Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/29 00:40:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365373.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_SRR5365373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365373_1.fastq.gz SRR5365373_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Nov 29 00:40:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	545,164,294
Mapped reads	512,912,537 / 94.08%
Unmapped reads	32,251,757 / 5.92%
Mapped paired reads	512,912,537 / 94.08%
Mapped reads, first in pair	256,874,333 / 47.12%
Mapped reads, second in pair	256,038,204 / 46.97%
Mapped reads, both in pair	507,137,432 / 93.02%
Mapped reads, singletons	5,775,105 / 1.06%
Secondary alignments	0
Supplementary alignments	10,928,236 / 2%
Read min/max/mean length	30 / 150 / 151.04
Duplicated reads (estimated)	197,072,872 / 36.15%
Duplication rate	36.88%
Clipped reads	229,871,116 / 42.17%

2.2. ACGT Content

Number/percentage of A's	19,150,725,706 / 27.08%
Number/percentage of C's	16,291,054,712 / 23.03%
Number/percentage of T's	18,449,970,065 / 26.09%
Number/percentage of G's	16,829,703,733 / 23.8%
Number/percentage of N's	1,645,838 / 0%

GC Percentage	46.83%

2.3. Coverage

Mean	22.8503
Standard Deviation	46.3744

2.4. Mapping Quality

Mean Mapping Quality	54.39

2.5. Insert size

Mean	90,737.39
Standard Deviation	2,996,923.16
P25/Median/P75	133 / 160 / 195

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	421,613,938
Insertions	6,369,417
Mapped reads with at least one insertion	1.21%
Deletions	4,994,050
Mapped reads with at least one deletion	0.94%
Homopolymer indels	41.55%

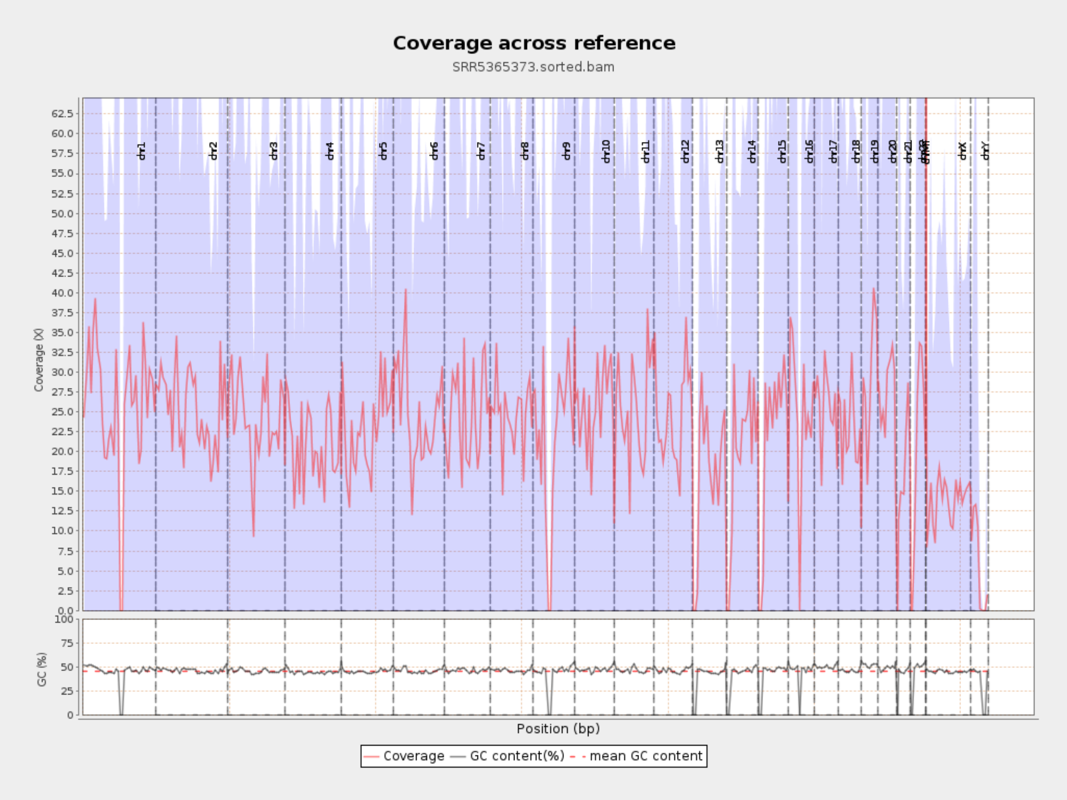
2.7. Chromosome stats

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

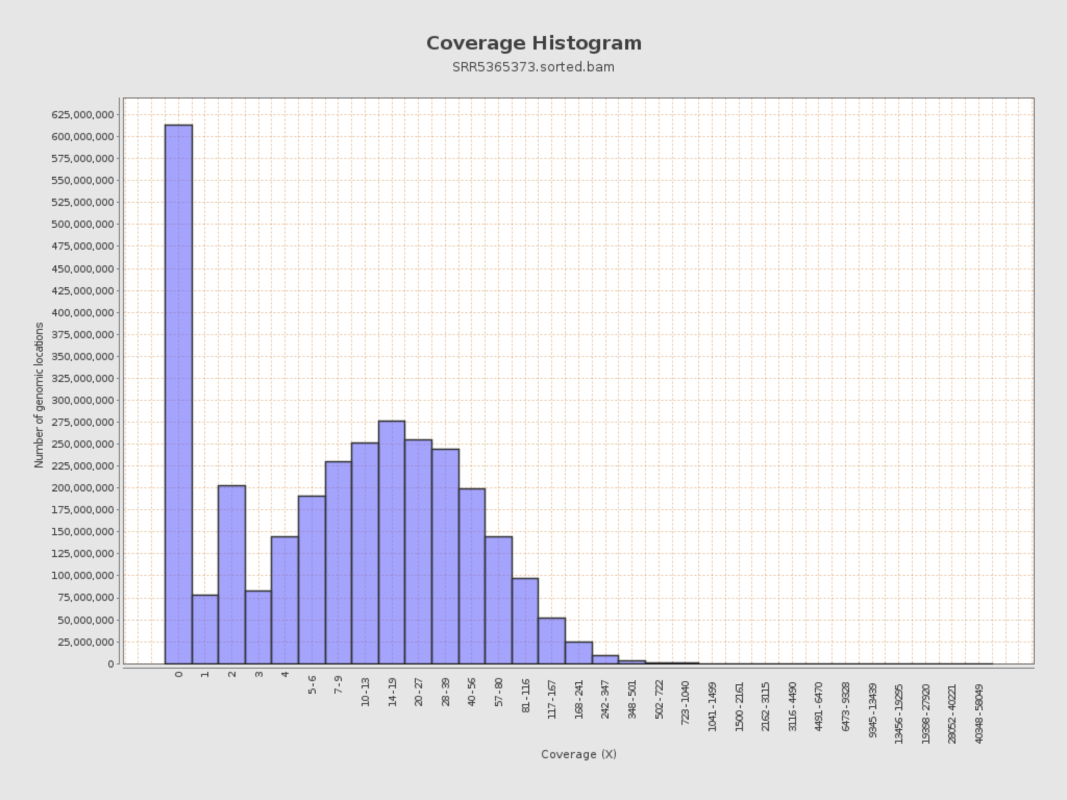
		bases	coverage	deviation
chr1	249250621	6436143887	25.822	52.5633
chr2	243199373	6155566555	25.3108	68.9518
chr3	198022430	4787419876	24.1761	38.3243
chr4	191154276	4022105480	21.0411	41.8669
chr5	180915260	4157363433	22.9796	41.3118
chr6	171115067	4228918311	24.7139	43.9513
chr7	159138663	3913794615	24.5936	43.0456
chr8	146364022	3589472995	24.5243	43.9518
chr9	141213431	3054927159	21.6334	40.5174
chr10	135534747	3509470639	25.8935	50.1867
chr11	135006516	3419553784	25.3288	42.6869
chr12	133851895	3325009608	24.841	43.6142
chr13	115169878	1980061274	17.1925	32.2894
chr14	107349540	2126933671	19.8132	38.6597
chr15	102531392	2191214274	21.3712	42.0643
chr16	90354753	2192835656	24.2692	43.331
chr17	81195210	2099955930	25.8631	52.0807
chr18	78077248	1788881909	22.9117	54.6958
chr19	59128983	1684004887	28.4802	56.1484
chr20	63025520	1722854878	27.3358	50.2973
chr21	48129895	808458978	16.7974	42.1246
chr22	51304566	1044363930	20.3562	50.3356
chrMT	16571	2919623	176.1887	84.5278
chrX	155270560	2147004225	13.8275	30.6849

chrY	59373566	348394658	5.8678	29.8485

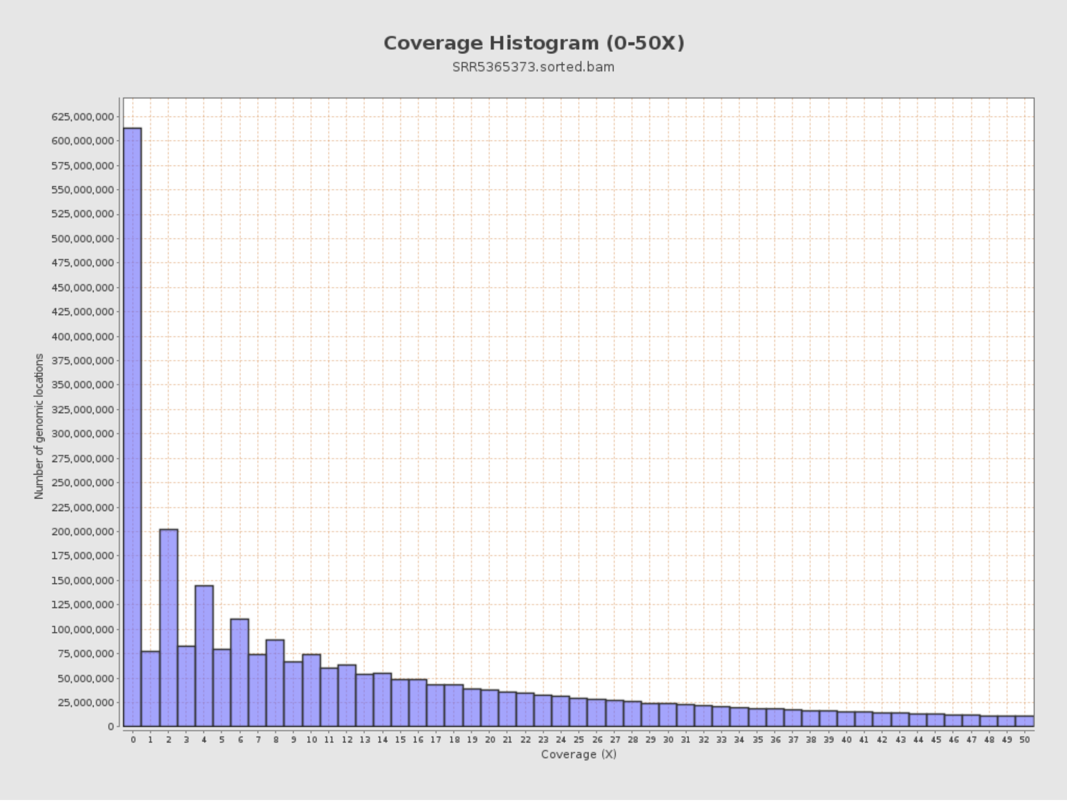
3. Results : Coverage across reference



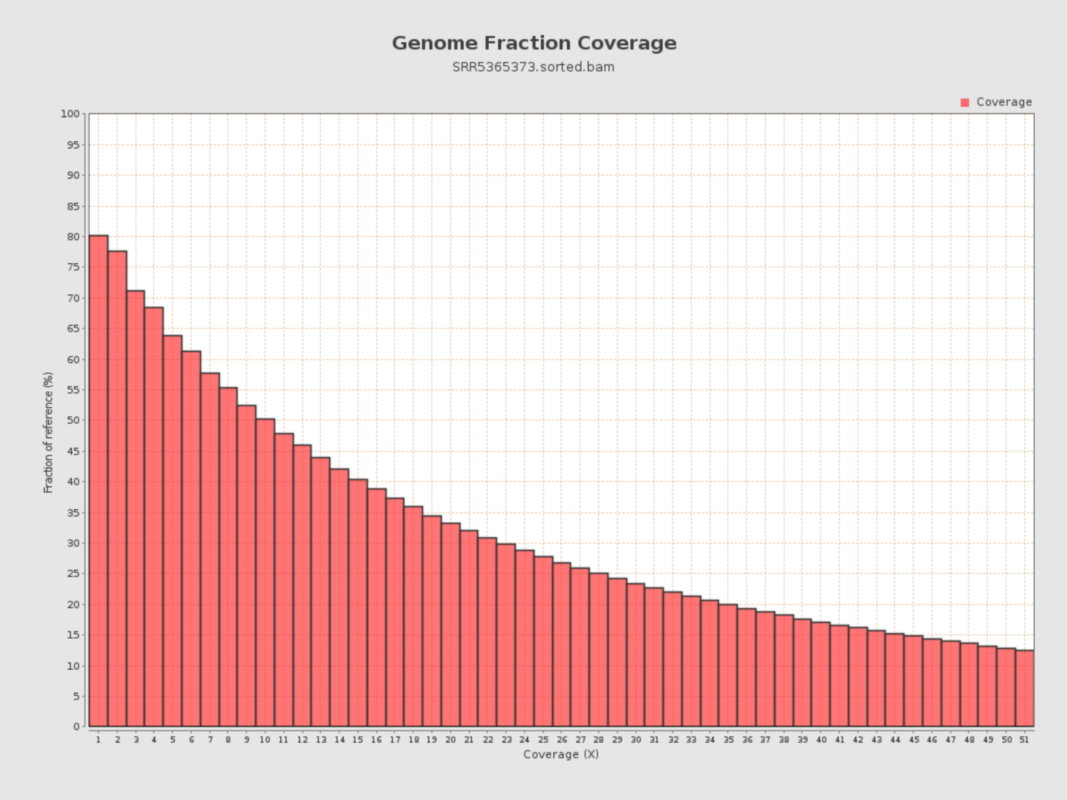
4. Results : Coverage Histogram



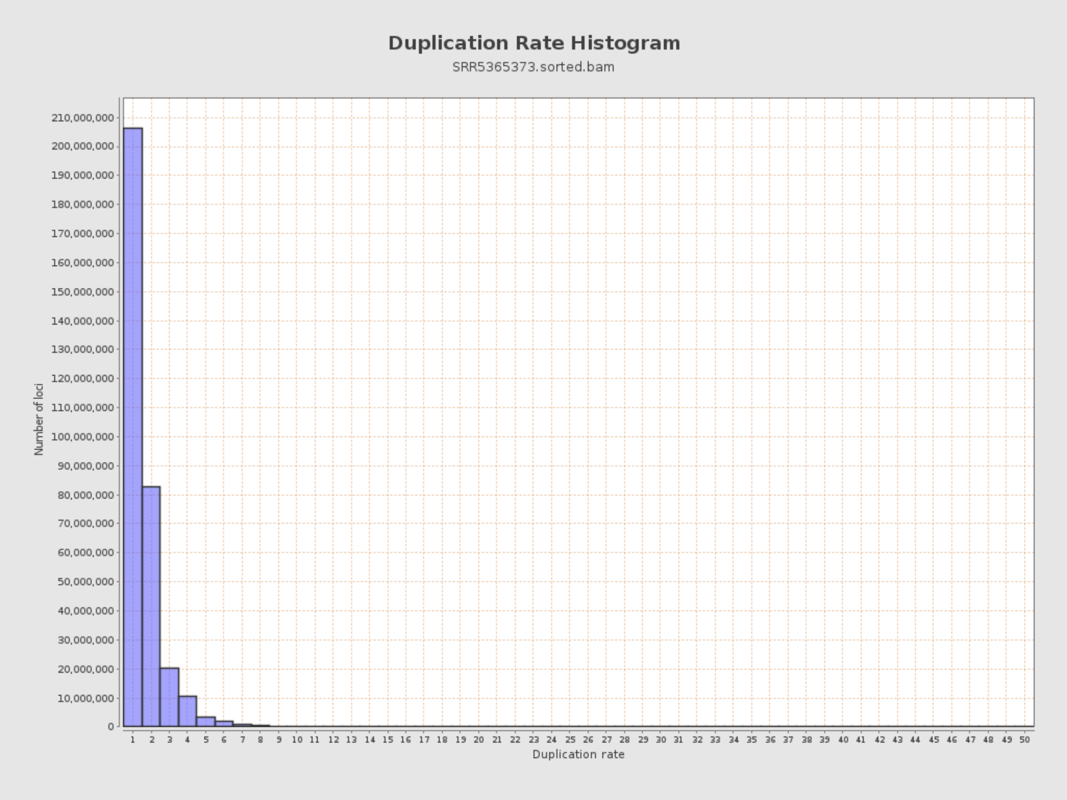
5. Results : Coverage Histogram (0-50X)



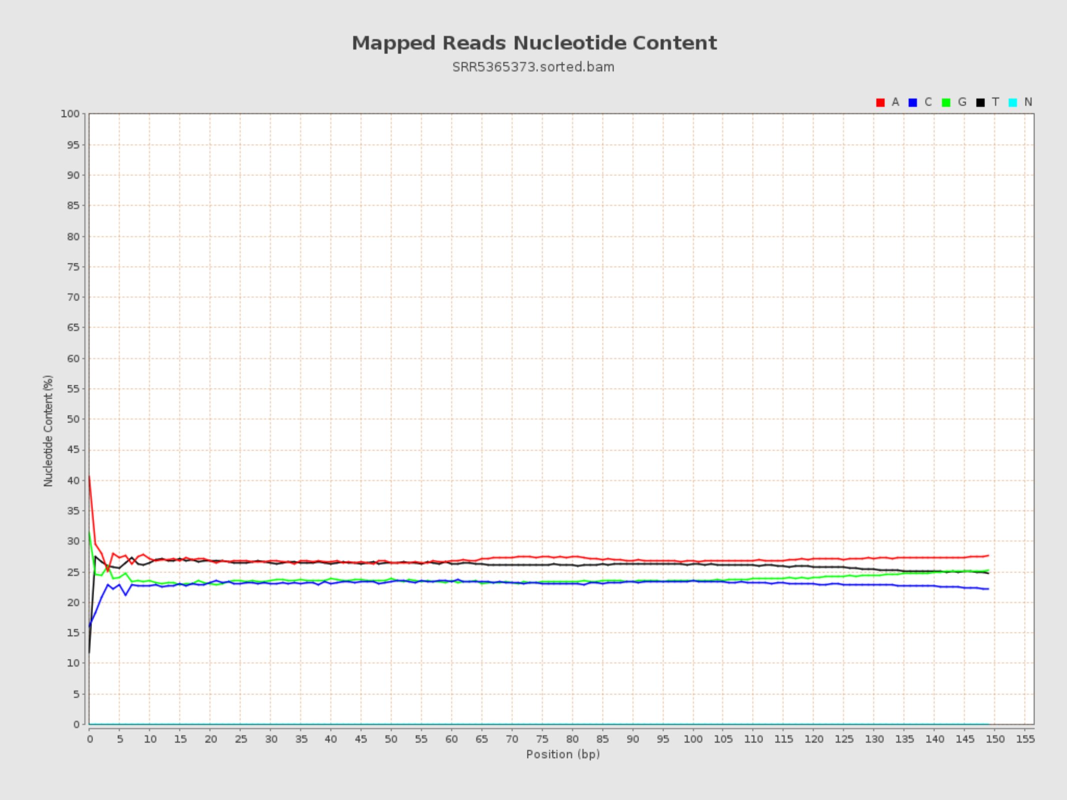
6. Results : Genome Fraction Coverage



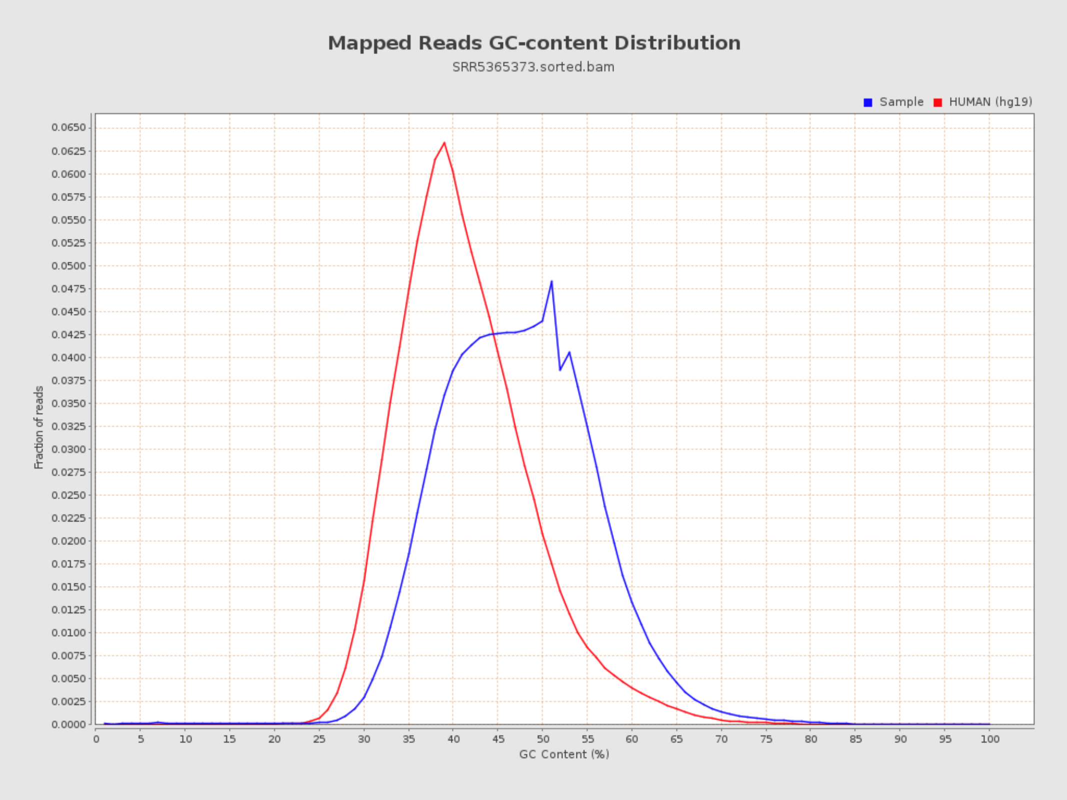
7. Results : Duplication Rate Histogram



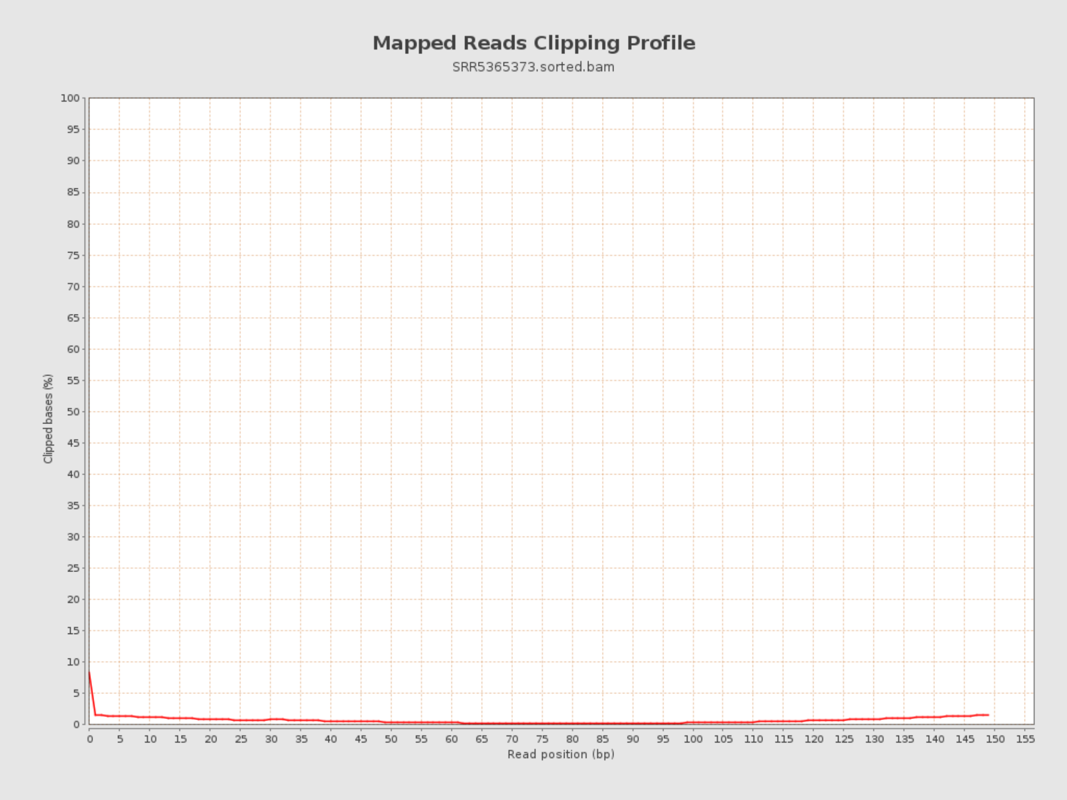
8. Results : Mapped Reads Nucleotide Content



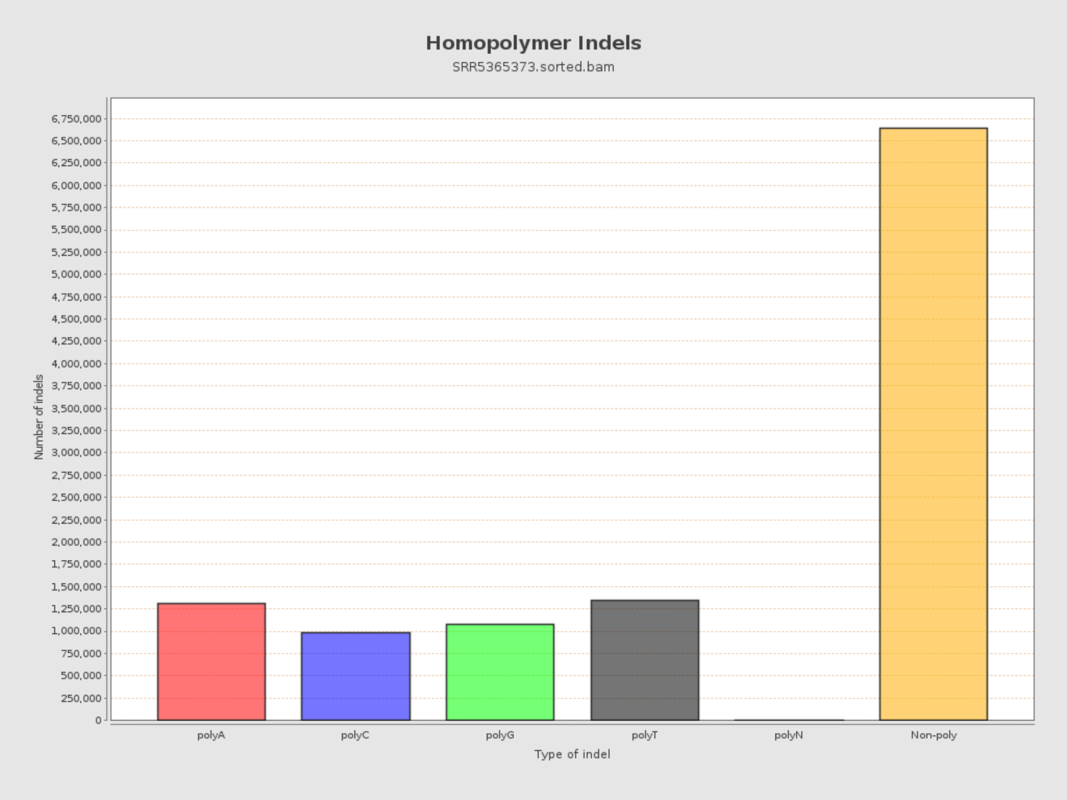
9. Results : Mapped Reads GC-content Distribution



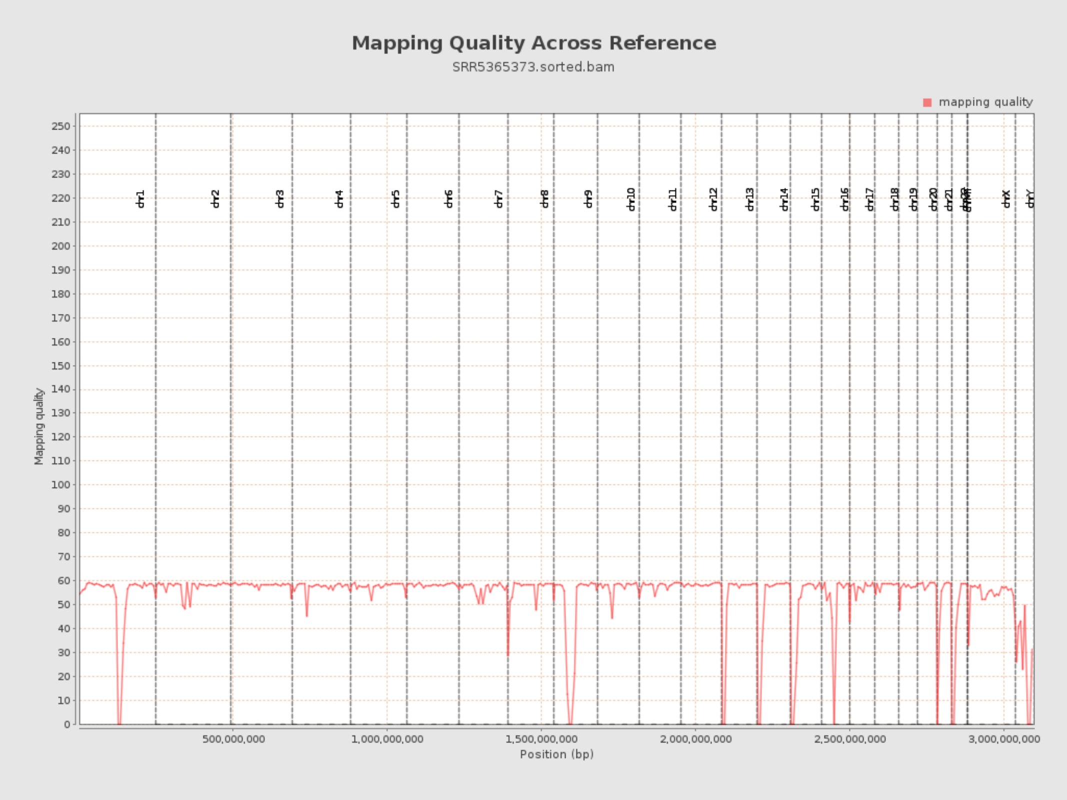
10. Results : Mapped Reads Clipping Profile



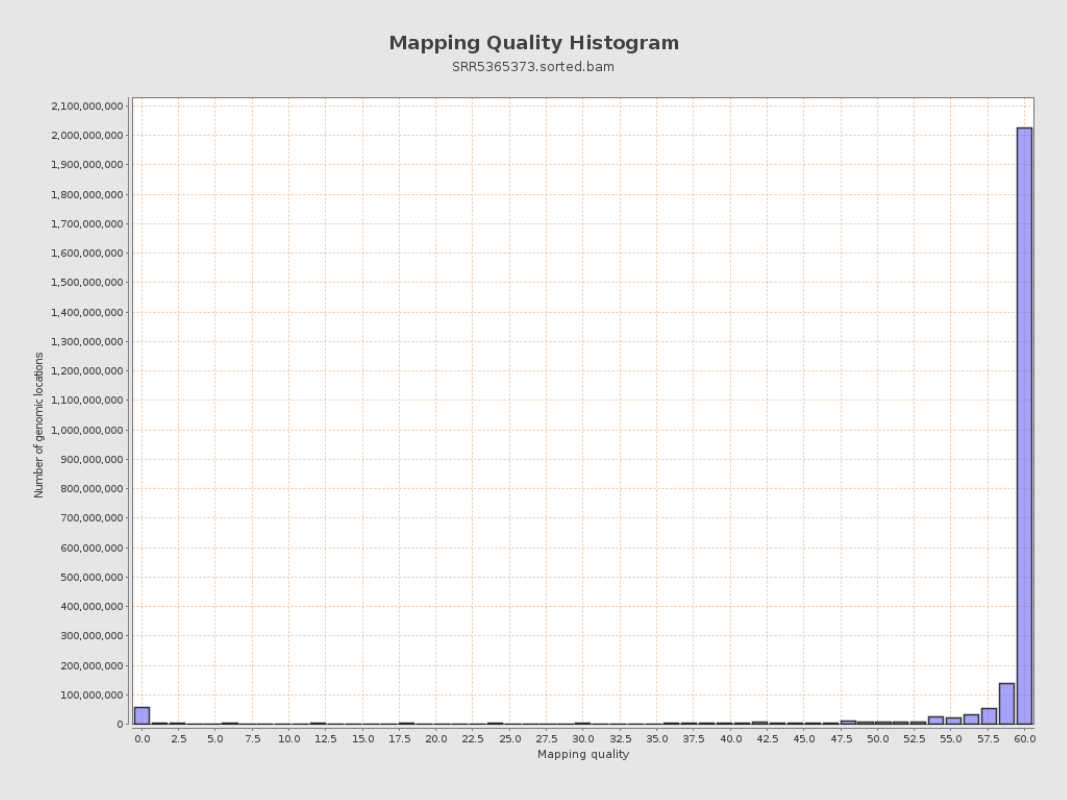
11. Results : Homopolymer Indels



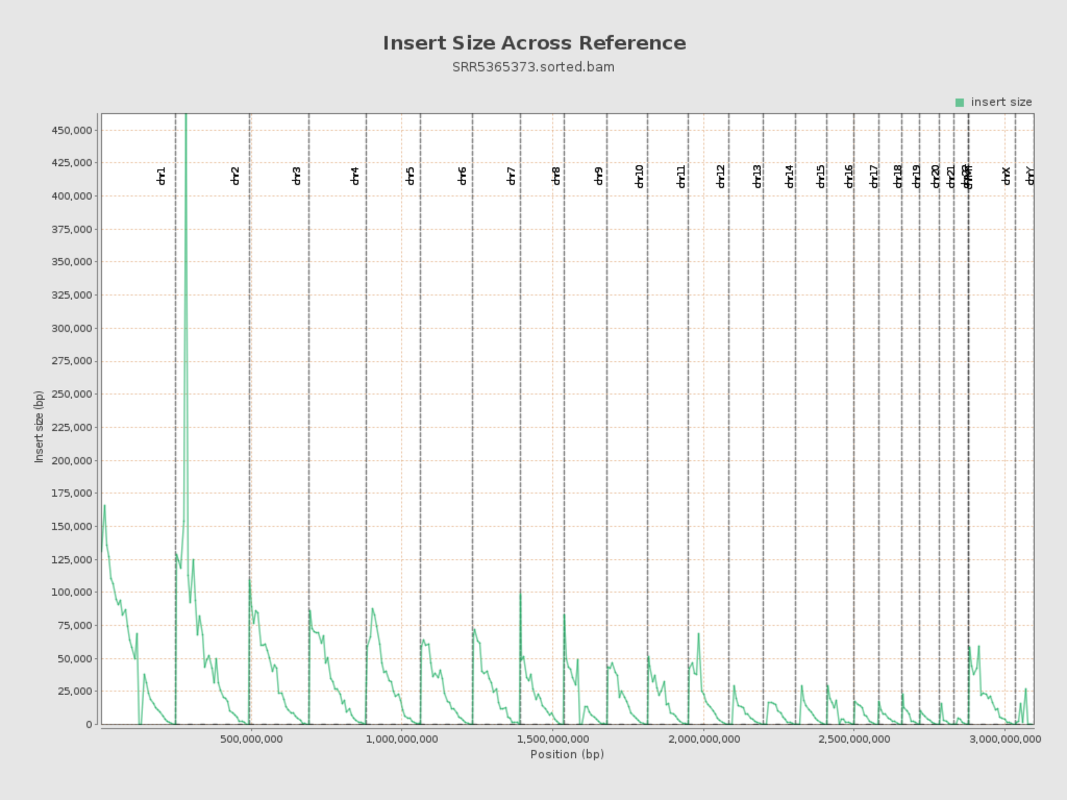
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram