Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 17:44:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779218.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_SRR1779218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779218_1.fastq.gz SRR1779218_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 17:44:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,770,922
Mapped reads	15,352,678 / 97.35%
Unmapped reads	418,244 / 2.65%
Mapped paired reads	15,352,678 / 97.35%
Mapped reads, first in pair	7,724,442 / 48.98%
Mapped reads, second in pair	7,628,236 / 48.37%
Mapped reads, both in pair	15,231,426 / 96.58%
Mapped reads, singletons	121,252 / 0.77%
Secondary alignments	0
Supplementary alignments	35,845 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	351,182 / 2.23%
Duplication rate	2.05%
Clipped reads	519,741 / 3.3%

2.2. ACGT Content

Number/percentage of A's	377,201,133 / 30.88%
Number/percentage of C's	231,899,835 / 18.99%
Number/percentage of T's	376,320,340 / 30.81%
Number/percentage of G's	235,811,159 / 19.31%
Number/percentage of N's	230,382 / 0.02%

GC Percentage	38.29%

2.3. Coverage

Mean	0.3946
Standard Deviation	1.3659

2.4. Mapping Quality

Mean Mapping Quality	52.7

2.5. Insert size

Mean	38,793.81
Standard Deviation	1,804,225.4
P25/Median/P75	145 / 194 / 266

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,569,836
Insertions	89,638
Mapped reads with at least one insertion	0.58%
Deletions	114,046
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.72%

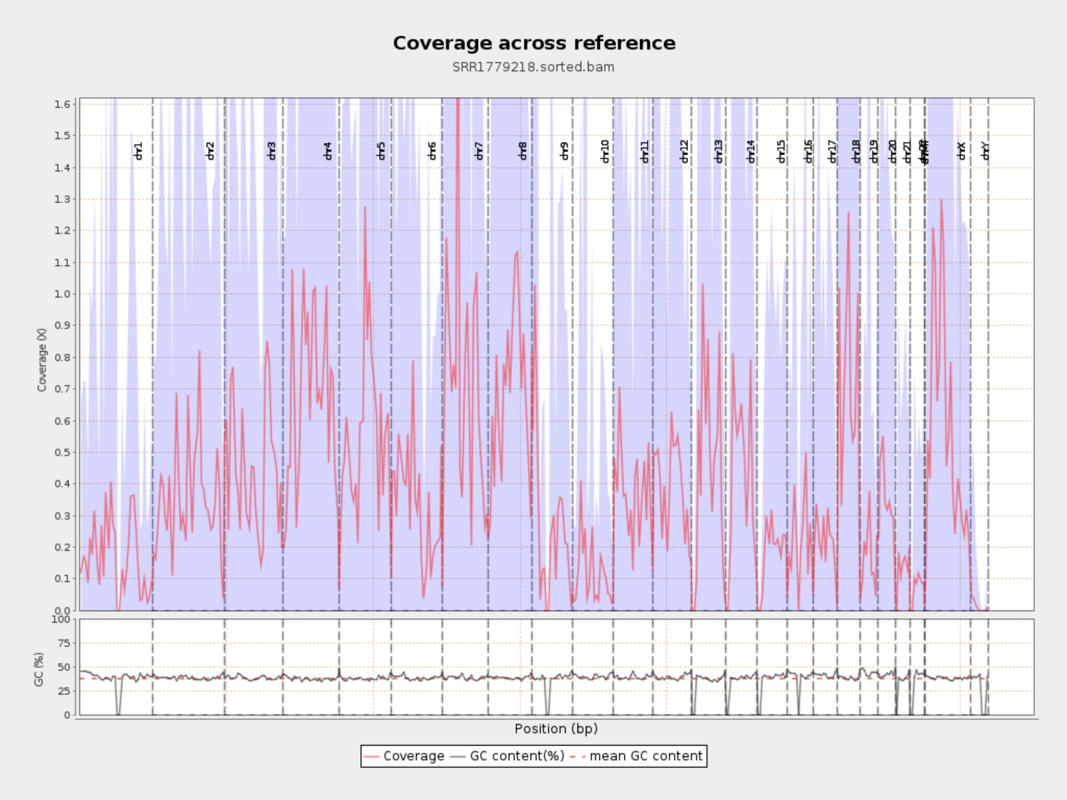
2.7. Chromosome stats

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

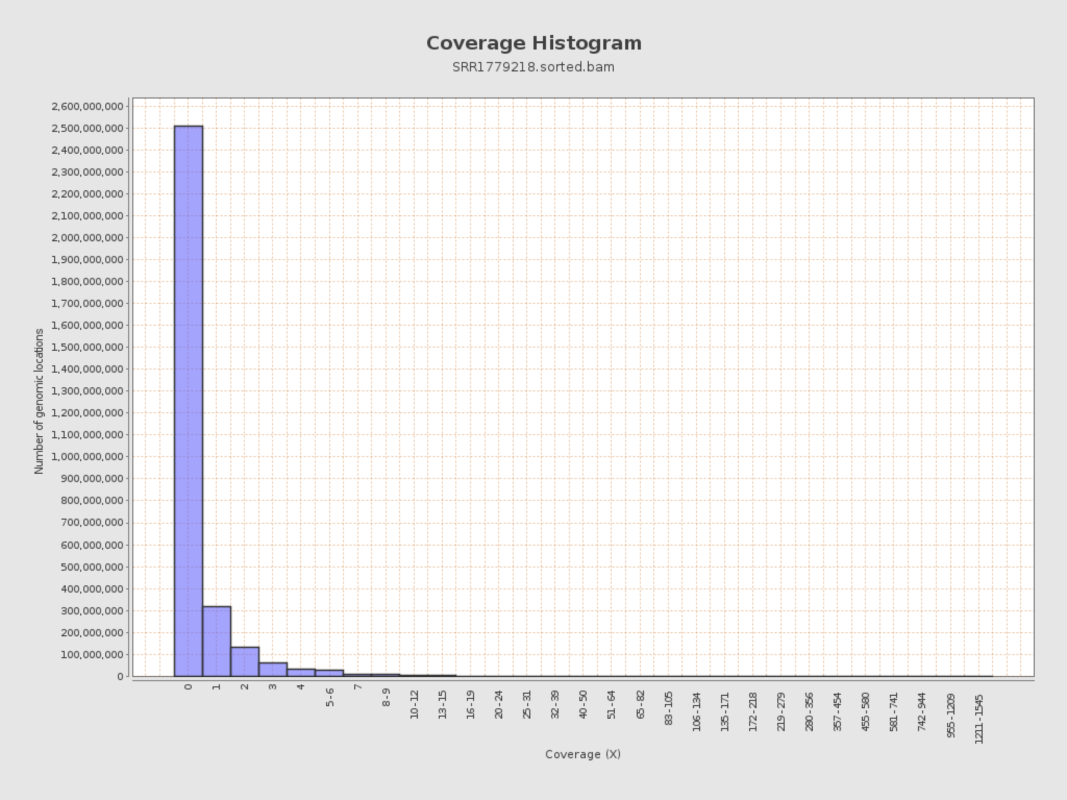
		bases	coverage	deviation
chr1	249250621	41463732	0.1664	1.7078
chr2	243199373	87693972	0.3606	1.0687
chr3	198022430	90358046	0.4563	1.1834
chr4	191154276	129543693	0.6777	1.4742
chr5	180915260	99579163	0.5504	1.3245
chr6	171115067	57549967	0.3363	1.0388
chr7	159138663	112991985	0.71	2.5929
chr8	146364022	102162853	0.698	1.5236
chr9	141213431	37185600	0.2633	1.0058
chr10	135534747	16024066	0.1182	1.6409
chr11	135006516	51013035	0.3779	1.0833
chr12	133851895	52839078	0.3948	1.1116
chr13	115169878	51988469	0.4514	1.1998
chr14	107349540	46004456	0.4285	1.1727
chr15	102531392	18641988	0.1818	0.675
chr16	90354753	18898712	0.2092	0.7478
chr17	81195210	17787887	0.2191	0.8778
chr18	78077248	58369552	0.7476	1.6236
chr19	59128983	9367192	0.1584	1.089
chr20	63025520	21690350	0.3442	0.9793
chr21	48129895	6675587	0.1387	0.5951
chr22	51304566	3742697	0.073	0.4345
chrMT	16571	775	0.0468	0.2723
chrX	155270560	89338189	0.5754	1.5497

chrY	59373566	787564	0.0133	0.2206

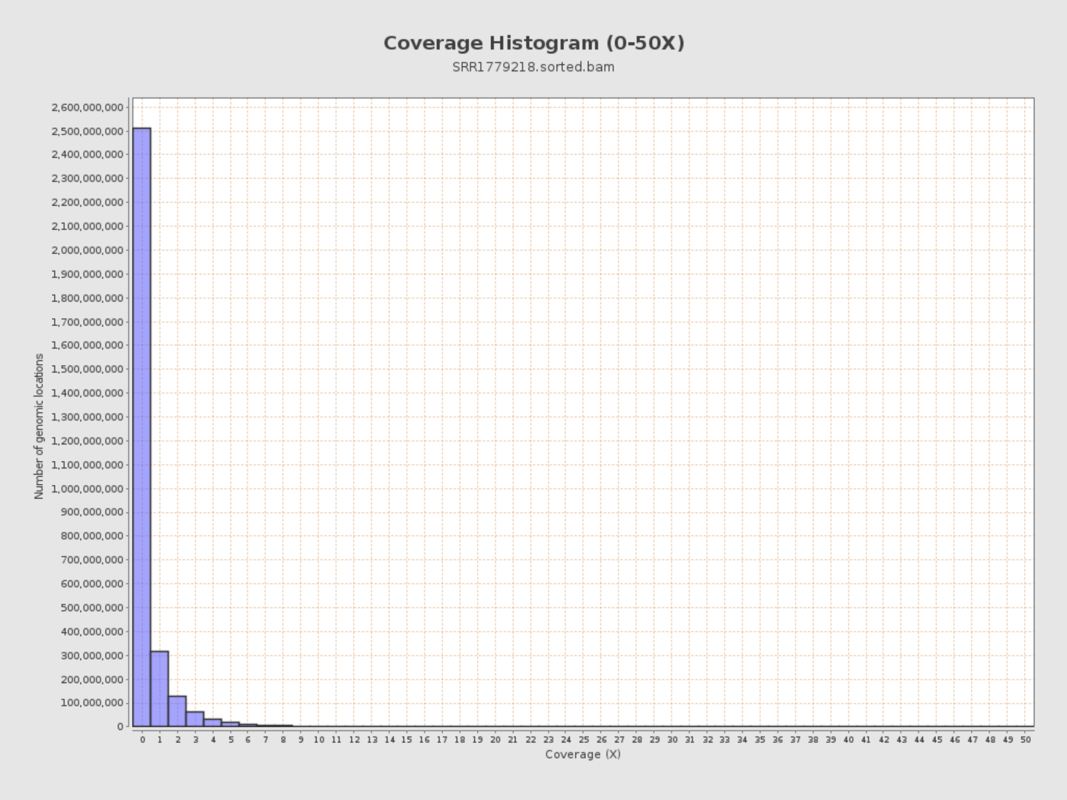
3. Results : Coverage across reference



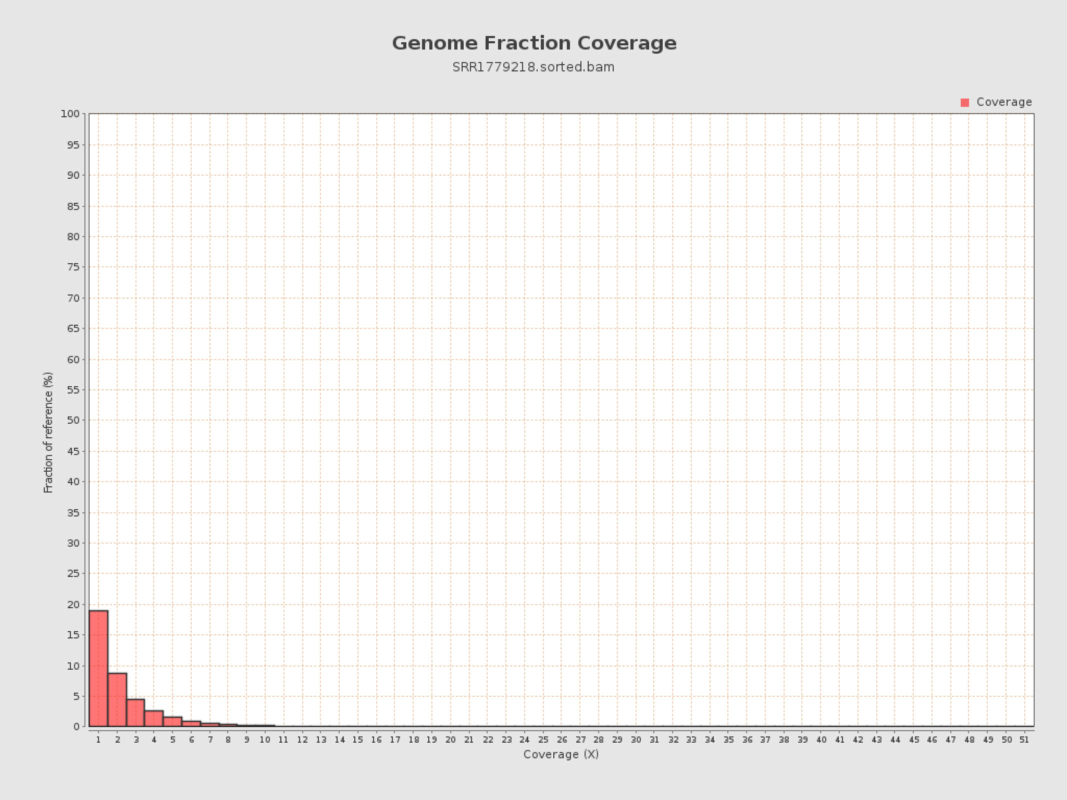
4. Results : Coverage Histogram



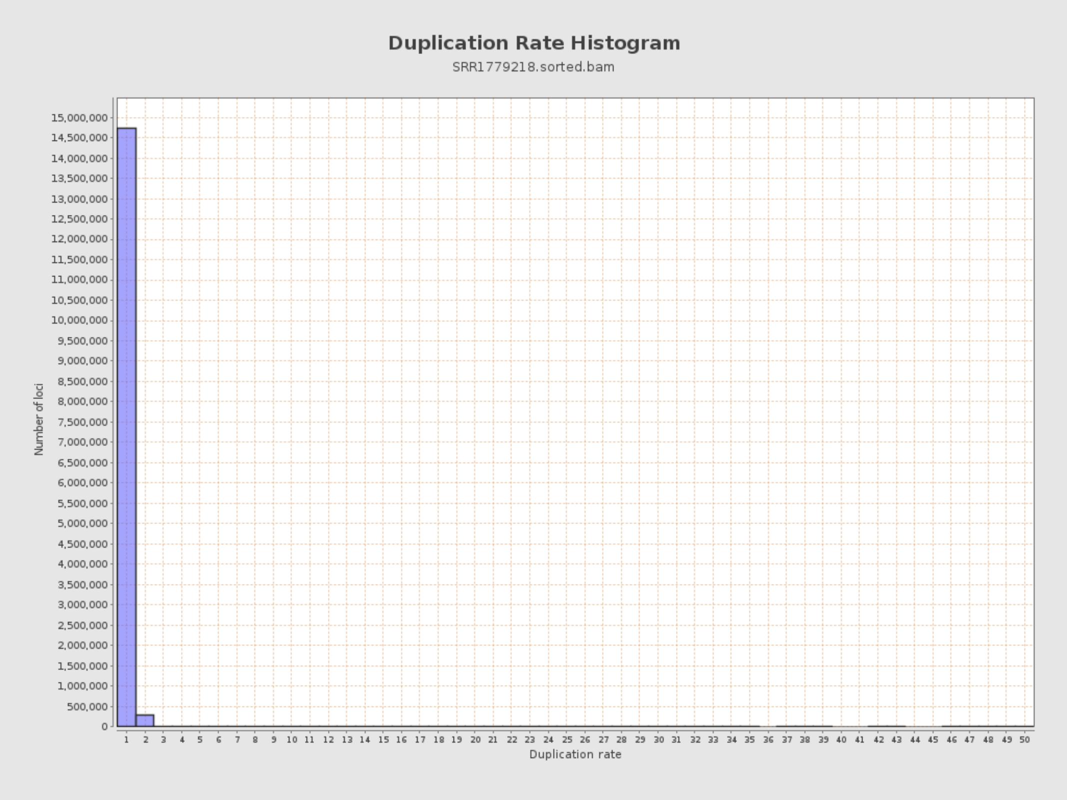
5. Results : Coverage Histogram (0-50X)



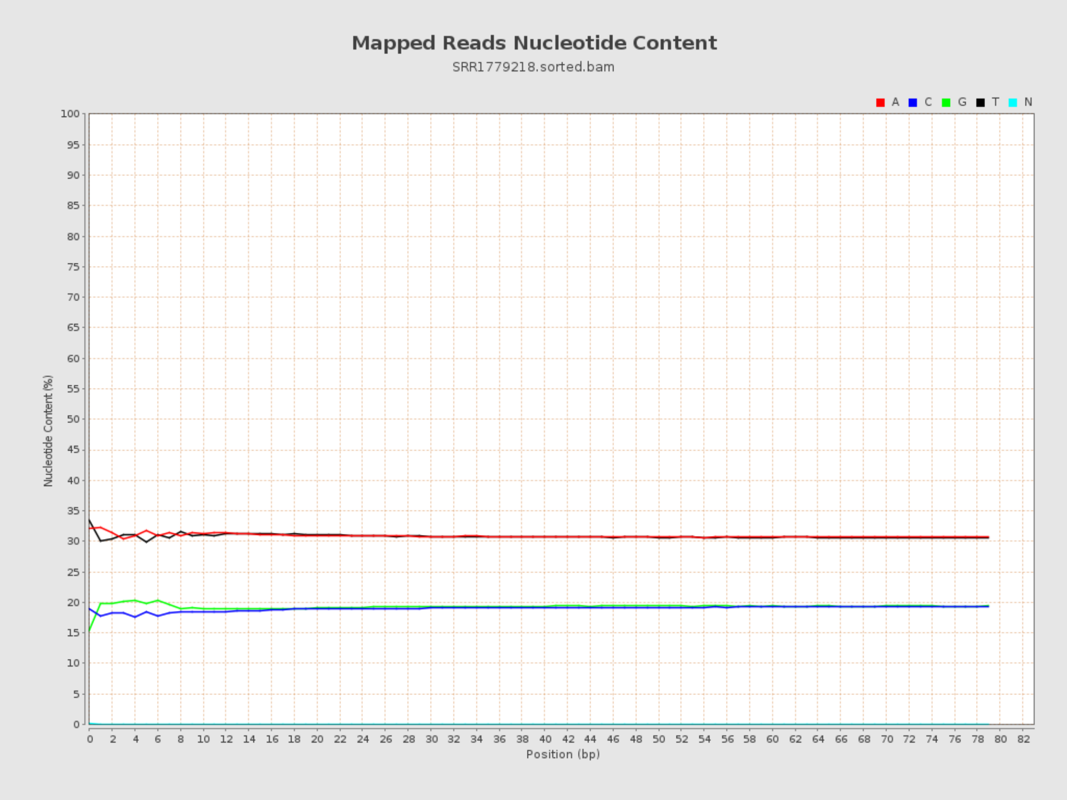
6. Results : Genome Fraction Coverage



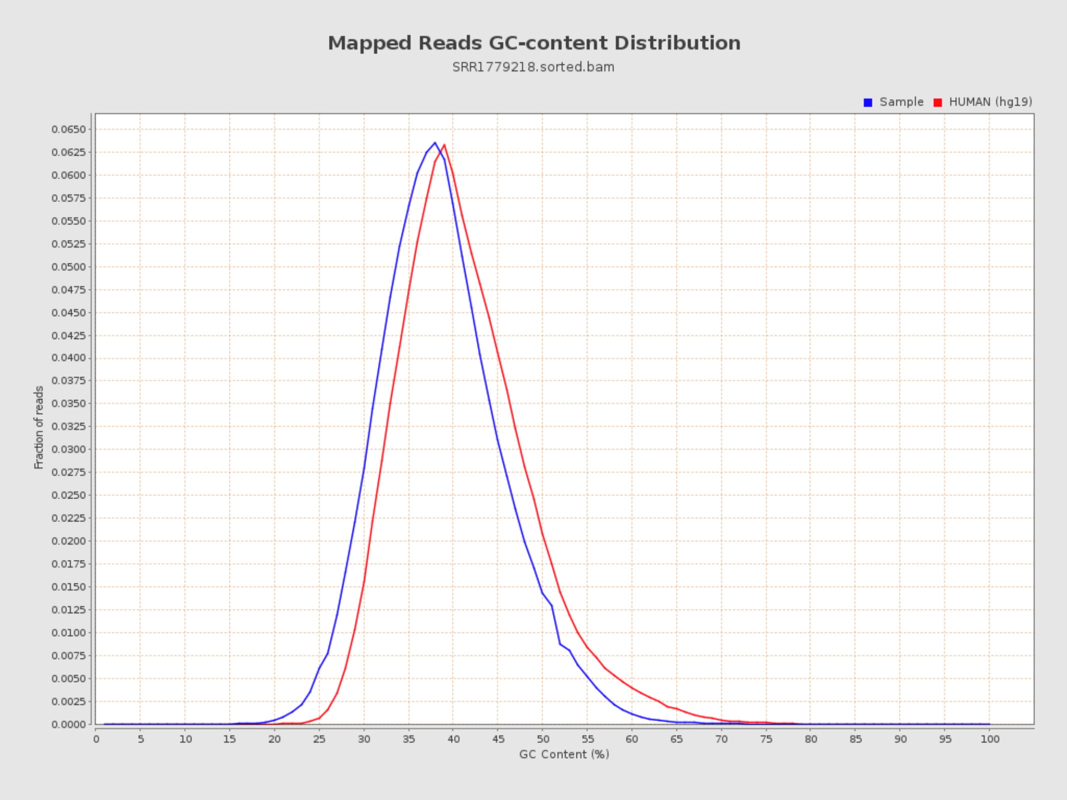
7. Results : Duplication Rate Histogram



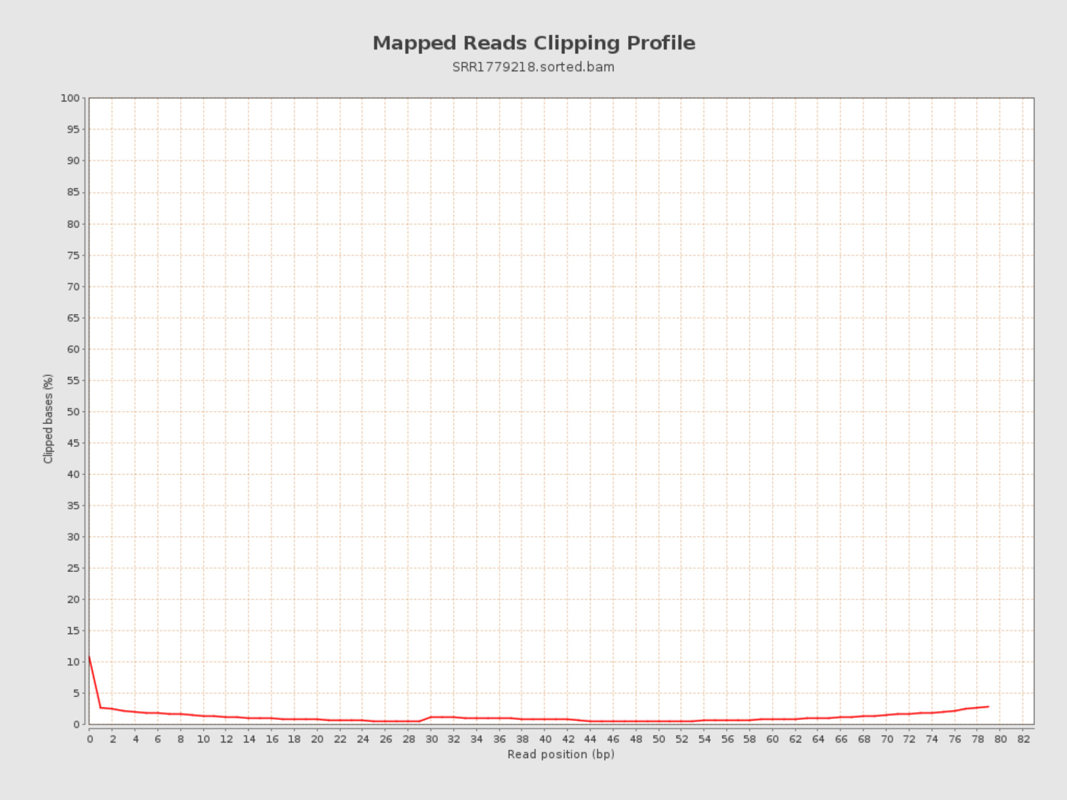
8. Results : Mapped Reads Nucleotide Content



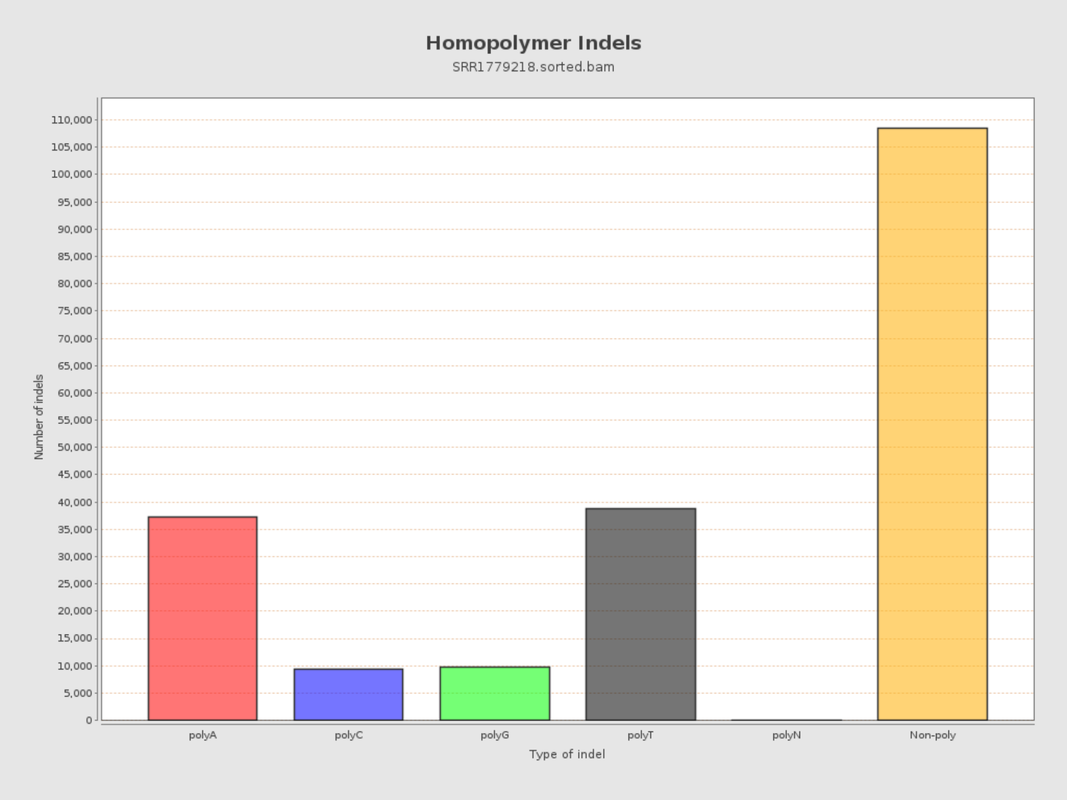
9. Results : Mapped Reads GC-content Distribution



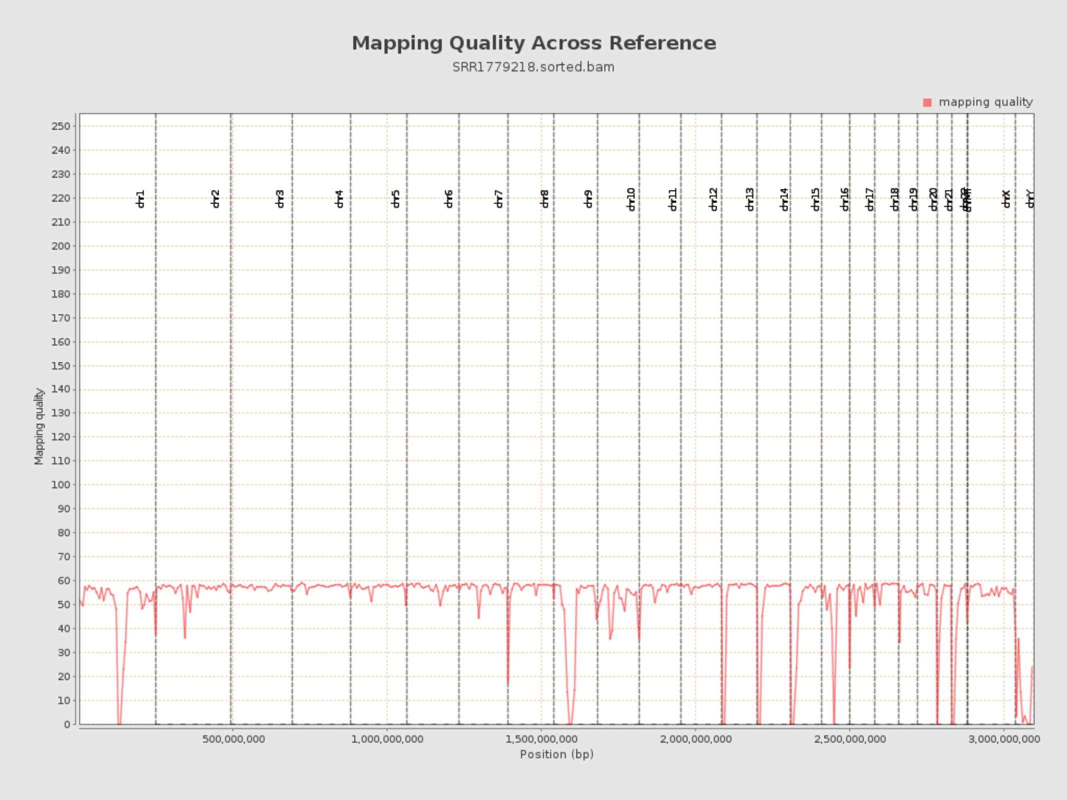
10. Results : Mapped Reads Clipping Profile



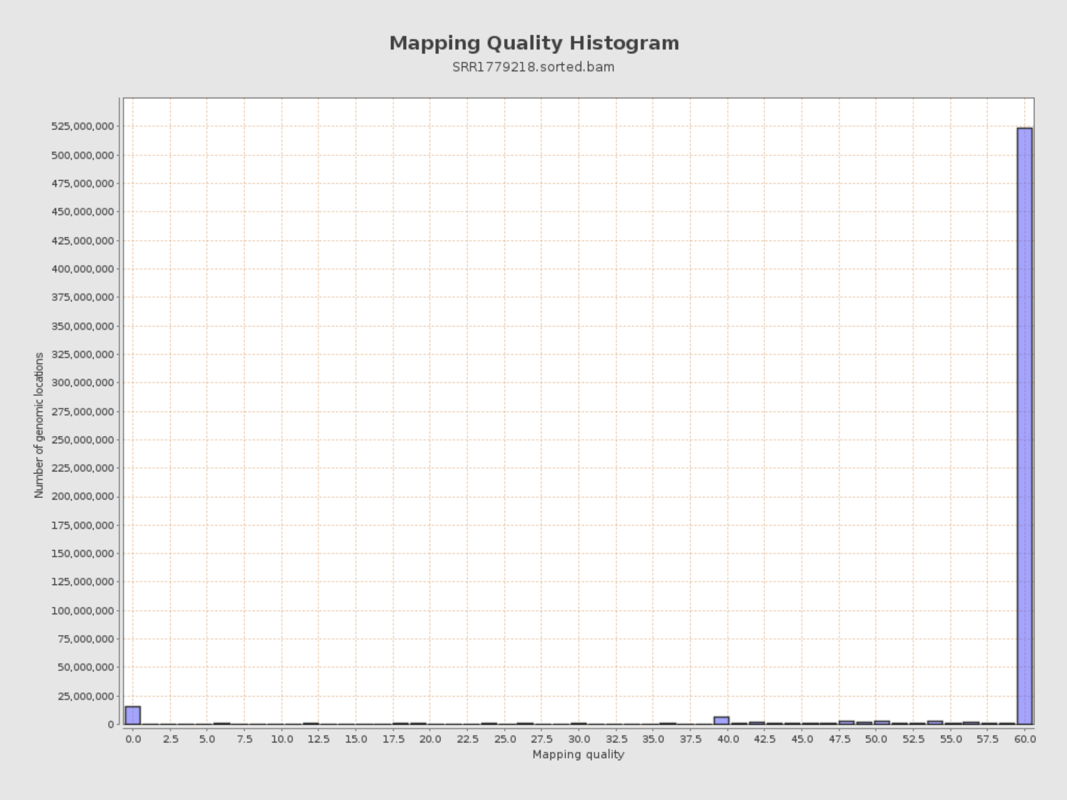
11. Results : Homopolymer Indels



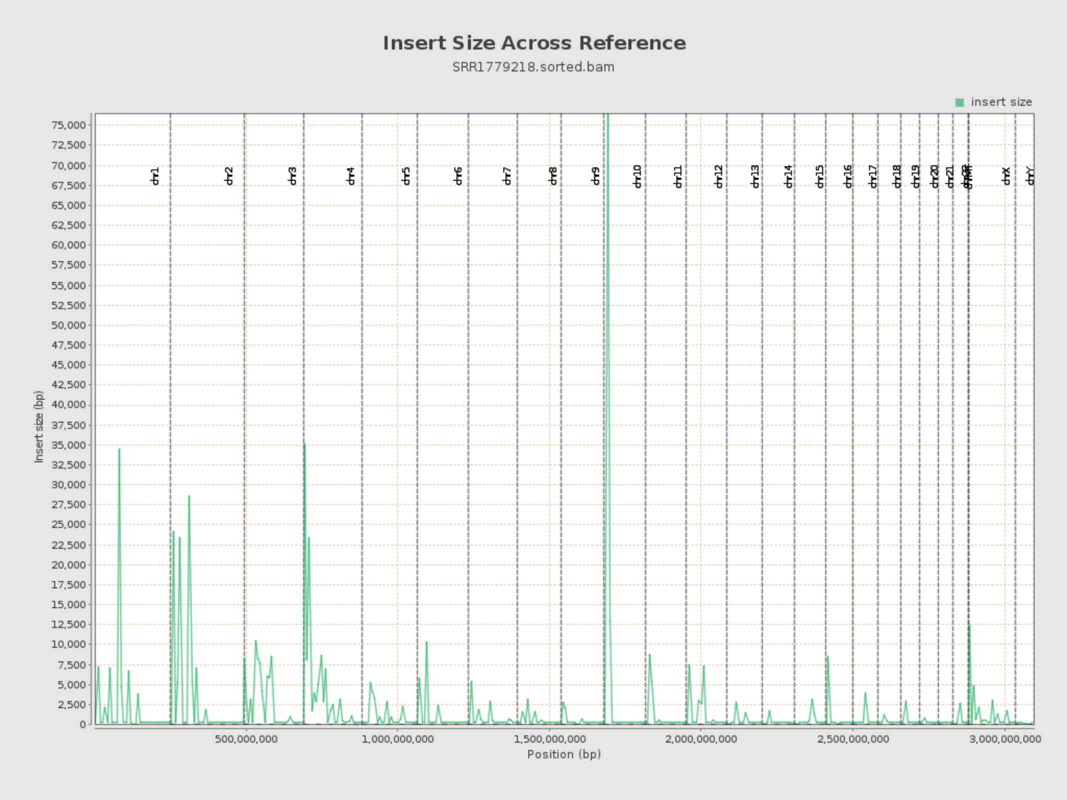
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram