Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 12:49:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779370.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_SRR1779370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779370_1.fastq.gz SRR1779370_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 12:49:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,477,826
Mapped reads	16,018,077 / 97.21%
Unmapped reads	459,749 / 2.79%
Mapped paired reads	16,018,077 / 97.21%
Mapped reads, first in pair	8,040,254 / 48.79%
Mapped reads, second in pair	7,977,823 / 48.42%
Mapped reads, both in pair	15,922,560 / 96.63%
Mapped reads, singletons	95,517 / 0.58%
Secondary alignments	0
Supplementary alignments	89,609 / 0.54%
Read min/max/mean length	30 / 80 / 80.2
Duplicated reads (estimated)	685,445 / 4.16%
Duplication rate	3.74%
Clipped reads	1,112,755 / 6.75%

2.2. ACGT Content

Number/percentage of A's	385,580,494 / 30.37%
Number/percentage of C's	248,656,347 / 19.59%
Number/percentage of T's	382,580,160 / 30.14%
Number/percentage of G's	252,360,728 / 19.88%
Number/percentage of N's	279,993 / 0.02%

GC Percentage	39.47%

2.3. Coverage

Mean	0.4102
Standard Deviation	1.9257

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	62,689.63
Standard Deviation	2,371,055.5
P25/Median/P75	115 / 151 / 195

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	4,122,757
Insertions	141,891
Mapped reads with at least one insertion	0.88%
Deletions	139,672
Mapped reads with at least one deletion	0.86%
Homopolymer indels	47.12%

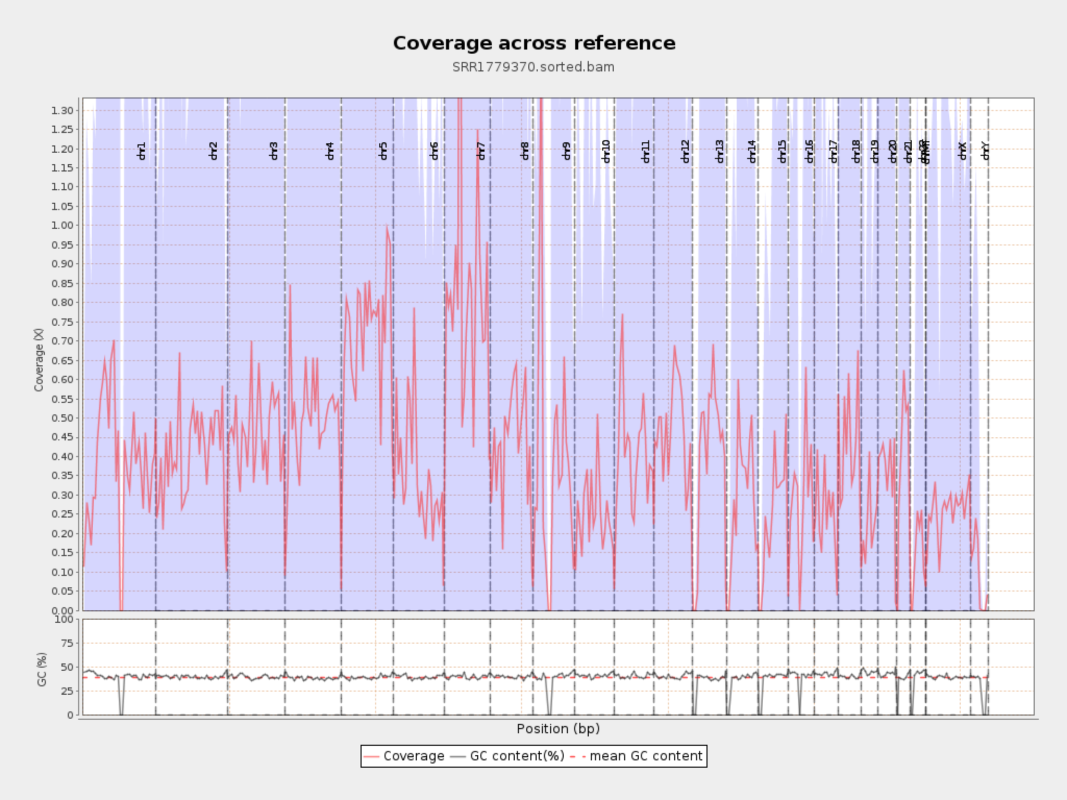
2.7. Chromosome stats

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

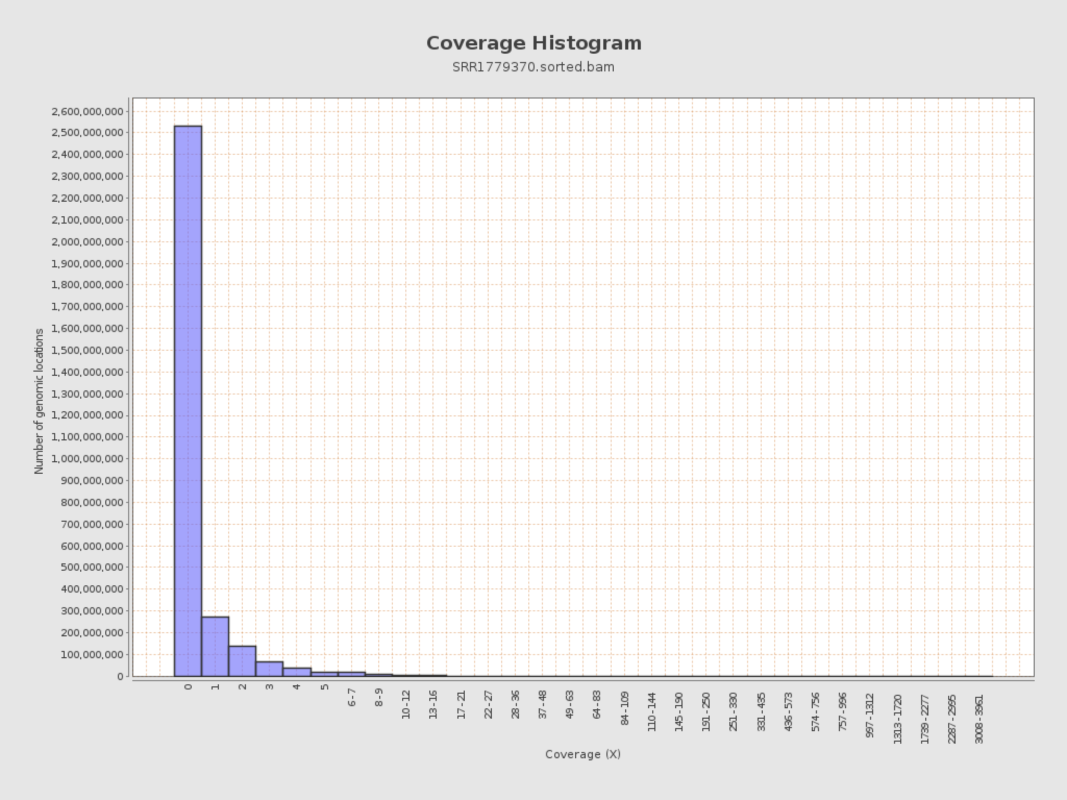
		bases	coverage	deviation
chr1	249250621	94993085	0.3811	4.1239
chr2	243199373	97811079	0.4022	1.2967
chr3	198022430	91695065	0.4631	1.244
chr4	191154276	96187295	0.5032	1.3181
chr5	180915260	128217743	0.7087	1.5242
chr6	171115067	60647207	0.3544	1.5077
chr7	159138663	134117724	0.8428	2.8537
chr8	146364022	64437587	0.4403	1.2637
chr9	141213431	56324336	0.3989	1.805
chr10	135534747	33734659	0.2489	2.8279
chr11	135006516	55999169	0.4148	1.3898
chr12	133851895	62357764	0.4659	1.2671
chr13	115169878	46875052	0.407	1.1557
chr14	107349540	32200231	0.3	1.0223
chr15	102531392	25492121	0.2486	0.8646
chr16	90354753	25210916	0.279	1.0251
chr17	81195210	20699426	0.2549	1.3607
chr18	78077248	33852336	0.4336	2.0049
chr19	59128983	13345327	0.2257	2.8577
chr20	63025520	23479359	0.3725	1.1456
chr21	48129895	18603312	0.3865	1.184
chr22	51304566	7406177	0.1444	0.7152
chrMT	16571	2571	0.1552	0.5046
chrX	155270560	40443888	0.2605	1.0802

chrY	59373566	5615104	0.0946	0.5277

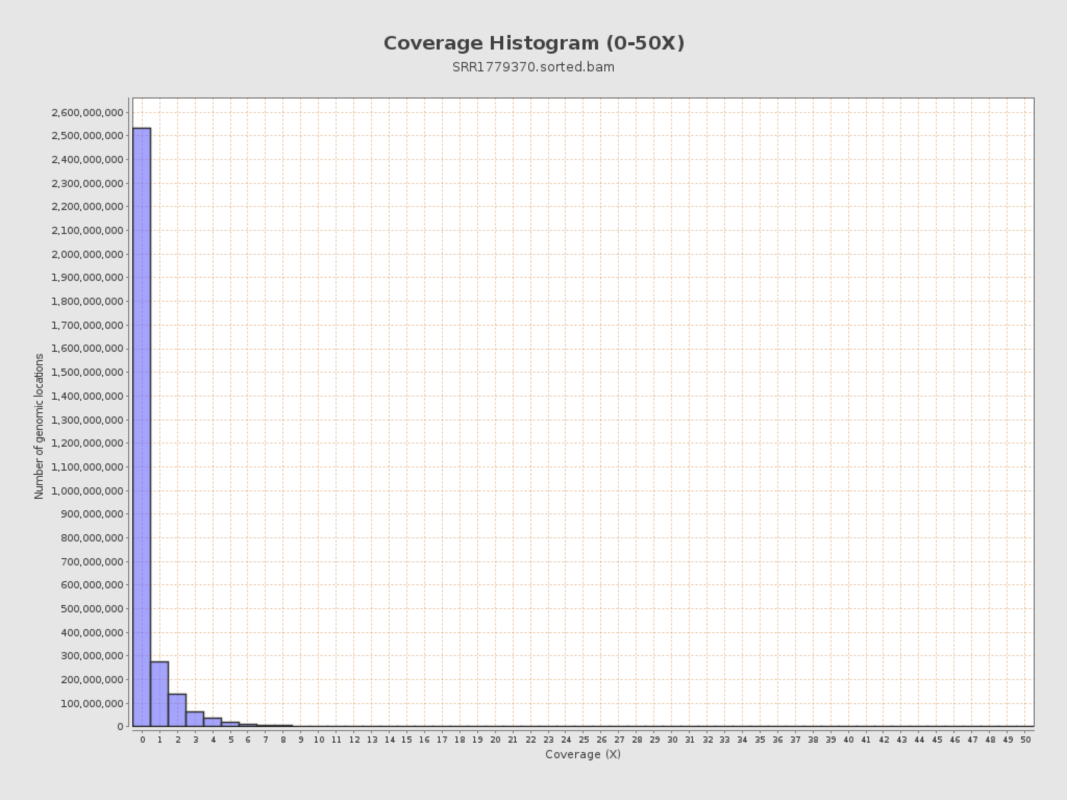
3. Results : Coverage across reference



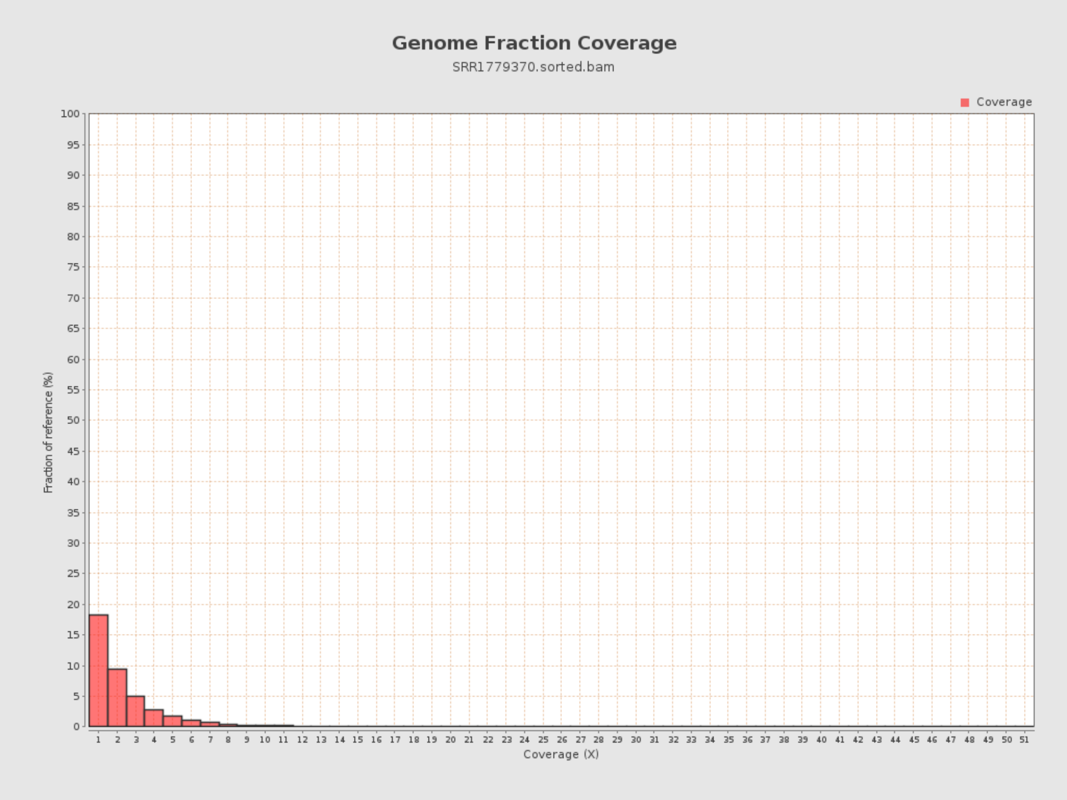
4. Results : Coverage Histogram



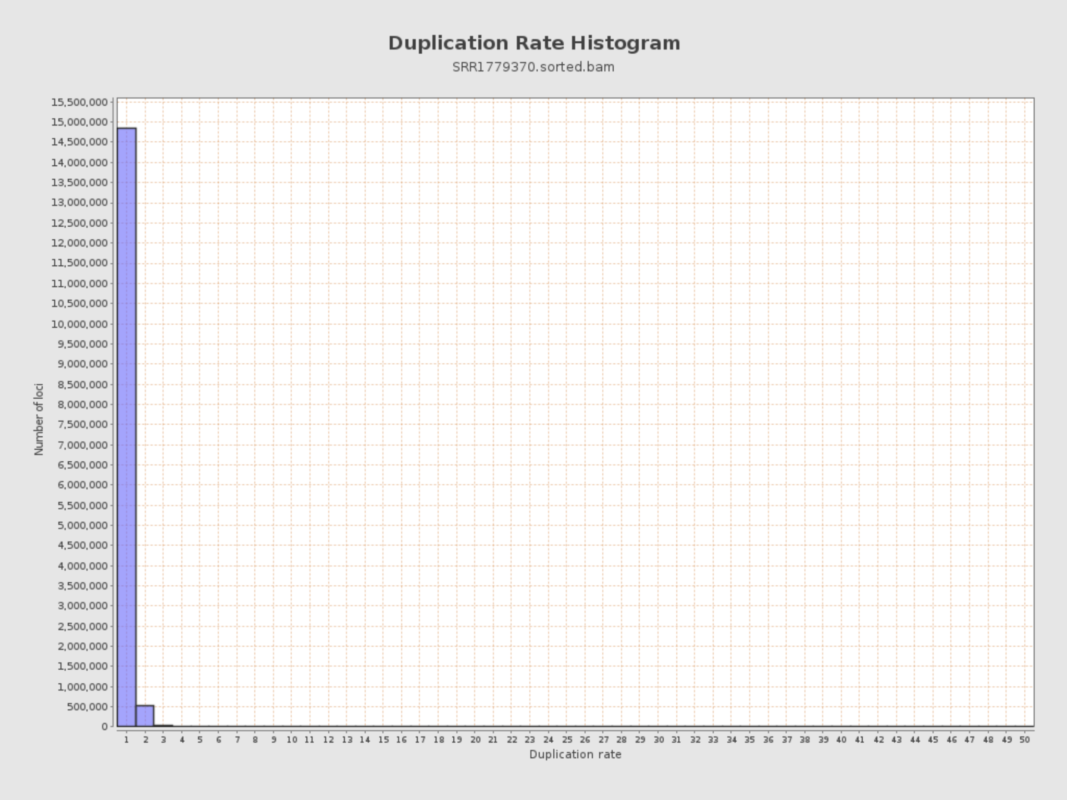
5. Results : Coverage Histogram (0-50X)



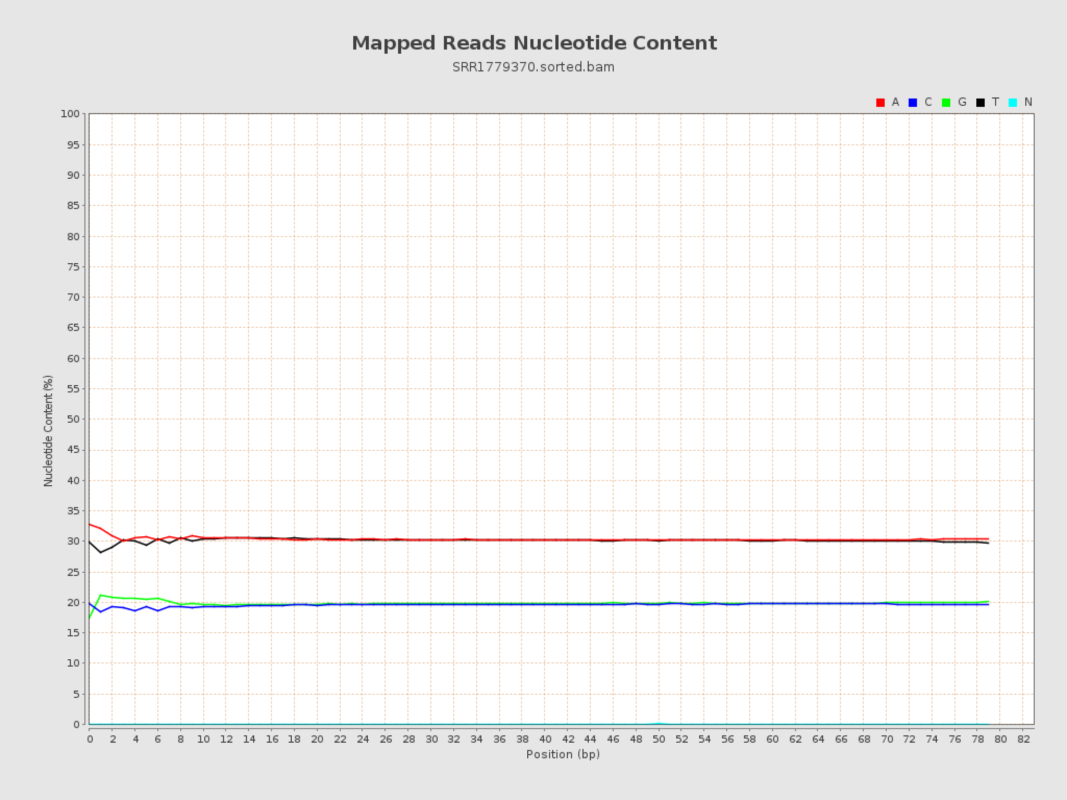
6. Results : Genome Fraction Coverage



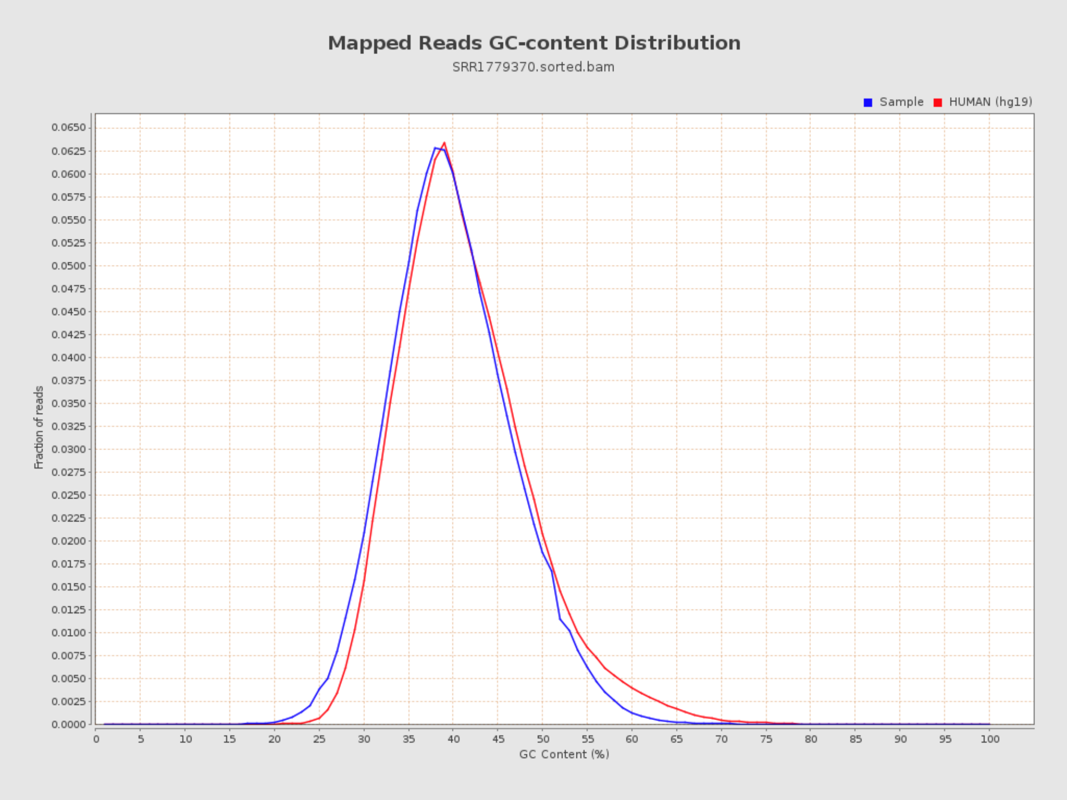
7. Results : Duplication Rate Histogram



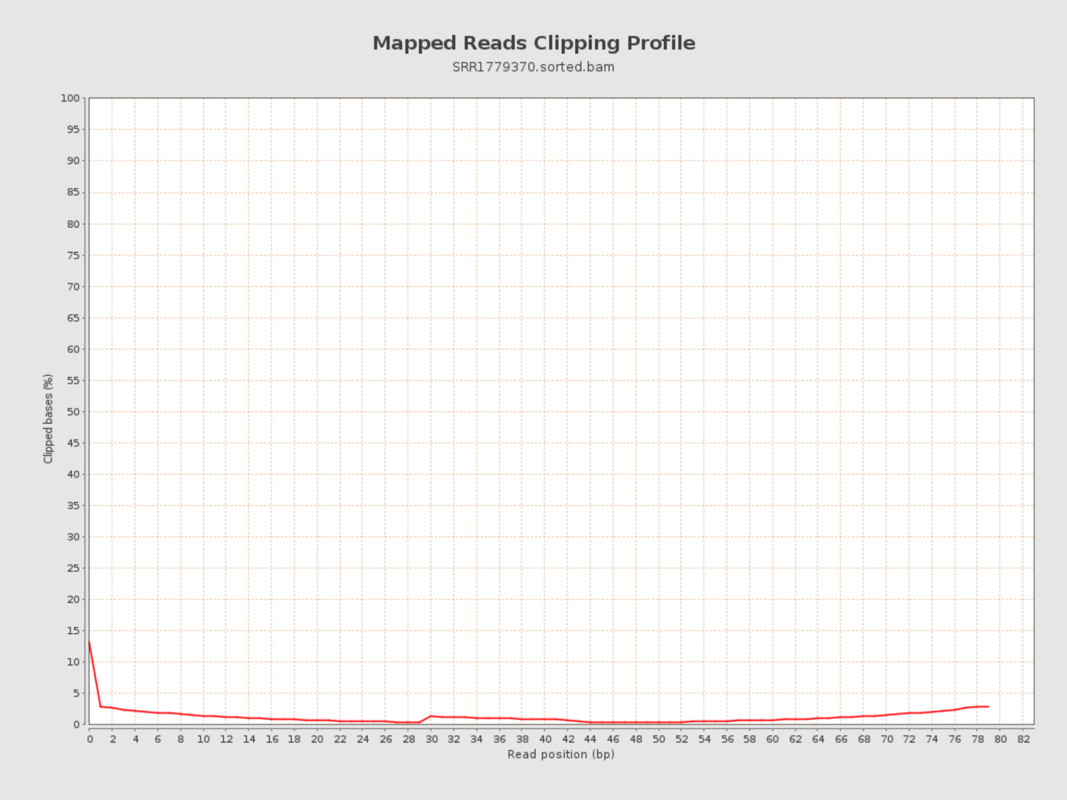
8. Results : Mapped Reads Nucleotide Content



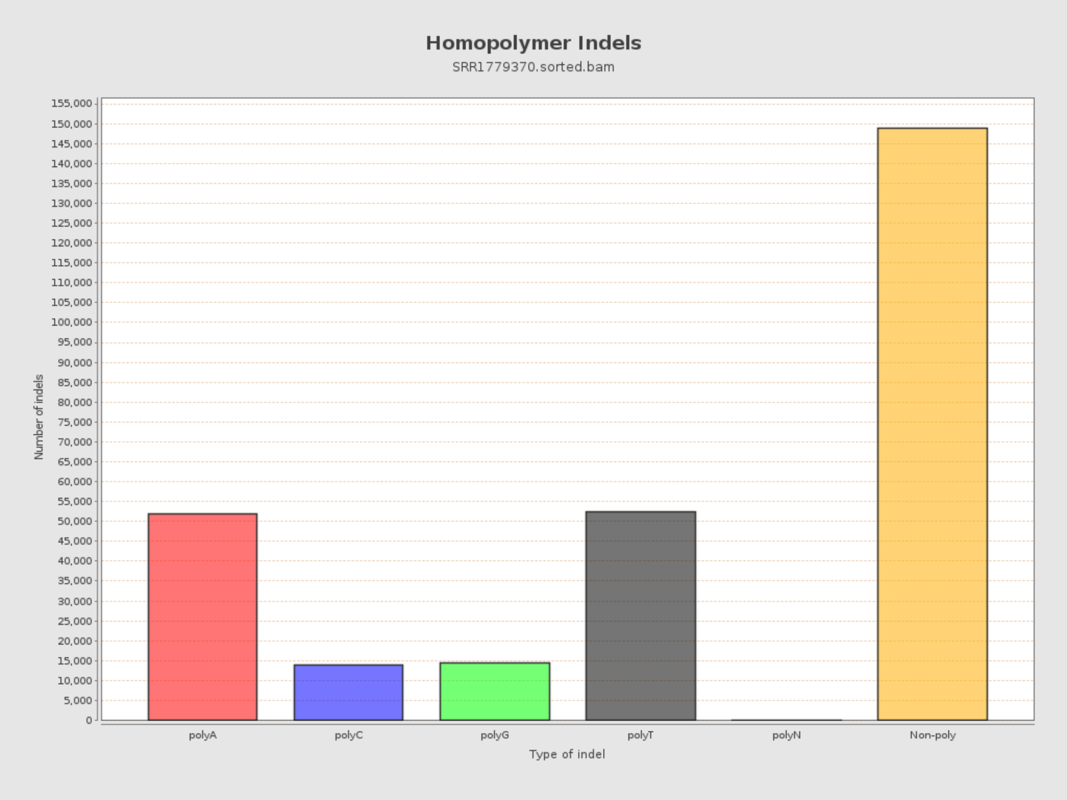
9. Results : Mapped Reads GC-content Distribution



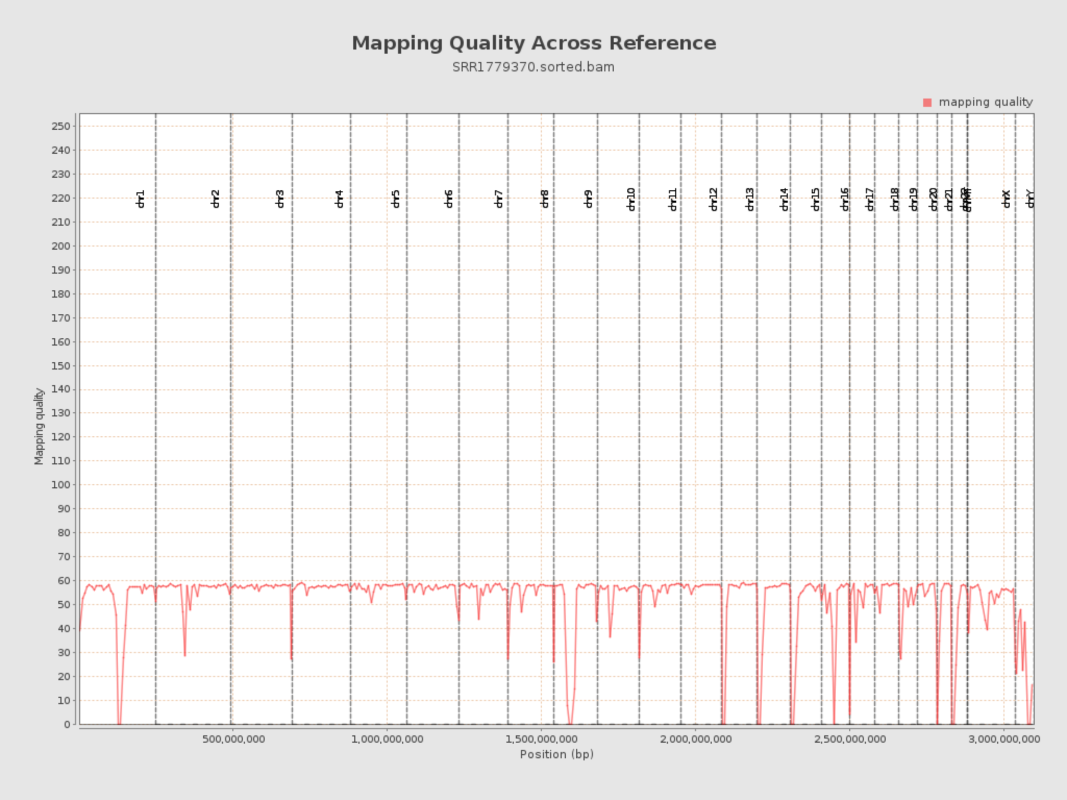
10. Results : Mapped Reads Clipping Profile



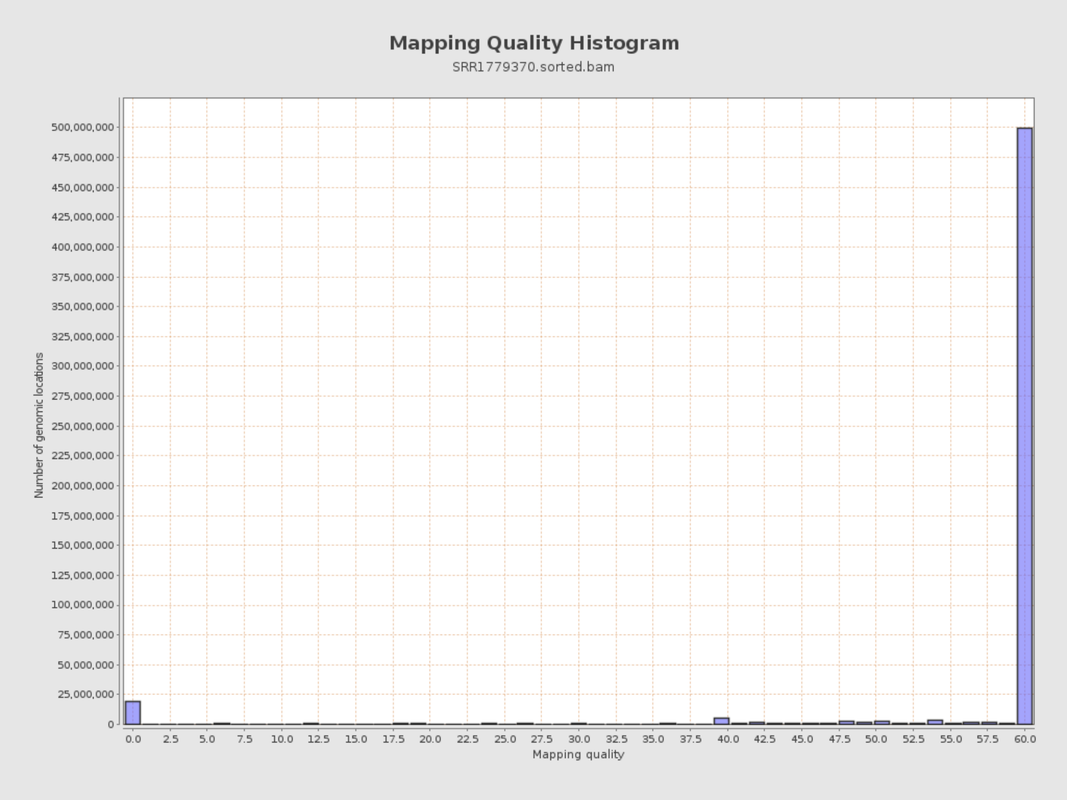
11. Results : Homopolymer Indels



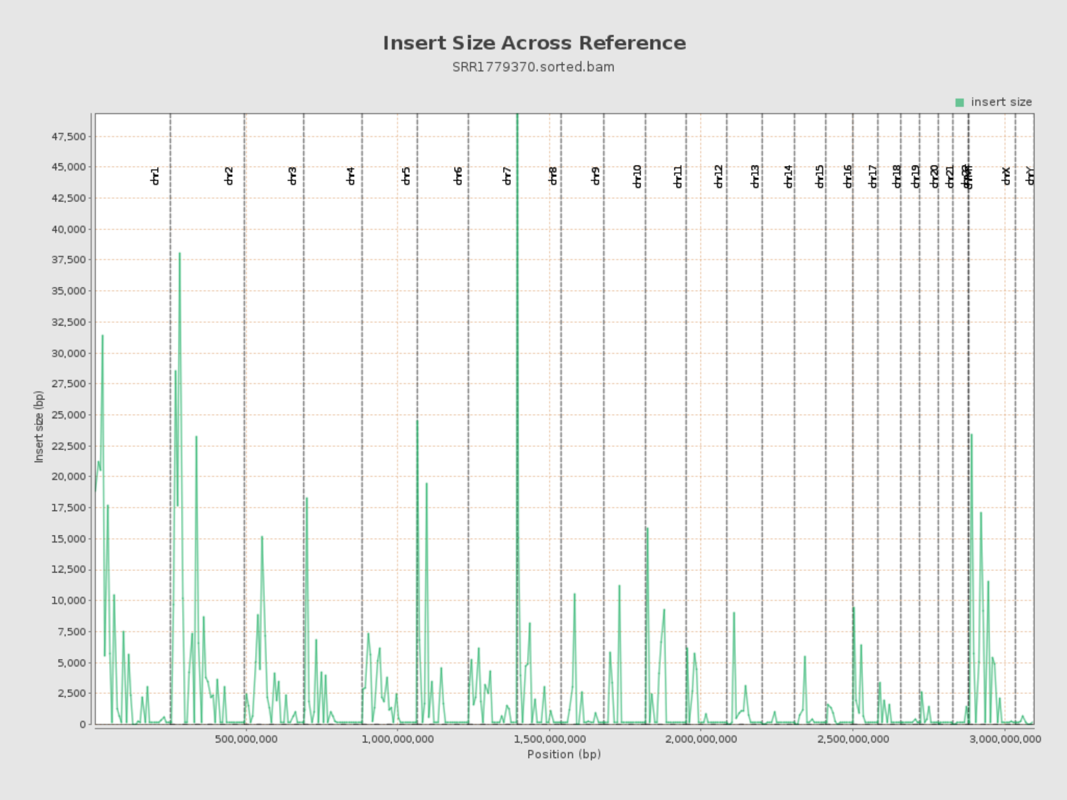
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram