Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 01:29:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779420.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_SRR1779420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779420_1.fastq.gz SRR1779420_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 01:29:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,722,832
Mapped reads	13,326,024 / 97.11%
Unmapped reads	396,808 / 2.89%
Mapped paired reads	13,326,024 / 97.11%
Mapped reads, first in pair	6,710,951 / 48.9%
Mapped reads, second in pair	6,615,073 / 48.2%
Mapped reads, both in pair	13,203,762 / 96.22%
Mapped reads, singletons	122,262 / 0.89%
Secondary alignments	0
Supplementary alignments	48,658 / 0.35%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	490,062 / 3.57%
Duplication rate	3.33%
Clipped reads	524,464 / 3.82%

2.2. ACGT Content

Number/percentage of A's	322,571,350 / 30.44%
Number/percentage of C's	207,558,923 / 19.59%
Number/percentage of T's	316,026,229 / 29.82%
Number/percentage of G's	213,239,149 / 20.12%
Number/percentage of N's	235,284 / 0.02%

GC Percentage	39.71%

2.3. Coverage

Mean	0.3424
Standard Deviation	1.4341

2.4. Mapping Quality

Mean Mapping Quality	53.2

2.5. Insert size

Mean	143,891.45
Standard Deviation	3,618,439.45
P25/Median/P75	152 / 193 / 243

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,458,914
Insertions	94,814
Mapped reads with at least one insertion	0.7%
Deletions	107,789
Mapped reads with at least one deletion	0.8%
Homopolymer indels	47.34%

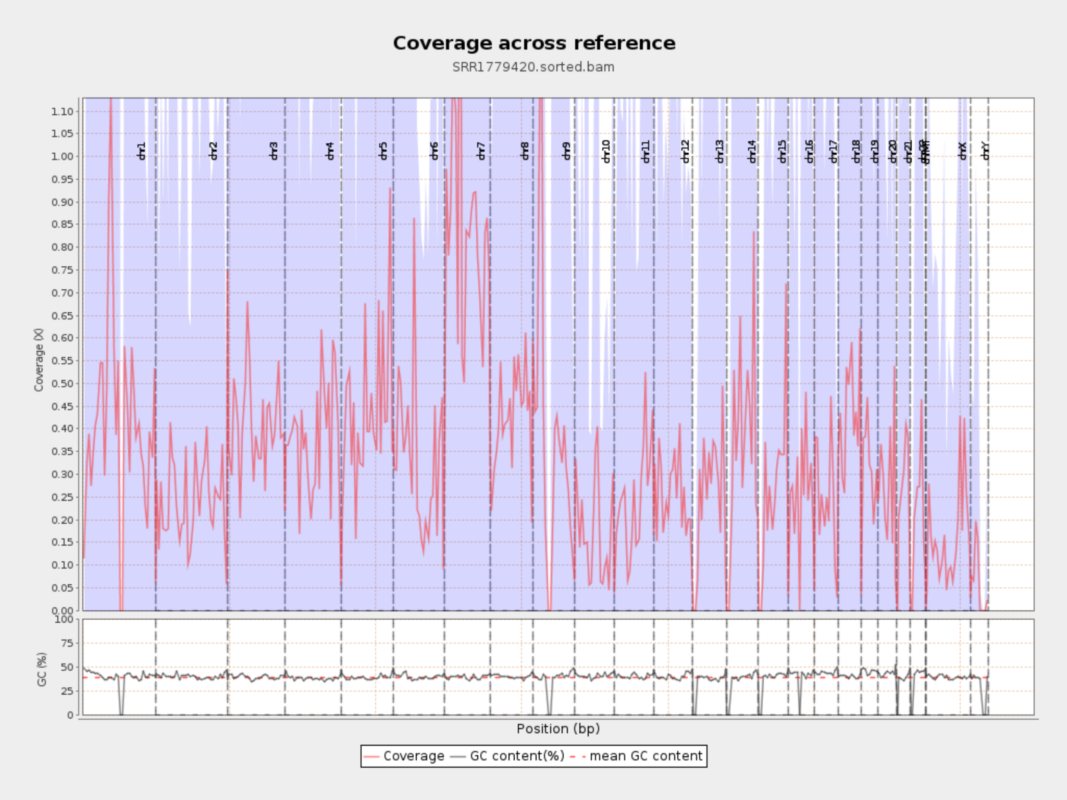
2.7. Chromosome stats

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

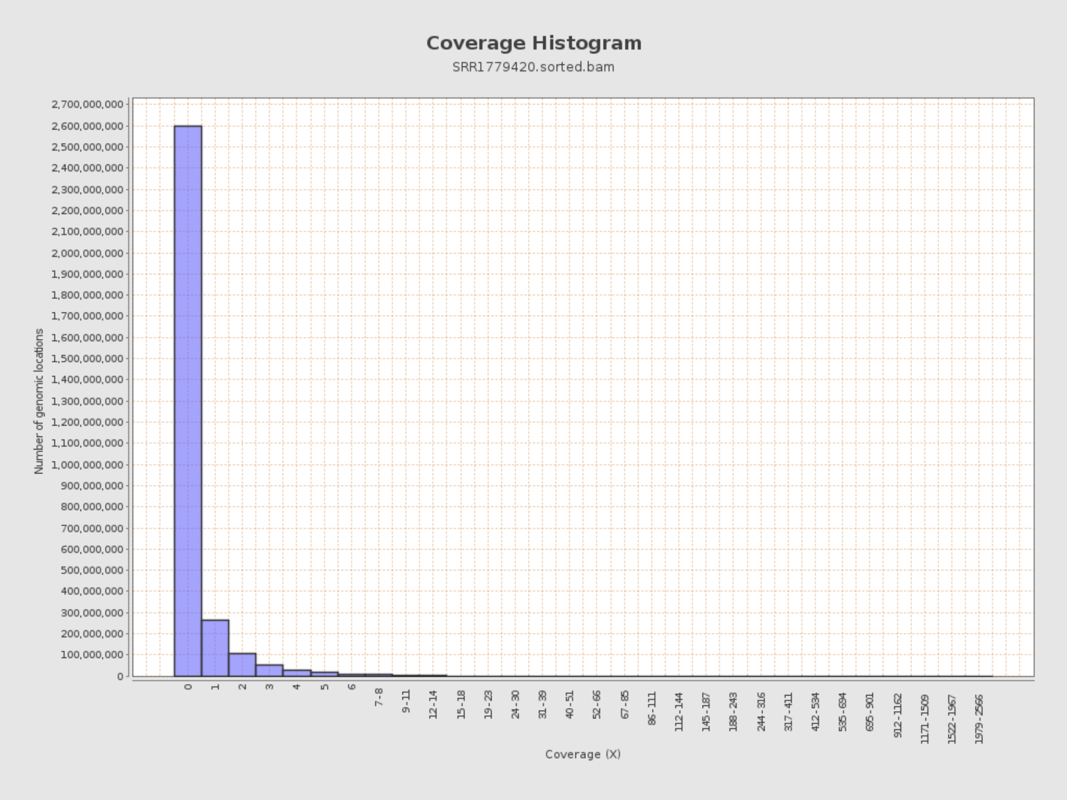
		bases	coverage	deviation
chr1	249250621	102790227	0.4124	2.8621
chr2	243199373	59499611	0.2447	0.9591
chr3	198022430	82084353	0.4145	1.1416
chr4	191154276	72441235	0.379	1.0846
chr5	180915260	78710597	0.4351	1.1434
chr6	171115067	56358569	0.3294	1.2382
chr7	159138663	135783385	0.8532	2.4364
chr8	146364022	62394239	0.4263	1.2393
chr9	141213431	54715139	0.3875	1.4303
chr10	135534747	23732042	0.1751	1.3698
chr11	135006516	33145362	0.2455	0.9679
chr12	133851895	34326025	0.2564	0.8368
chr13	115169878	29283179	0.2543	0.9689
chr14	107349540	40653209	0.3787	1.2022
chr15	102531392	27304191	0.2663	0.982
chr16	90354753	22923942	0.2537	0.9018
chr17	81195210	20732752	0.2553	1.1763
chr18	78077248	33657075	0.4311	1.4672
chr19	59128983	18892085	0.3195	1.7361
chr20	63025520	18108694	0.2873	0.9496
chr21	48129895	12270679	0.2549	0.9427
chr22	51304566	10739146	0.2093	0.8117
chrMT	16571	80	0.0048	0.0693
chrX	155270560	25469562	0.164	0.7147

chrY	59373566	3838549	0.0647	0.4069

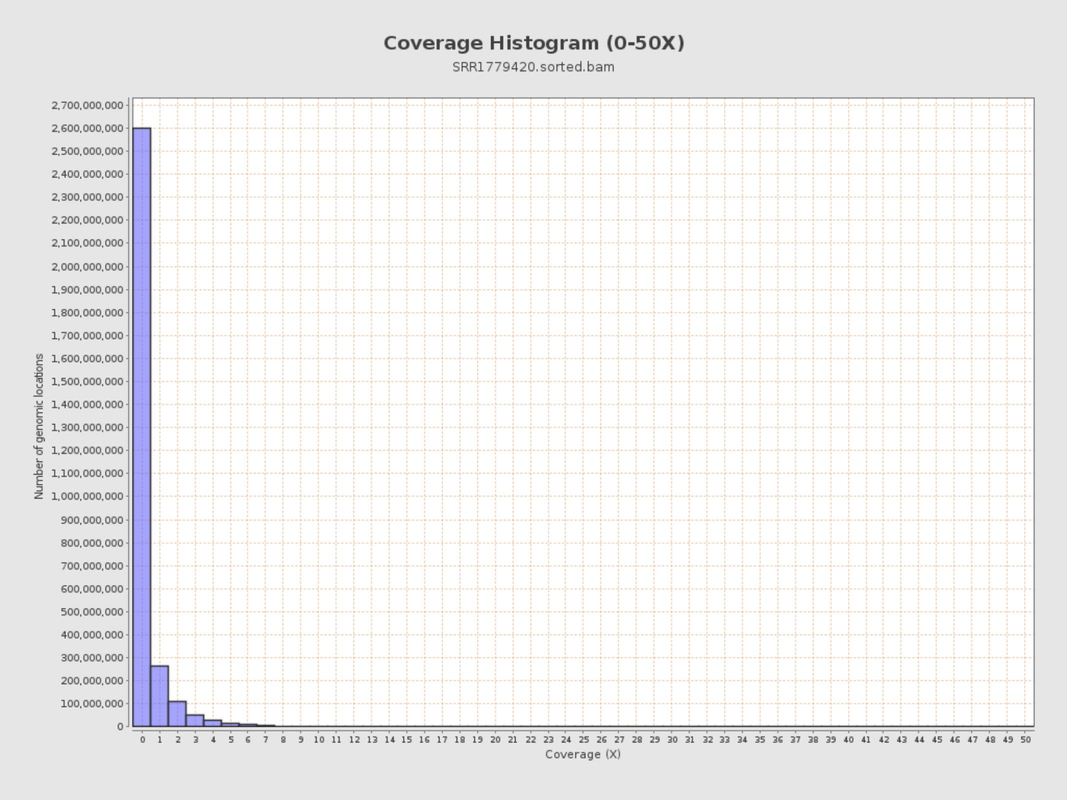
3. Results : Coverage across reference



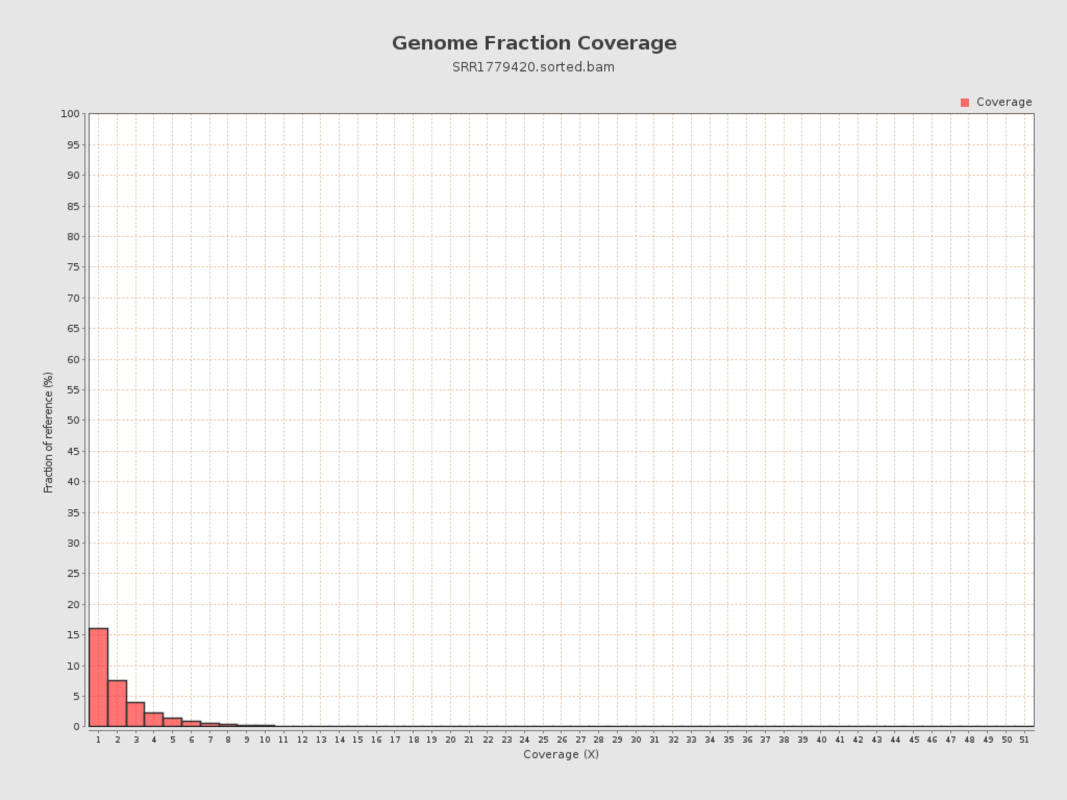
4. Results : Coverage Histogram



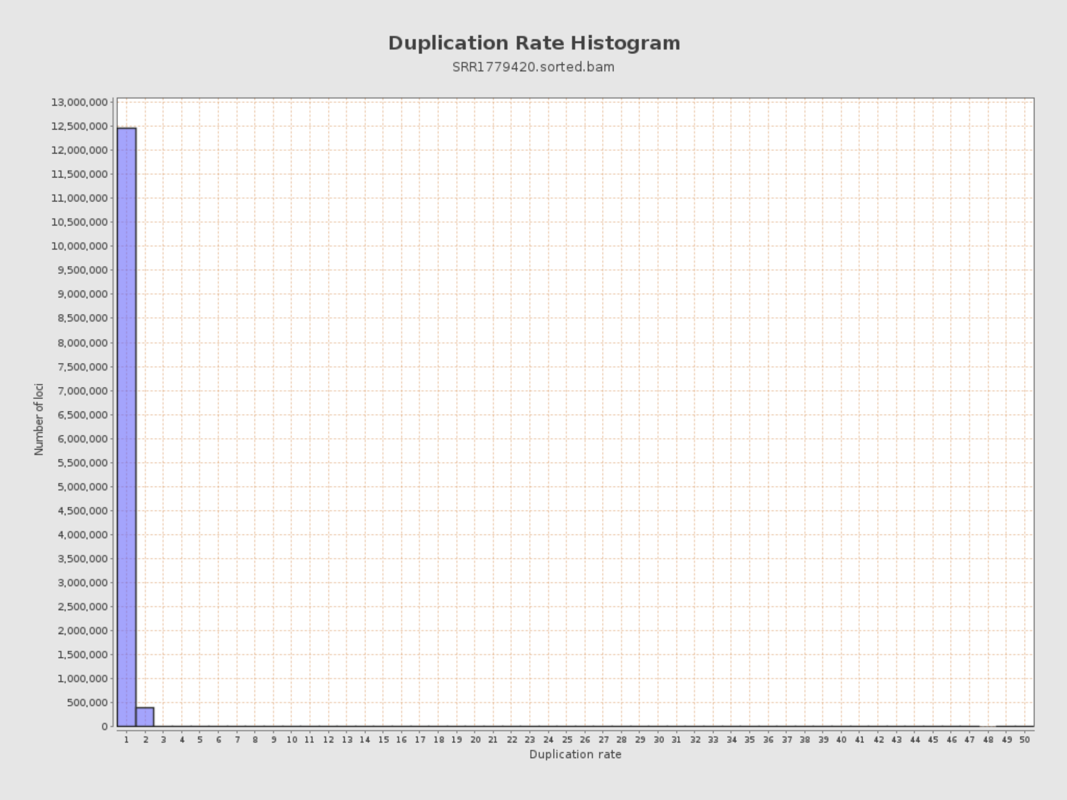
5. Results : Coverage Histogram (0-50X)



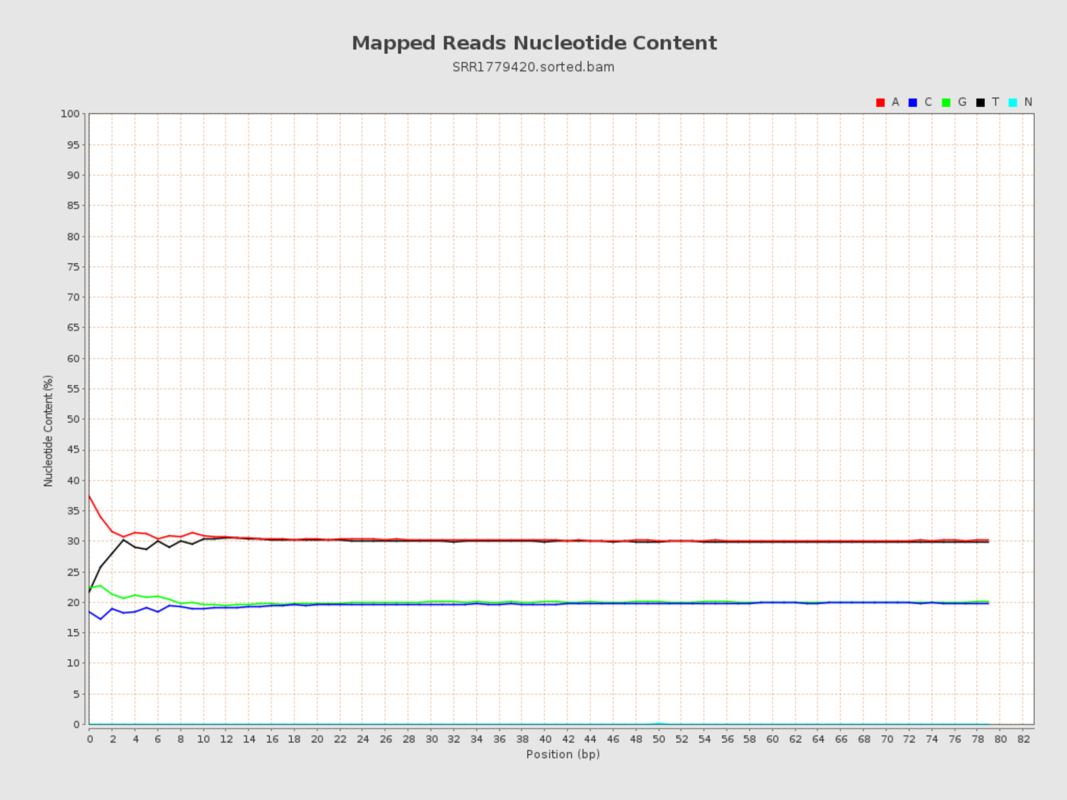
6. Results : Genome Fraction Coverage



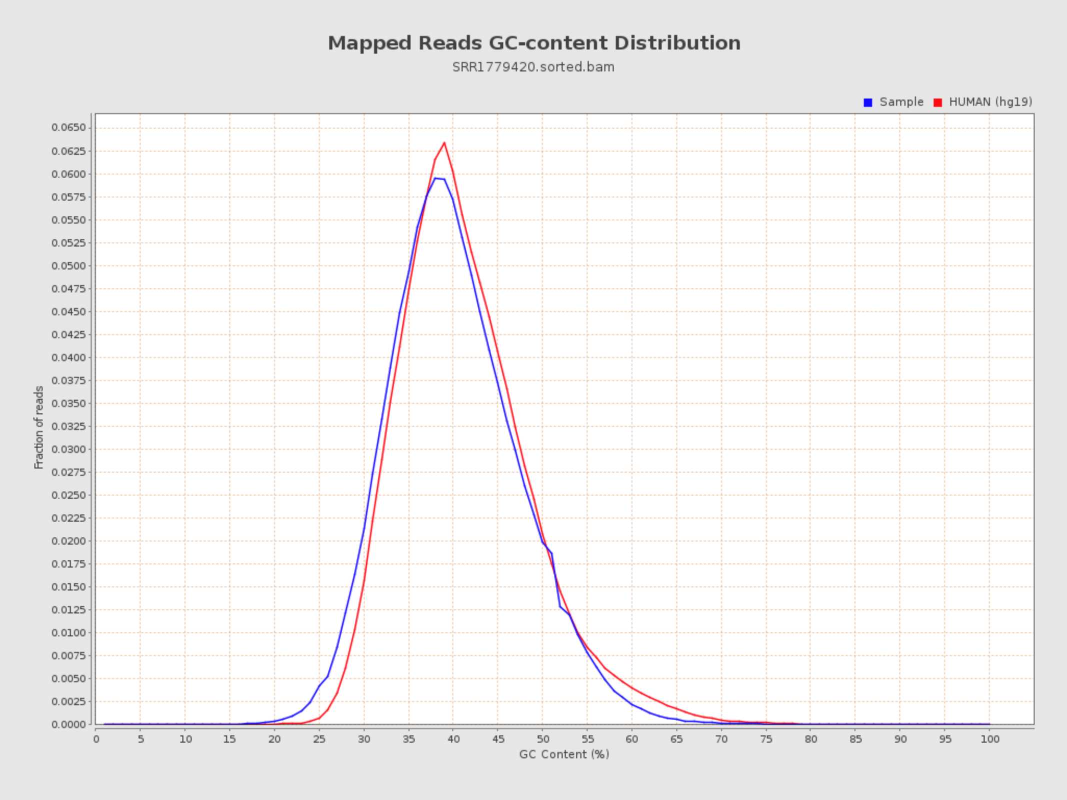
7. Results : Duplication Rate Histogram



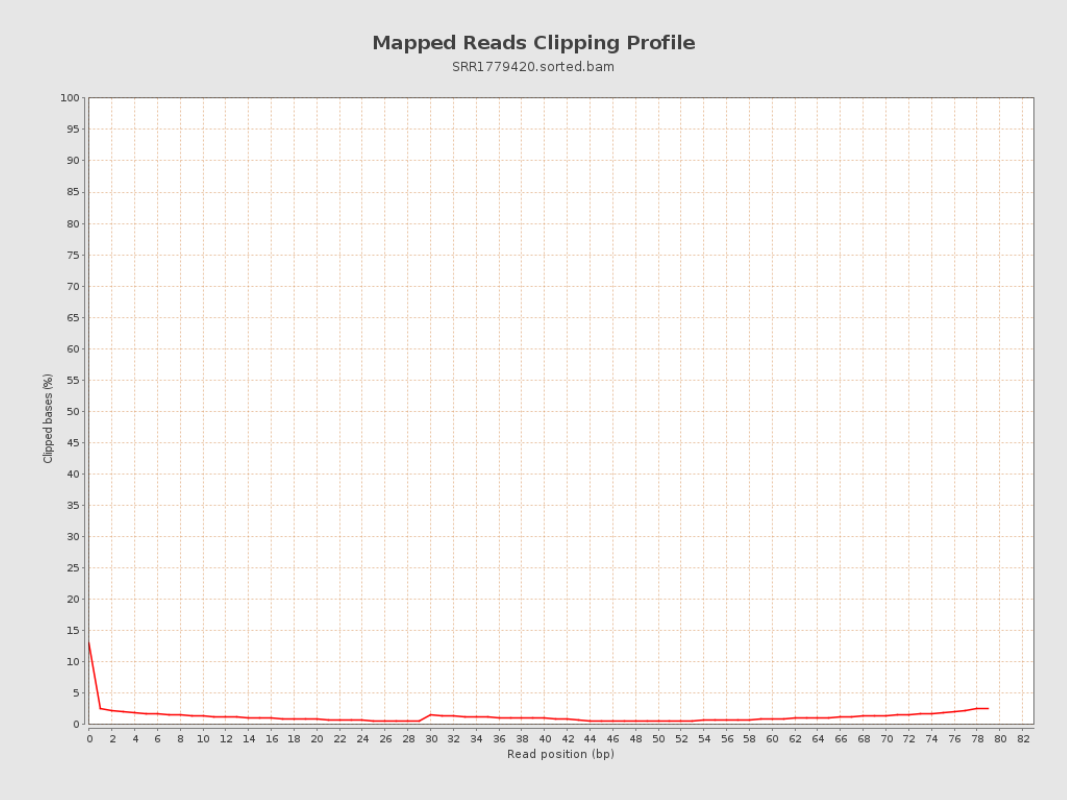
8. Results : Mapped Reads Nucleotide Content



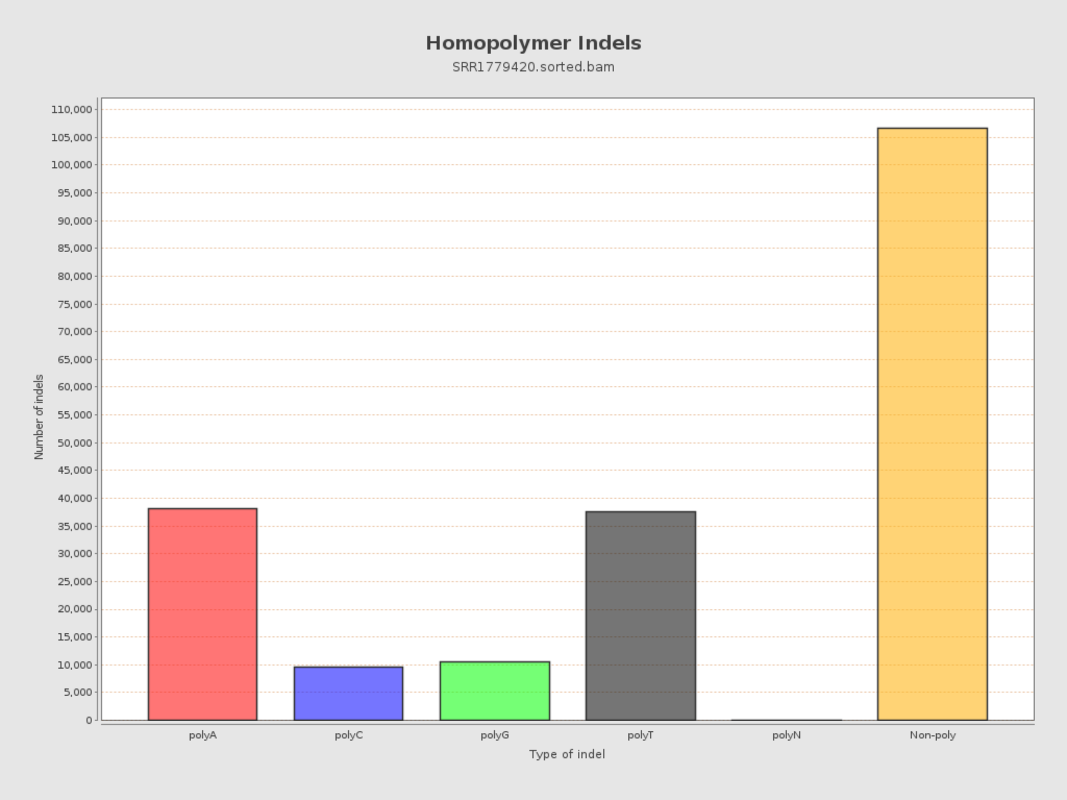
9. Results : Mapped Reads GC-content Distribution



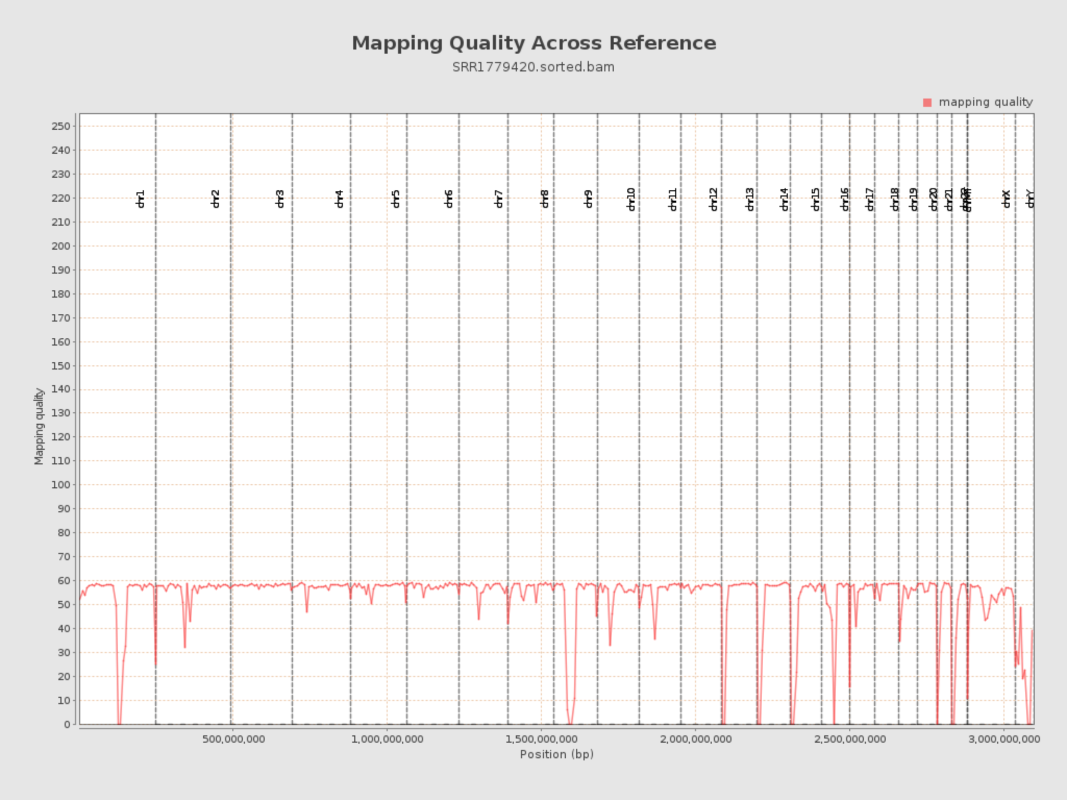
10. Results : Mapped Reads Clipping Profile



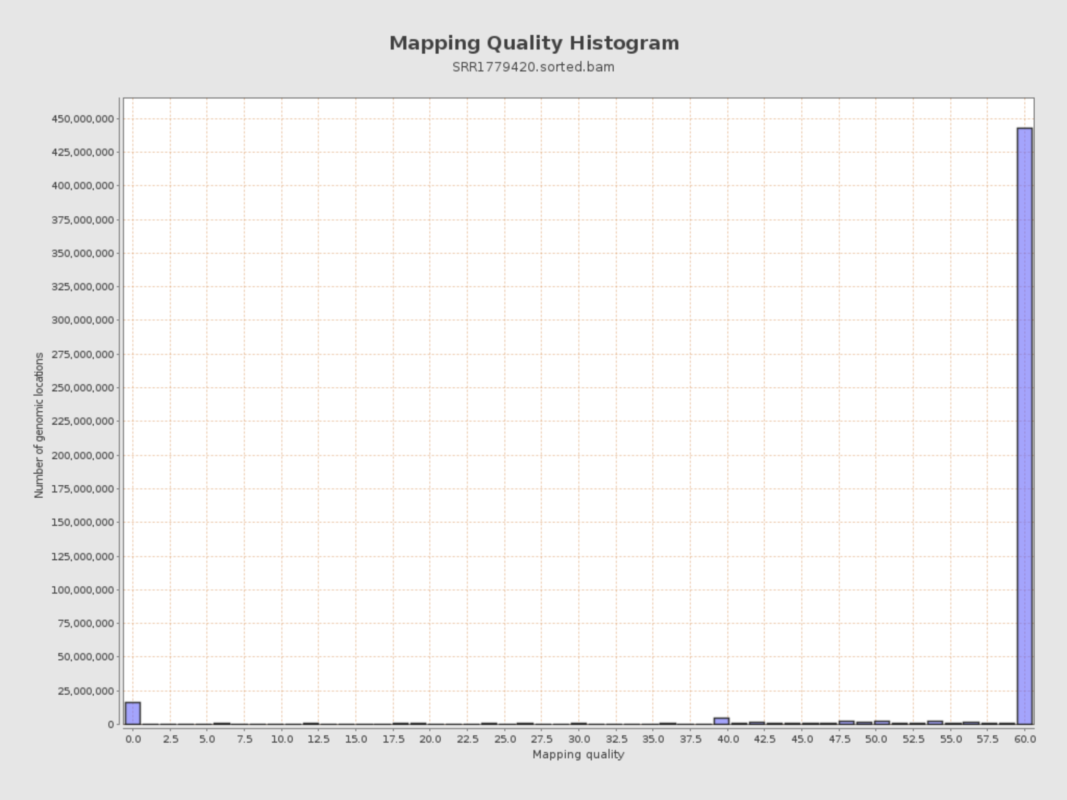
11. Results : Homopolymer Indels



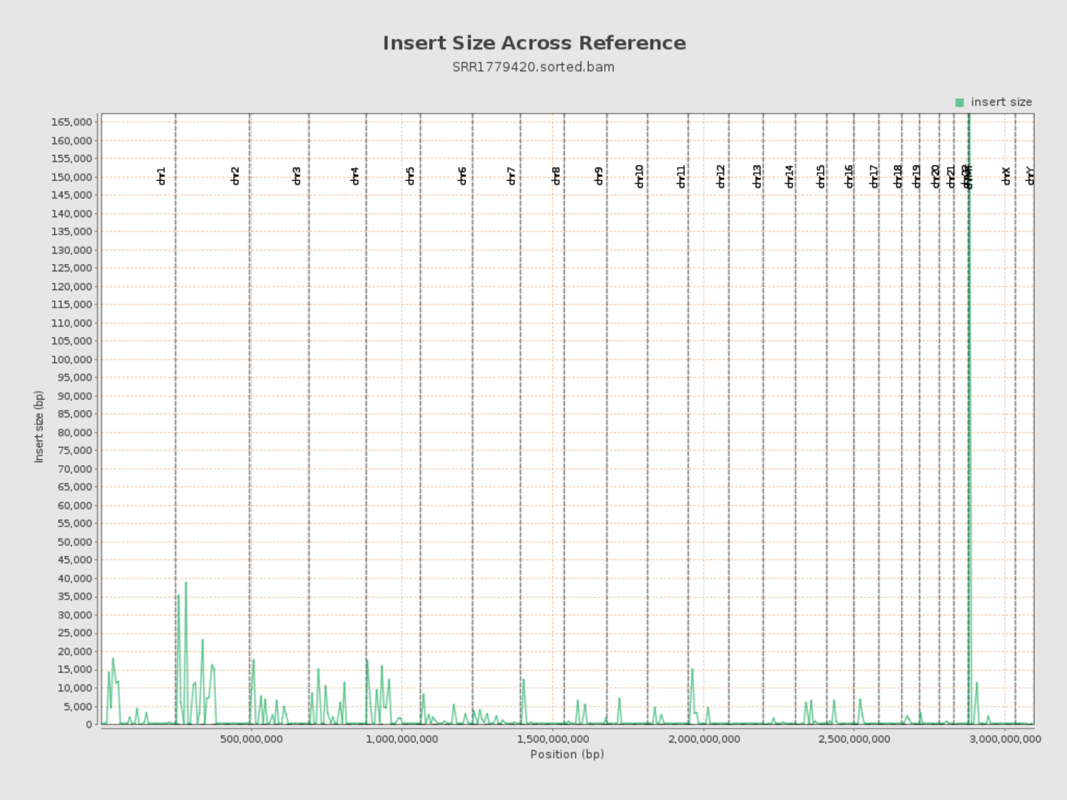
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram