Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 15:59:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779211.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_SRR1779211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779211_1.fastq.gz SRR1779211_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 15:59:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,035,392
Mapped reads	13,556,144 / 96.59%
Unmapped reads	479,248 / 3.41%
Mapped paired reads	13,556,144 / 96.59%
Mapped reads, first in pair	6,867,581 / 48.93%
Mapped reads, second in pair	6,688,563 / 47.65%
Mapped reads, both in pair	13,360,430 / 95.19%
Mapped reads, singletons	195,714 / 1.39%
Secondary alignments	0
Supplementary alignments	27,243 / 0.19%
Read min/max/mean length	30 / 80 / 80.07
Duplicated reads (estimated)	207,211 / 1.48%
Duplication rate	1.42%
Clipped reads	449,051 / 3.2%

2.2. ACGT Content

Number/percentage of A's	331,578,496 / 30.75%
Number/percentage of C's	205,882,575 / 19.09%
Number/percentage of T's	330,491,206 / 30.65%
Number/percentage of G's	210,236,102 / 19.5%
Number/percentage of N's	198,129 / 0.02%

GC Percentage	38.59%

2.3. Coverage

Mean	0.3484
Standard Deviation	1.0037

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	41,467.09
Standard Deviation	1,957,097.32
P25/Median/P75	210 / 278 / 352

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	4,681,602
Insertions	79,653
Mapped reads with at least one insertion	0.58%
Deletions	100,929
Mapped reads with at least one deletion	0.73%
Homopolymer indels	47.23%

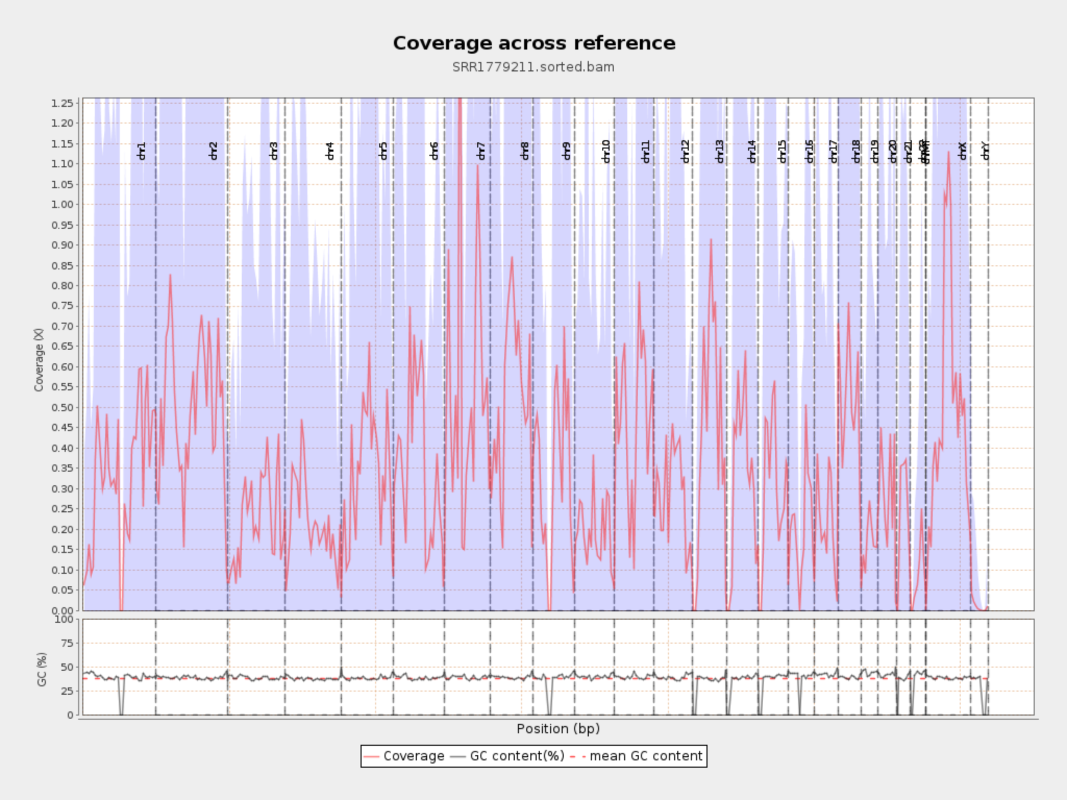
2.7. Chromosome stats

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

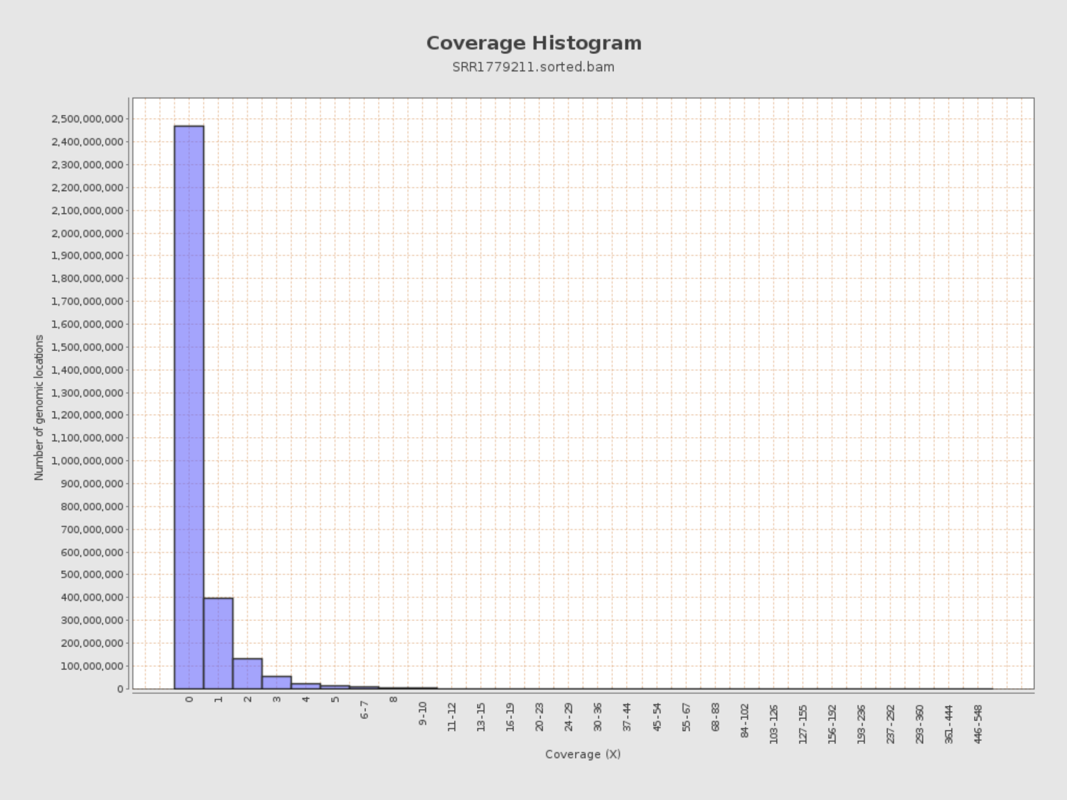
		bases	coverage	deviation
chr1	249250621	81423718	0.3267	1.0196
chr2	243199373	122697364	0.5045	1.0871
chr3	198022430	44796395	0.2262	0.685
chr4	191154276	41996535	0.2197	0.6555
chr5	180915260	60814563	0.3361	0.8484
chr6	171115067	63232868	0.3695	0.918
chr7	159138663	90702570	0.57	2.0303
chr8	146364022	76903582	0.5254	1.1071
chr9	141213431	47539162	0.3366	0.9058
chr10	135534747	26985048	0.1991	0.8826
chr11	135006516	63620058	0.4712	1.0635
chr12	133851895	38368657	0.2867	0.7867
chr13	115169878	52336647	0.4544	1.0186
chr14	107349540	35281366	0.3287	0.922
chr15	102531392	30444522	0.2969	0.8557
chr16	90354753	18328226	0.2028	0.6222
chr17	81195210	17820726	0.2195	0.6817
chr18	78077248	40891510	0.5237	1.054
chr19	59128983	10151021	0.1717	0.6397
chr20	63025520	18919601	0.3002	0.8297
chr21	48129895	11328906	0.2354	0.6852
chr22	51304566	4704479	0.0917	0.4108
chrMT	16571	36	0.0022	0.0466
chrX	155270560	78690658	0.5068	1.2185

chrY	59373566	616659	0.0104	0.1415

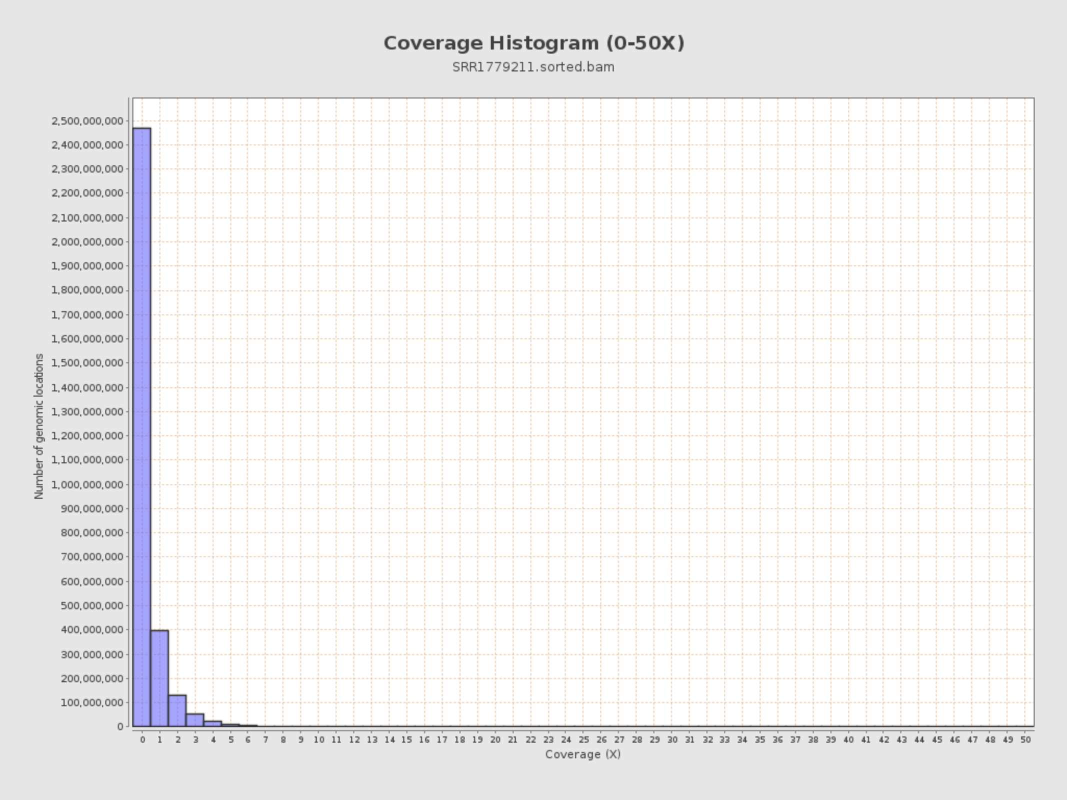
3. Results : Coverage across reference



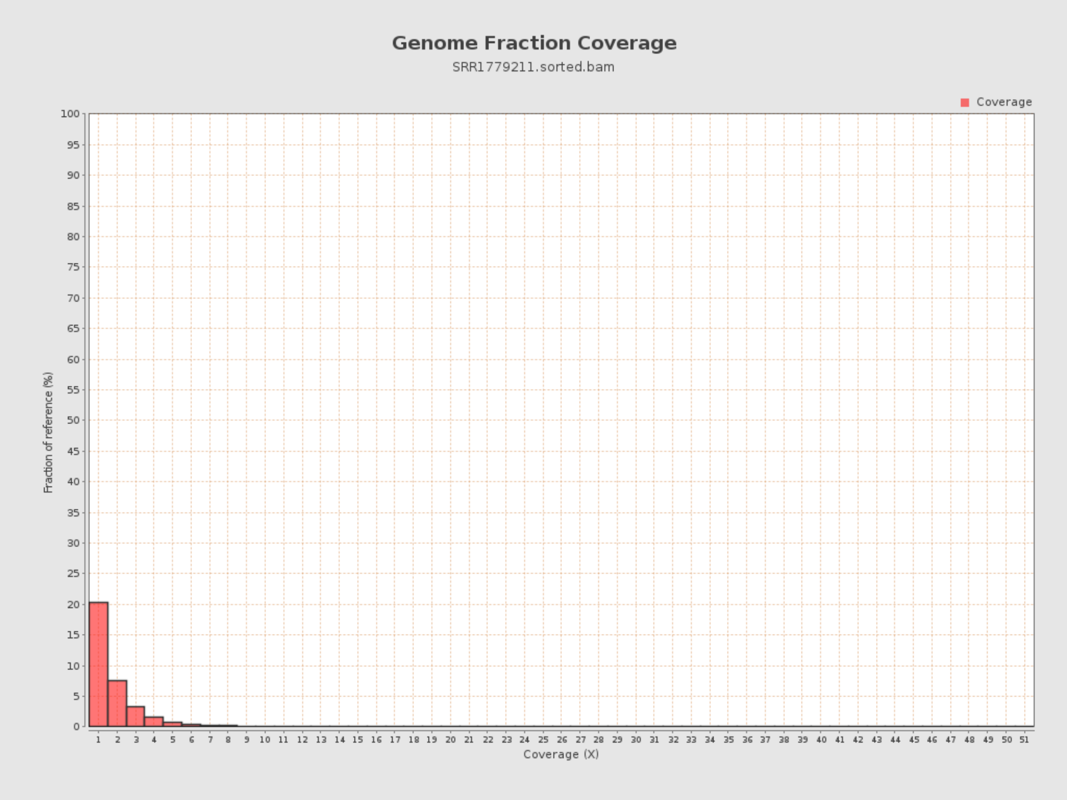
4. Results : Coverage Histogram



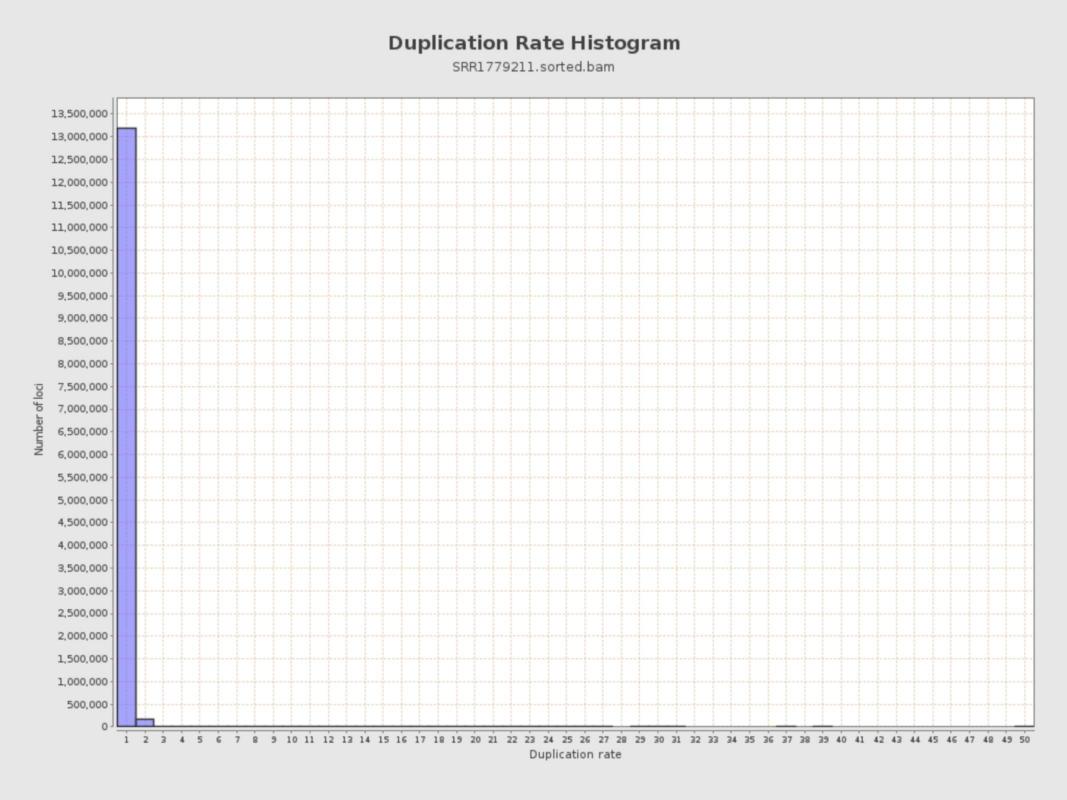
5. Results : Coverage Histogram (0-50X)



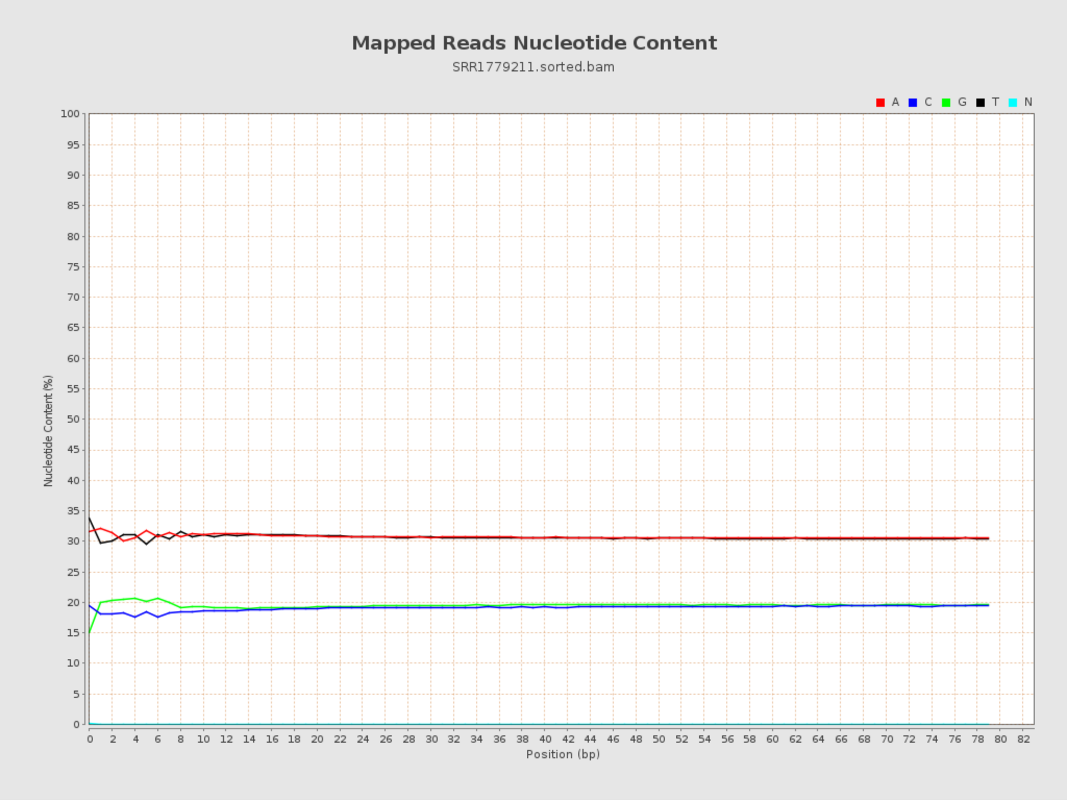
6. Results : Genome Fraction Coverage



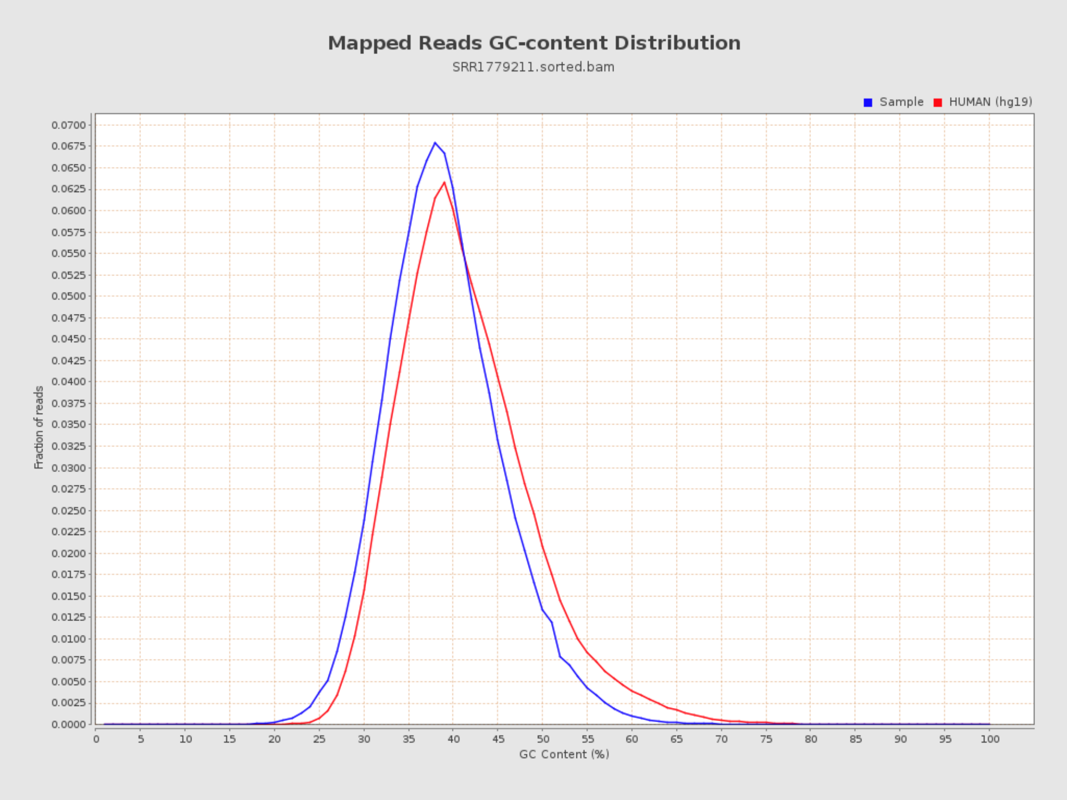
7. Results : Duplication Rate Histogram



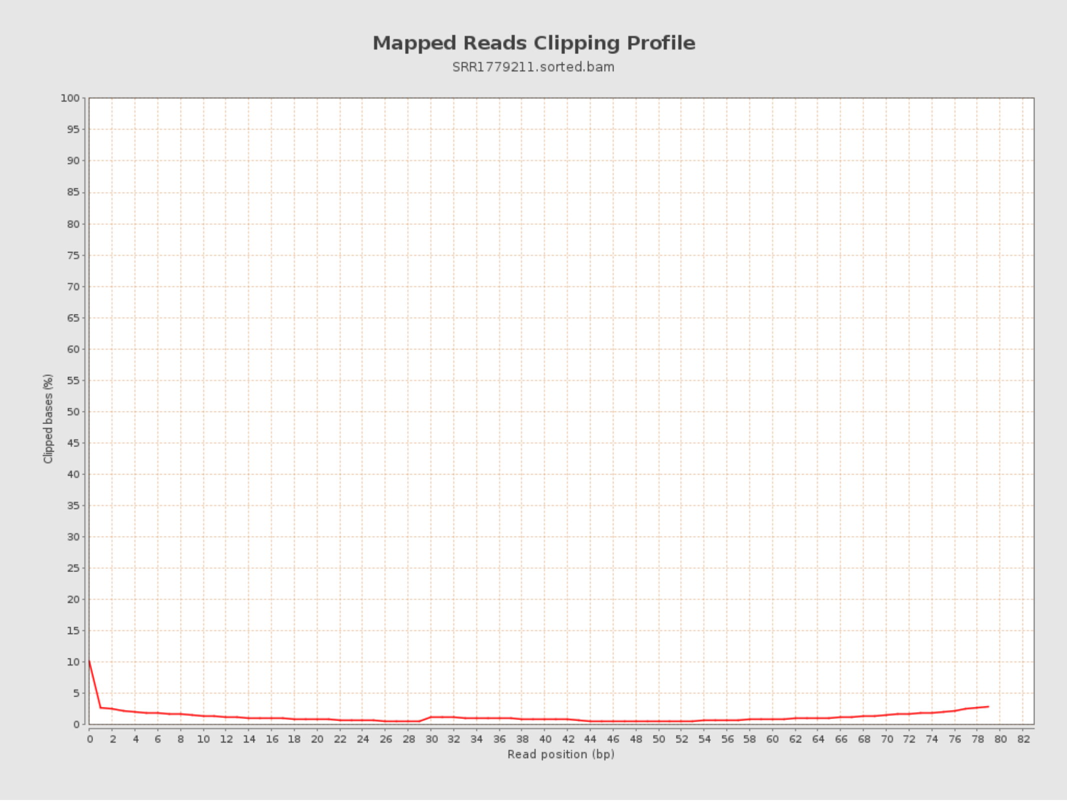
8. Results : Mapped Reads Nucleotide Content



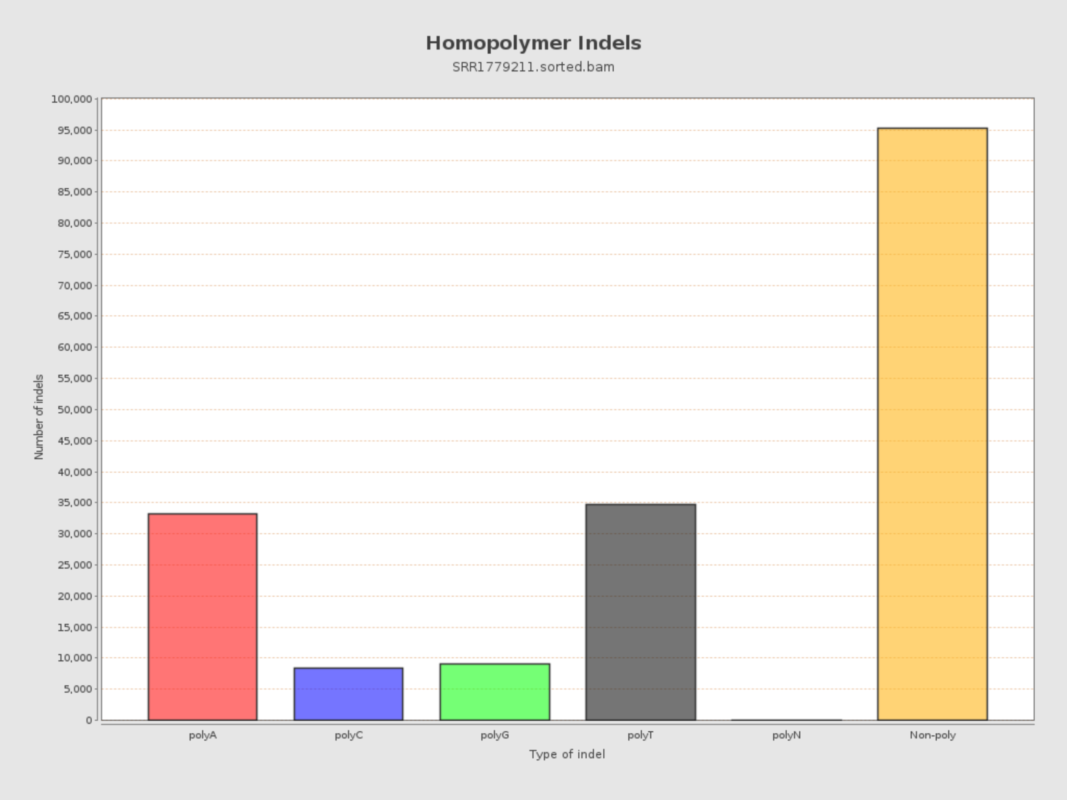
9. Results : Mapped Reads GC-content Distribution



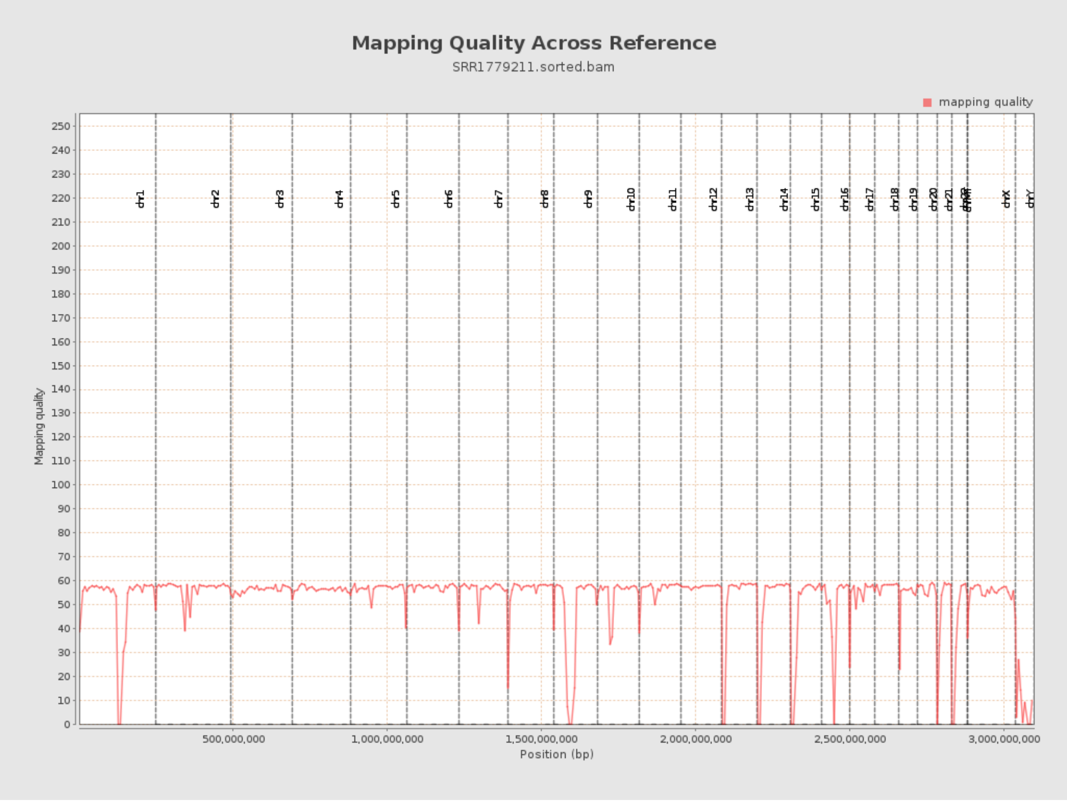
10. Results : Mapped Reads Clipping Profile



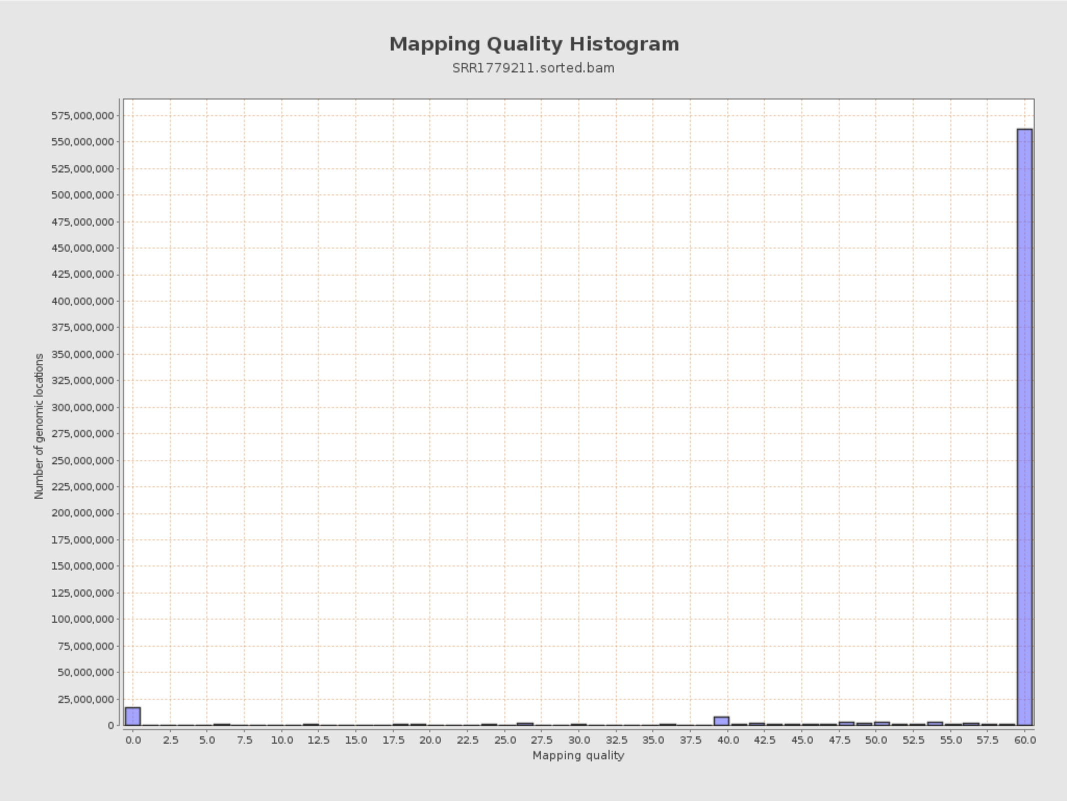
11. Results : Homopolymer Indels



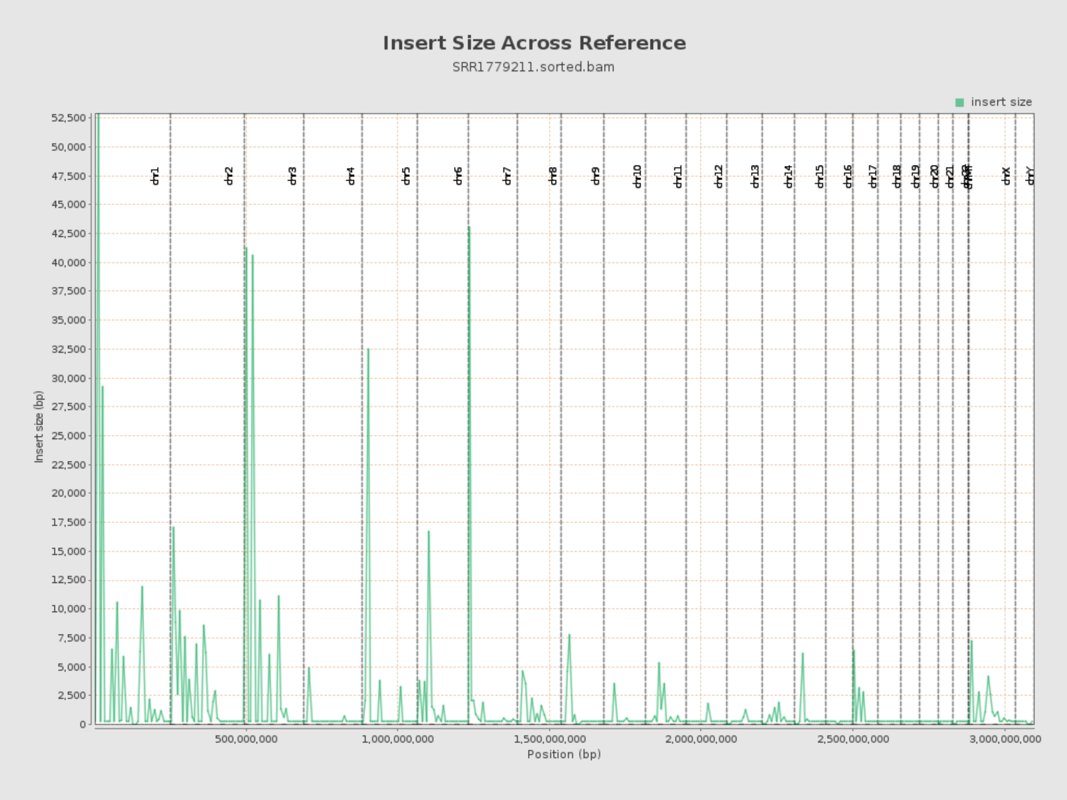
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram