Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/11/10 19:56:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365349.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_SRR5365349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365349_1.fastq.gz SRR5365349_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Nov 10 19:56:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5365349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	516,081,342
Mapped reads	486,922,596 / 94.35%
Unmapped reads	29,158,746 / 5.65%
Mapped paired reads	486,922,596 / 94.35%
Mapped reads, first in pair	244,036,888 / 47.29%
Mapped reads, second in pair	242,885,708 / 47.06%
Mapped reads, both in pair	484,084,054 / 93.8%
Mapped reads, singletons	2,838,542 / 0.55%
Secondary alignments	0
Supplementary alignments	1,992,911 / 0.39%
Read min/max/mean length	30 / 125 / 125.16
Duplicated reads (estimated)	366,685,795 / 71.05%
Duplication rate	43.01%
Clipped reads	343,411,047 / 66.54%

2.2. ACGT Content

Number/percentage of A's	15,012,578,487 / 30.09%
Number/percentage of C's	9,704,809,710 / 19.45%
Number/percentage of T's	14,537,050,100 / 29.14%
Number/percentage of G's	10,624,221,356 / 21.3%
Number/percentage of N's	6,999,975 / 0.01%

GC Percentage	40.75%

2.3. Coverage

Mean	16.12
Standard Deviation	162.1095

2.4. Mapping Quality

Mean Mapping Quality	53.74

2.5. Insert size

Mean	60,830.67
Standard Deviation	2,350,454.58
P25/Median/P75	129 / 198 / 300

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	293,741,252
Insertions	15,121,203
Mapped reads with at least one insertion	3.03%
Deletions	8,033,552
Mapped reads with at least one deletion	1.61%
Homopolymer indels	49.76%

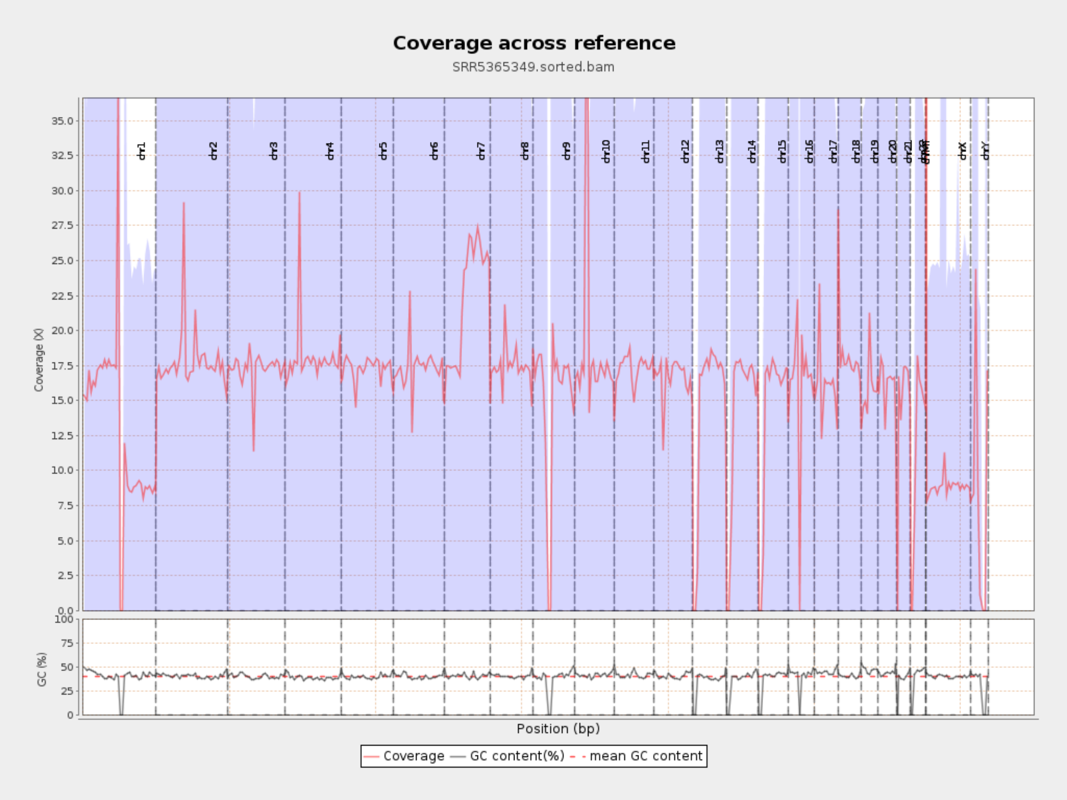
2.7. Chromosome stats

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

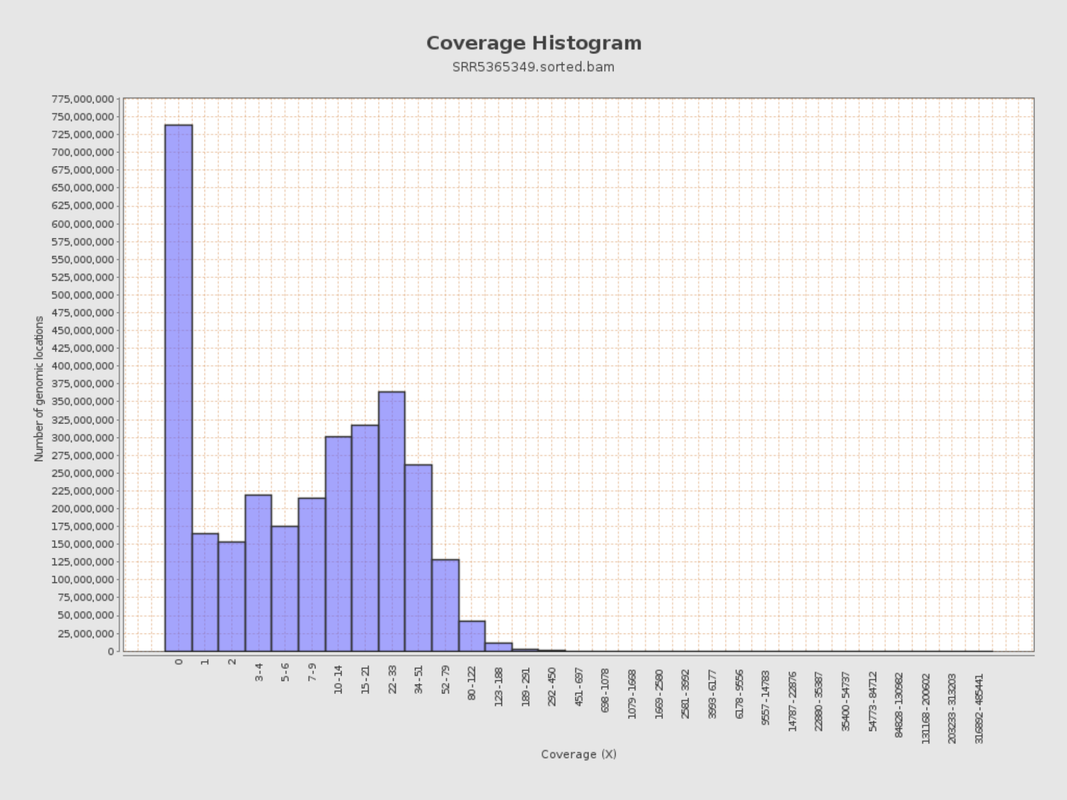
		bases	coverage	deviation
chr1	249250621	3239427634	12.9967	452.9752
chr2	243199373	4348924306	17.8821	95.9112
chr3	198022430	3418616173	17.2638	26.8429
chr4	191154276	3469667286	18.1511	103.5676
chr5	180915260	3120300475	17.2473	24.284
chr6	171115067	2971824998	17.3674	68.8126
chr7	159138663	3550151828	22.3085	105.7374
chr8	146364022	2550446907	17.4254	54.4992
chr9	141213431	2126840400	15.0612	125.1057
chr10	135534747	2555804277	18.8572	265.7178
chr11	135006516	2334130962	17.289	99.926
chr12	133851895	2231642469	16.6725	35.7027
chr13	115169878	1673986803	14.5349	21.0141
chr14	107349540	1532911152	14.2796	22.8291
chr15	102531392	1399450165	13.649	23.9932
chr16	90354753	1437050778	15.9045	59.5422
chr17	81195210	1319758274	16.2541	94.8151
chr18	78077248	1413573261	18.1048	168.2214
chr19	59128983	943444825	15.9557	226.4354
chr20	63025520	1021100823	16.2014	34.1584
chr21	48129895	709626857	14.744	60.1345
chr22	51304566	583639828	11.376	45.1938
chrMT	16571	67077282	4,047.8717	776.9577
chrX	155270560	1375224790	8.857	38.2075

chrY	59373566	507980247	8.5557	183.9138

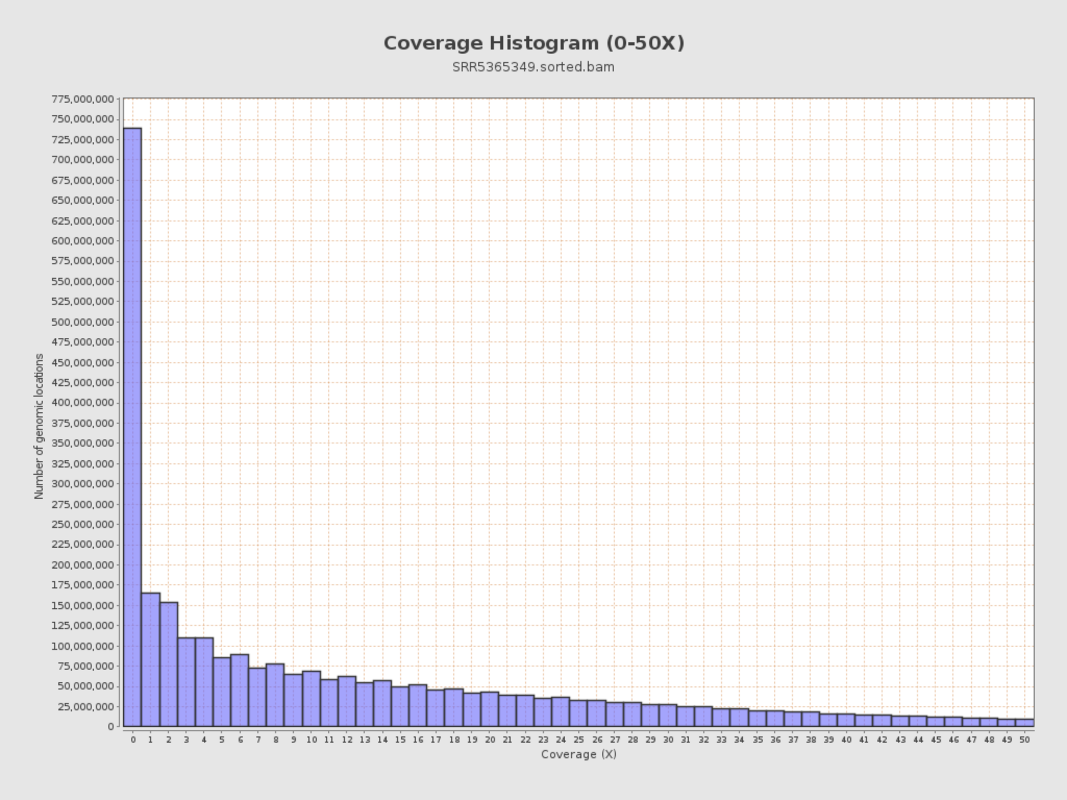
3. Results : Coverage across reference



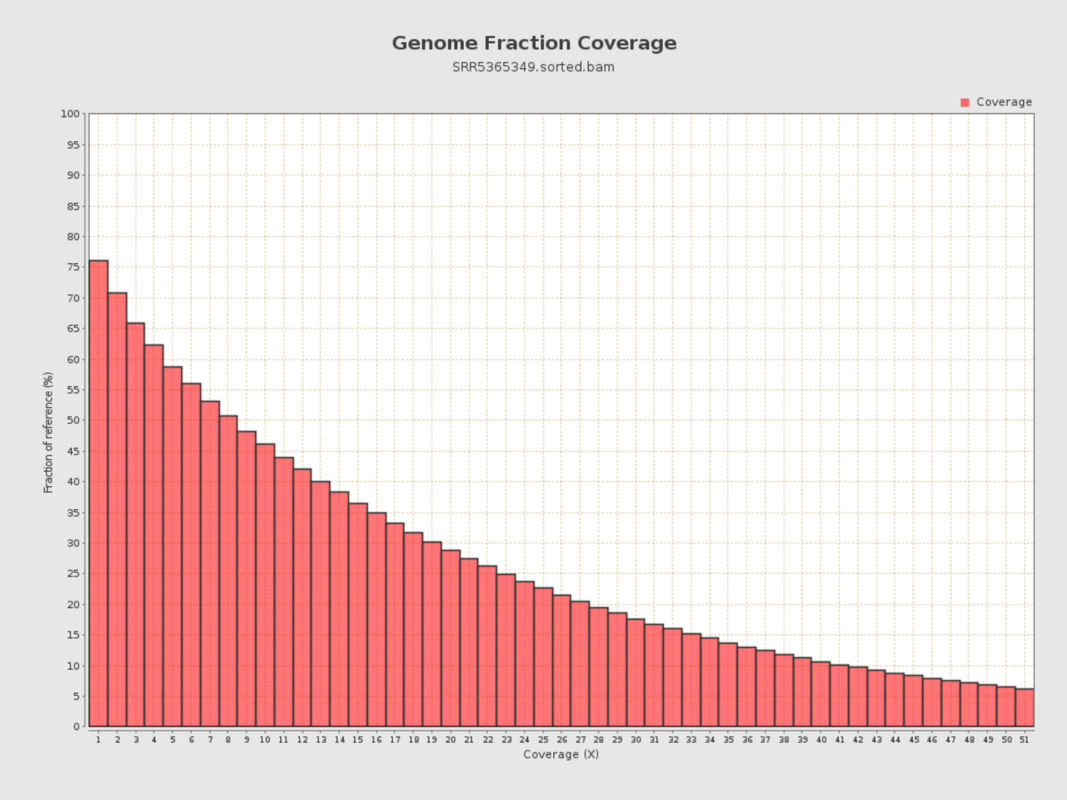
4. Results : Coverage Histogram



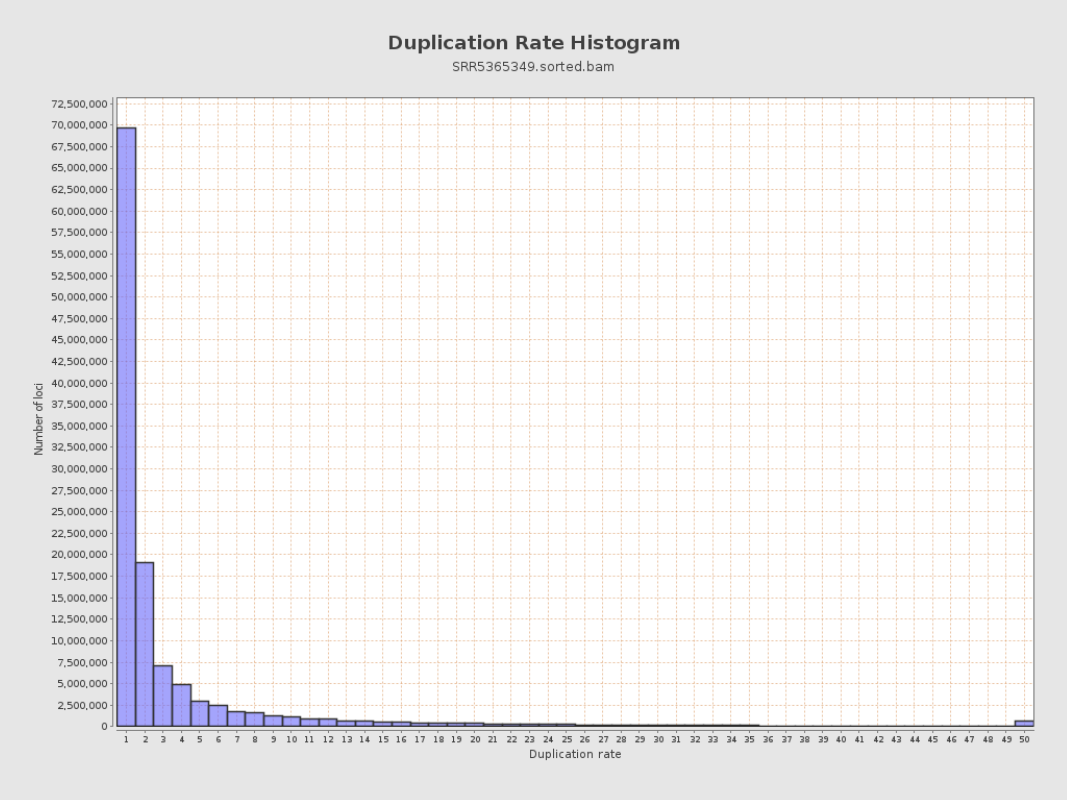
5. Results : Coverage Histogram (0-50X)



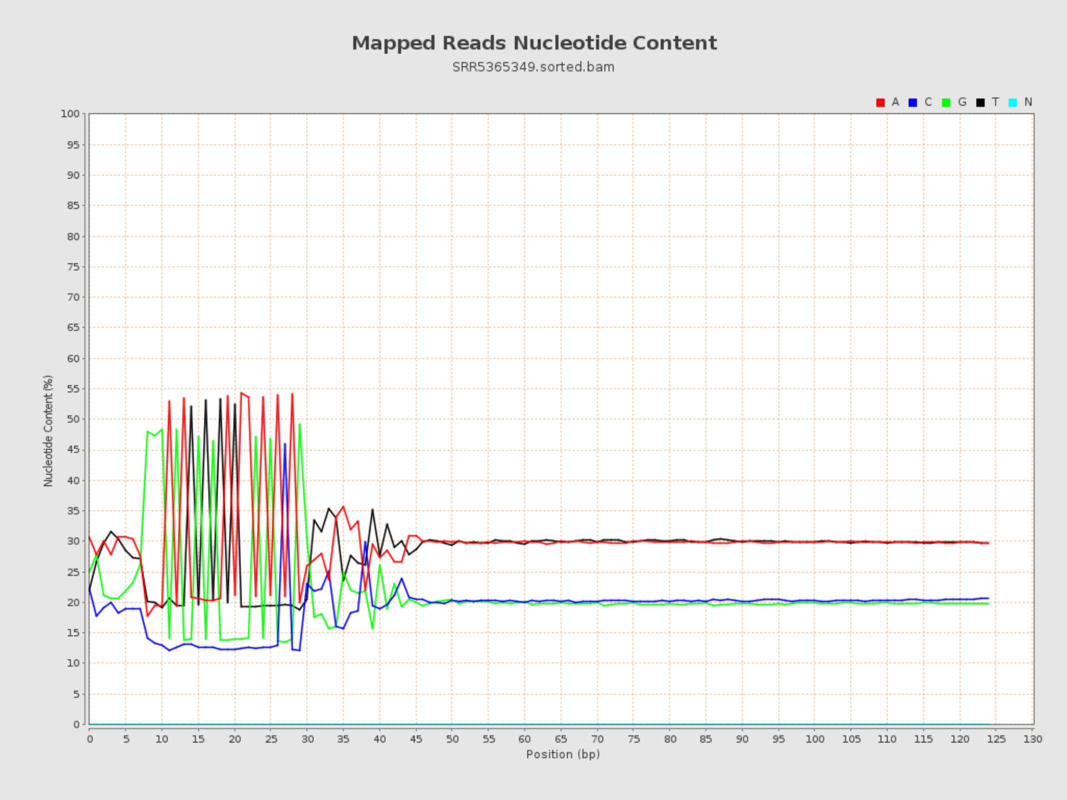
6. Results : Genome Fraction Coverage



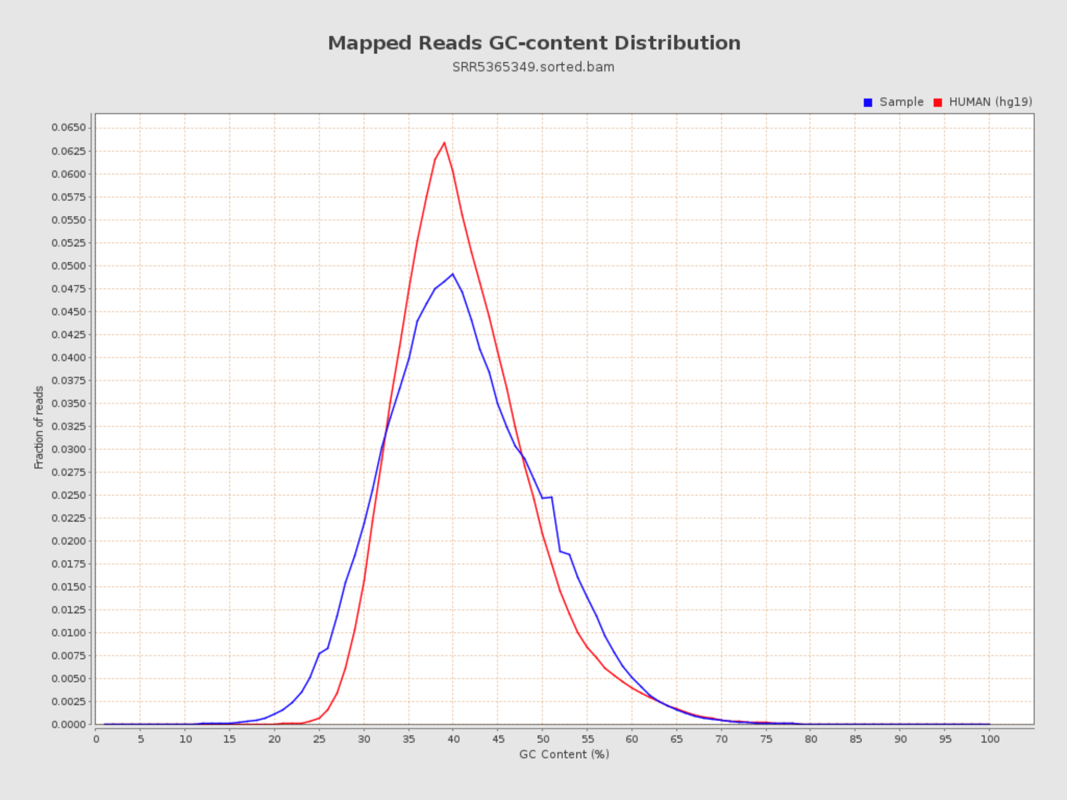
7. Results : Duplication Rate Histogram



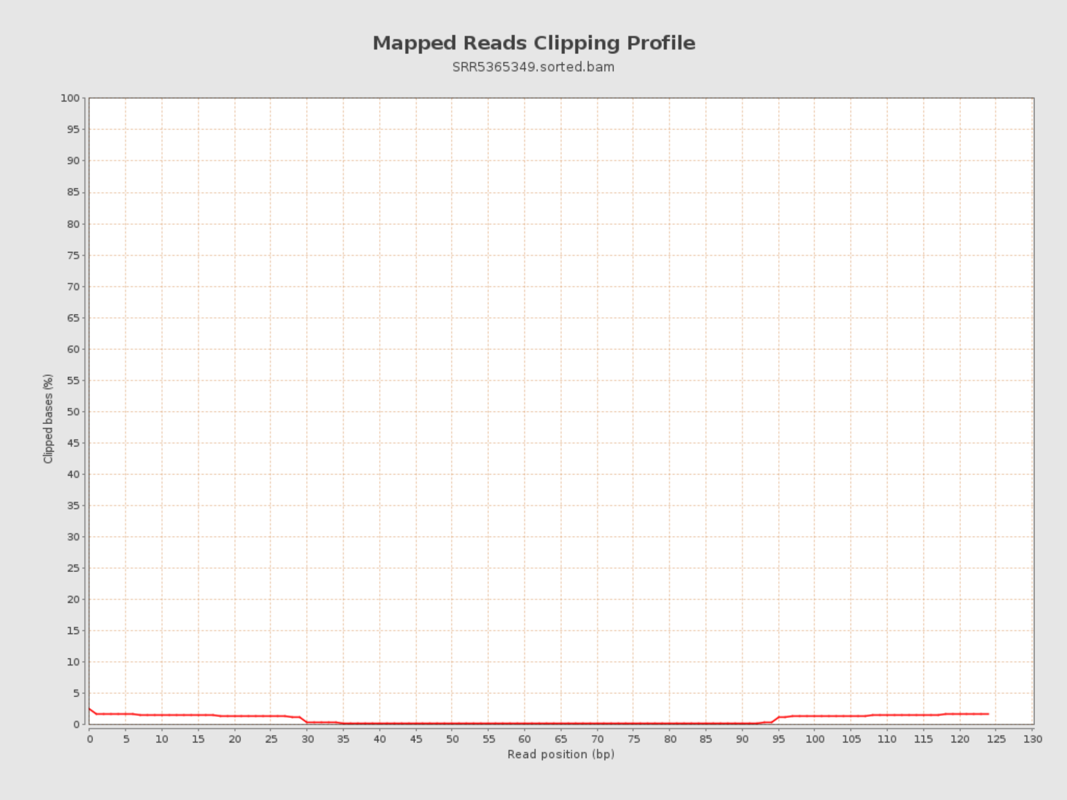
8. Results : Mapped Reads Nucleotide Content



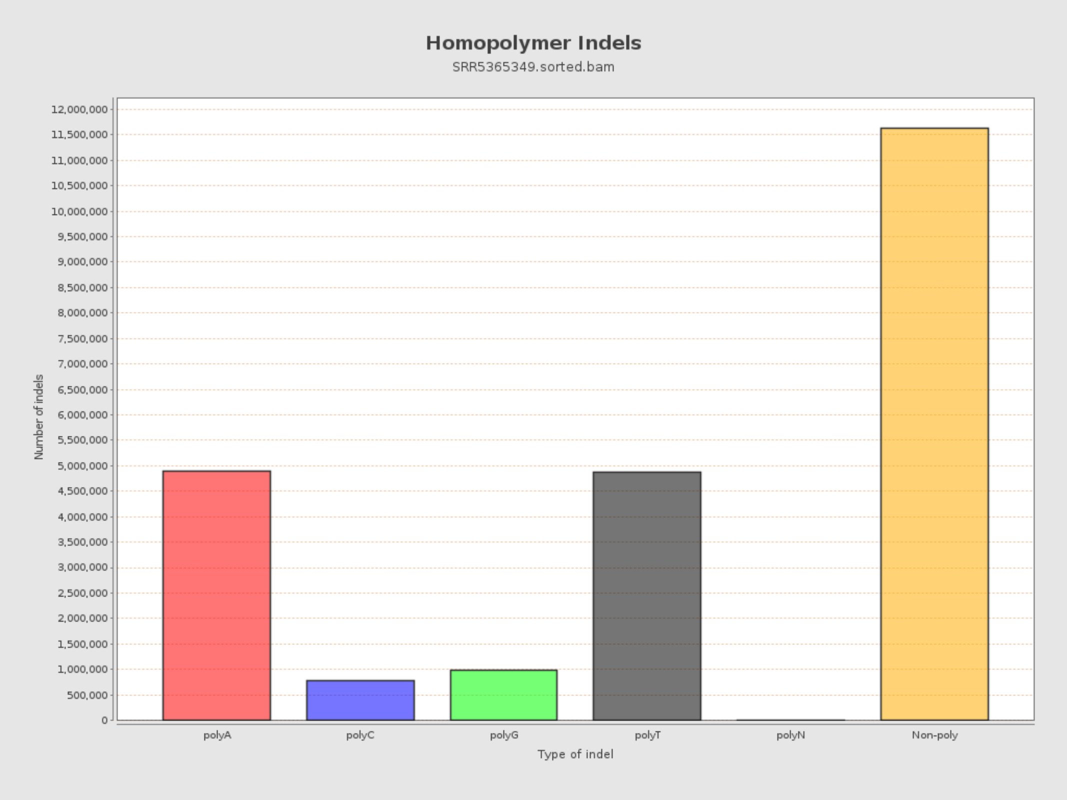
9. Results : Mapped Reads GC-content Distribution



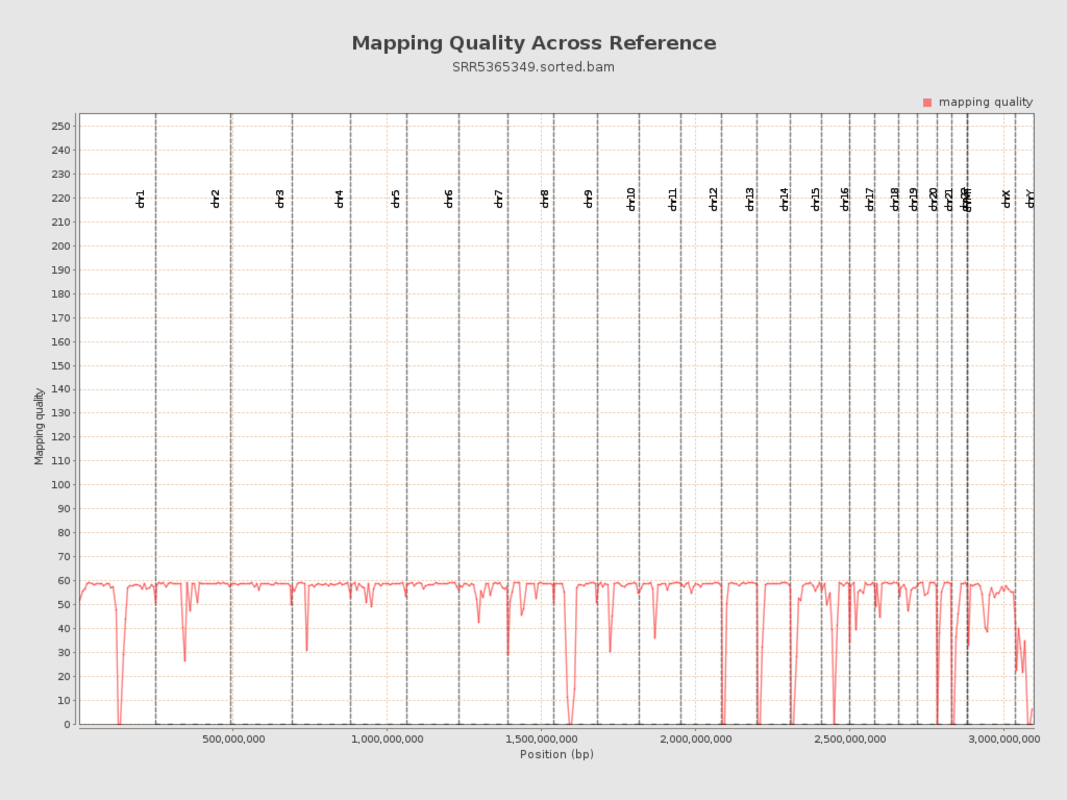
10. Results : Mapped Reads Clipping Profile



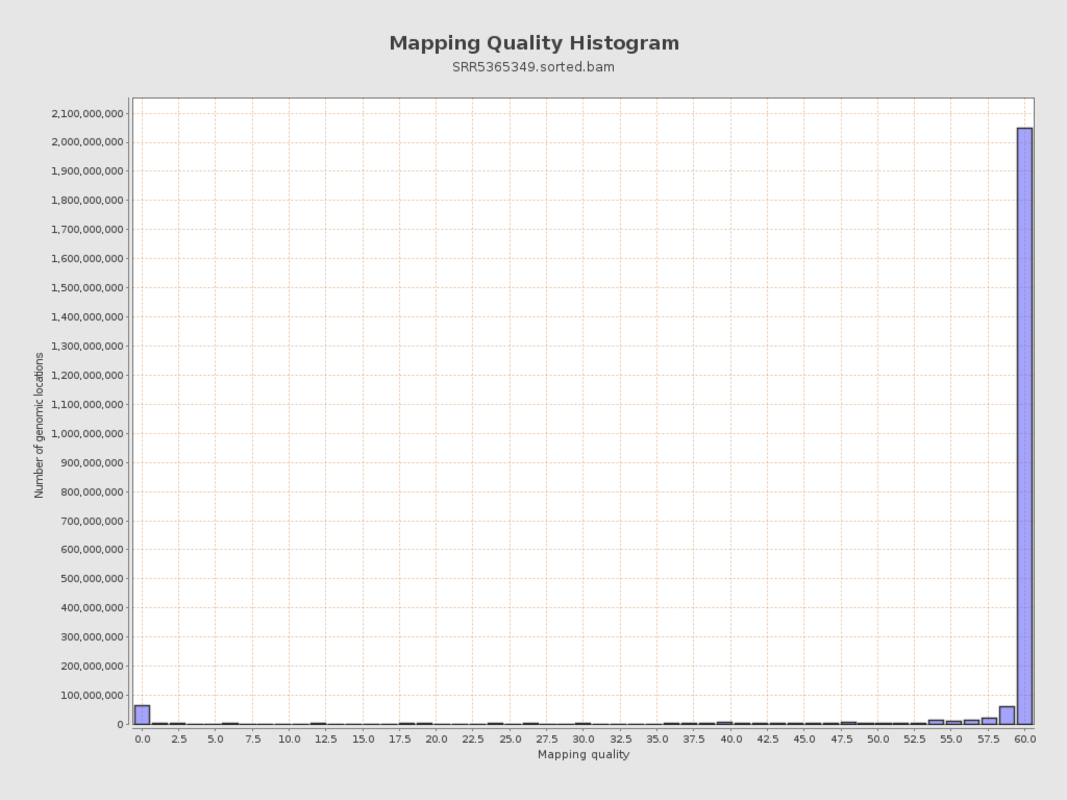
11. Results : Homopolymer Indels



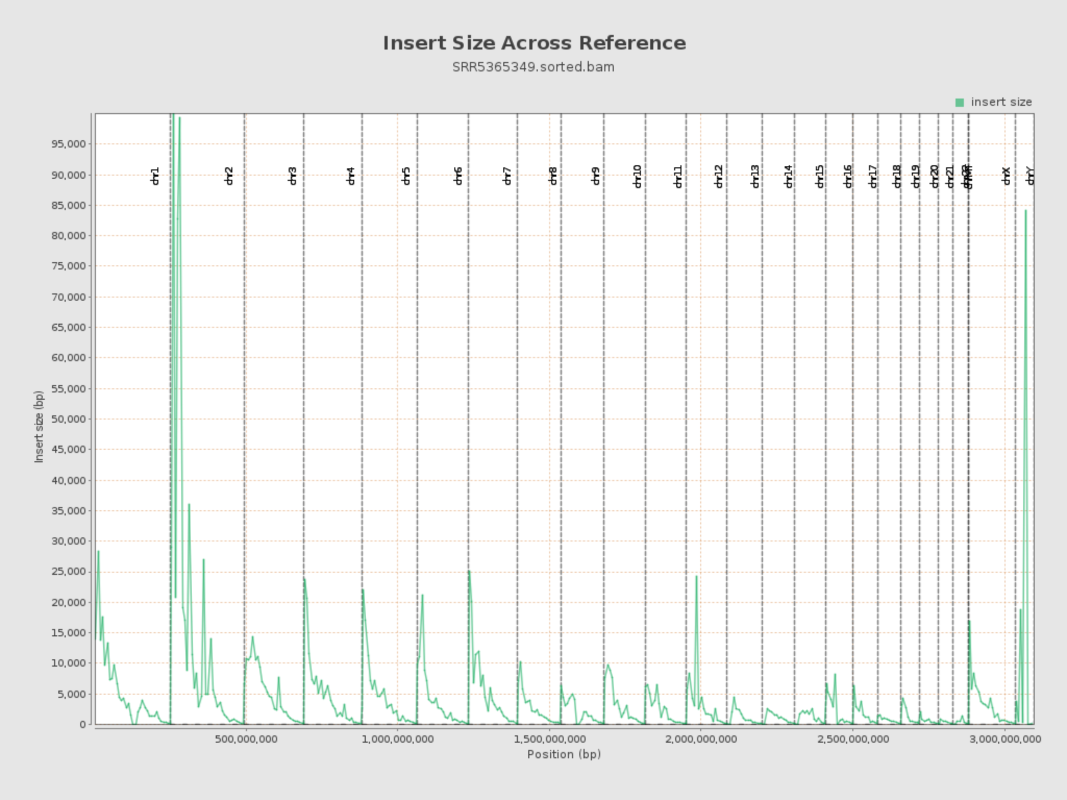
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram