Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:35:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819126.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_SRR1819126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:35:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	935,654
Mapped reads	857,023 / 91.6%
Unmapped reads	78,631 / 8.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,916 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	25,201 / 2.69%
Duplication rate	2.2%
Clipped reads	858,108 / 91.71%

2.2. ACGT Content

Number/percentage of A's	12,330,533 / 24.66%
Number/percentage of C's	9,389,805 / 18.78%
Number/percentage of T's	16,045,728 / 32.09%
Number/percentage of G's	12,229,215 / 24.46%
Number/percentage of N's	664 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.1766

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

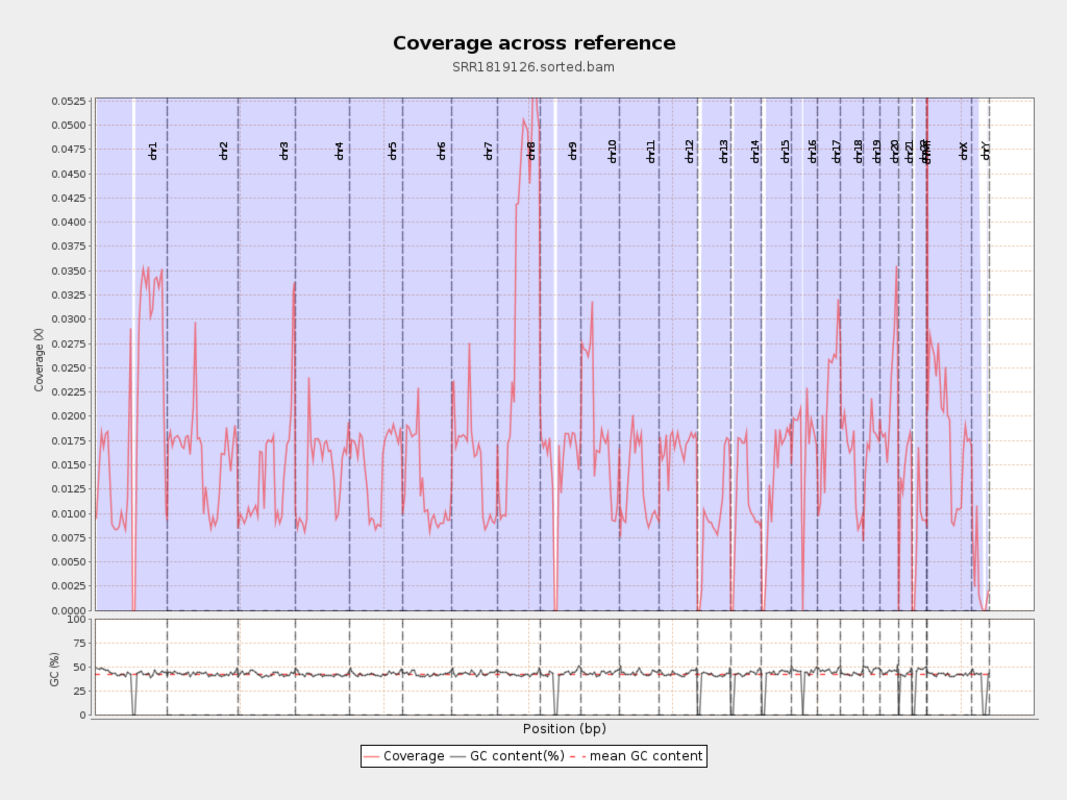
General error rate	0.52%
Mismatches	254,978
Insertions	3,192
Mapped reads with at least one insertion	0.37%
Deletions	9,323
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.13%

2.6. Chromosome stats

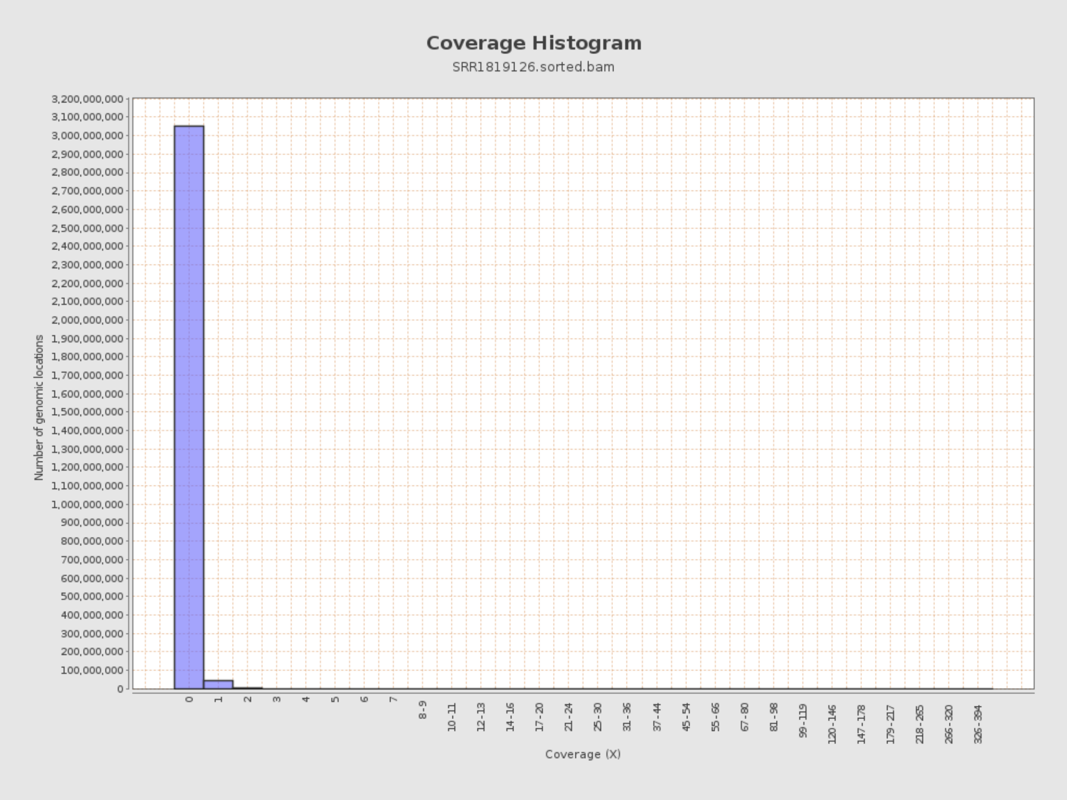
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4854572	0.0195	0.3062
chr2	243199373	3878060	0.0159	0.1887
chr3	198022430	2730156	0.0138	0.1246
chr4	191154276	2761794	0.0144	0.1401
chr5	180915260	2731442	0.0151	0.1306
chr6	171115067	2144189	0.0125	0.1404
chr7	159138663	2472976	0.0155	0.205

chr8	146364022	5042191	0.0344	0.2194
chr9	141213431	2087161	0.0148	0.1513
chr10	135534747	2593153	0.0191	0.1825
chr11	135006516	1714075	0.0127	0.1581
chr12	133851895	2278423	0.017	0.1391
chr13	115169878	1098538	0.0095	0.1028
chr14	107349540	1198377	0.0112	0.1137
chr15	102531392	1327675	0.0129	0.1204
chr16	90354753	1543841	0.0171	0.1438
chr17	81195210	1734796	0.0214	0.1603
chr18	78077248	1165250	0.0149	0.2594
chr19	59128983	1020513	0.0173	0.2277
chr20	63025520	1423624	0.0226	0.1599
chr21	48129895	674429	0.014	0.1354
chr22	51304566	415238	0.0081	0.095
chrMT	16571	2632	0.1588	0.4279
chrX	155270560	2943418	0.019	0.1557
chrY	59373566	175128	0.0029	0.0992

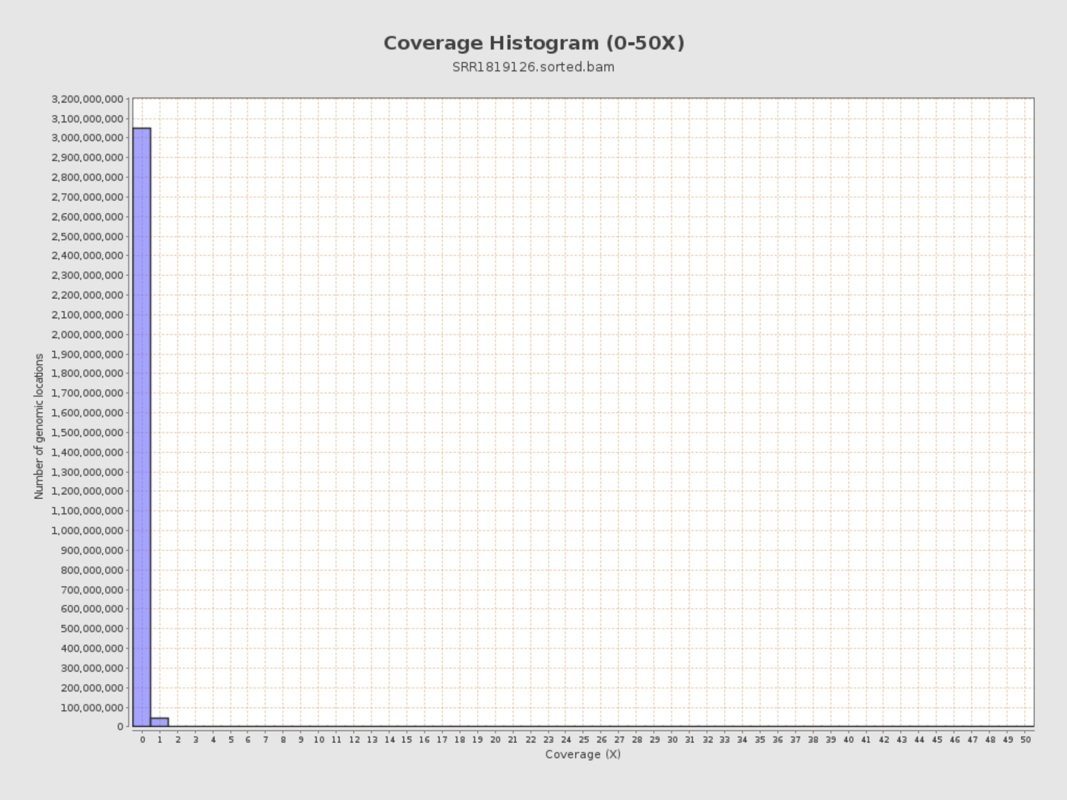
3. Results : Coverage across reference



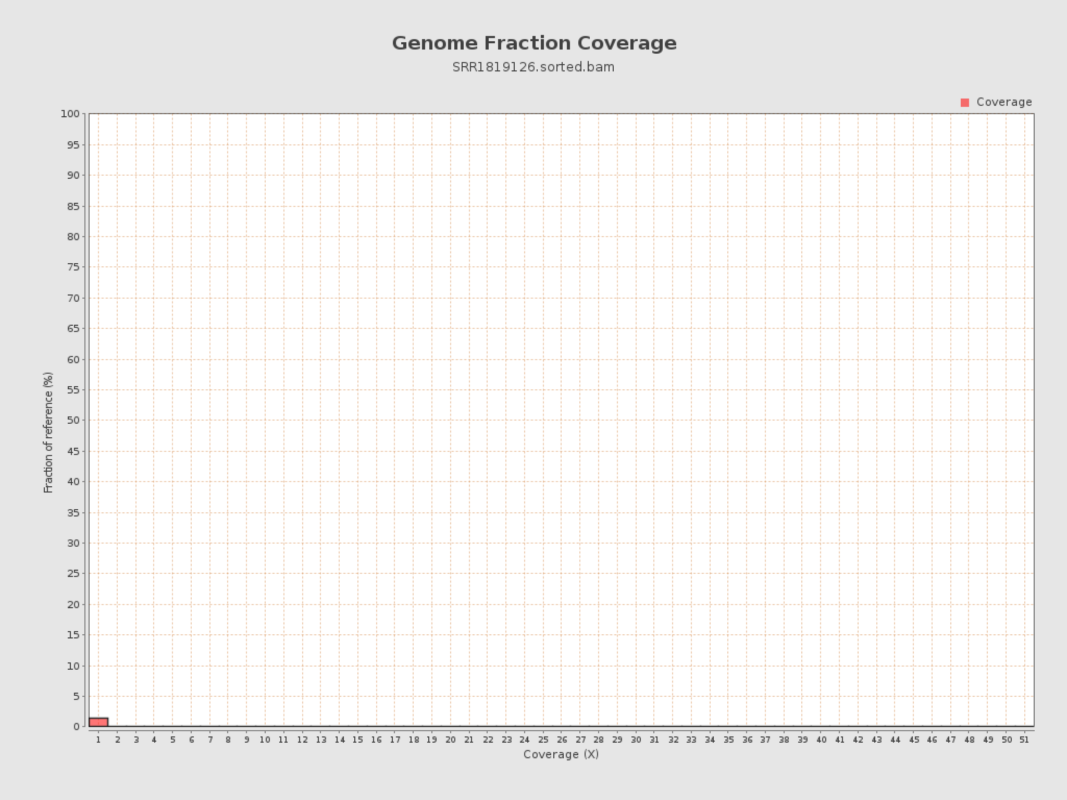
4. Results : Coverage Histogram



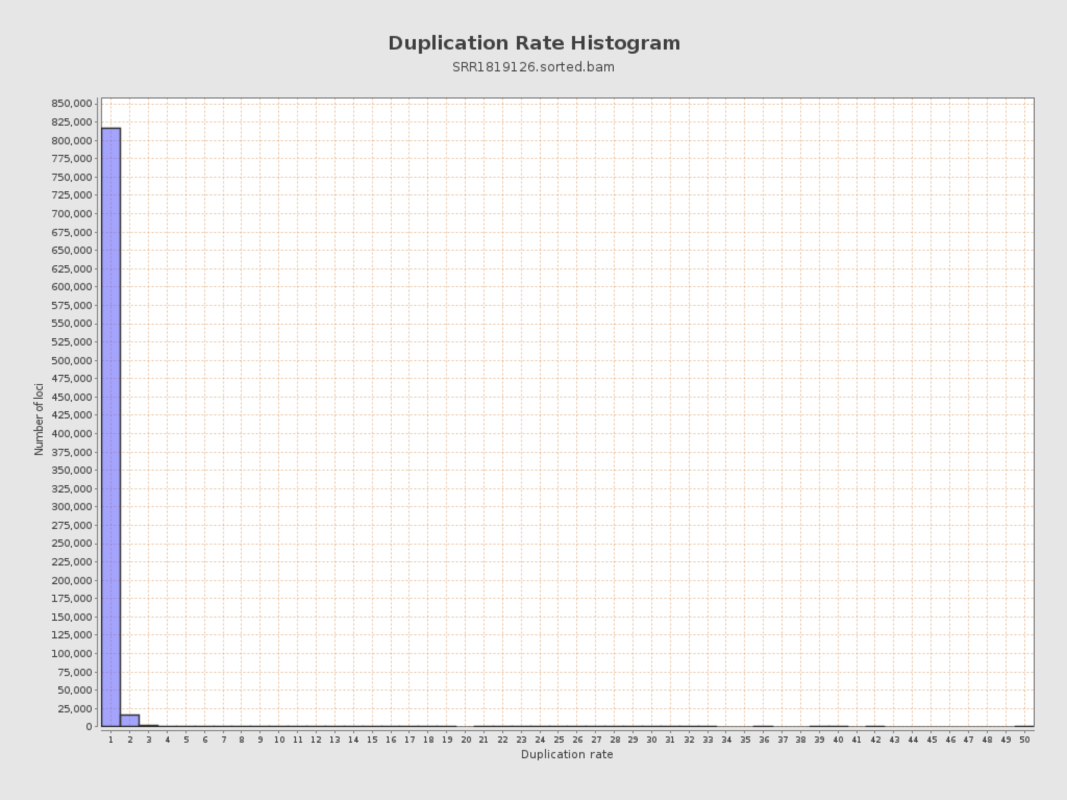
5. Results : Coverage Histogram (0-50X)



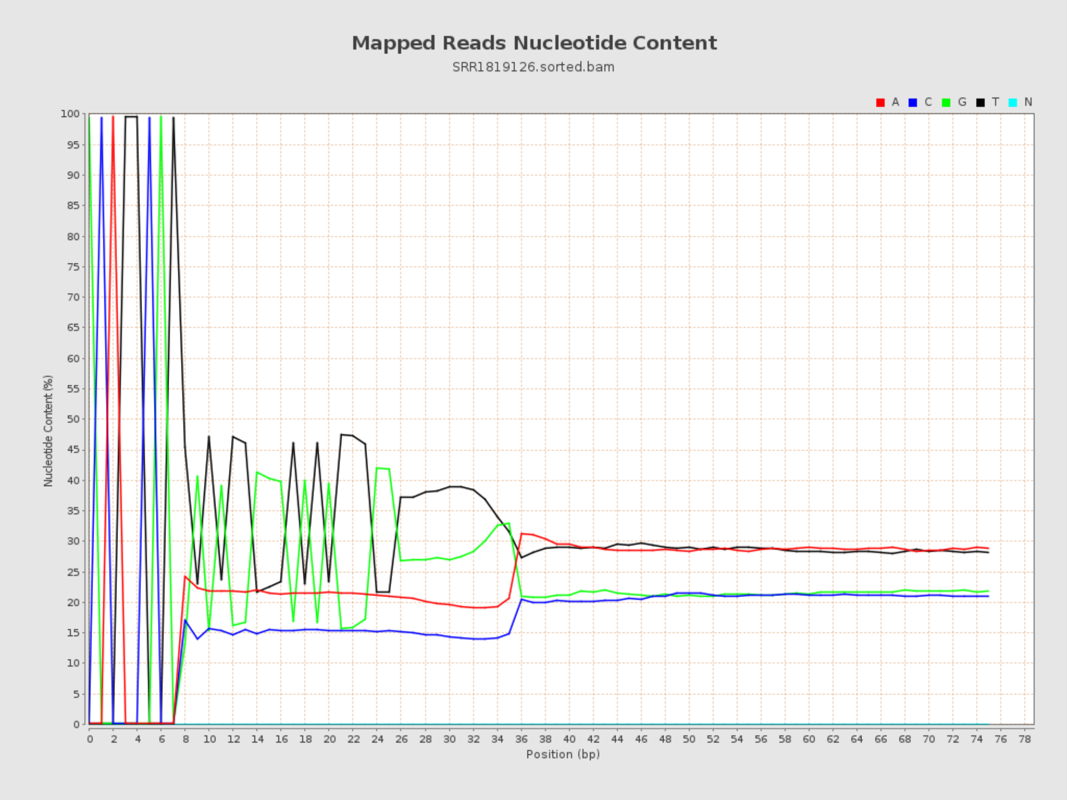
6. Results : Genome Fraction Coverage



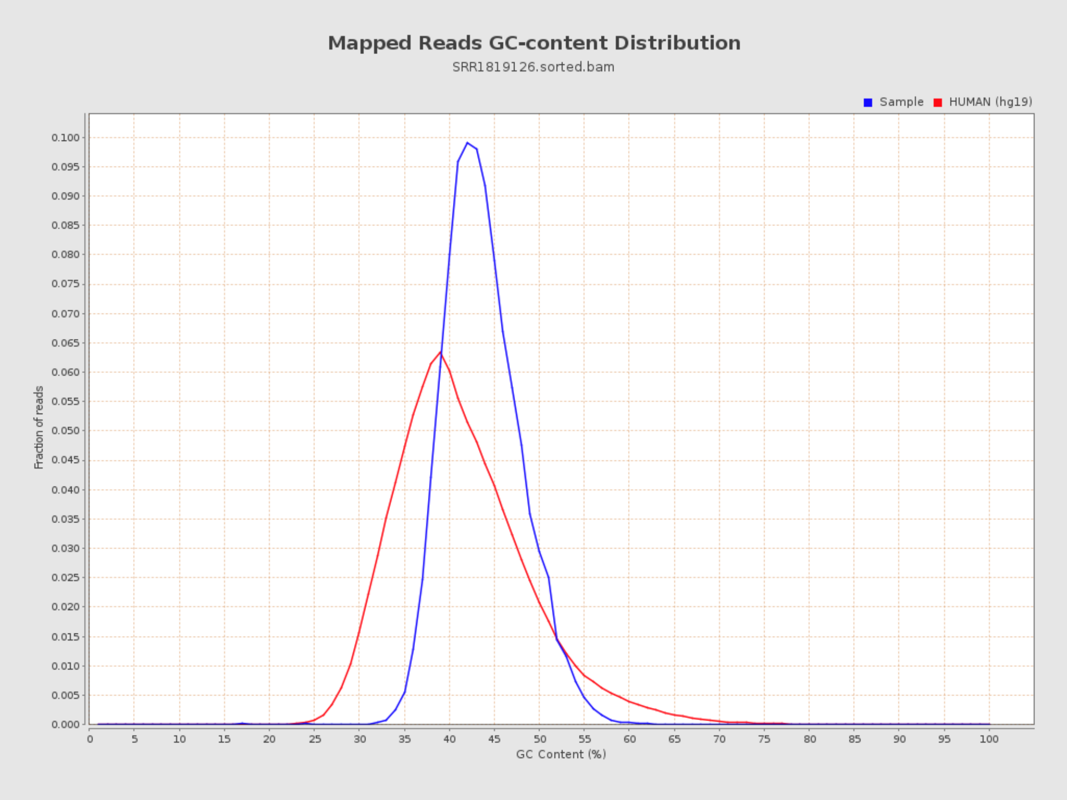
7. Results : Duplication Rate Histogram



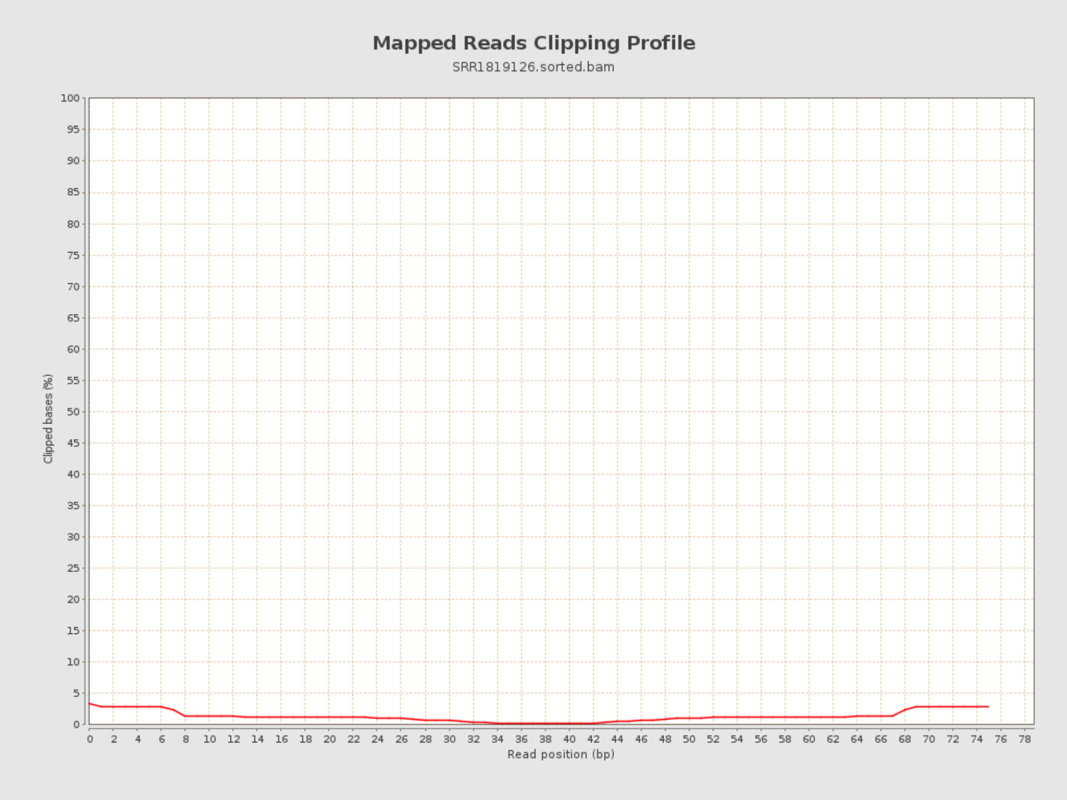
8. Results : Mapped Reads Nucleotide Content



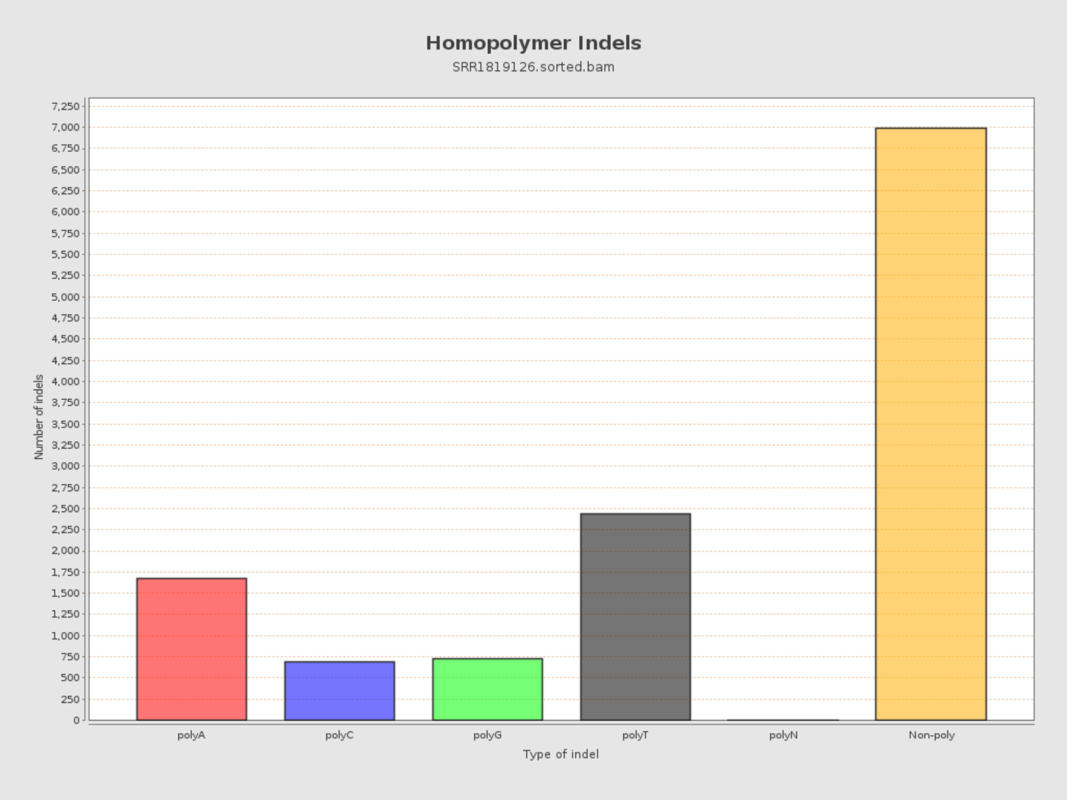
9. Results : Mapped Reads GC-content Distribution



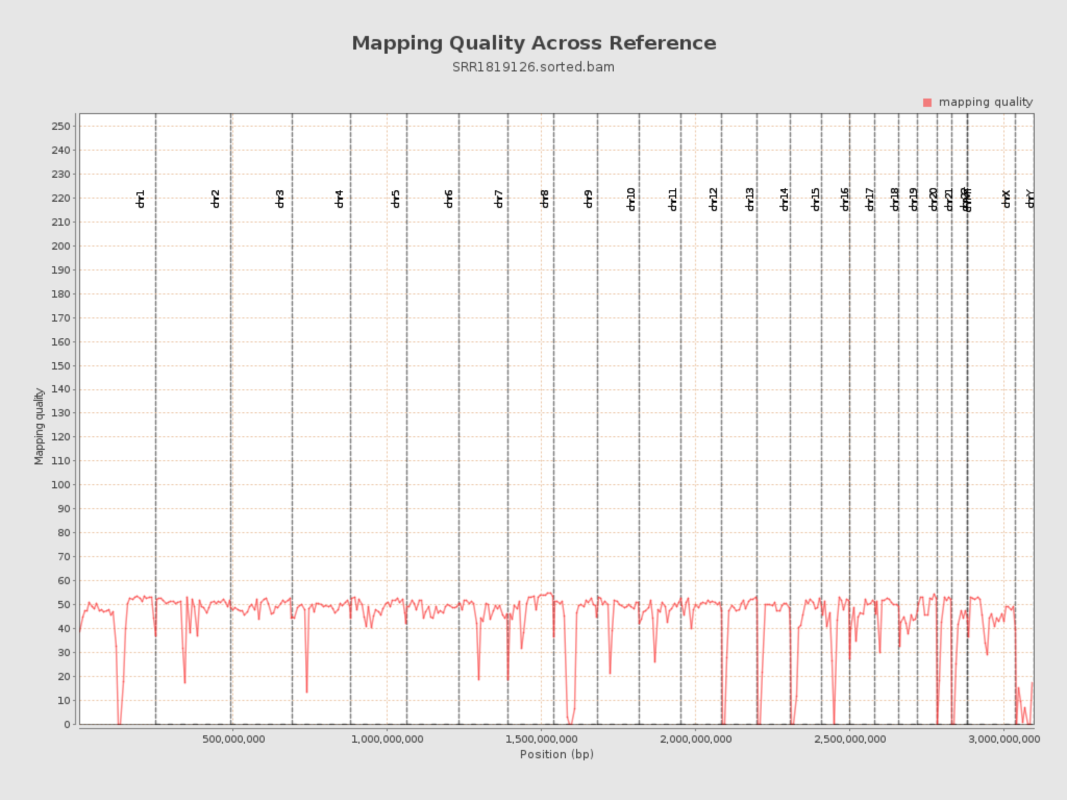
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram