Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 20:23:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779274.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_SRR1779274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779274_1.fastq.gz SRR1779274_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 20:23:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,079,276
Mapped reads	10,740,991 / 96.95%
Unmapped reads	338,285 / 3.05%
Mapped paired reads	10,740,991 / 96.95%
Mapped reads, first in pair	5,414,032 / 48.87%
Mapped reads, second in pair	5,326,959 / 48.08%
Mapped reads, both in pair	10,638,924 / 96.03%
Mapped reads, singletons	102,067 / 0.92%
Secondary alignments	0
Supplementary alignments	24,760 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	124,158 / 1.12%
Duplication rate	1.06%
Clipped reads	355,934 / 3.21%

2.2. ACGT Content

Number/percentage of A's	259,572,219 / 30.37%
Number/percentage of C's	166,689,464 / 19.5%
Number/percentage of T's	258,669,087 / 30.27%
Number/percentage of G's	169,524,423 / 19.84%
Number/percentage of N's	161,735 / 0.02%

GC Percentage	39.34%

2.3. Coverage

Mean	0.2761
Standard Deviation	0.8015

2.4. Mapping Quality

Mean Mapping Quality	53.14

2.5. Insert size

Mean	45,735.12
Standard Deviation	2,045,294.98
P25/Median/P75	153 / 200 / 265

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,286,193
Insertions	61,163
Mapped reads with at least one insertion	0.56%
Deletions	77,301
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.56%

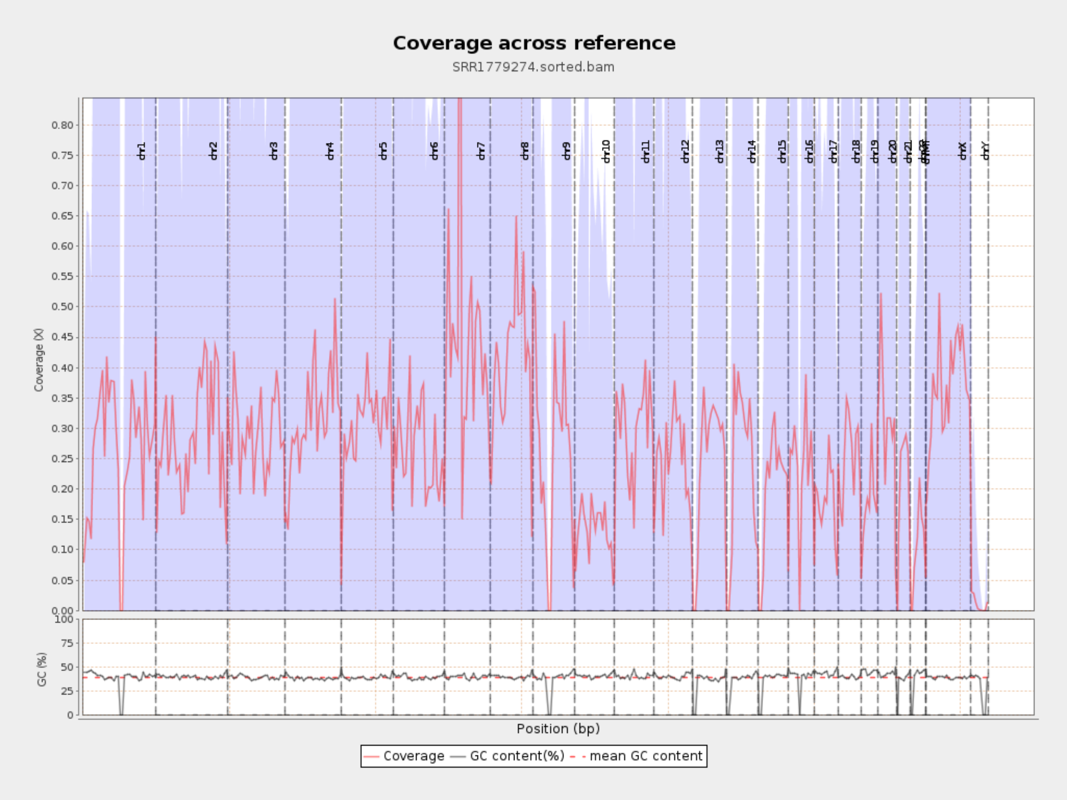
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

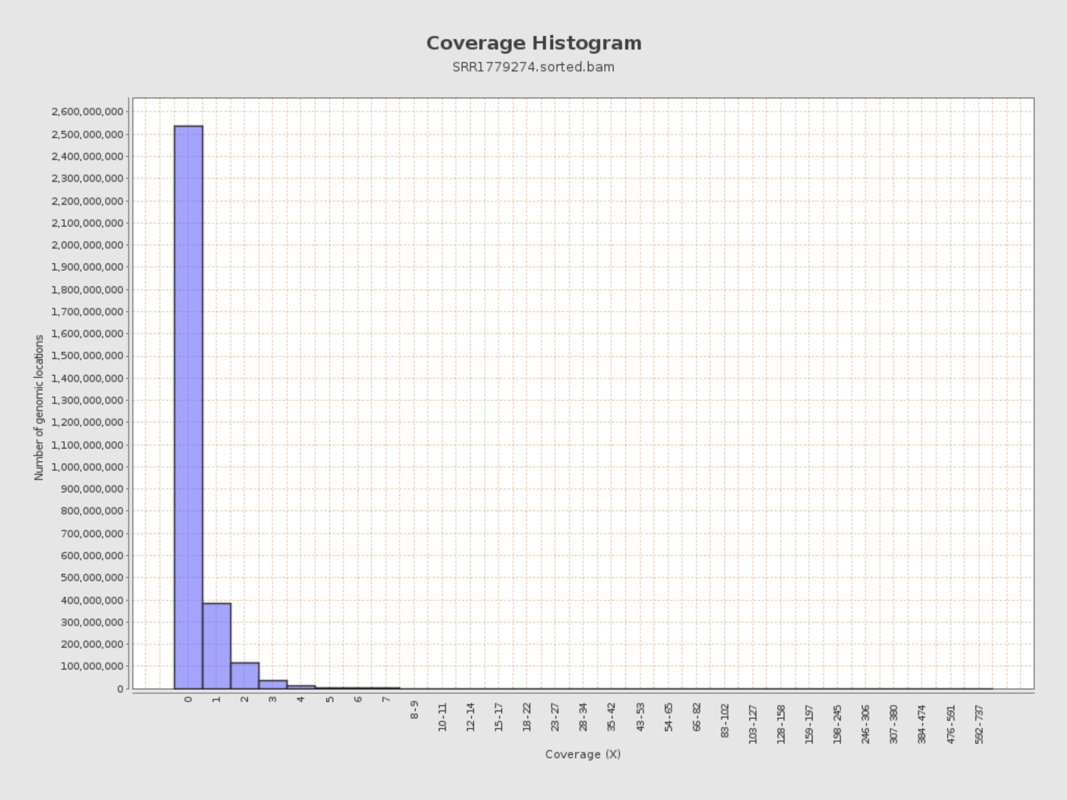
		bases	coverage	deviation
chr1	249250621	66194869	0.2656	1.0095
chr2	243199373	68870344	0.2832	0.7338
chr3	198022430	58217925	0.294	0.7399
chr4	191154276	60506060	0.3165	0.76
chr5	180915260	55383525	0.3061	0.7349
chr6	171115067	46064384	0.2692	0.7029
chr7	159138663	73440745	0.4615	1.388
chr8	146364022	60838330	0.4157	0.8838
chr9	141213431	37368939	0.2646	0.7242
chr10	135534747	18369778	0.1355	0.8571
chr11	135006516	40347140	0.2989	0.7479
chr12	133851895	33452589	0.2499	0.6653
chr13	115169878	28669317	0.2489	0.67
chr14	107349540	26511160	0.247	0.6892
chr15	102531392	20385811	0.1988	0.583
chr16	90354753	20614911	0.2282	0.6361
chr17	81195210	15067448	0.1856	0.5827
chr18	78077248	19805735	0.2537	0.6935
chr19	59128983	10885208	0.1841	0.7687
chr20	63025520	20314745	0.3223	0.7686
chr21	48129895	9876702	0.2052	0.6157
chr22	51304566	5521693	0.1076	0.417
chrMT	16571	2907	0.1754	0.4452
chrX	155270560	57457345	0.37	0.8492

chrY	59373566	610680	0.0103	0.1456

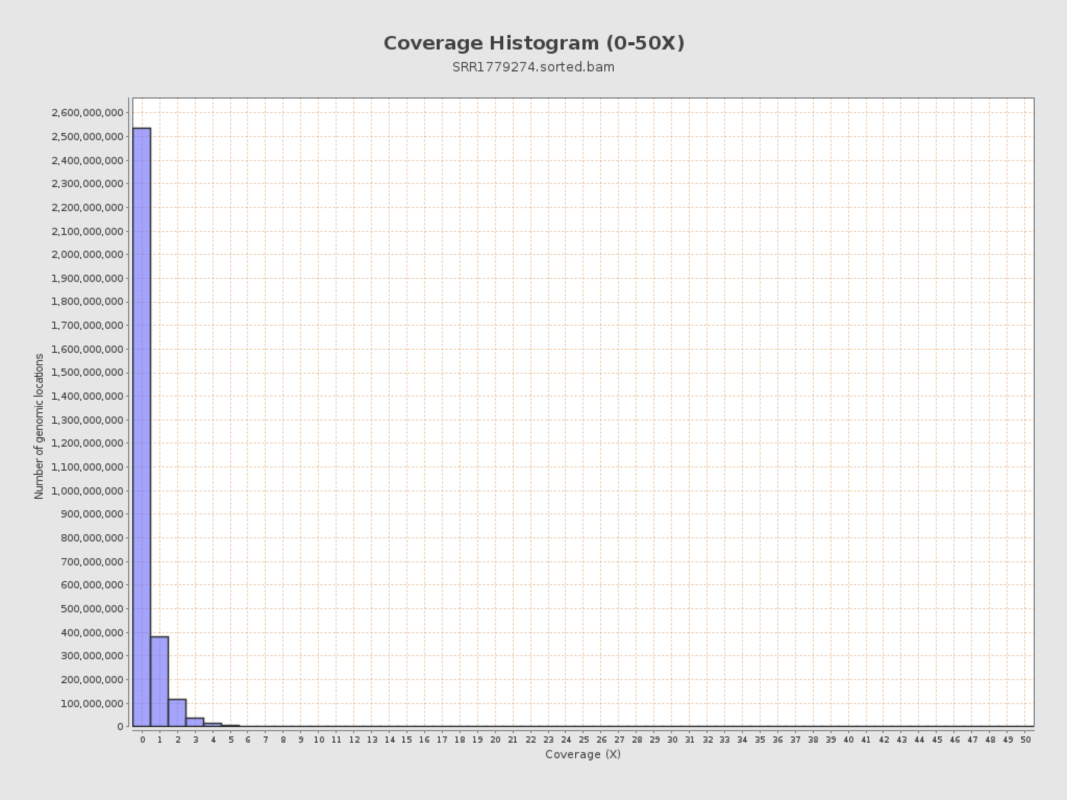
3. Results : Coverage across reference



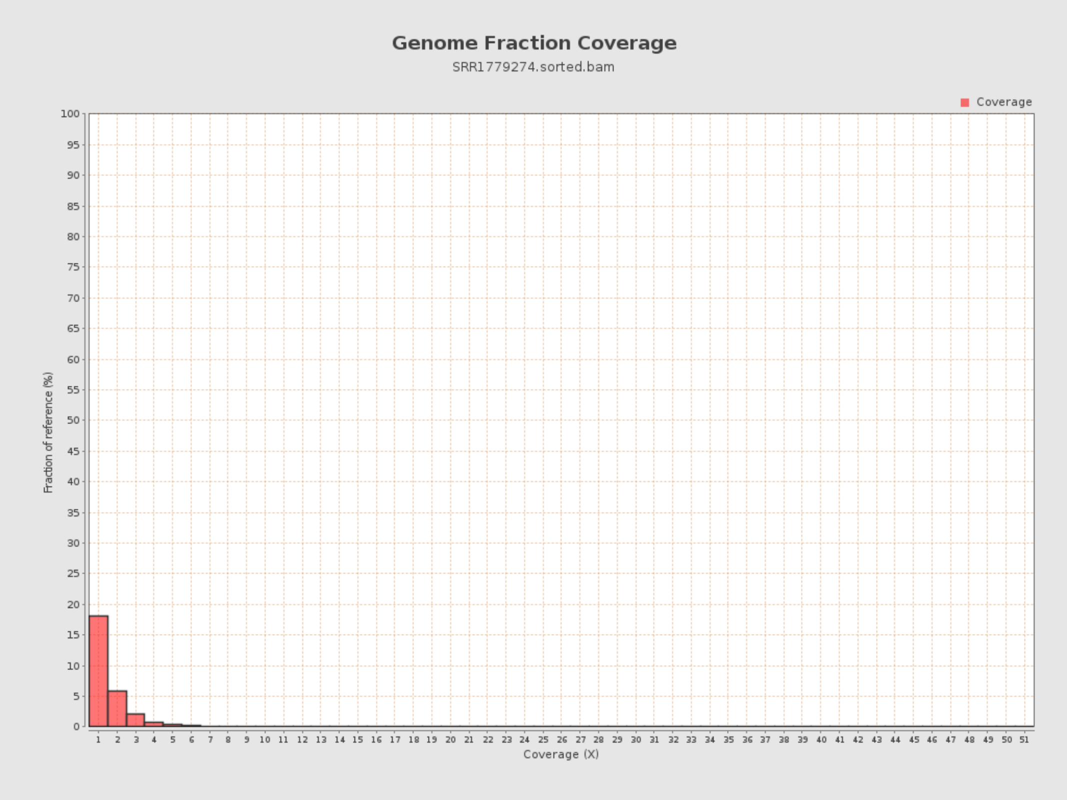
4. Results : Coverage Histogram



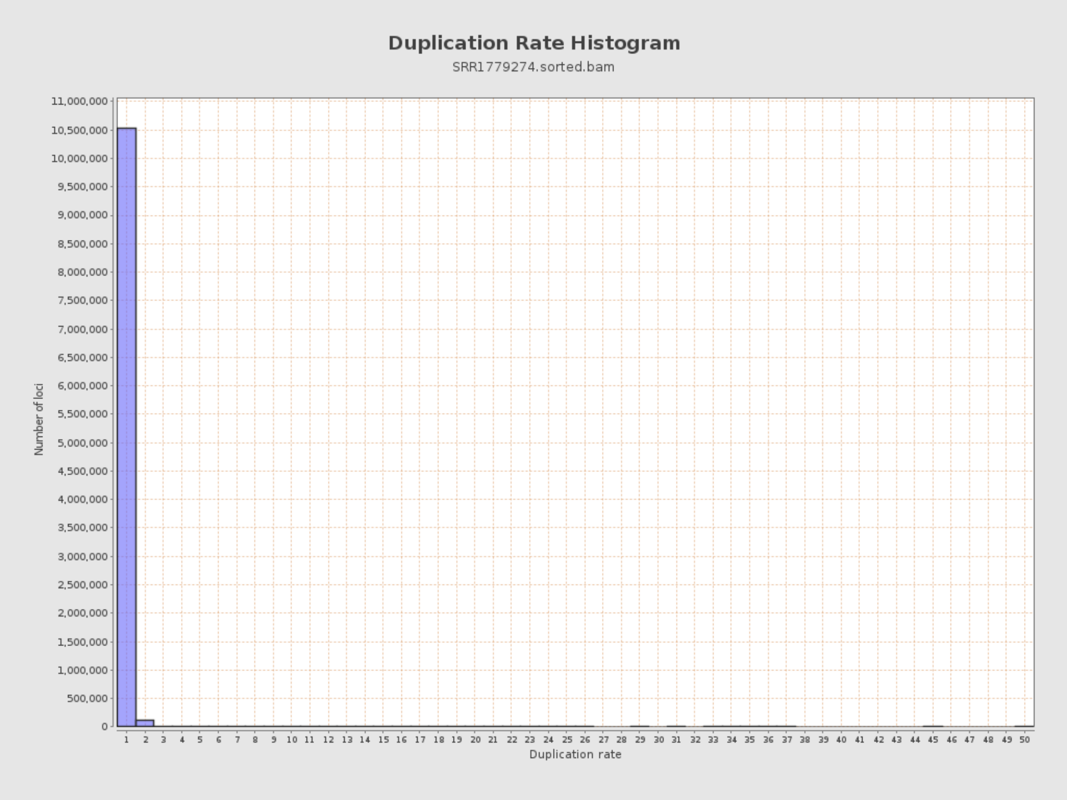
5. Results : Coverage Histogram (0-50X)



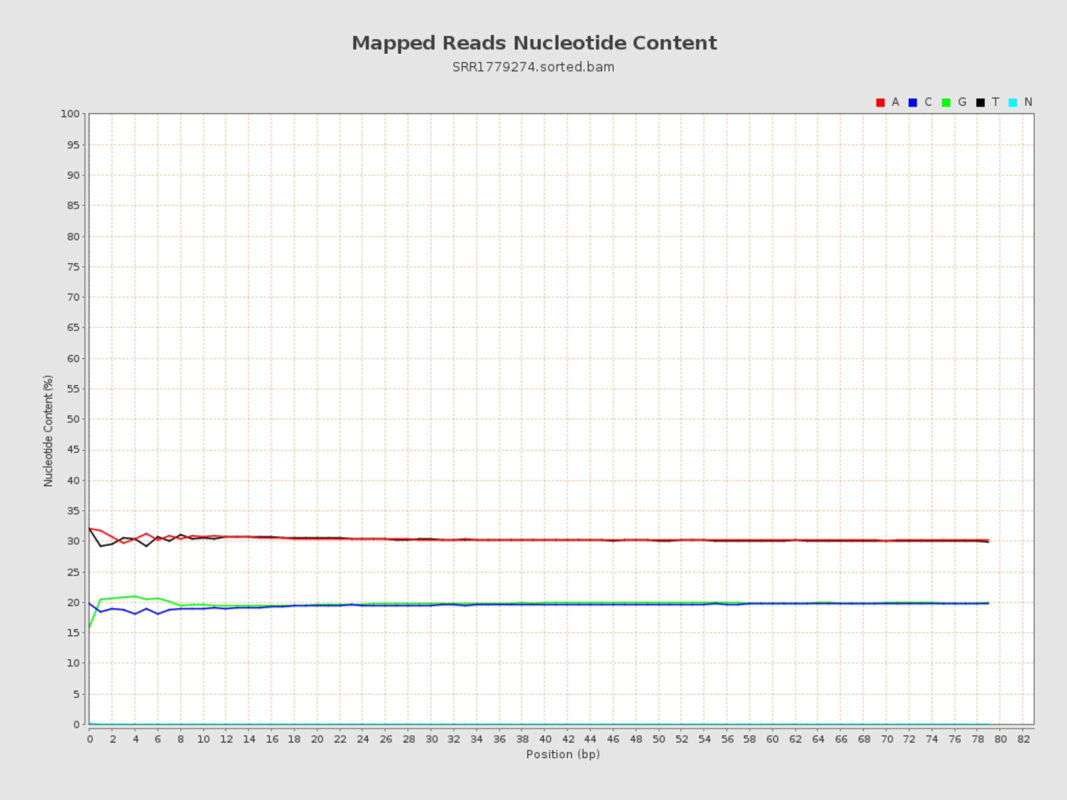
6. Results : Genome Fraction Coverage



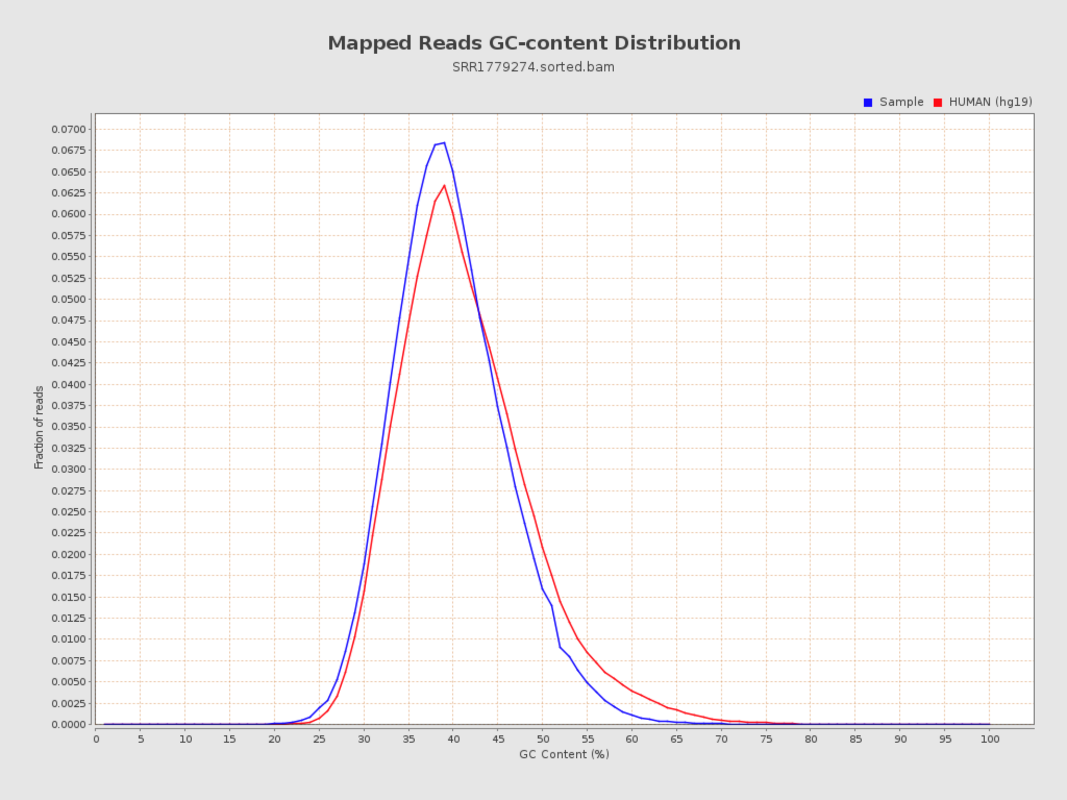
7. Results : Duplication Rate Histogram



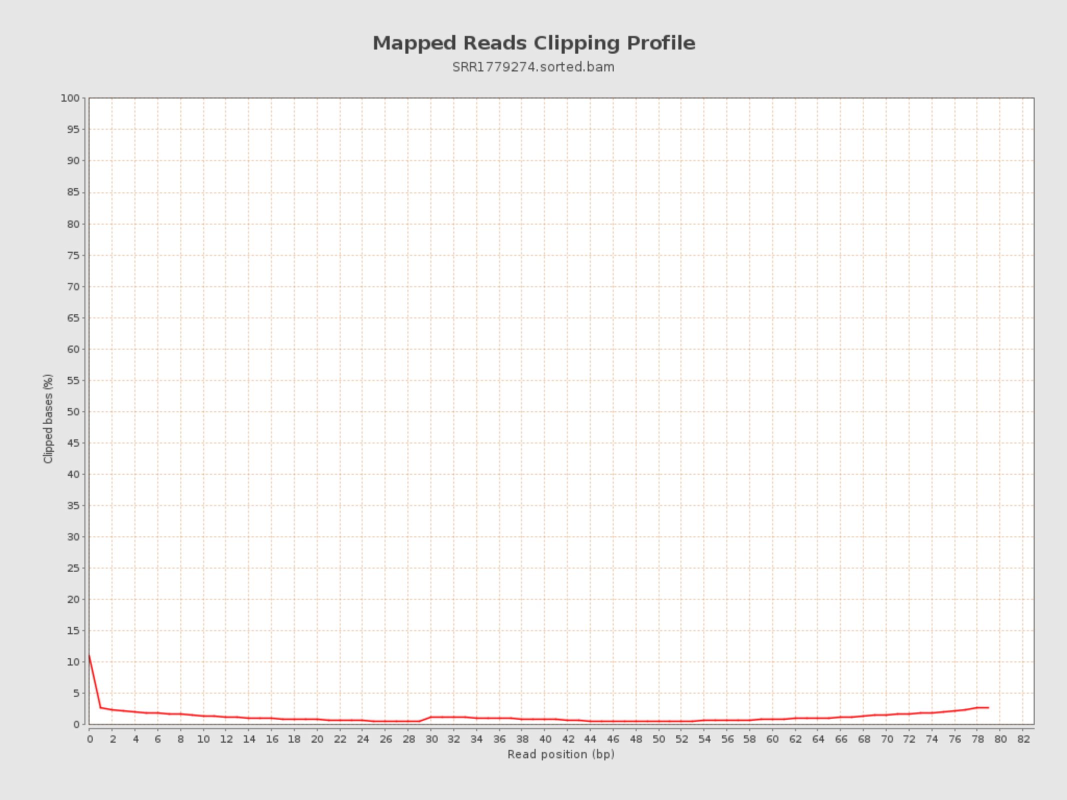
8. Results : Mapped Reads Nucleotide Content



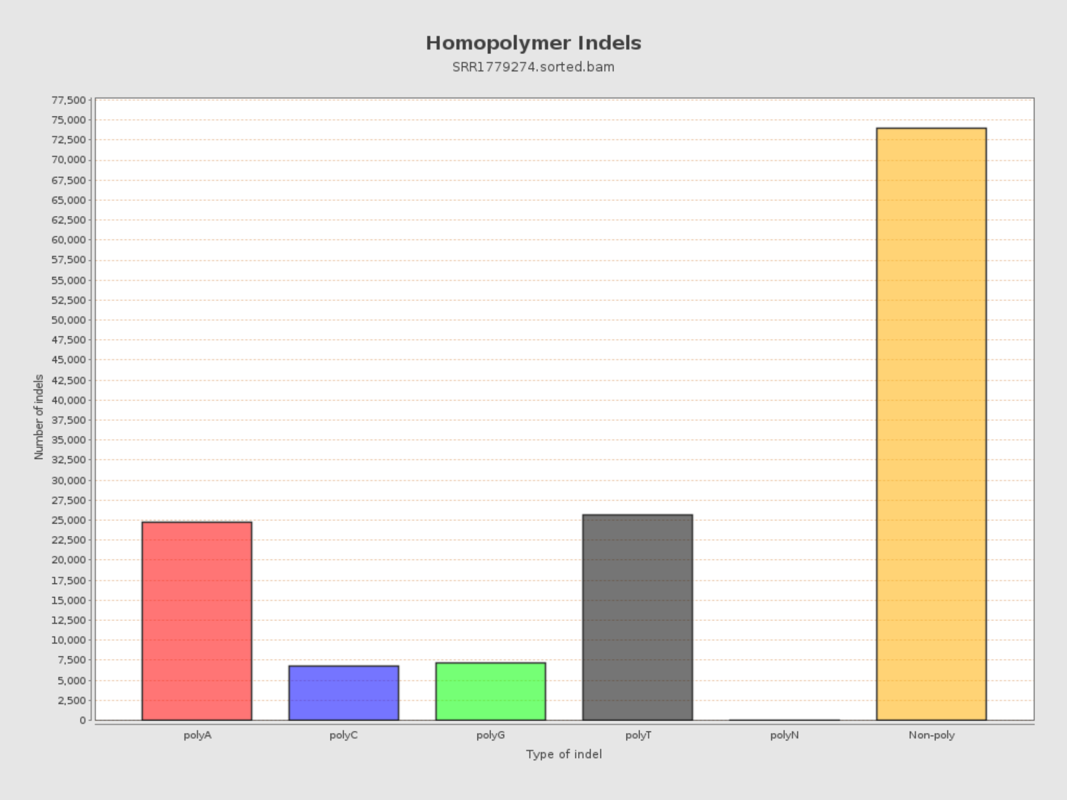
9. Results : Mapped Reads GC-content Distribution



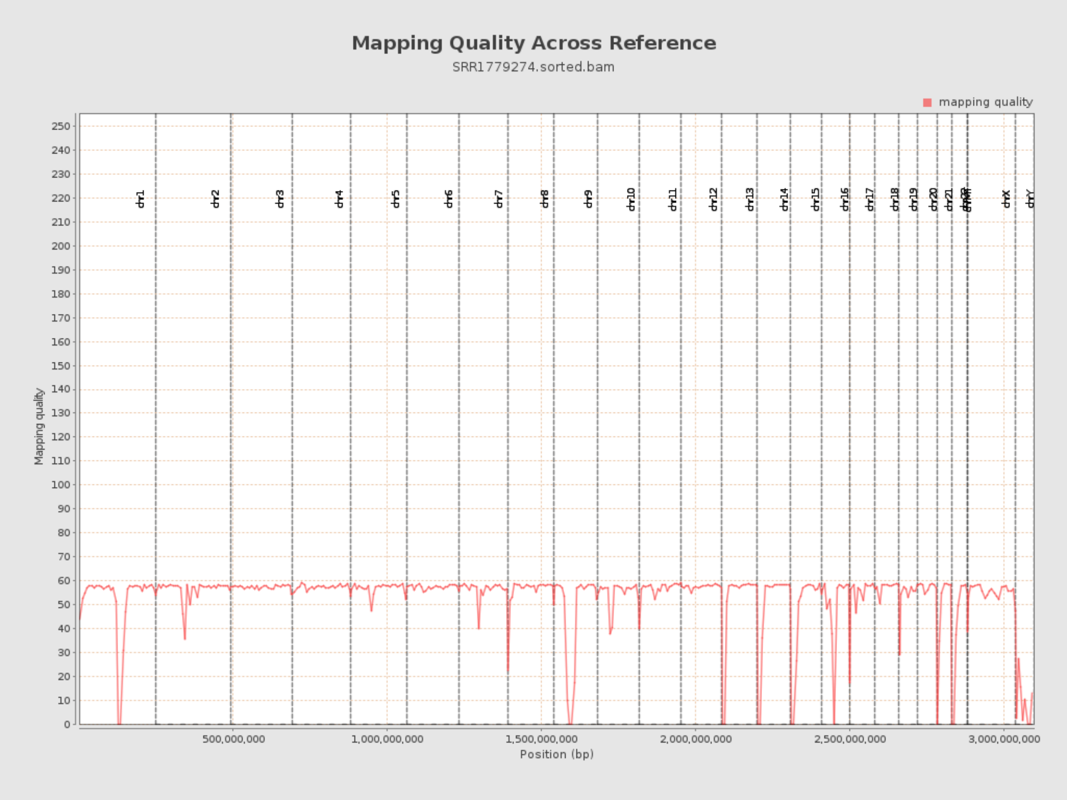
10. Results : Mapped Reads Clipping Profile



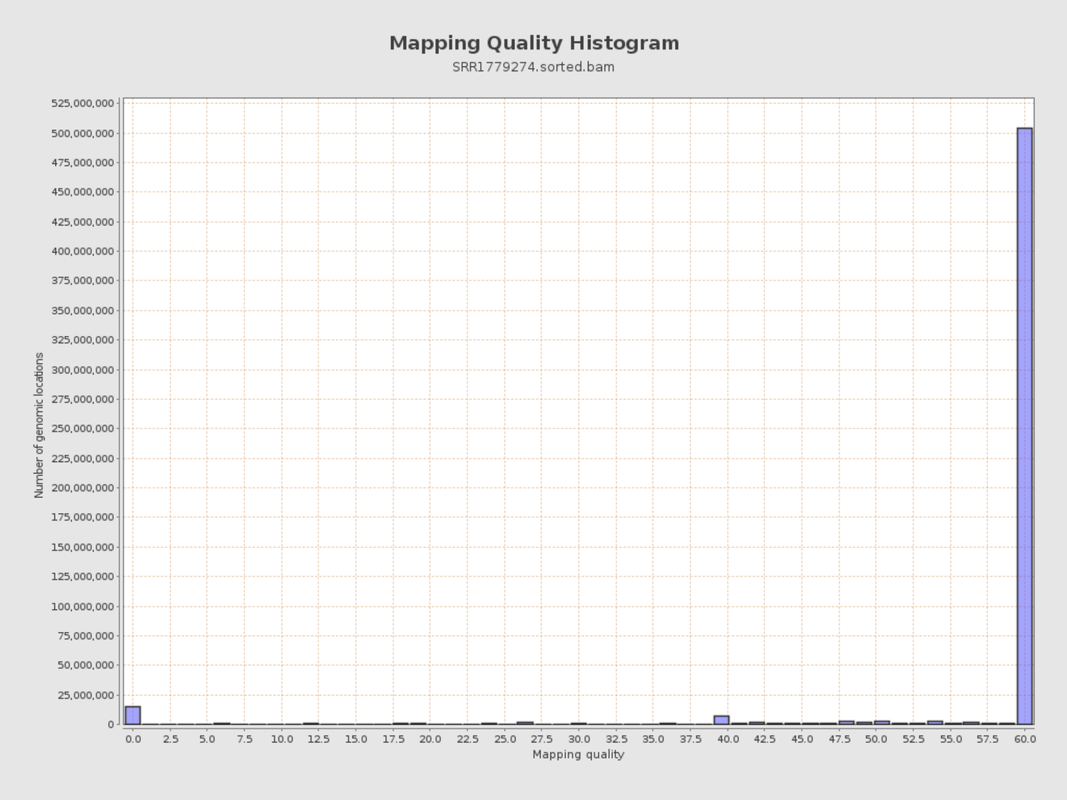
11. Results : Homopolymer Indels



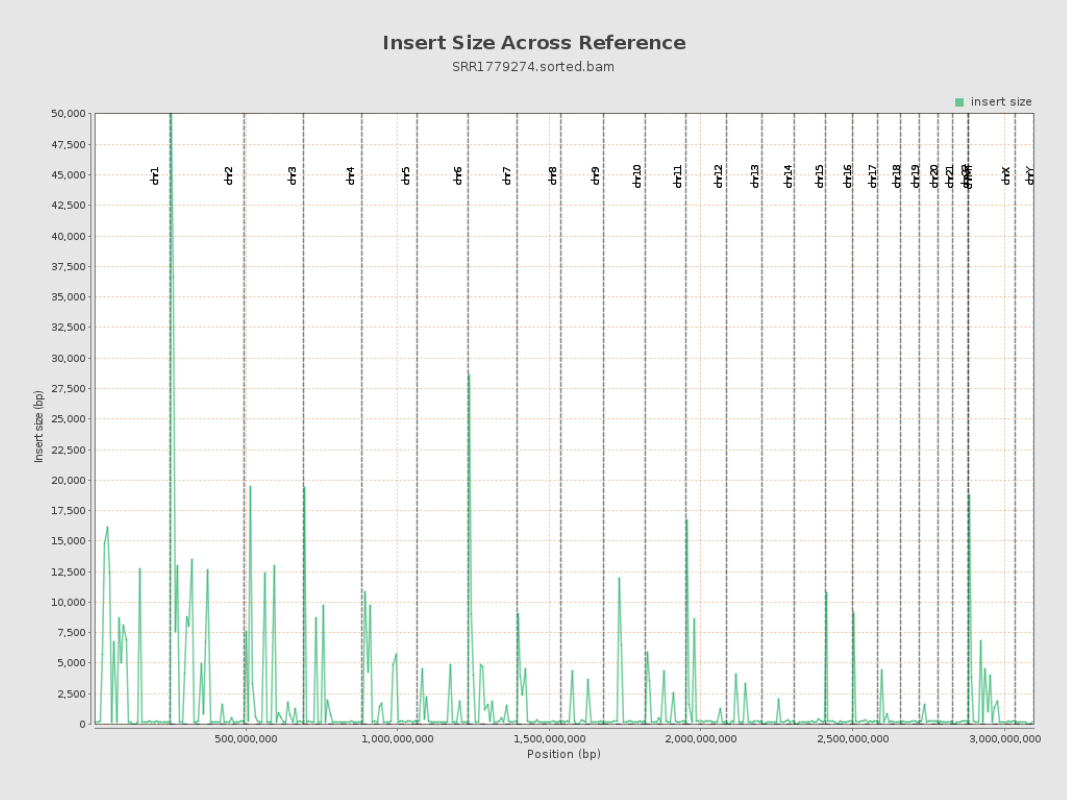
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram