Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 23:15:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779413.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_SRR1779413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779413_1.fastq.gz SRR1779413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 23:15:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,624,788
Mapped reads	17,119,559 / 97.13%
Unmapped reads	505,229 / 2.87%
Mapped paired reads	17,119,559 / 97.13%
Mapped reads, first in pair	8,618,415 / 48.9%
Mapped reads, second in pair	8,501,144 / 48.23%
Mapped reads, both in pair	16,970,576 / 96.29%
Mapped reads, singletons	148,983 / 0.85%
Secondary alignments	0
Supplementary alignments	73,599 / 0.42%
Read min/max/mean length	30 / 80 / 80.15
Duplicated reads (estimated)	749,708 / 4.25%
Duplication rate	3.69%
Clipped reads	711,995 / 4.04%

2.2. ACGT Content

Number/percentage of A's	414,060,461 / 30.42%
Number/percentage of C's	266,660,917 / 19.59%
Number/percentage of T's	406,582,049 / 29.87%
Number/percentage of G's	273,544,130 / 20.1%
Number/percentage of N's	303,314 / 0.02%

GC Percentage	39.69%

2.3. Coverage

Mean	0.4398
Standard Deviation	2.0911

2.4. Mapping Quality

Mean Mapping Quality	53.24

2.5. Insert size

Mean	121,567.35
Standard Deviation	3,278,501.6
P25/Median/P75	156 / 199 / 250

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,654,624
Insertions	123,911
Mapped reads with at least one insertion	0.72%
Deletions	140,223
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.1%

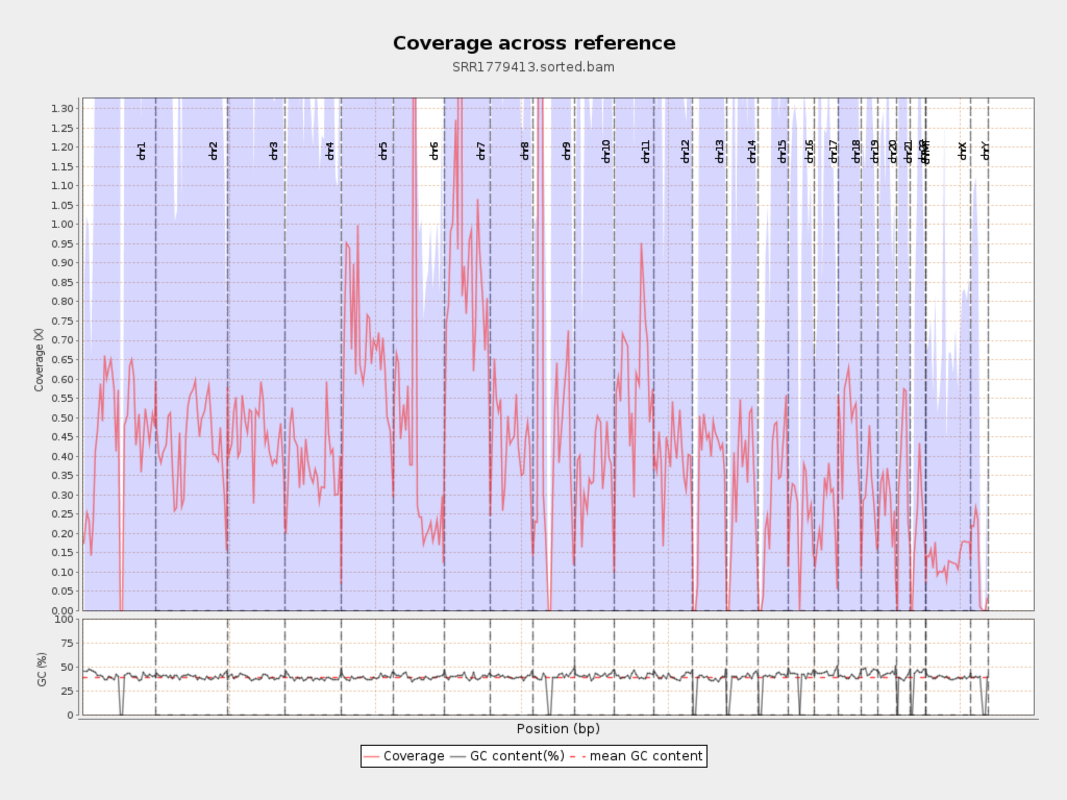
2.7. Chromosome stats

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

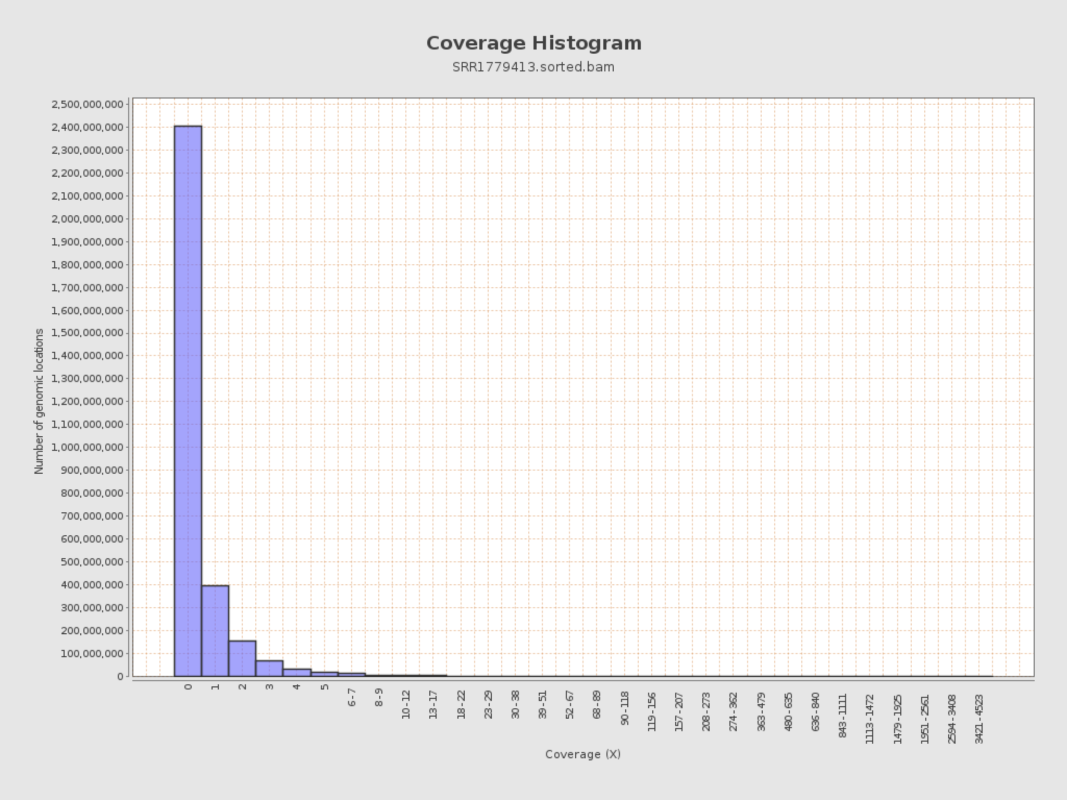
		bases	coverage	deviation
chr1	249250621	110367638	0.4428	4.6476
chr2	243199373	106084926	0.4362	1.0882
chr3	198022430	90519996	0.4571	1.0438
chr4	191154276	72954450	0.3817	0.9506
chr5	180915260	121265170	0.6703	1.3098
chr6	171115067	72304719	0.4226	1.4865
chr7	159138663	171908891	1.0802	4.9739
chr8	146364022	63760009	0.4356	1.0427
chr9	141213431	89406691	0.6331	2.2769
chr10	135534747	48628456	0.3588	1.5311
chr11	135006516	82306656	0.6096	1.3667
chr12	133851895	52966570	0.3957	1.0109
chr13	115169878	42030569	0.3649	0.928
chr14	107349540	35365098	0.3294	0.9327
chr15	102531392	30470599	0.2972	0.8517
chr16	90354753	22247328	0.2462	0.7699
chr17	81195210	19676910	0.2423	0.9184
chr18	78077248	38225784	0.4896	1.4754
chr19	59128983	17835761	0.3016	2.5361
chr20	63025520	17321964	0.2748	0.8257
chr21	48129895	16944505	0.3521	1.0045
chr22	51304566	11013609	0.2147	0.7369
chrMT	16571	1200	0.0724	0.3927
chrX	155270560	20758639	0.1337	0.5825

chrY	59373566	7074035	0.1191	0.5557

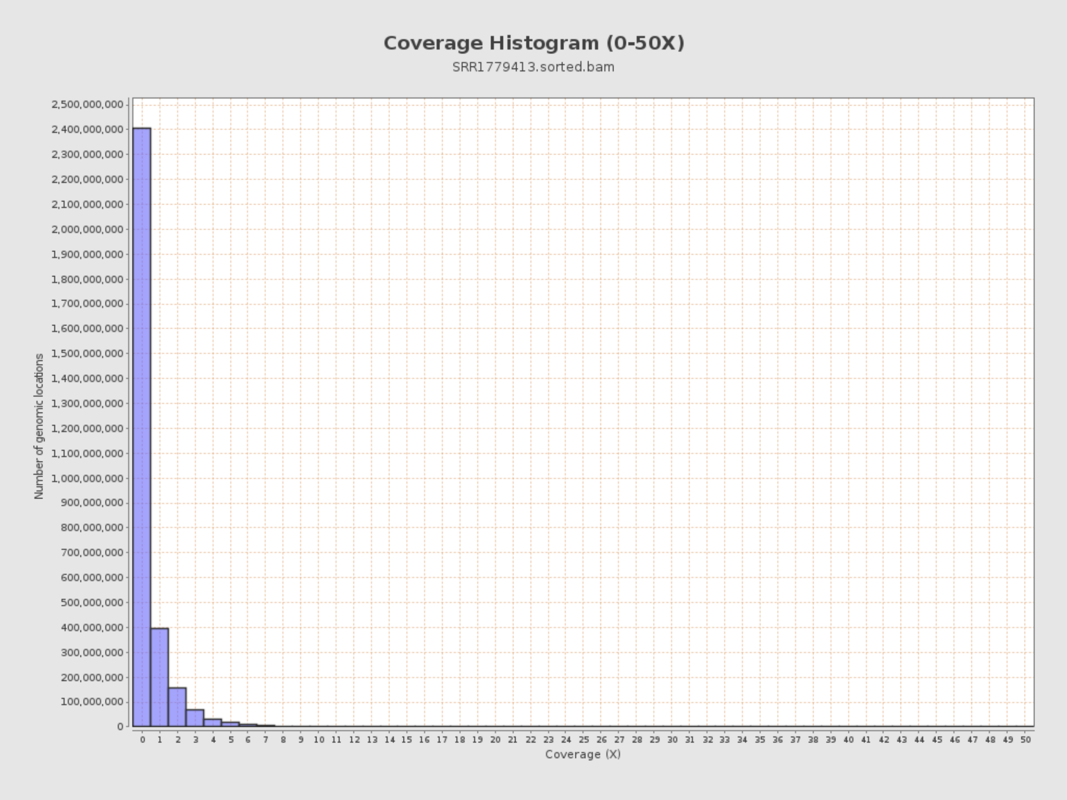
3. Results : Coverage across reference



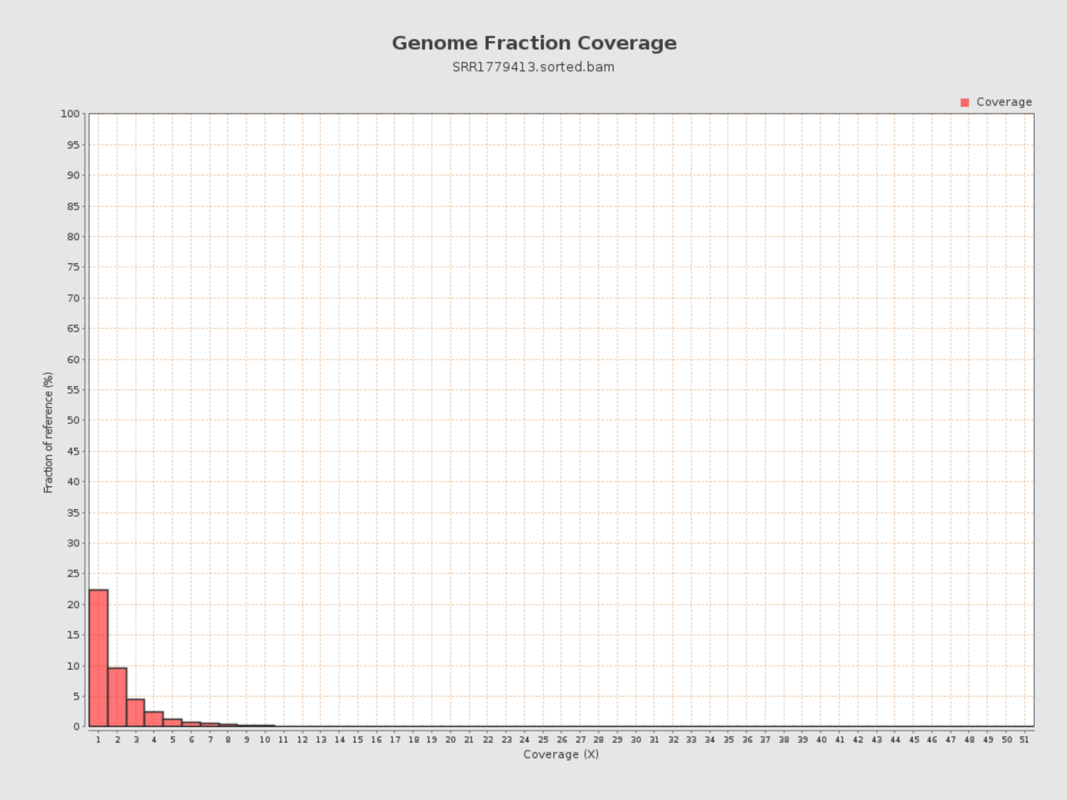
4. Results : Coverage Histogram



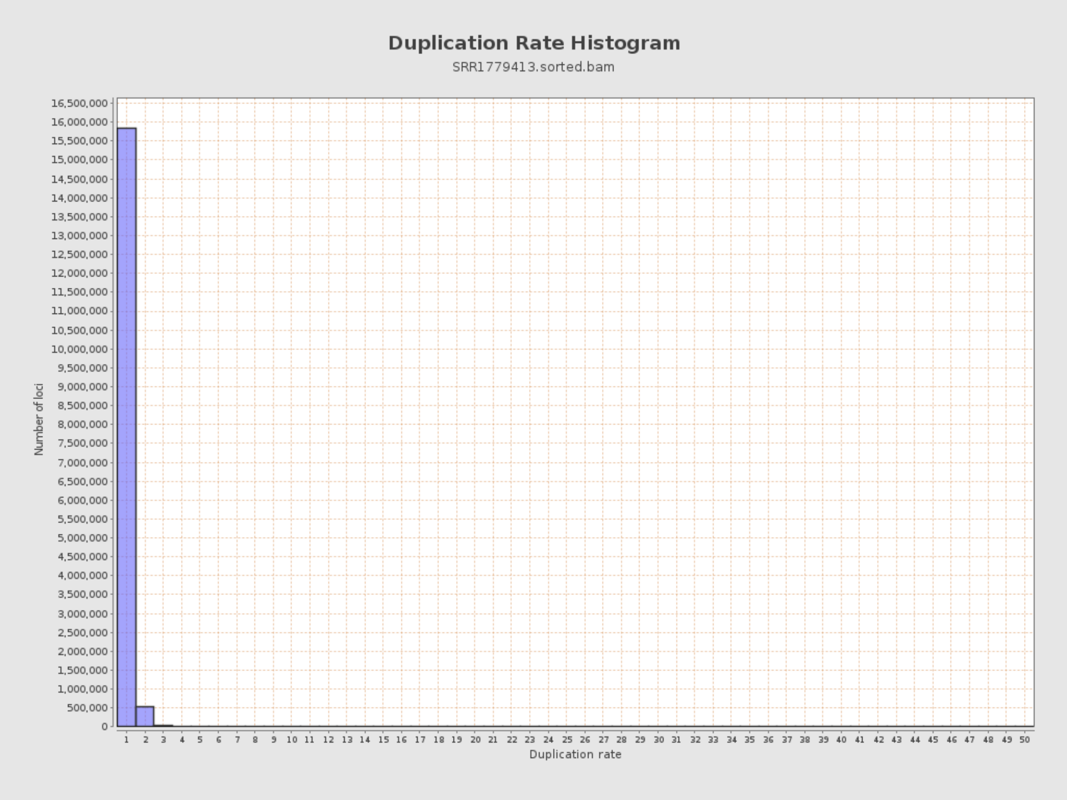
5. Results : Coverage Histogram (0-50X)



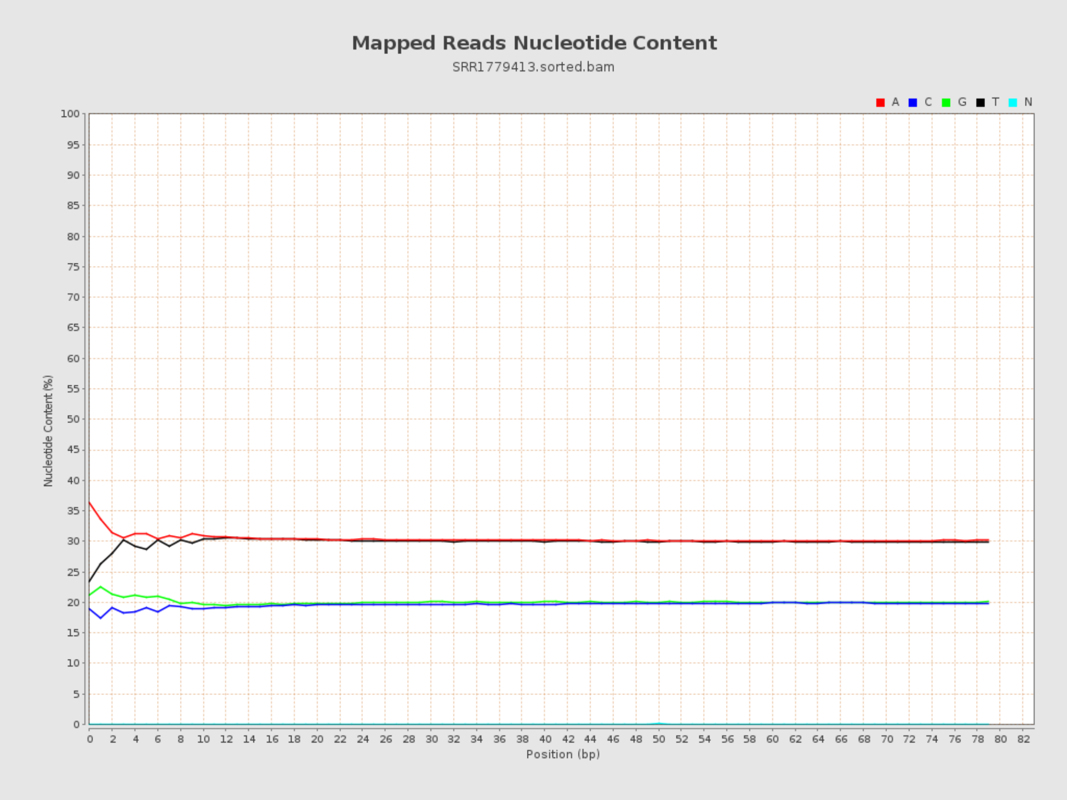
6. Results : Genome Fraction Coverage



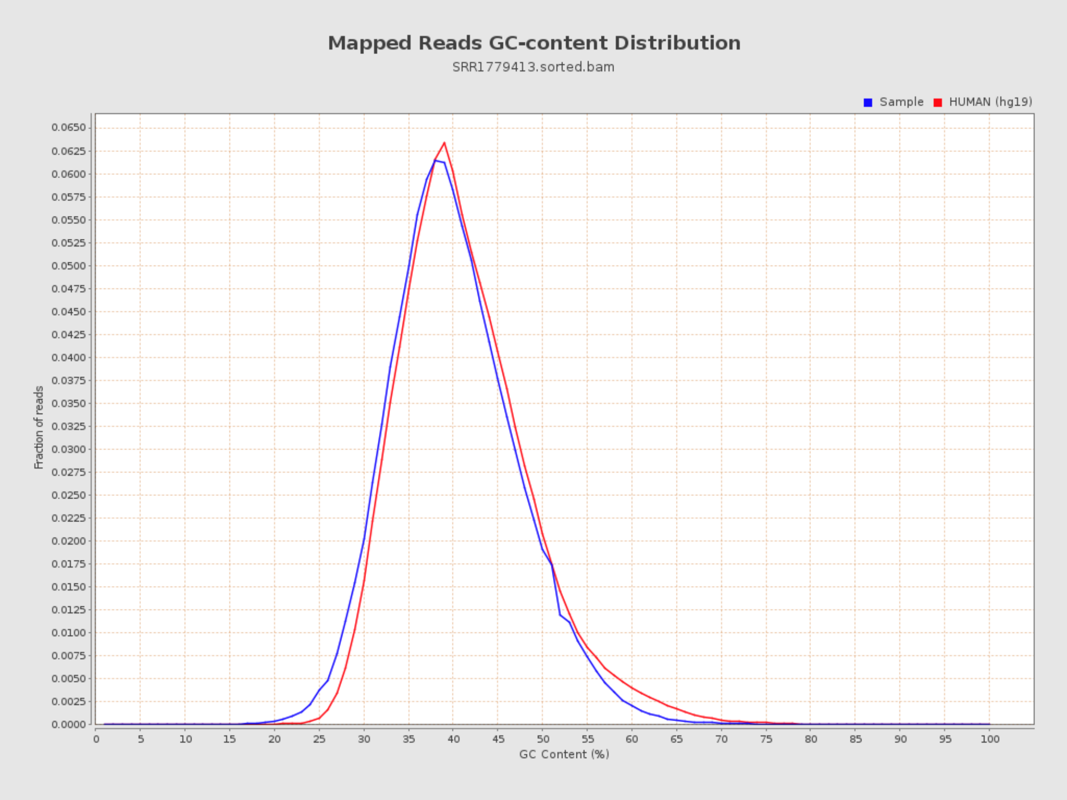
7. Results : Duplication Rate Histogram



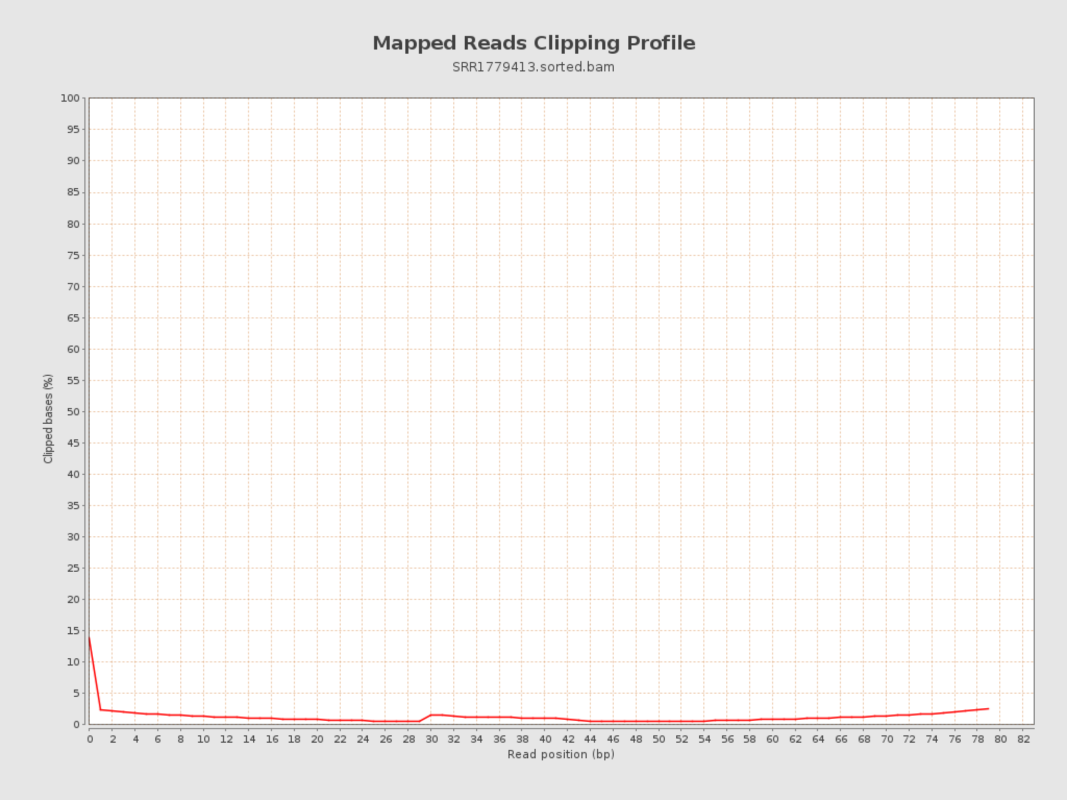
8. Results : Mapped Reads Nucleotide Content



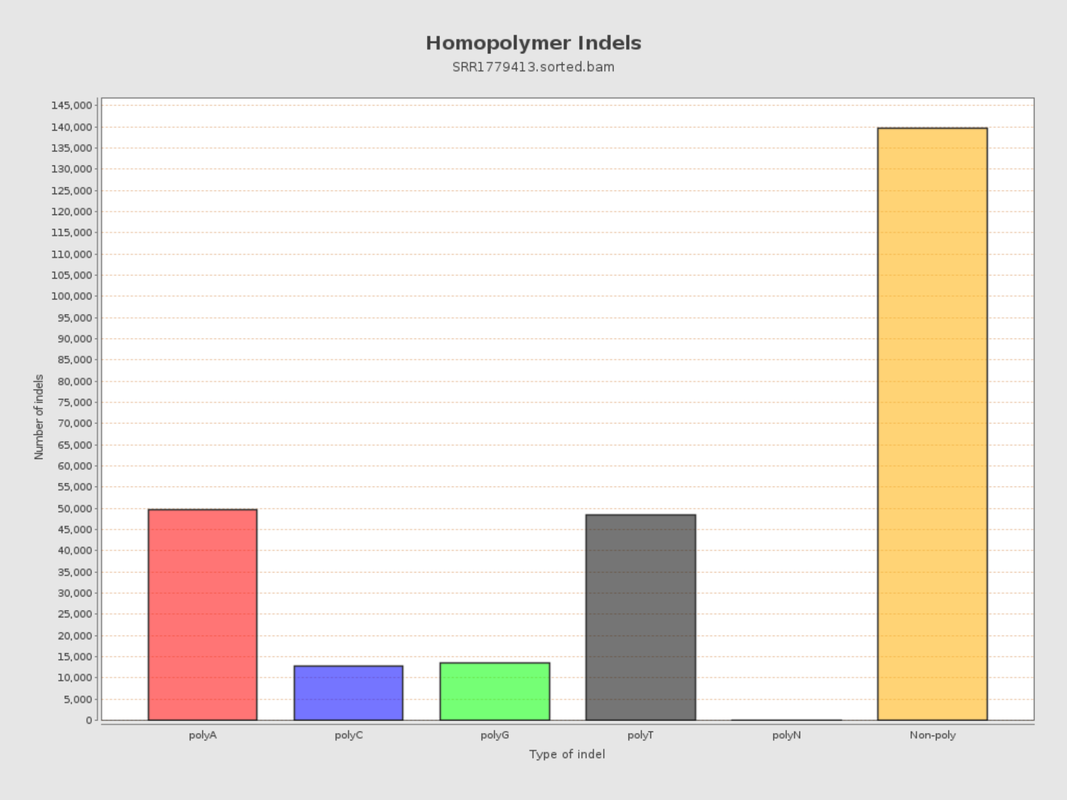
9. Results : Mapped Reads GC-content Distribution



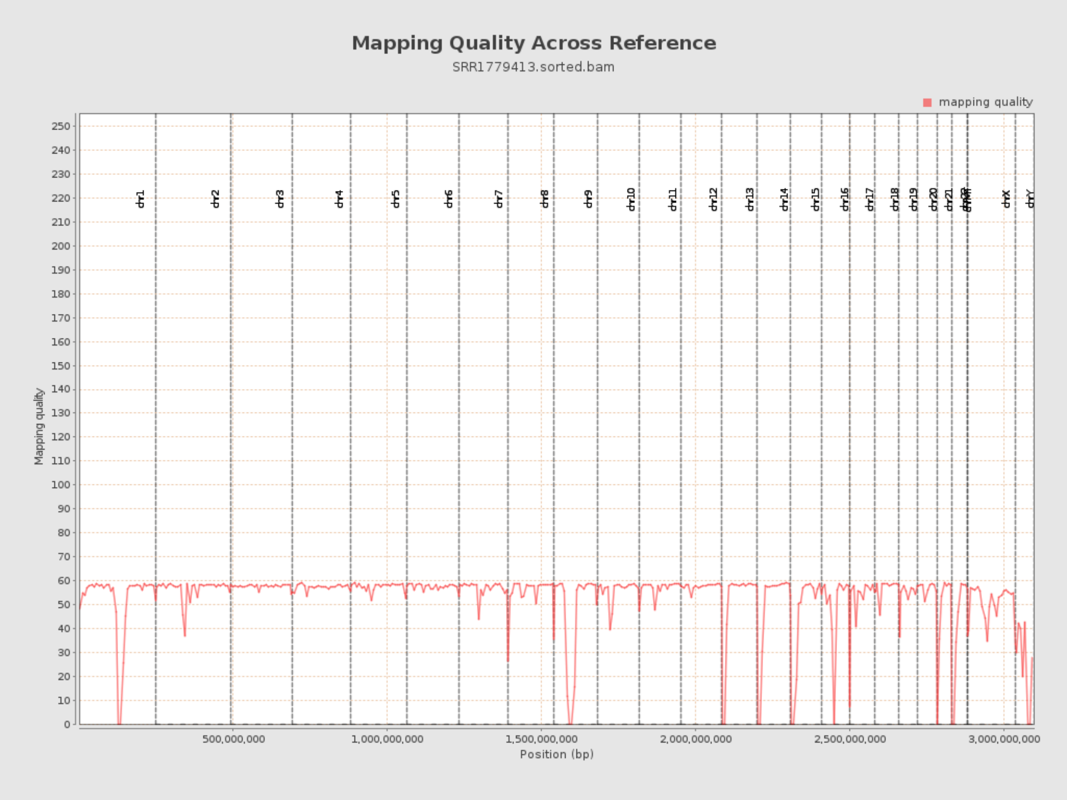
10. Results : Mapped Reads Clipping Profile



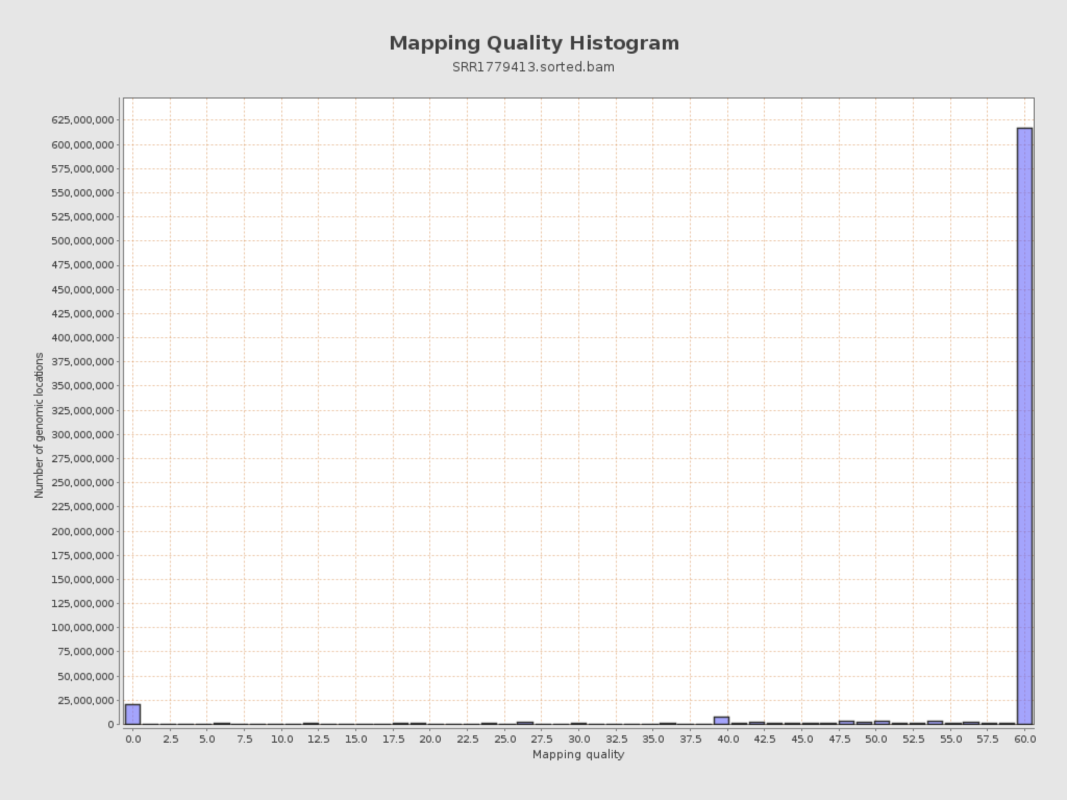
11. Results : Homopolymer Indels



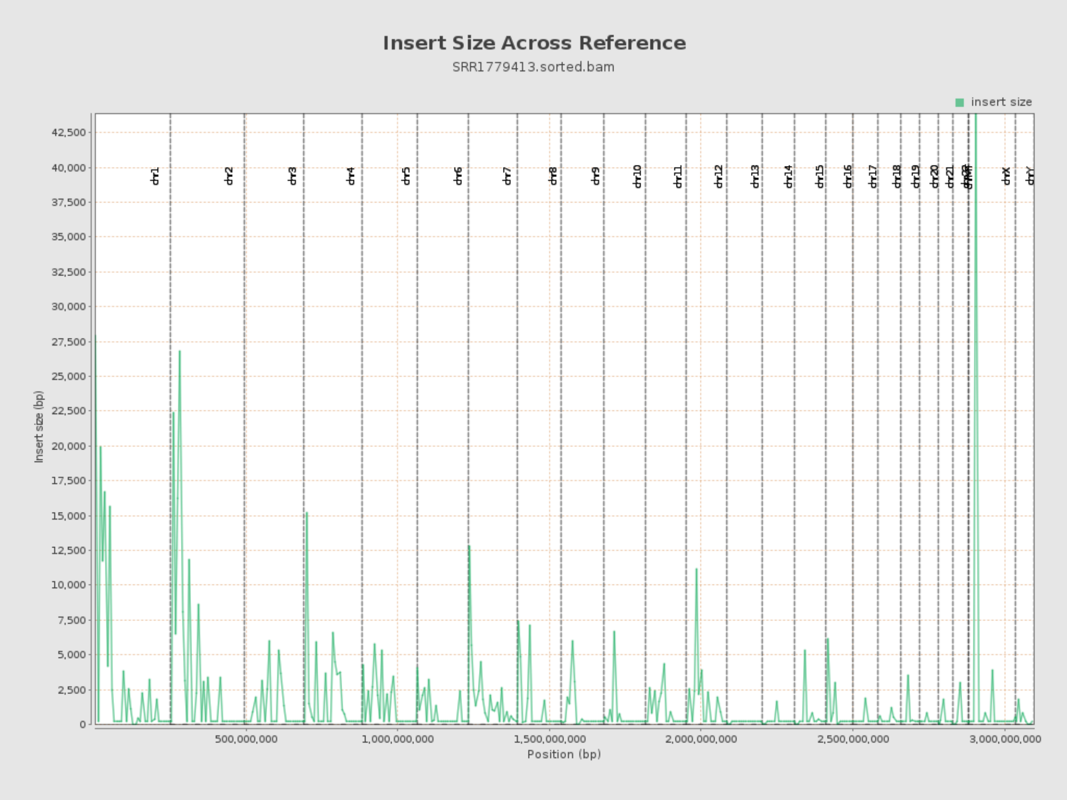
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram