Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:38:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819027.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_SRR1819027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:38:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	597,218
Mapped reads	535,031 / 89.59%
Unmapped reads	62,187 / 10.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,346 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	7,561 / 1.27%
Duplication rate	1.09%
Clipped reads	535,579 / 89.68%

2.2. ACGT Content

Number/percentage of A's	7,683,549 / 25.3%
Number/percentage of C's	5,864,104 / 19.31%
Number/percentage of T's	9,525,860 / 31.36%
Number/percentage of G's	7,298,171 / 24.03%
Number/percentage of N's	673 / 0%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1121

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Mismatches and indels

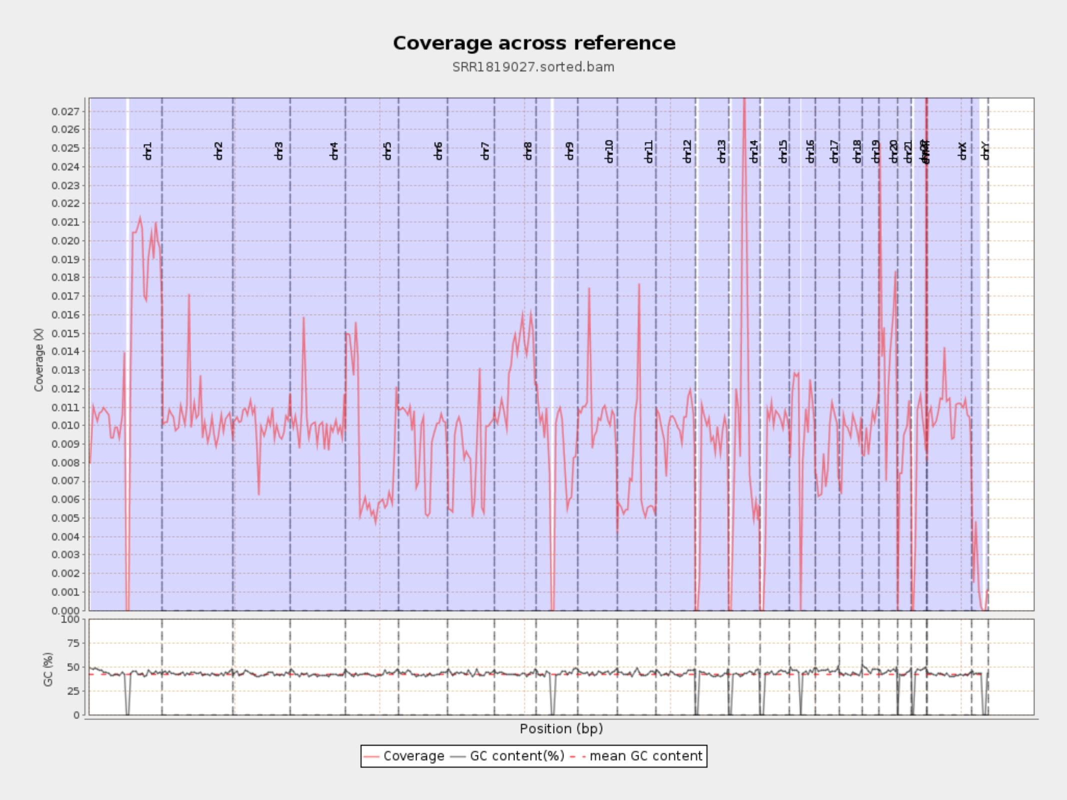
General error rate	0.5%
Mismatches	148,836
Insertions	2,240
Mapped reads with at least one insertion	0.42%
Deletions	4,992
Mapped reads with at least one deletion	0.93%
Homopolymer indels	41.23%

2.6. Chromosome stats

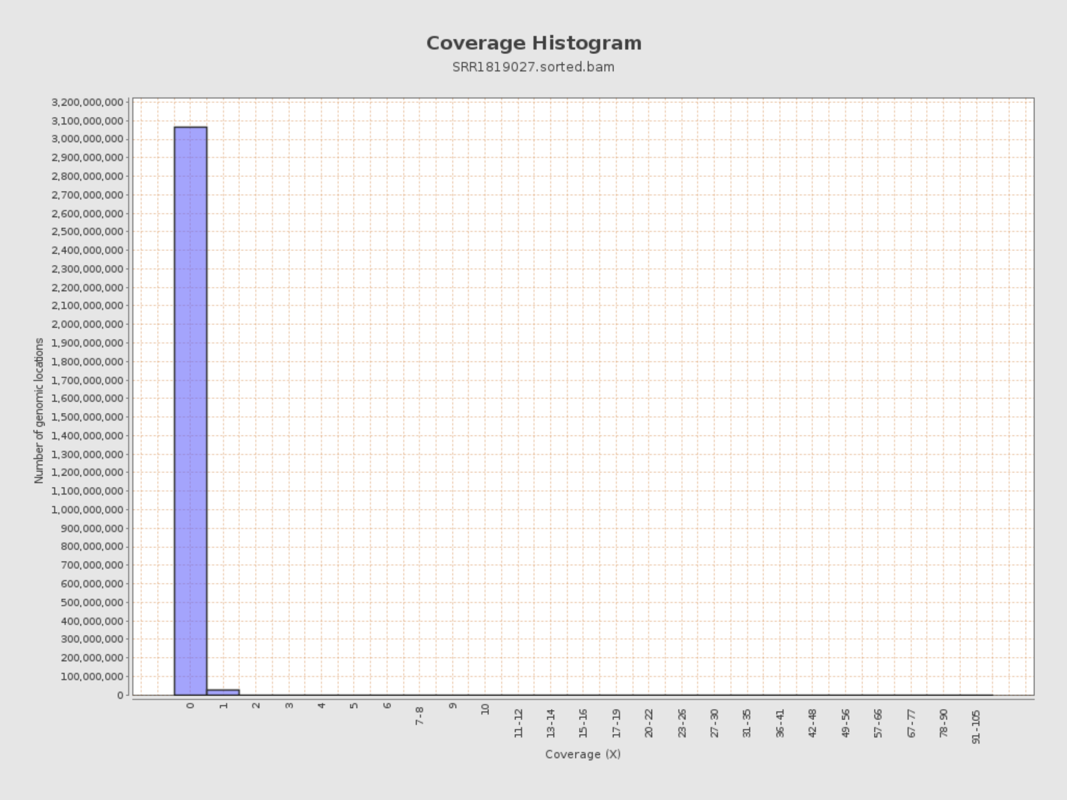
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3398455	0.0136	0.149
chr2	243199373	2549442	0.0105	0.1232
chr3	198022430	1988302	0.01	0.1032
chr4	191154276	1937111	0.0101	0.1073
chr5	180915260	1509728	0.0083	0.0947
chr6	171115067	1590398	0.0093	0.1012
chr7	159138663	1325930	0.0083	0.1031

chr8	146364022	1924772	0.0132	0.124
chr9	141213431	1131974	0.008	0.1064
chr10	135534747	1460102	0.0108	0.1233
chr11	135006516	944529	0.007	0.0967
chr12	133851895	1358492	0.0101	0.1041
chr13	115169878	940918	0.0082	0.0928
chr14	107349540	1065520	0.0099	0.1063
chr15	102531392	867344	0.0085	0.0948
chr16	90354753	918180	0.0102	0.1074
chr17	81195210	682061	0.0084	0.0954
chr18	78077248	740661	0.0095	0.1582
chr19	59128983	581357	0.0098	0.1197
chr20	63025520	929301	0.0147	0.1267
chr21	48129895	394506	0.0082	0.0961
chr22	51304566	370567	0.0072	0.0875
chrMT	16571	1649	0.0995	0.344
chrX	155270560	1680902	0.0108	0.1132
chrY	59373566	88444	0.0015	0.0481

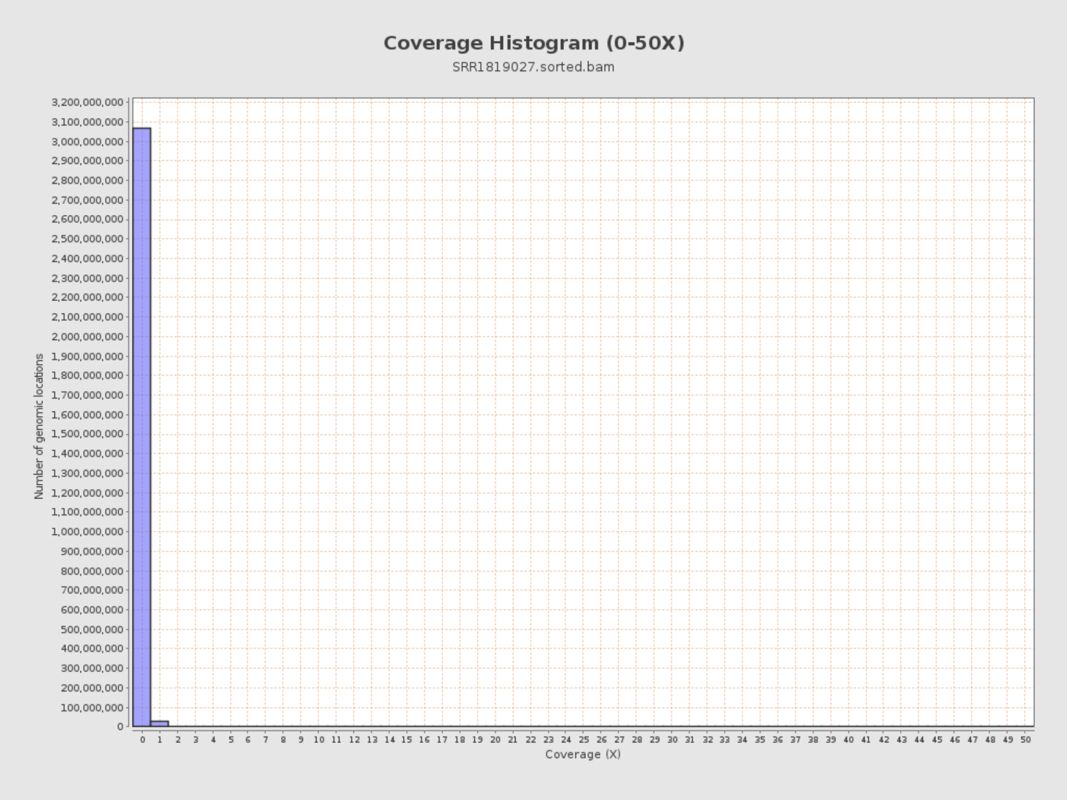
3. Results : Coverage across reference



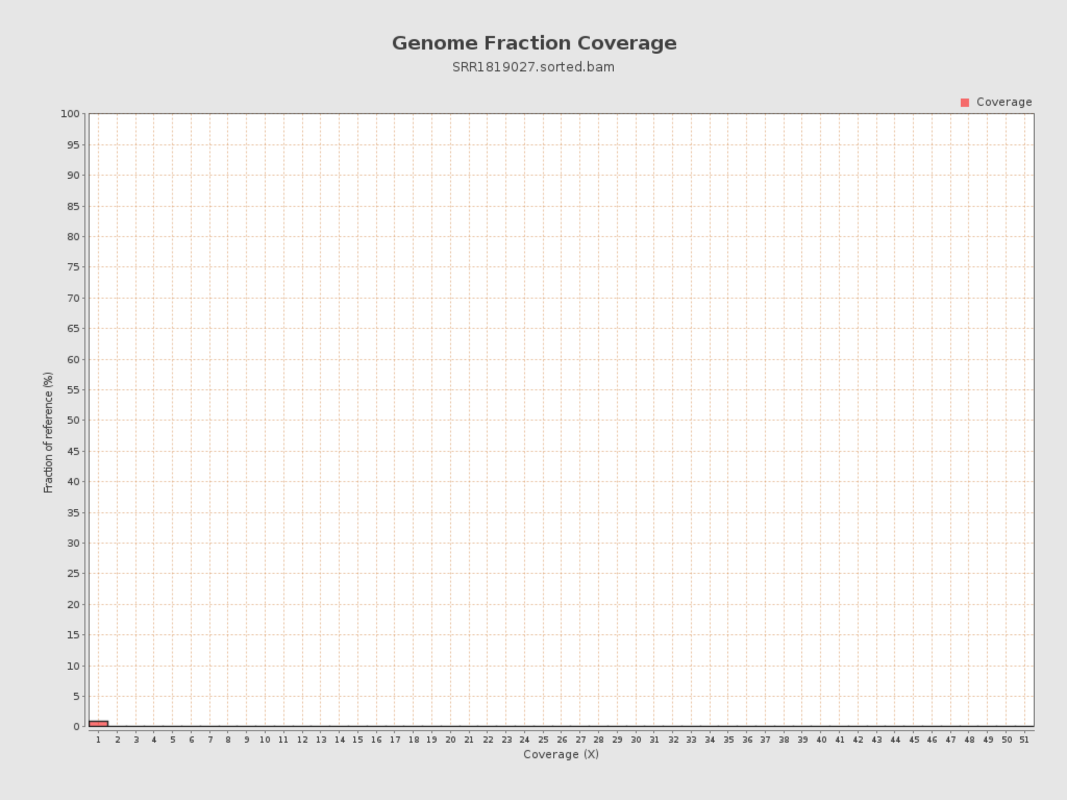
4. Results : Coverage Histogram



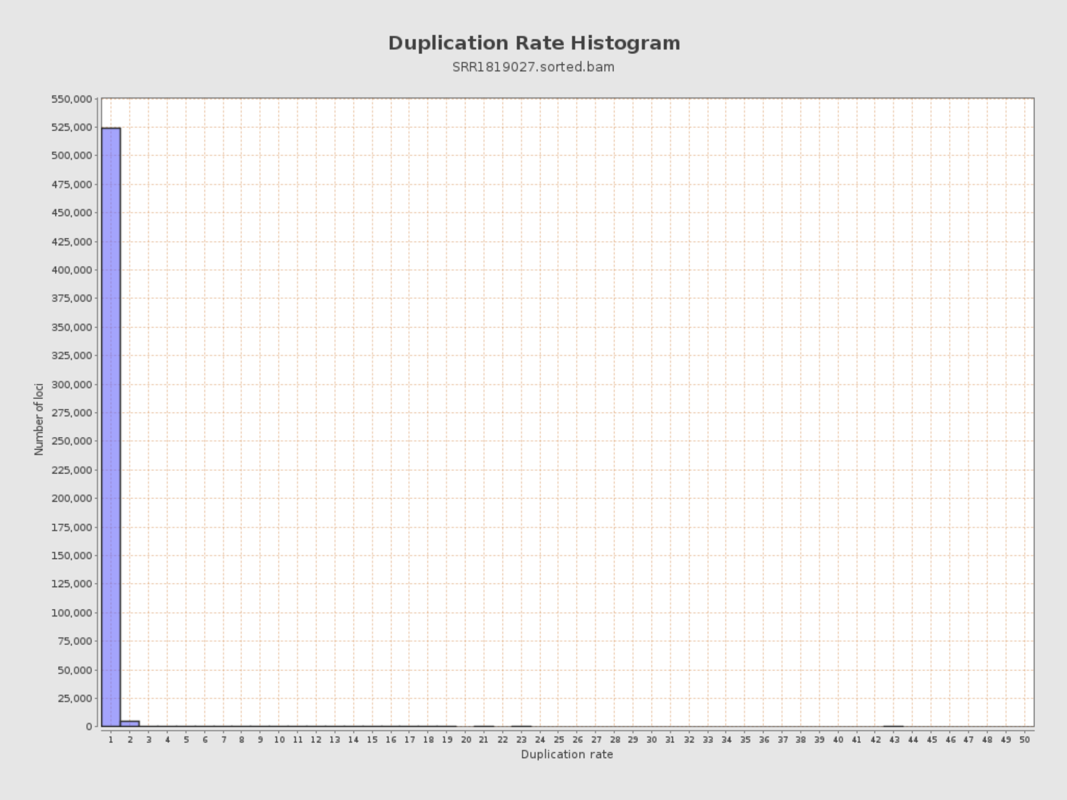
5. Results : Coverage Histogram (0-50X)



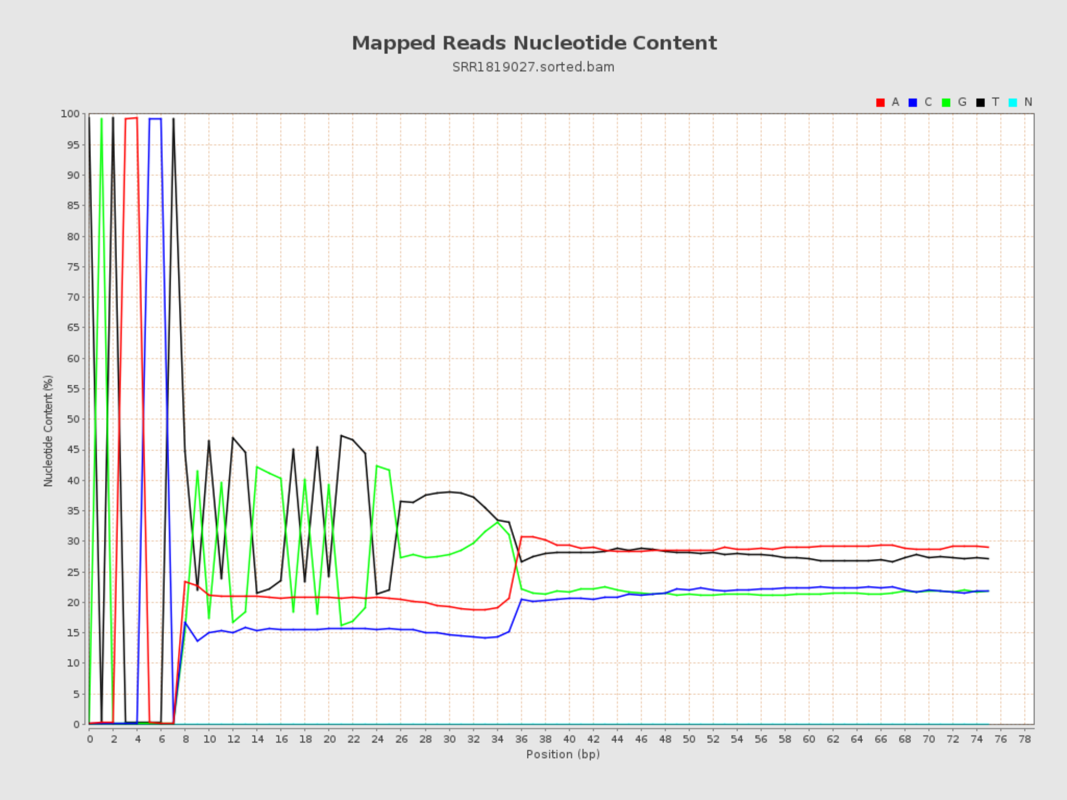
6. Results : Genome Fraction Coverage



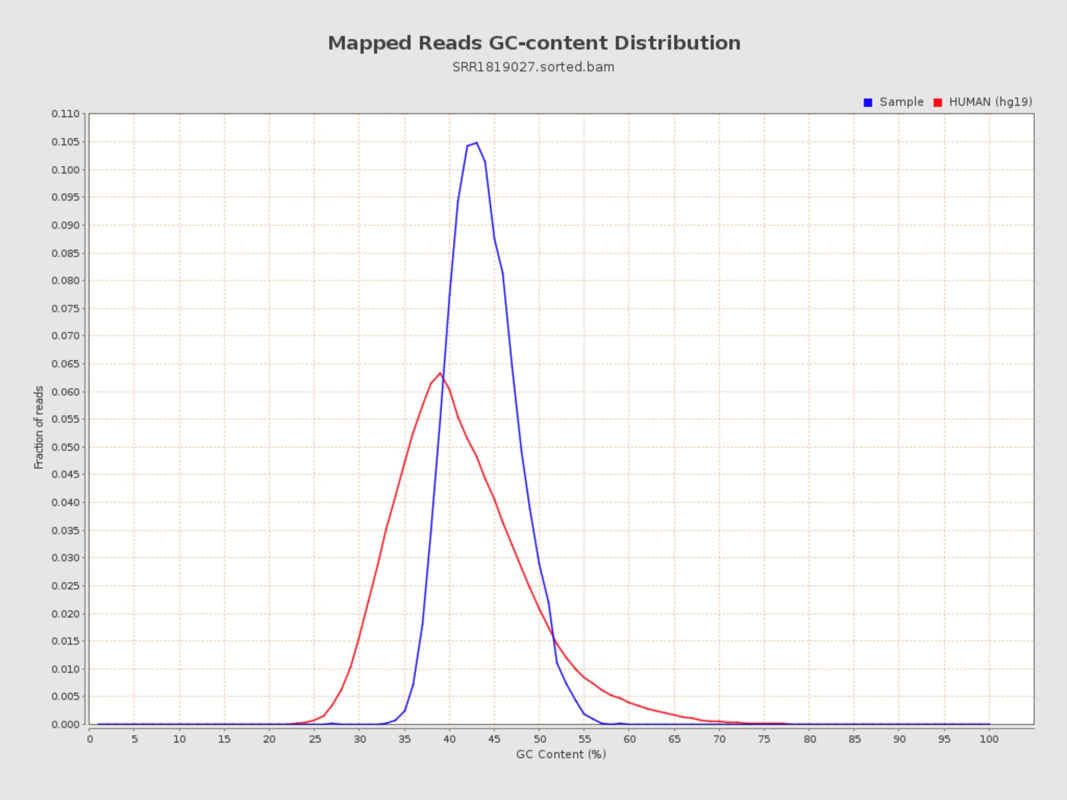
7. Results : Duplication Rate Histogram



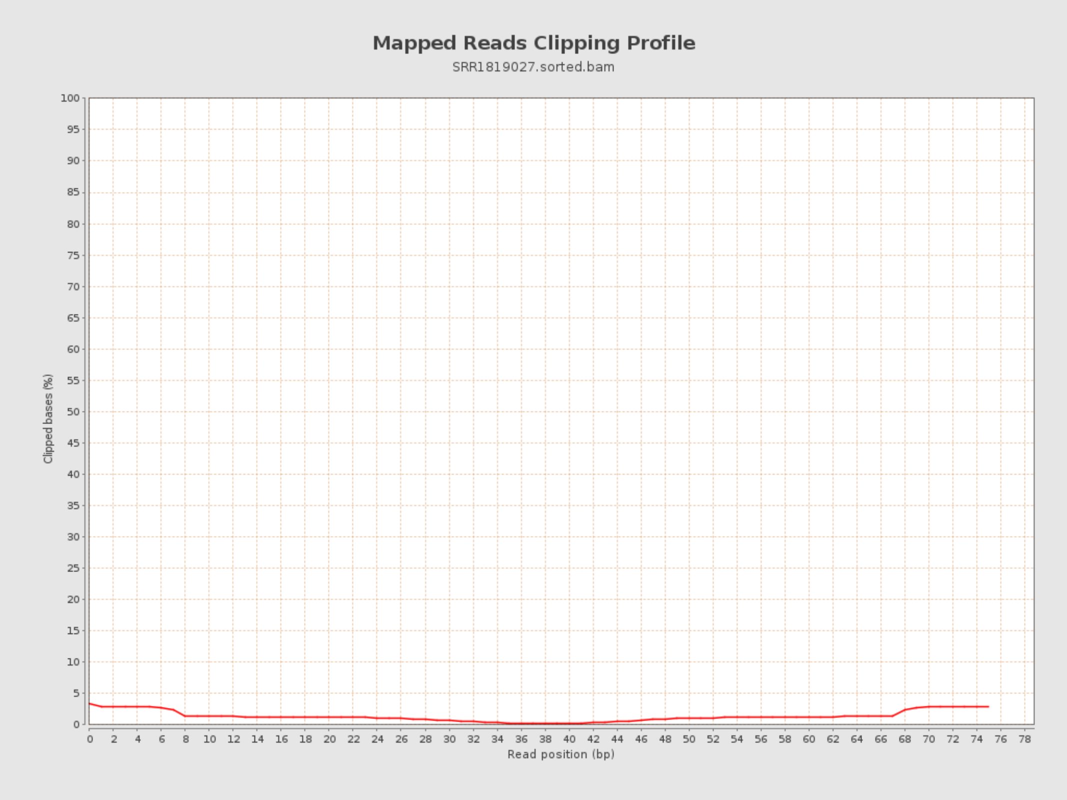
8. Results : Mapped Reads Nucleotide Content



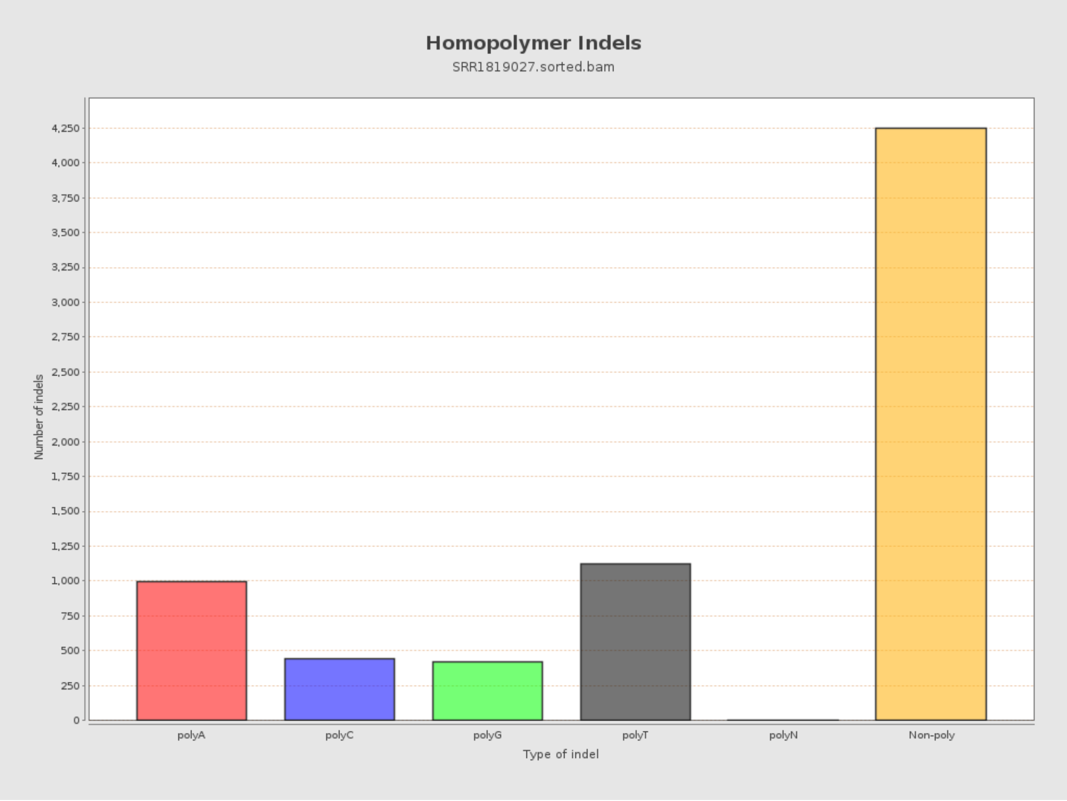
9. Results : Mapped Reads GC-content Distribution



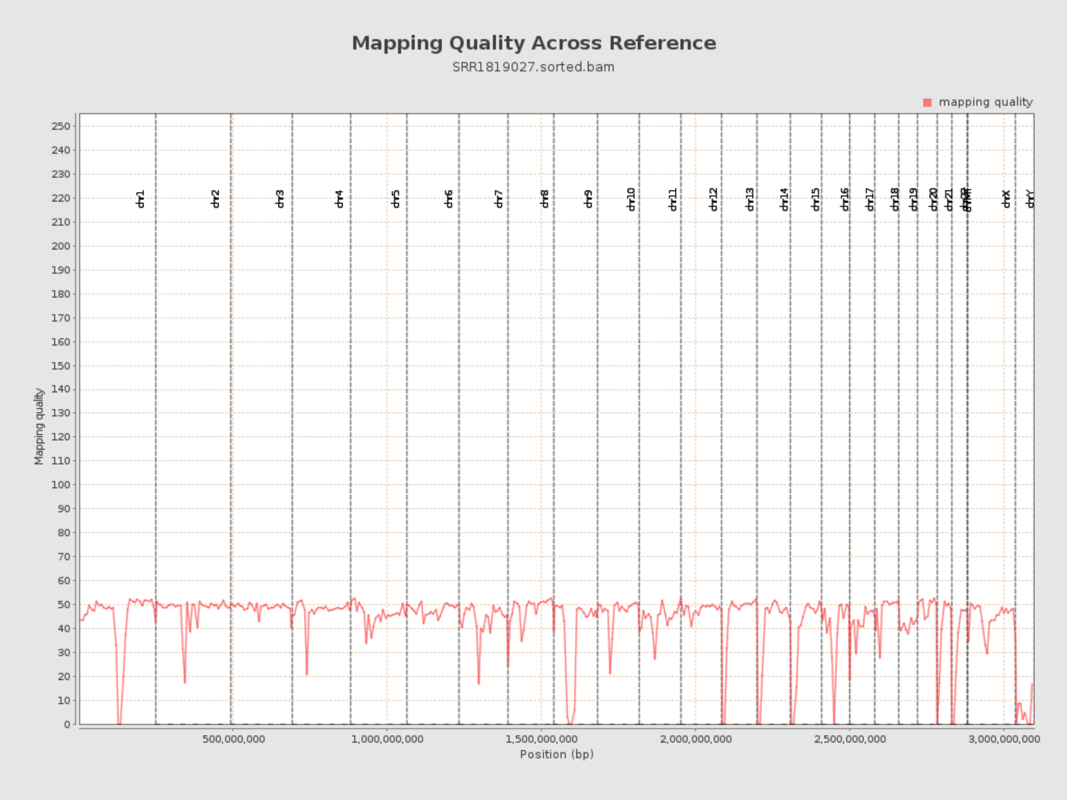
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram