Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 23:22:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124819.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_SRR3124819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124819_1.fastq.gz SRR3124819_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 23:22:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,236,344
Mapped reads	22,421,096 / 96.49%
Unmapped reads	815,248 / 3.51%
Mapped paired reads	22,421,096 / 96.49%
Mapped reads, first in pair	11,300,882 / 48.63%
Mapped reads, second in pair	11,120,214 / 47.86%
Mapped reads, both in pair	22,004,738 / 94.7%
Mapped reads, singletons	416,358 / 1.79%
Secondary alignments	0
Supplementary alignments	30,145 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	2,512,241 / 10.81%
Duplication rate	7.02%
Clipped reads	8,141,979 / 35.04%

2.2. ACGT Content

Number/percentage of A's	415,384,309 / 28.39%
Number/percentage of C's	266,100,264 / 18.19%
Number/percentage of T's	440,831,345 / 30.13%
Number/percentage of G's	340,759,405 / 23.29%
Number/percentage of N's	45,949 / 0%

GC Percentage	41.48%

2.3. Coverage

Mean	0.4728
Standard Deviation	4.0991

2.4. Mapping Quality

Mean Mapping Quality	51.92

2.5. Insert size

Mean	42,382.45
Standard Deviation	1,956,974.6
P25/Median/P75	147 / 194 / 266

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	11,927,349
Insertions	167,919
Mapped reads with at least one insertion	0.74%
Deletions	450,001
Mapped reads with at least one deletion	1.98%
Homopolymer indels	48.27%

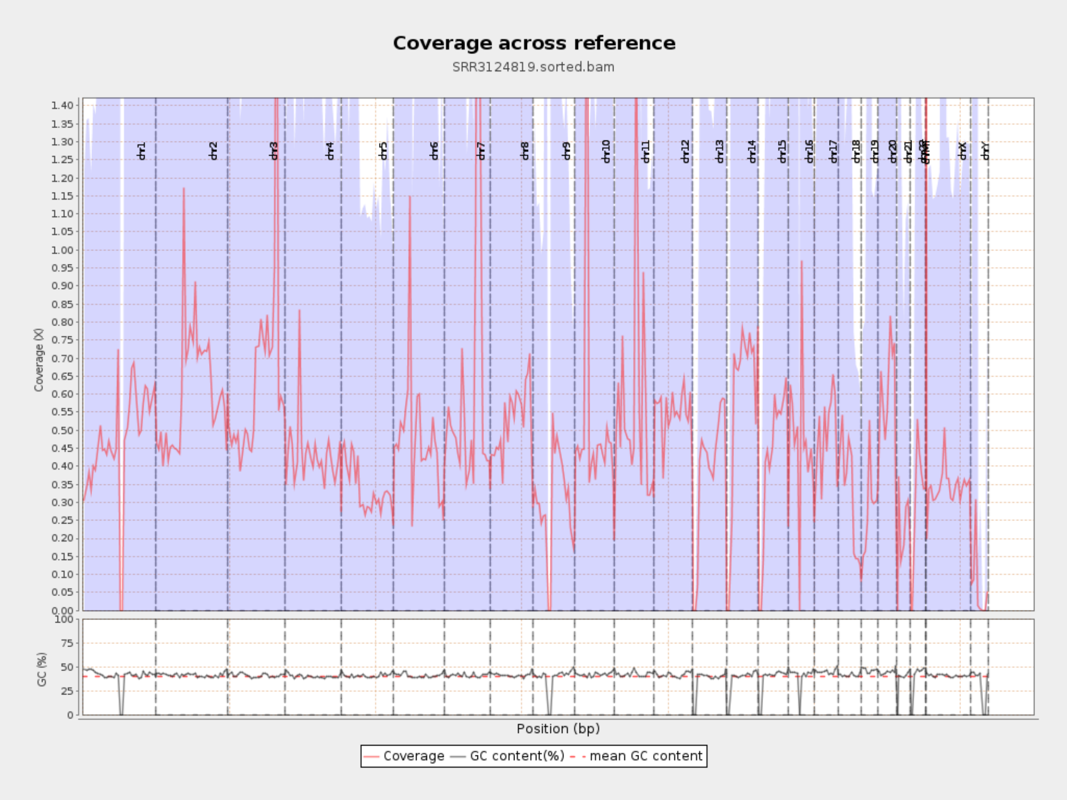
2.7. Chromosome stats

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

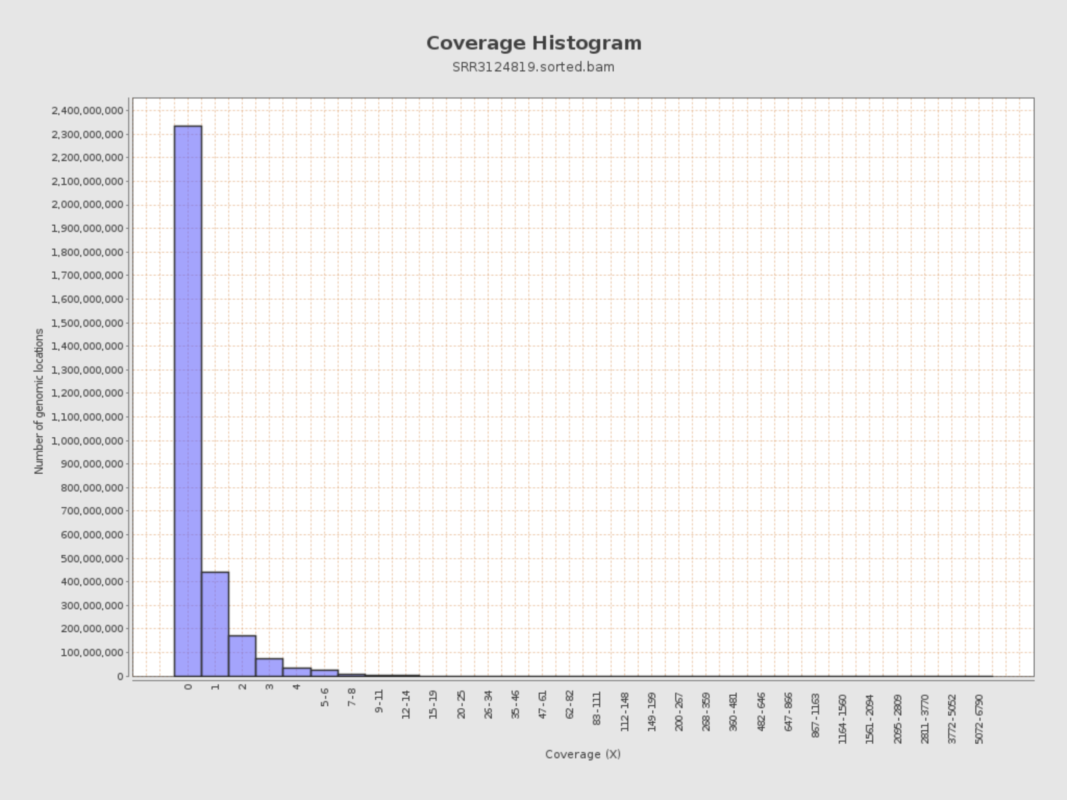
		bases	coverage	deviation
chr1	249250621	117210999	0.4703	4.2563
chr2	243199373	148185831	0.6093	4.0785
chr3	198022430	130020092	0.6566	1.5859
chr4	191154276	83404668	0.4363	2.1485
chr5	180915260	61255869	0.3386	0.9151
chr6	171115067	82759793	0.4836	5.8769
chr7	159138663	102860257	0.6464	5.9623
chr8	146364022	77458111	0.5292	1.7267
chr9	141213431	42619612	0.3018	3.7011
chr10	135534747	71303072	0.5261	12.1014
chr11	135006516	76762610	0.5686	2.6415
chr12	133851895	74086248	0.5535	1.2141
chr13	115169878	44900145	0.3899	0.9563
chr14	107349540	62245156	0.5798	1.432
chr15	102531392	42782930	0.4173	1.0537
chr16	90354753	41867000	0.4634	4.1585
chr17	81195210	40044552	0.4932	3.0311
chr18	78077248	25848728	0.3311	5.1733
chr19	59128983	16405744	0.2775	3.0467
chr20	63025520	38644784	0.6132	1.3947
chr21	48129895	10903824	0.2265	1.4393
chr22	51304566	15267982	0.2976	0.9023
chrMT	16571	104779	6.323	4.6088
chrX	155270560	52885955	0.3406	1.5122

chrY	59373566	3968093	0.0668	3.9776

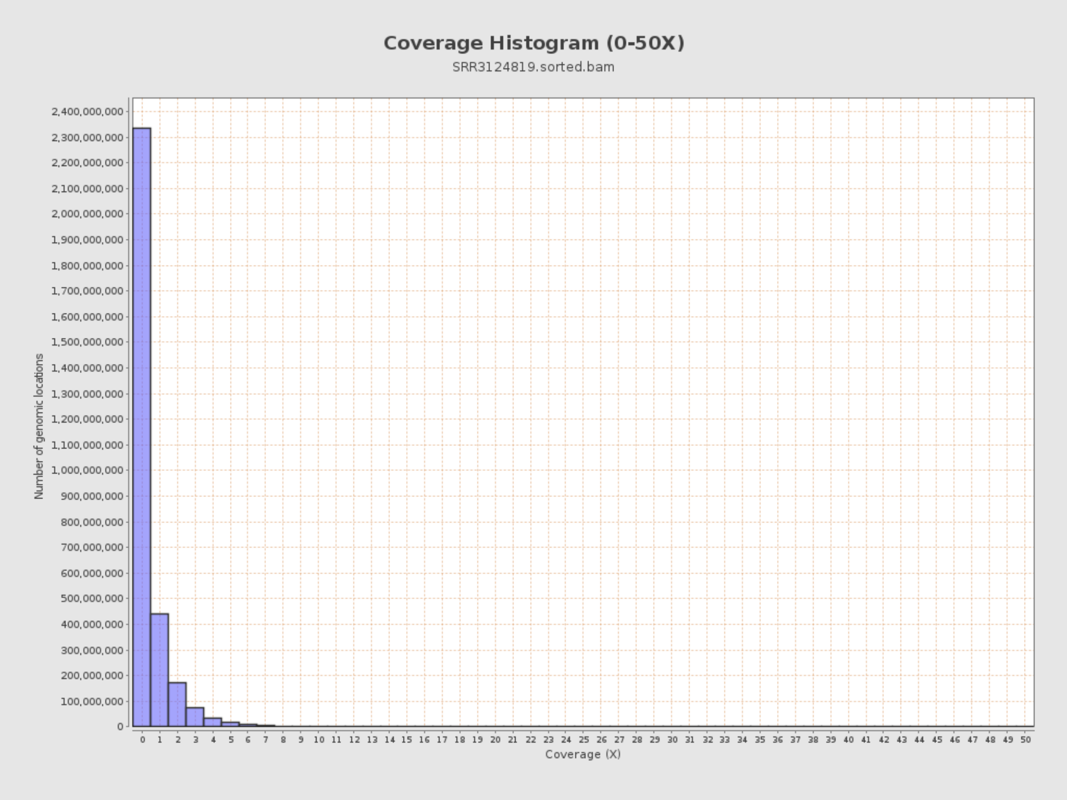
3. Results : Coverage across reference



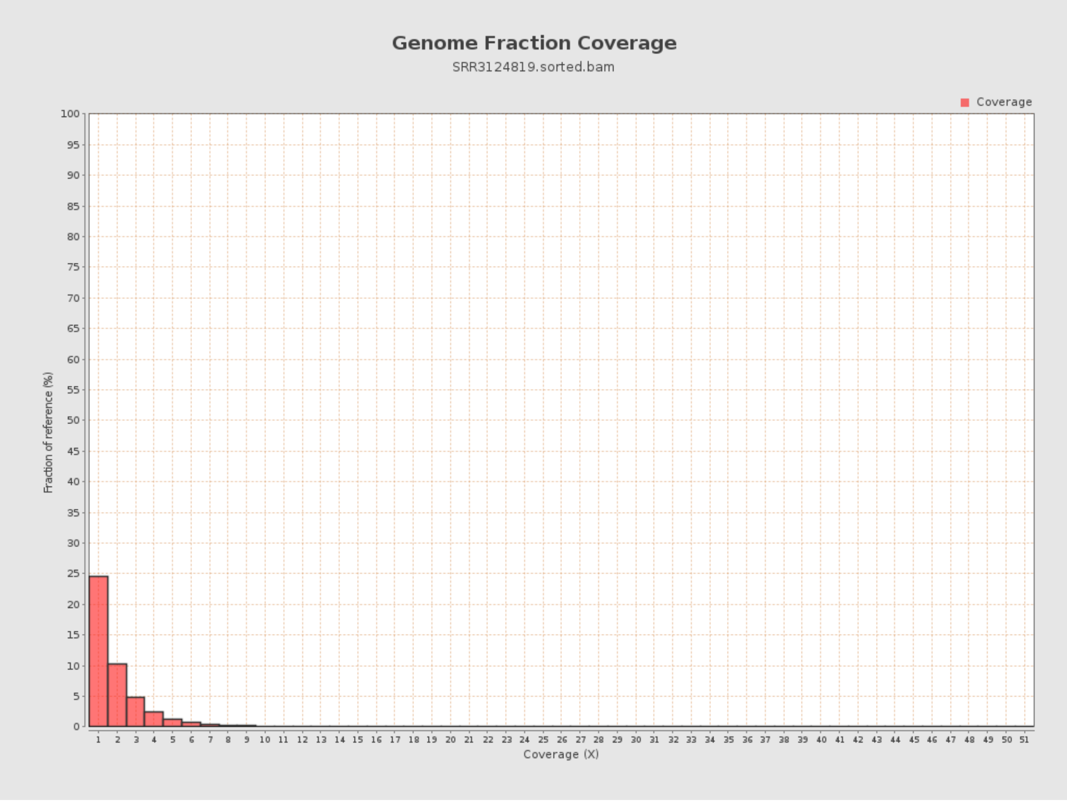
4. Results : Coverage Histogram



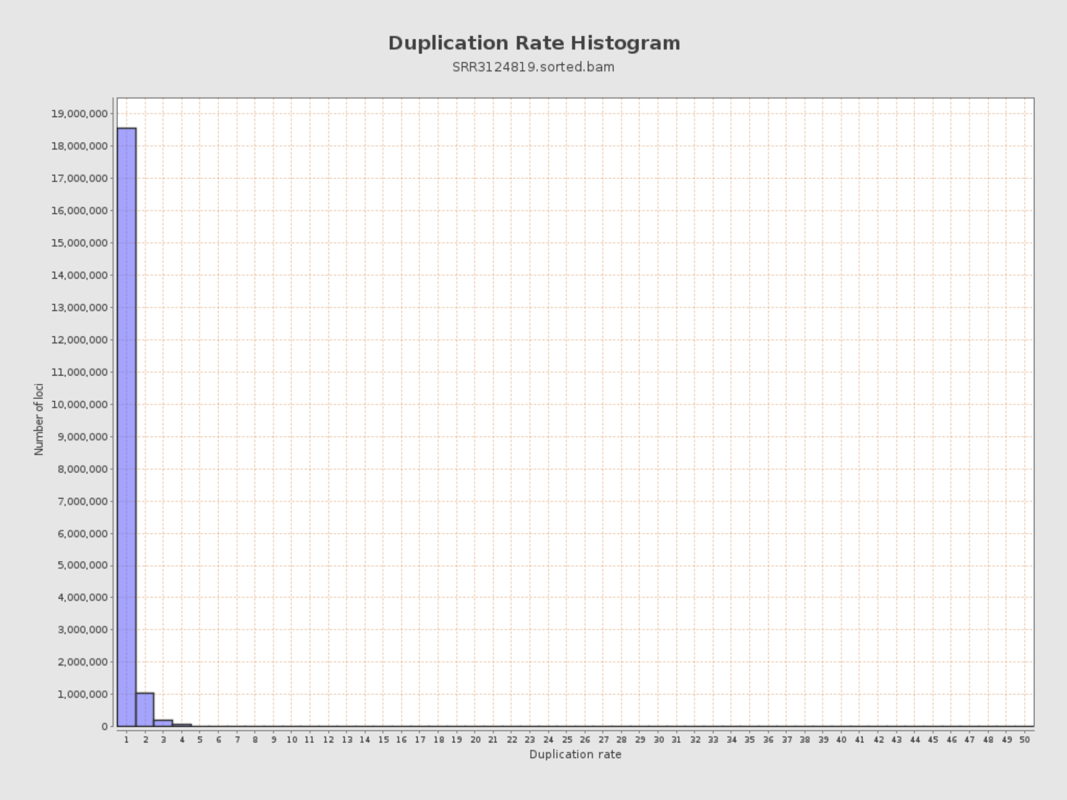
5. Results : Coverage Histogram (0-50X)



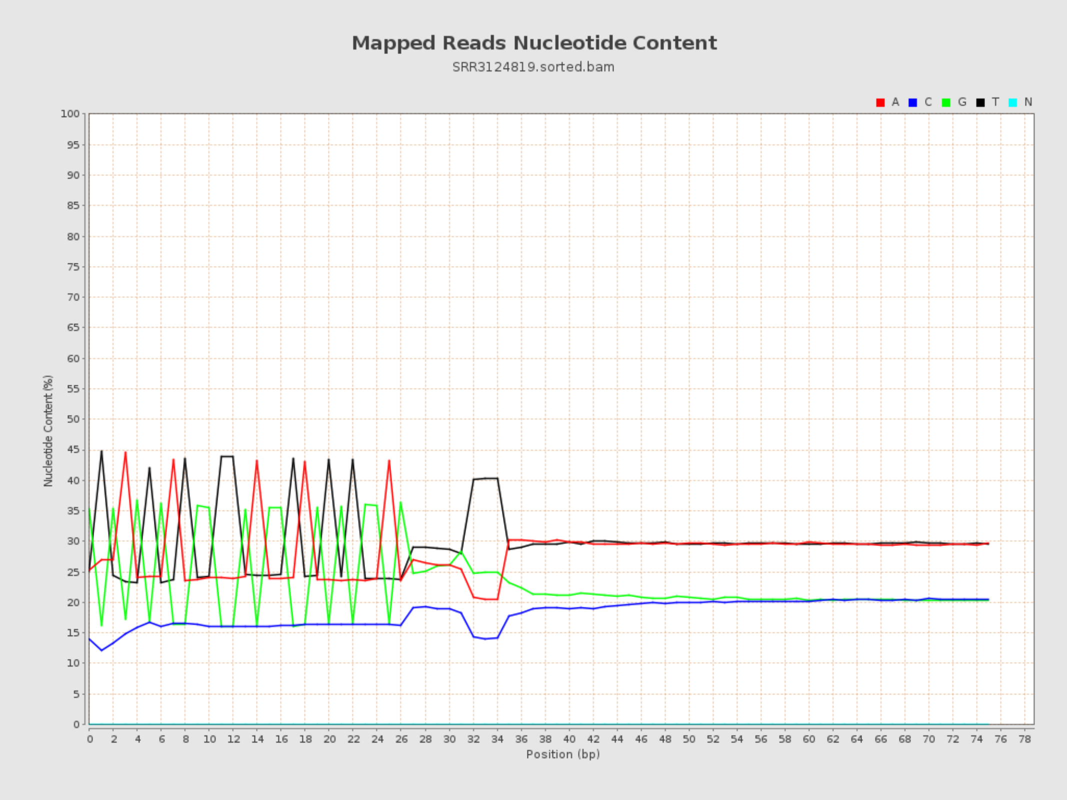
6. Results : Genome Fraction Coverage



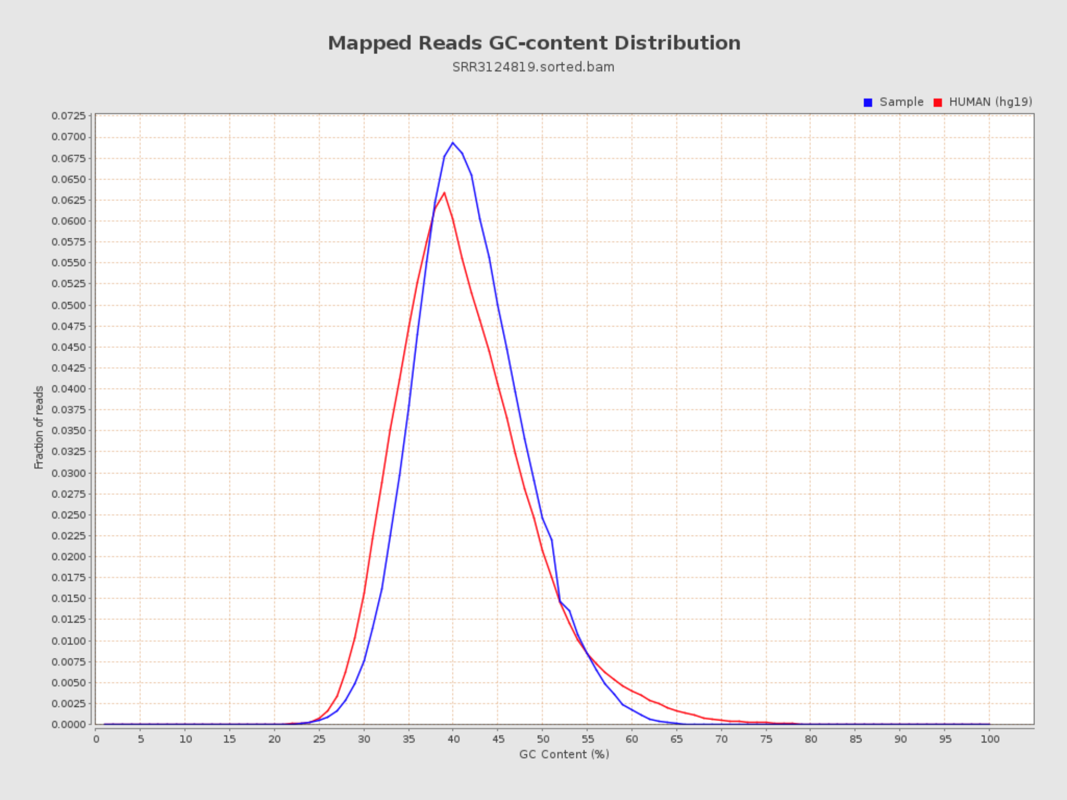
7. Results : Duplication Rate Histogram



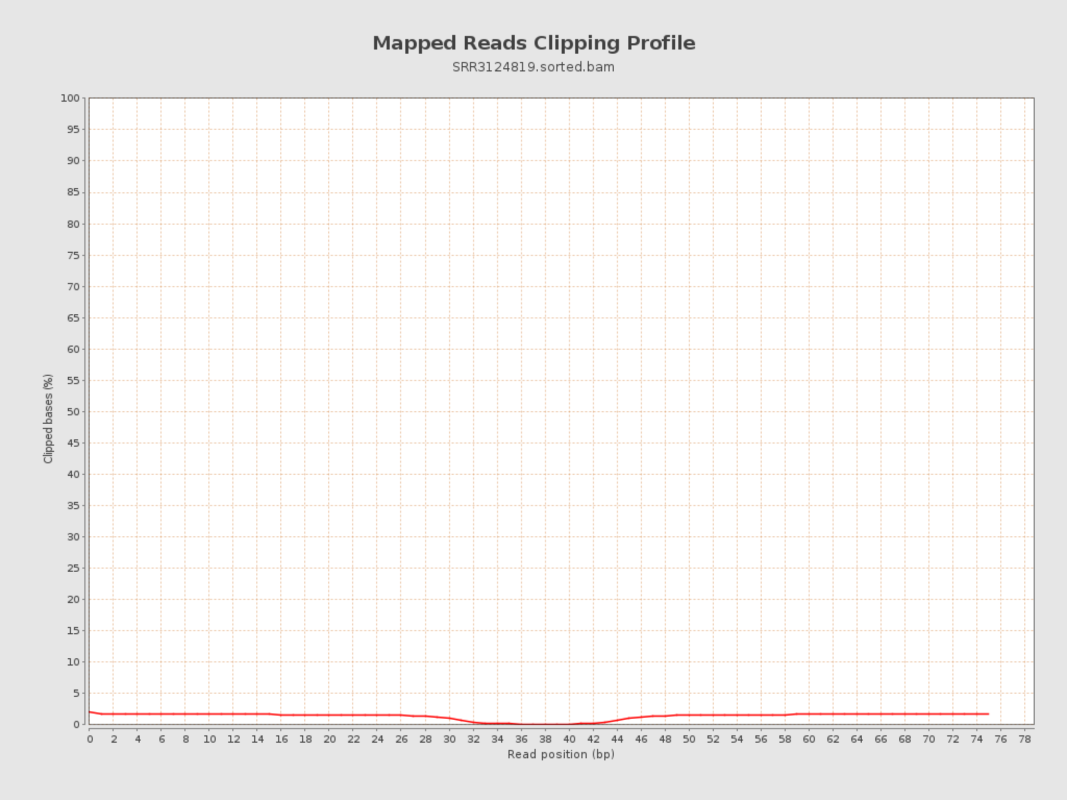
8. Results : Mapped Reads Nucleotide Content



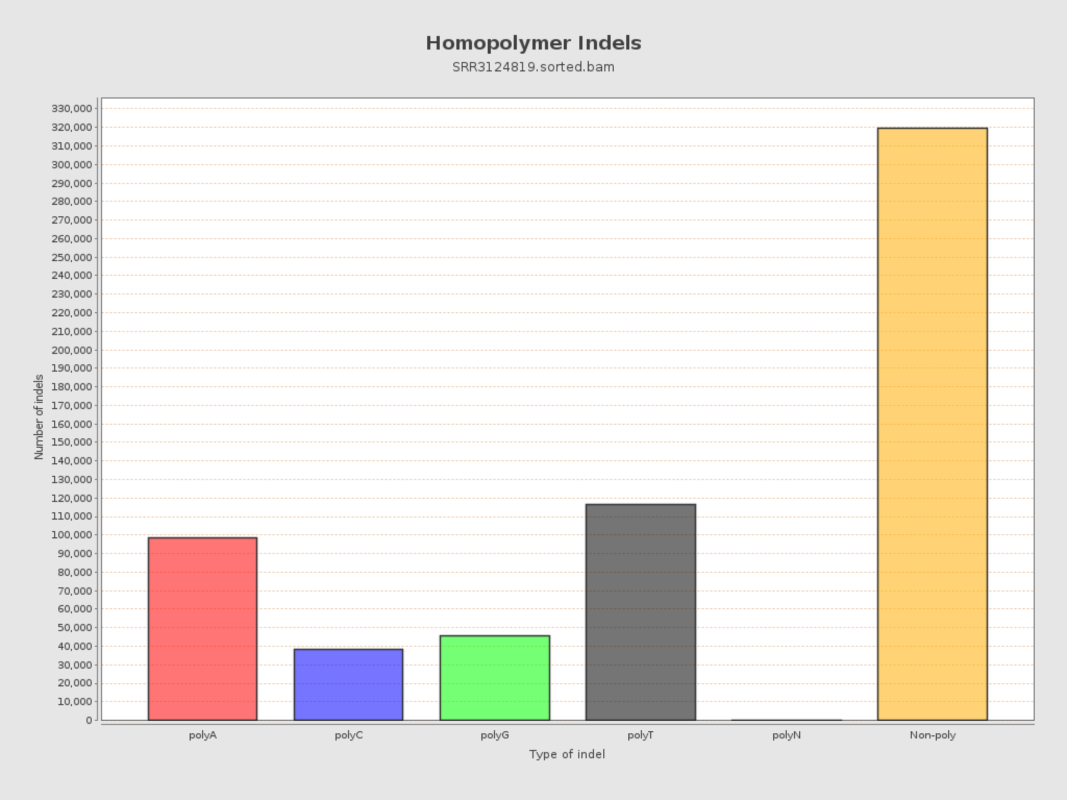
9. Results : Mapped Reads GC-content Distribution



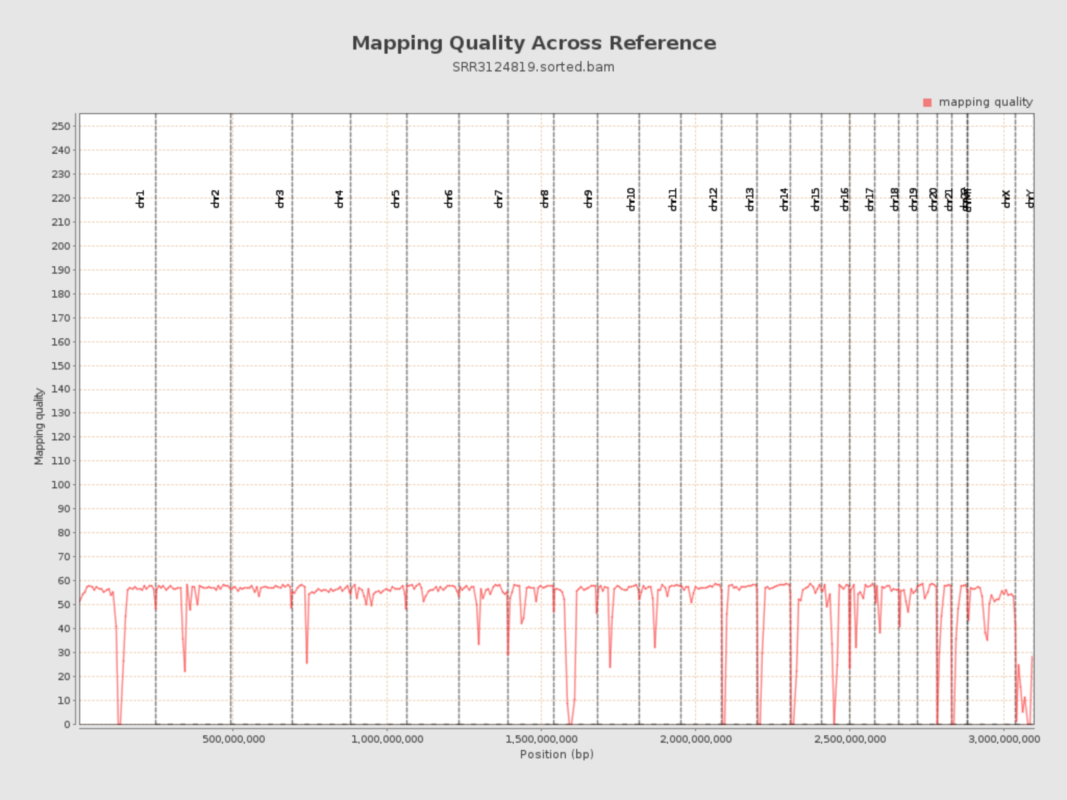
10. Results : Mapped Reads Clipping Profile



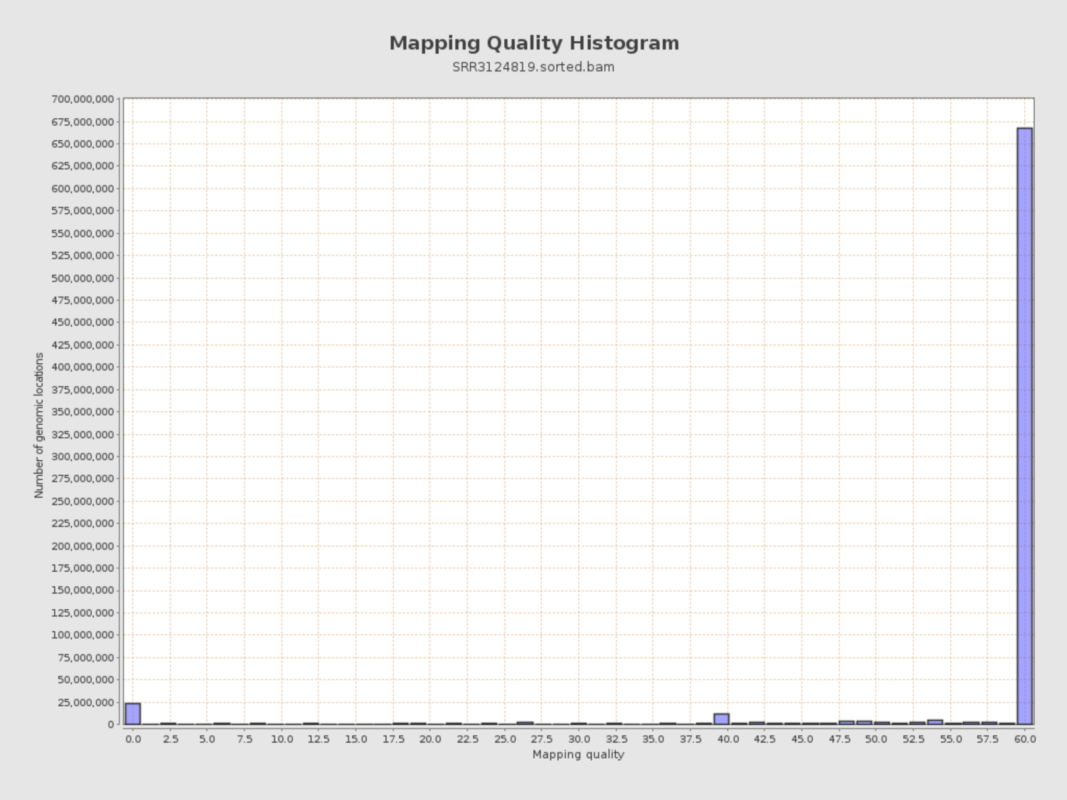
11. Results : Homopolymer Indels



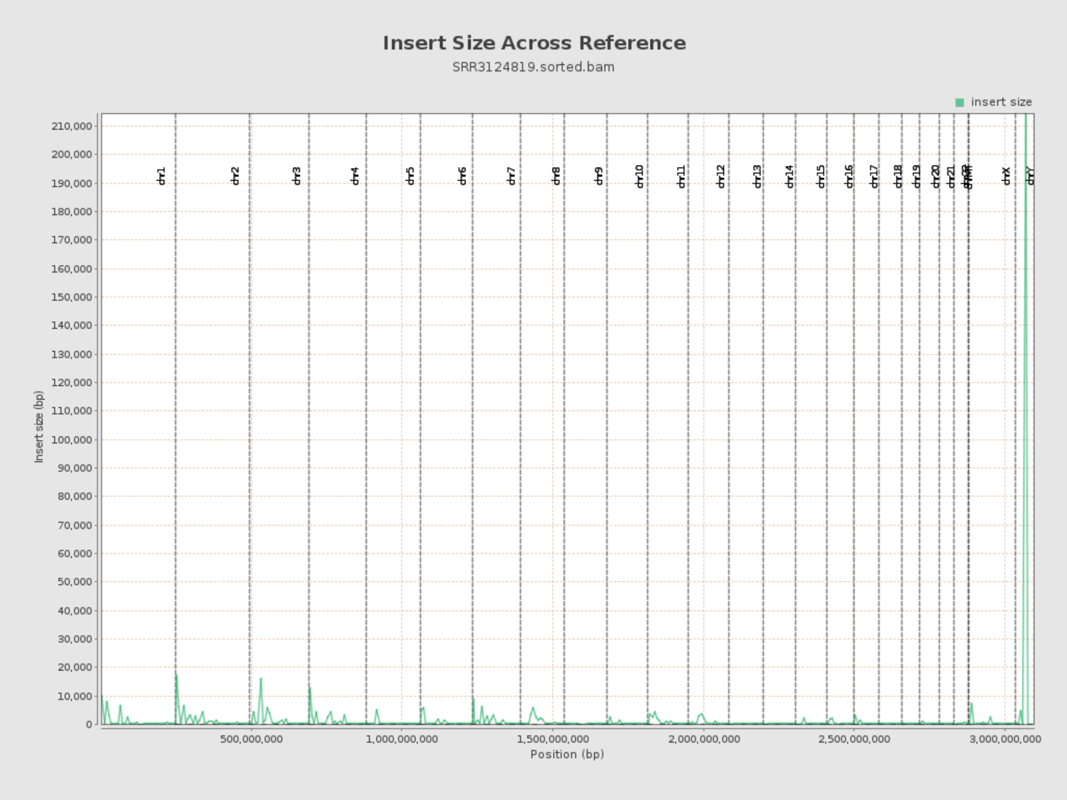
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram