Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:01:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819033.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_SRR1819033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:01:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,009,137
Mapped reads	908,924 / 90.07%
Unmapped reads	100,213 / 9.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,568 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	14,973 / 1.48%
Duplication rate	1.27%
Clipped reads	910,849 / 90.26%

2.2. ACGT Content

Number/percentage of A's	12,755,154 / 24.56%
Number/percentage of C's	10,283,730 / 19.8%
Number/percentage of T's	16,040,284 / 30.88%
Number/percentage of G's	12,856,586 / 24.75%
Number/percentage of N's	1,173 / 0%
GC Percentage	44.55%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1527

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

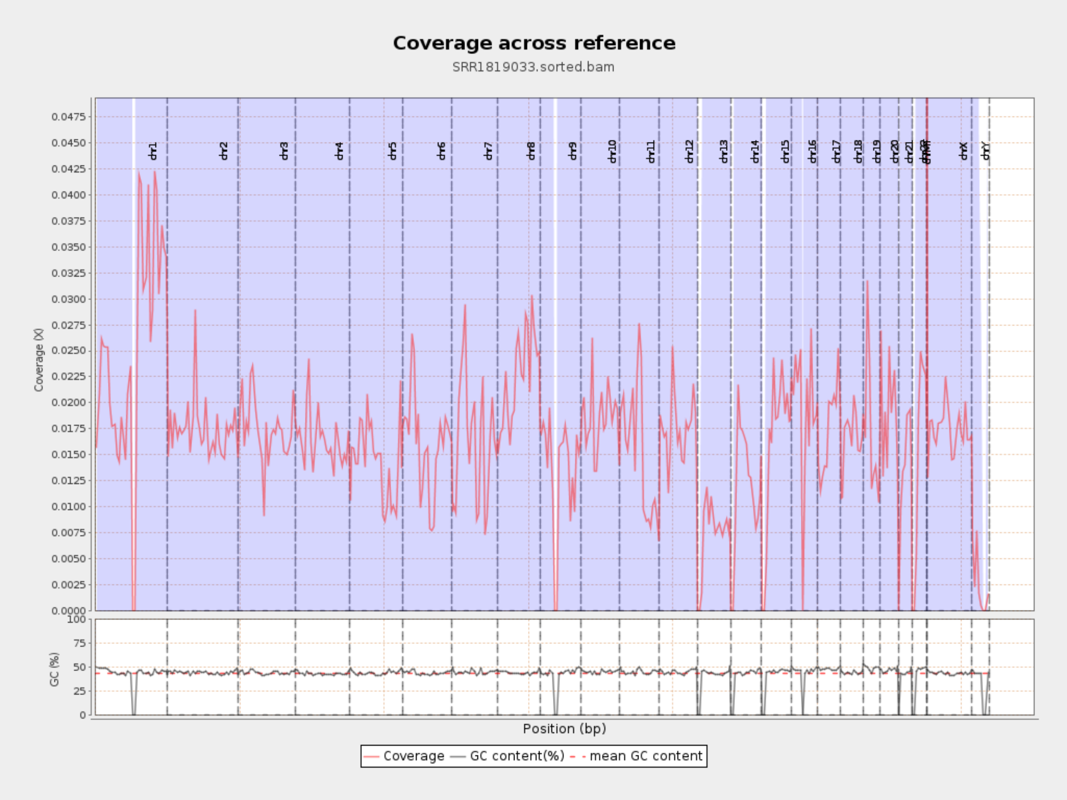
General error rate	0.5%
Mismatches	253,890
Insertions	3,317
Mapped reads with at least one insertion	0.36%
Deletions	8,308
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.09%

2.6. Chromosome stats

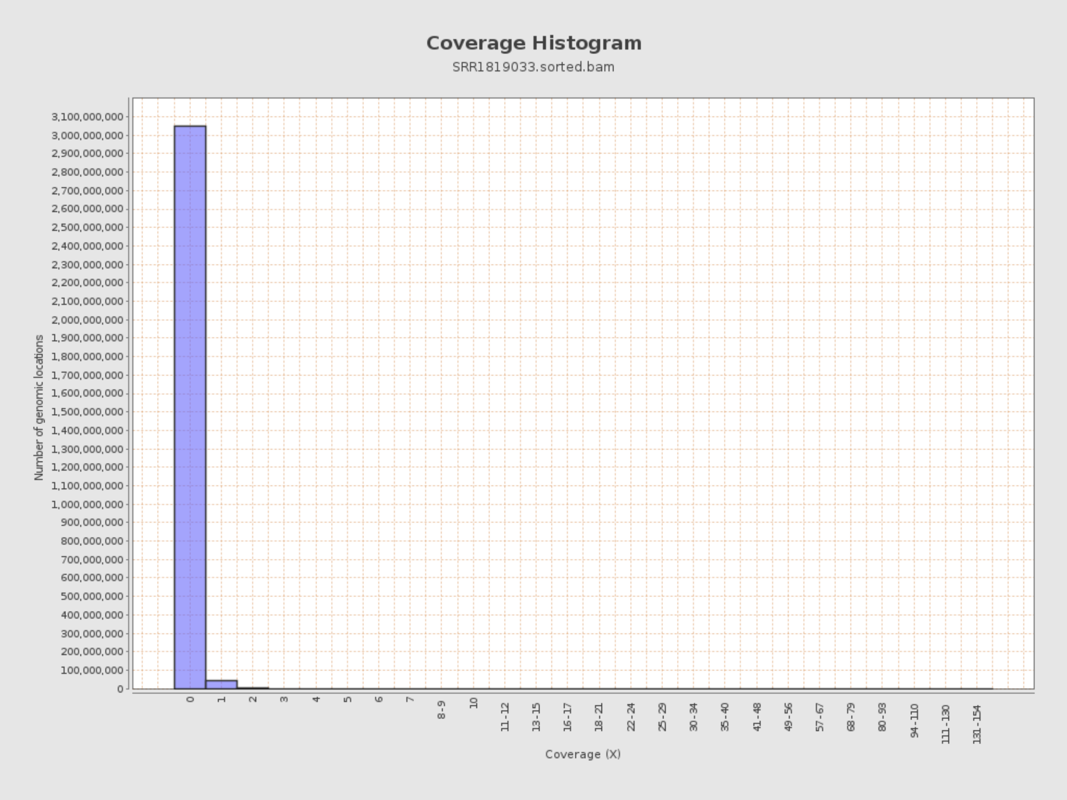
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6254776	0.0251	0.2062
chr2	243199373	4258260	0.0175	0.1705
chr3	198022430	3459659	0.0175	0.139
chr4	191154276	3146141	0.0165	0.1405
chr5	180915260	2627767	0.0145	0.127
chr6	171115067	2735558	0.016	0.1369
chr7	159138663	2609575	0.0164	0.145

chr8	146364022	3288160	0.0225	0.1656
chr9	141213431	1895309	0.0134	0.151
chr10	135534747	2522340	0.0186	0.1739
chr11	135006516	2118356	0.0157	0.1552
chr12	133851895	2358686	0.0176	0.1401
chr13	115169878	846520	0.0074	0.0894
chr14	107349540	1254004	0.0117	0.1194
chr15	102531392	1621370	0.0158	0.1326
chr16	90354753	1730703	0.0192	0.1522
chr17	81195210	1407216	0.0173	0.1403
chr18	78077248	1288591	0.0165	0.228
chr19	59128983	1030362	0.0174	0.1667
chr20	63025520	1205428	0.0191	0.1458
chr21	48129895	655051	0.0136	0.128
chr22	51304566	773264	0.0151	0.1296
chrMT	16571	1202	0.0725	0.2912
chrX	155270560	2720801	0.0175	0.1469
chrY	59373566	141954	0.0024	0.0633

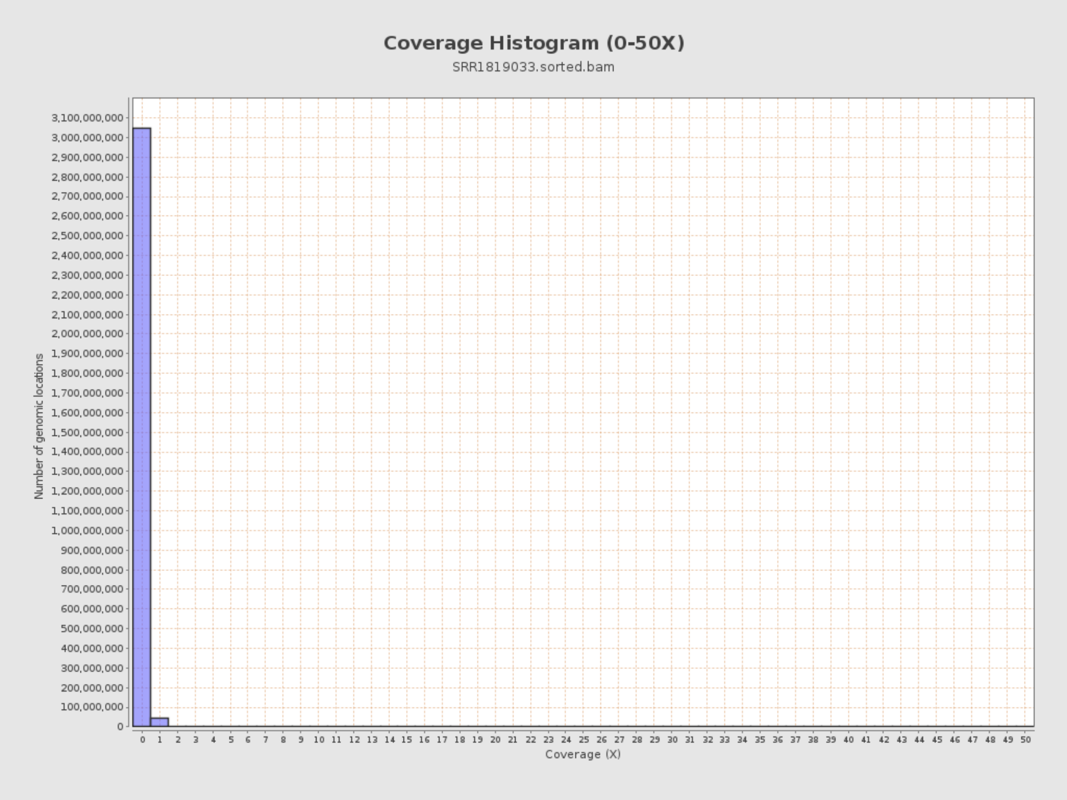
3. Results : Coverage across reference



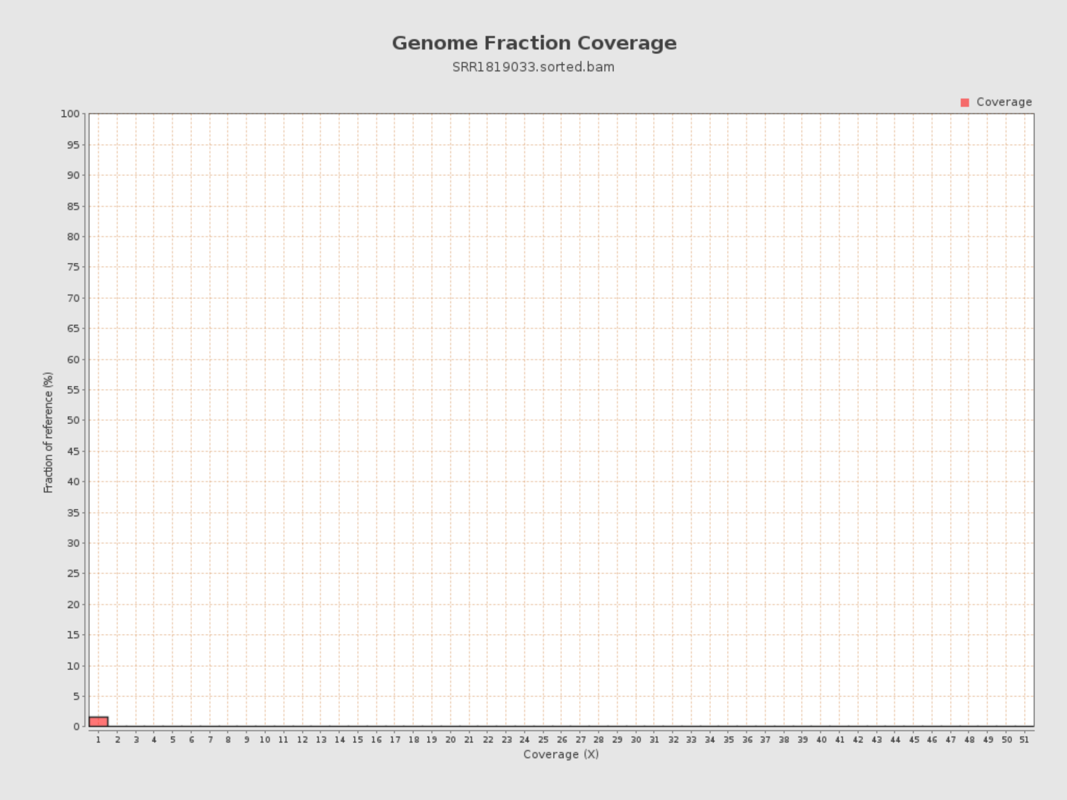
4. Results : Coverage Histogram



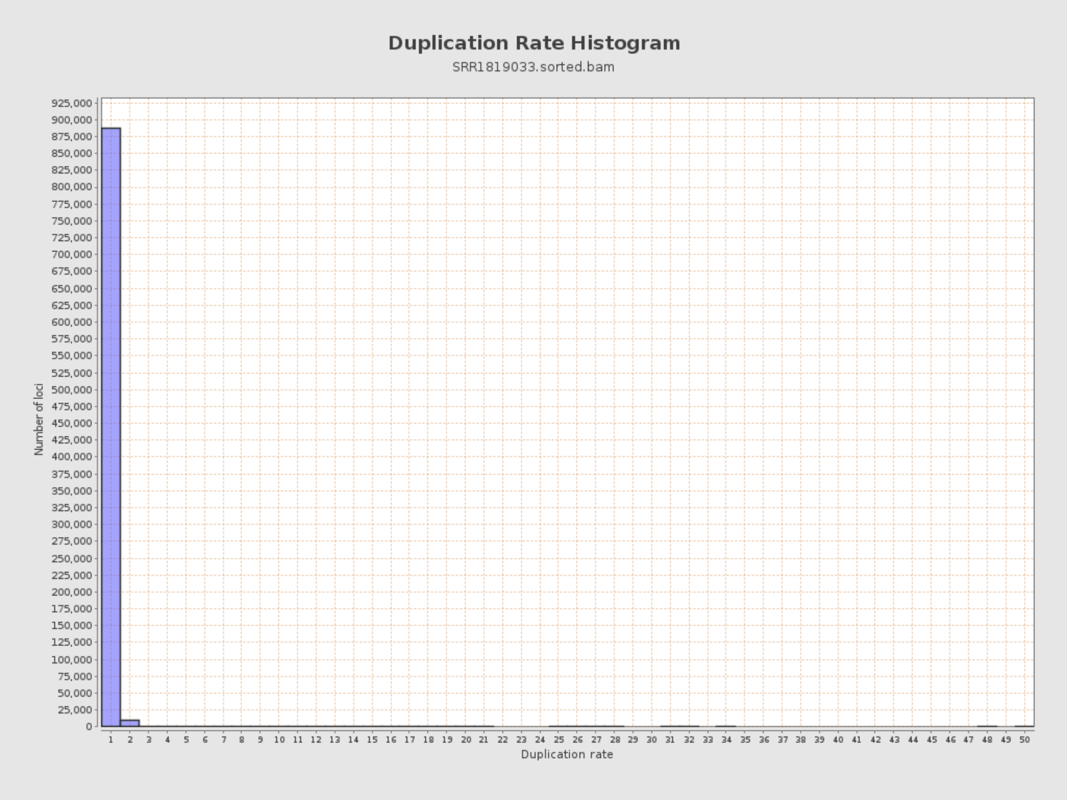
5. Results : Coverage Histogram (0-50X)



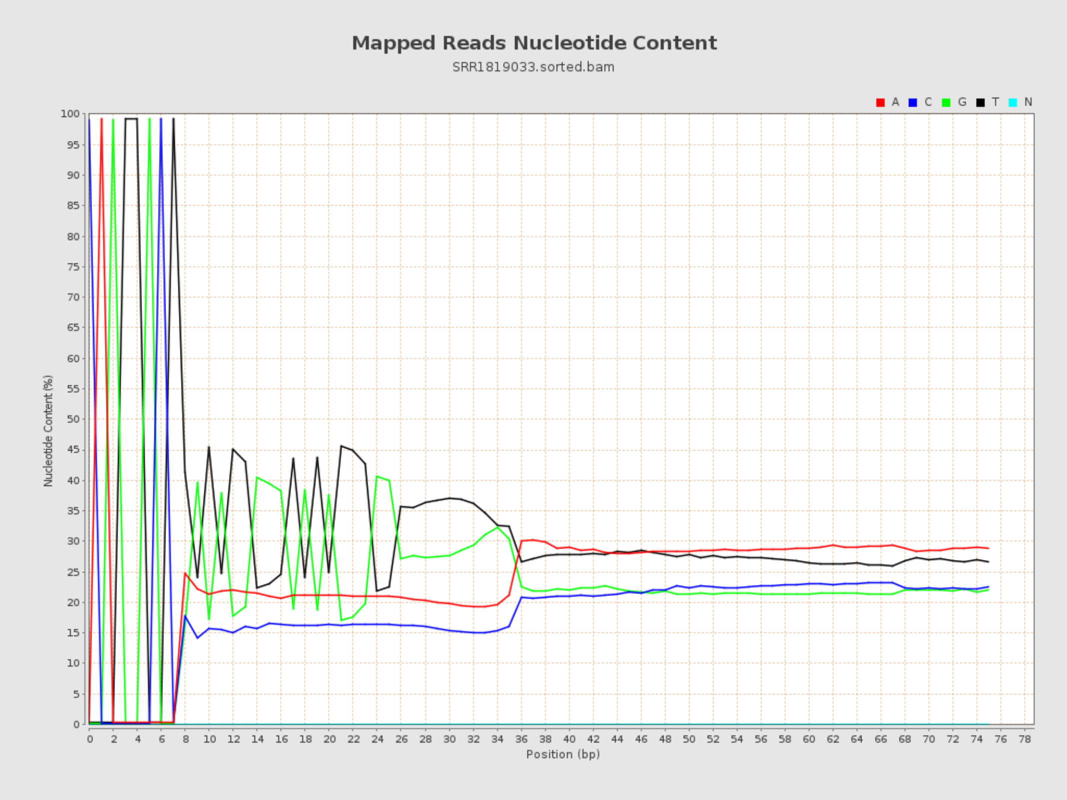
6. Results : Genome Fraction Coverage



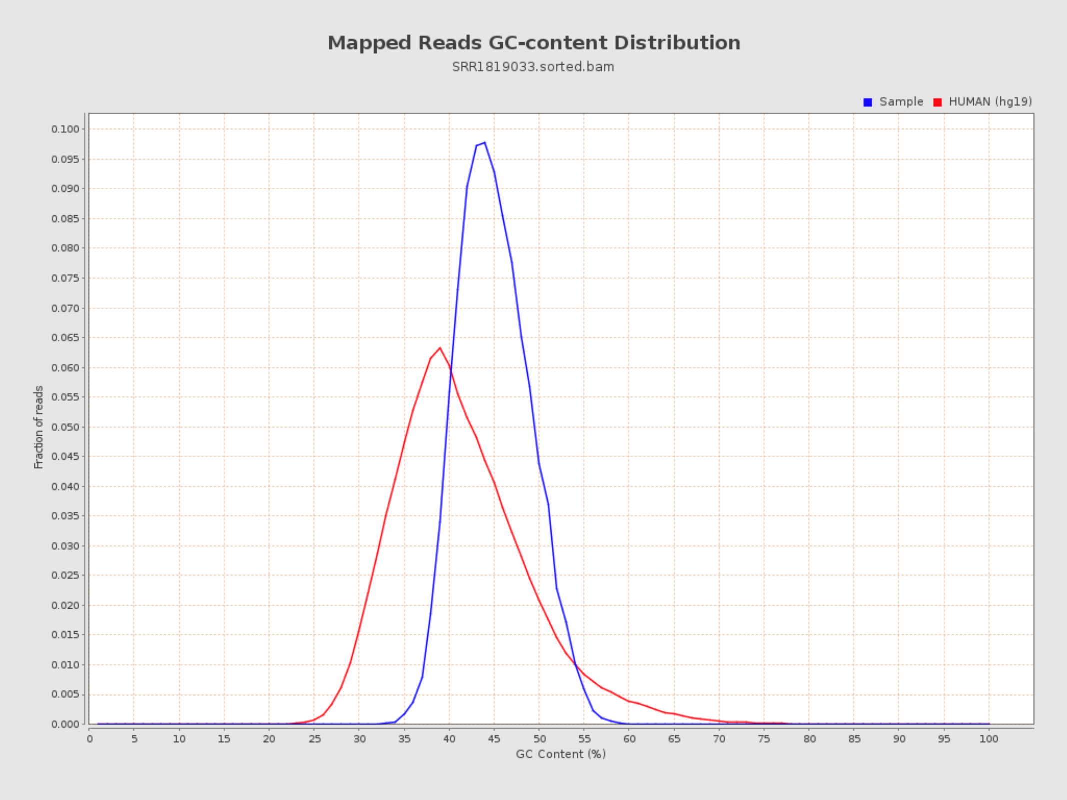
7. Results : Duplication Rate Histogram



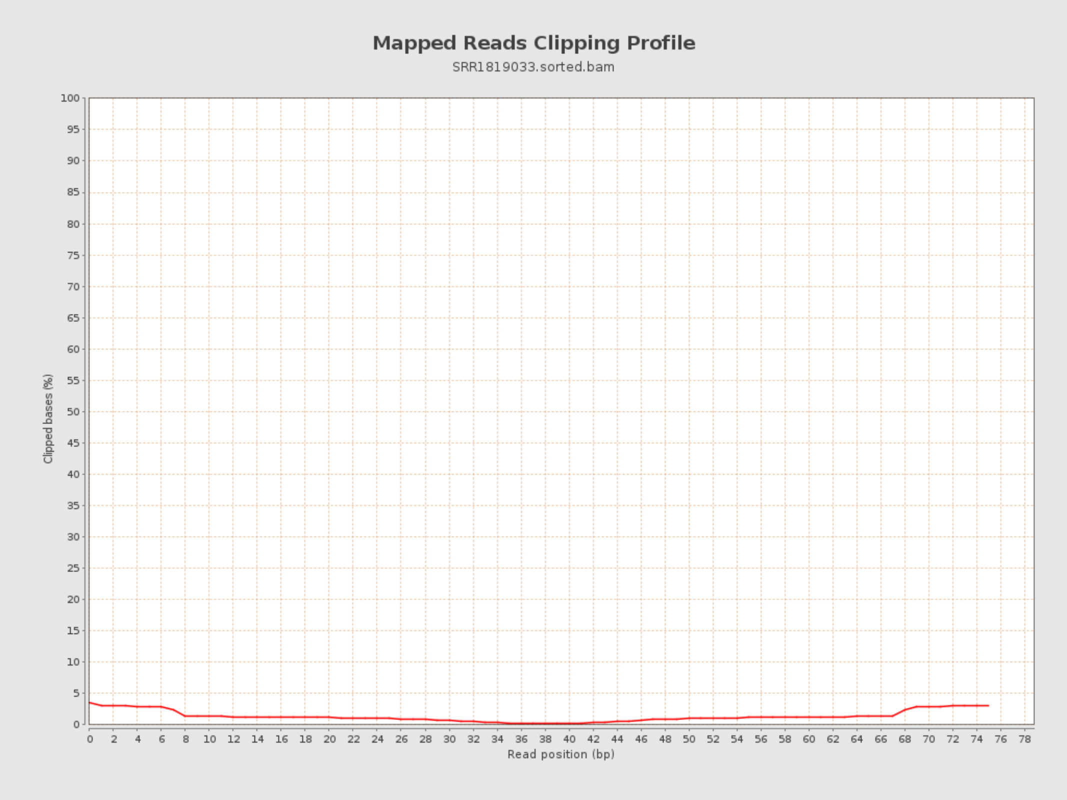
8. Results : Mapped Reads Nucleotide Content



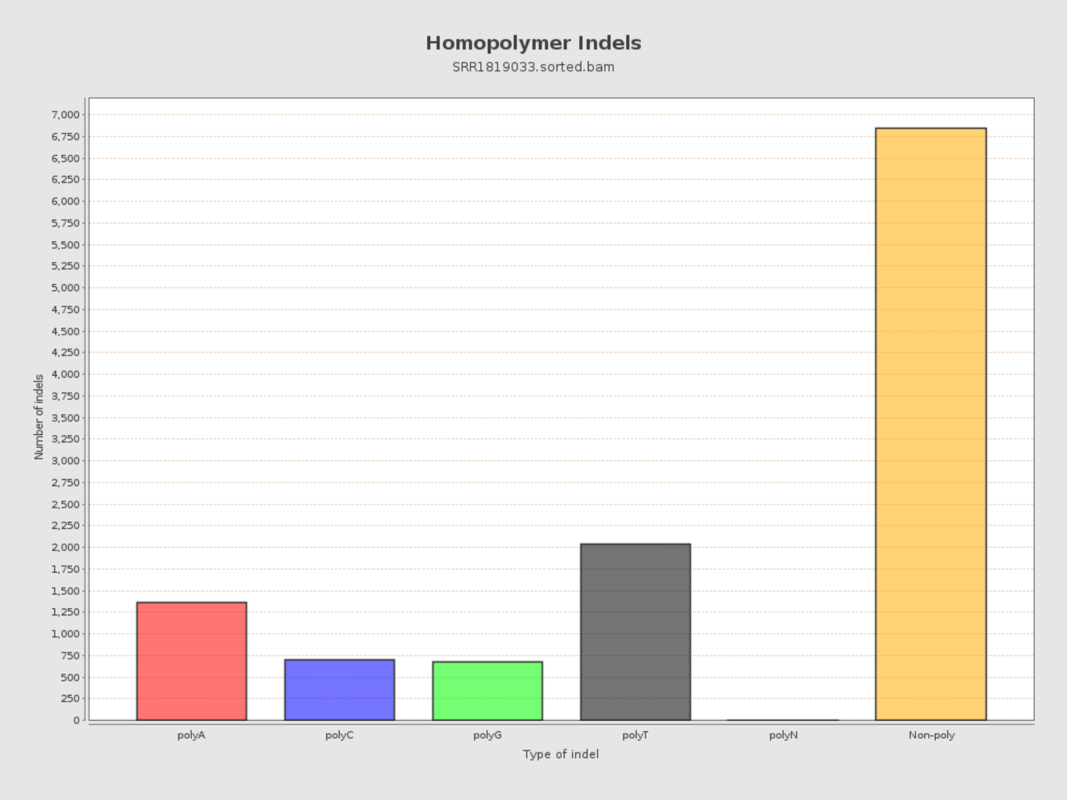
9. Results : Mapped Reads GC-content Distribution



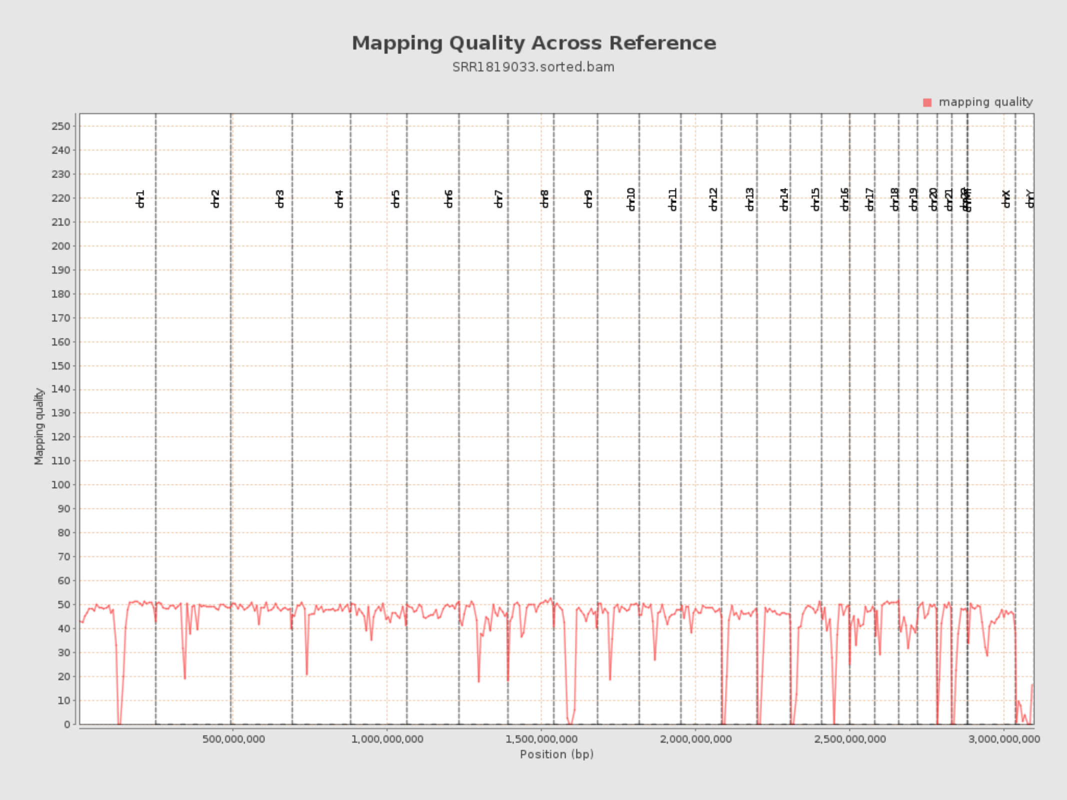
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram