Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 17:08:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779215.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_SRR1779215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779215_1.fastq.gz SRR1779215_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 17:08:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,134,572
Mapped reads	5,892,925 / 96.06%
Unmapped reads	241,647 / 3.94%
Mapped paired reads	5,892,925 / 96.06%
Mapped reads, first in pair	2,987,231 / 48.7%
Mapped reads, second in pair	2,905,694 / 47.37%
Mapped reads, both in pair	5,802,996 / 94.59%
Mapped reads, singletons	89,929 / 1.47%
Secondary alignments	0
Supplementary alignments	13,286 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	39,157 / 0.64%
Duplication rate	0.61%
Clipped reads	204,558 / 3.33%

2.2. ACGT Content

Number/percentage of A's	143,653,105 / 30.65%
Number/percentage of C's	89,901,458 / 19.18%
Number/percentage of T's	143,518,495 / 30.62%
Number/percentage of G's	91,499,575 / 19.52%
Number/percentage of N's	86,226 / 0.02%

GC Percentage	38.71%

2.3. Coverage

Mean	0.1514
Standard Deviation	0.5049

2.4. Mapping Quality

Mean Mapping Quality	52.95

2.5. Insert size

Mean	57,796.55
Standard Deviation	2,277,217.97
P25/Median/P75	200 / 261 / 330

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	2,063,290
Insertions	36,134
Mapped reads with at least one insertion	0.61%
Deletions	45,268
Mapped reads with at least one deletion	0.76%
Homopolymer indels	46.81%

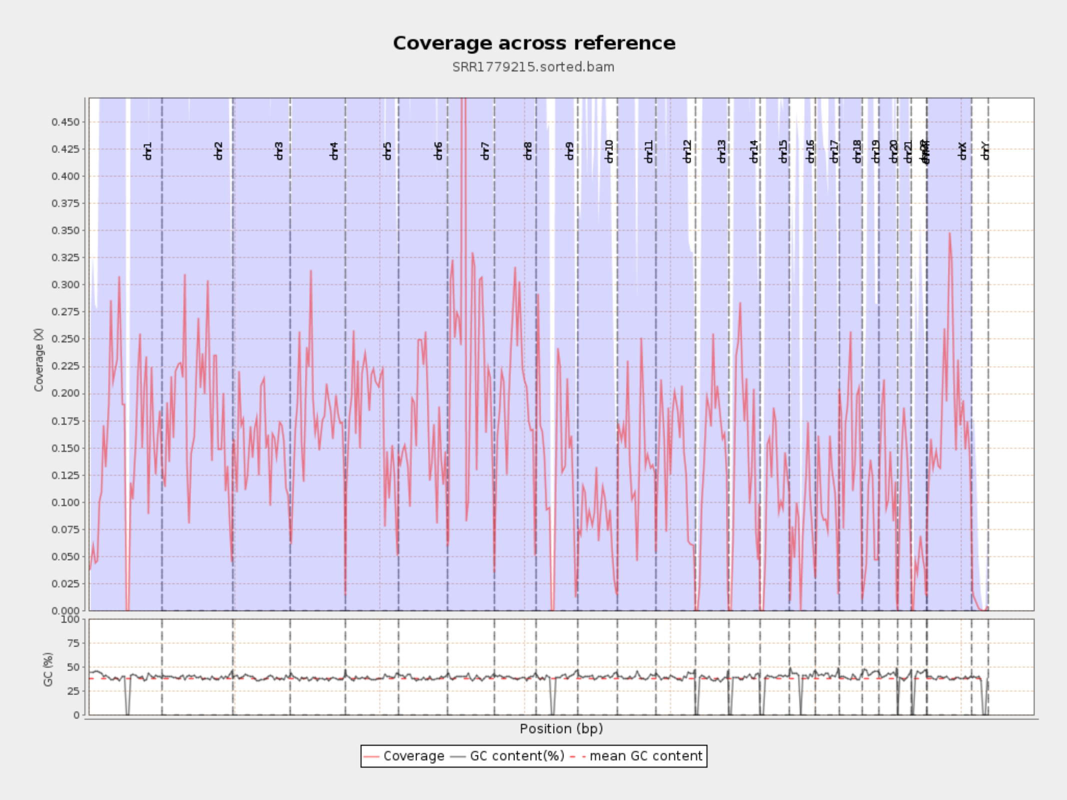
2.7. Chromosome stats

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

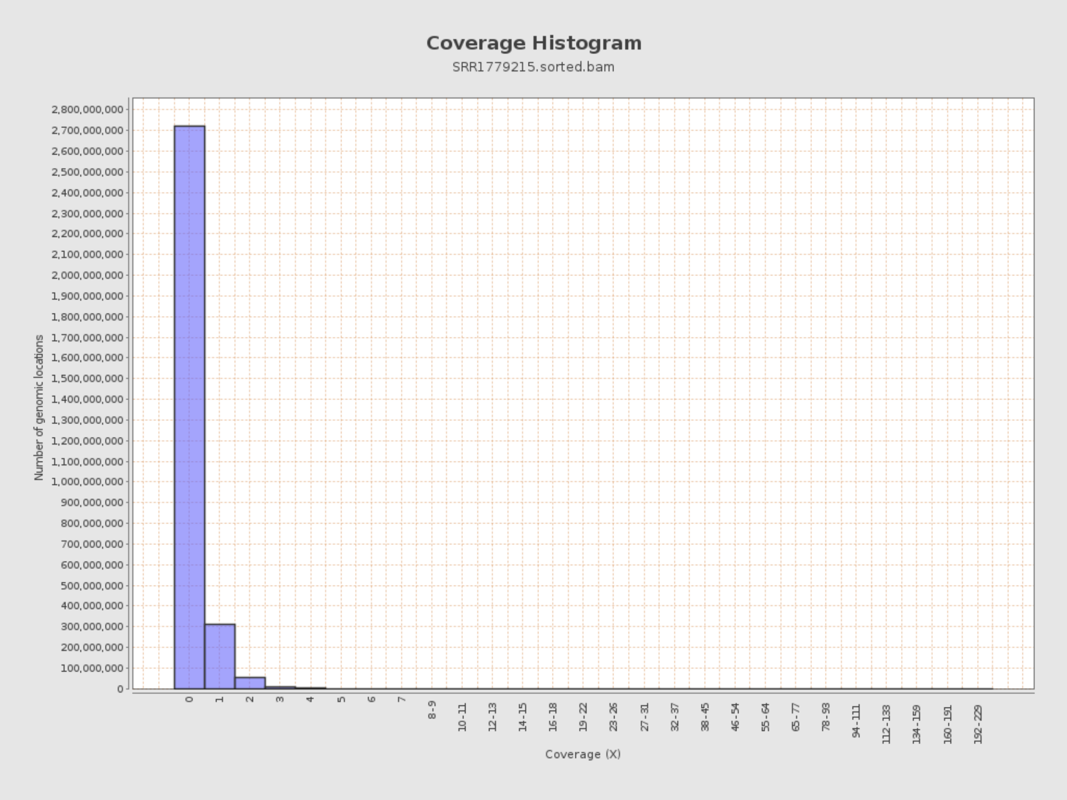
		bases	coverage	deviation
chr1	249250621	38289821	0.1536	0.5054
chr2	243199373	44444569	0.1827	0.4934
chr3	198022430	30451851	0.1538	0.4393
chr4	191154276	34478787	0.1804	0.4782
chr5	180915260	32039311	0.1771	0.4775
chr6	171115067	27944430	0.1633	0.459
chr7	159138663	44079394	0.277	1.1086
chr8	146364022	29199465	0.1995	0.5131
chr9	141213431	19160370	0.1357	0.4322
chr10	135534747	11343382	0.0837	0.4603
chr11	135006516	19597095	0.1452	0.4351
chr12	133851895	18646157	0.1393	0.4244
chr13	115169878	16118966	0.14	0.4206
chr14	107349540	15436460	0.1438	0.4432
chr15	102531392	11152865	0.1088	0.3814
chr16	90354753	7000013	0.0775	0.3117
chr17	81195210	7884307	0.0971	0.3612
chr18	78077248	12989730	0.1664	0.465
chr19	59128983	4410839	0.0746	0.338
chr20	63025520	8155203	0.1294	0.4218
chr21	48129895	5384303	0.1119	0.3923
chr22	51304566	1856888	0.0362	0.2146
chrMT	16571	240	0.0145	0.1195
chrX	155270560	28385415	0.1828	0.5063

chrY	59373566	303659	0.0051	0.0911

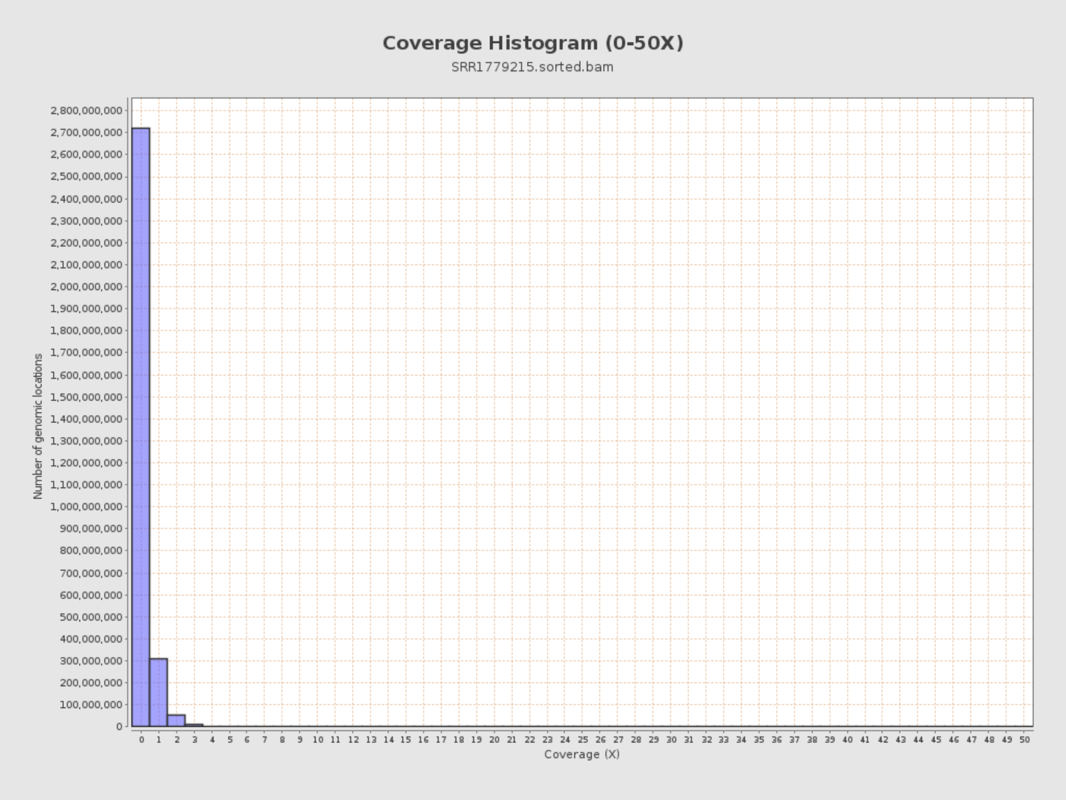
3. Results : Coverage across reference



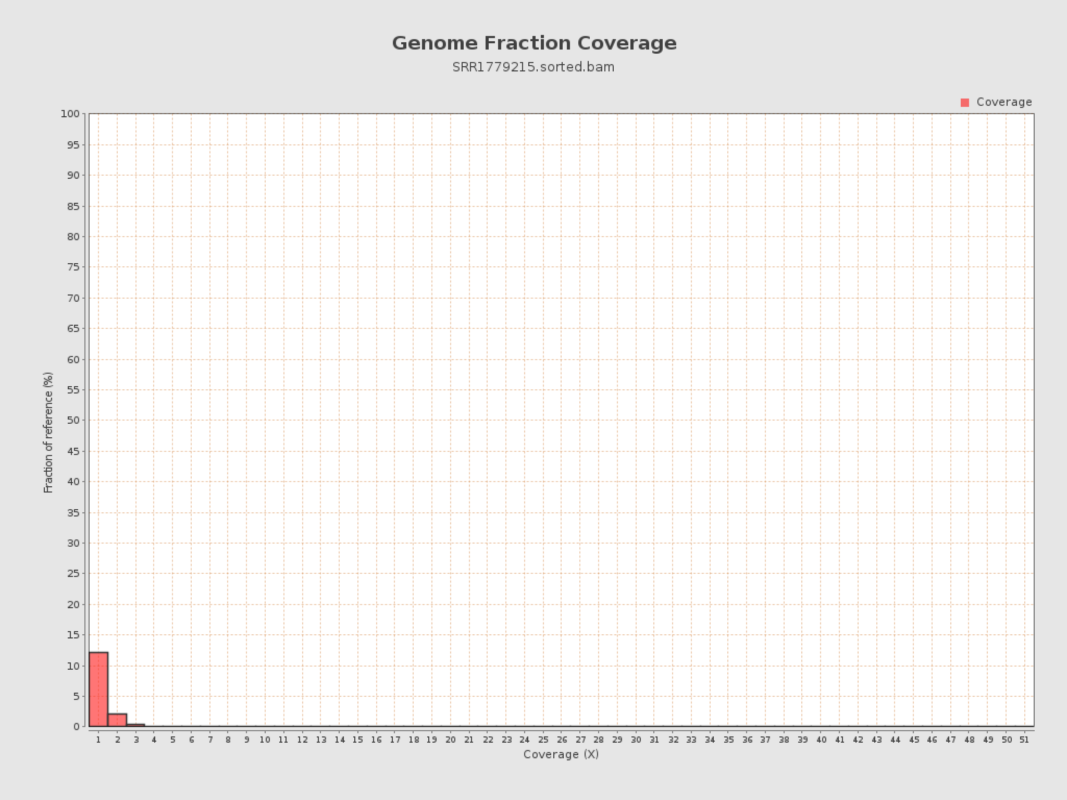
4. Results : Coverage Histogram



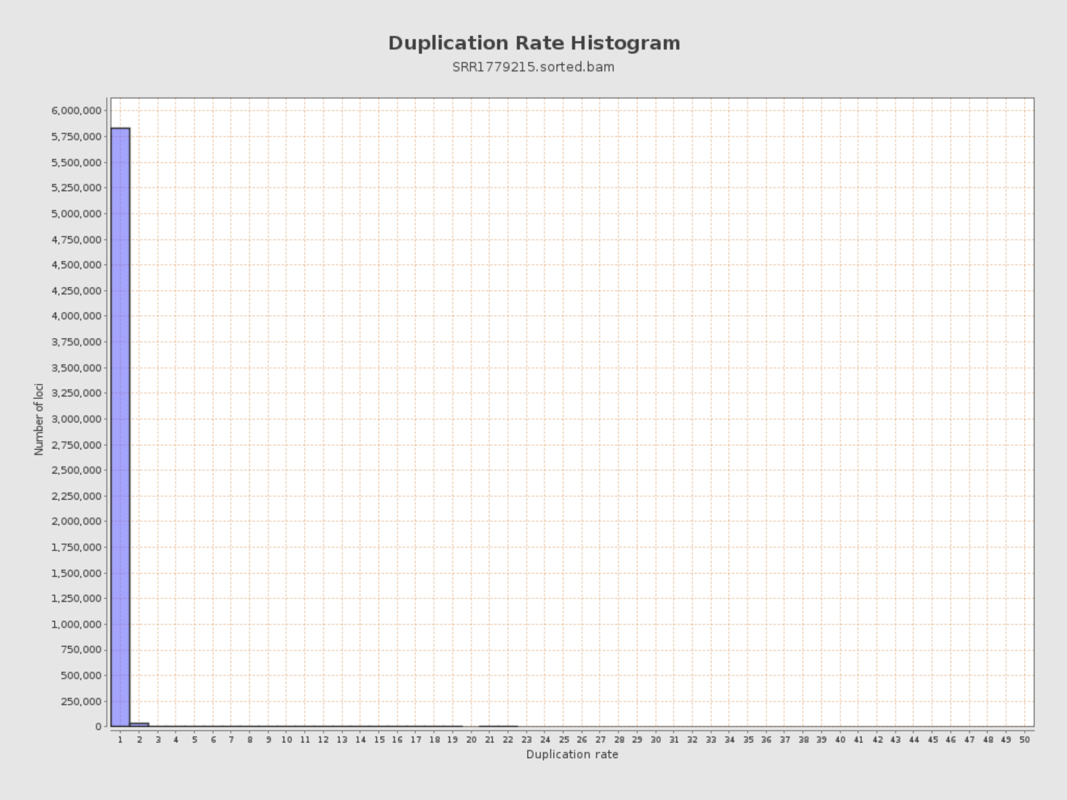
5. Results : Coverage Histogram (0-50X)



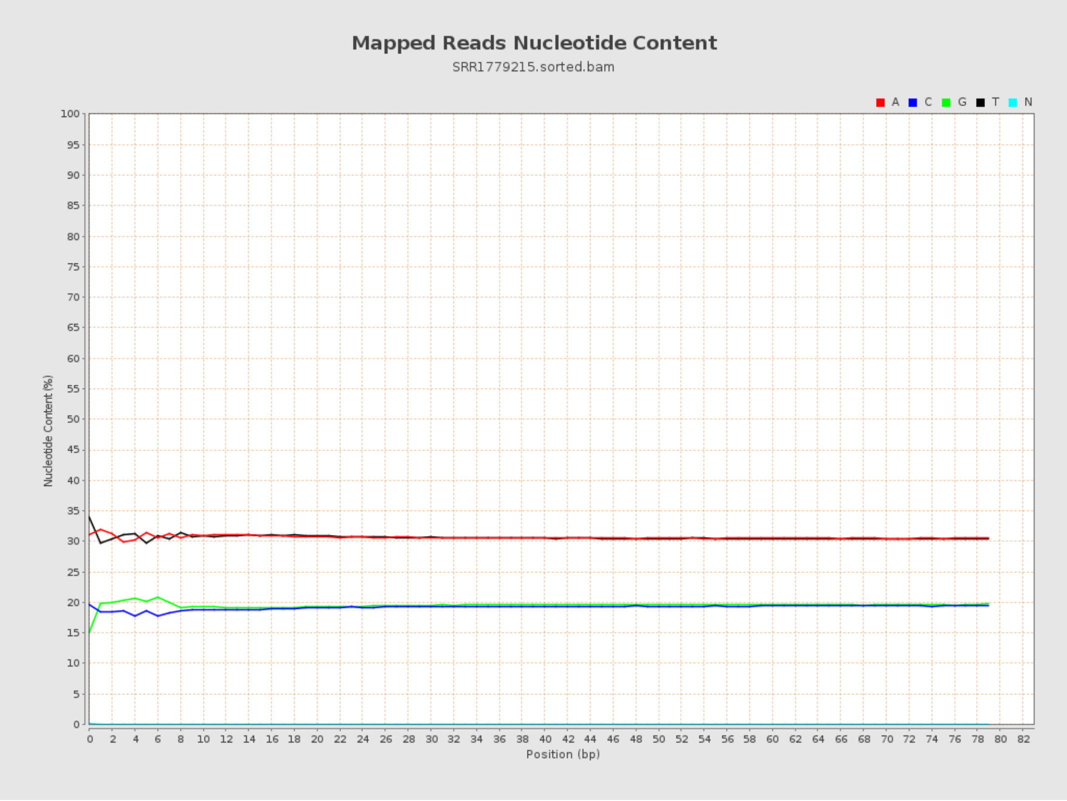
6. Results : Genome Fraction Coverage



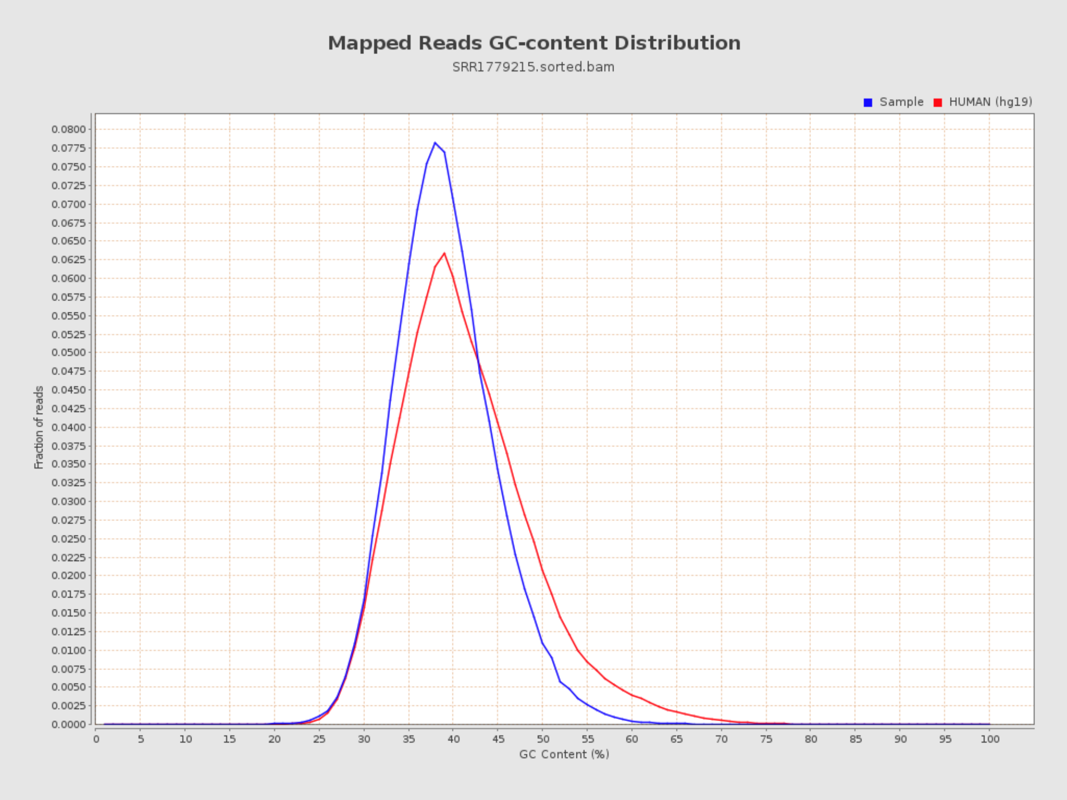
7. Results : Duplication Rate Histogram



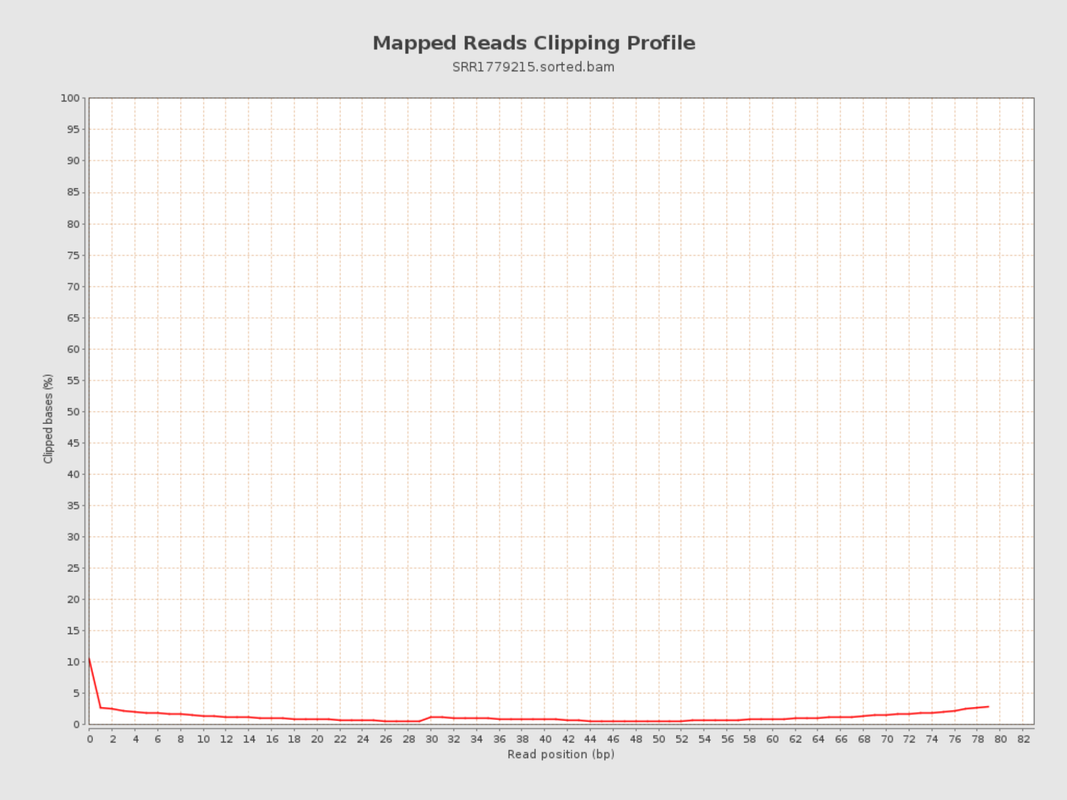
8. Results : Mapped Reads Nucleotide Content



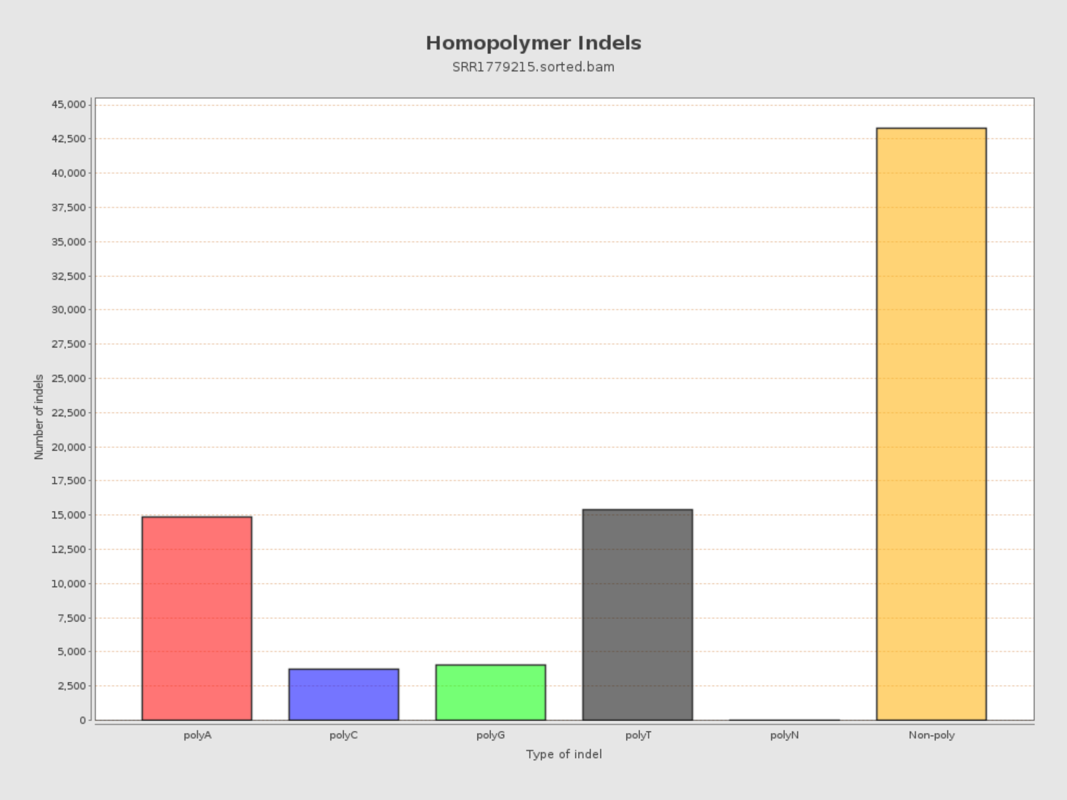
9. Results : Mapped Reads GC-content Distribution



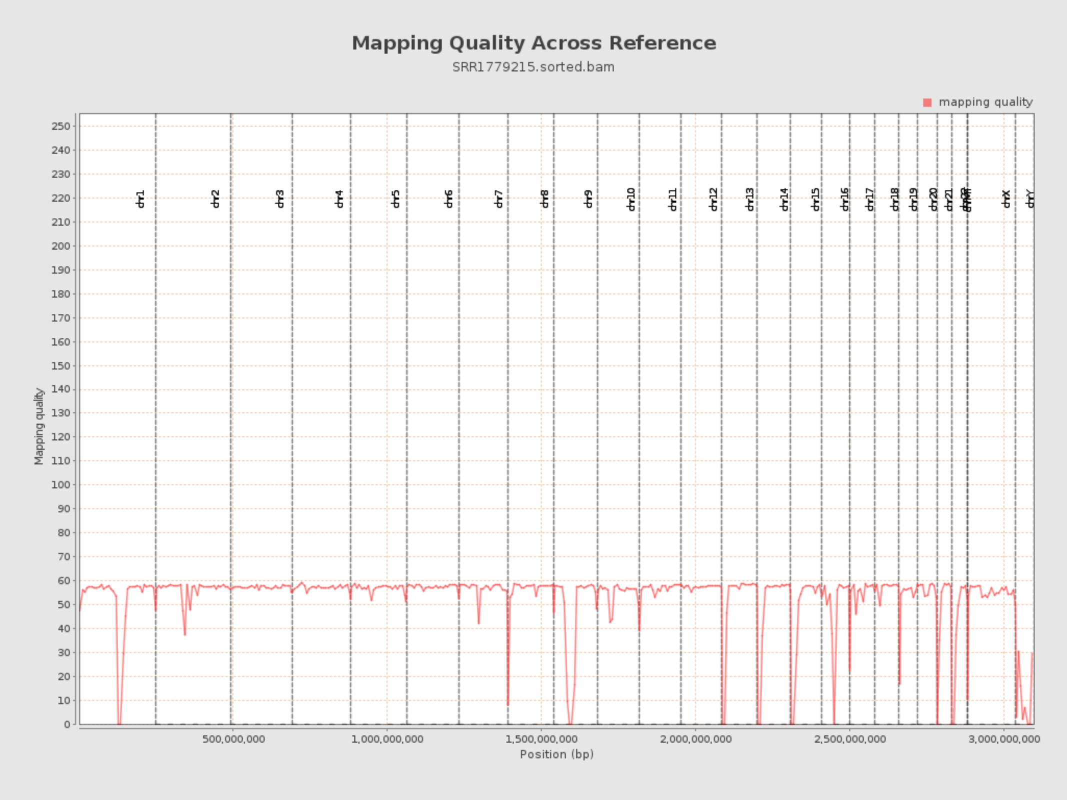
10. Results : Mapped Reads Clipping Profile



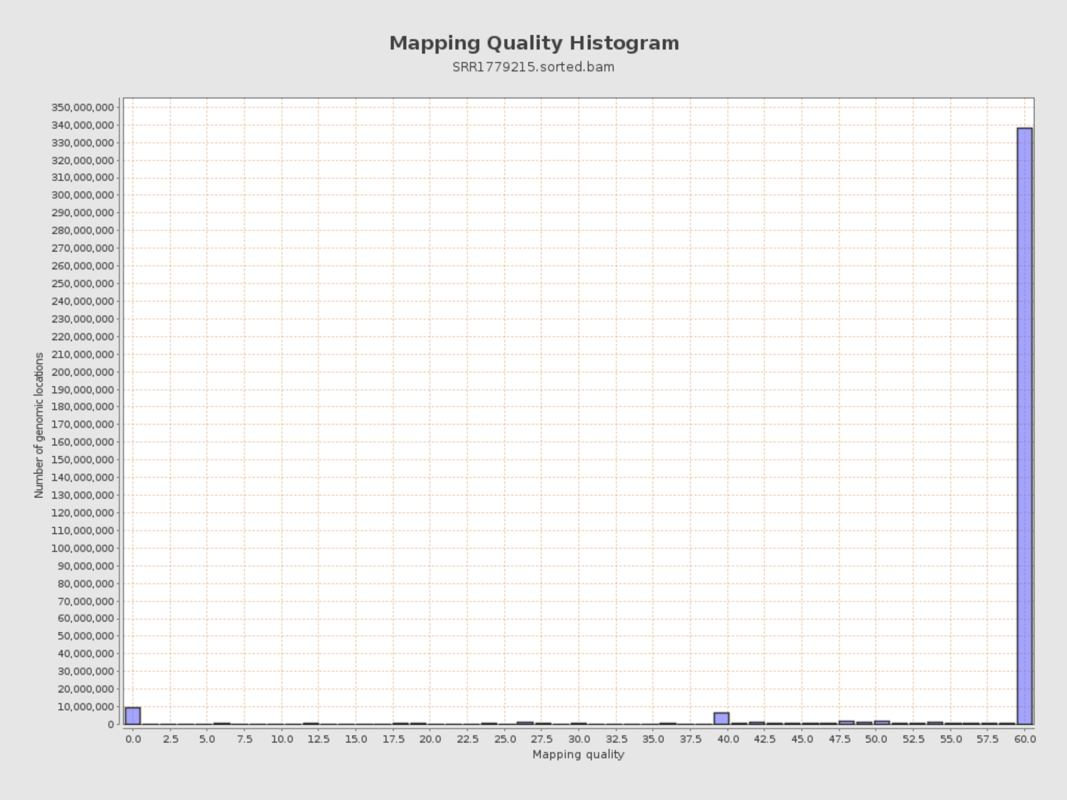
11. Results : Homopolymer Indels



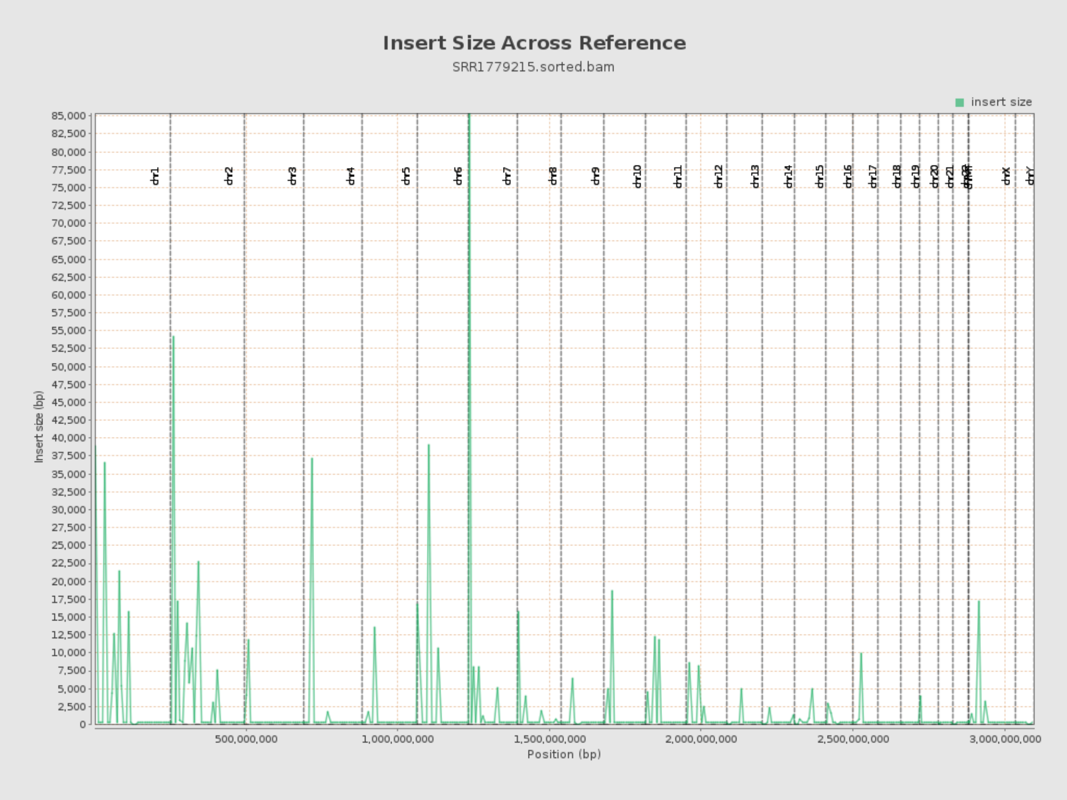
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram