Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 18:04:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779220.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_SRR1779220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779220_1.fastq.gz SRR1779220_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 18:04:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,378,630
Mapped reads	11,020,108 / 96.85%
Unmapped reads	358,522 / 3.15%
Mapped paired reads	11,020,108 / 96.85%
Mapped reads, first in pair	5,564,729 / 48.91%
Mapped reads, second in pair	5,455,379 / 47.94%
Mapped reads, both in pair	10,893,870 / 95.74%
Mapped reads, singletons	126,238 / 1.11%
Secondary alignments	0
Supplementary alignments	28,554 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	173,780 / 1.53%
Duplication rate	1.4%
Clipped reads	382,976 / 3.37%

2.2. ACGT Content

Number/percentage of A's	266,459,044 / 30.39%
Number/percentage of C's	170,851,410 / 19.49%
Number/percentage of T's	265,082,285 / 30.24%
Number/percentage of G's	174,117,055 / 19.86%
Number/percentage of N's	165,897 / 0.02%

GC Percentage	39.35%

2.3. Coverage

Mean	0.2832
Standard Deviation	0.9438

2.4. Mapping Quality

Mean Mapping Quality	53.03

2.5. Insert size

Mean	50,899.39
Standard Deviation	2,154,796.44
P25/Median/P75	146 / 195 / 264

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	3,337,557
Insertions	63,747
Mapped reads with at least one insertion	0.57%
Deletions	80,476
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.65%

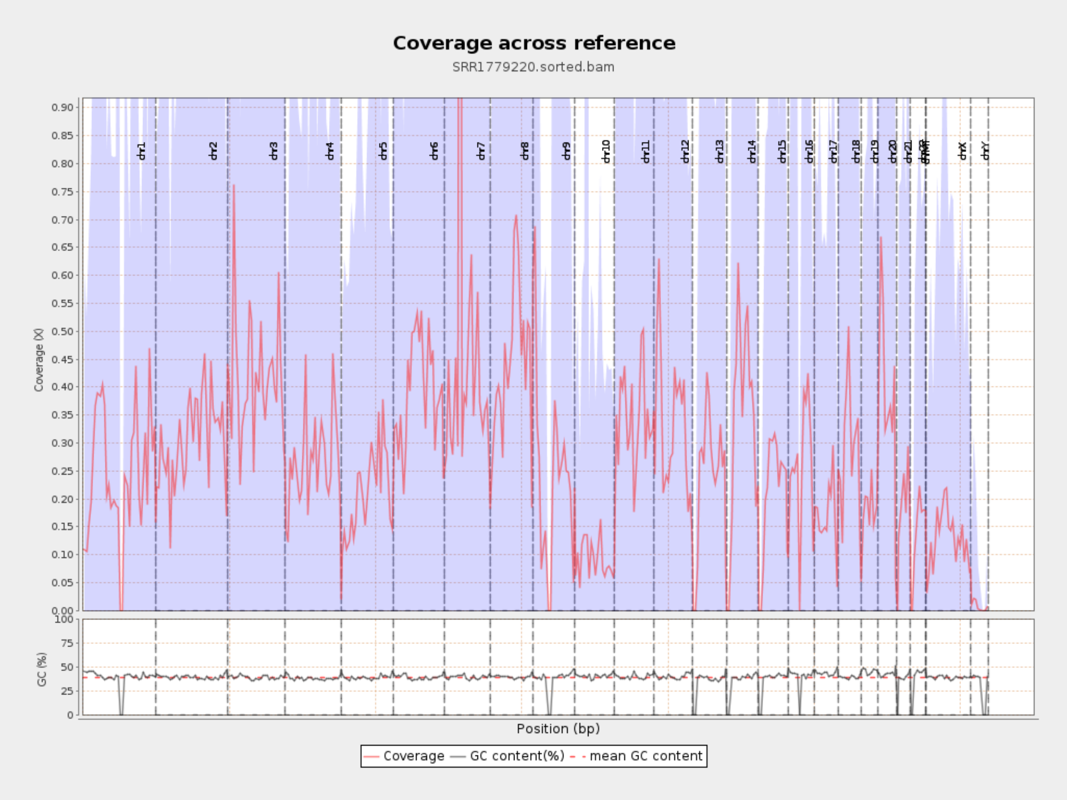
2.7. Chromosome stats

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

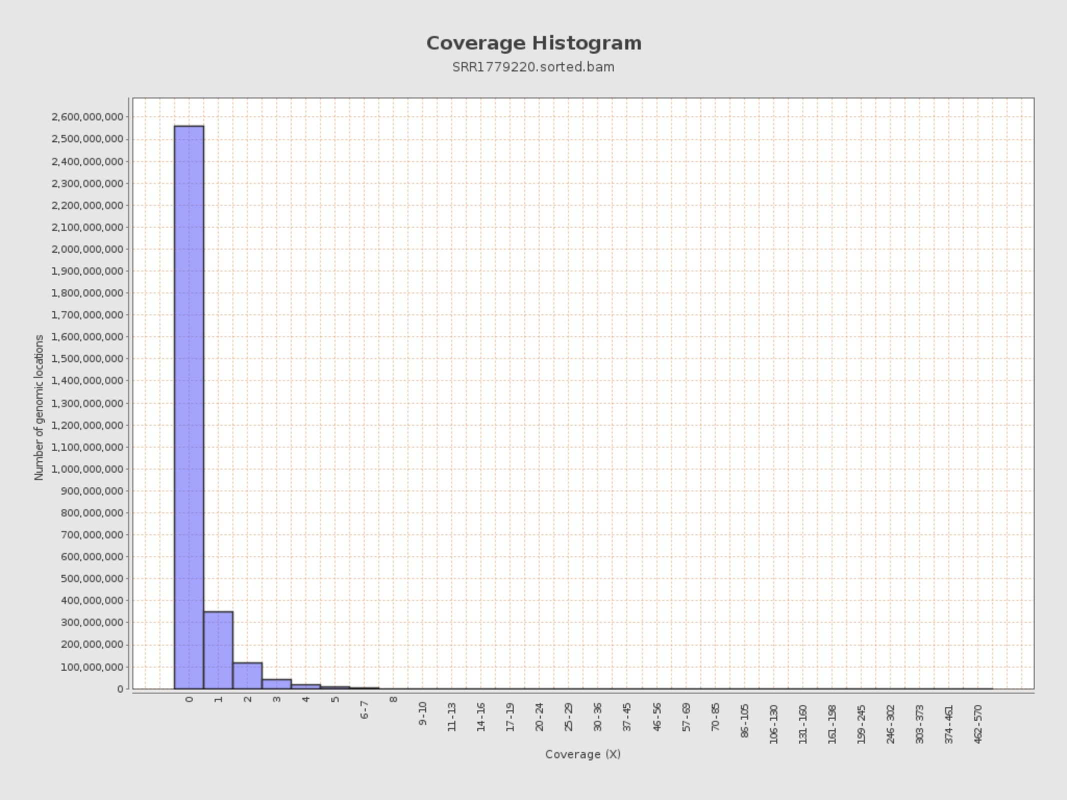
		bases	**coverage**	**deviation**
chr1	249250621	60728555	0.2436	0.8036
chr2	243199373	73931368	0.304	0.7922
chr3	198022430	82710648	0.4177	0.9335
chr4	191154276	51347606	0.2686	0.722
chr5	180915260	38127519	0.2107	0.6271
chr6	171115067	67884360	0.3967	0.9174
chr7	159138663	80873554	0.5082	2.4212
chr8	146364022	65034101	0.4443	0.9584
chr9	141213431	32747678	0.2319	0.7455
chr10	135534747	12382940	0.0914	0.949
chr11	135006516	46236201	0.3425	0.8585
chr12	133851895	44474239	0.3323	0.8147
chr13	115169878	28201042	0.2449	0.6723
chr14	107349540	37924328	0.3533	0.8605
chr15	102531392	21286701	0.2076	0.6382
chr16	90354753	22565209	0.2497	0.7115
chr17	81195210	14282699	0.1759	0.5853
chr18	78077248	23150024	0.2965	0.8059
chr19	59128983	10909099	0.1845	0.7211
chr20	63025520	25898822	0.4109	0.9751
chr21	48129895	8680590	0.1804	0.6011
chr22	51304566	6938964	0.1353	0.4873
chrMT	16571	2416	0.1458	0.4173
chrX	155270560	20056709	0.1292	0.5212

chrY	59373566	467869	0.0079	0.1432

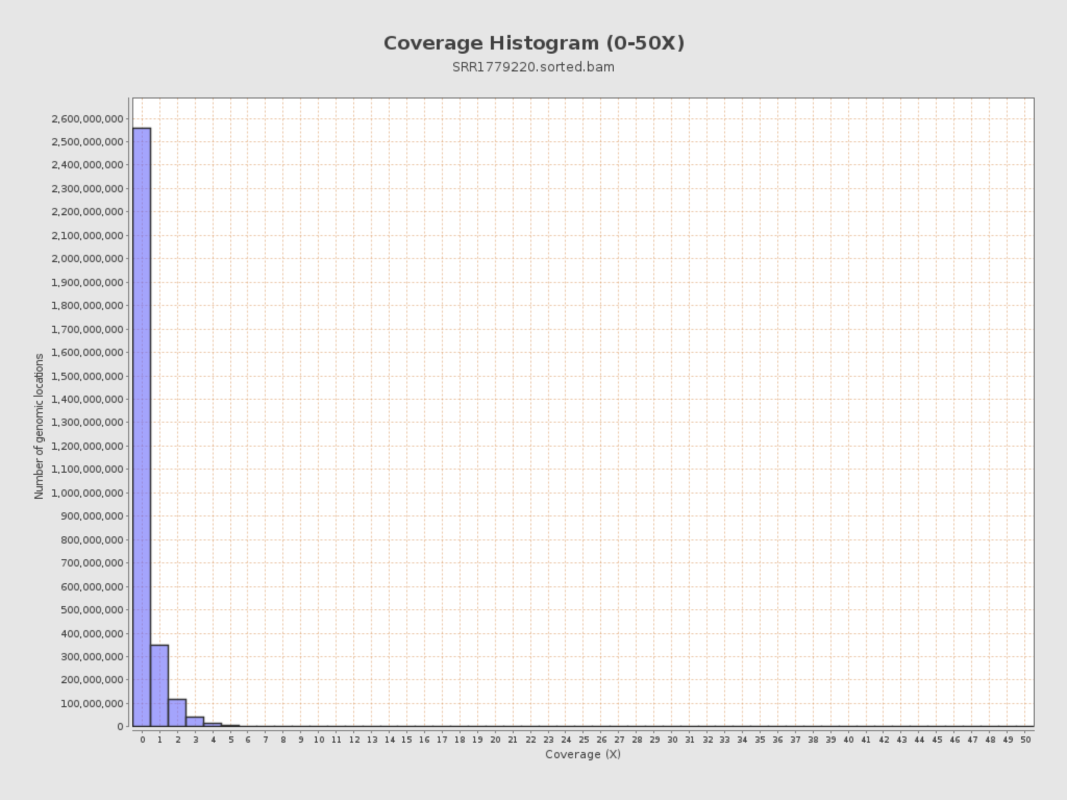
3. Results : Coverage across reference



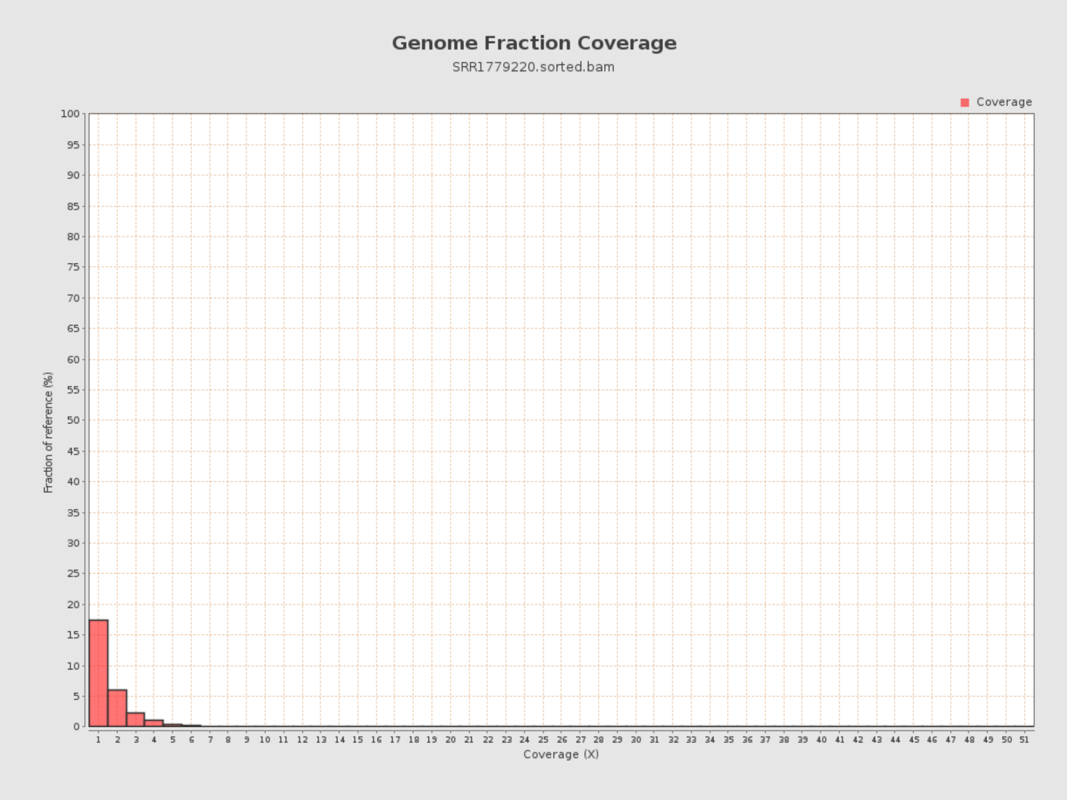
4. Results : Coverage Histogram



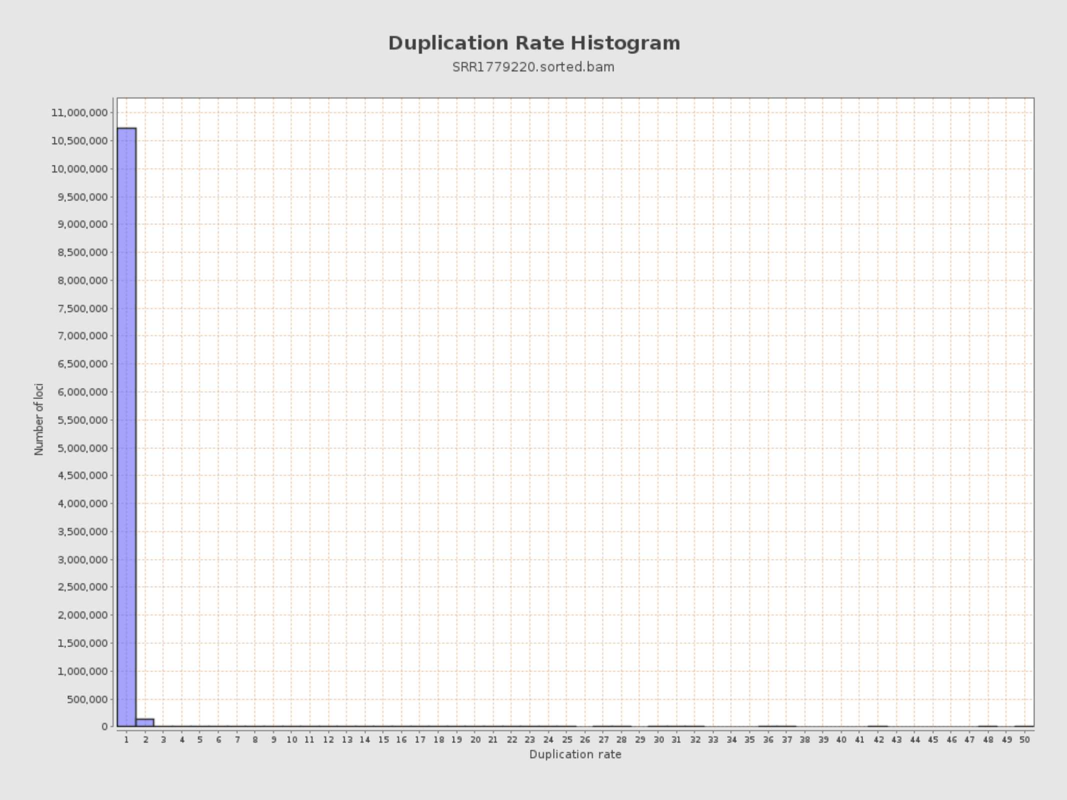
5. Results : Coverage Histogram (0-50X)



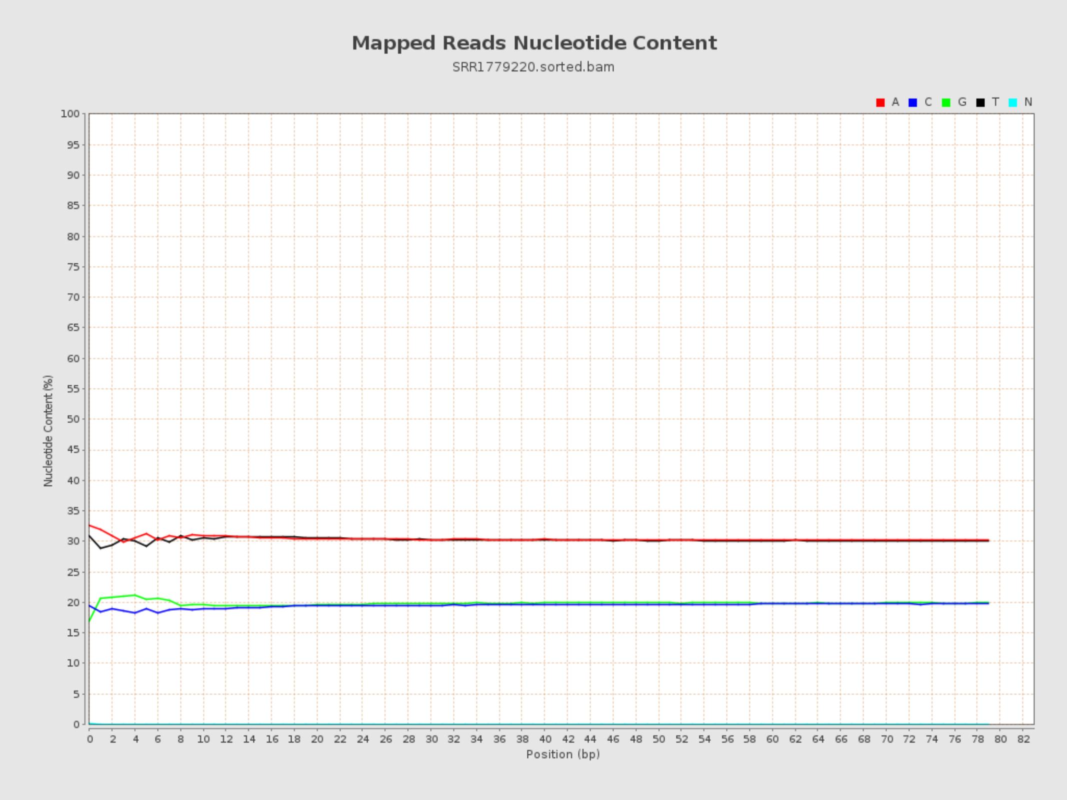
6. Results : Genome Fraction Coverage



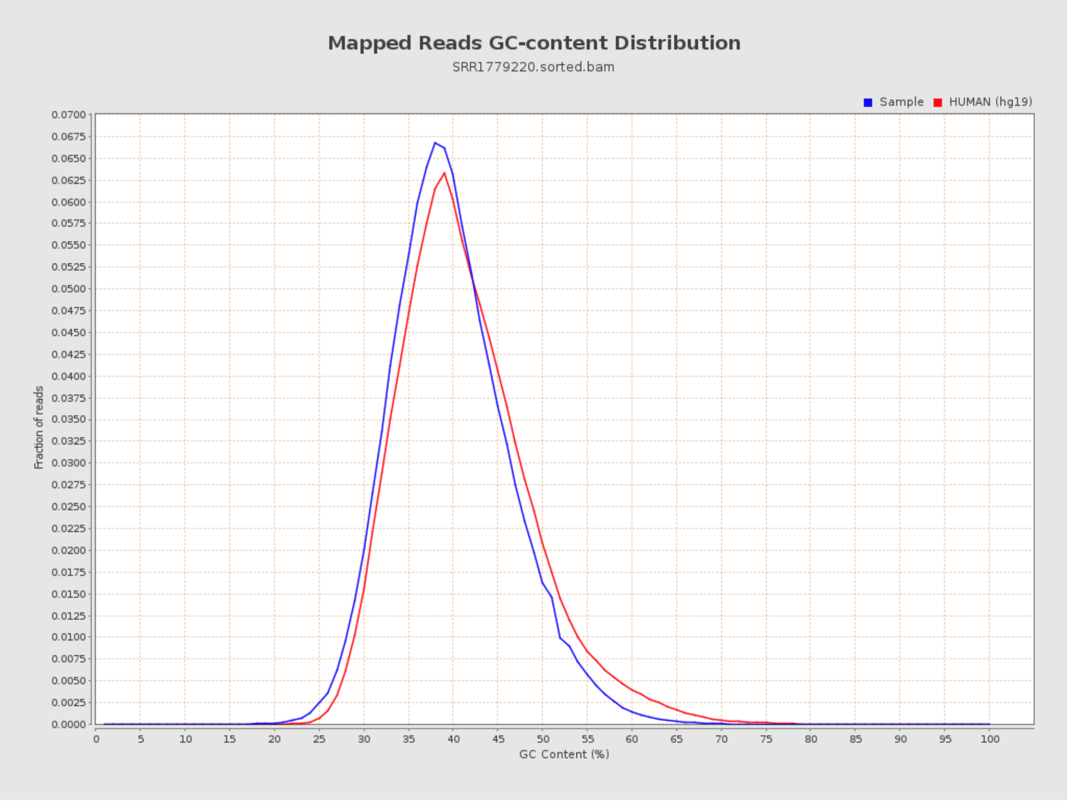
7. Results : Duplication Rate Histogram



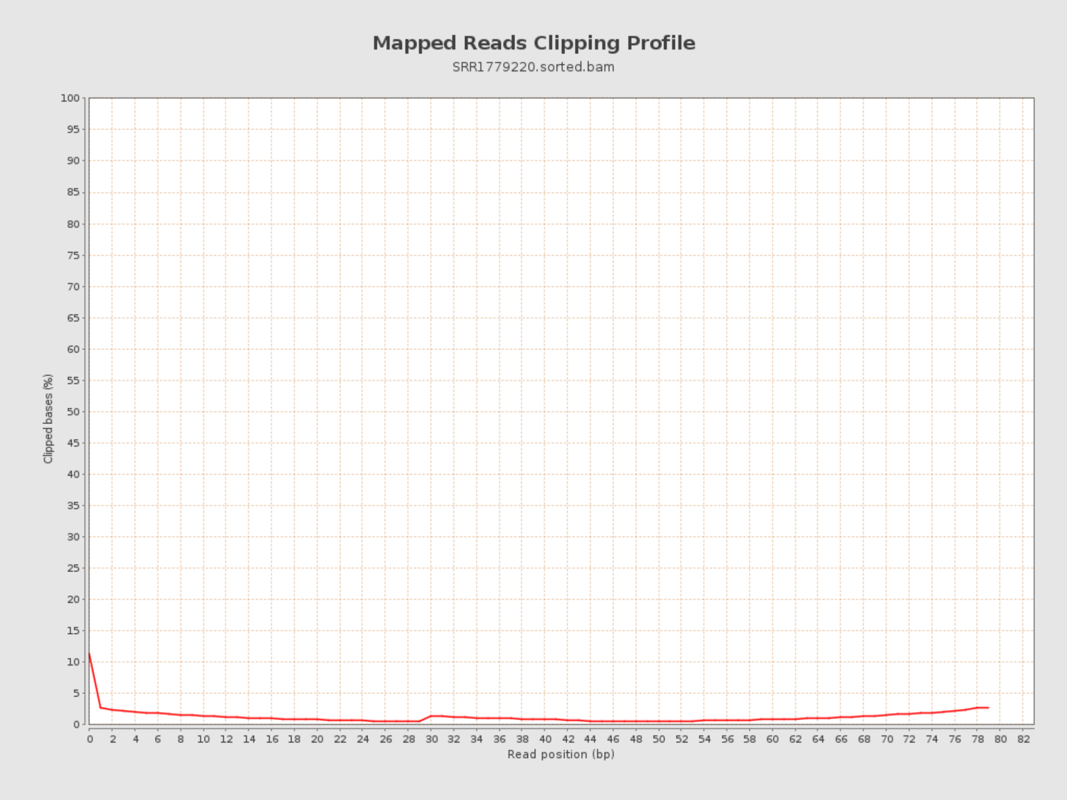
8. Results : Mapped Reads Nucleotide Content



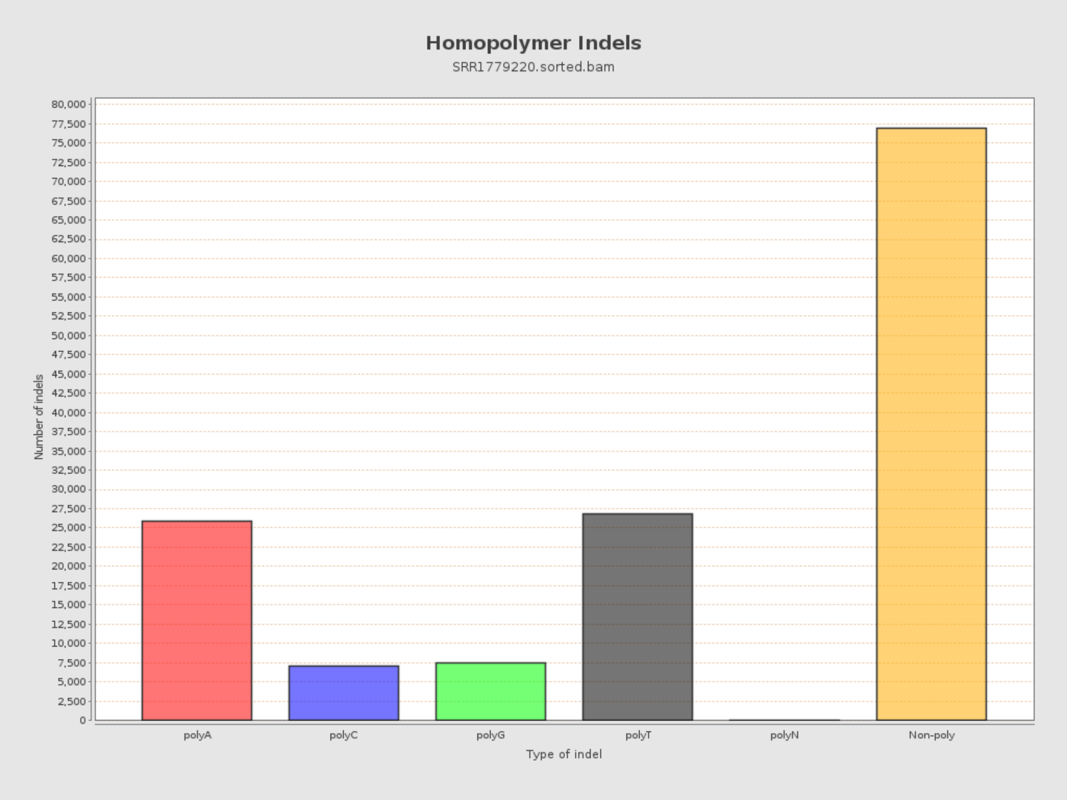
9. Results : Mapped Reads GC-content Distribution



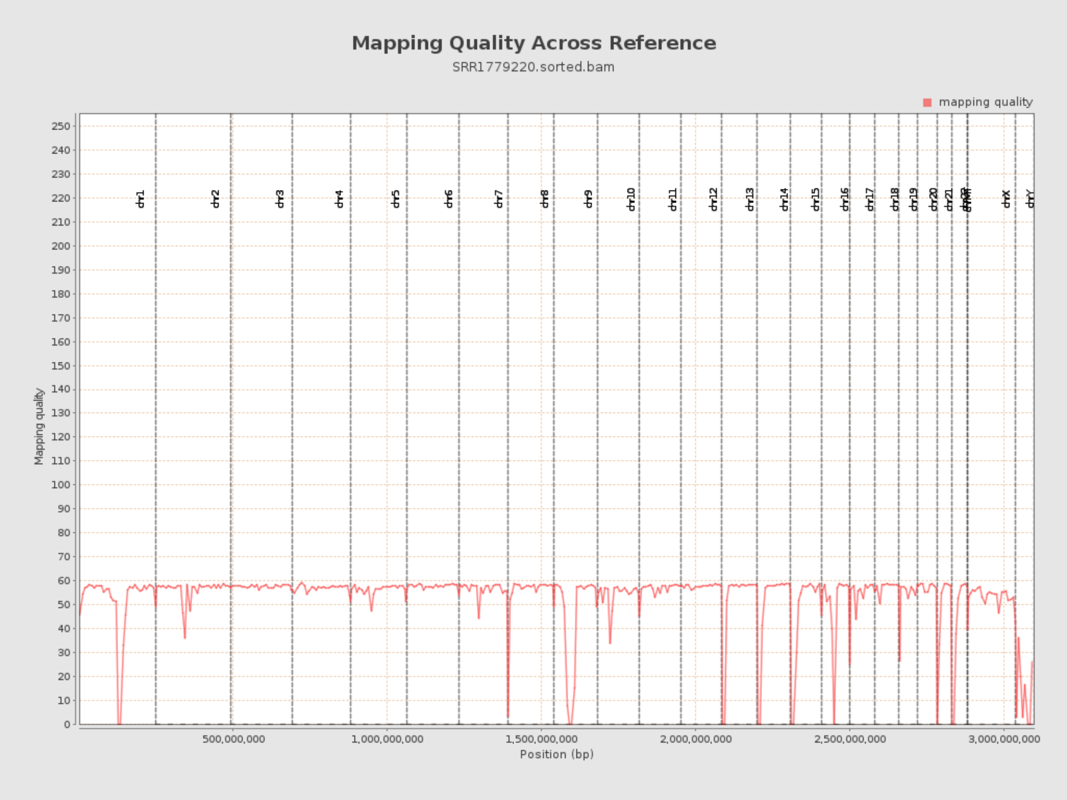
10. Results : Mapped Reads Clipping Profile



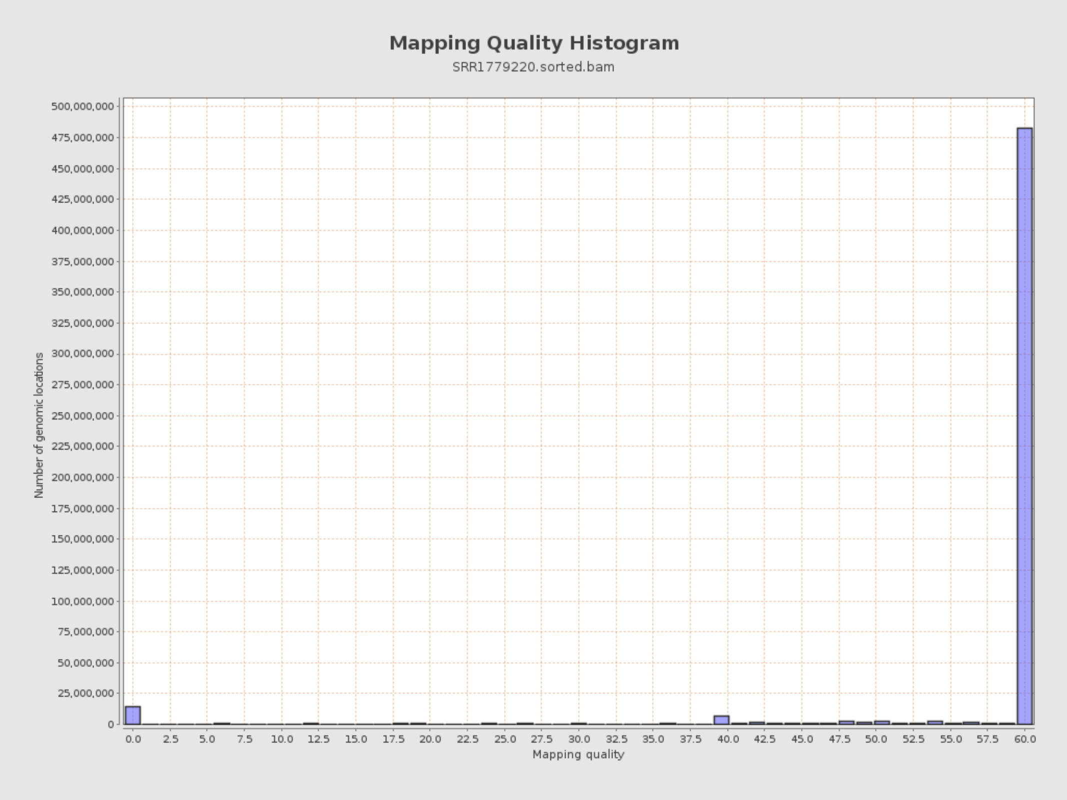
11. Results : Homopolymer Indels



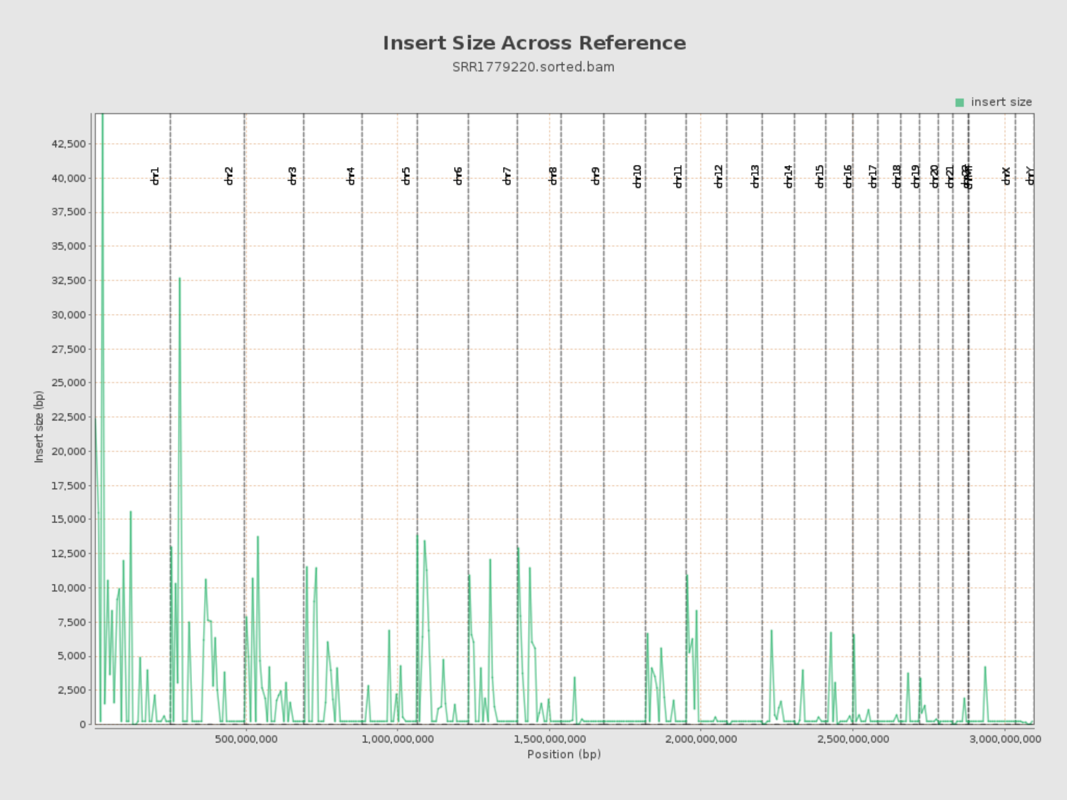
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram