Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 05:16:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779162.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_SRR1779162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779162_1.fastq.gz SRR1779162_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 05:16:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,125,028
Mapped reads	4,997,137 / 97.5%
Unmapped reads	127,891 / 2.5%
Mapped paired reads	4,997,137 / 97.5%
Mapped reads, first in pair	2,513,510 / 49.04%
Mapped reads, second in pair	2,483,627 / 48.46%
Mapped reads, both in pair	4,950,602 / 96.6%
Mapped reads, singletons	46,535 / 0.91%
Secondary alignments	0
Supplementary alignments	29,011 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	62,207 / 1.21%
Duplication rate	1.13%
Clipped reads	308,341 / 6.02%

2.2. ACGT Content

Number/percentage of A's	153,040,187 / 30.66%
Number/percentage of C's	96,085,767 / 19.25%
Number/percentage of T's	152,490,769 / 30.55%
Number/percentage of G's	97,378,810 / 19.51%
Number/percentage of N's	205,892 / 0.04%

GC Percentage	38.75%

2.3. Coverage

Mean	0.1613
Standard Deviation	0.5516

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	63,617.89
Standard Deviation	2,354,347.32
P25/Median/P75	157 / 209 / 284

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	2,036,391
Insertions	41,280
Mapped reads with at least one insertion	0.81%
Deletions	49,958
Mapped reads with at least one deletion	0.98%
Homopolymer indels	46.84%

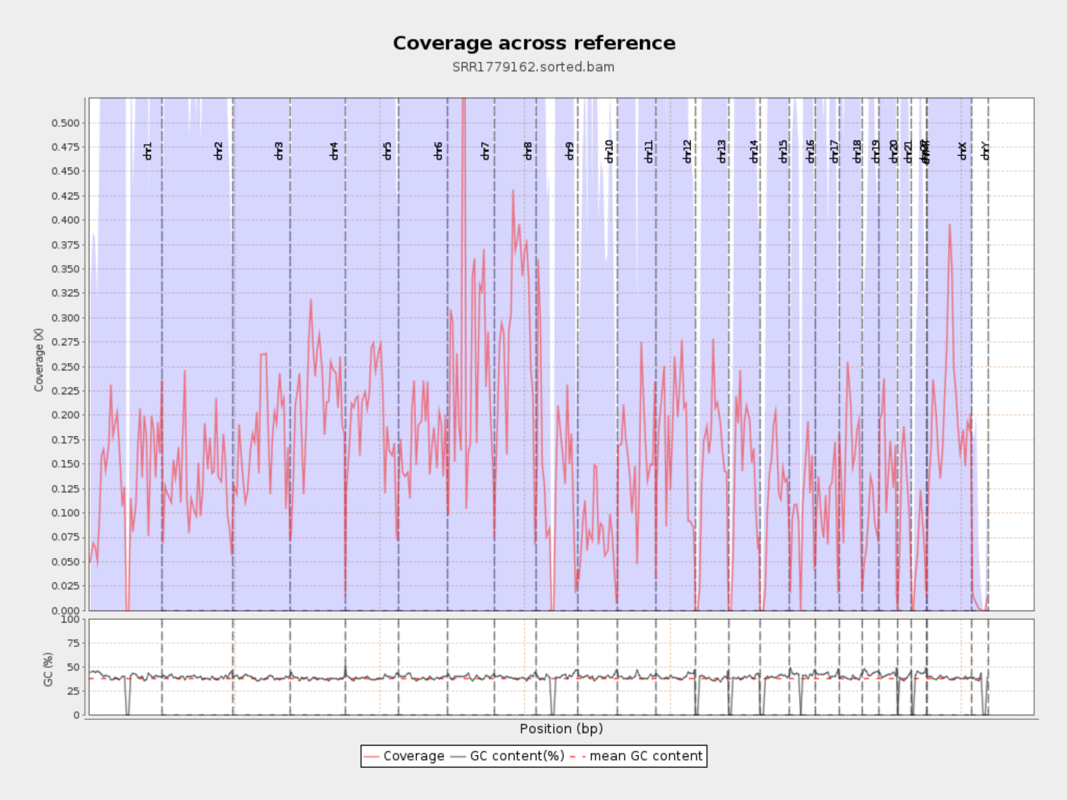
2.7. Chromosome stats

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

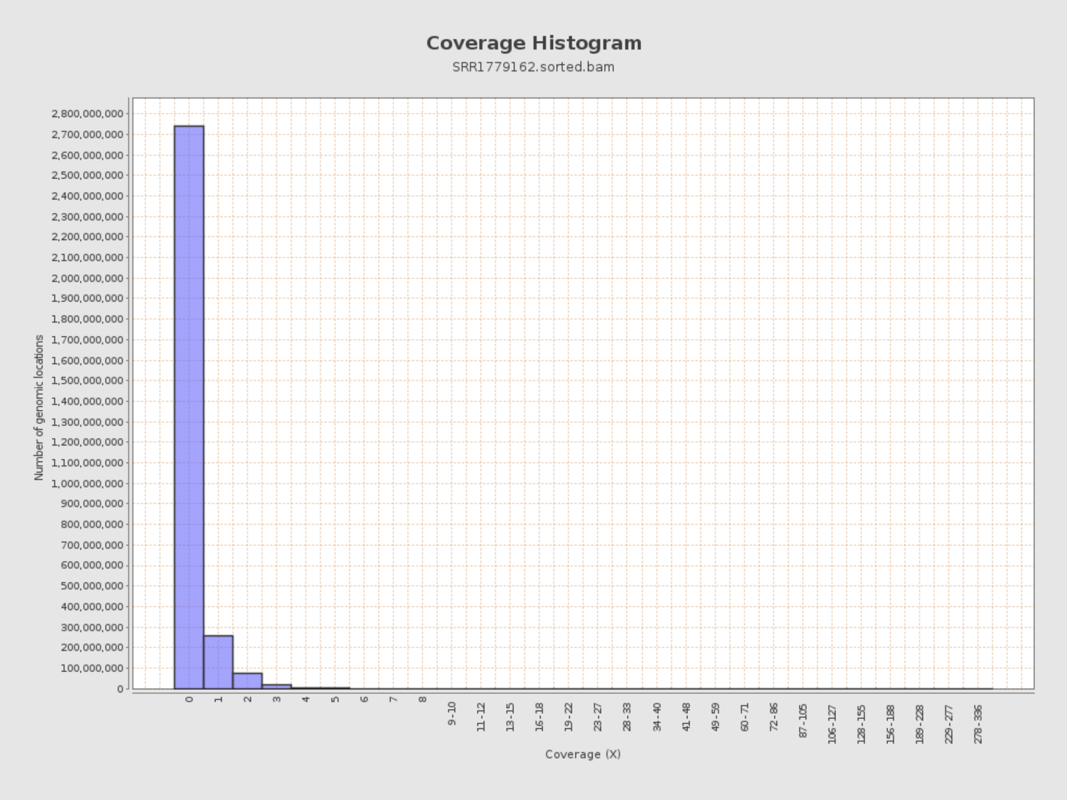
		bases	coverage	deviation
chr1	249250621	33834205	0.1357	0.5416
chr2	243199373	32773419	0.1348	0.496
chr3	198022430	34715288	0.1753	0.526
chr4	191154276	42283332	0.2212	0.5966
chr5	180915260	35886969	0.1984	0.5619
chr6	171115067	29868729	0.1746	0.5317
chr7	159138663	42147554	0.2648	0.8879
chr8	146364022	42281239	0.2889	0.6919
chr9	141213431	20293068	0.1437	0.4964
chr10	135534747	10805514	0.0797	0.614
chr11	135006516	21640791	0.1603	0.5124
chr12	133851895	23595575	0.1763	0.539
chr13	115169878	17078954	0.1483	0.4871
chr14	107349540	15031597	0.14	0.4817
chr15	102531392	11529878	0.1125	0.4389
chr16	90354753	9349780	0.1035	0.403
chr17	81195210	8347389	0.1028	0.4255
chr18	78077248	12669620	0.1623	0.5079
chr19	59128983	5198090	0.0879	0.4045
chr20	63025520	10044751	0.1594	0.5201
chr21	48129895	5228444	0.1086	0.4148
chr22	51304566	2854411	0.0556	0.293
chrMT	16571	239	0.0144	0.119
chrX	155270560	31474398	0.2027	0.5852

chrY	59373566	380119	0.0064	0.1194

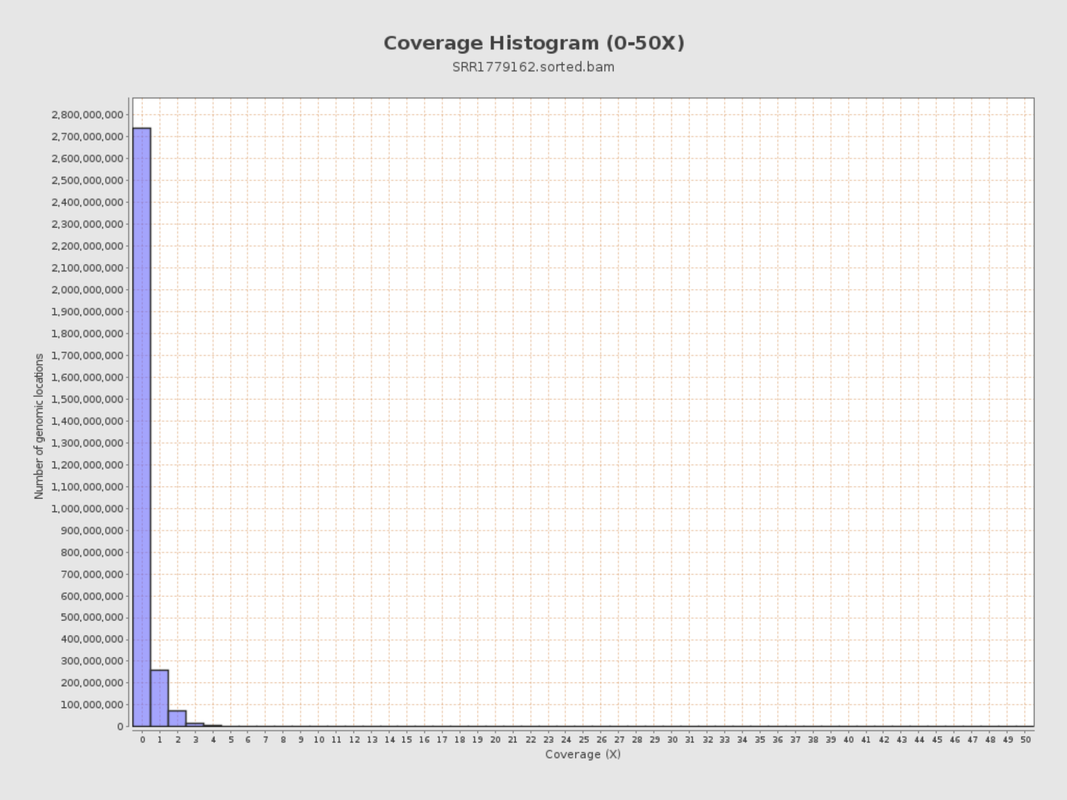
3. Results : Coverage across reference



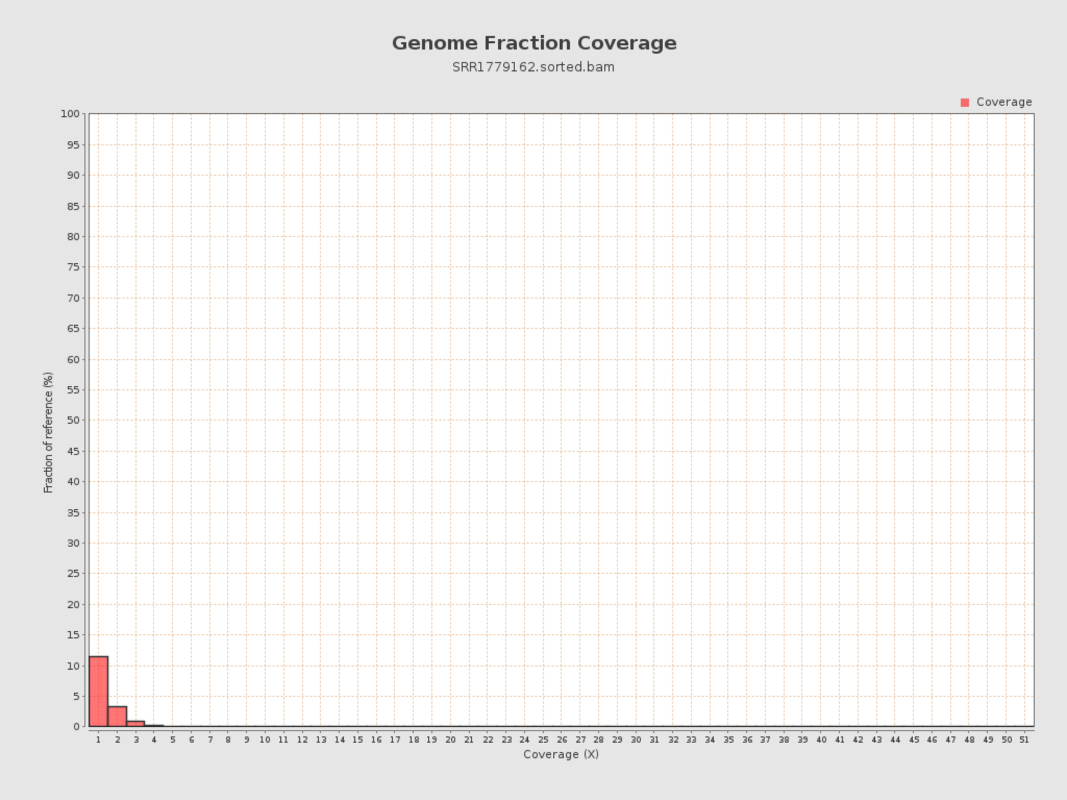
4. Results : Coverage Histogram



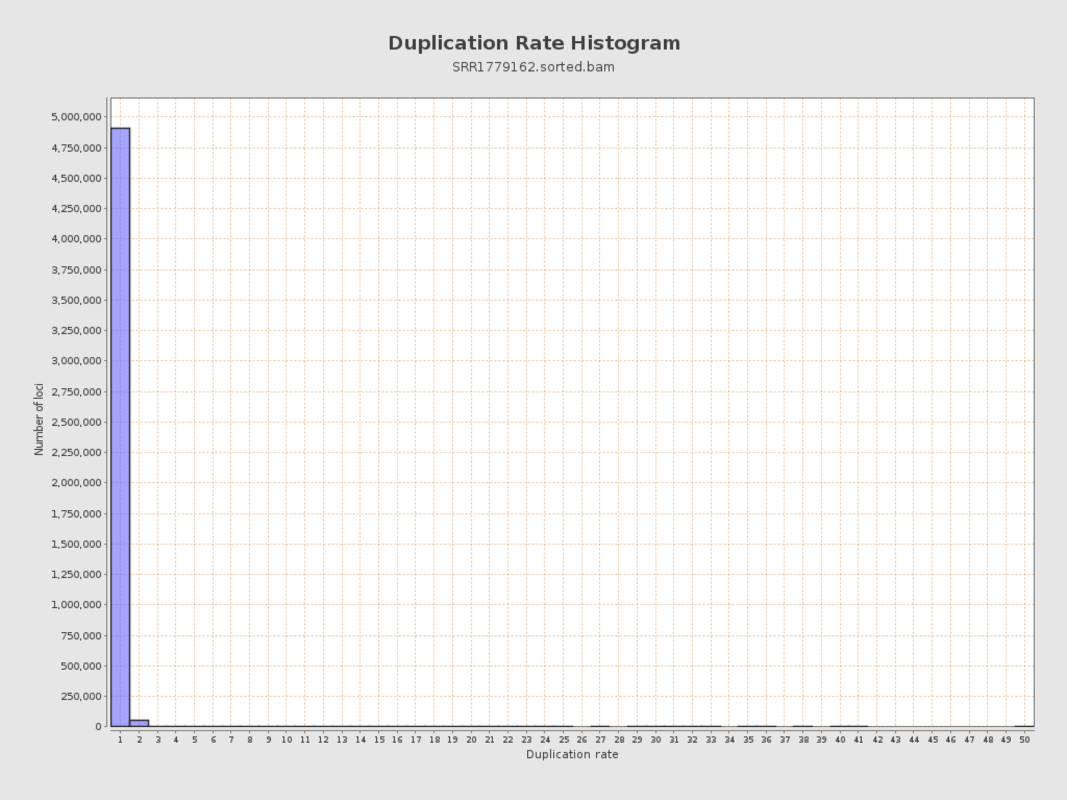
5. Results : Coverage Histogram (0-50X)



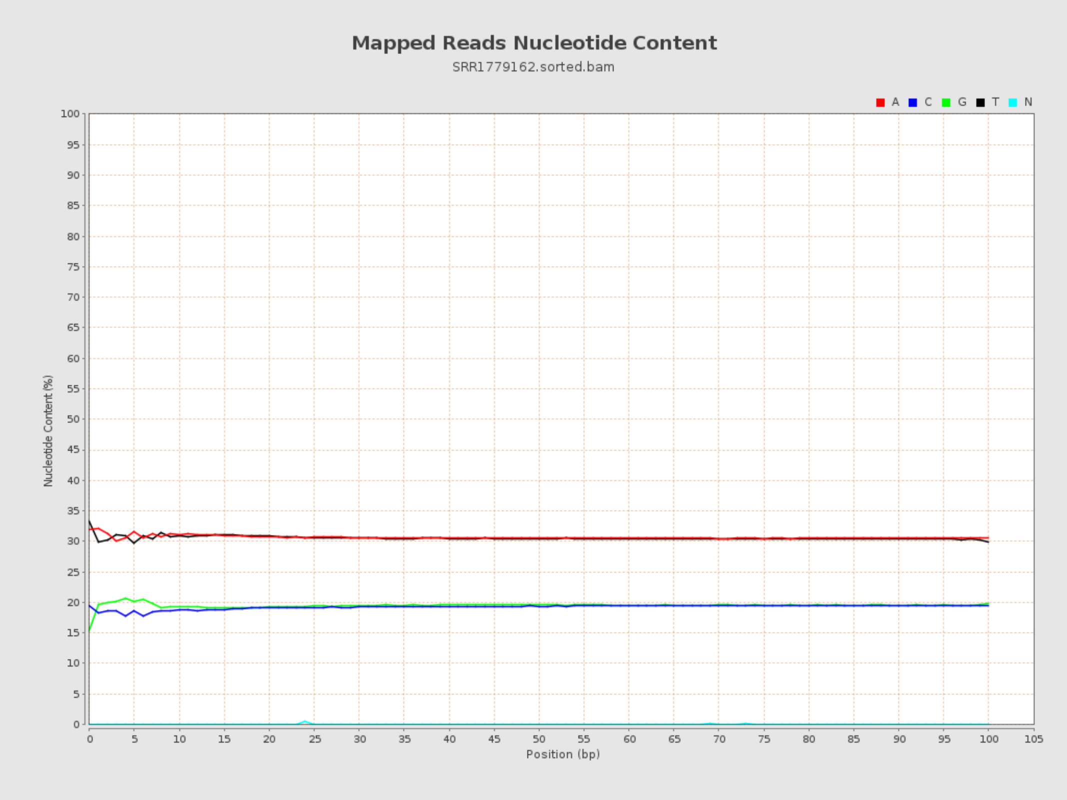
6. Results : Genome Fraction Coverage



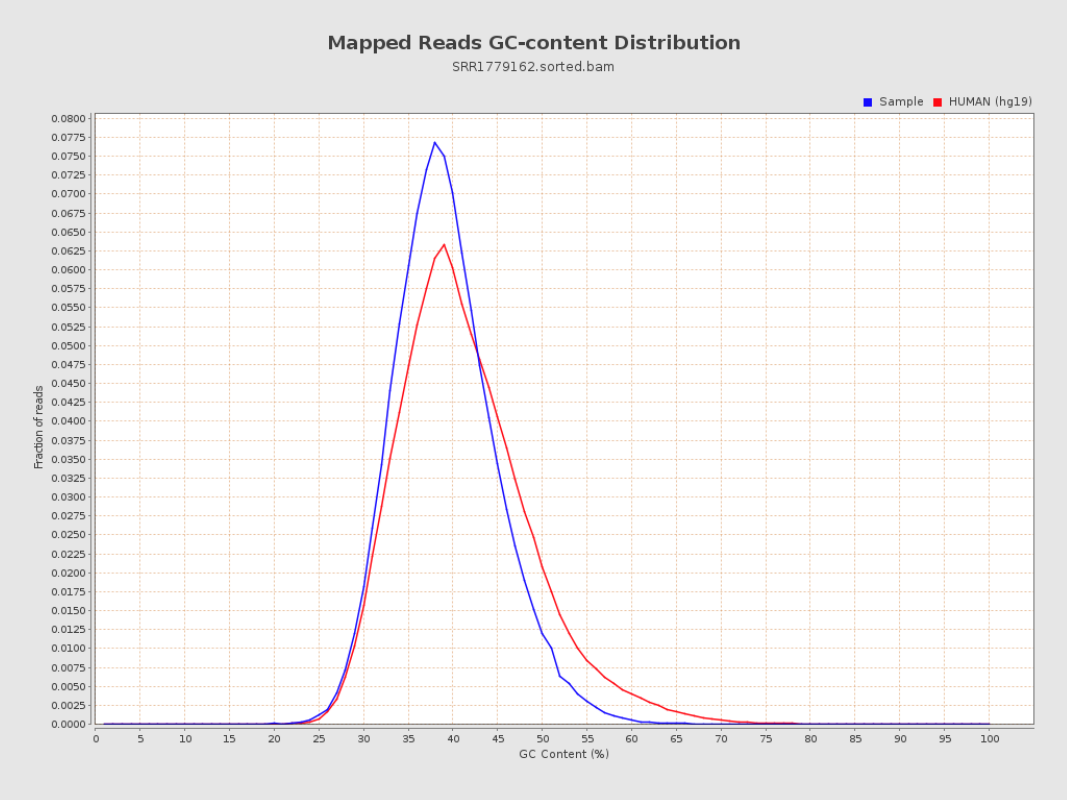
7. Results : Duplication Rate Histogram



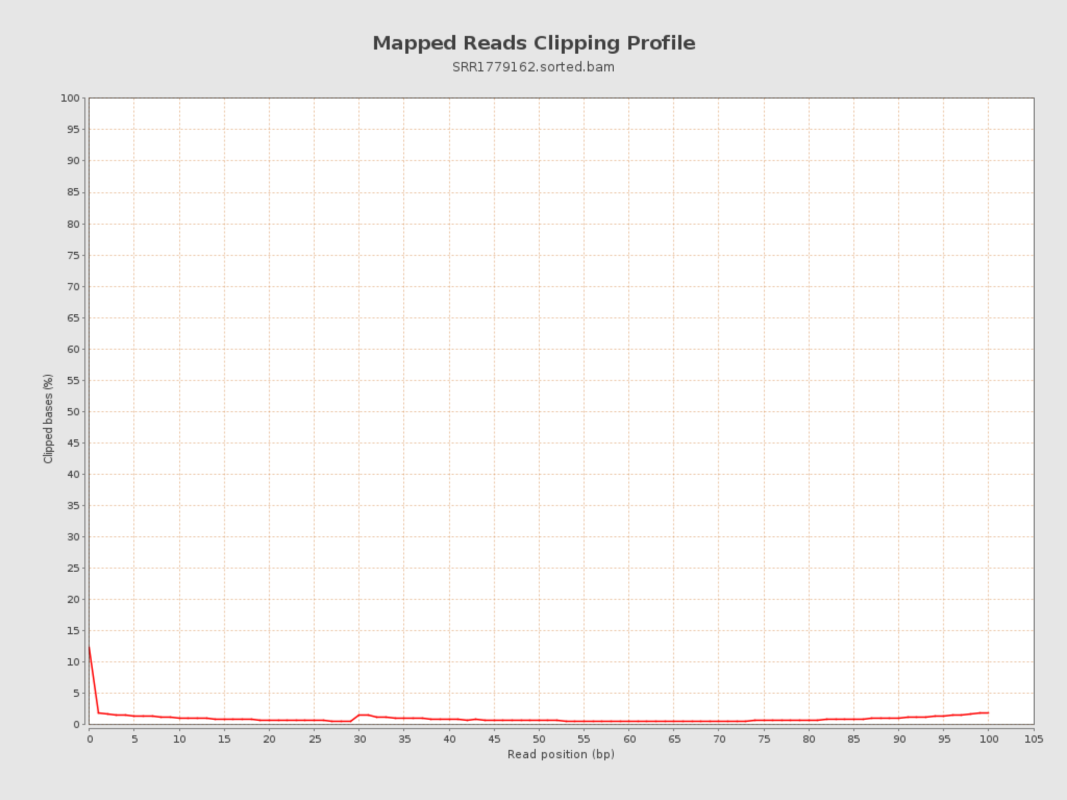
8. Results : Mapped Reads Nucleotide Content



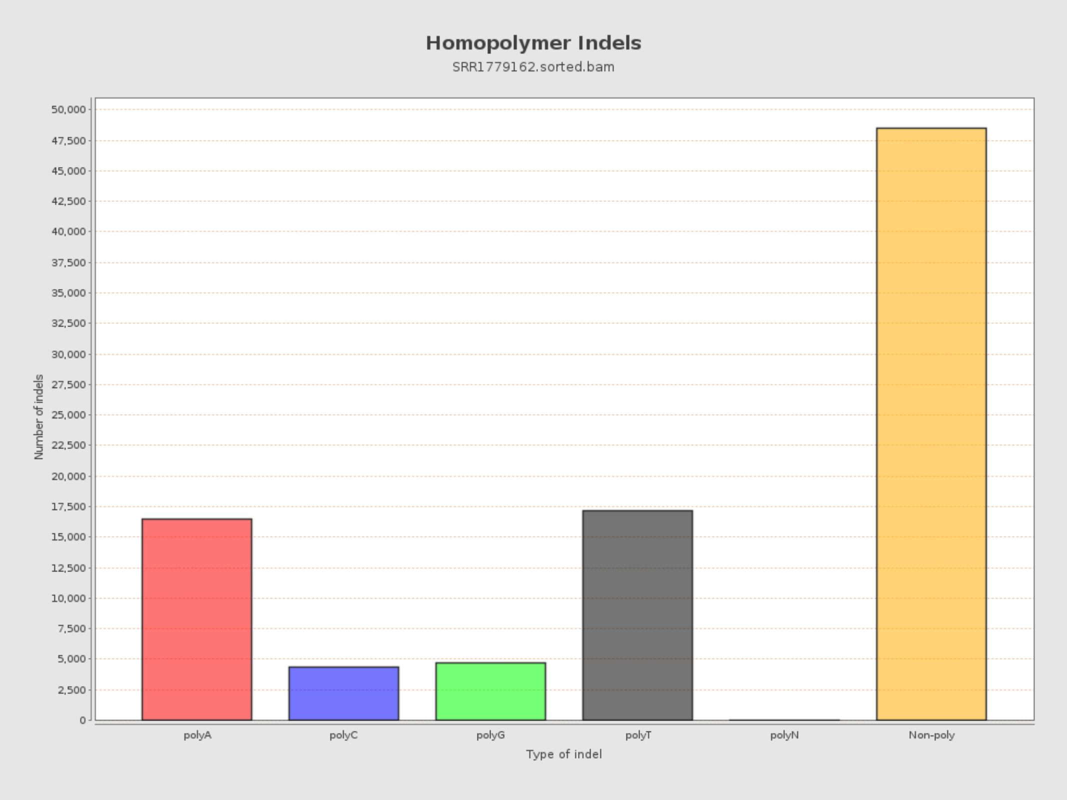
9. Results : Mapped Reads GC-content Distribution



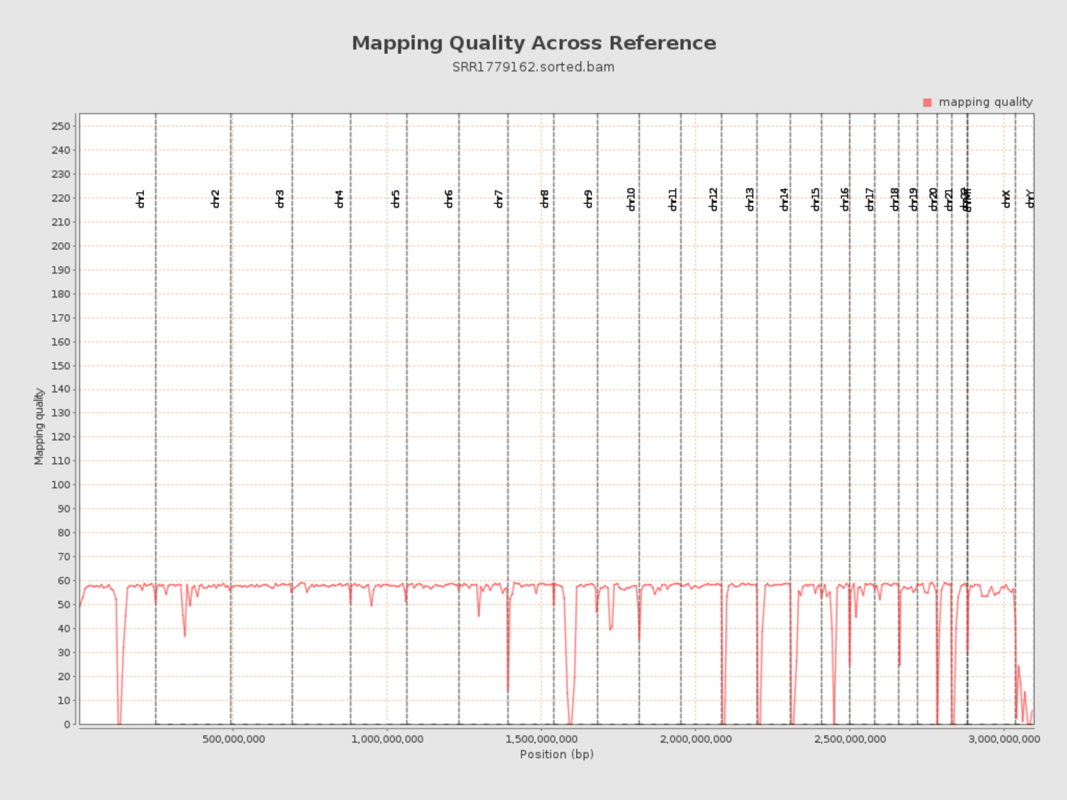
10. Results : Mapped Reads Clipping Profile



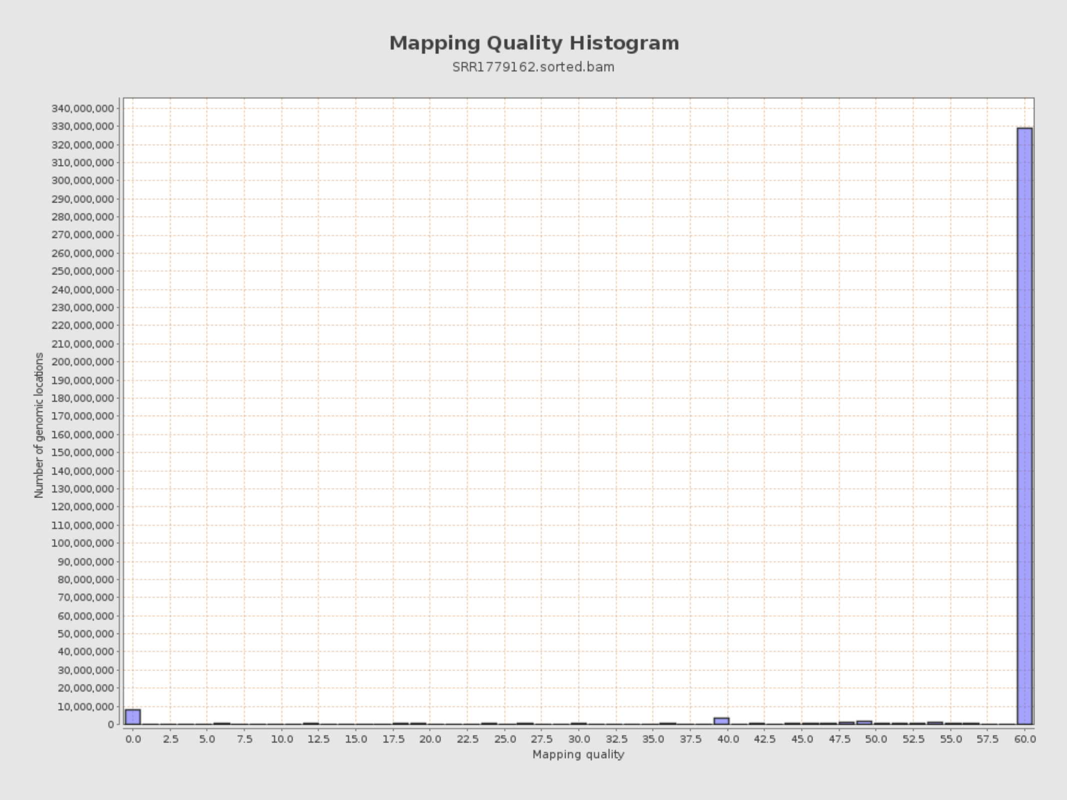
11. Results : Homopolymer Indels



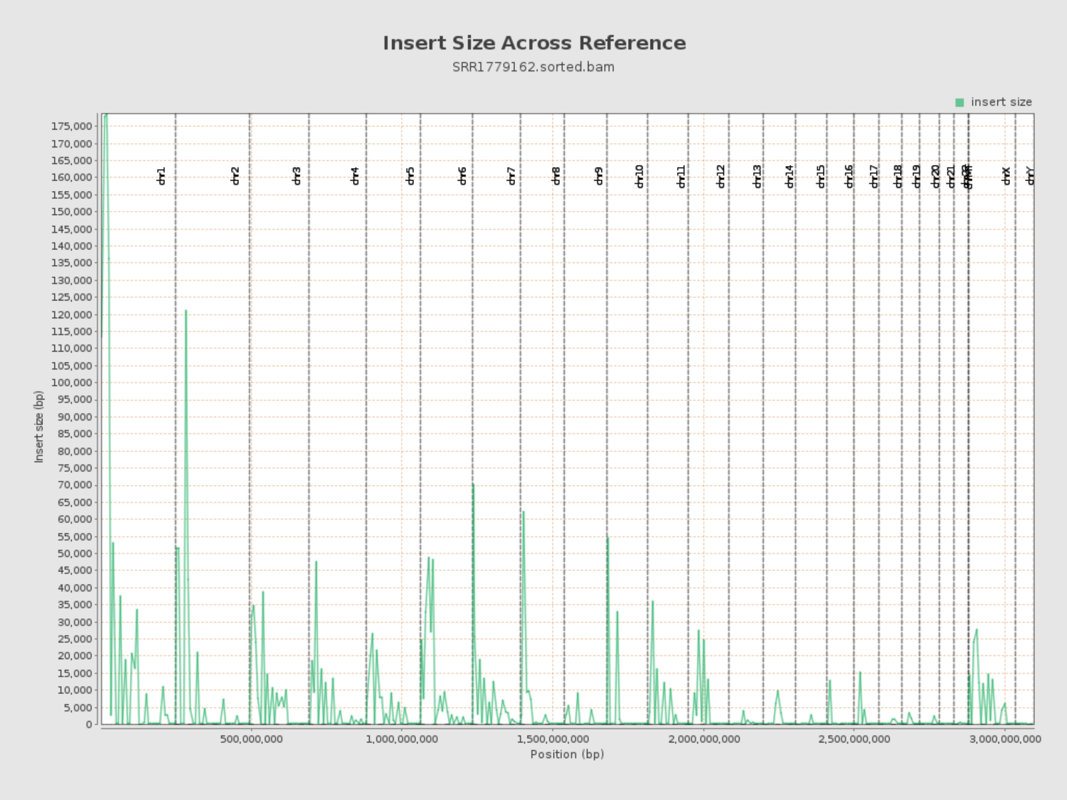
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram