Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/01 06:02:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365377.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_SRR5365377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365377_1.fastq.gz SRR5365377_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 01 06:02:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,103,368,040
Mapped reads	1,067,313,091 / 96.73%
Unmapped reads	36,054,949 / 3.27%
Mapped paired reads	1,067,313,091 / 96.73%
Mapped reads, first in pair	537,159,897 / 48.68%
Mapped reads, second in pair	530,153,194 / 48.05%
Mapped reads, both in pair	1,058,517,910 / 95.94%
Mapped reads, singletons	8,795,181 / 0.8%
Secondary alignments	0
Supplementary alignments	8,172,626 / 0.74%
Read min/max/mean length	30 / 125 / 125.33
Duplicated reads (estimated)	290,021,449 / 26.29%
Duplication rate	23.05%
Clipped reads	205,897,825 / 18.66%

2.2. ACGT Content

Number/percentage of A's	38,101,860,088 / 29.72%
Number/percentage of C's	26,051,149,962 / 20.32%
Number/percentage of T's	37,558,944,157 / 29.29%
Number/percentage of G's	26,491,759,630 / 20.66%
Number/percentage of N's	12,378,041 / 0.01%

GC Percentage	40.98%

2.3. Coverage

Mean	41.4316
Standard Deviation	541.169

2.4. Mapping Quality

Mean Mapping Quality	54.04

2.5. Insert size

Mean	74,014.75
Standard Deviation	2,640,061.44
P25/Median/P75	143 / 199 / 280

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	686,849,744
Insertions	13,374,586
Mapped reads with at least one insertion	1.19%
Deletions	16,205,031
Mapped reads with at least one deletion	1.46%
Homopolymer indels	40.72%

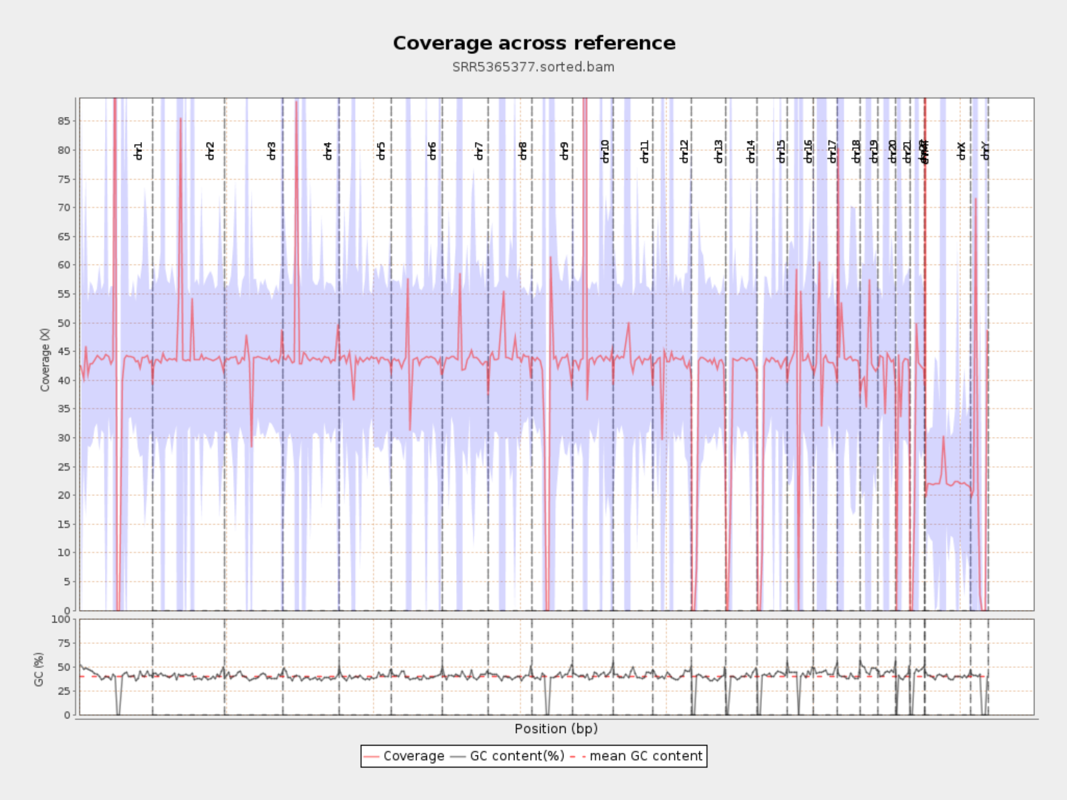
2.7. Chromosome stats

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

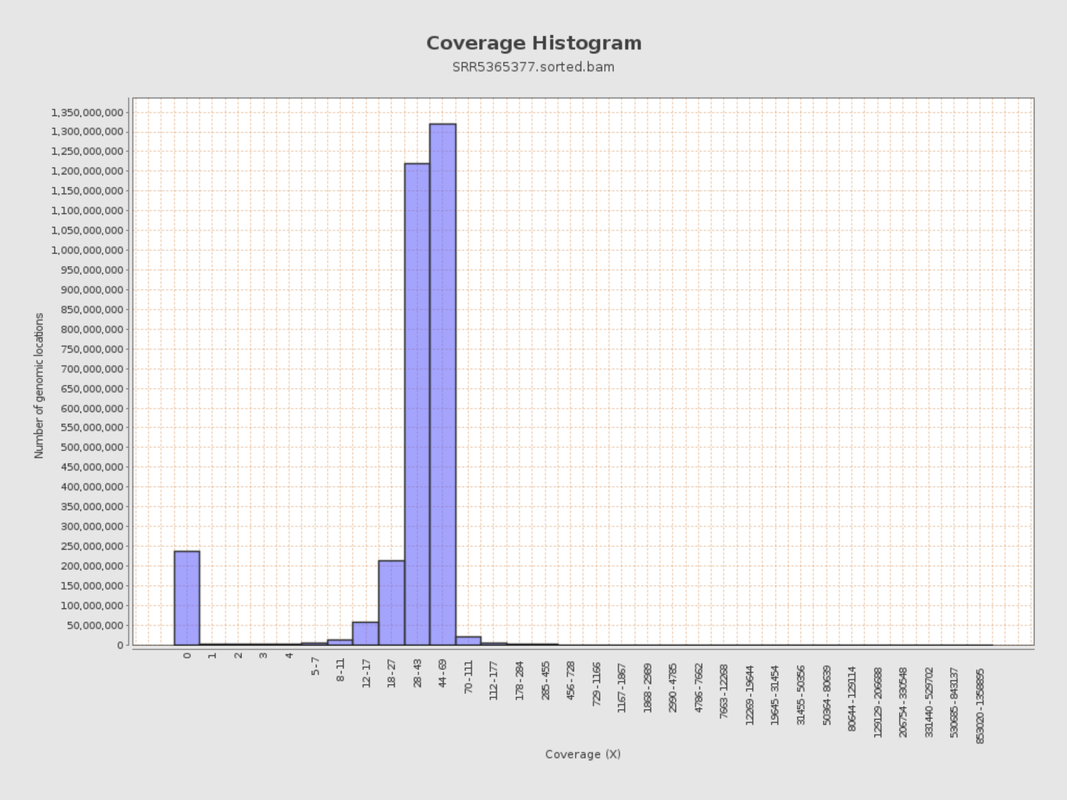
		bases	coverage	deviation
chr1	249250621	10634124742	42.6644	1,392.8115
chr2	243199373	11086500742	45.5861	289.4805
chr3	198022430	8575498464	43.3057	63.5403
chr4	191154276	8738914595	45.7166	391.0116
chr5	180915260	7831450987	43.288	34.465
chr6	171115067	7463822244	43.6187	166.7998
chr7	159138663	7023914799	44.1371	346.0992
chr8	146364022	6575298309	44.9243	469.1427
chr9	141213431	5469222461	38.7302	487.1049
chr10	135534747	6990372706	51.5762	1,173.2596
chr11	135006516	5940469581	44.0014	291.3264
chr12	133851895	5717995381	42.7188	64.5877
chr13	115169878	4154791713	36.0753	20.507
chr14	107349540	3897204051	36.3039	33.8839
chr15	102531392	3556487500	34.6868	29.4835
chr16	90354753	3789374211	41.9388	167.8225
chr17	81195210	3526454402	43.4318	238.3605
chr18	78077248	3611568173	46.2563	539.0822
chr19	59128983	2517365049	42.5741	625.439
chr20	63025520	2668171607	42.3348	111.5328
chr21	48129895	1818609109	37.7854	188.8609
chr22	51304566	1570136183	30.6042	126.9191
chrMT	16571	231270794	13,956.3571	1,124.3539
chrX	155270560	3481189100	22.4201	110.3824

chrY	59373566	1389242552	23.3983	616.0236

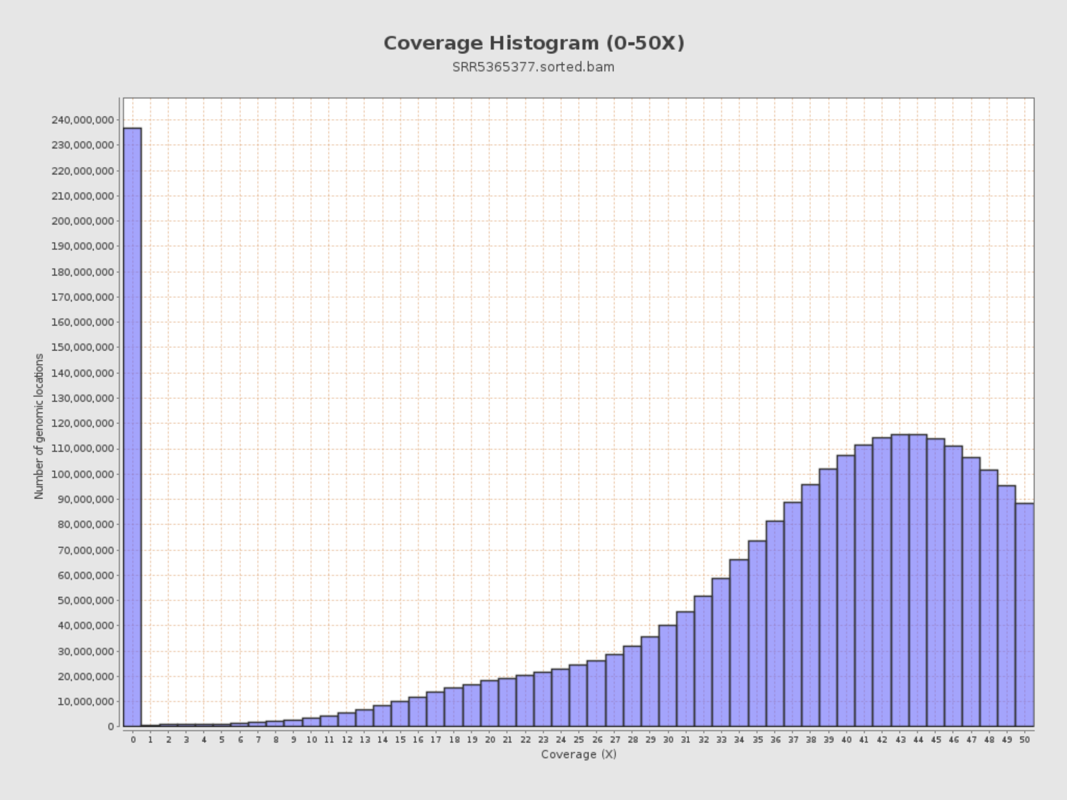
3. Results : Coverage across reference



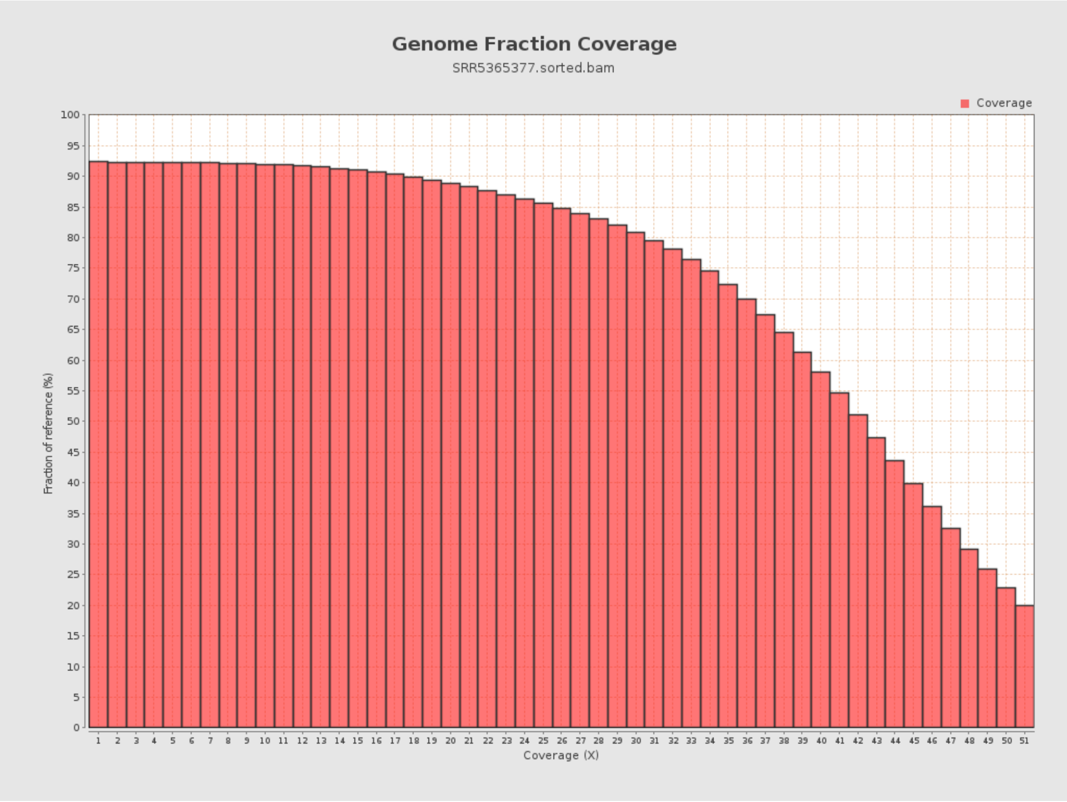
4. Results : Coverage Histogram



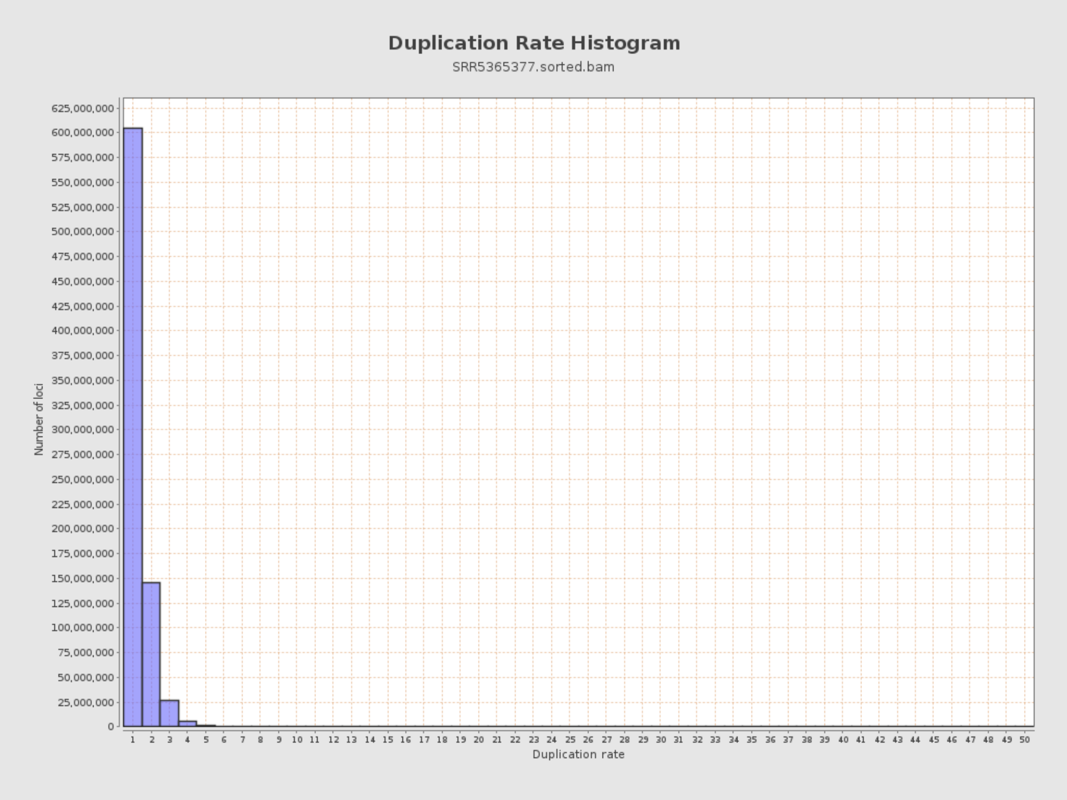
5. Results : Coverage Histogram (0-50X)



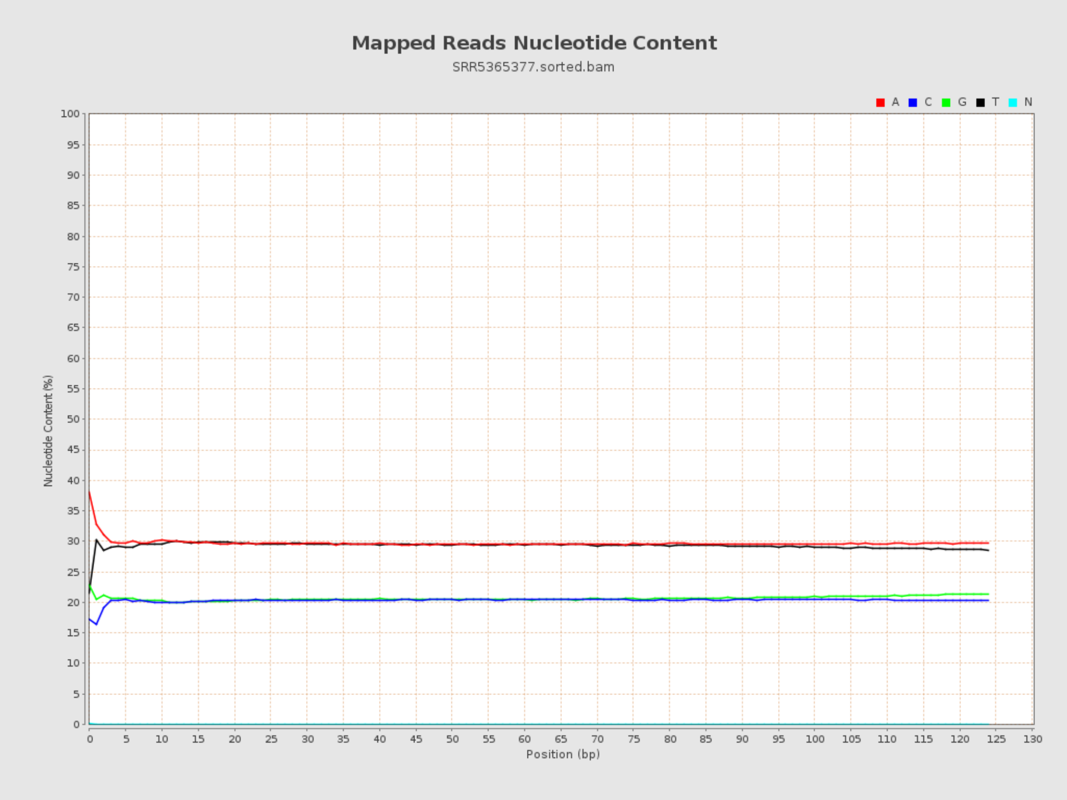
6. Results : Genome Fraction Coverage



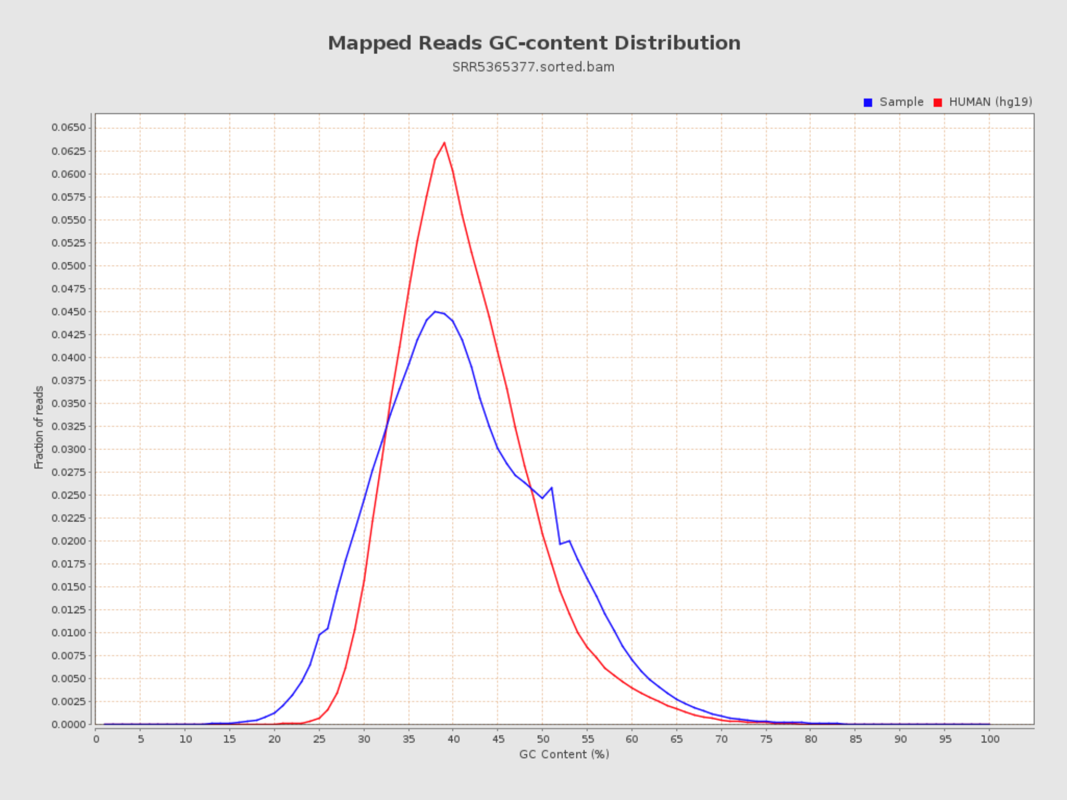
7. Results : Duplication Rate Histogram



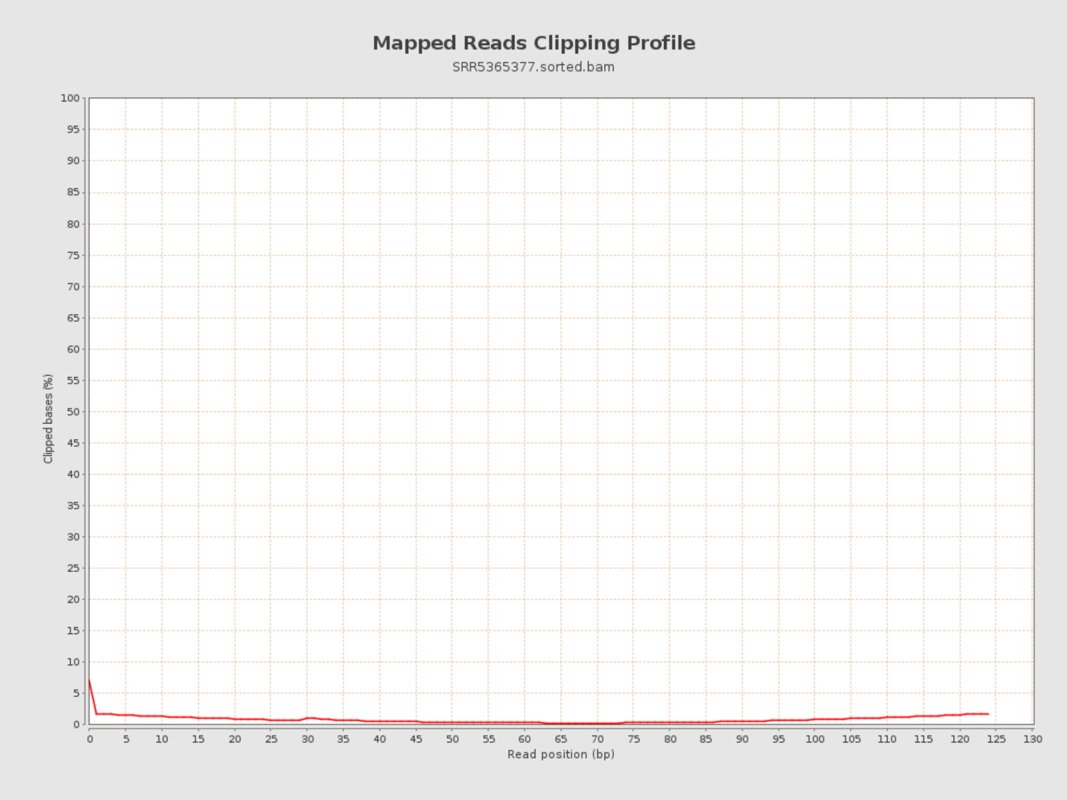
8. Results : Mapped Reads Nucleotide Content



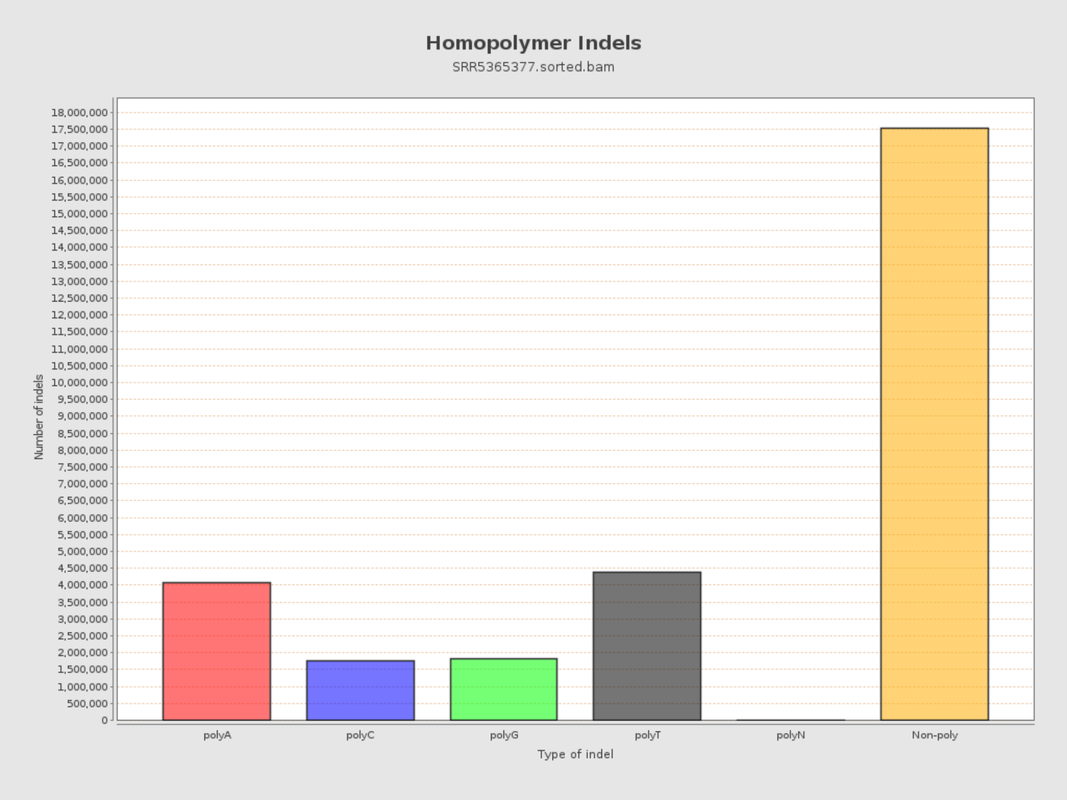
9. Results : Mapped Reads GC-content Distribution



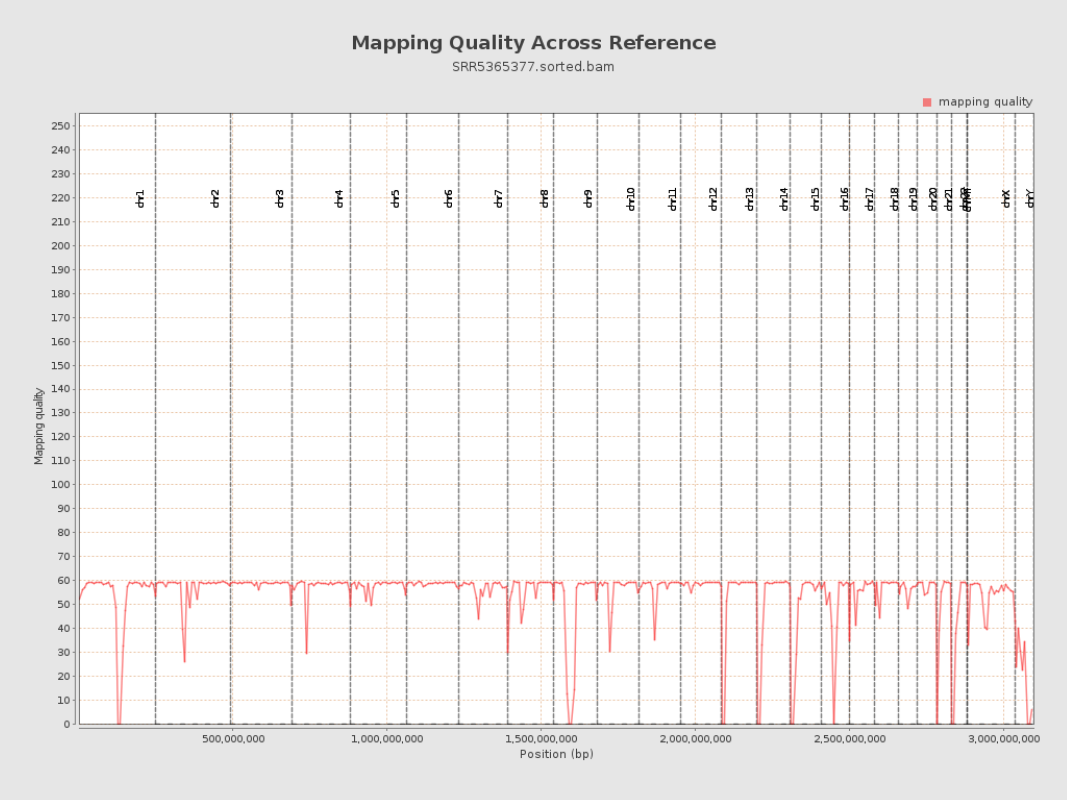
10. Results : Mapped Reads Clipping Profile



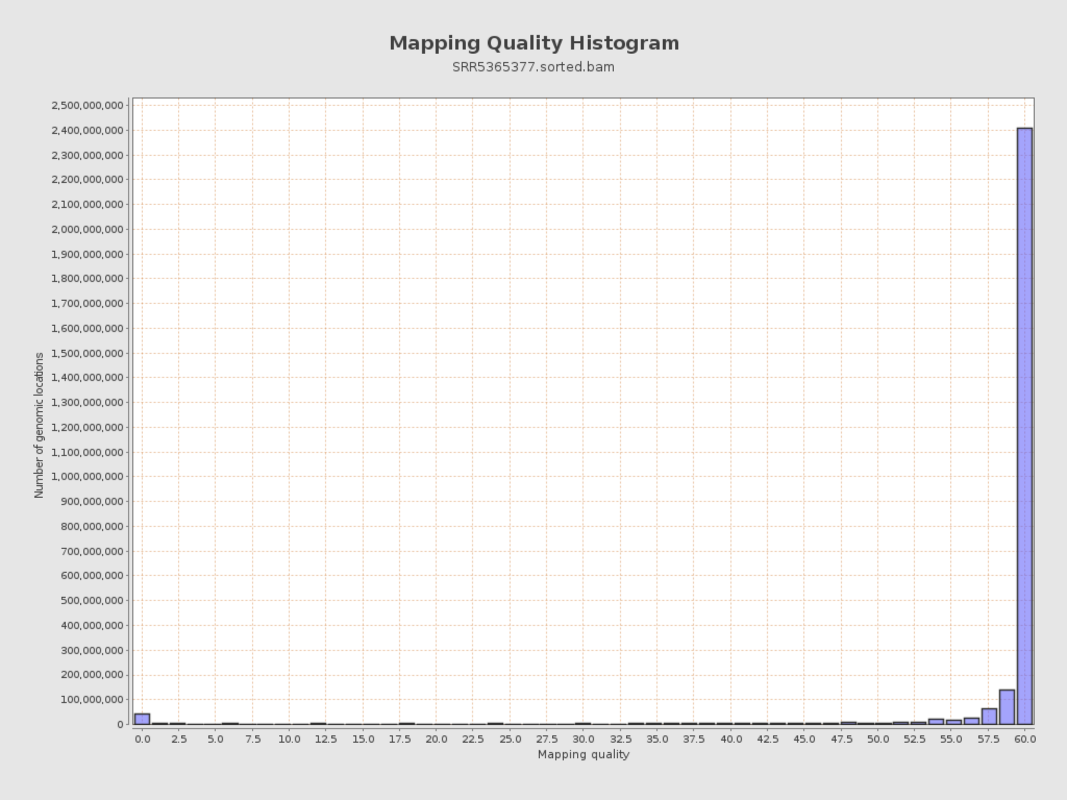
11. Results : Homopolymer Indels



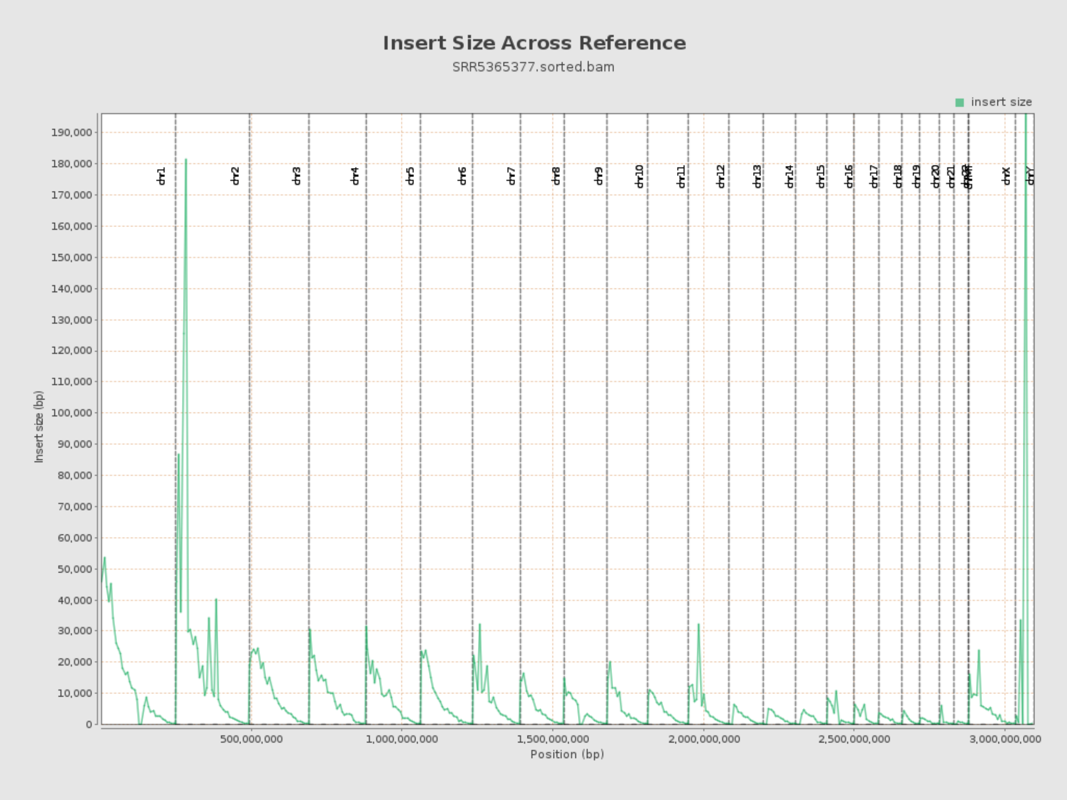
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram