Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819046.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_SRR1819046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,989,240
Mapped reads	1,270,952 / 63.89%
Unmapped reads	718,288 / 36.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,451 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	30,043 / 1.51%
Duplication rate	1.73%
Clipped reads	1,274,354 / 64.06%

2.2. ACGT Content

Number/percentage of A's	18,019,452 / 25.18%
Number/percentage of C's	14,479,542 / 20.24%
Number/percentage of T's	21,836,916 / 30.52%
Number/percentage of G's	17,213,351 / 24.06%
Number/percentage of N's	1,623 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.1982

2.4. Mapping Quality

Mean Mapping Quality	42.73

2.5. Mismatches and indels

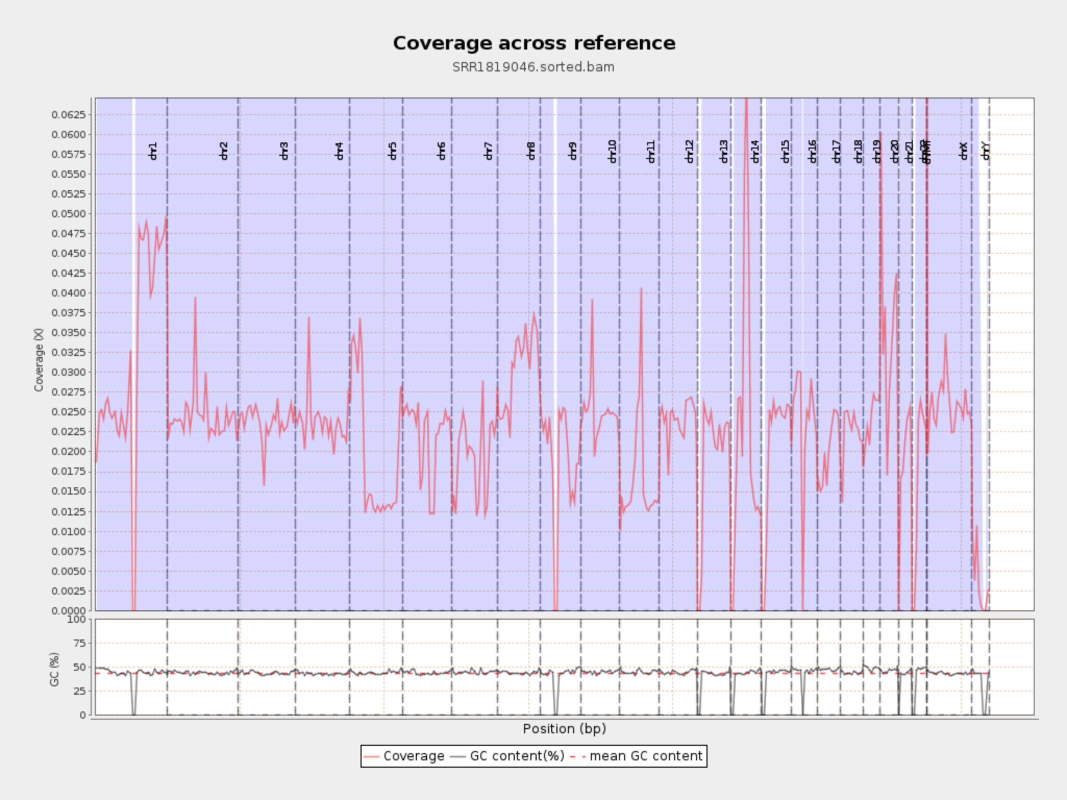
General error rate	0.51%
Mismatches	356,799
Insertions	4,781
Mapped reads with at least one insertion	0.37%
Deletions	11,650
Mapped reads with at least one deletion	0.91%
Homopolymer indels	39.97%

2.6. Chromosome stats

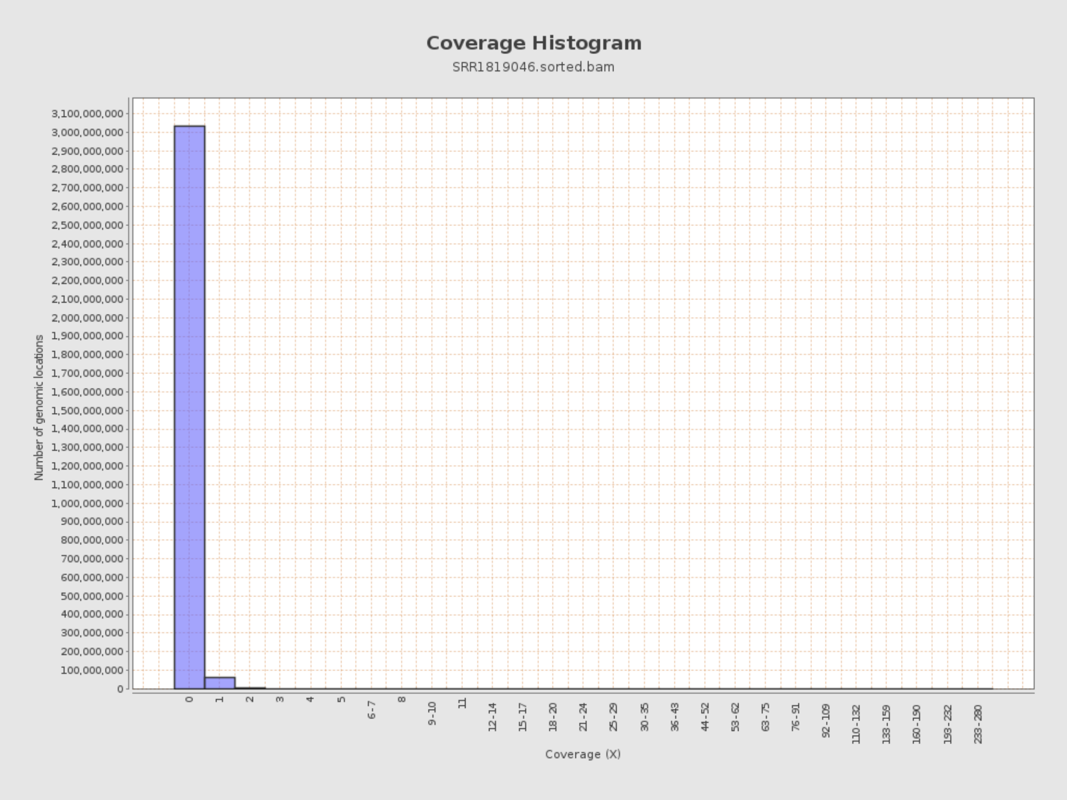
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7976984	0.032	0.2822
chr2	243199373	5970575	0.0246	0.2241
chr3	198022430	4714274	0.0238	0.1658
chr4	191154276	4572132	0.0239	0.179
chr5	180915260	3548857	0.0196	0.1519
chr6	171115067	3749926	0.0219	0.1661
chr7	159138663	3103843	0.0195	0.1739

chr8	146364022	4455291	0.0304	0.209
chr9	141213431	2622059	0.0186	0.2036
chr10	135534747	3406632	0.0251	0.2179
chr11	135006516	2276989	0.0169	0.1834
chr12	133851895	3235207	0.0242	0.1706
chr13	115169878	2206183	0.0192	0.1473
chr14	107349540	2514642	0.0234	0.1756
chr15	102531392	2079581	0.0203	0.1537
chr16	90354753	2130596	0.0236	0.1796
chr17	81195210	1633583	0.0201	0.1715
chr18	78077248	1734371	0.0222	0.3509
chr19	59128983	1427058	0.0241	0.2269
chr20	63025520	2200868	0.0349	0.2053
chr21	48129895	912629	0.019	0.1582
chr22	51304566	862412	0.0168	0.1395
chrMT	16571	1383	0.0835	0.3146
chrX	155270560	4030571	0.026	0.1906
chrY	59373566	203668	0.0034	0.0851

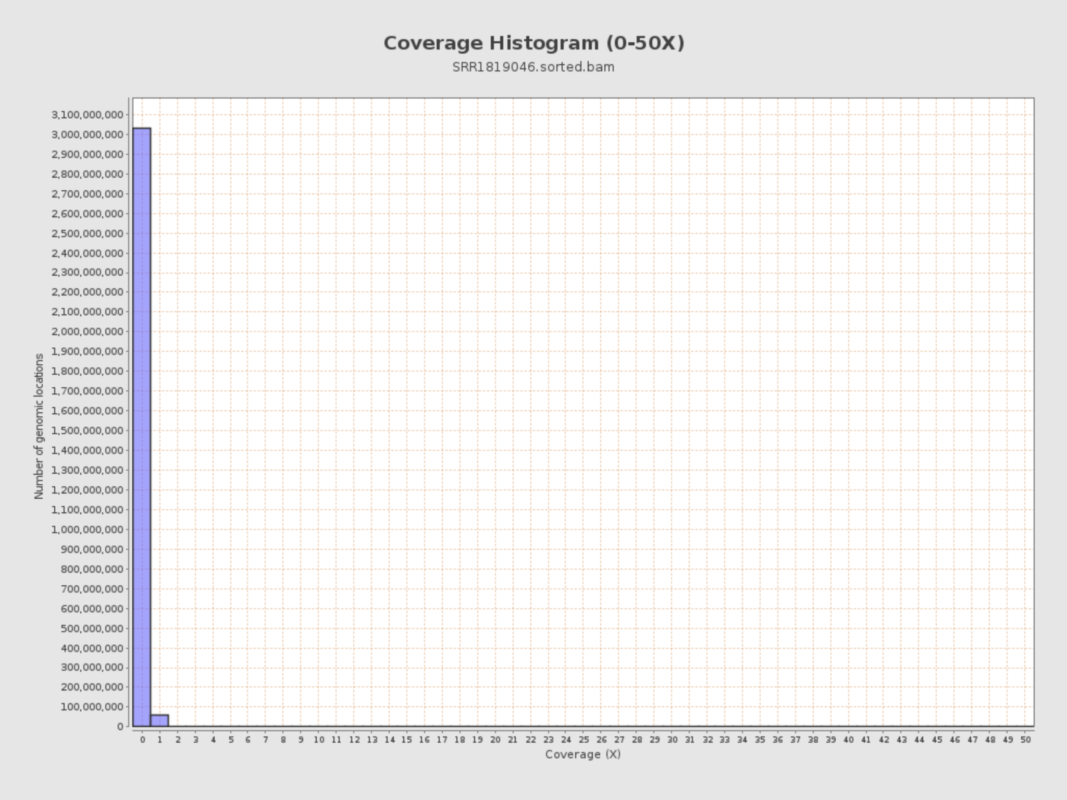
3. Results : Coverage across reference



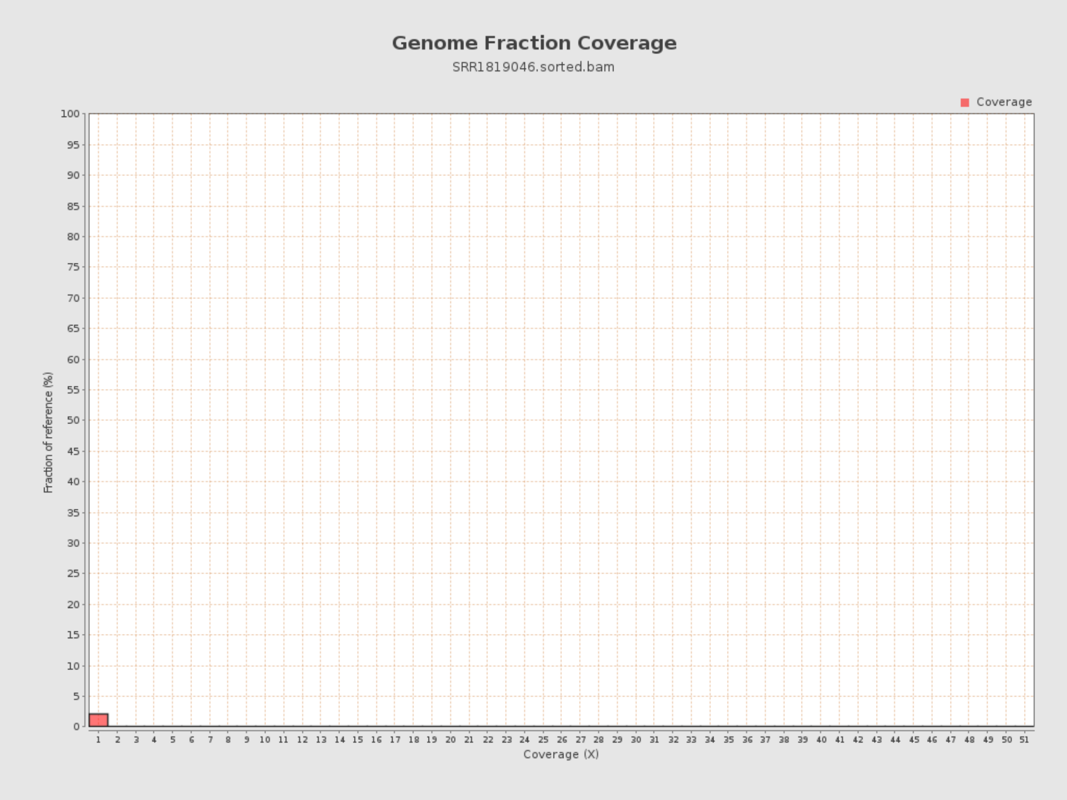
4. Results : Coverage Histogram



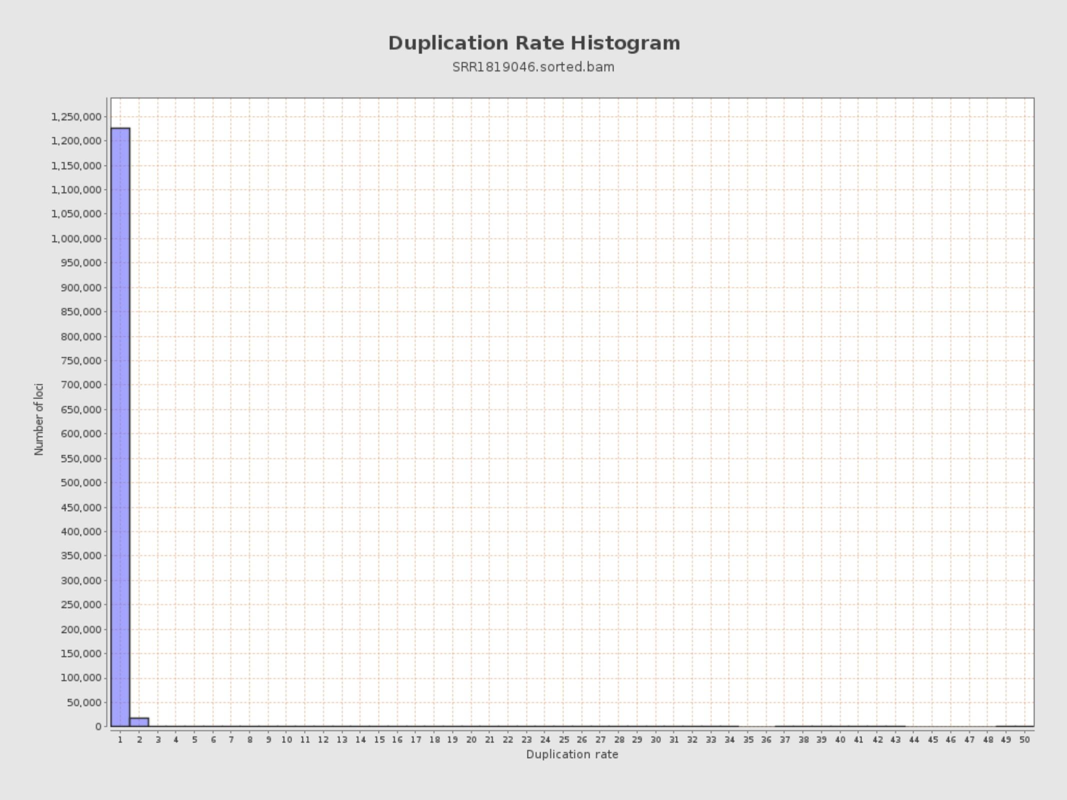
5. Results : Coverage Histogram (0-50X)



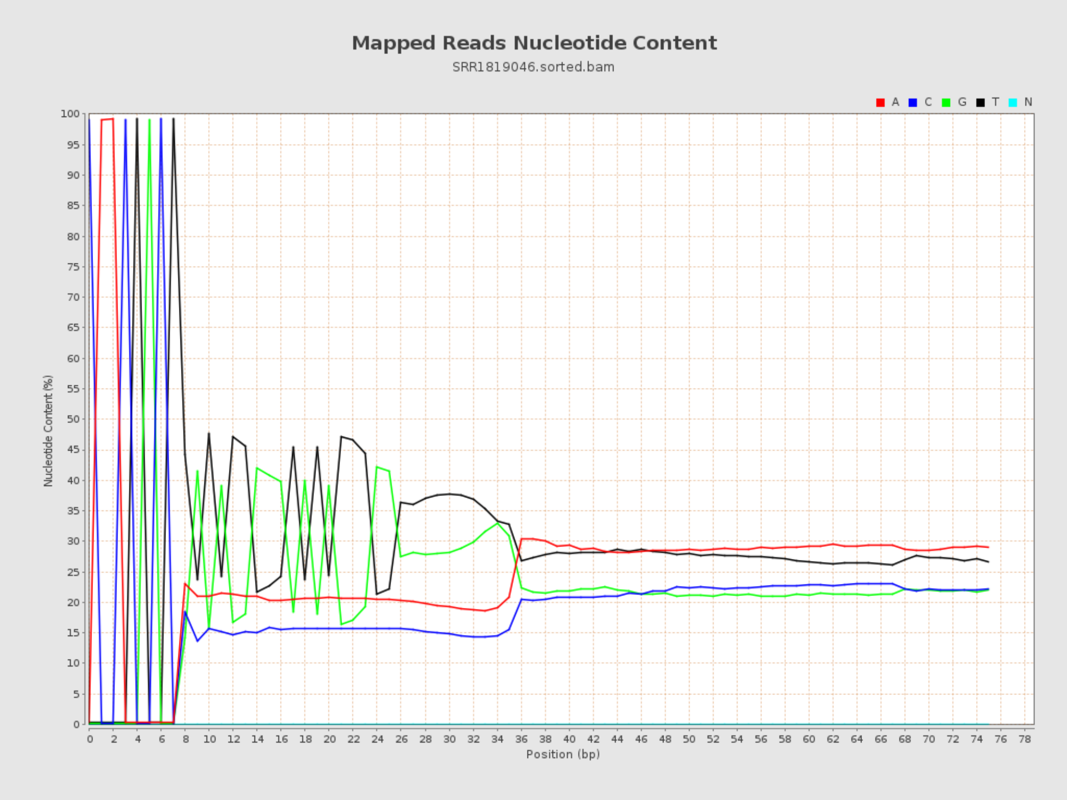
6. Results : Genome Fraction Coverage



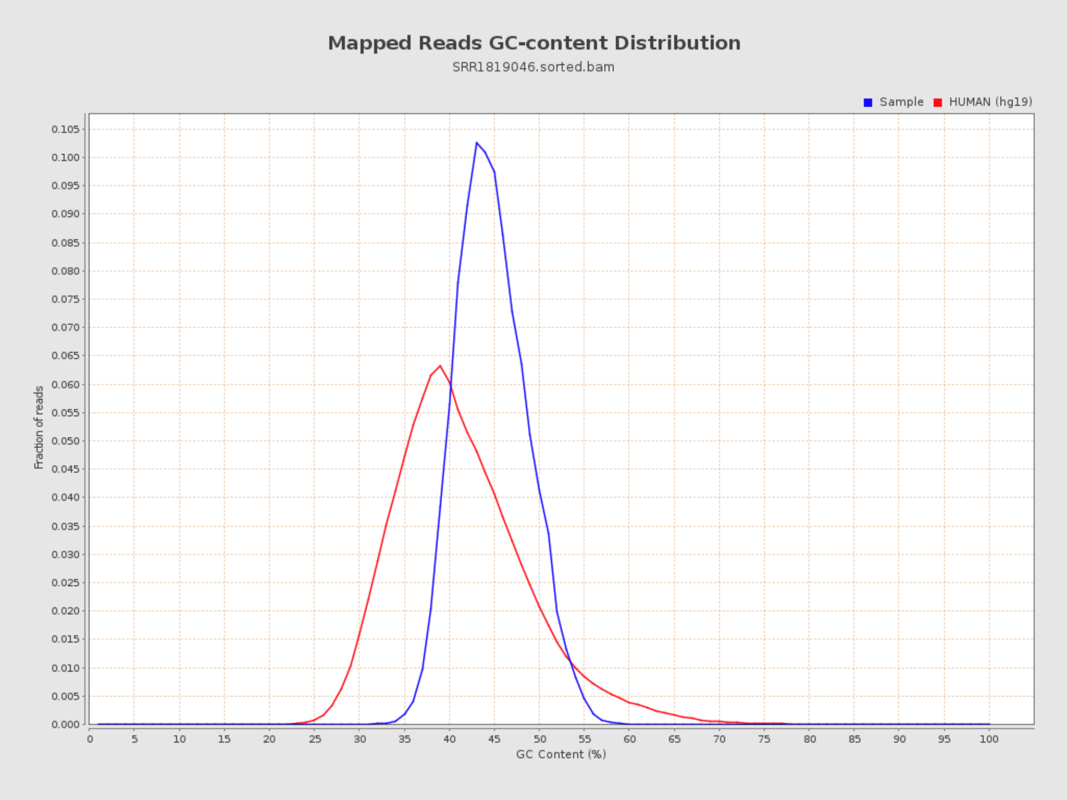
7. Results : Duplication Rate Histogram



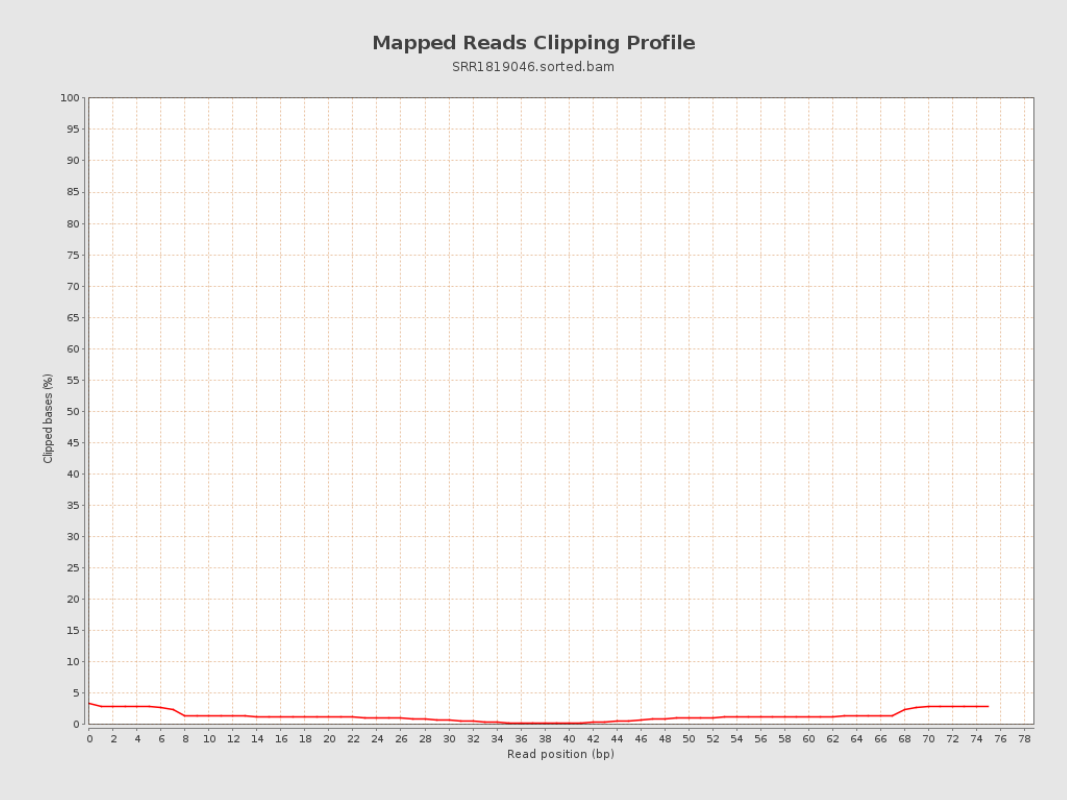
8. Results : Mapped Reads Nucleotide Content



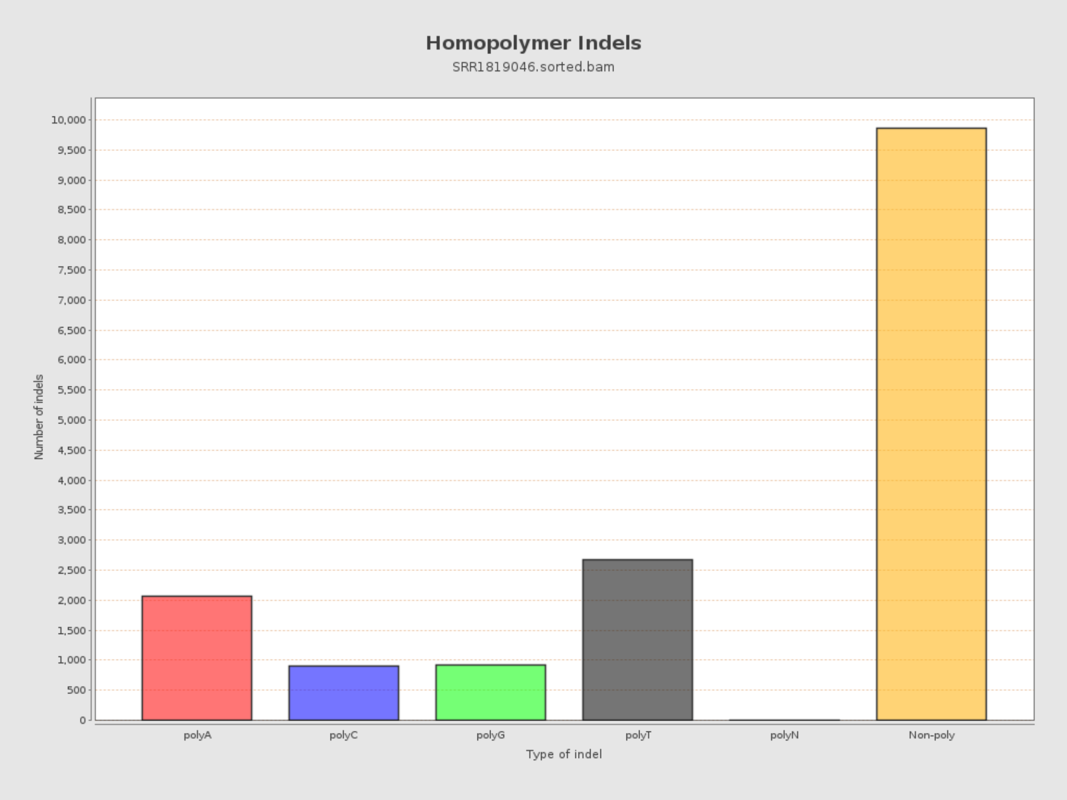
9. Results : Mapped Reads GC-content Distribution



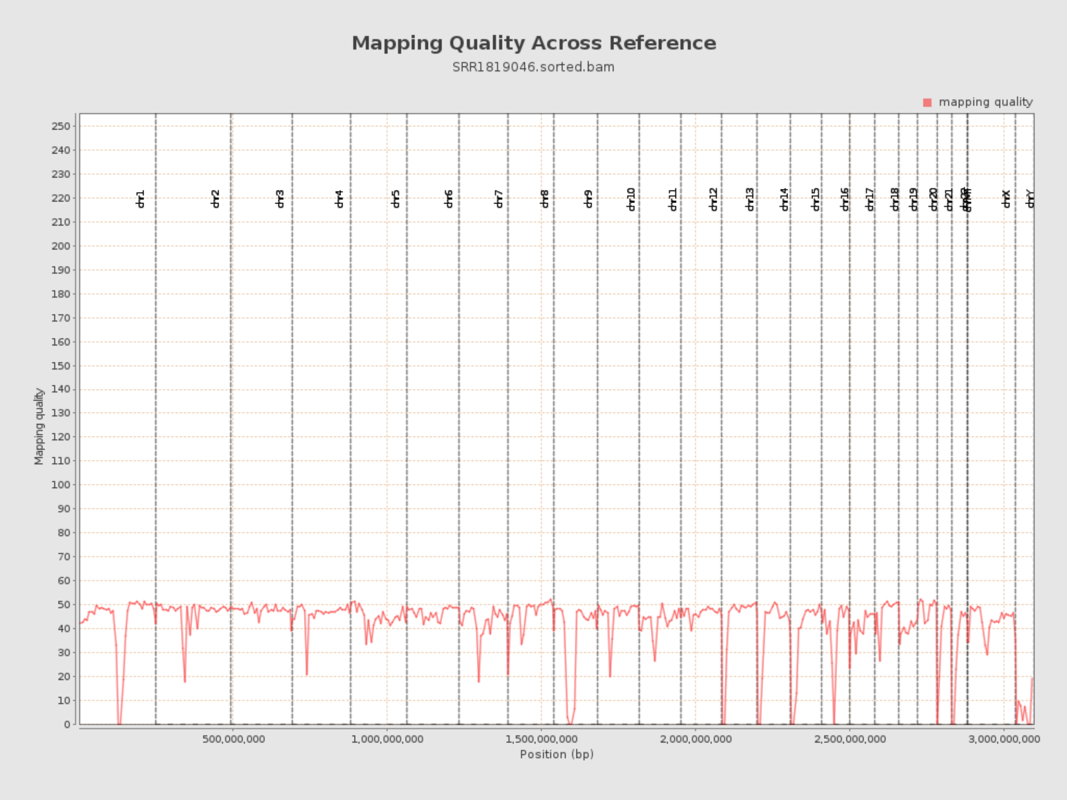
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram