Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 15:12:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779205.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_SRR1779205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779205_1.fastq.gz SRR1779205_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 15:12:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,988,722
Mapped reads	7,717,790 / 96.61%
Unmapped reads	270,932 / 3.39%
Mapped paired reads	7,717,790 / 96.61%
Mapped reads, first in pair	3,912,166 / 48.97%
Mapped reads, second in pair	3,805,624 / 47.64%
Mapped reads, both in pair	7,596,288 / 95.09%
Mapped reads, singletons	121,502 / 1.52%
Secondary alignments	0
Supplementary alignments	28,098 / 0.35%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	85,437 / 1.07%
Duplication rate	0.84%
Clipped reads	353,179 / 4.42%

2.2. ACGT Content

Number/percentage of A's	184,566,102 / 30.11%
Number/percentage of C's	120,703,744 / 19.69%
Number/percentage of T's	184,043,753 / 30.02%
Number/percentage of G's	123,582,104 / 20.16%
Number/percentage of N's	112,770 / 0.02%

GC Percentage	39.85%

2.3. Coverage

Mean	0.1981
Standard Deviation	0.8239

2.4. Mapping Quality

Mean Mapping Quality	53.34

2.5. Insert size

Mean	55,766.83
Standard Deviation	2,276,071.8
P25/Median/P75	212 / 277 / 347

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	3,050,030
Insertions	54,298
Mapped reads with at least one insertion	0.7%
Deletions	63,717
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.03%

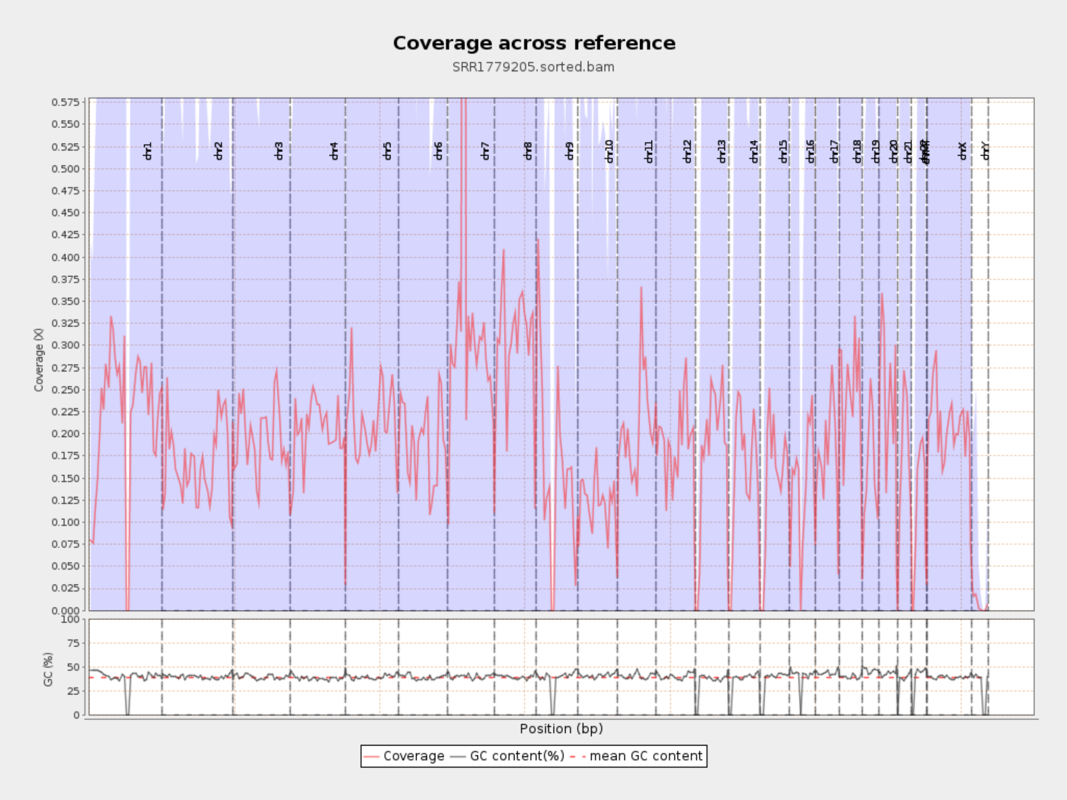
2.7. Chromosome stats

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

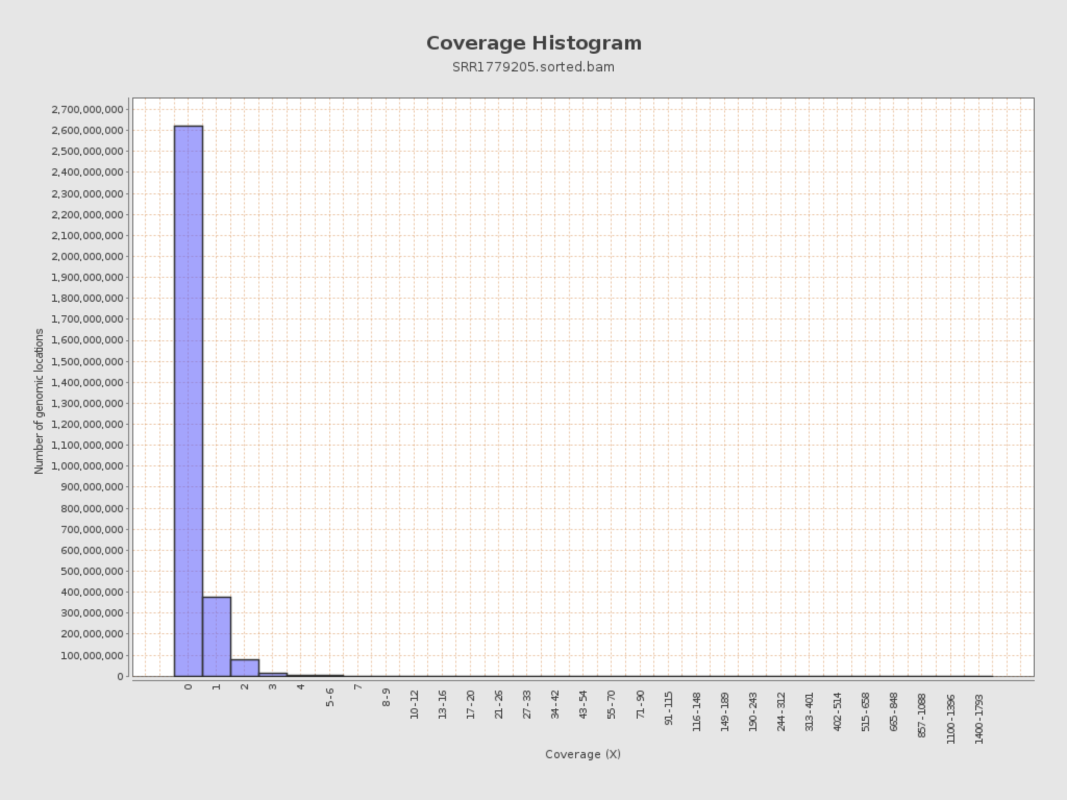
		bases	coverage	deviation
chr1	249250621	54908972	0.2203	1.8275
chr2	243199373	40672668	0.1672	0.505
chr3	198022430	38701463	0.1954	0.5016
chr4	191154276	39090222	0.2045	0.5141
chr5	180915260	38732605	0.2141	0.5276
chr6	171115067	32435623	0.1896	0.5431
chr7	159138663	59841550	0.376	1.5074
chr8	146364022	44426301	0.3035	0.6561
chr9	141213431	22742384	0.161	0.5574
chr10	135534747	16785168	0.1238	0.8099
chr11	135006516	27848465	0.2063	0.5519
chr12	133851895	25559896	0.191	0.5011
chr13	115169878	20592331	0.1788	0.4877
chr14	107349540	16877261	0.1572	0.4586
chr15	102531392	15045329	0.1467	0.4438
chr16	90354753	13133151	0.1454	0.4502
chr17	81195210	14346842	0.1767	0.8191
chr18	78077248	19494710	0.2497	0.6882
chr19	59128983	9571863	0.1619	1.2415
chr20	63025520	15591688	0.2474	0.5848
chr21	48129895	8019441	0.1666	0.4818
chr22	51304566	6103722	0.119	0.4041
chrMT	16571	480	0.029	0.1677
chrX	155270560	32149847	0.2071	0.5606

chrY	59373566	468787	0.0079	0.1294

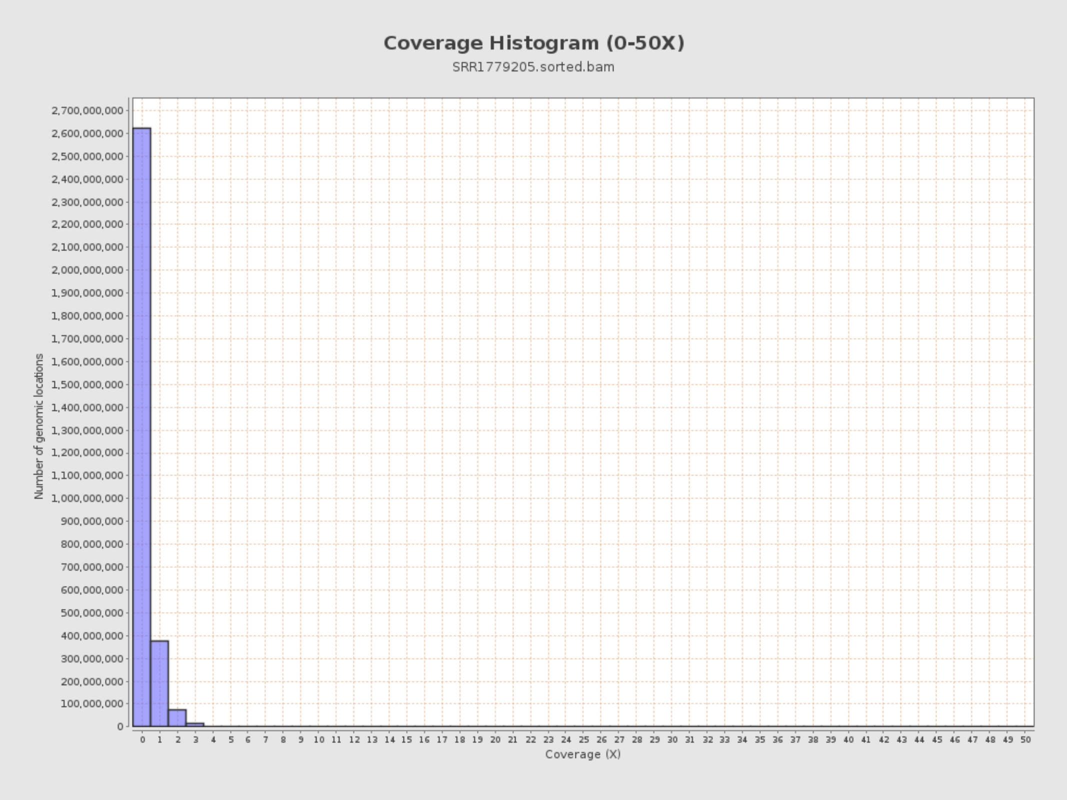
3. Results : Coverage across reference



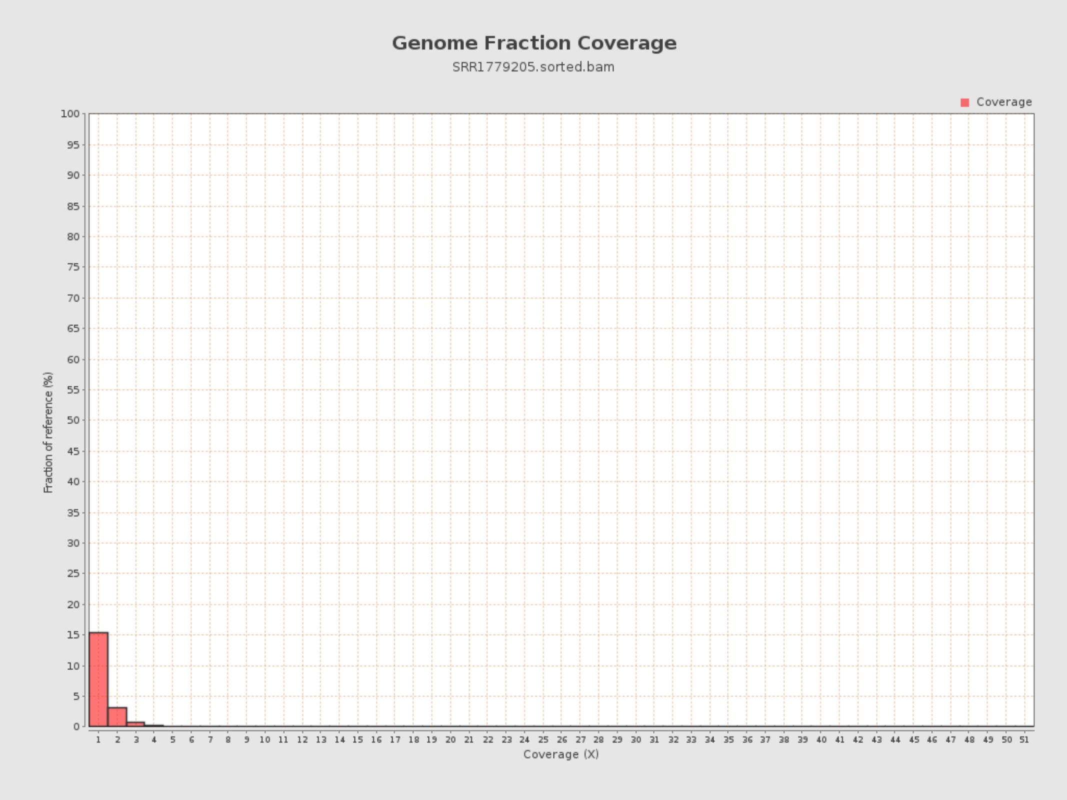
4. Results : Coverage Histogram



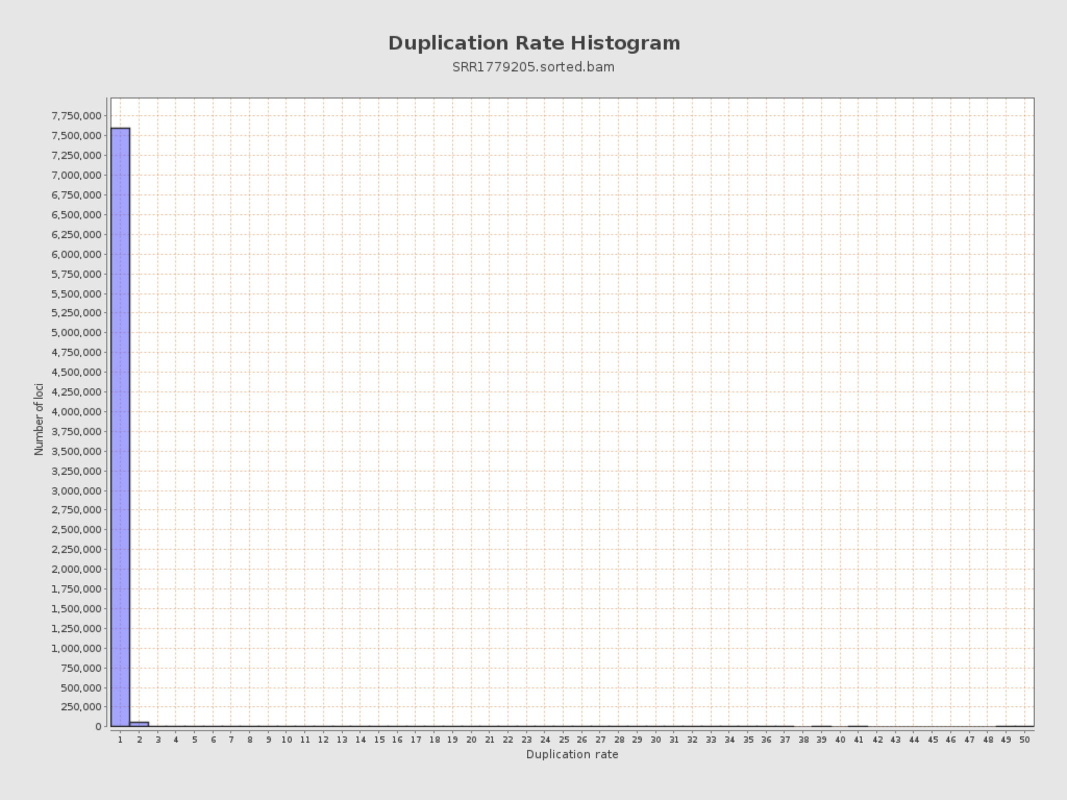
5. Results : Coverage Histogram (0-50X)



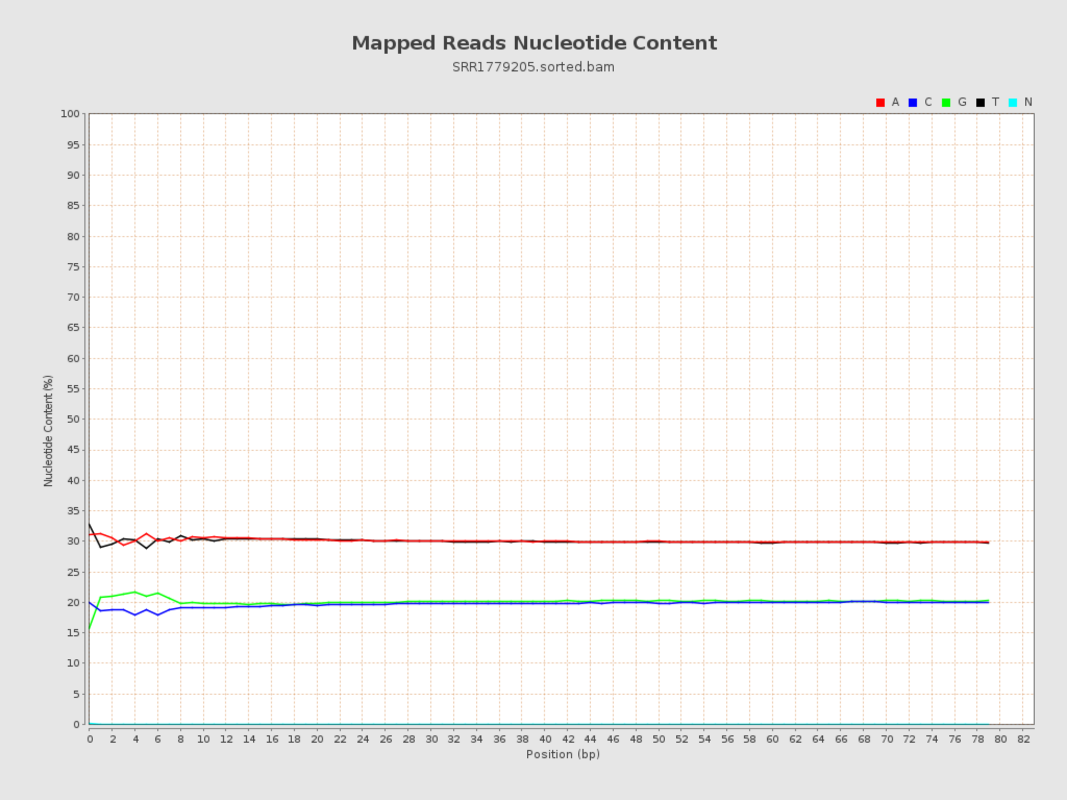
6. Results : Genome Fraction Coverage



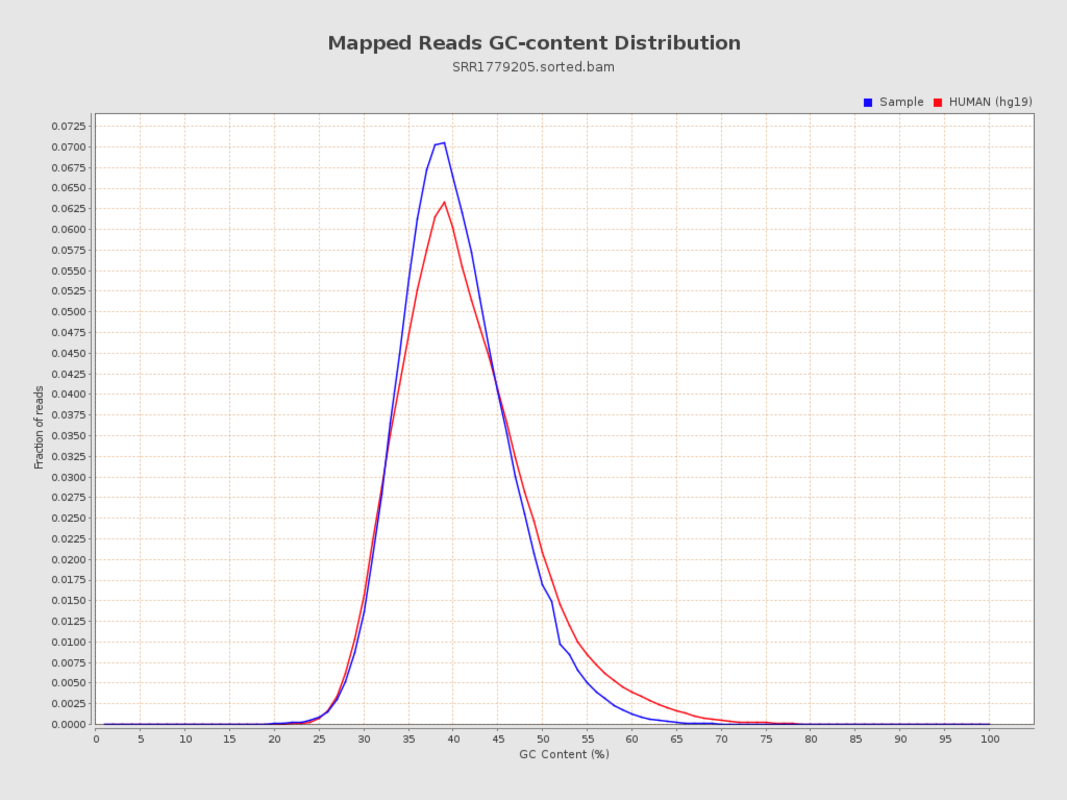
7. Results : Duplication Rate Histogram



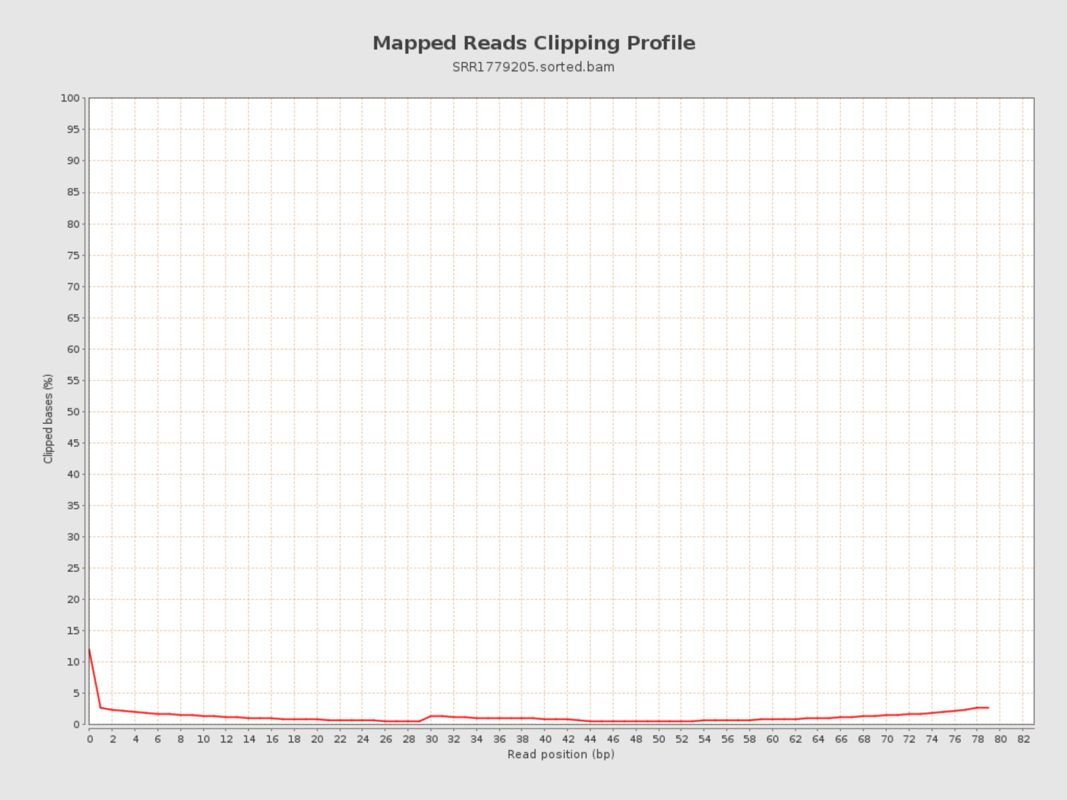
8. Results : Mapped Reads Nucleotide Content



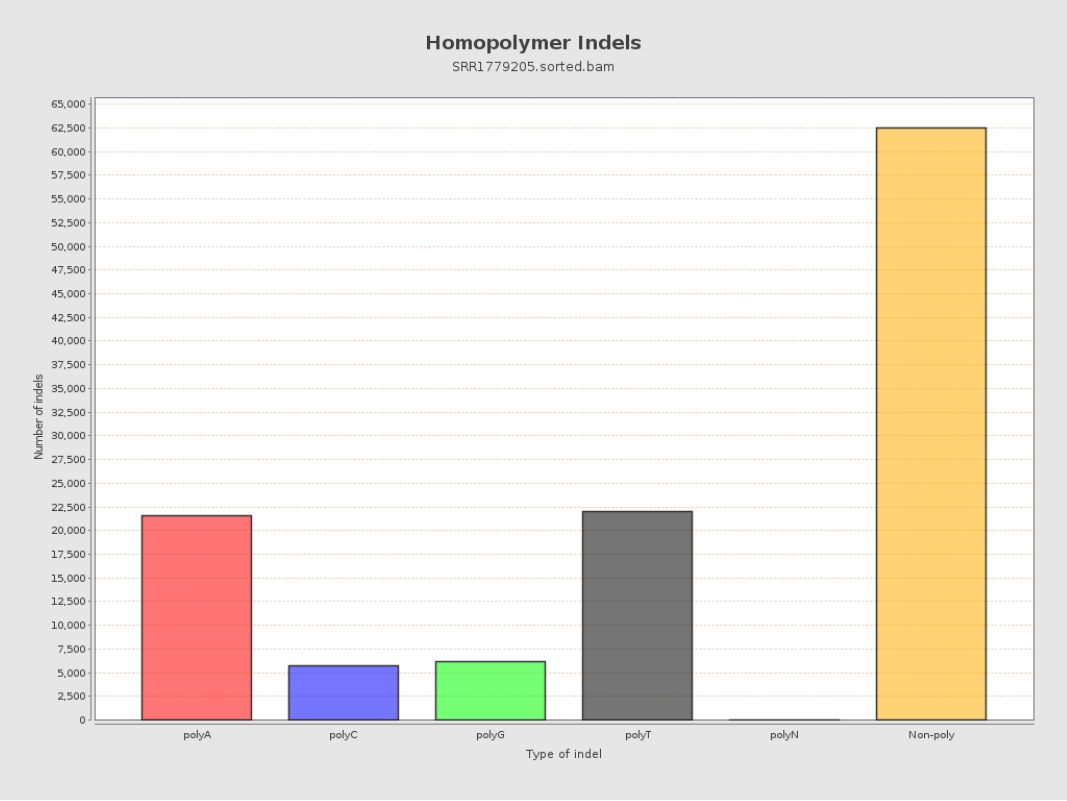
9. Results : Mapped Reads GC-content Distribution



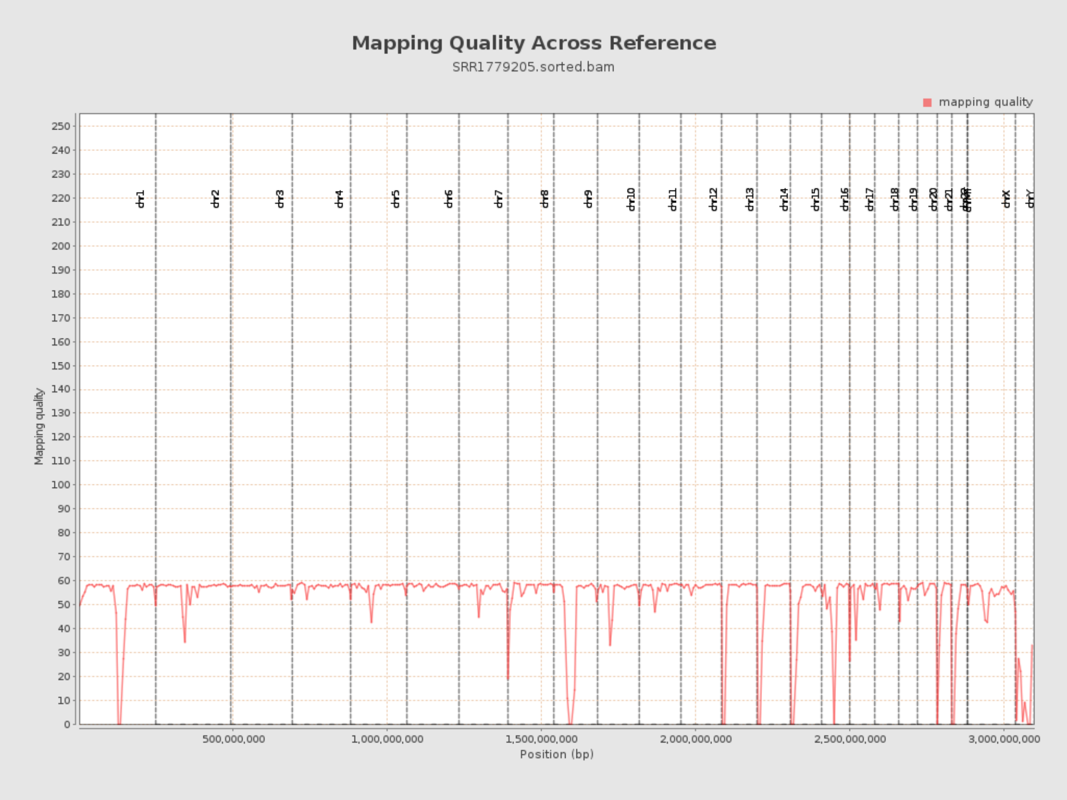
10. Results : Mapped Reads Clipping Profile



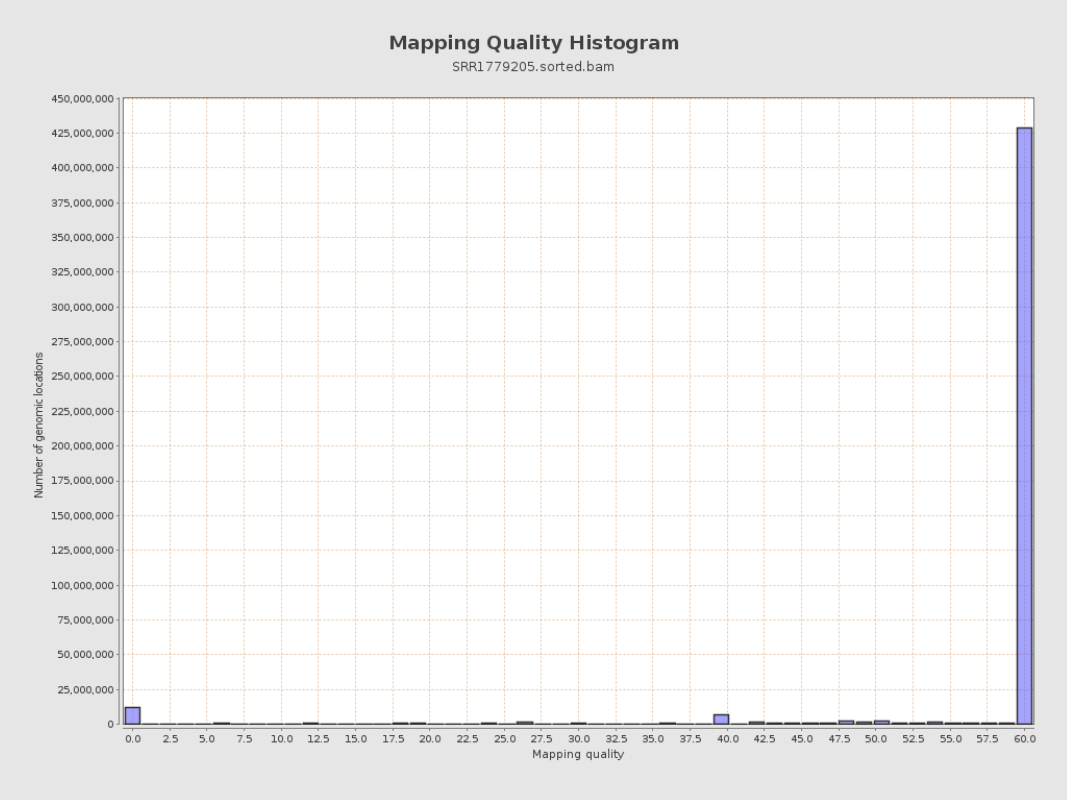
11. Results : Homopolymer Indels



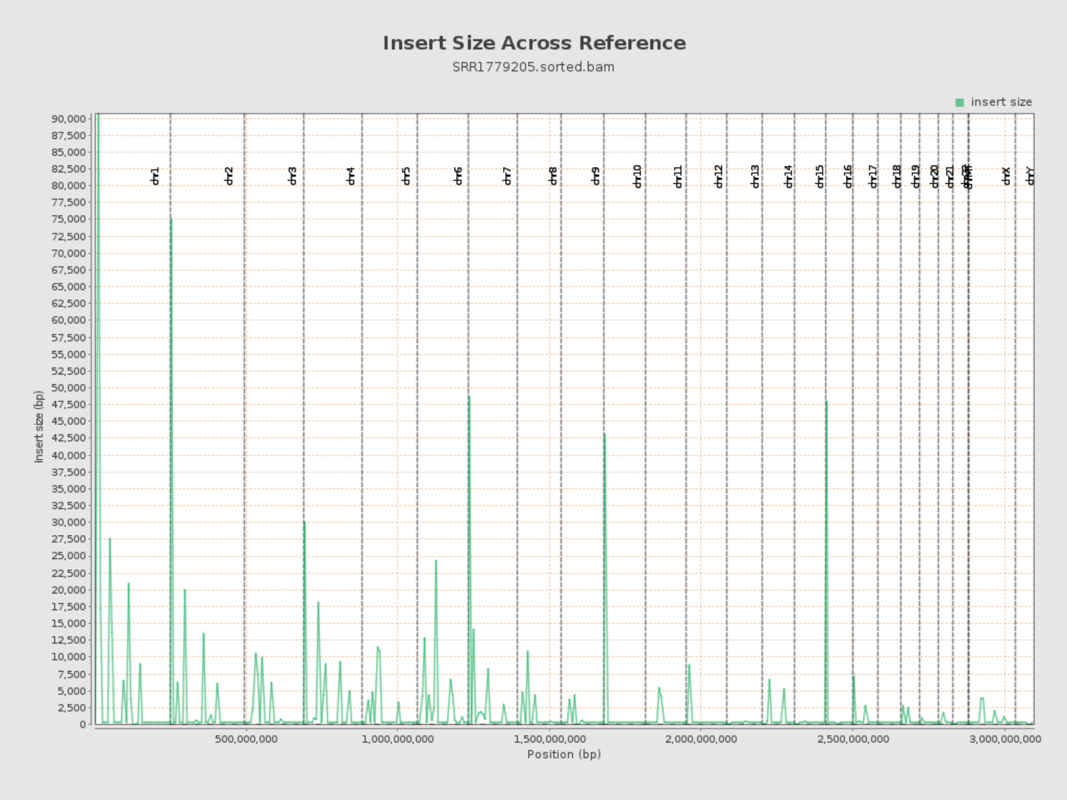
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram