Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819122.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_SRR1819122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,156,945
Mapped reads	1,037,490 / 89.67%
Unmapped reads	119,455 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,507 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	28,131 / 2.43%
Duplication rate	1.83%
Clipped reads	1,038,982 / 89.8%

2.2. ACGT Content

Number/percentage of A's	14,420,186 / 24.16%
Number/percentage of C's	10,836,897 / 18.16%
Number/percentage of T's	18,415,049 / 30.85%
Number/percentage of G's	16,013,091 / 26.83%
Number/percentage of N's	892 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.2022

2.4. Mapping Quality

Mean Mapping Quality	42.63

2.5. Mismatches and indels

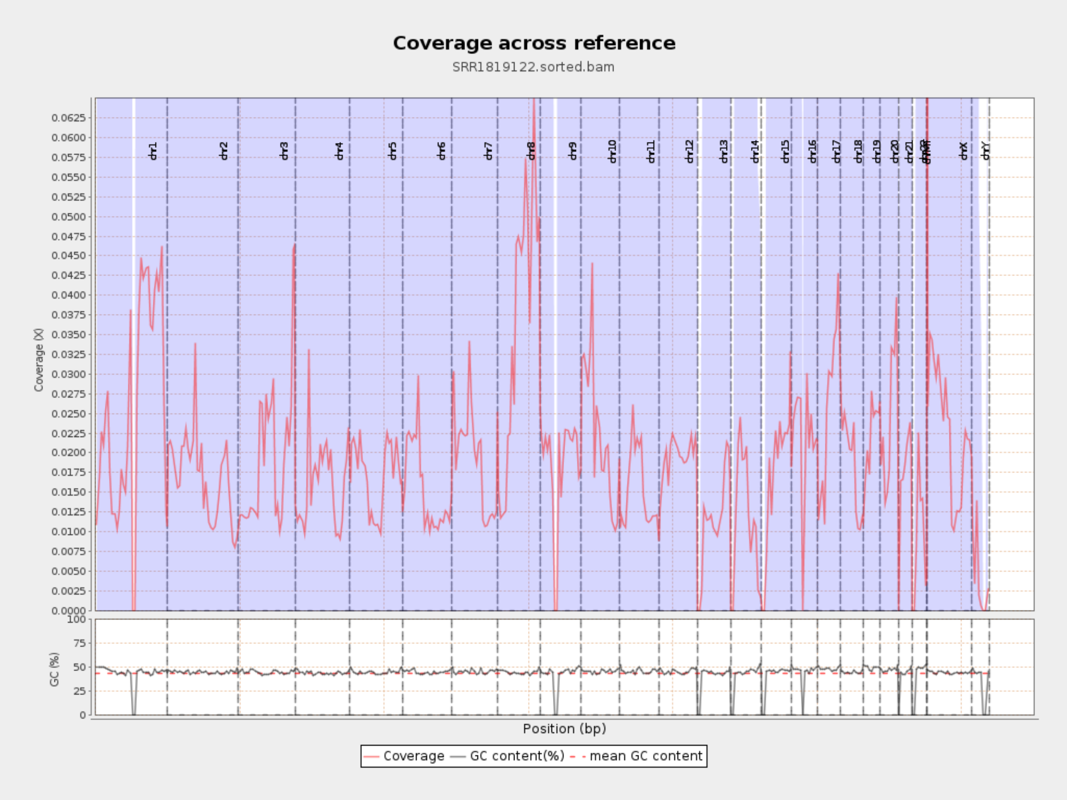
General error rate	0.54%
Mismatches	313,550
Insertions	4,012
Mapped reads with at least one insertion	0.38%
Deletions	10,330
Mapped reads with at least one deletion	0.99%
Homopolymer indels	41.75%

2.6. Chromosome stats

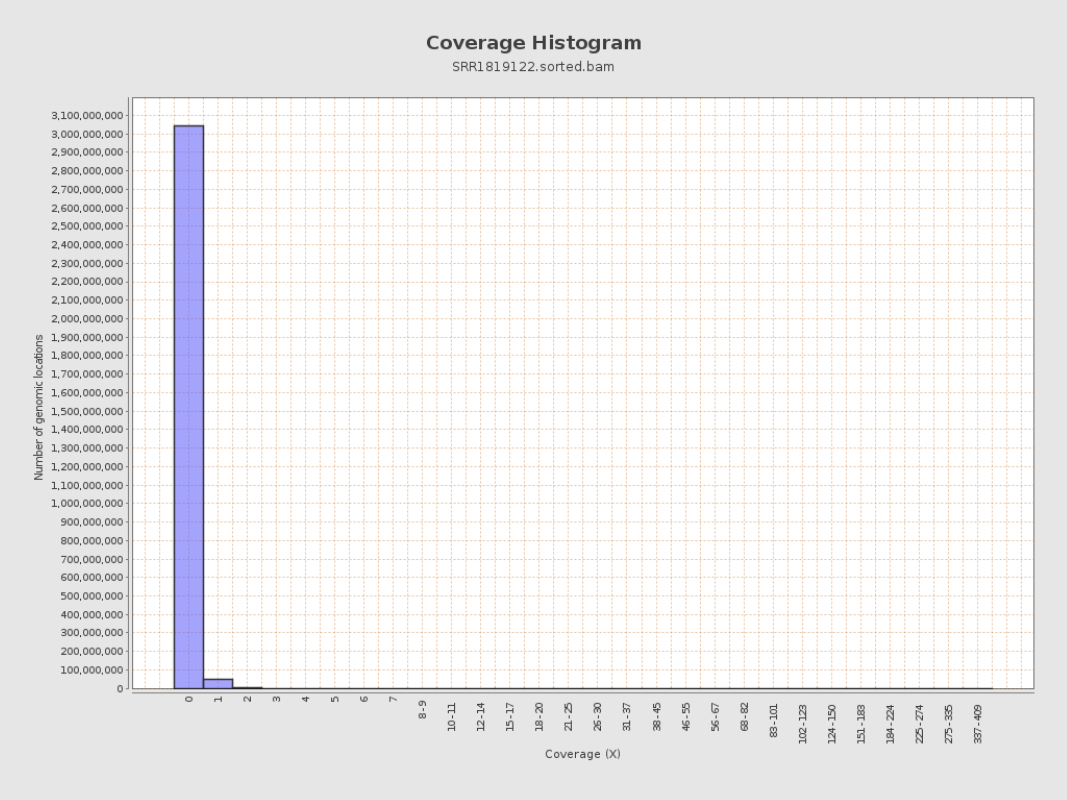
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6344199	0.0255	0.3374
chr2	243199373	4143505	0.017	0.2282
chr3	198022430	3754761	0.019	0.1492
chr4	191154276	3070123	0.0161	0.1518
chr5	180915260	3133651	0.0173	0.1405
chr6	171115067	2629871	0.0154	0.1667
chr7	159138663	3109360	0.0195	0.2431

chr8	146364022	5377318	0.0367	0.2288
chr9	141213431	2593122	0.0184	0.1847
chr10	135534747	3092079	0.0228	0.2327
chr11	135006516	2090690	0.0155	0.1906
chr12	133851895	2608075	0.0195	0.1501
chr13	115169878	1315480	0.0114	0.114
chr14	107349540	1243696	0.0116	0.1182
chr15	102531392	1737691	0.0169	0.1462
chr16	90354753	1931989	0.0214	0.1725
chr17	81195210	2070769	0.0255	0.1767
chr18	78077248	1448642	0.0186	0.3119
chr19	59128983	1305907	0.0221	0.2532
chr20	63025520	1539917	0.0244	0.1707
chr21	48129895	847168	0.0176	0.1529
chr22	51304566	487859	0.0095	0.105
chrMT	16571	12620	0.7616	0.9807
chrX	155270560	3584123	0.0231	0.1786
chrY	59373566	230770	0.0039	0.1194

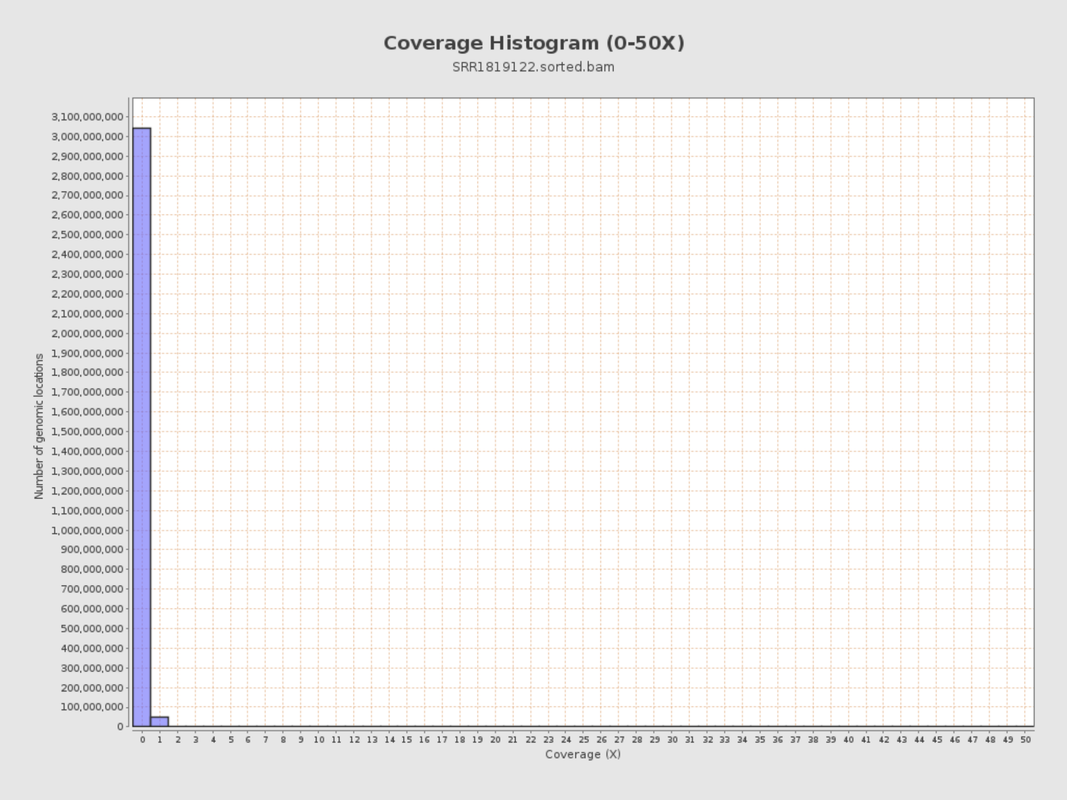
3. Results : Coverage across reference



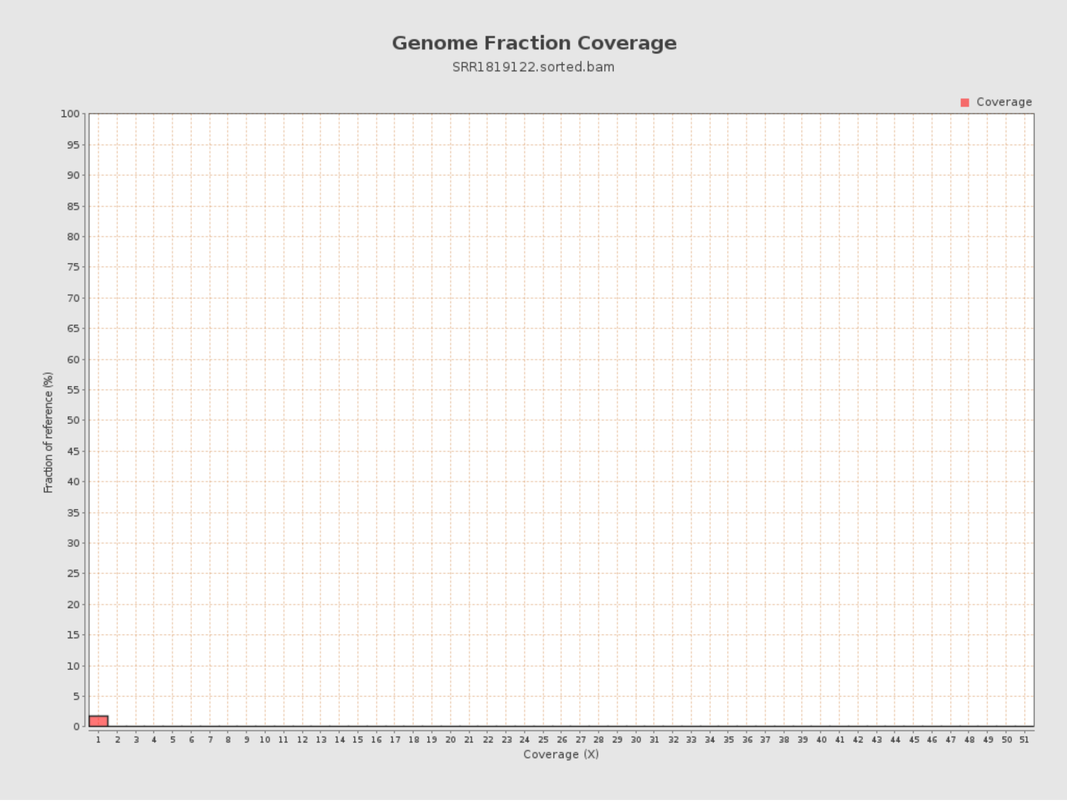
4. Results : Coverage Histogram



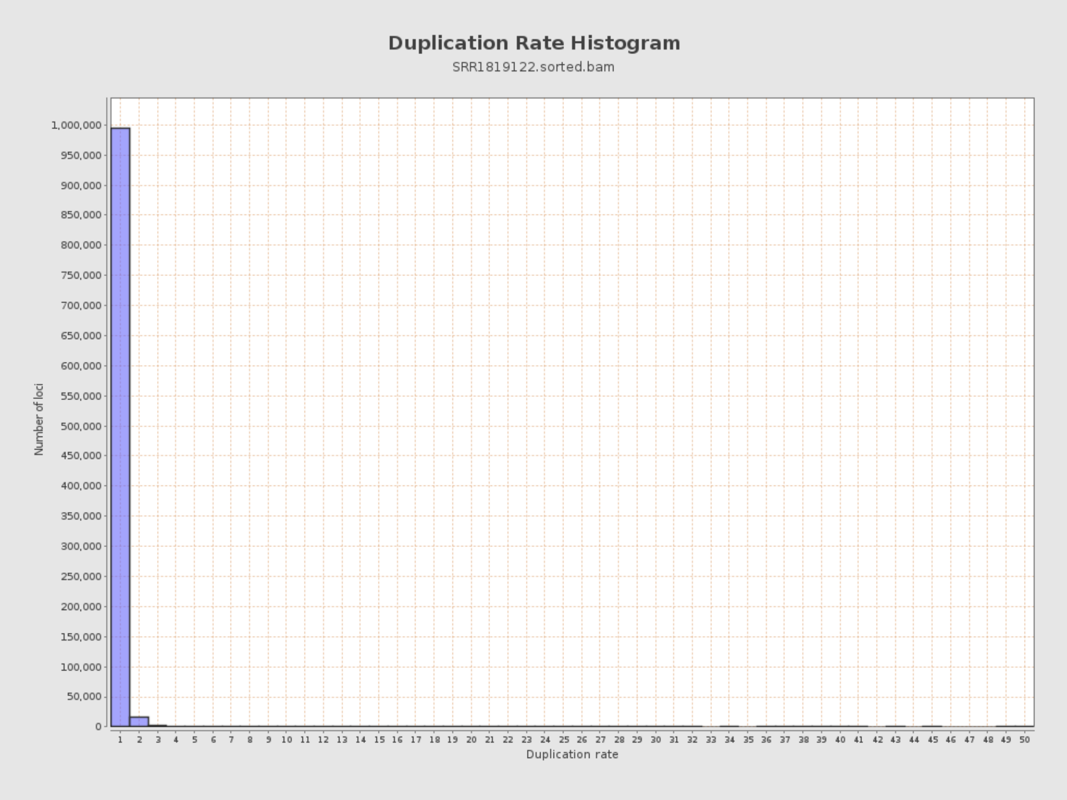
5. Results : Coverage Histogram (0-50X)



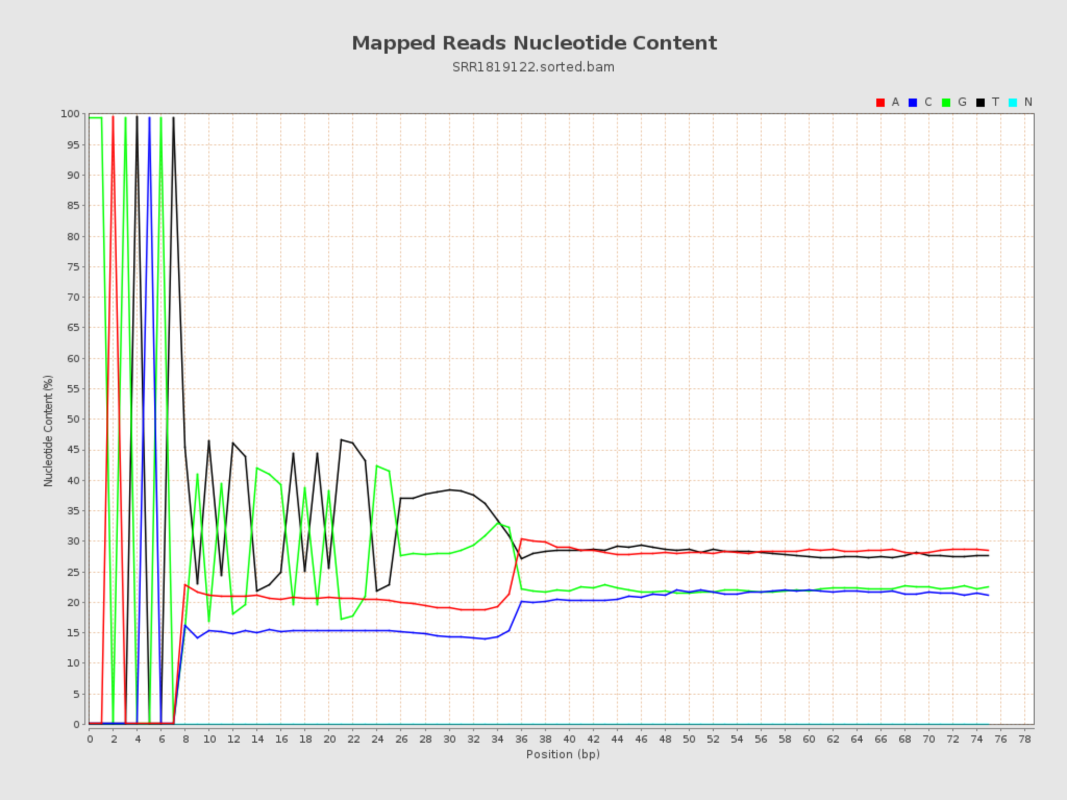
6. Results : Genome Fraction Coverage



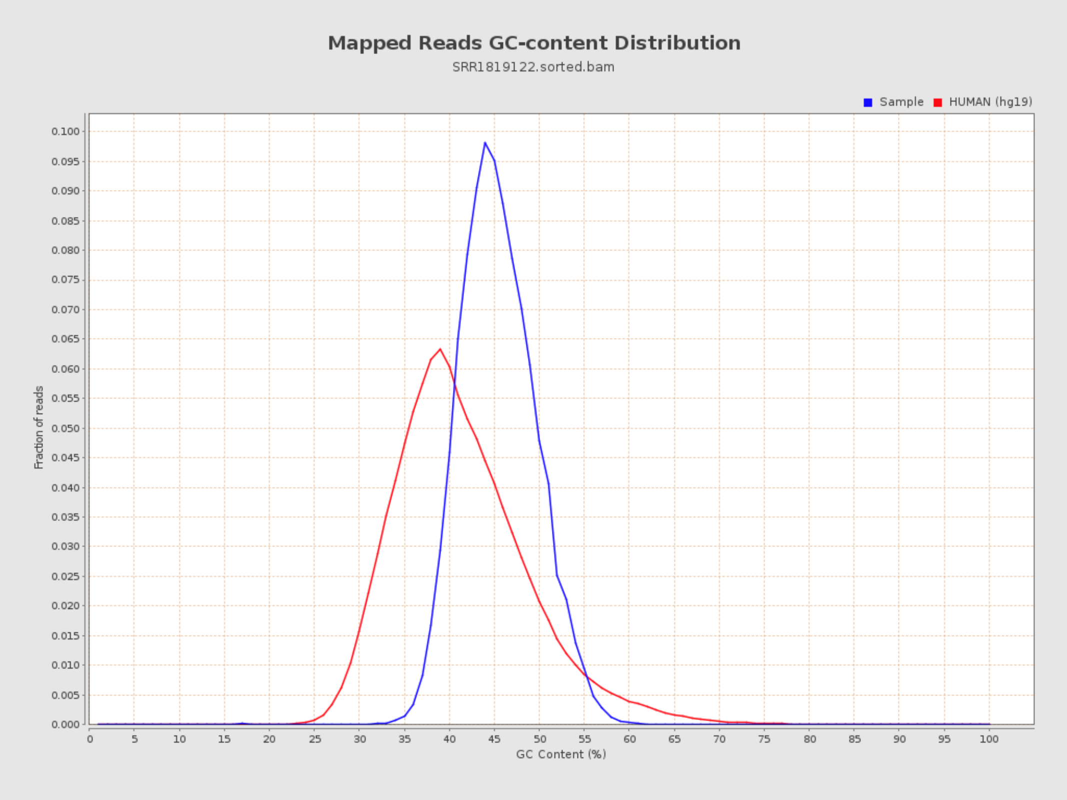
7. Results : Duplication Rate Histogram



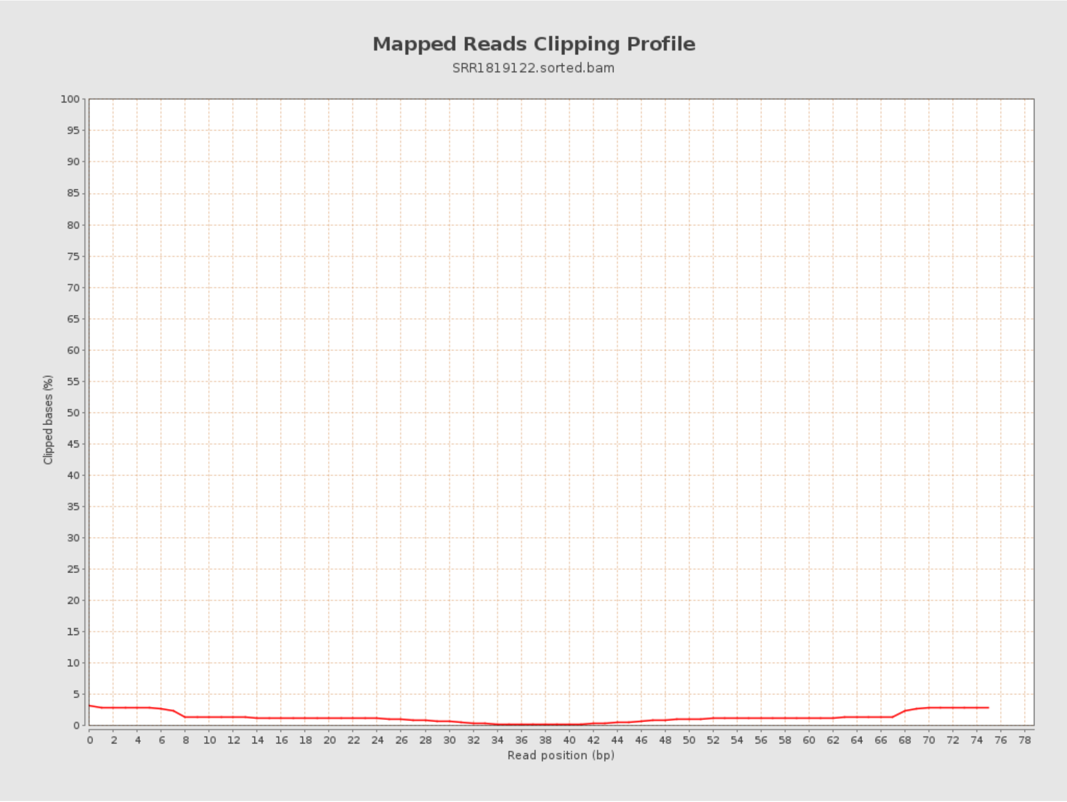
8. Results : Mapped Reads Nucleotide Content



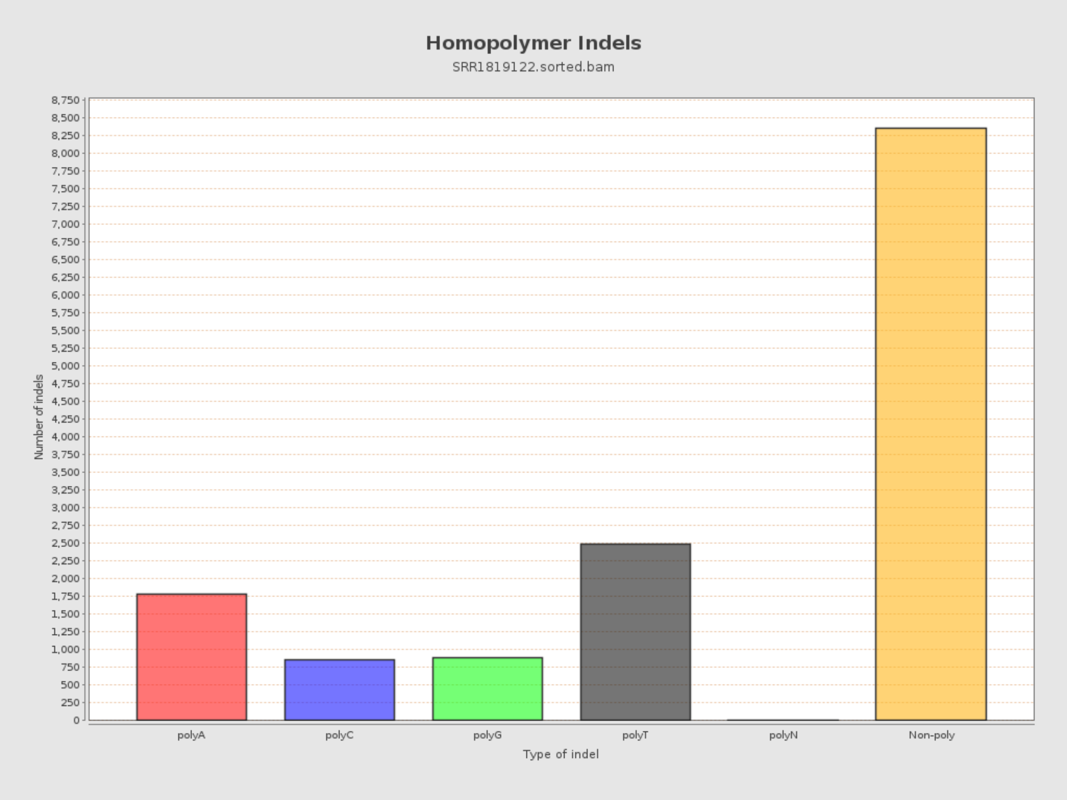
9. Results : Mapped Reads GC-content Distribution



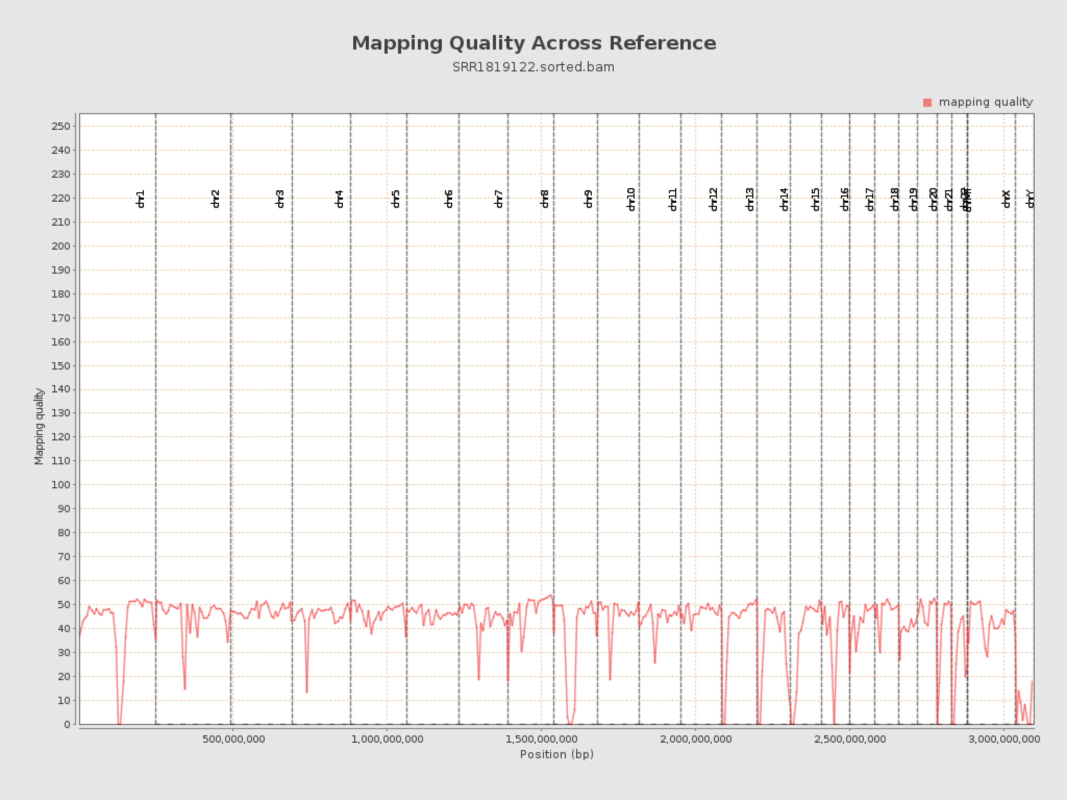
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram