Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 16:41:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779213.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_SRR1779213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779213_1.fastq.gz SRR1779213_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 16:41:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,546,502
Mapped reads	7,285,073 / 96.54%
Unmapped reads	261,429 / 3.46%
Mapped paired reads	7,285,073 / 96.54%
Mapped reads, first in pair	3,685,986 / 48.84%
Mapped reads, second in pair	3,599,087 / 47.69%
Mapped reads, both in pair	7,189,144 / 95.26%
Mapped reads, singletons	95,929 / 1.27%
Secondary alignments	0
Supplementary alignments	15,718 / 0.21%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	58,600 / 0.78%
Duplication rate	0.77%
Clipped reads	247,046 / 3.27%

2.2. ACGT Content

Number/percentage of A's	178,858,995 / 30.87%
Number/percentage of C's	109,957,451 / 18.98%
Number/percentage of T's	178,515,957 / 30.81%
Number/percentage of G's	112,008,775 / 19.33%
Number/percentage of N's	104,873 / 0.02%

GC Percentage	38.31%

2.3. Coverage

Mean	0.1872
Standard Deviation	0.5916

2.4. Mapping Quality

Mean Mapping Quality	52.79

2.5. Insert size

Mean	53,312.84
Standard Deviation	2,188,649.04
P25/Median/P75	209 / 275 / 346

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	2,484,873
Insertions	44,076
Mapped reads with at least one insertion	0.6%
Deletions	55,676
Mapped reads with at least one deletion	0.75%
Homopolymer indels	46.68%

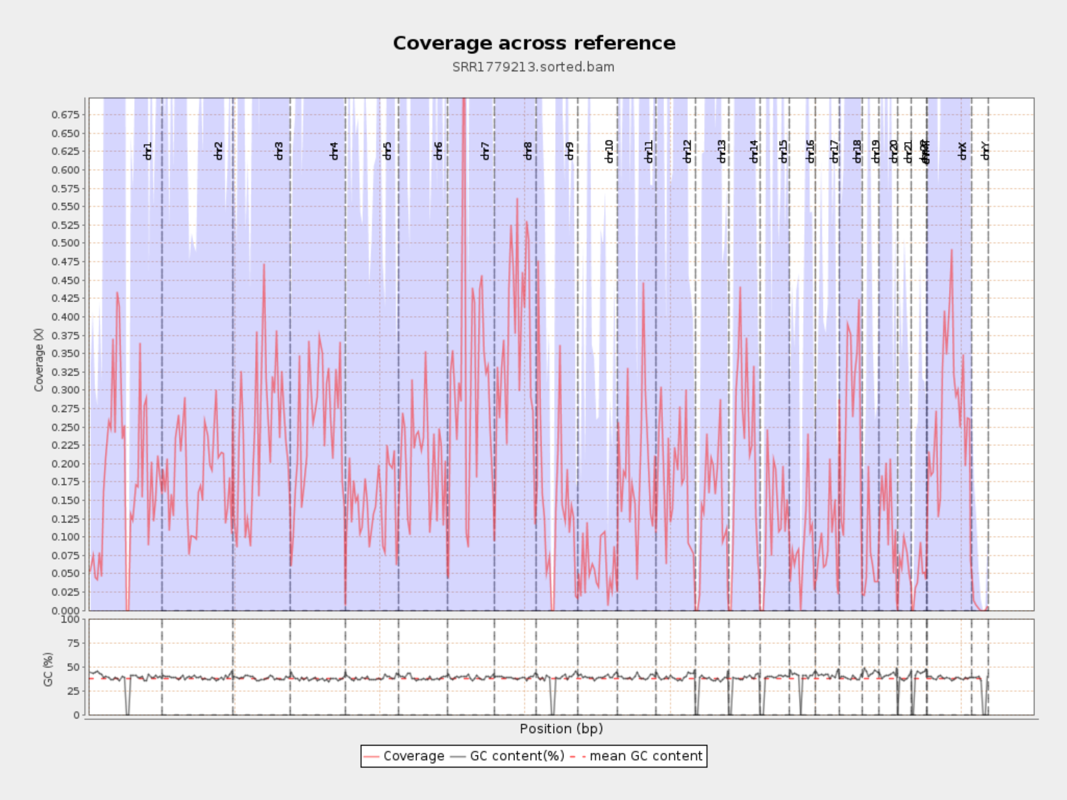
2.7. Chromosome stats

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

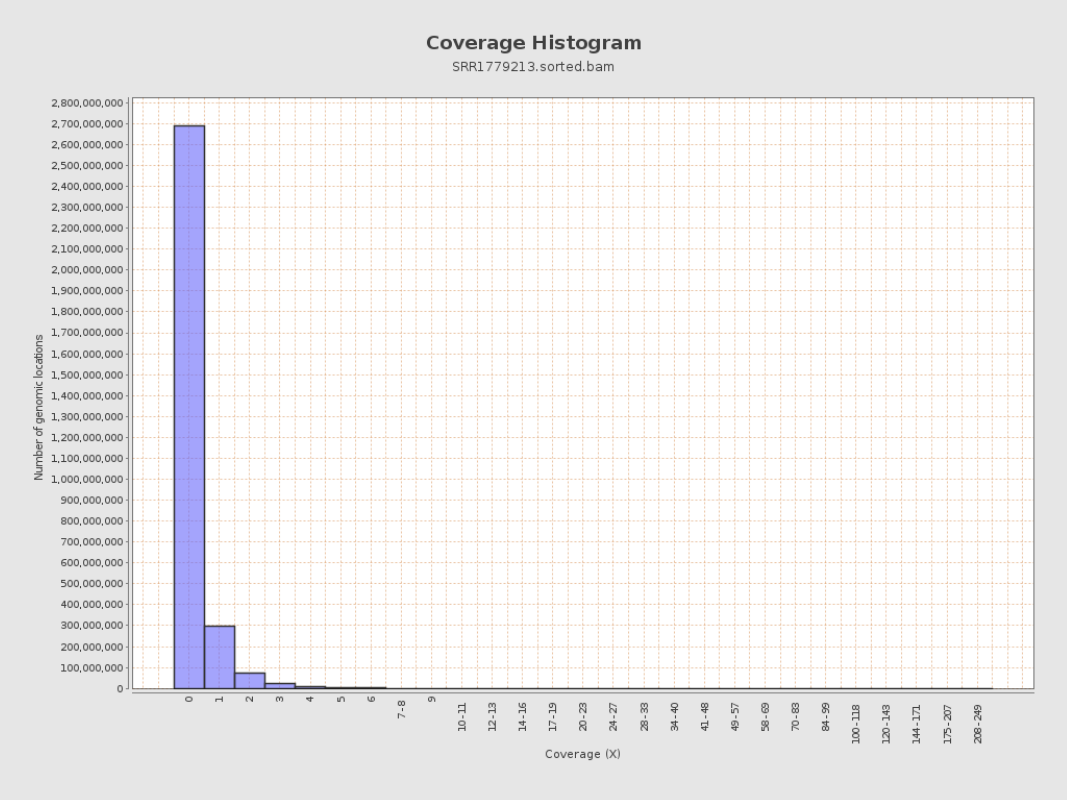
		bases	**coverage**	**deviation**
chr1	249250621	45218263	0.1814	0.618
chr2	243199373	44603606	0.1834	0.5461
chr3	198022430	48160899	0.2432	0.6431
chr4	191154276	47917392	0.2507	0.647
chr5	180915260	26068565	0.1441	0.4769
chr6	171115067	35190814	0.2057	0.5912
chr7	159138663	50442288	0.317	0.9391
chr8	146364022	53633193	0.3664	0.7968
chr9	141213431	21297817	0.1508	0.5276
chr10	135534747	8151163	0.0601	0.3509
chr11	135006516	26479892	0.1961	0.5851
chr12	133851895	23389828	0.1747	0.5411
chr13	115169878	15915946	0.1382	0.4721
chr14	107349540	23388698	0.2179	0.626
chr15	102531392	12804048	0.1249	0.4625
chr16	90354753	7967337	0.0882	0.3681
chr17	81195210	7203041	0.0887	0.3843
chr18	78077248	21569061	0.2763	0.6762
chr19	59128983	3994424	0.0676	0.3526
chr20	63025520	8356855	0.1326	0.4716
chr21	48129895	2965910	0.0616	0.3055
chr22	51304566	2140590	0.0417	0.2384
chrMT	16571	1381	0.0833	0.4212
chrX	155270560	42279795	0.2723	0.7106

chrY	59373566	421208	0.0071	0.1061

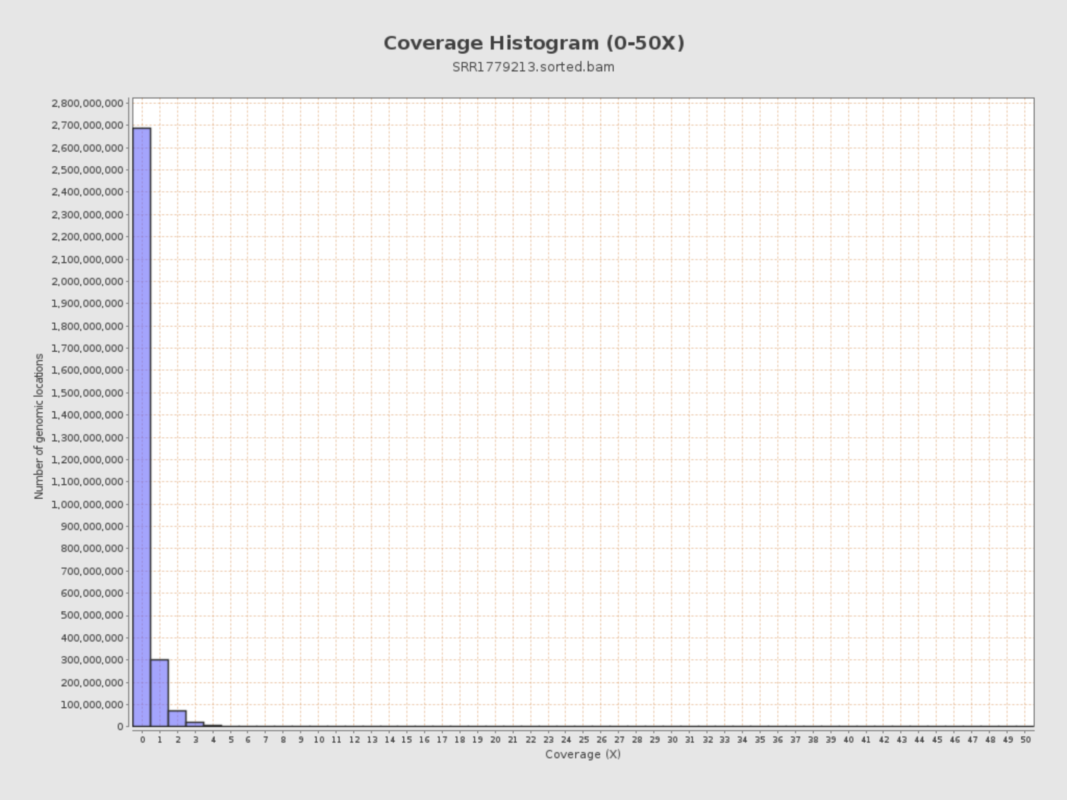
3. Results : Coverage across reference



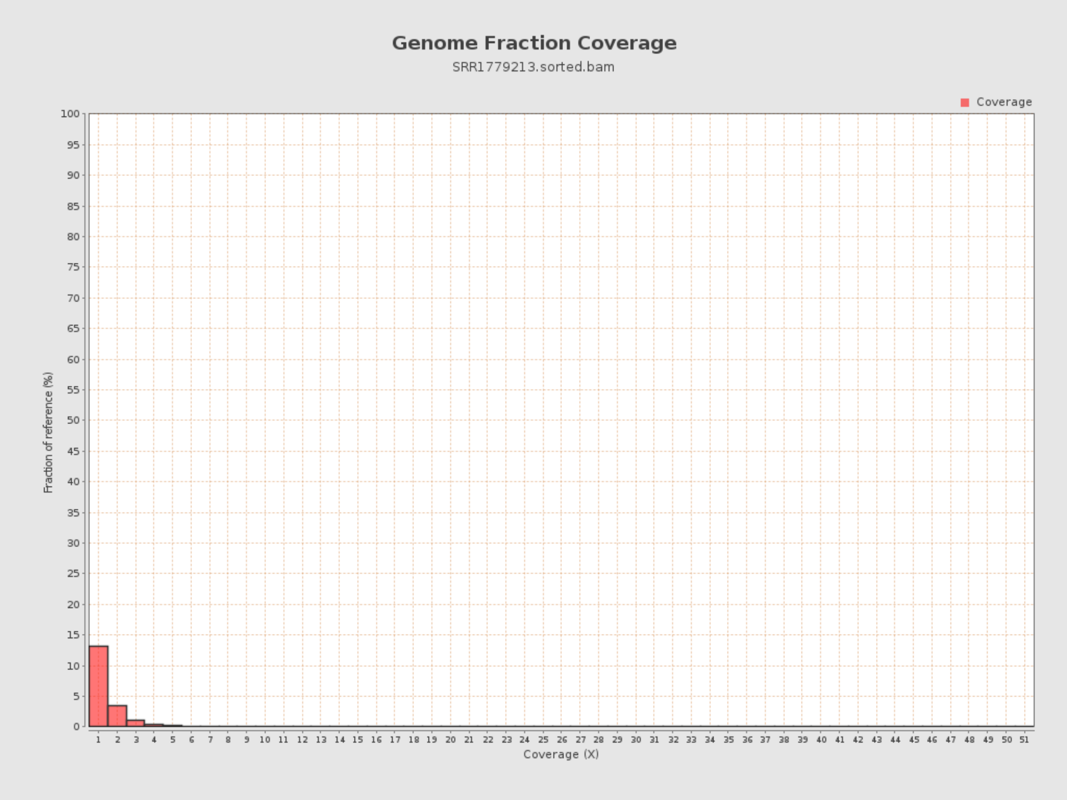
4. Results : Coverage Histogram



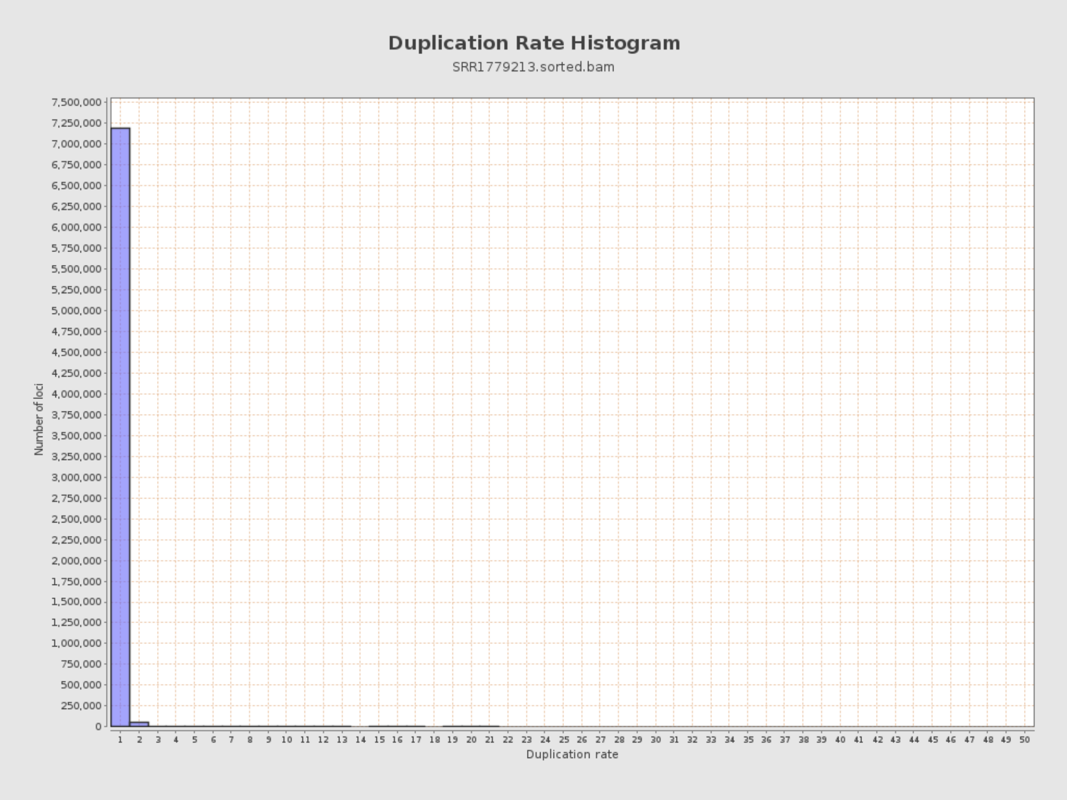
5. Results : Coverage Histogram (0-50X)



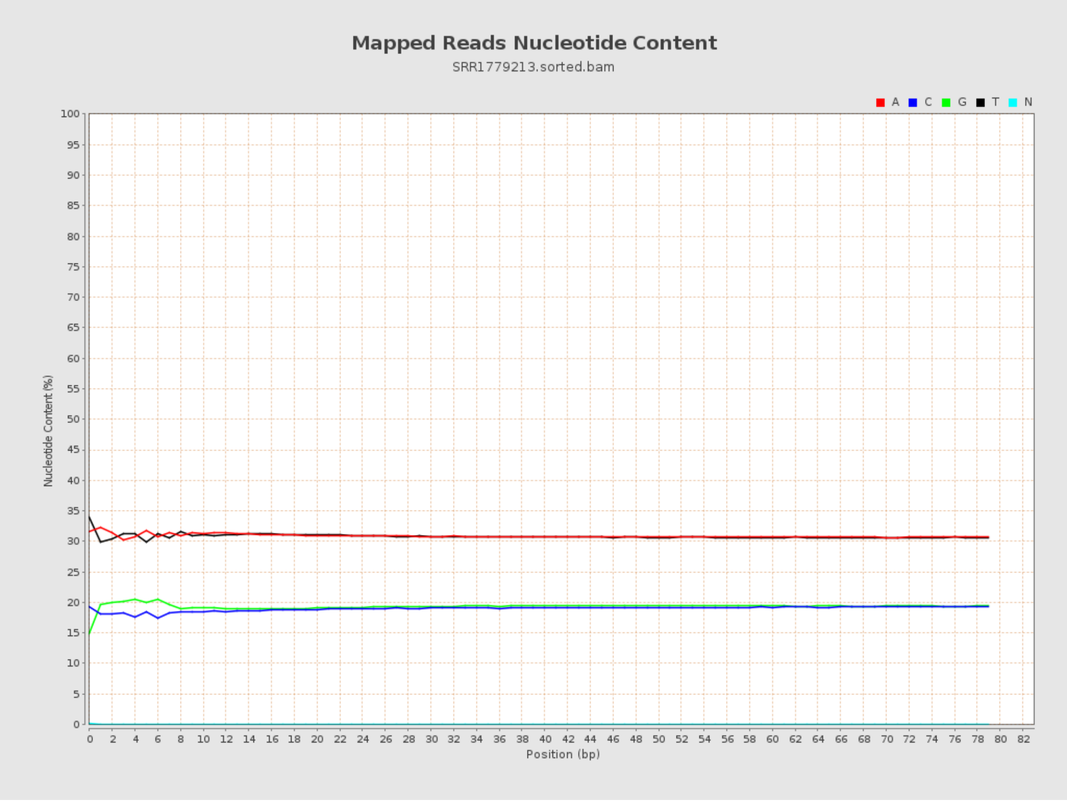
6. Results : Genome Fraction Coverage



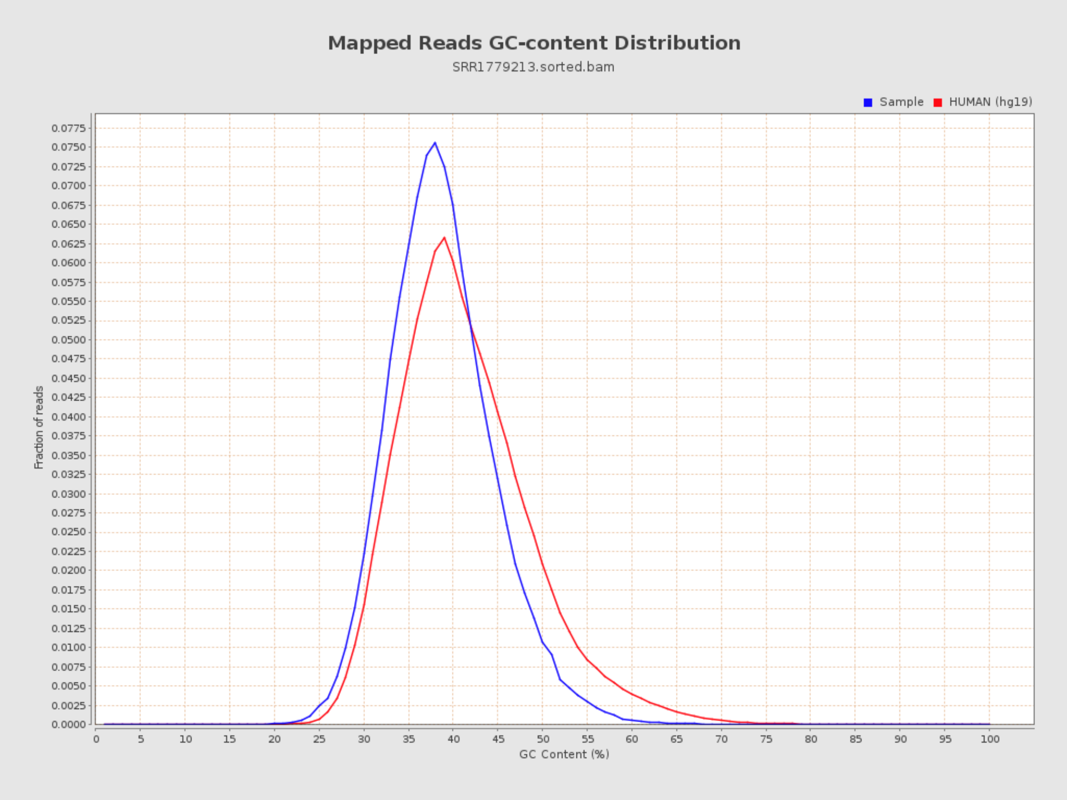
7. Results : Duplication Rate Histogram



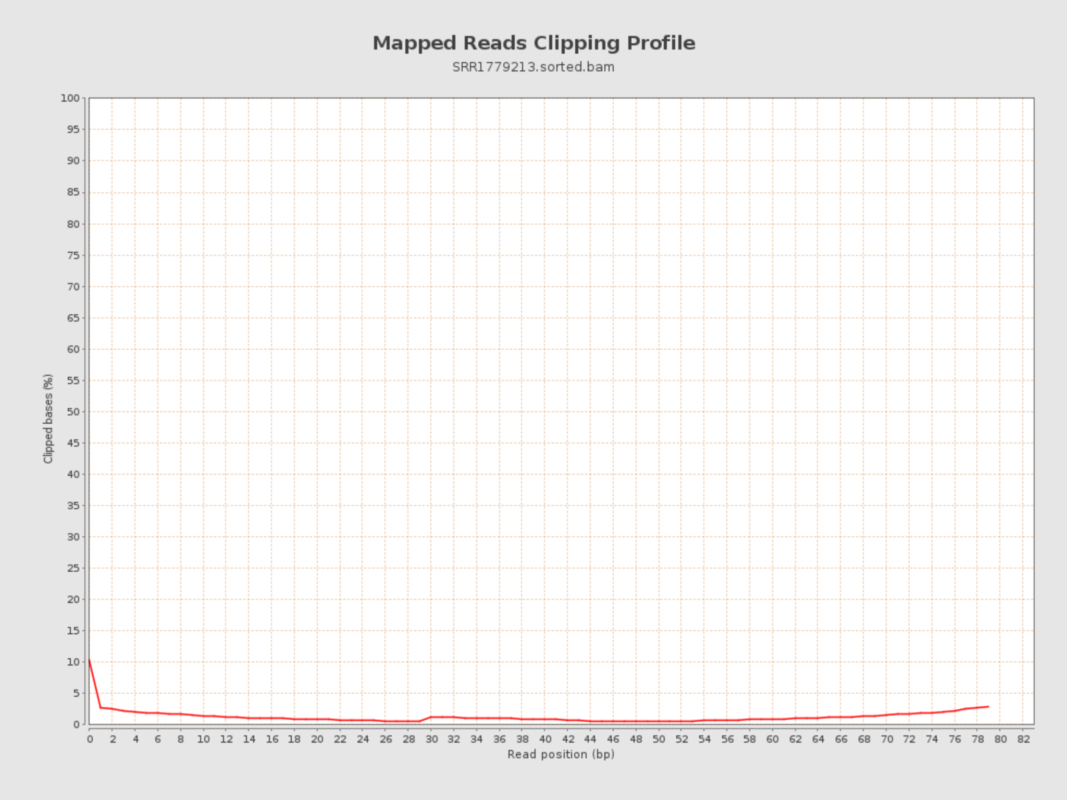
8. Results : Mapped Reads Nucleotide Content



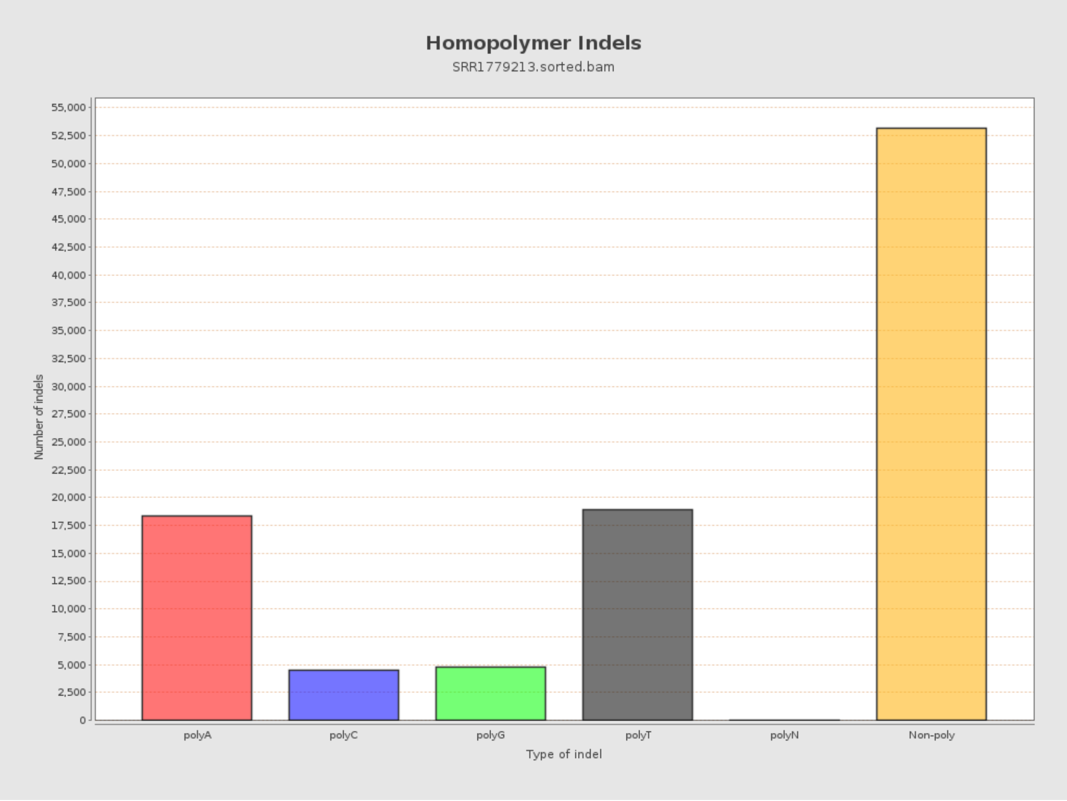
9. Results : Mapped Reads GC-content Distribution



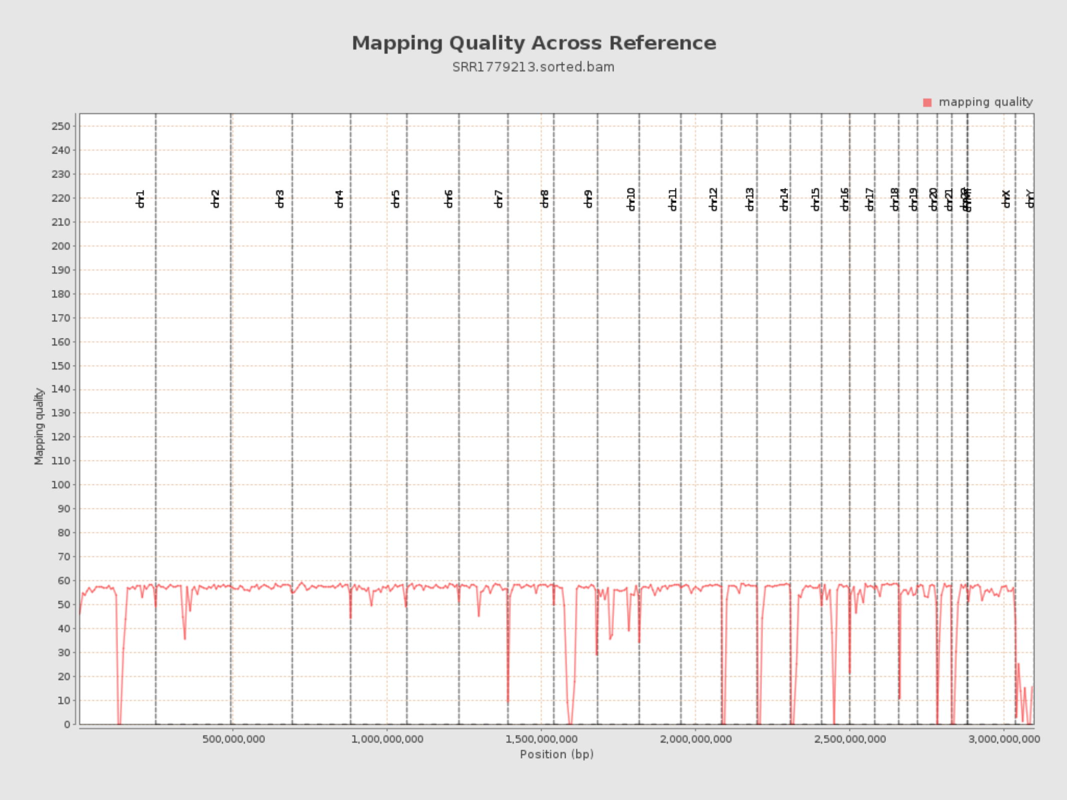
10. Results : Mapped Reads Clipping Profile



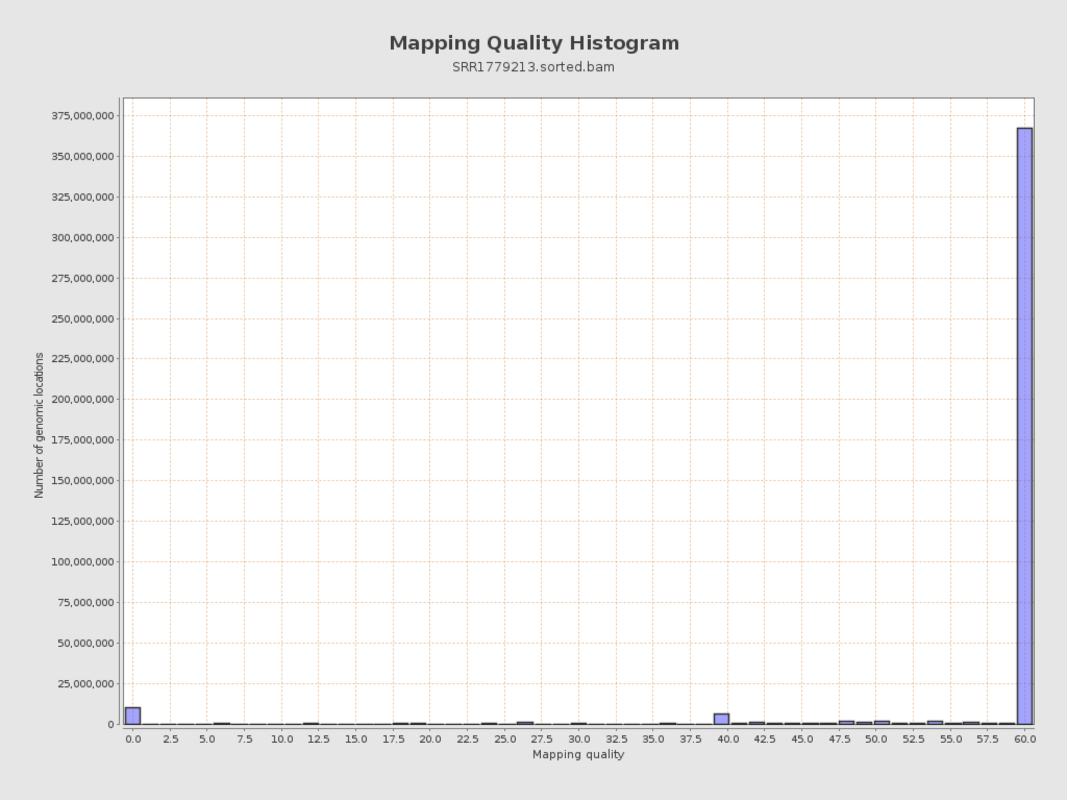
11. Results : Homopolymer Indels



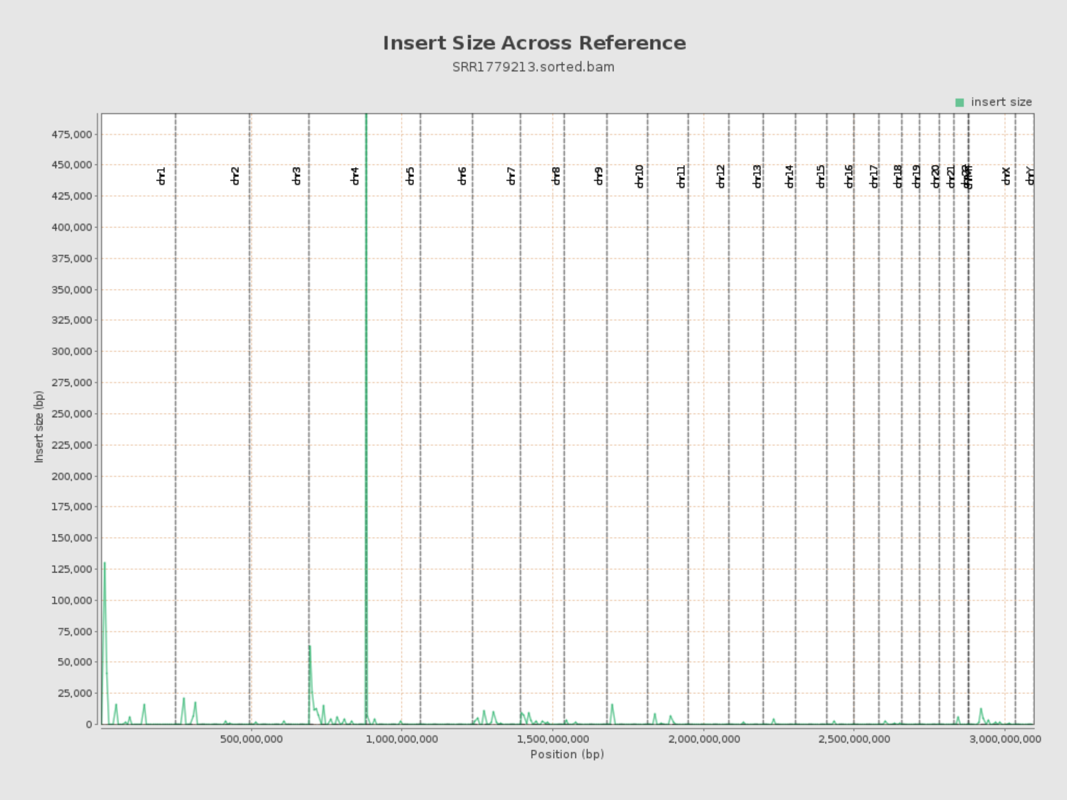
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram