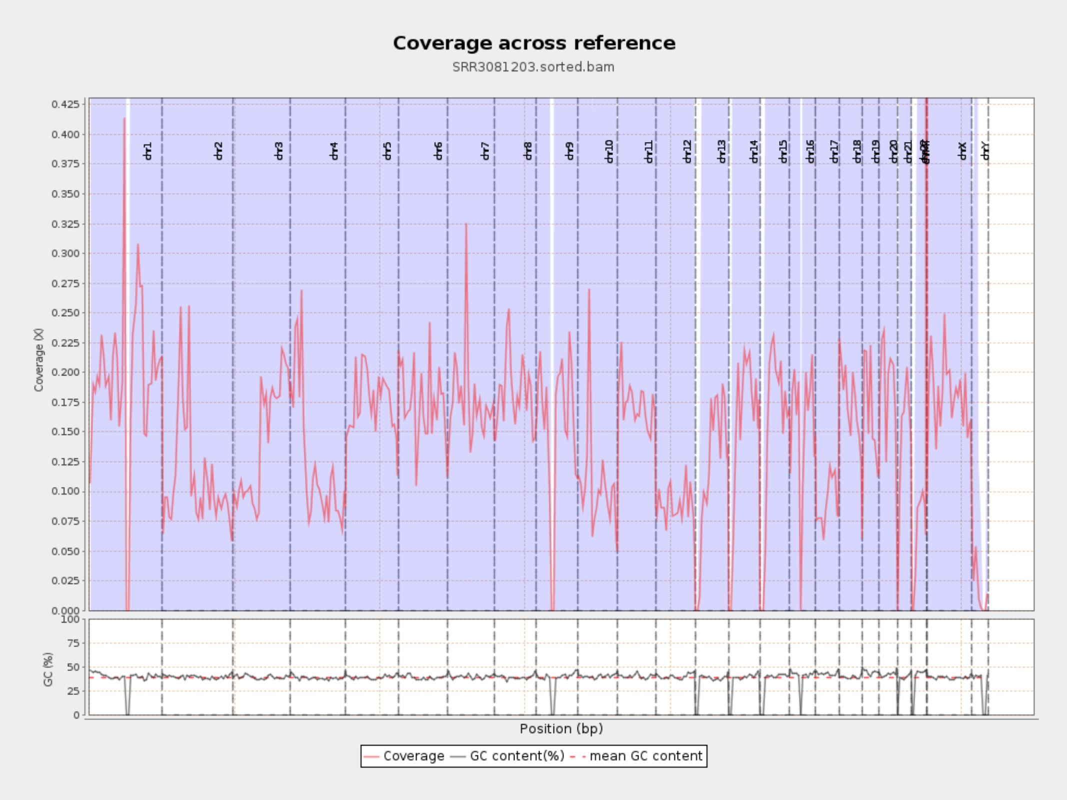
General error rate	1.02%
Mismatches	4,628,605
Insertions	34,790
Mapped reads with at least one insertion	0.52%
Deletions	108,929
Mapped reads with at least one deletion	1.62%
Homopolymer indels	48.28%

2.6. Chromosome stats

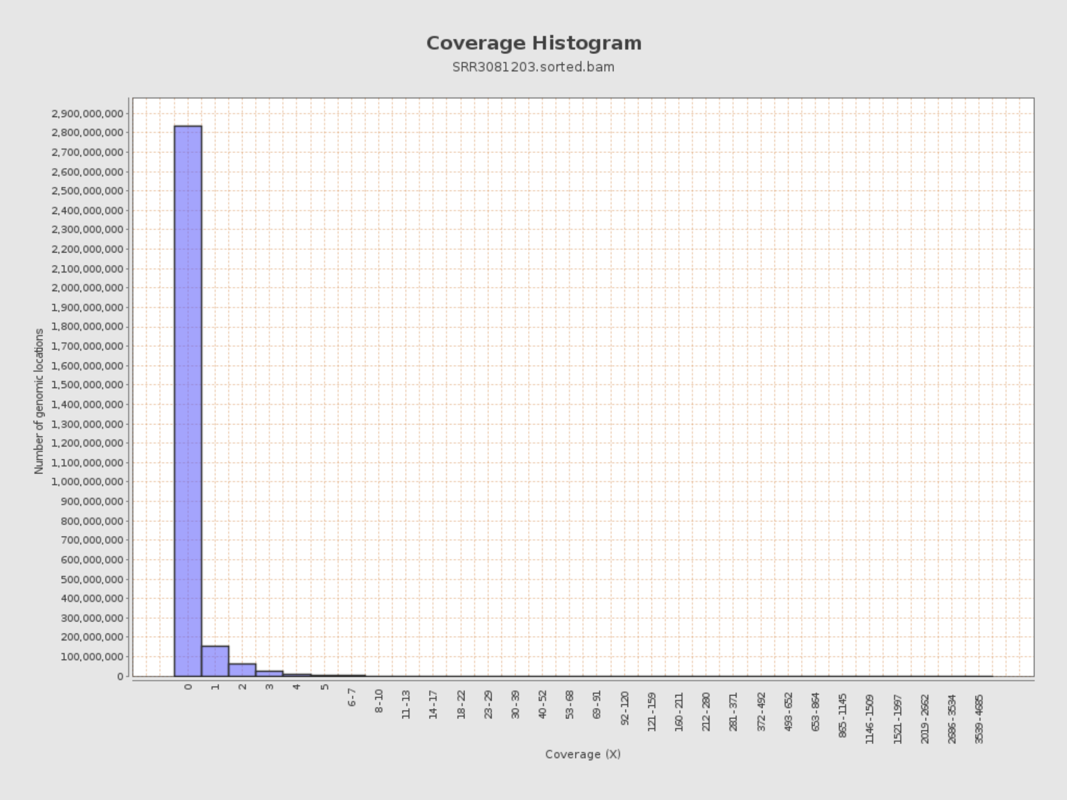
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49134793	0.1971	4.0615
chr2	243199373	27279254	0.1122	1.1443
chr3	198022430	28175910	0.1423	0.5995
chr4	191154276	23824285	0.1246	0.5968
chr5	180915260	31704507	0.1752	0.6703
chr6	171115067	29953916	0.1751	0.9536
chr7	159138663	28299231	0.1778	2.4285

chr8	146364022	26814338	0.1832	2.7958
chr9	141213431	22198490	0.1572	1.1477
chr10	135534747	14437561	0.1065	1.4766
chr11	135006516	23096214	0.1711	1.3449
chr12	133851895	11936697	0.0892	0.5056
chr13	115169878	13516871	0.1174	0.5185
chr14	107349540	16220113	0.1511	0.6975
chr15	102531392	15623339	0.1524	0.5884
chr16	90354753	14133891	0.1564	0.7221
chr17	81195210	7313644	0.0901	0.5774
chr18	78077248	13859522	0.1775	2.1593
chr19	59128983	9779038	0.1654	2.4414
chr20	63025520	11871734	0.1884	0.6917
chr21	48129895	6942328	0.1442	0.6875
chr22	51304566	3216338	0.0627	0.3611
chrMT	16571	194600	11.7434	8.4934
chrX	155270560	27929205	0.1799	0.838
chrY	59373566	1048123	0.0177	0.3878

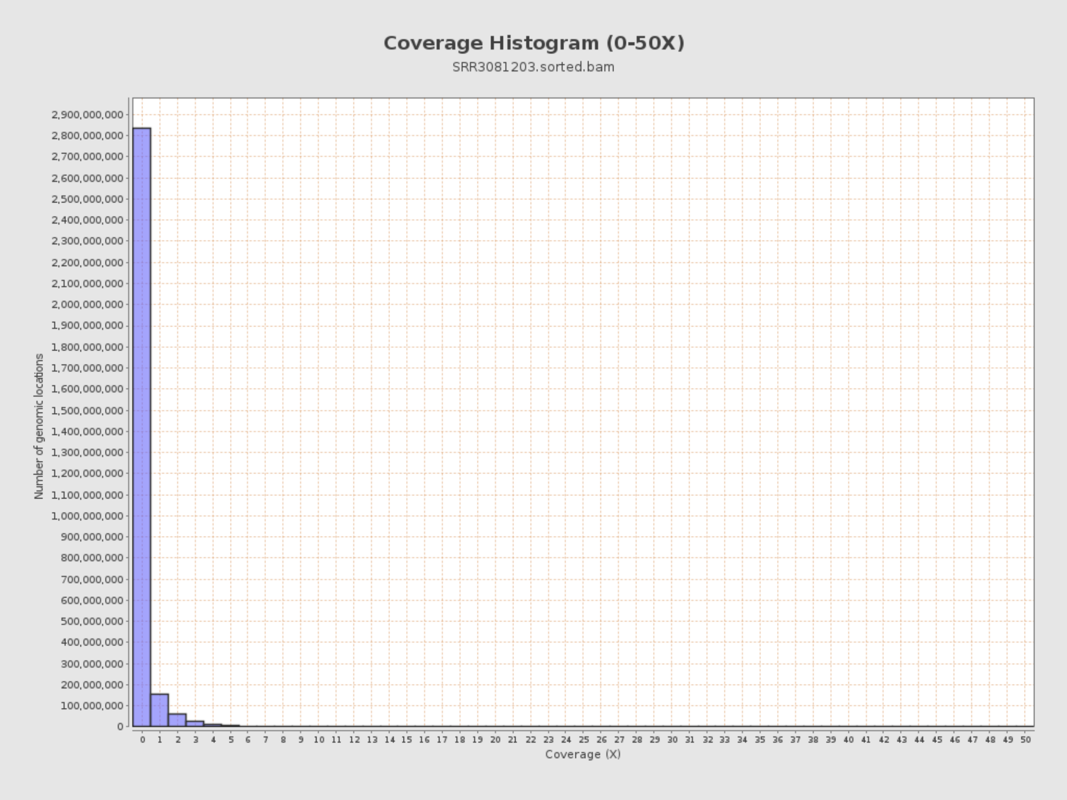
3. Results : Coverage across reference



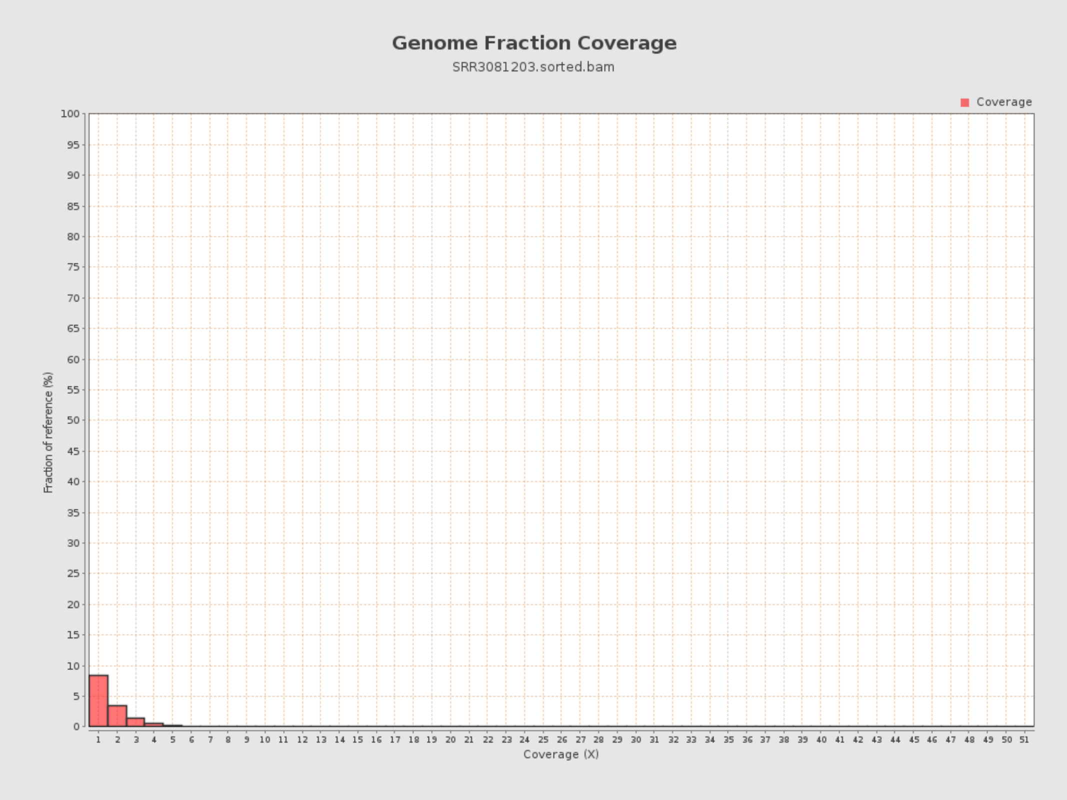
4. Results : Coverage Histogram



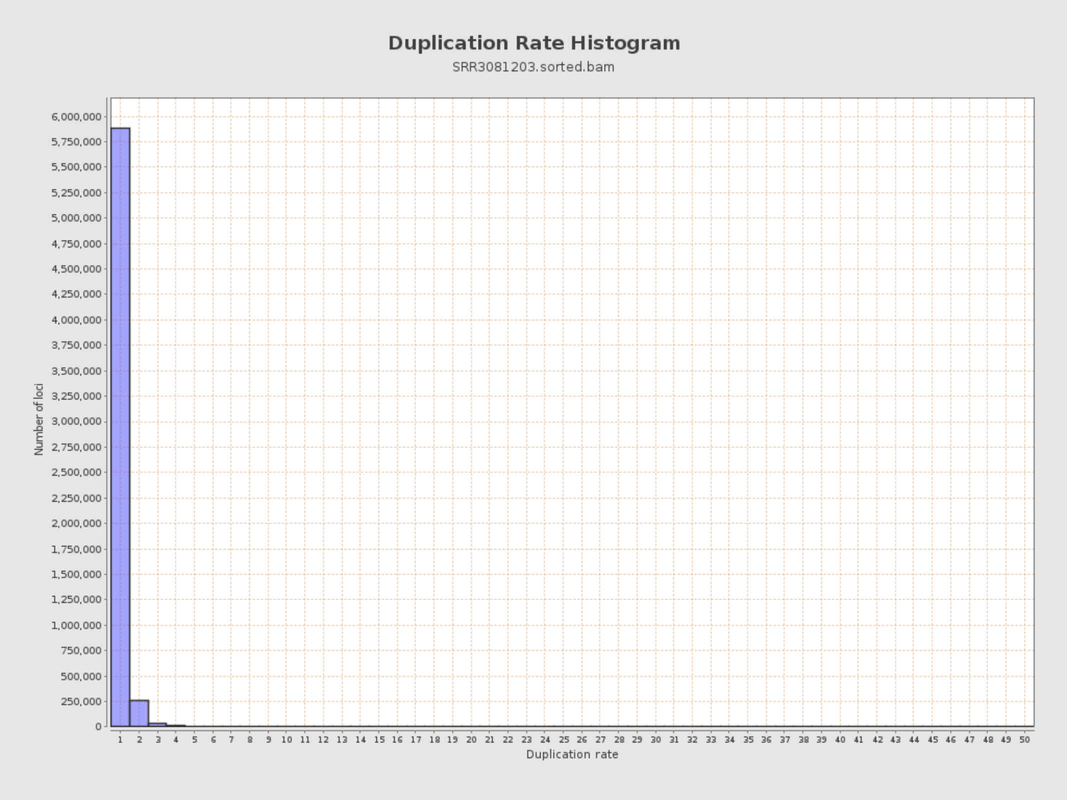
5. Results : Coverage Histogram (0-50X)



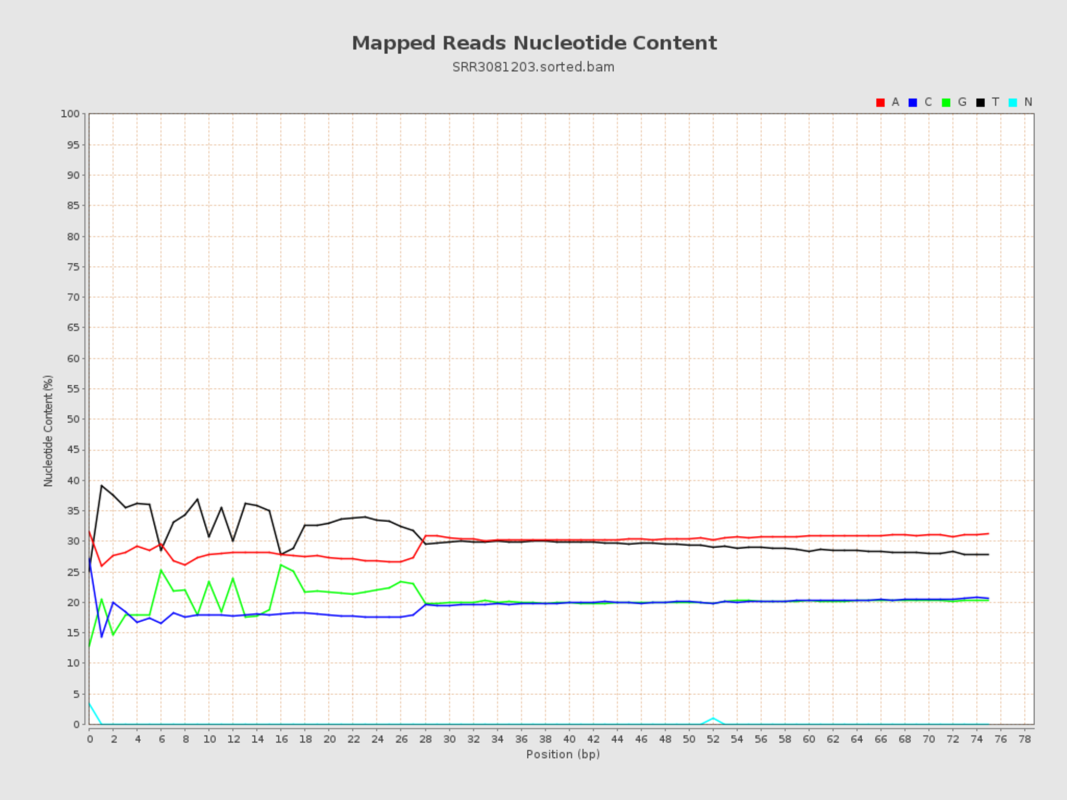
6. Results : Genome Fraction Coverage



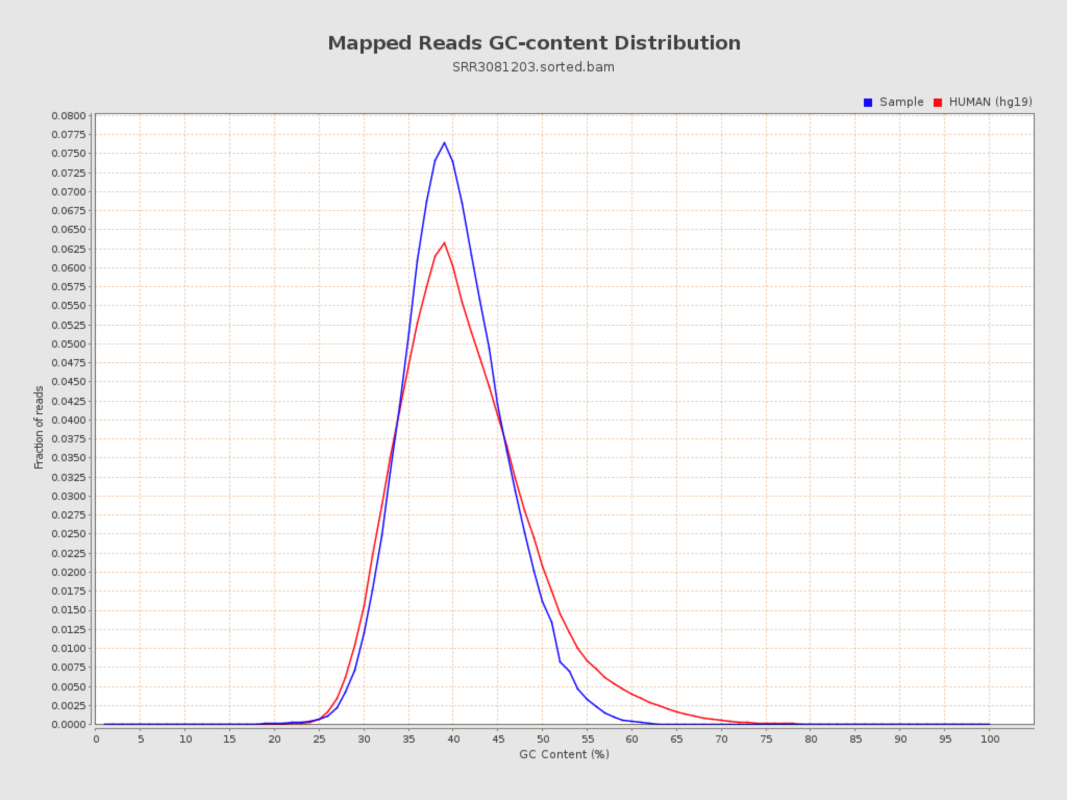
7. Results : Duplication Rate Histogram



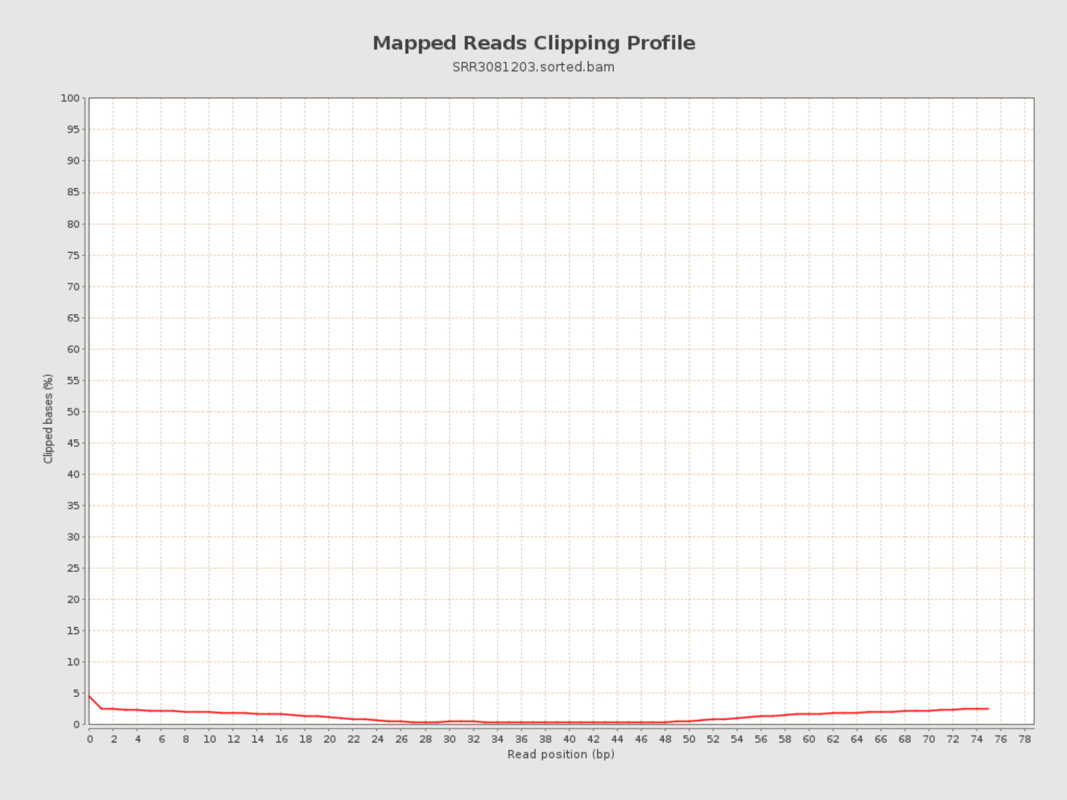
8. Results : Mapped Reads Nucleotide Content



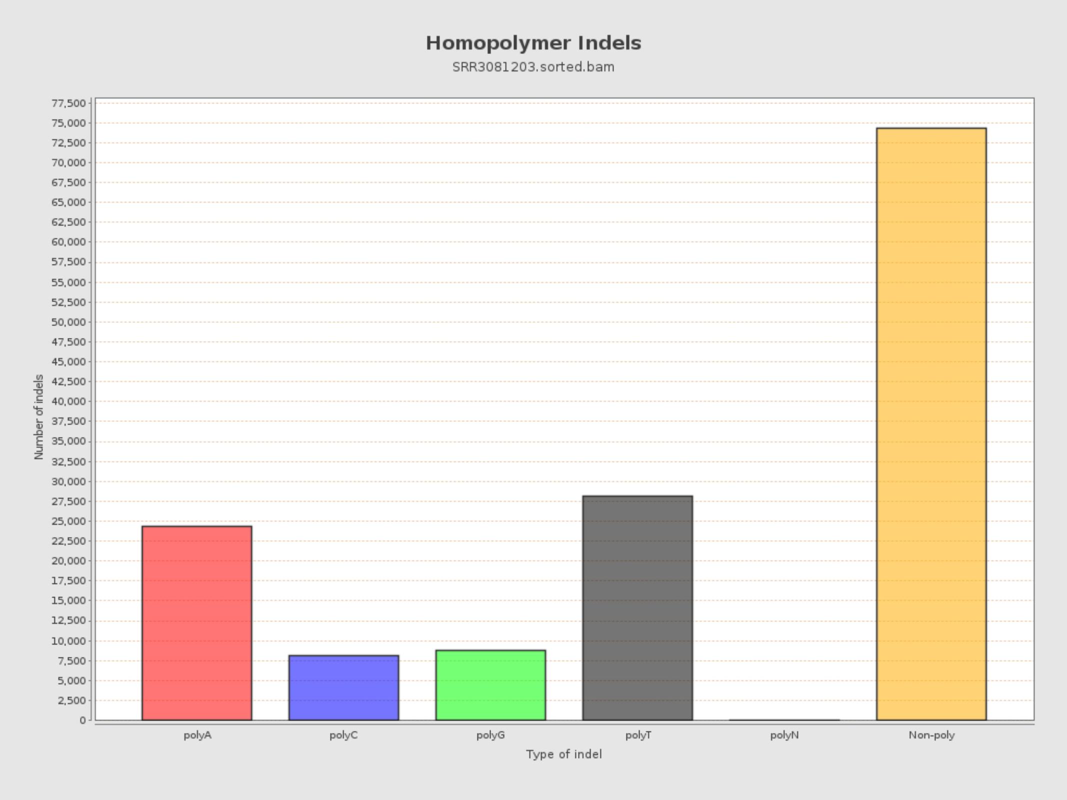
9. Results : Mapped Reads GC-content Distribution



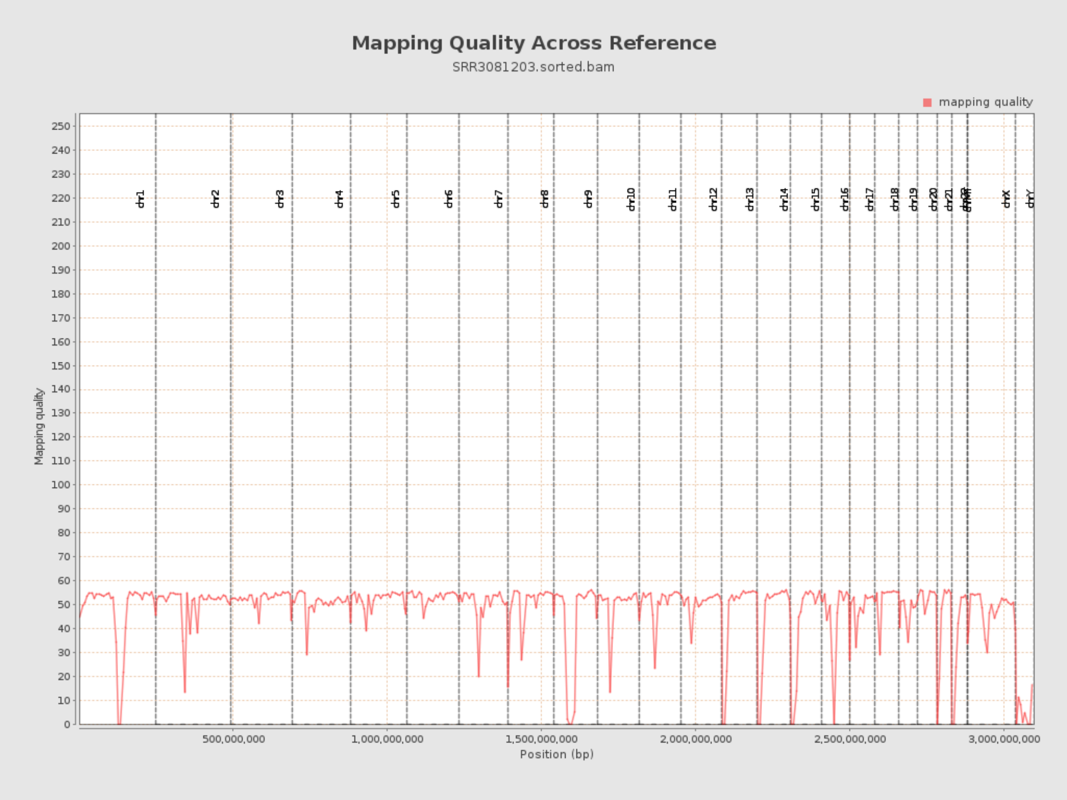
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram