Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 15:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779207.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_SRR1779207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779207_1.fastq.gz SRR1779207_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 15:27:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,482,370
Mapped reads	8,219,882 / 96.91%
Unmapped reads	262,488 / 3.09%
Mapped paired reads	8,219,882 / 96.91%
Mapped reads, first in pair	4,156,436 / 49%
Mapped reads, second in pair	4,063,446 / 47.9%
Mapped reads, both in pair	8,114,474 / 95.66%
Mapped reads, singletons	105,408 / 1.24%
Secondary alignments	0
Supplementary alignments	20,726 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	72,677 / 0.86%
Duplication rate	0.8%
Clipped reads	306,876 / 3.62%

2.2. ACGT Content

Number/percentage of A's	199,164,438 / 30.48%
Number/percentage of C's	126,454,374 / 19.35%
Number/percentage of T's	199,048,835 / 30.46%
Number/percentage of G's	128,718,342 / 19.7%
Number/percentage of N's	120,393 / 0.02%

GC Percentage	39.05%

2.3. Coverage

Mean	0.2111
Standard Deviation	0.6488

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	53,772.53
Standard Deviation	2,189,405.56
P25/Median/P75	195 / 256 / 326

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	2,887,095
Insertions	51,549
Mapped reads with at least one insertion	0.62%
Deletions	64,988
Mapped reads with at least one deletion	0.78%
Homopolymer indels	47.16%

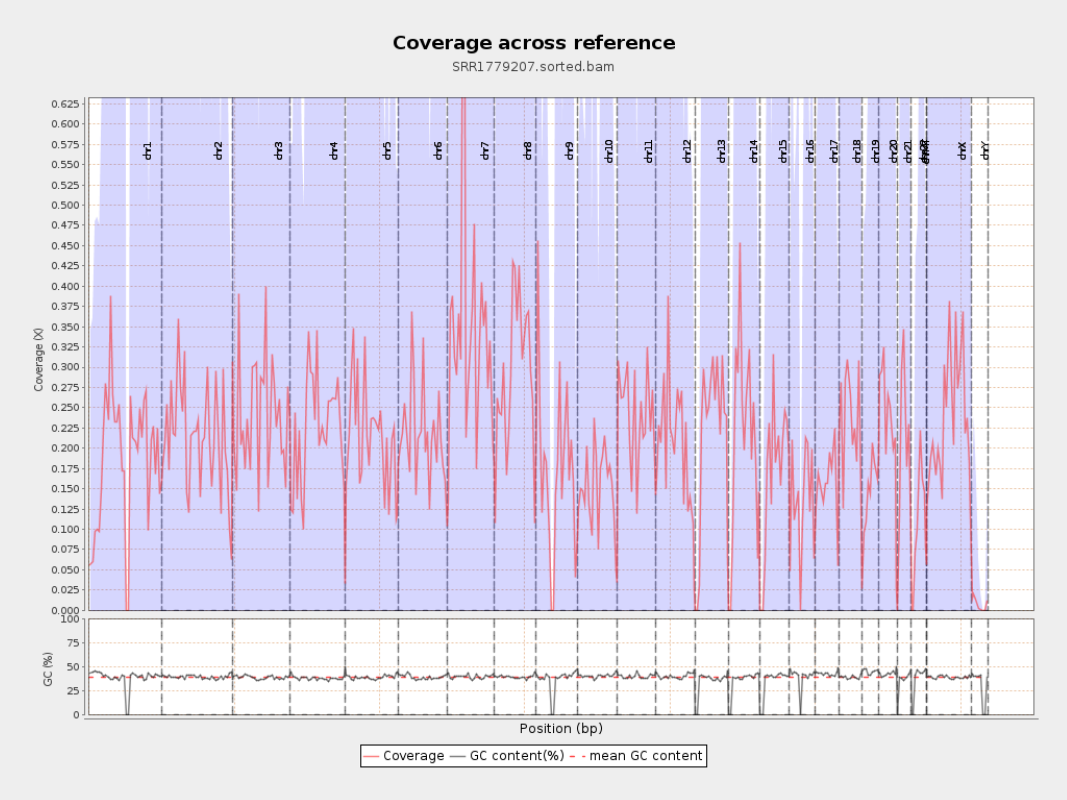
2.7. Chromosome stats

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

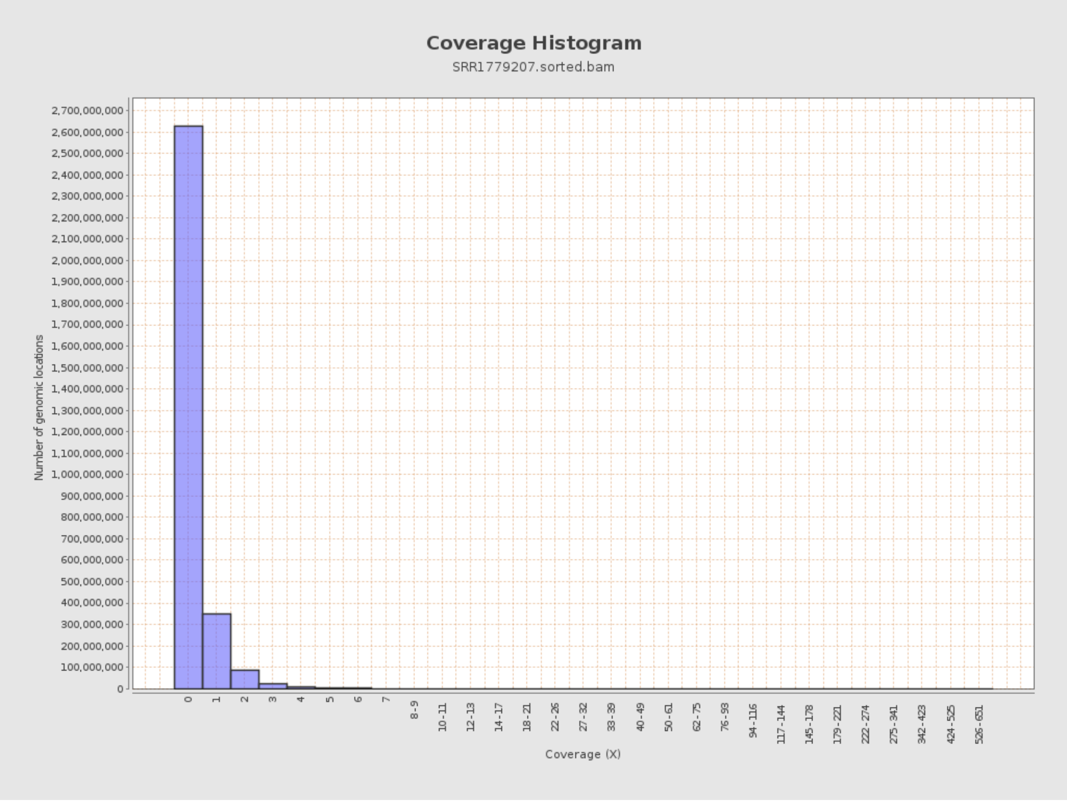
		bases	coverage	deviation
chr1	249250621	46397651	0.1861	0.8327
chr2	243199373	52040320	0.214	0.5783
chr3	198022430	47874114	0.2418	0.6206
chr4	191154276	43255126	0.2263	0.6056
chr5	180915260	38948715	0.2153	0.5838
chr6	171115067	36992929	0.2162	0.5944
chr7	159138663	56255361	0.3535	1.0244
chr8	146364022	42577772	0.2909	0.6799
chr9	141213431	24619750	0.1743	0.5527
chr10	135534747	20955534	0.1546	0.7941
chr11	135006516	31867034	0.236	0.6137
chr12	133851895	27748044	0.2073	0.5738
chr13	115169878	25171947	0.2186	0.5875
chr14	107349540	22598099	0.2105	0.5784
chr15	102531392	17358368	0.1693	0.521
chr16	90354753	11981756	0.1326	0.459
chr17	81195210	12544031	0.1545	0.4921
chr18	78077248	18425141	0.236	0.6165
chr19	59128983	8656996	0.1464	0.6638
chr20	63025520	15231105	0.2417	0.6549
chr21	48129895	9465937	0.1967	0.5746
chr22	51304566	5594335	0.109	0.4077
chrMT	16571	931	0.0562	0.2782
chrX	155270560	36629936	0.2359	0.6341

chrY	59373566	449734	0.0076	0.1178

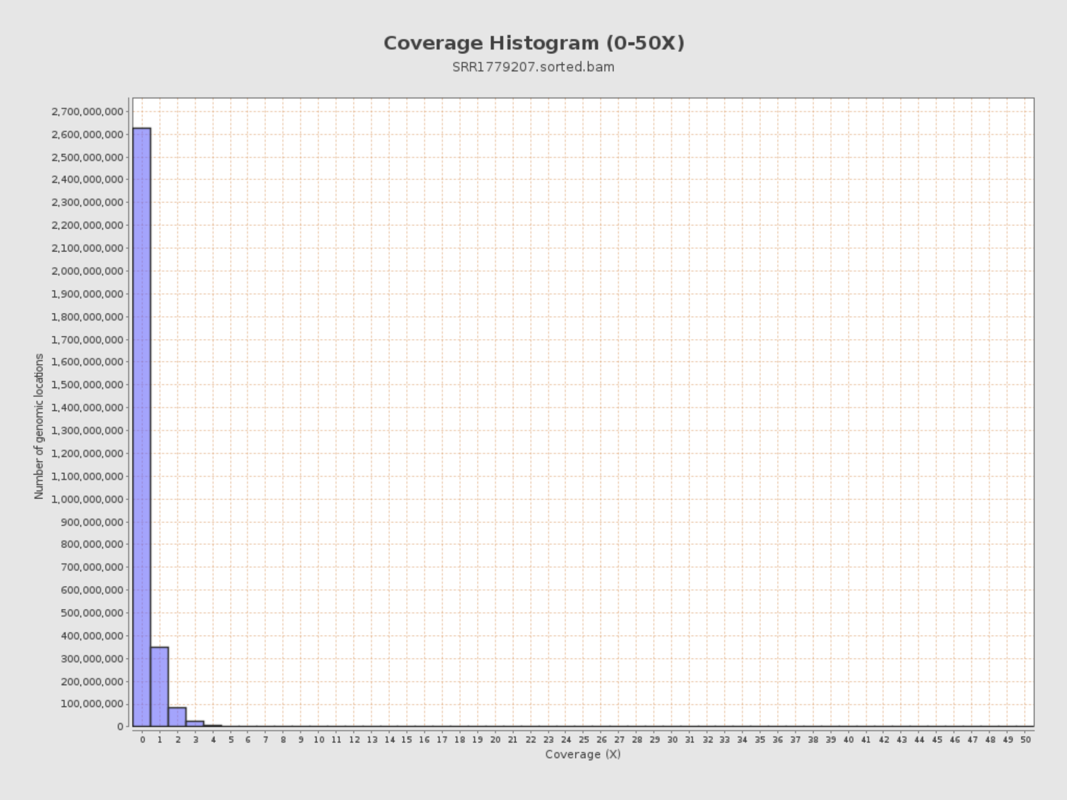
3. Results : Coverage across reference



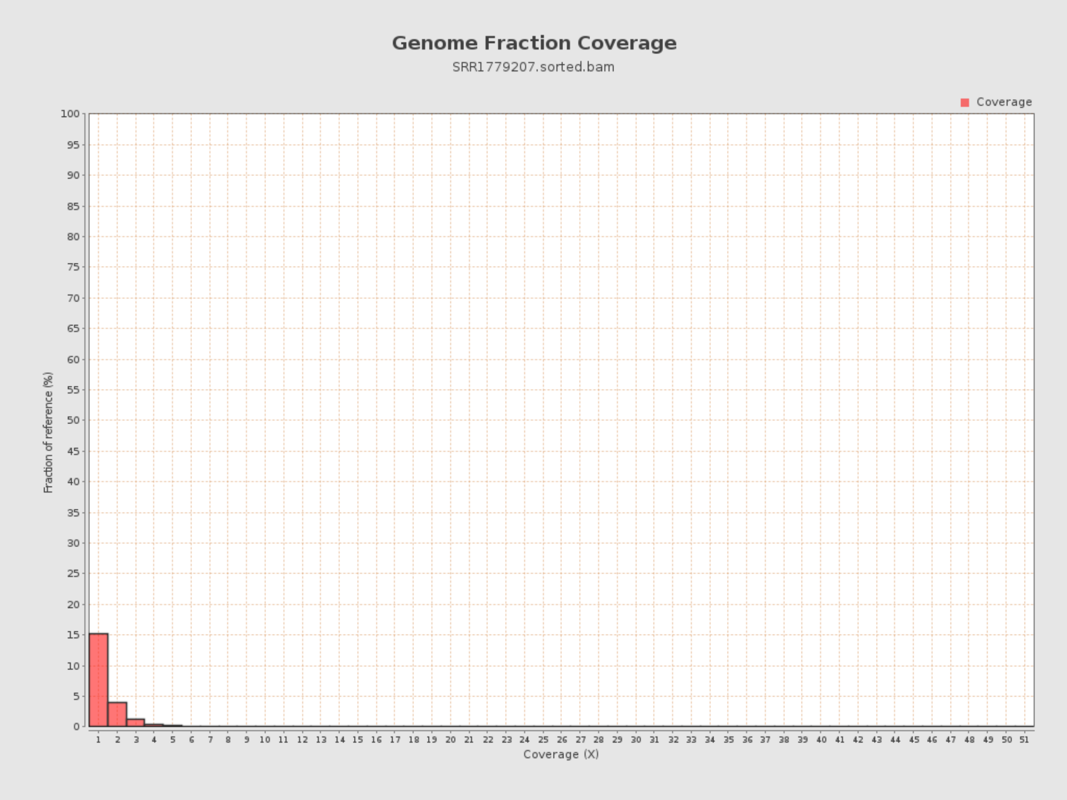
4. Results : Coverage Histogram



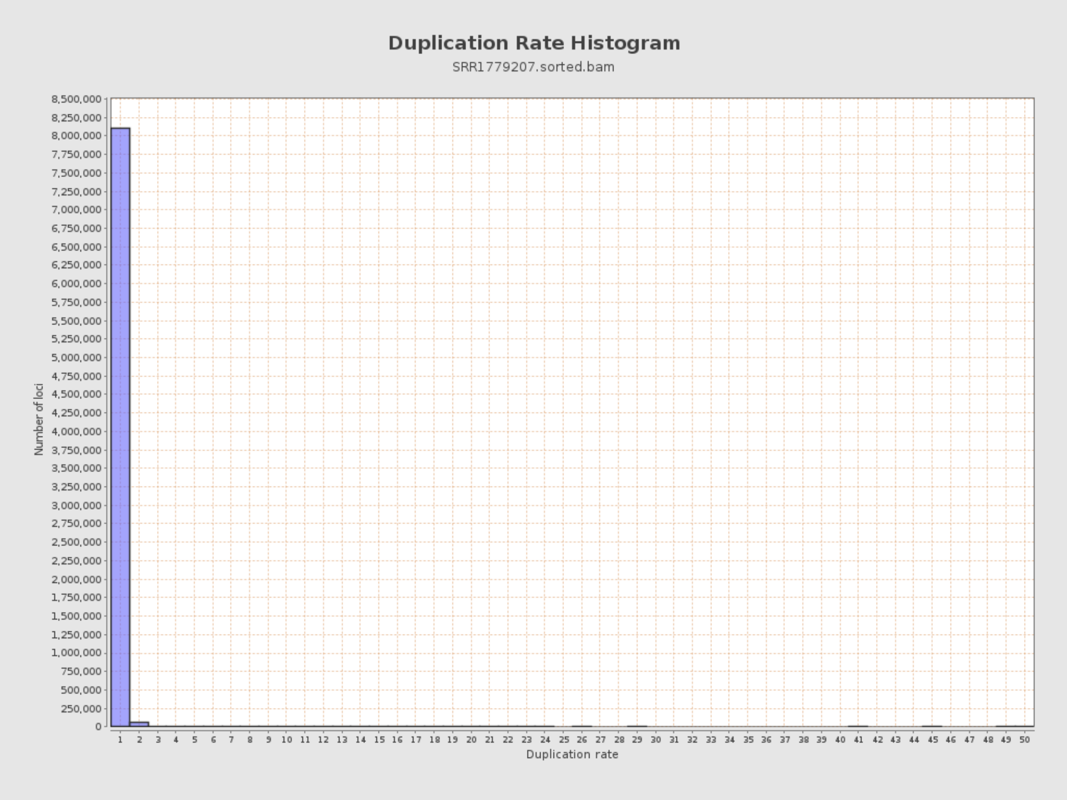
5. Results : Coverage Histogram (0-50X)



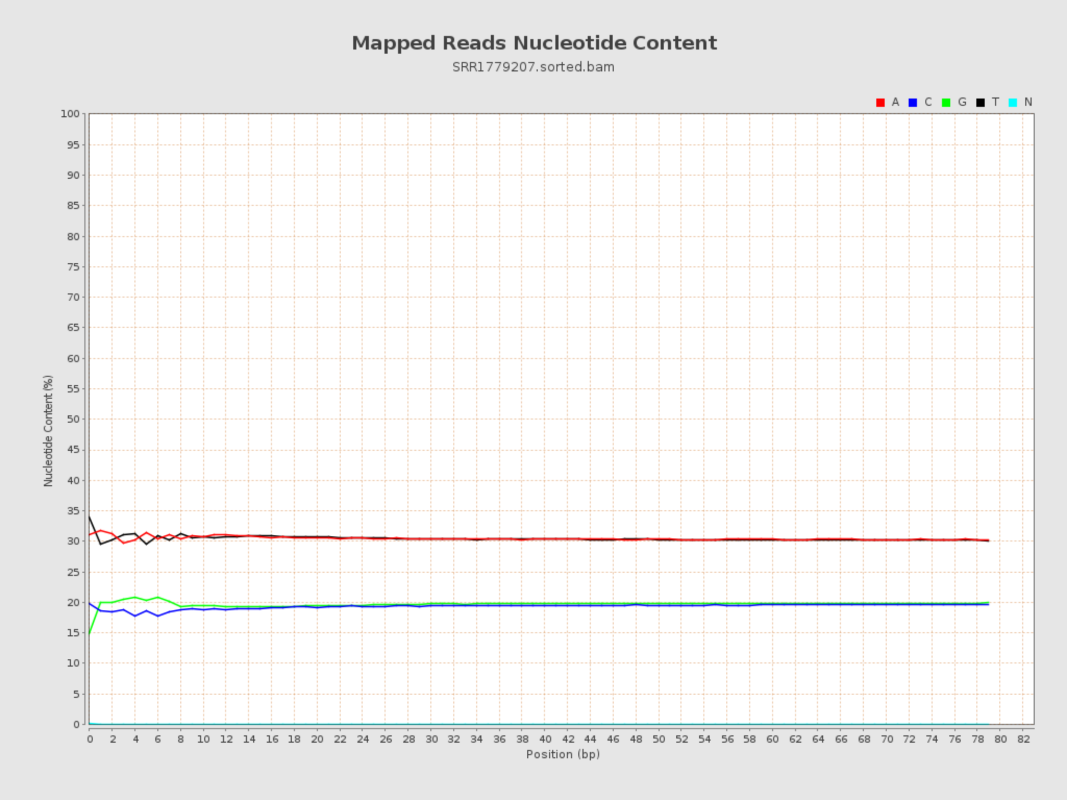
6. Results : Genome Fraction Coverage



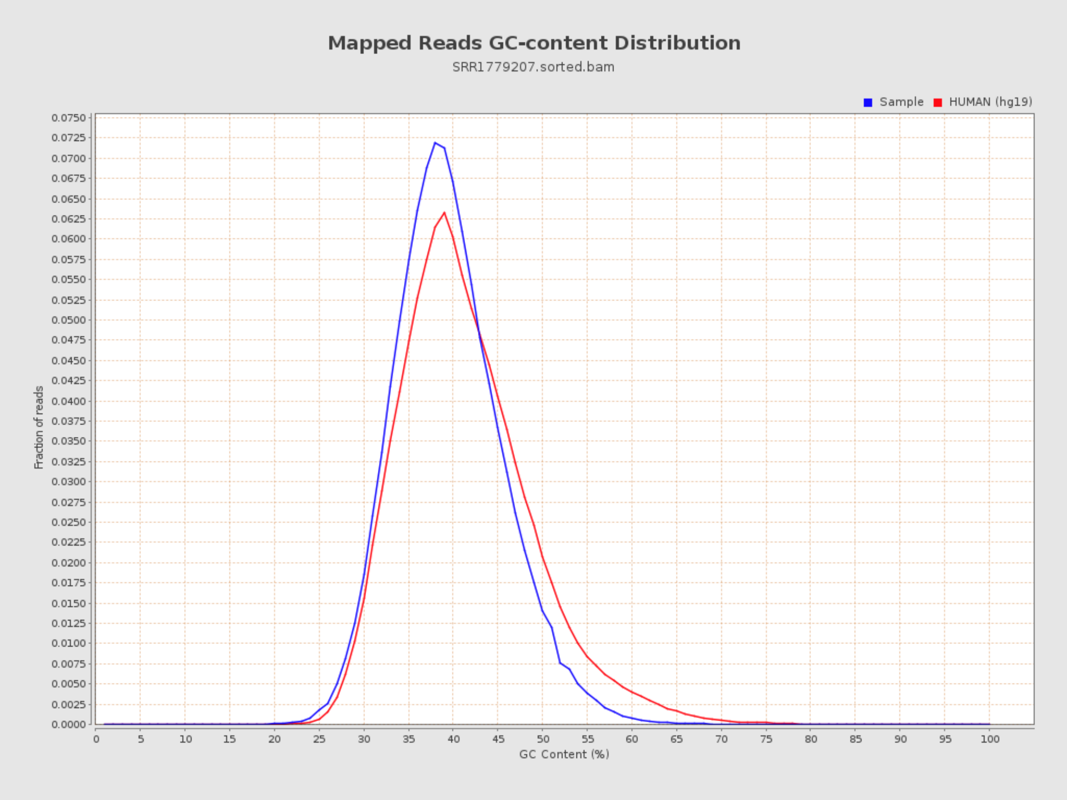
7. Results : Duplication Rate Histogram



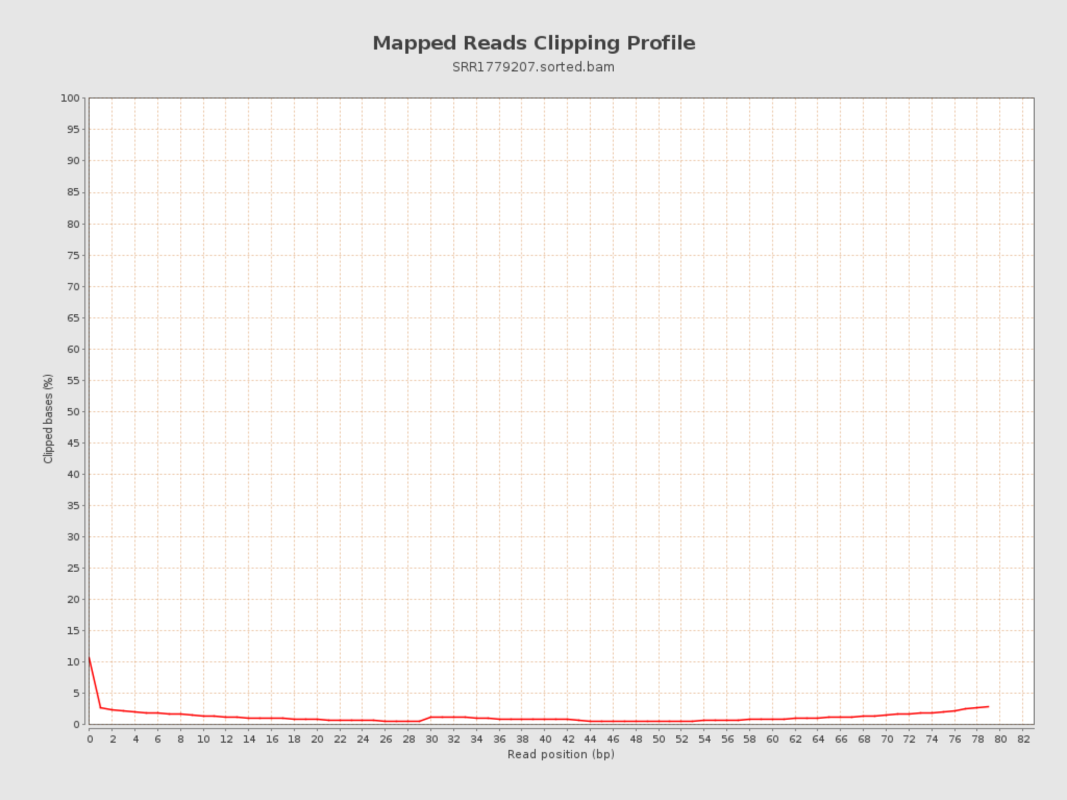
8. Results : Mapped Reads Nucleotide Content



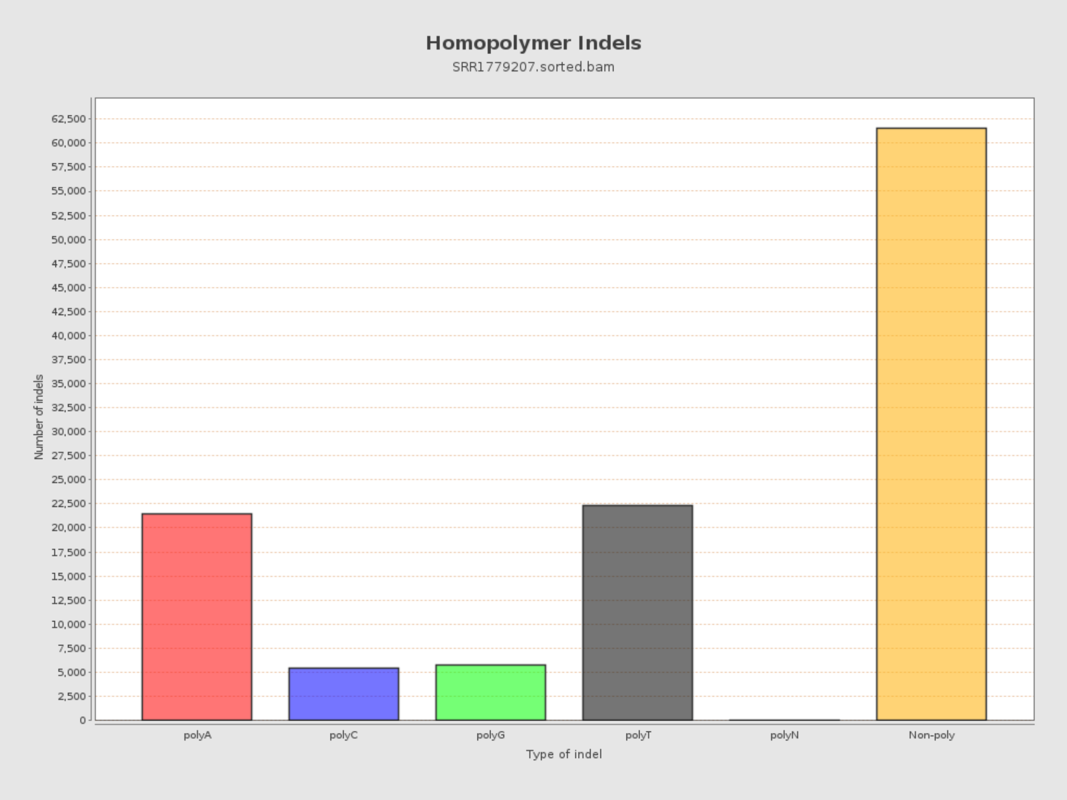
9. Results : Mapped Reads GC-content Distribution



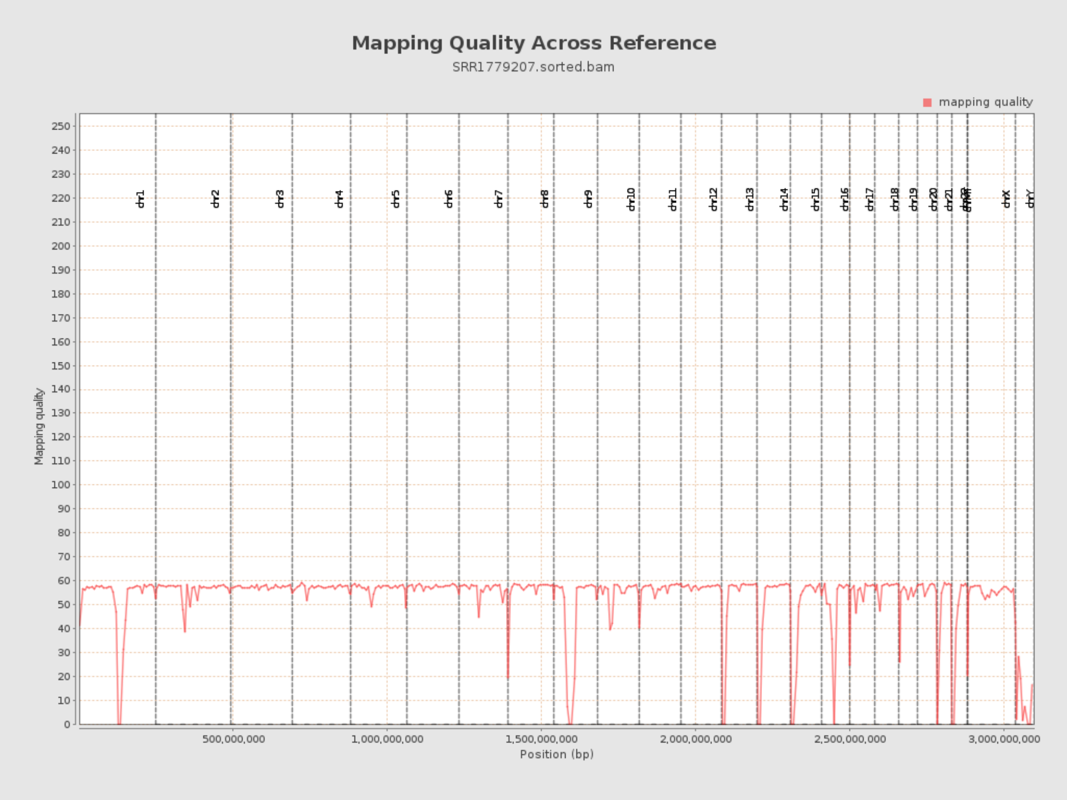
10. Results : Mapped Reads Clipping Profile



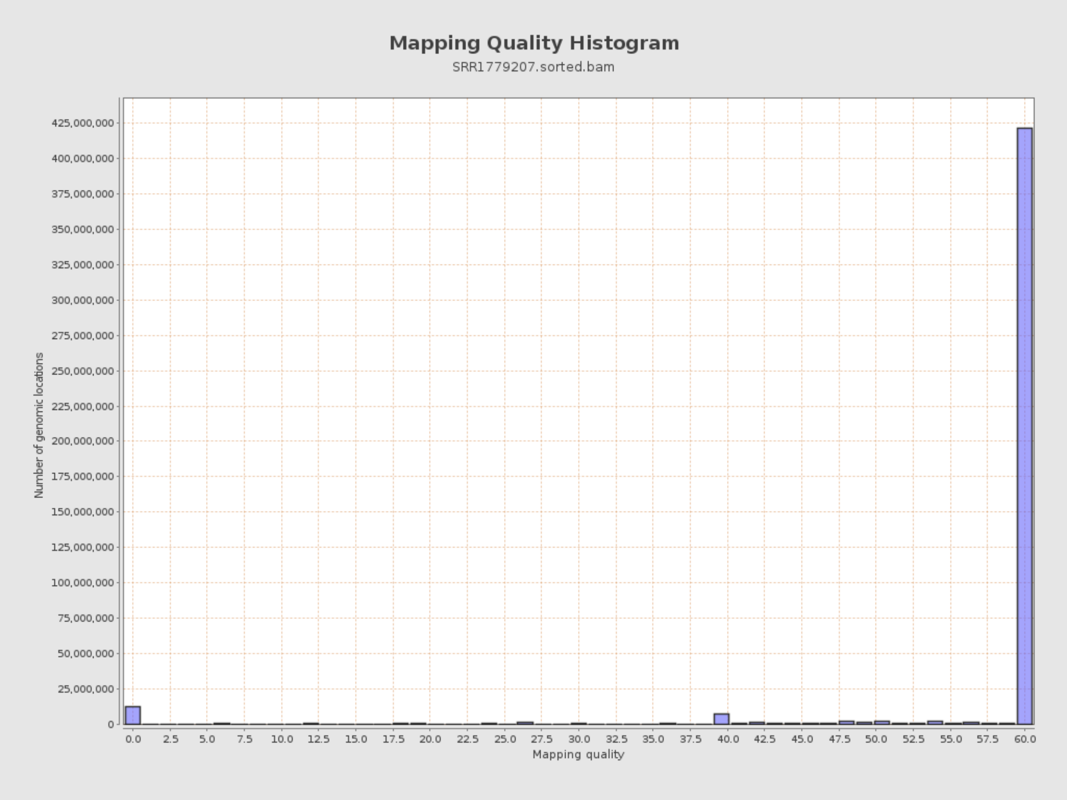
11. Results : Homopolymer Indels



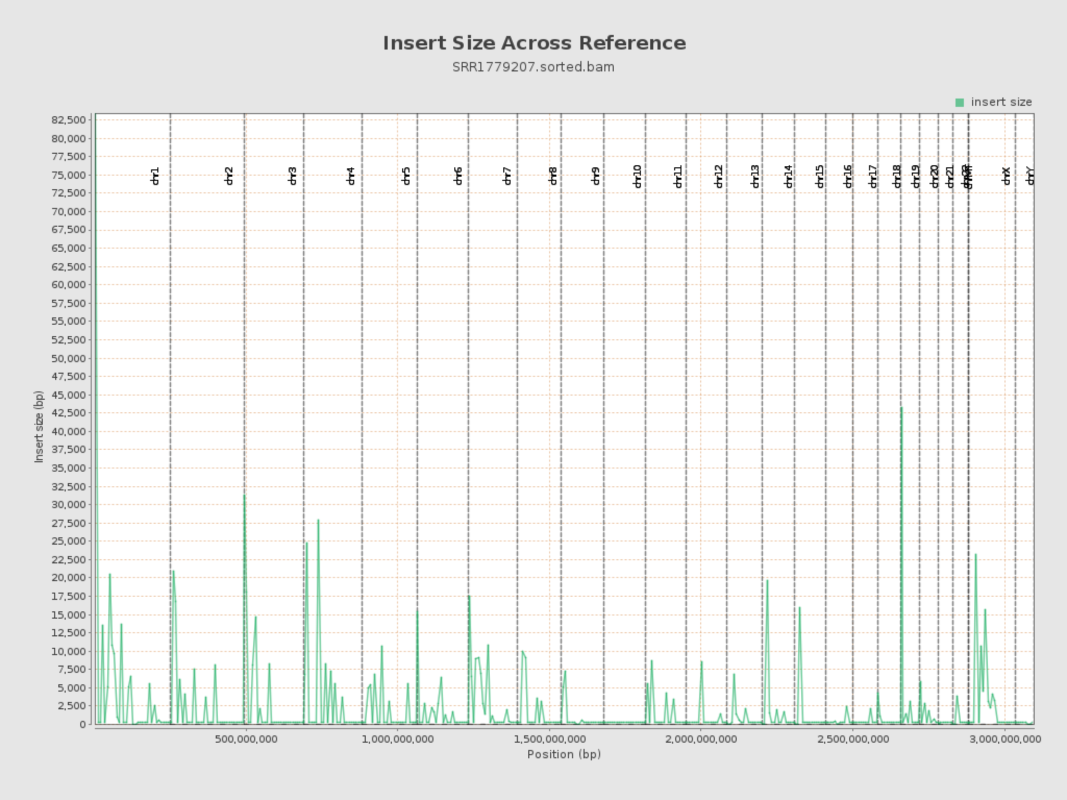
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram