Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818779.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_SRR1818779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:58:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,064,506
Mapped reads	1,033,299 / 97.07%
Unmapped reads	31,207 / 2.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,223 / 0.87%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	408,203 / 38.35%
Duplication rate	35.07%
Clipped reads	1,034,553 / 97.19%

2.2. ACGT Content

Number/percentage of A's	20,453,287 / 29.21%
Number/percentage of C's	15,375,065 / 21.96%
Number/percentage of T's	19,861,670 / 28.37%
Number/percentage of G's	14,316,502 / 20.45%
Number/percentage of N's	4,380 / 0.01%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.3115

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

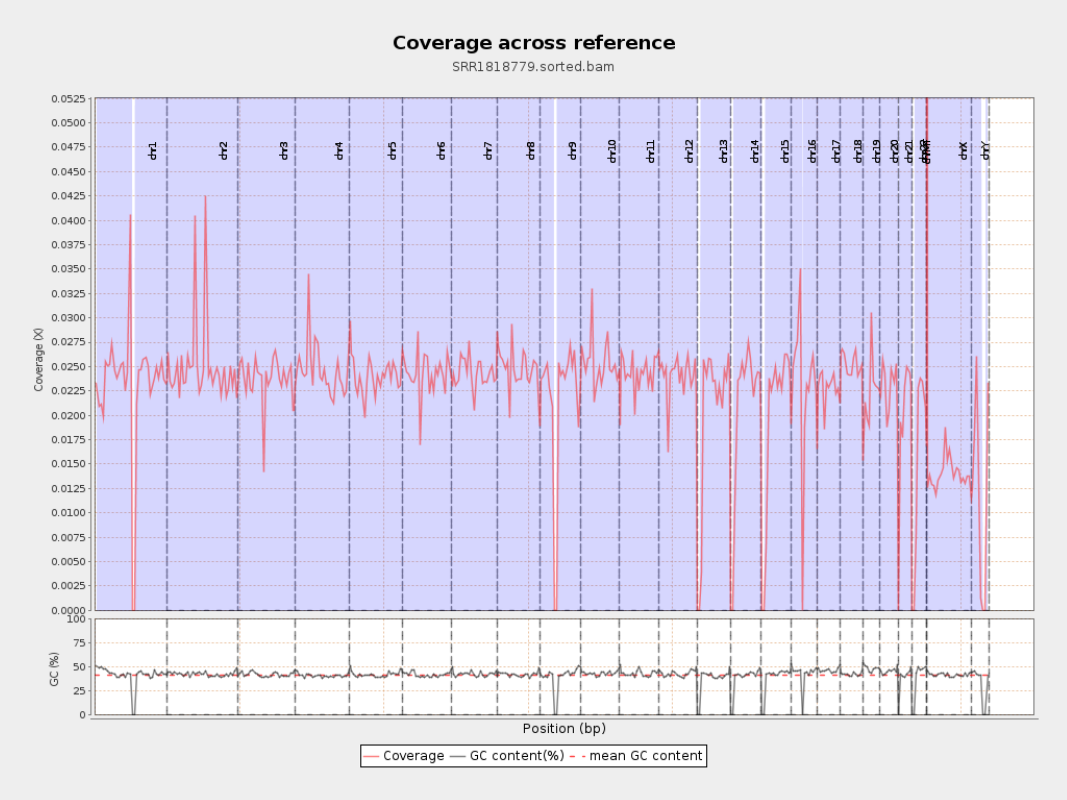
General error rate	0.55%
Mismatches	367,972
Insertions	7,841
Mapped reads with at least one insertion	0.75%
Deletions	17,828
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.31%

2.6. Chromosome stats

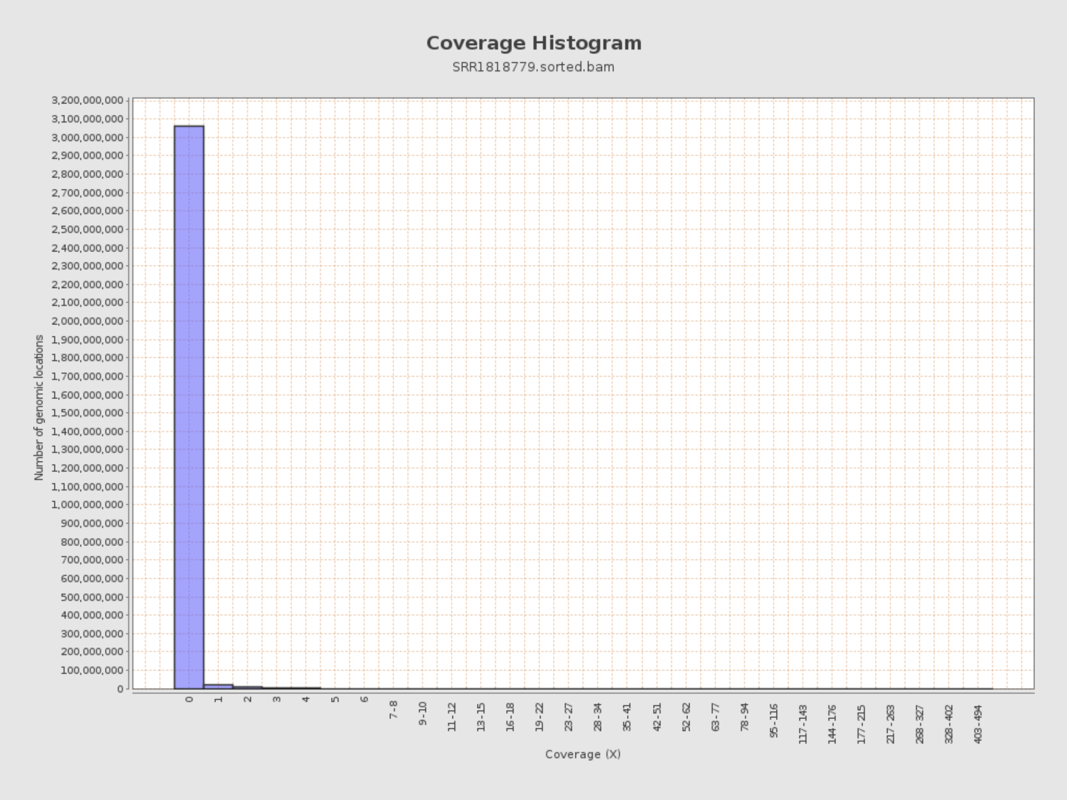
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5740974	0.023	0.4305
chr2	243199373	6103453	0.0251	0.4506
chr3	198022430	4706508	0.0238	0.2553
chr4	191154276	4697834	0.0246	0.2824
chr5	180915260	4328563	0.0239	0.2598
chr6	171115067	4151147	0.0243	0.2782
chr7	159138663	3874816	0.0243	0.3043

chr8	146364022	3625529	0.0248	0.2901
chr9	141213431	3022834	0.0214	0.2695
chr10	135534747	3443140	0.0254	0.3239
chr11	135006516	3282508	0.0243	0.2791
chr12	133851895	3215228	0.024	0.2669
chr13	115169878	2306888	0.02	0.2348
chr14	107349540	2193769	0.0204	0.2515
chr15	102531392	1993952	0.0194	0.2323
chr16	90354753	2050225	0.0227	0.3203
chr17	81195210	1857133	0.0229	0.265
chr18	78077248	1975150	0.0253	0.3528
chr19	59128983	1327593	0.0225	0.3672
chr20	63025520	1446122	0.0229	0.2609
chr21	48129895	957559	0.0199	0.2449
chr22	51304566	798608	0.0156	0.2168
chrMT	16571	50841	3.0681	3.3987
chrX	155270560	2183322	0.0141	0.2086
chrY	59373566	705195	0.0119	0.4405

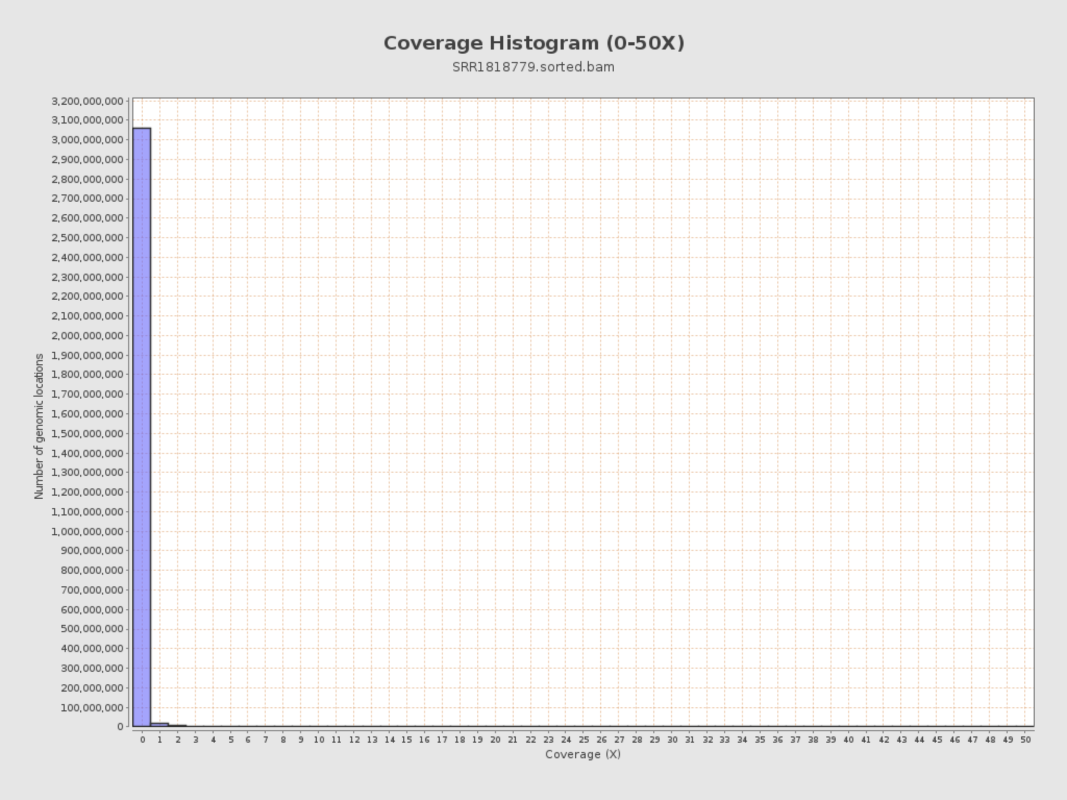
3. Results : Coverage across reference



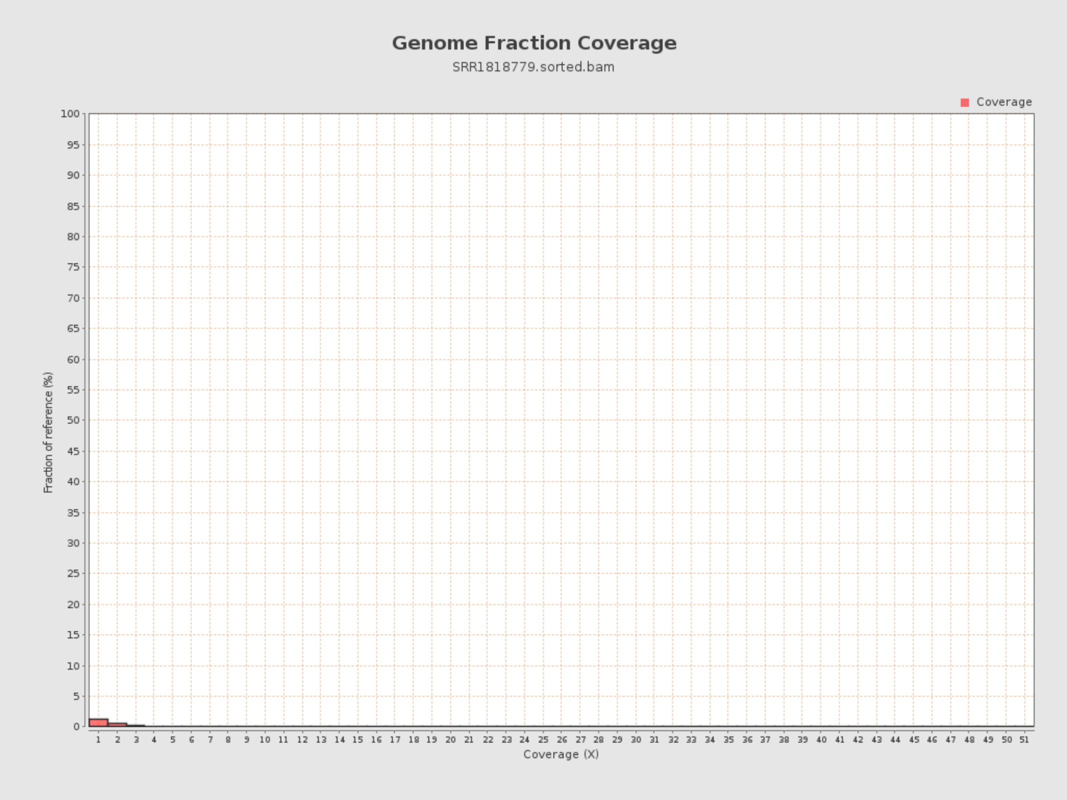
4. Results : Coverage Histogram



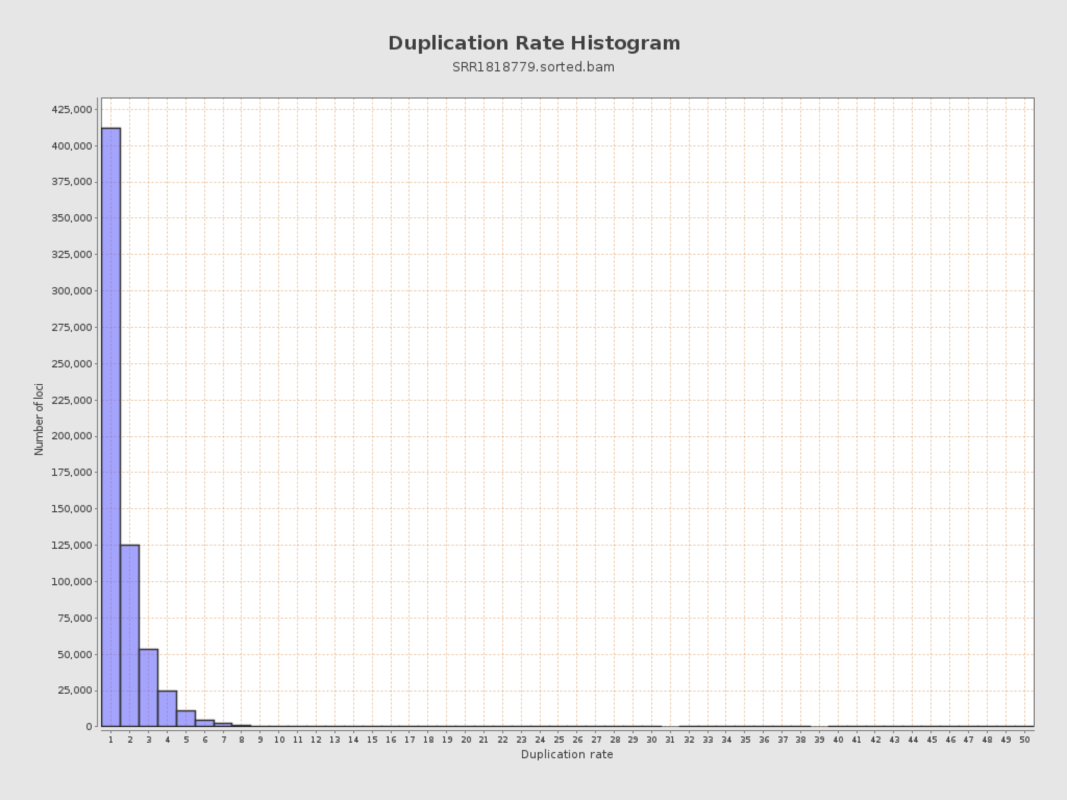
5. Results : Coverage Histogram (0-50X)



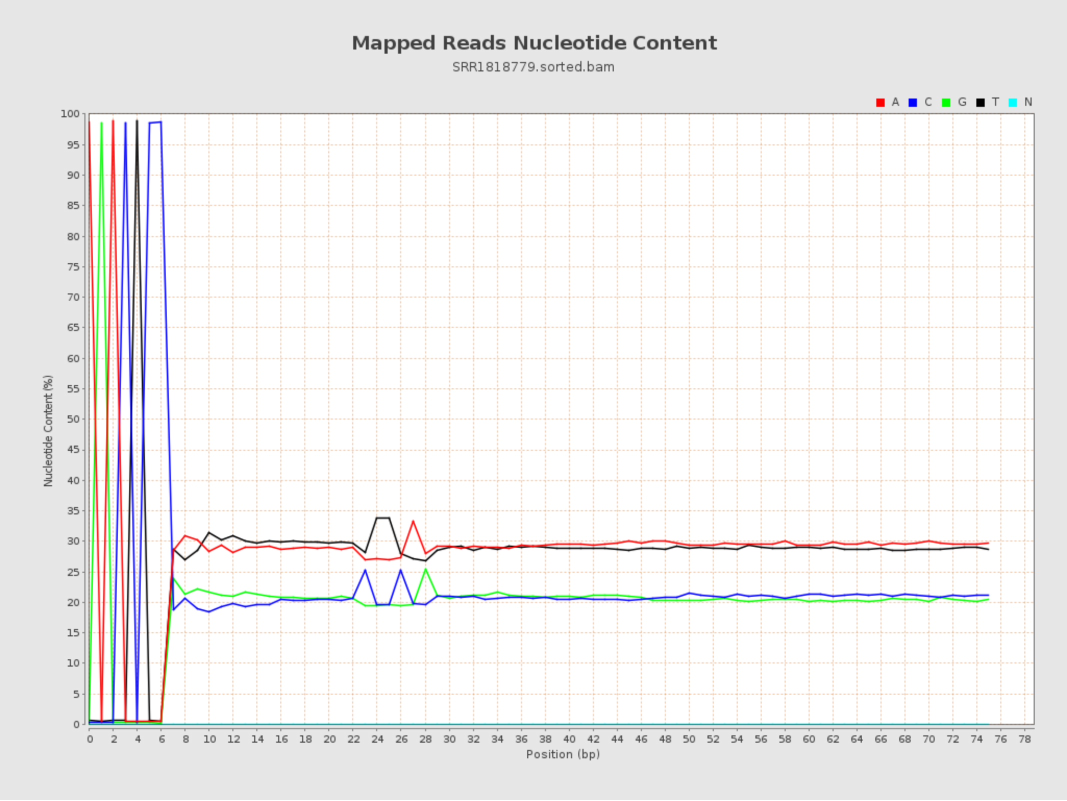
6. Results : Genome Fraction Coverage



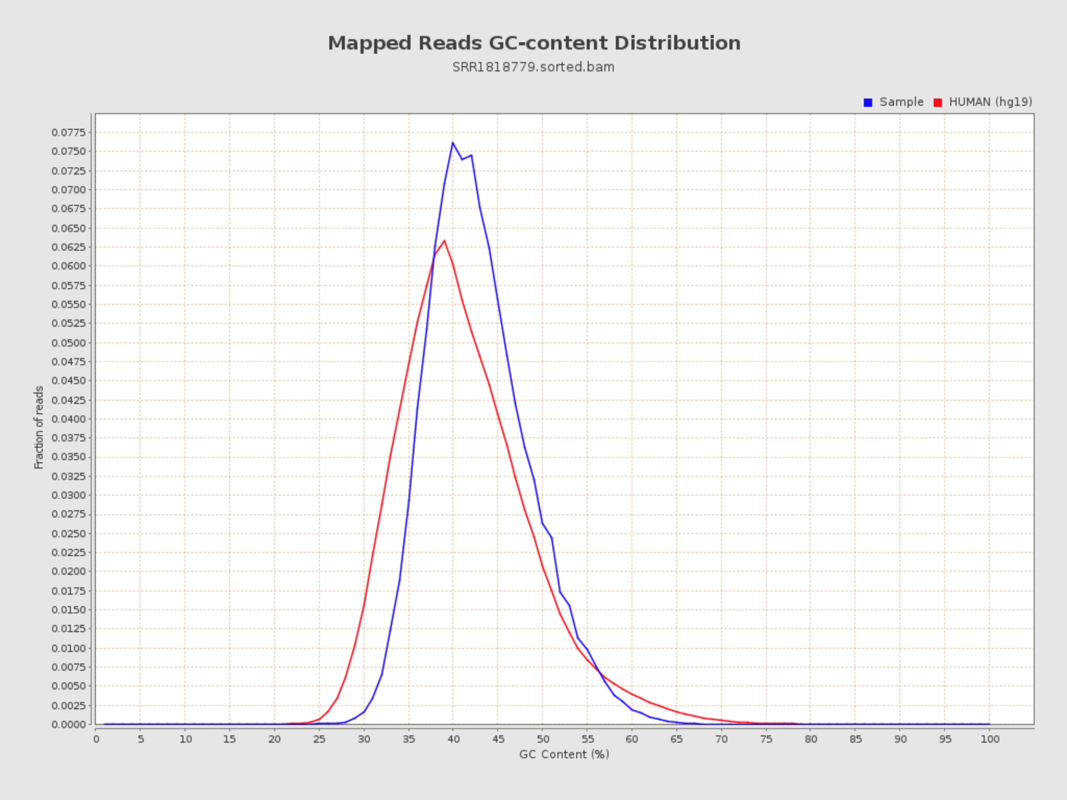
7. Results : Duplication Rate Histogram



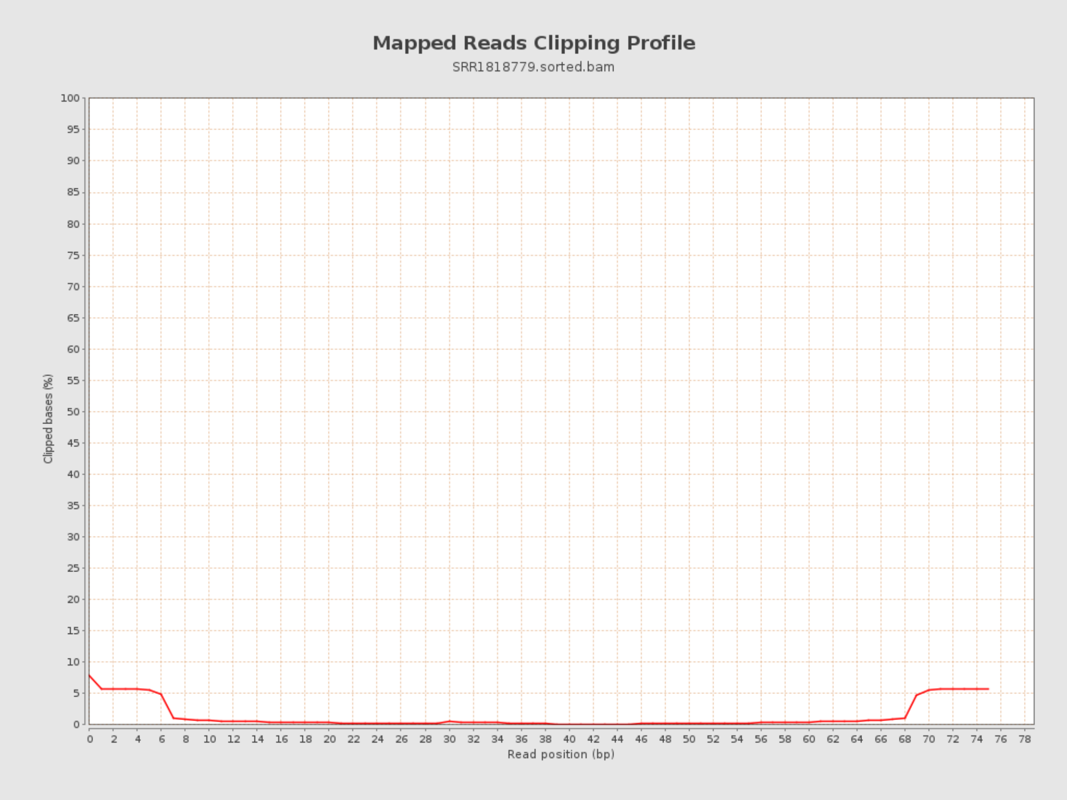
8. Results : Mapped Reads Nucleotide Content



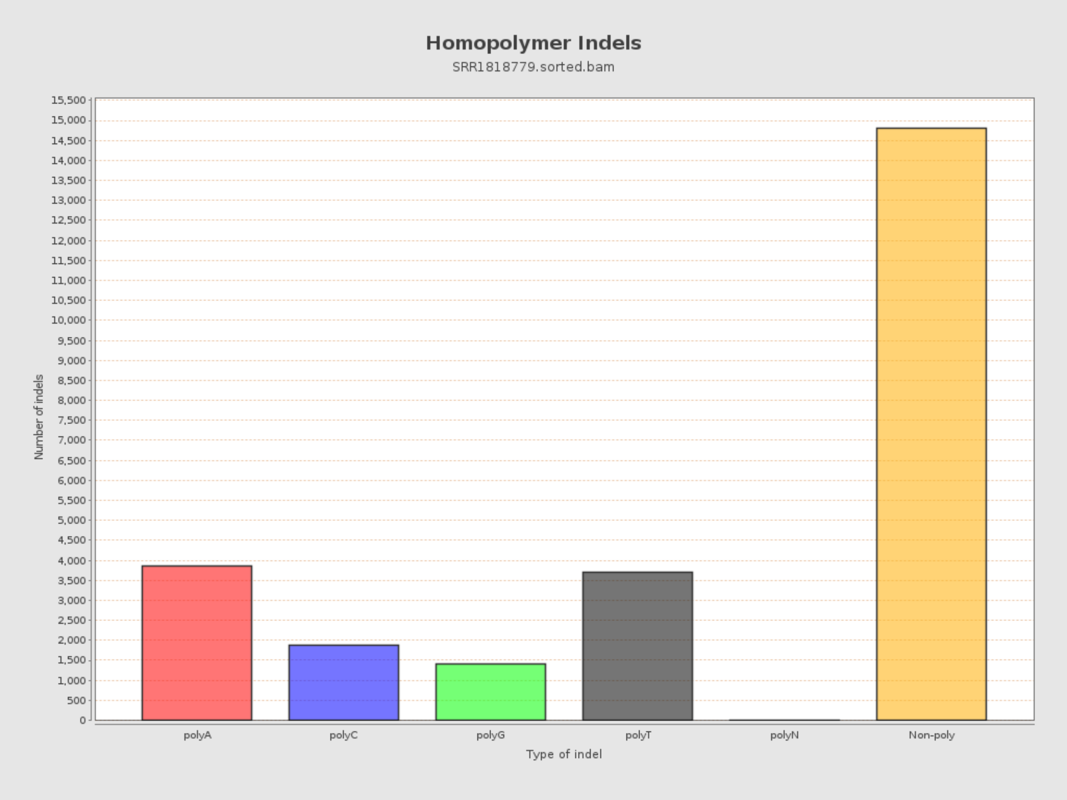
9. Results : Mapped Reads GC-content Distribution



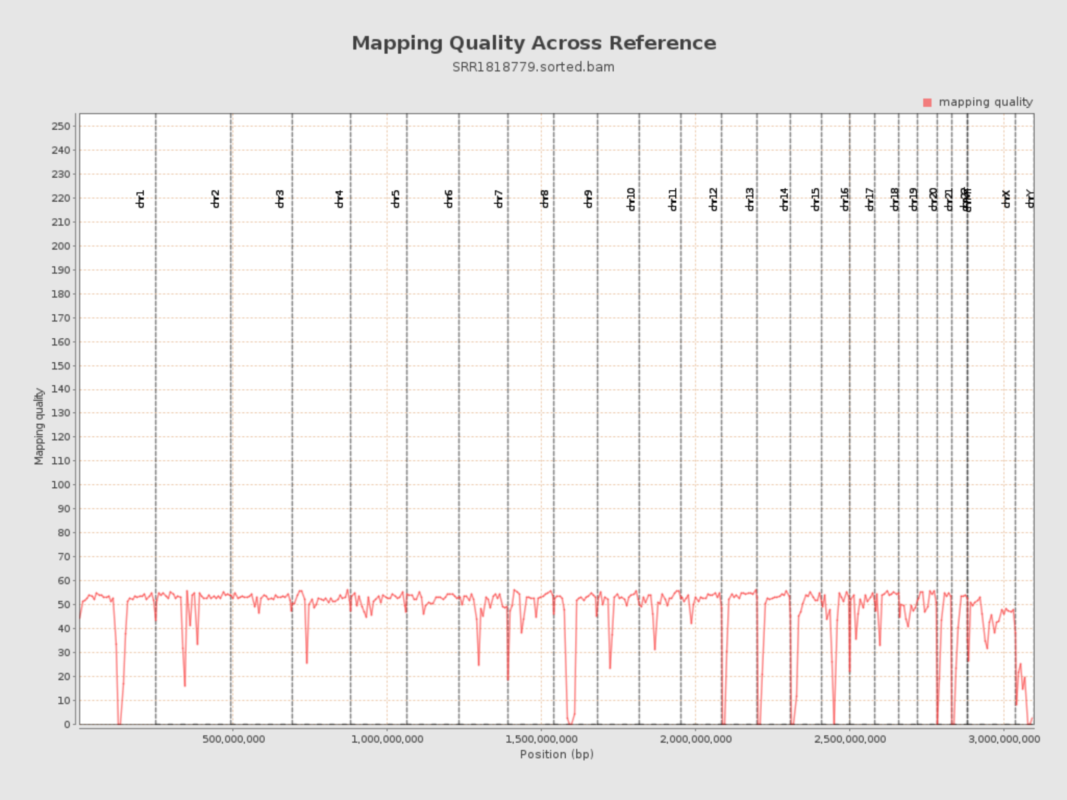
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram