Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 01:09:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779419.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_SRR1779419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779419_1.fastq.gz SRR1779419_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 01:09:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,248,636
Mapped reads	13,743,137 / 96.45%
Unmapped reads	505,499 / 3.55%
Mapped paired reads	13,743,137 / 96.45%
Mapped reads, first in pair	6,937,391 / 48.69%
Mapped reads, second in pair	6,805,746 / 47.76%
Mapped reads, both in pair	13,584,552 / 95.34%
Mapped reads, singletons	158,585 / 1.11%
Secondary alignments	0
Supplementary alignments	48,792 / 0.34%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	393,298 / 2.76%
Duplication rate	2.58%
Clipped reads	550,482 / 3.86%

2.2. ACGT Content

Number/percentage of A's	331,894,097 / 30.38%
Number/percentage of C's	214,847,360 / 19.67%
Number/percentage of T's	324,656,401 / 29.72%
Number/percentage of G's	220,663,971 / 20.2%
Number/percentage of N's	240,407 / 0.02%

GC Percentage	39.87%

2.3. Coverage

Mean	0.3529
Standard Deviation	1.1479

2.4. Mapping Quality

Mean Mapping Quality	53.28

2.5. Insert size

Mean	191,367.52
Standard Deviation	4,203,064.63
P25/Median/P75	156 / 199 / 251

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,589,831
Insertions	96,445
Mapped reads with at least one insertion	0.7%
Deletions	110,639
Mapped reads with at least one deletion	0.79%
Homopolymer indels	47.26%

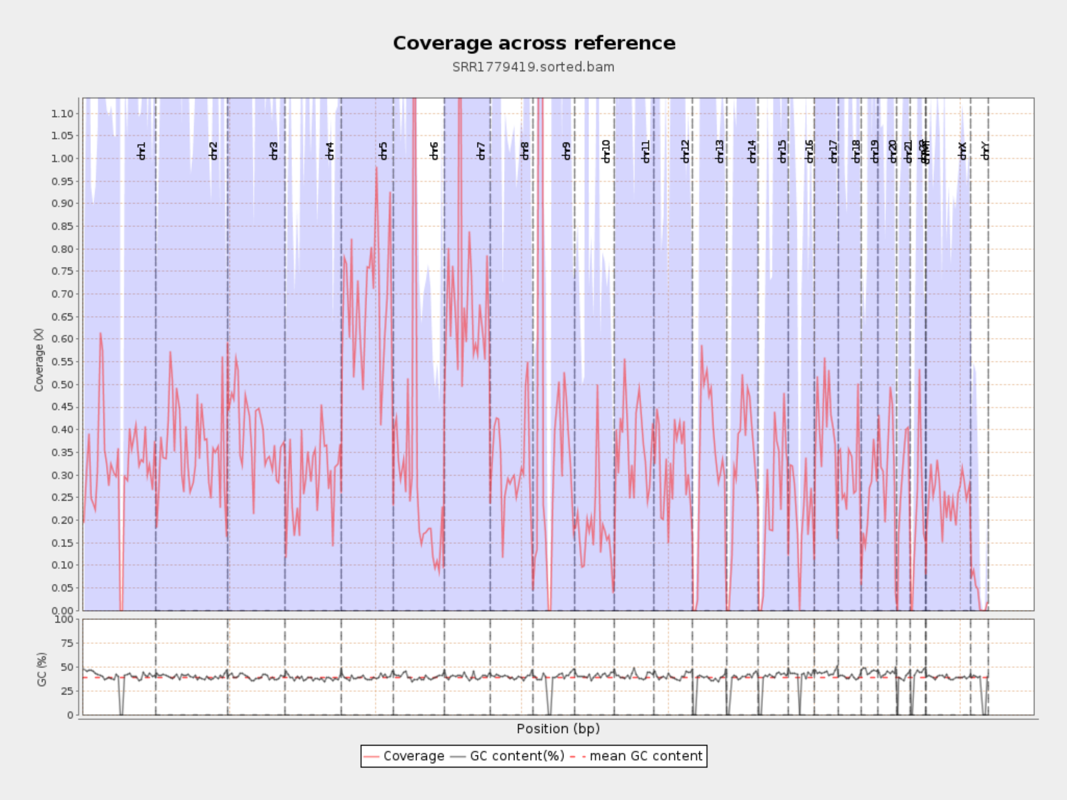
2.7. Chromosome stats

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

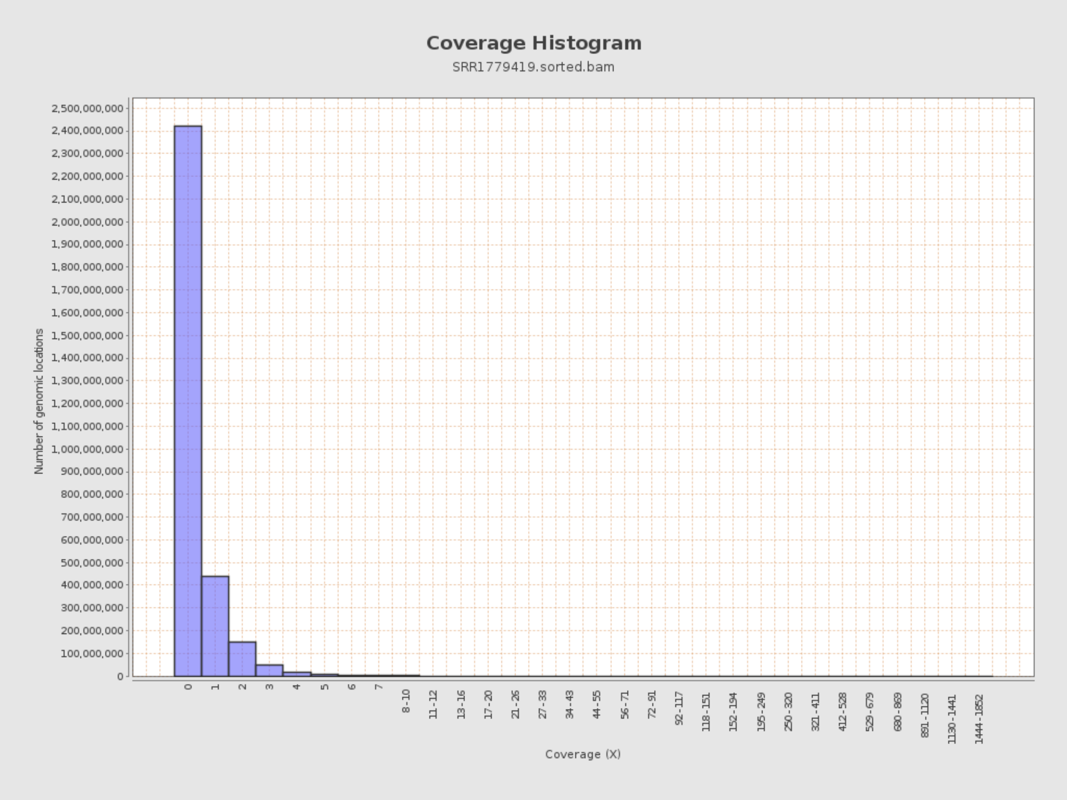
		bases	coverage	deviation
chr1	249250621	78948242	0.3167	2.0361
chr2	243199373	86765556	0.3568	0.849
chr3	198022430	77939250	0.3936	0.8362
chr4	191154276	55788332	0.2918	0.7011
chr5	180915260	121114998	0.6695	1.0866
chr6	171115067	51161113	0.299	1.0866
chr7	159138663	110327711	0.6933	1.8217
chr8	146364022	46882229	0.3203	0.7564
chr9	141213431	71782187	0.5083	1.7736
chr10	135534747	24513353	0.1809	1.3948
chr11	135006516	49041185	0.3633	0.8833
chr12	133851895	42542314	0.3178	0.7502
chr13	115169878	38138610	0.3312	0.7713
chr14	107349540	34646552	0.3227	0.7653
chr15	102531392	24975514	0.2436	0.6931
chr16	90354753	19541478	0.2163	0.6415
chr17	81195210	33651255	0.4144	1.0867
chr18	78077248	24130432	0.3091	1.0043
chr19	59128983	14270810	0.2414	1.3653
chr20	63025520	20892133	0.3315	0.7659
chr21	48129895	12965798	0.2694	0.7236
chr22	51304566	11168373	0.2177	0.6641
chrMT	16571	1309	0.079	0.374
chrX	155270560	39322760	0.2533	0.6745

chrY	59373566	2018331	0.034	0.2875

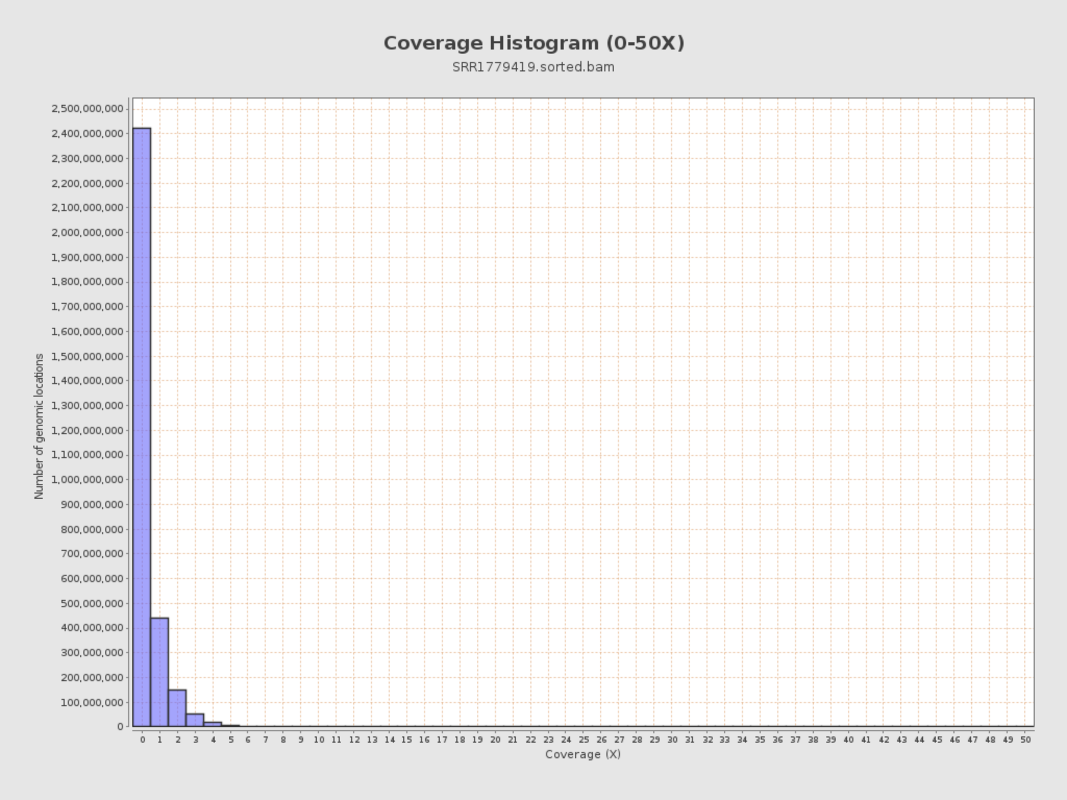
3. Results : Coverage across reference



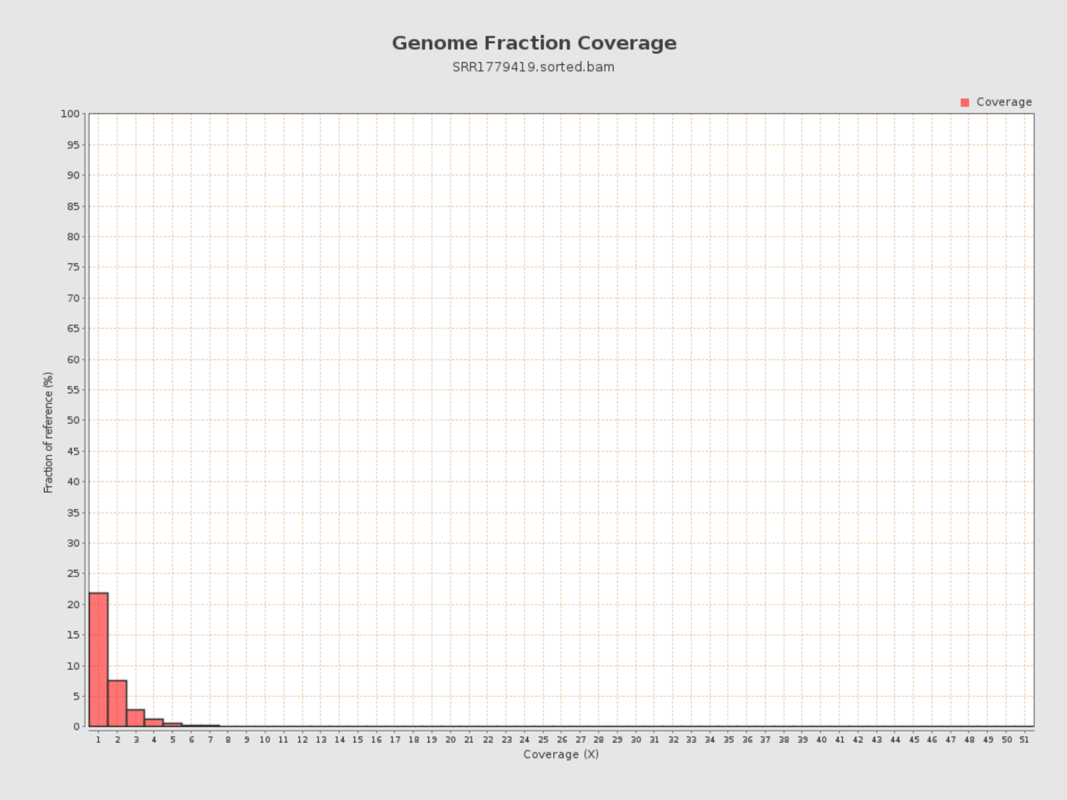
4. Results : Coverage Histogram



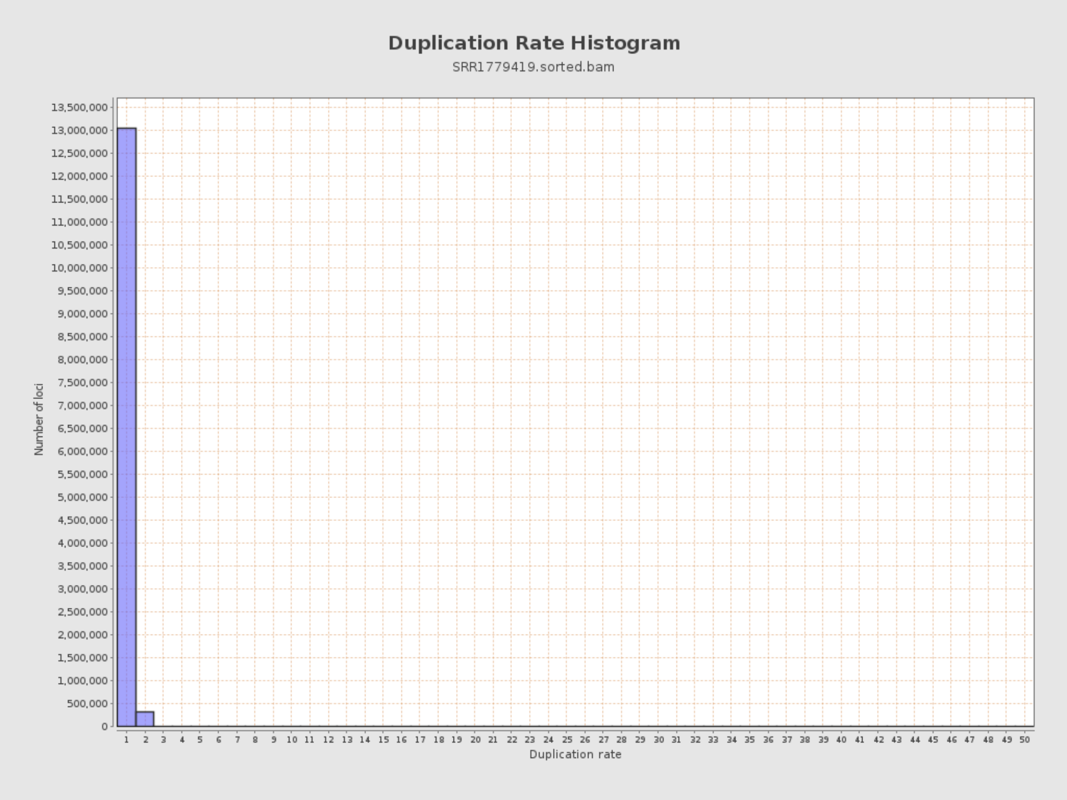
5. Results : Coverage Histogram (0-50X)



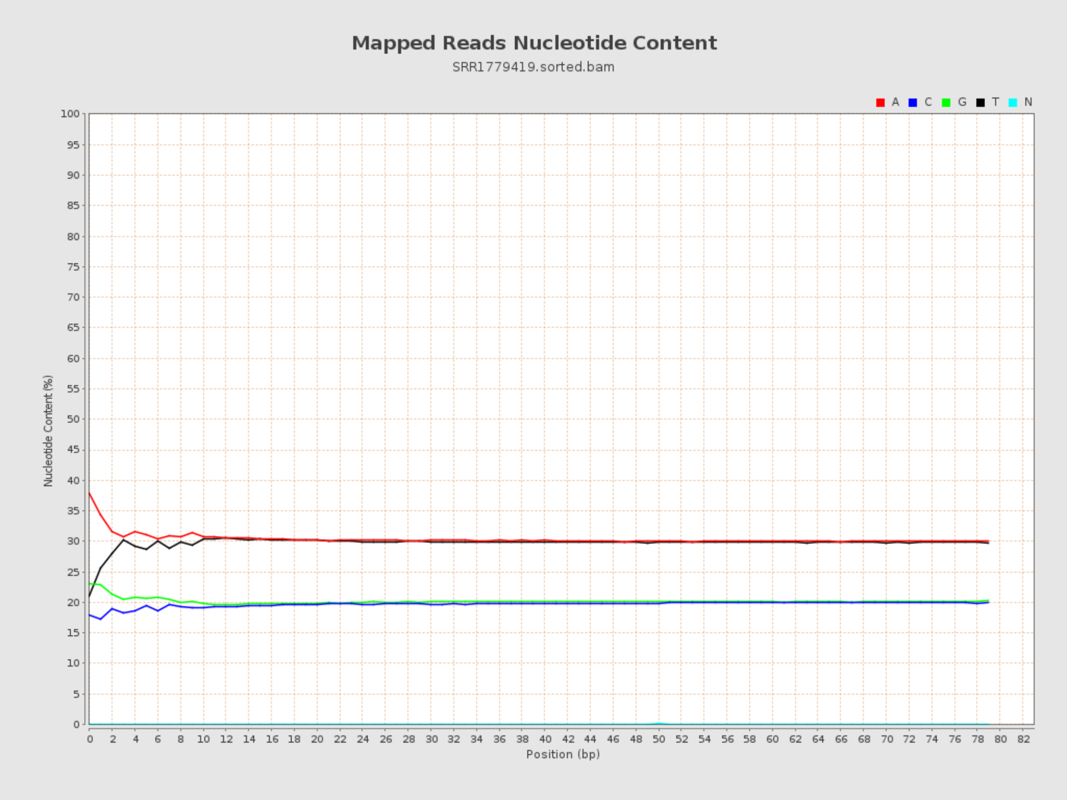
6. Results : Genome Fraction Coverage



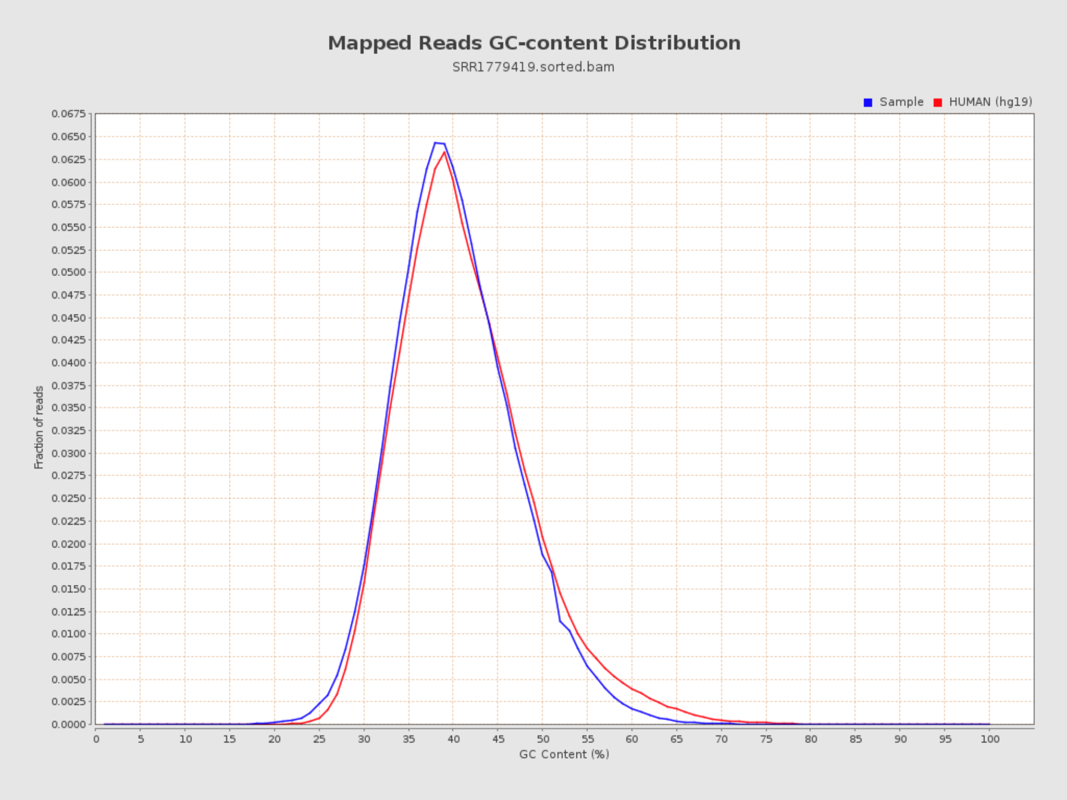
7. Results : Duplication Rate Histogram



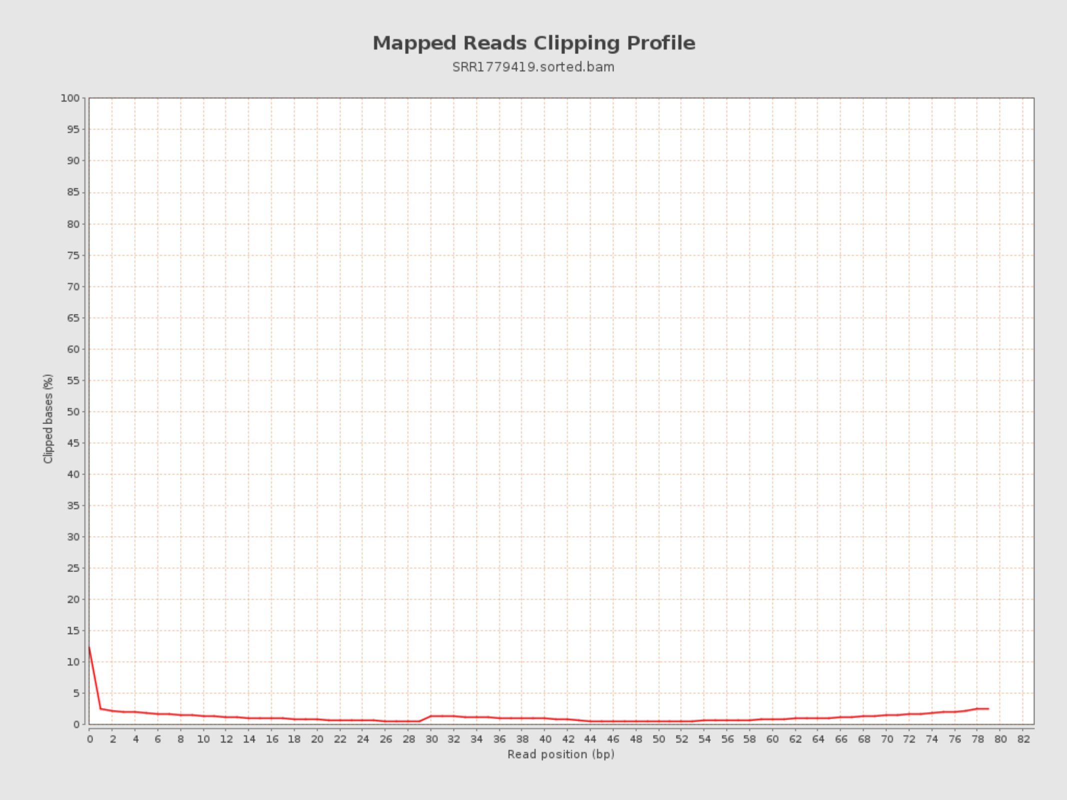
8. Results : Mapped Reads Nucleotide Content



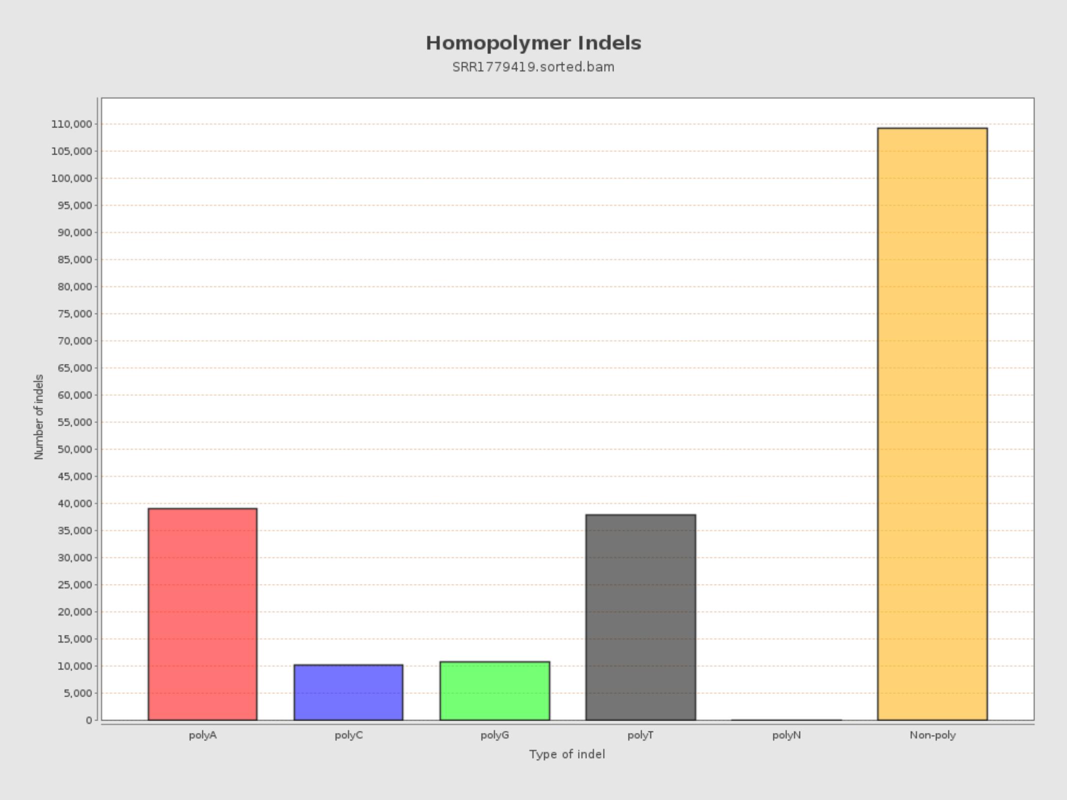
9. Results : Mapped Reads GC-content Distribution



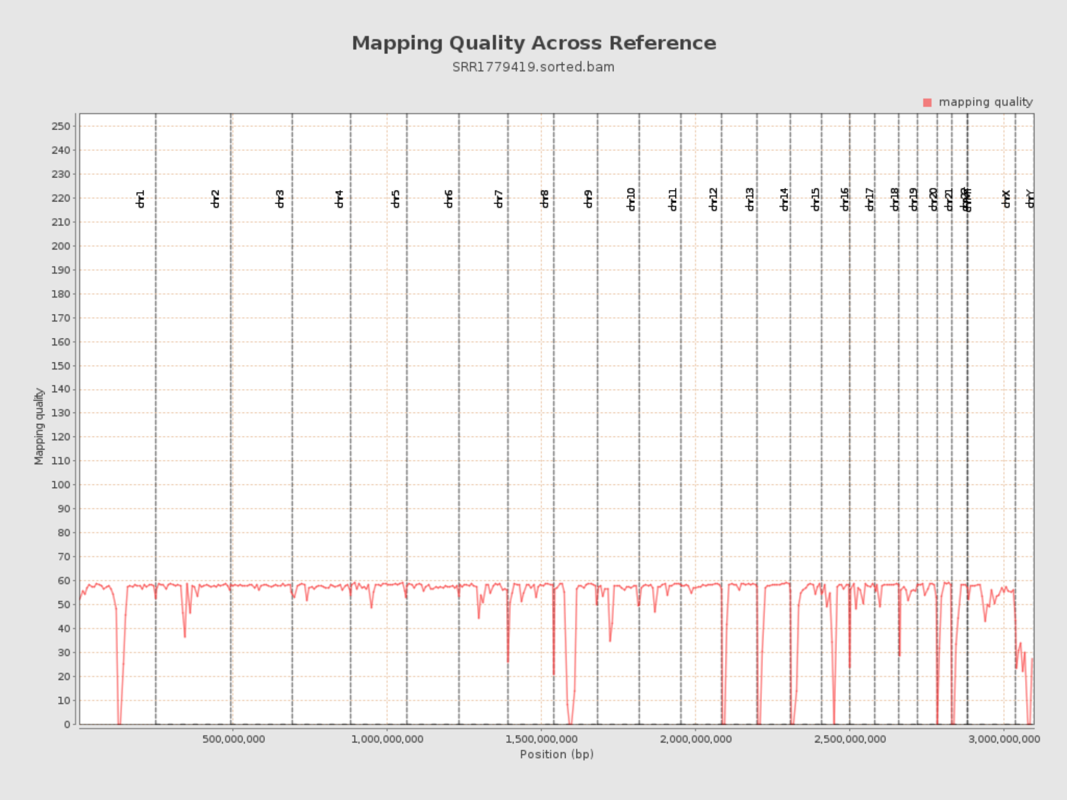
10. Results : Mapped Reads Clipping Profile



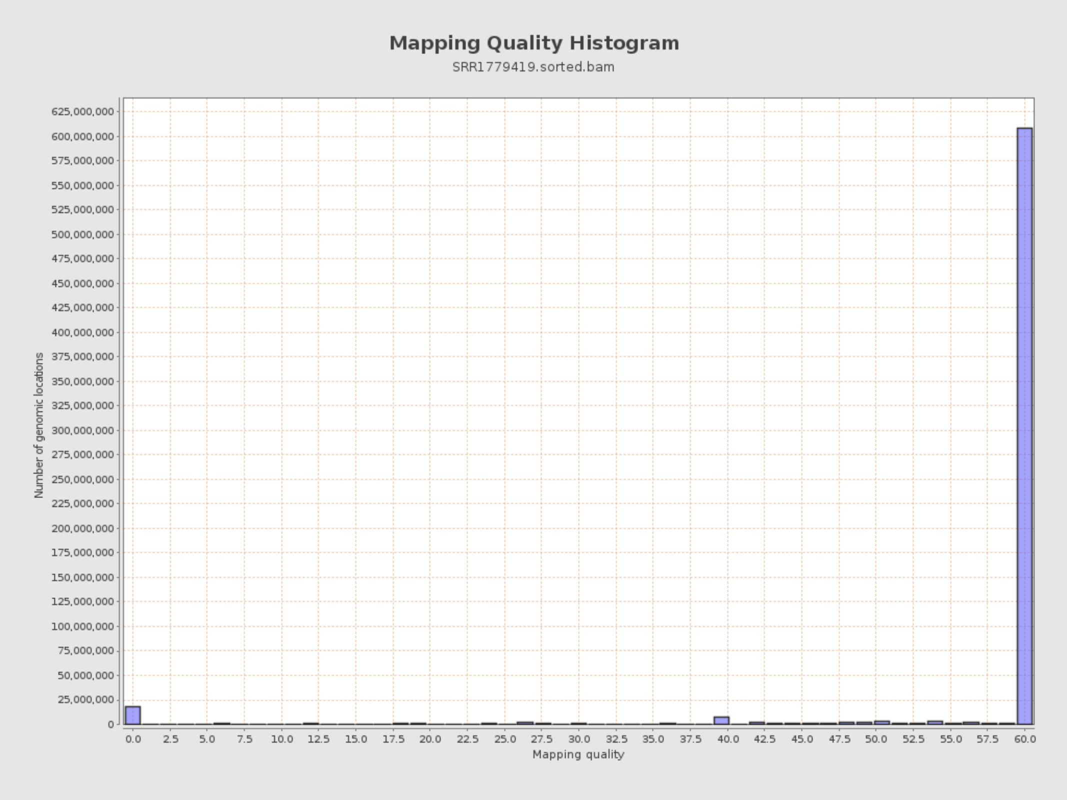
11. Results : Homopolymer Indels



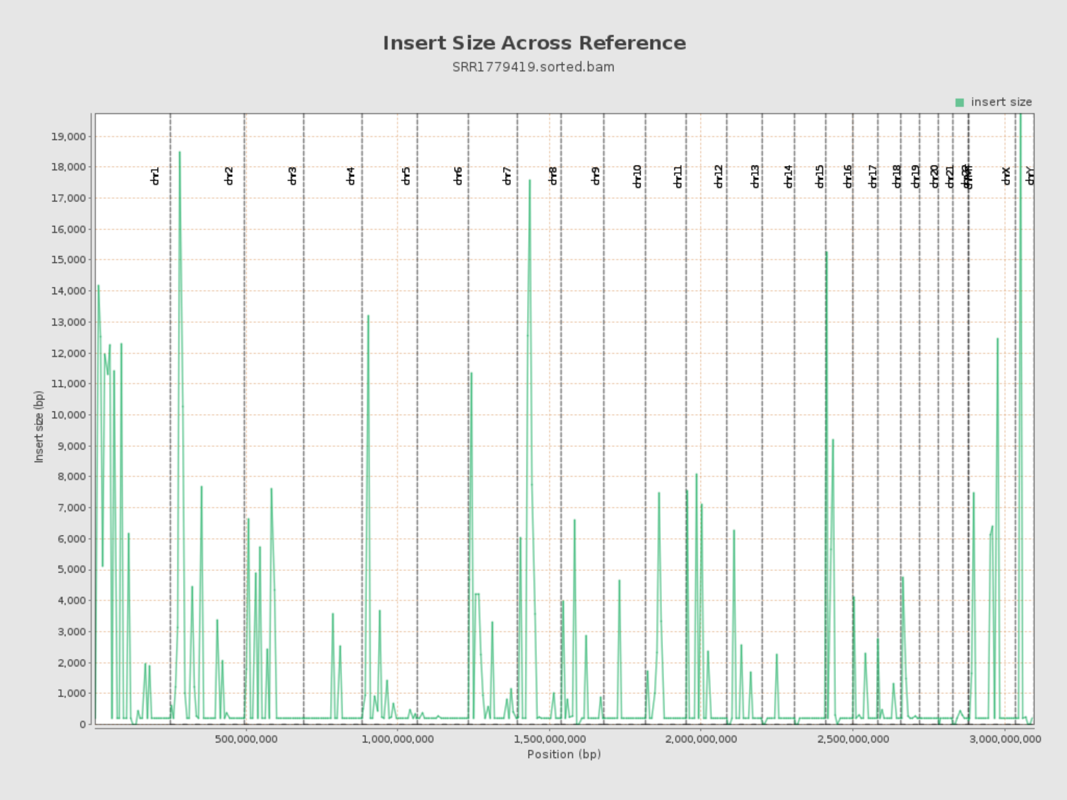
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram