Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 18:25:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779222.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_SRR1779222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779222_1.fastq.gz SRR1779222_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 18:25:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,170,782
Mapped reads	9,863,225 / 96.98%
Unmapped reads	307,557 / 3.02%
Mapped paired reads	9,863,225 / 96.98%
Mapped reads, first in pair	4,968,515 / 48.85%
Mapped reads, second in pair	4,894,710 / 48.13%
Mapped reads, both in pair	9,775,410 / 96.11%
Mapped reads, singletons	87,815 / 0.86%
Secondary alignments	0
Supplementary alignments	24,610 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	157,429 / 1.55%
Duplication rate	1.46%
Clipped reads	334,211 / 3.29%

2.2. ACGT Content

Number/percentage of A's	239,242,961 / 30.49%
Number/percentage of C's	152,432,195 / 19.43%
Number/percentage of T's	236,855,196 / 30.19%
Number/percentage of G's	155,995,313 / 19.88%
Number/percentage of N's	148,547 / 0.02%

GC Percentage	39.31%

2.3. Coverage

Mean	0.2535
Standard Deviation	0.8799

2.4. Mapping Quality

Mean Mapping Quality	53.18

2.5. Insert size

Mean	54,468.07
Standard Deviation	2,217,101.6
P25/Median/P75	153 / 204 / 279

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,001,163
Insertions	56,400
Mapped reads with at least one insertion	0.57%
Deletions	71,884
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.7%

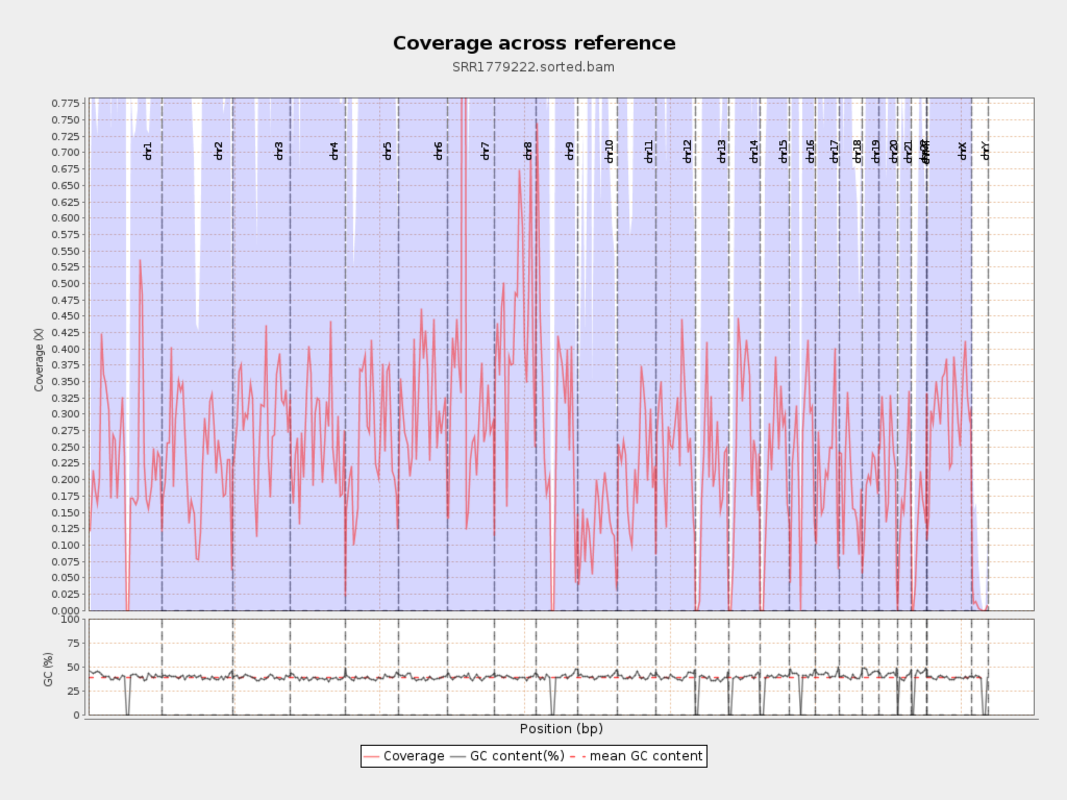
2.7. Chromosome stats

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

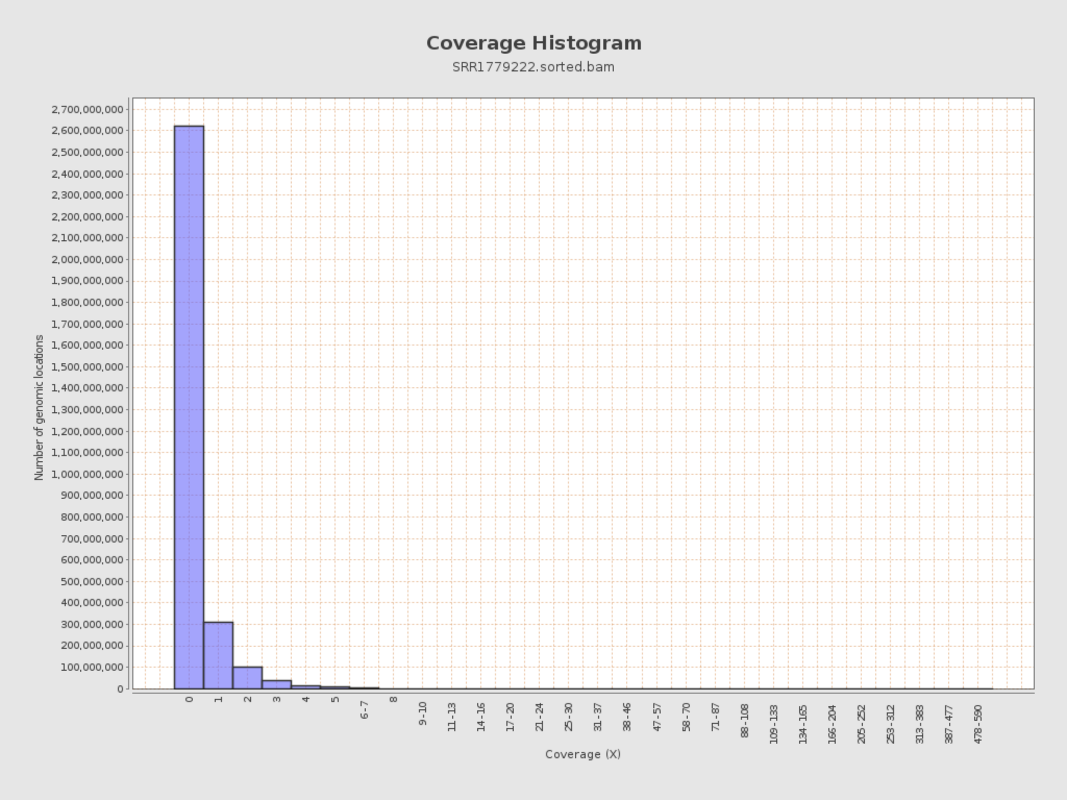
		bases	**coverage**	**deviation**
chr1	249250621	57172961	0.2294	0.9066
chr2	243199373	55661064	0.2289	0.6944
chr3	198022430	57887940	0.2923	0.7829
chr4	191154276	50466881	0.264	0.7426
chr5	180915260	47076774	0.2602	0.7424
chr6	171115067	53332700	0.3117	0.8284
chr7	159138663	63166649	0.3969	2.0143
chr8	146364022	63790401	0.4358	0.9992
chr9	141213431	40668414	0.288	0.832
chr10	135534747	17267788	0.1274	0.8766
chr11	135006516	30461736	0.2256	0.6968
chr12	133851895	35958824	0.2686	0.7554
chr13	115169878	22340532	0.194	0.6469
chr14	107349540	27028377	0.2518	0.7464
chr15	102531392	22093705	0.2155	0.6968
chr16	90354753	21923102	0.2426	0.7239
chr17	81195210	16671225	0.2053	0.6548
chr18	78077248	14558527	0.1865	0.6328
chr19	59128983	11162521	0.1888	0.6902
chr20	63025520	14538125	0.2307	0.6938
chr21	48129895	8345905	0.1734	0.6116
chr22	51304566	5644582	0.11	0.4409
chrMT	16571	5504	0.3321	0.6475
chrX	155270560	47145322	0.3036	0.8732

chrY	59373566	453424	0.0076	0.1093

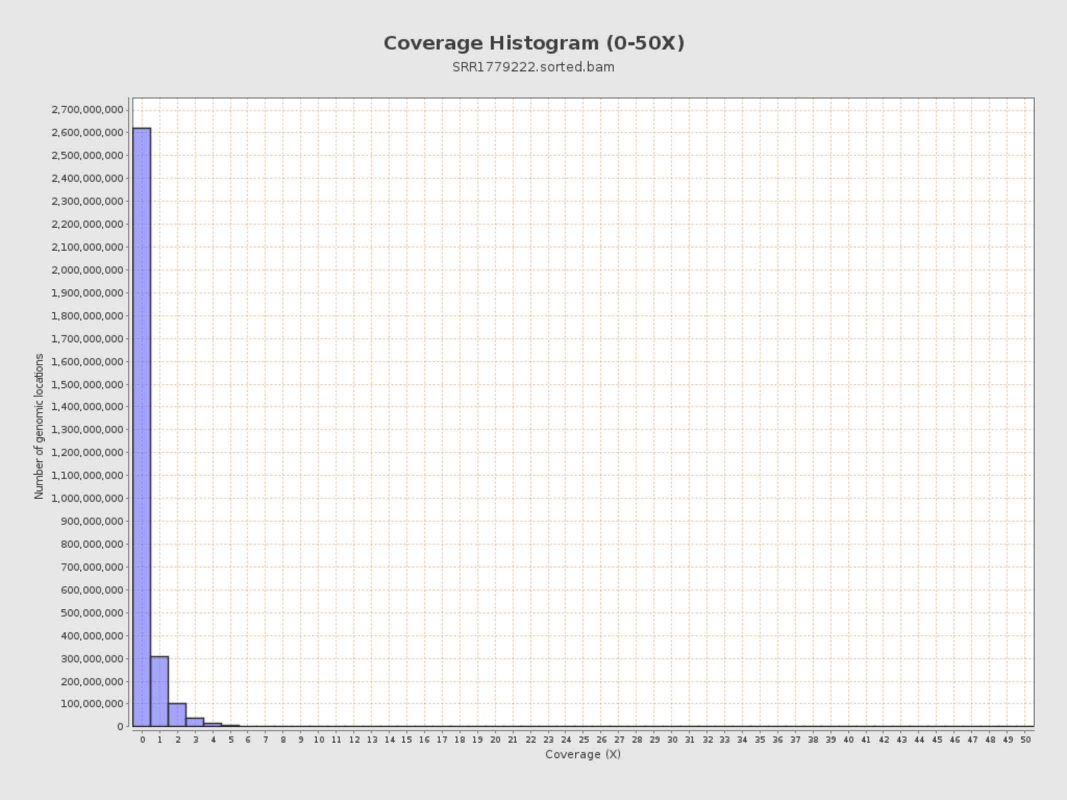
3. Results : Coverage across reference



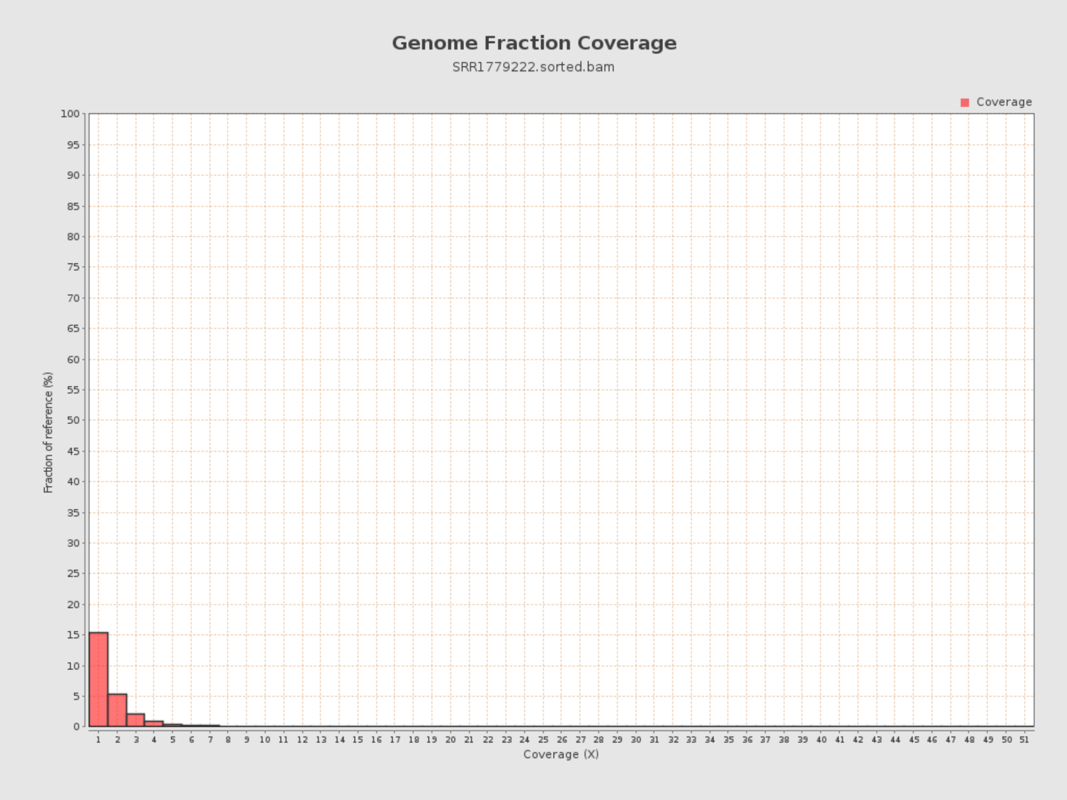
4. Results : Coverage Histogram



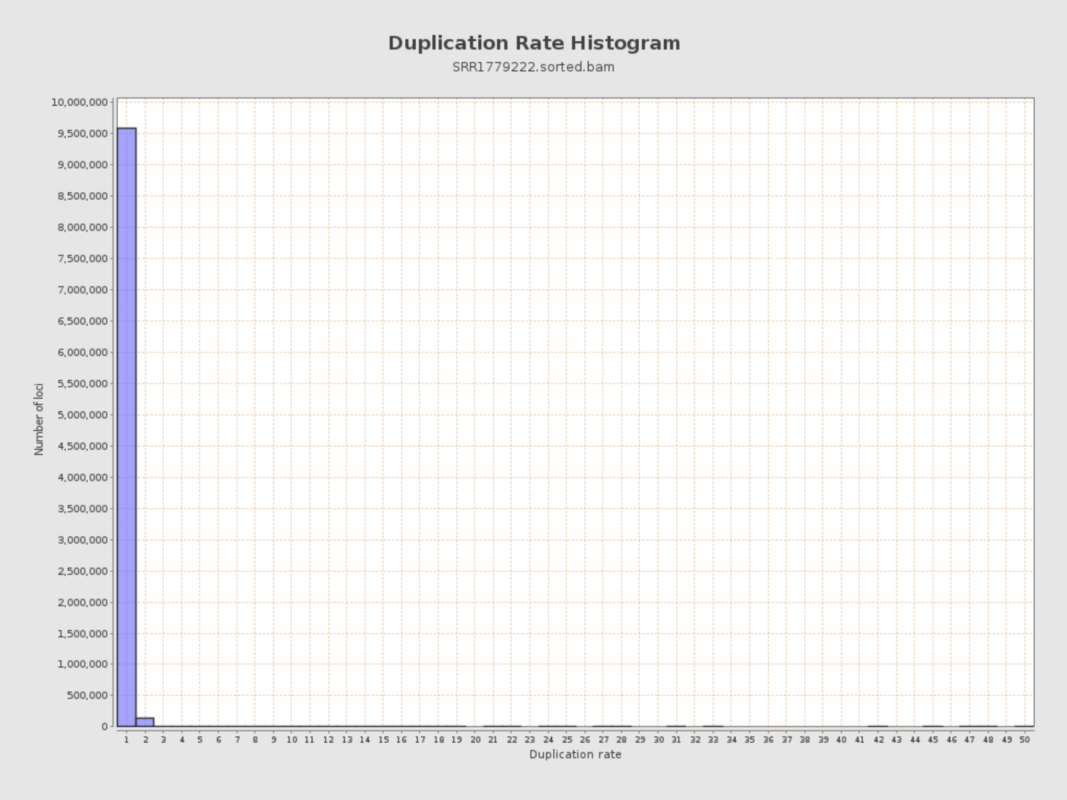
5. Results : Coverage Histogram (0-50X)



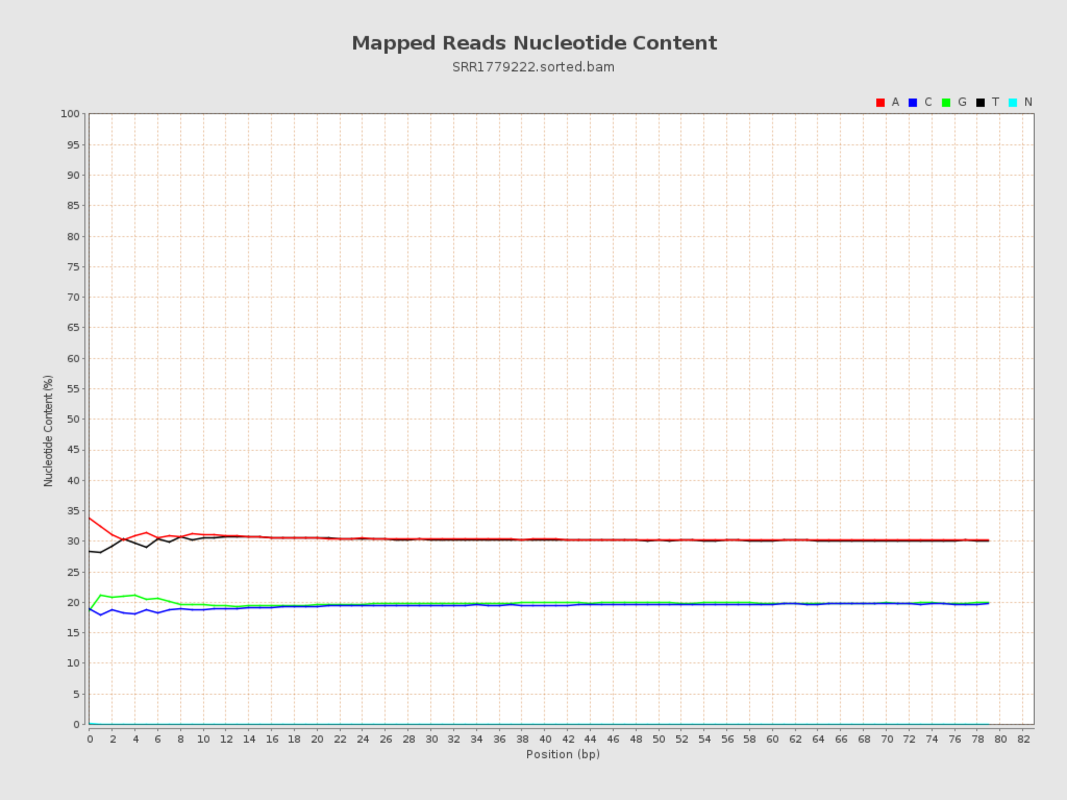
6. Results : Genome Fraction Coverage



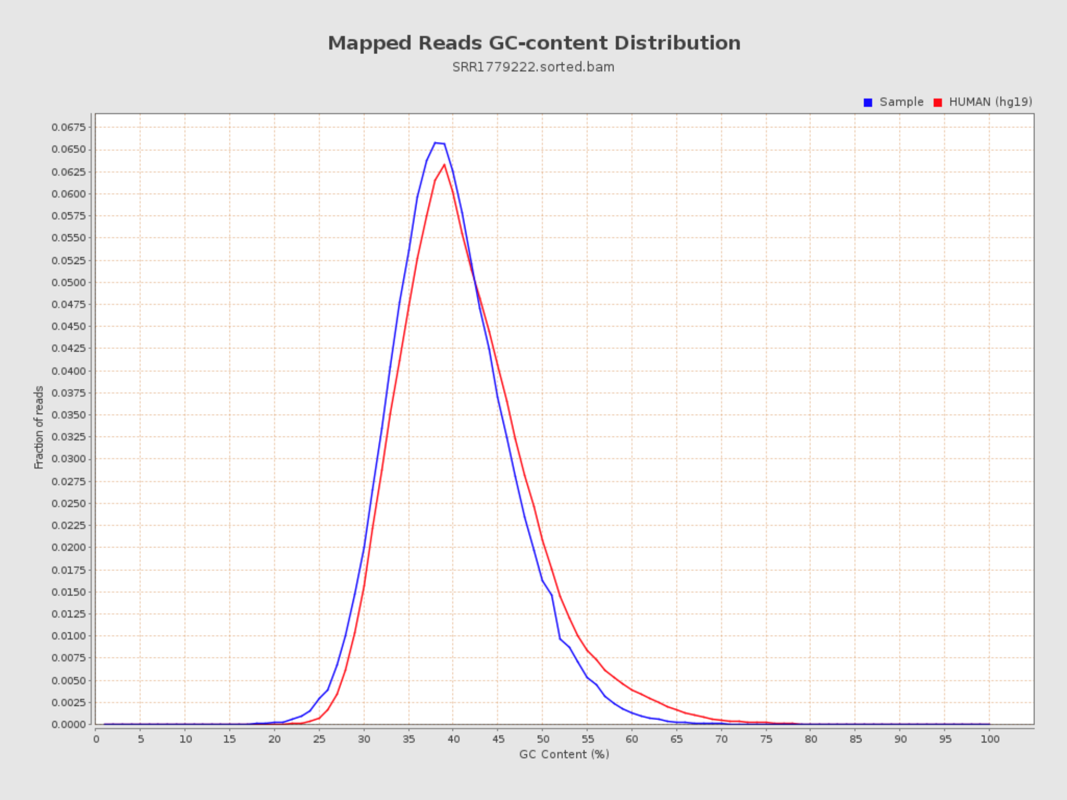
7. Results : Duplication Rate Histogram



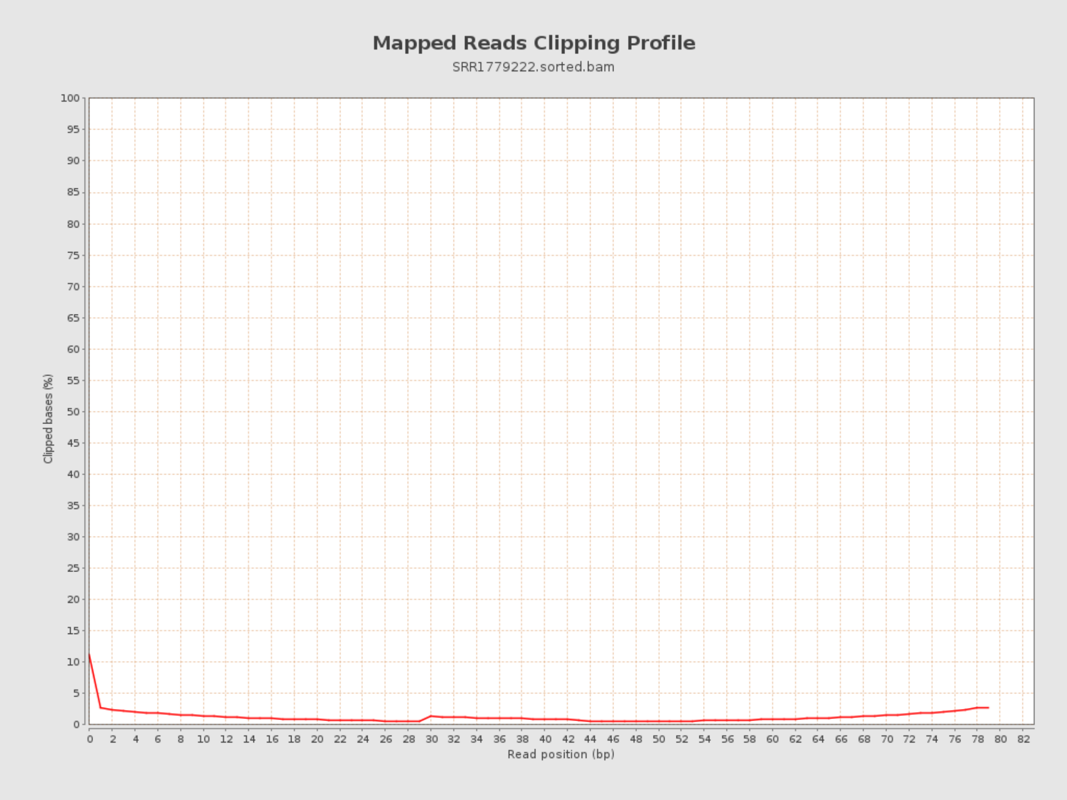
8. Results : Mapped Reads Nucleotide Content



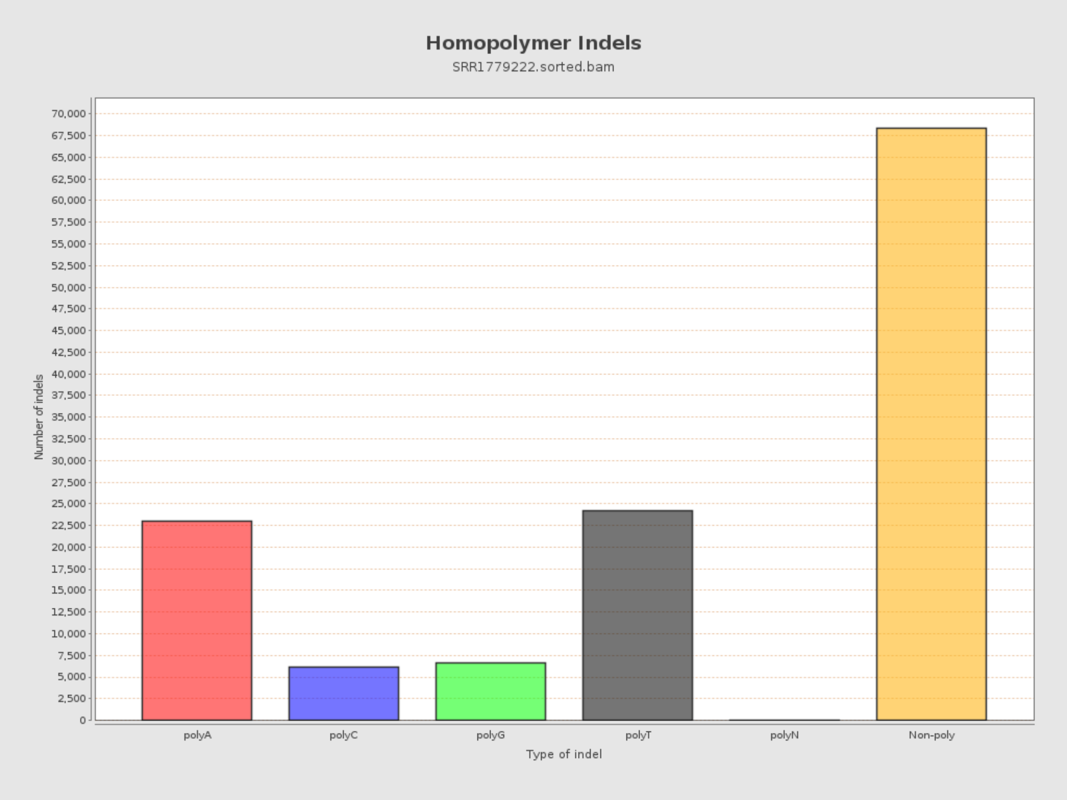
9. Results : Mapped Reads GC-content Distribution



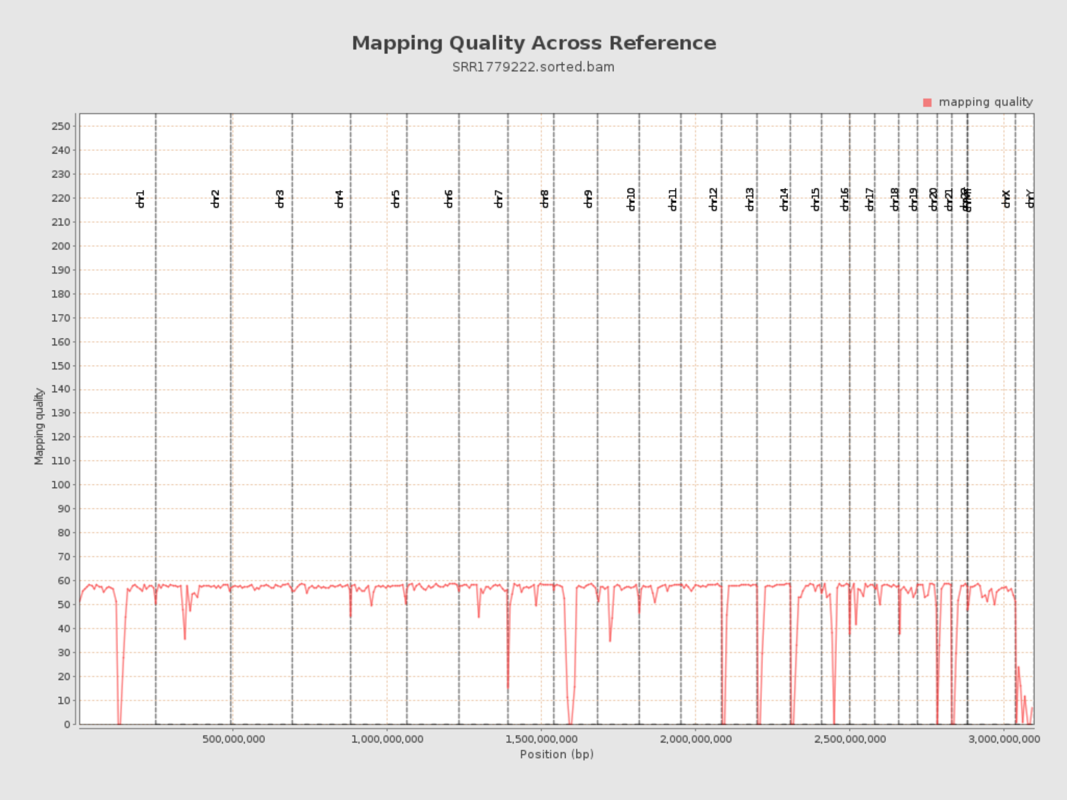
10. Results : Mapped Reads Clipping Profile



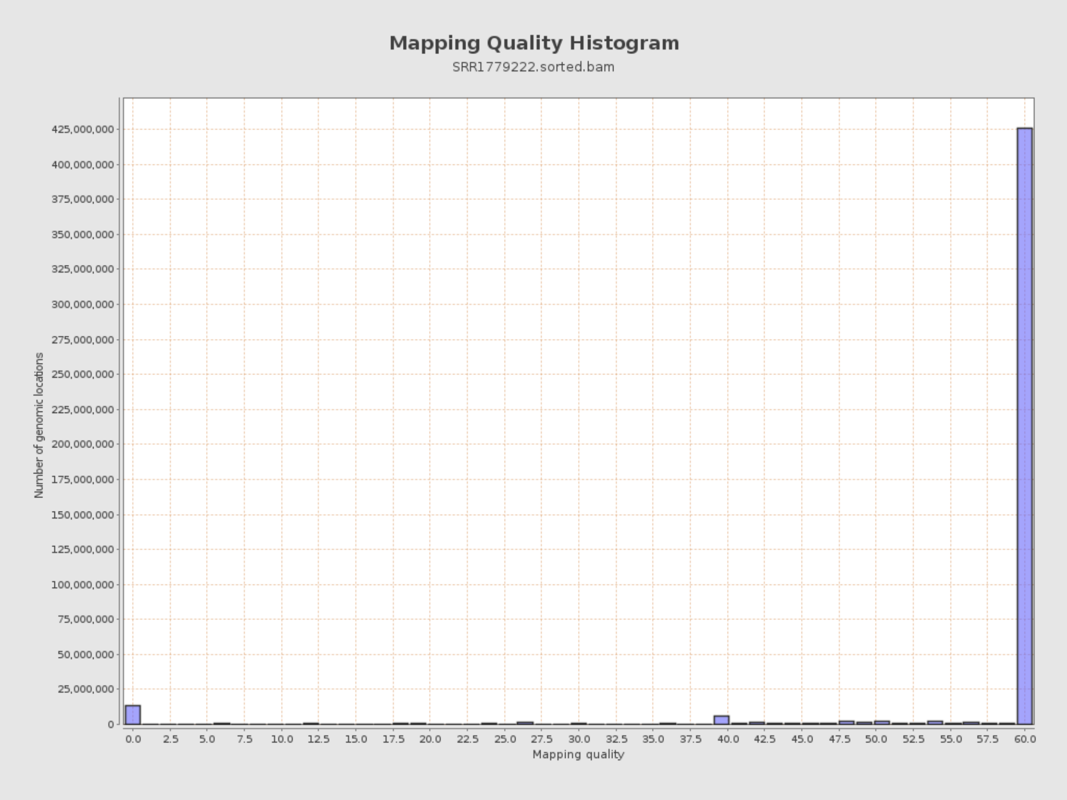
11. Results : Homopolymer Indels



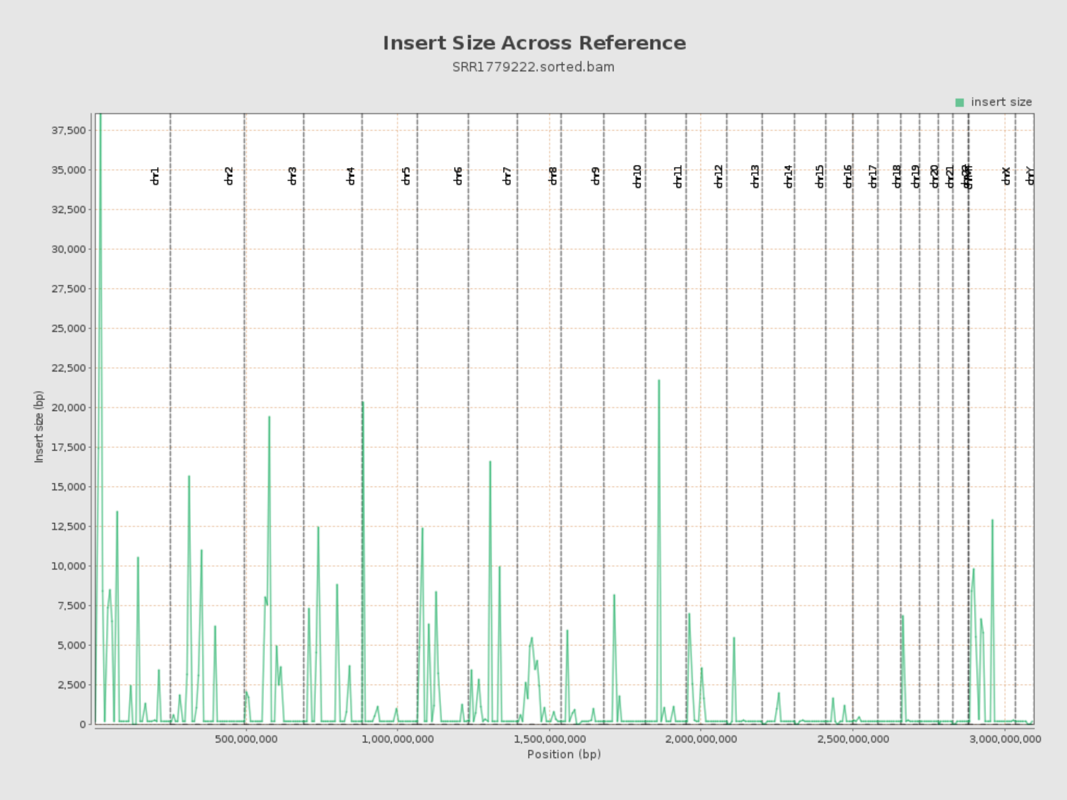
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram