Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:39:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472485.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_SRR3472485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472485_1.fastq.gz SRR3472485_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:39:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,267,396
Mapped reads	13,120,089 / 98.89%
Unmapped reads	147,307 / 1.11%
Mapped paired reads	13,120,089 / 98.89%
Mapped reads, first in pair	6,585,100 / 49.63%
Mapped reads, second in pair	6,534,989 / 49.26%
Mapped reads, both in pair	13,037,162 / 98.26%
Mapped reads, singletons	82,927 / 0.63%
Secondary alignments	0
Supplementary alignments	50,756 / 0.38%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	7,766,866 / 58.54%
Duplication rate	44.31%
Clipped reads	849,687 / 6.4%

2.2. ACGT Content

Number/percentage of A's	364,018,475 / 28.08%
Number/percentage of C's	285,859,432 / 22.05%
Number/percentage of T's	362,664,194 / 27.97%
Number/percentage of G's	283,701,687 / 21.88%
Number/percentage of N's	197,631 / 0.02%

GC Percentage	43.93%

2.3. Coverage

Mean	0.4188
Standard Deviation	14.5568

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	27,428.39
Standard Deviation	1,593,168.92
P25/Median/P75	188 / 254 / 335

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	8,282,153
Insertions	76,256
Mapped reads with at least one insertion	0.58%
Deletions	71,378
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.27%

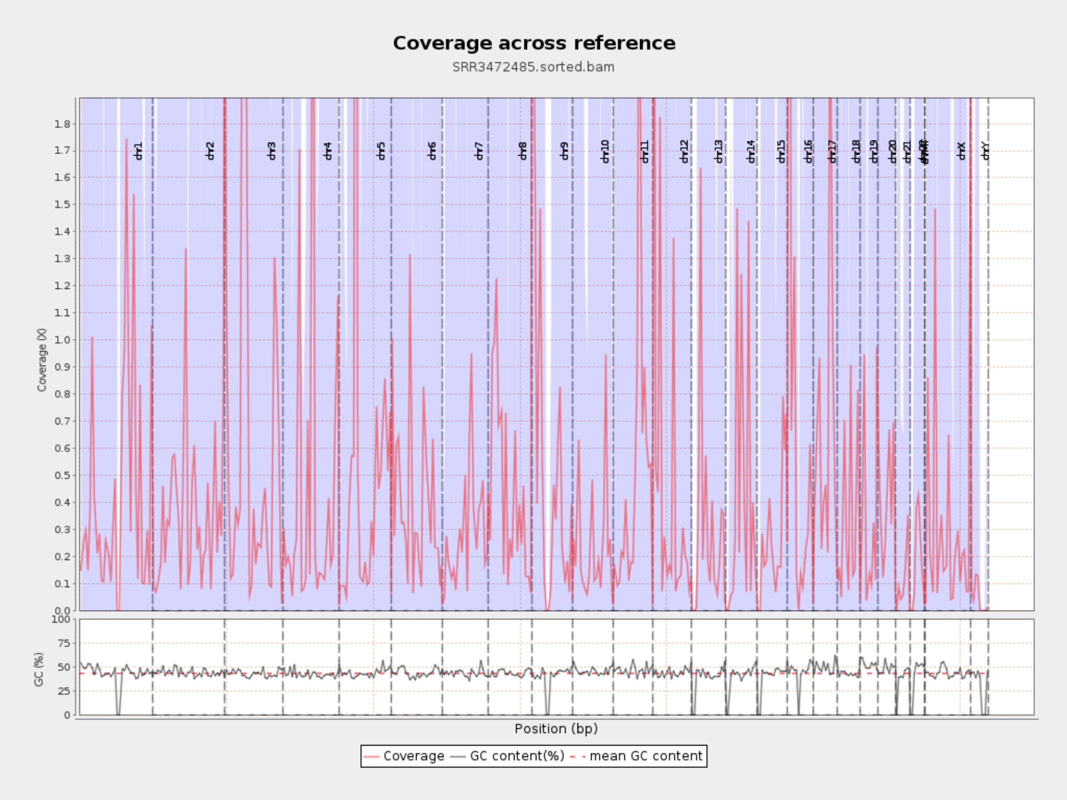
2.7. Chromosome stats

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

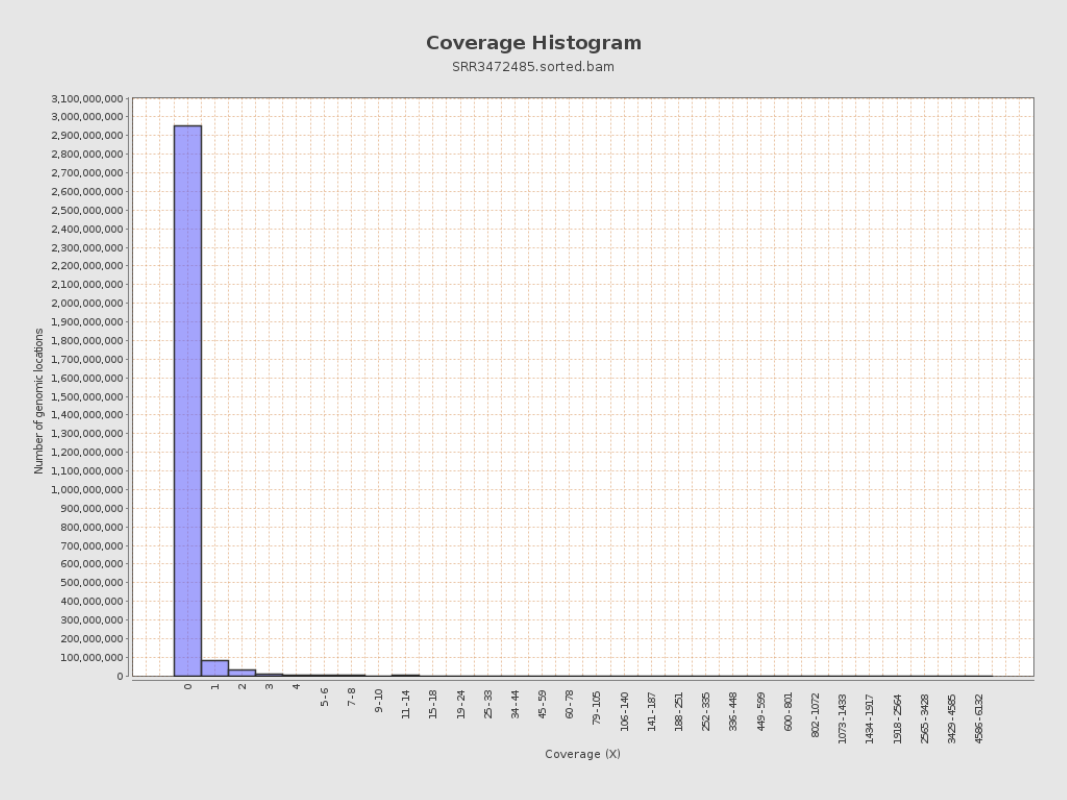
		bases	coverage	deviation
chr1	249250621	109454257	0.4391	14.3509
chr2	243199373	84487744	0.3474	9.8568
chr3	198022430	128602999	0.6494	14.4994
chr4	191154276	82606880	0.4321	21.7736
chr5	180915260	99858519	0.552	17.015
chr6	171115067	67566279	0.3949	11.1454
chr7	159138663	46307479	0.291	9.317
chr8	146364022	66450855	0.454	13.4088
chr9	141213431	81000196	0.5736	16.5086
chr10	135534747	33372246	0.2462	10.2452
chr11	135006516	69273717	0.5131	19.1687
chr12	133851895	69109600	0.5163	19.6489
chr13	115169878	35755266	0.3105	13.1475
chr14	107349540	44918616	0.4184	22.0572
chr15	102531392	27014935	0.2635	7.0045
chr16	90354753	61273931	0.6781	18.6367
chr17	81195210	53721753	0.6616	18.1003
chr18	78077248	27254712	0.3491	11.8234
chr19	59128983	17545419	0.2967	9.3548
chr20	63025520	25973949	0.4121	10.6501
chr21	48129895	5469594	0.1136	3.9787
chr22	51304566	8617999	0.168	4.964
chrMT	16571	2402	0.145	0.4934
chrX	155270560	48212290	0.3105	11.444

chrY	59373566	2767921	0.0466	1.8214

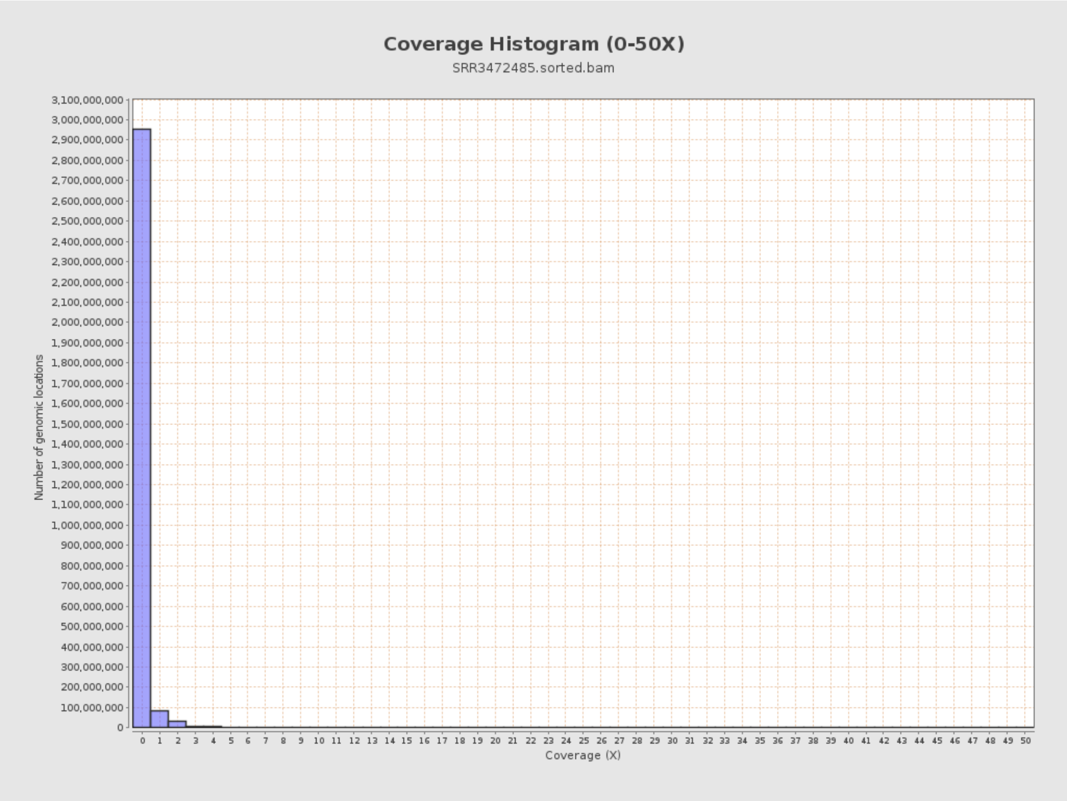
3. Results : Coverage across reference



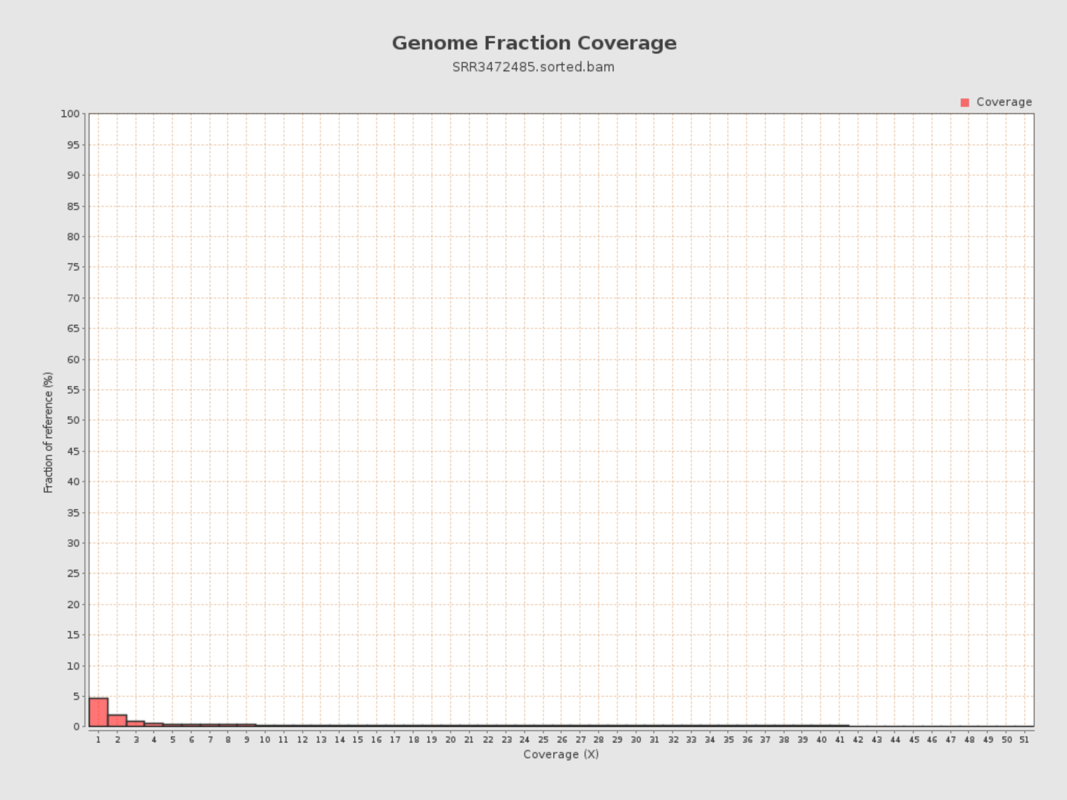
4. Results : Coverage Histogram



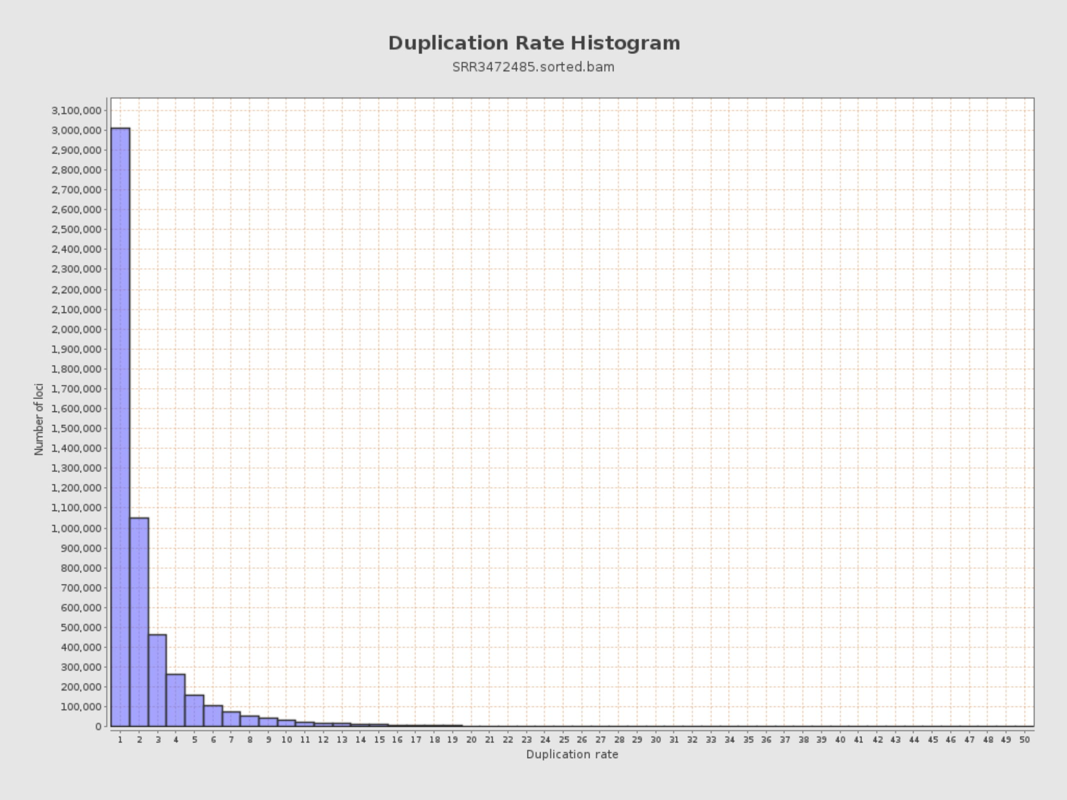
5. Results : Coverage Histogram (0-50X)



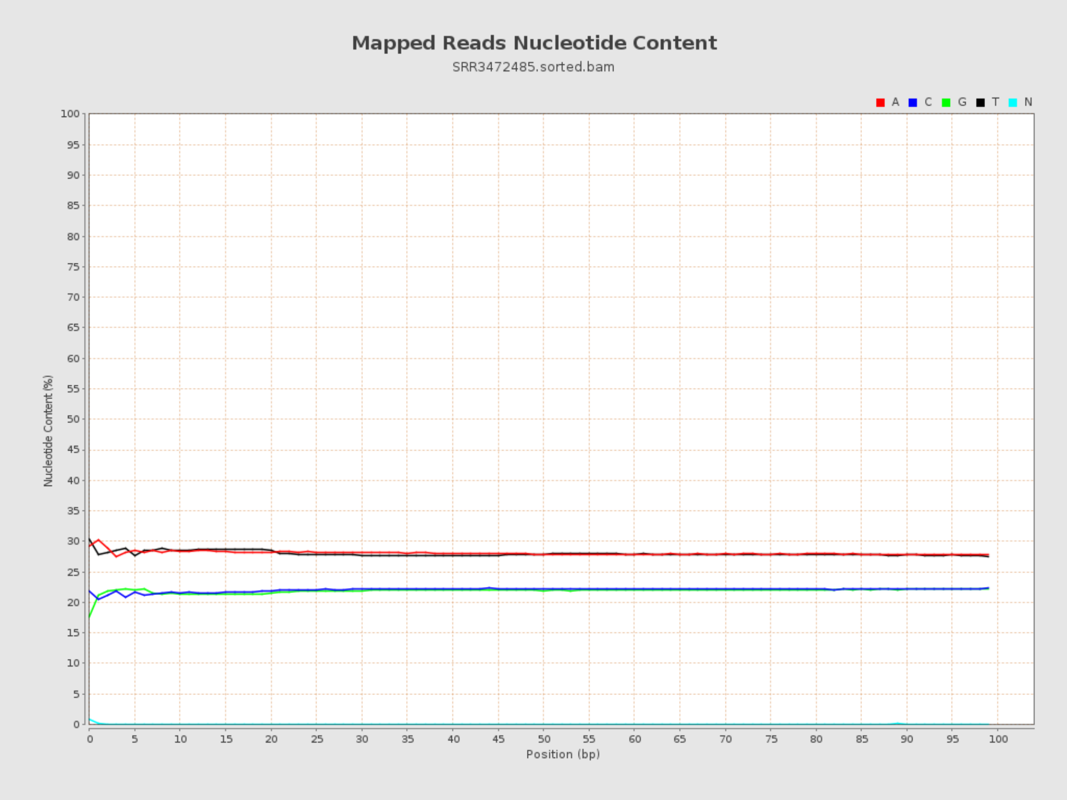
6. Results : Genome Fraction Coverage



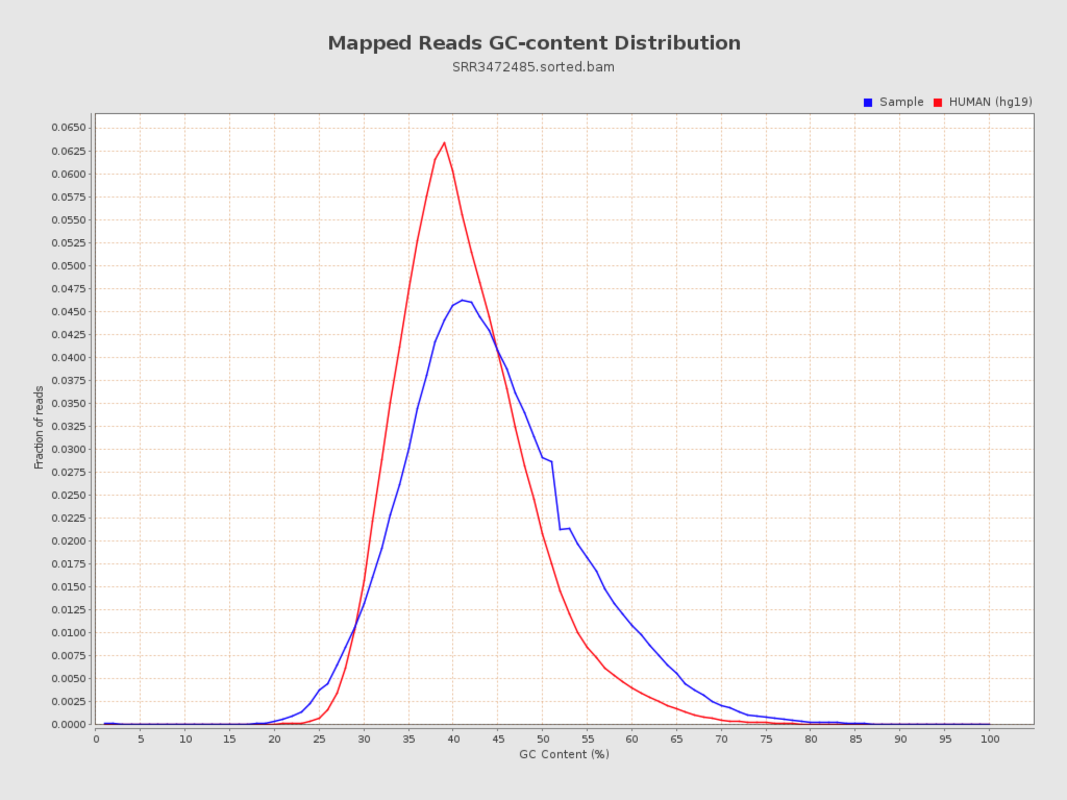
7. Results : Duplication Rate Histogram



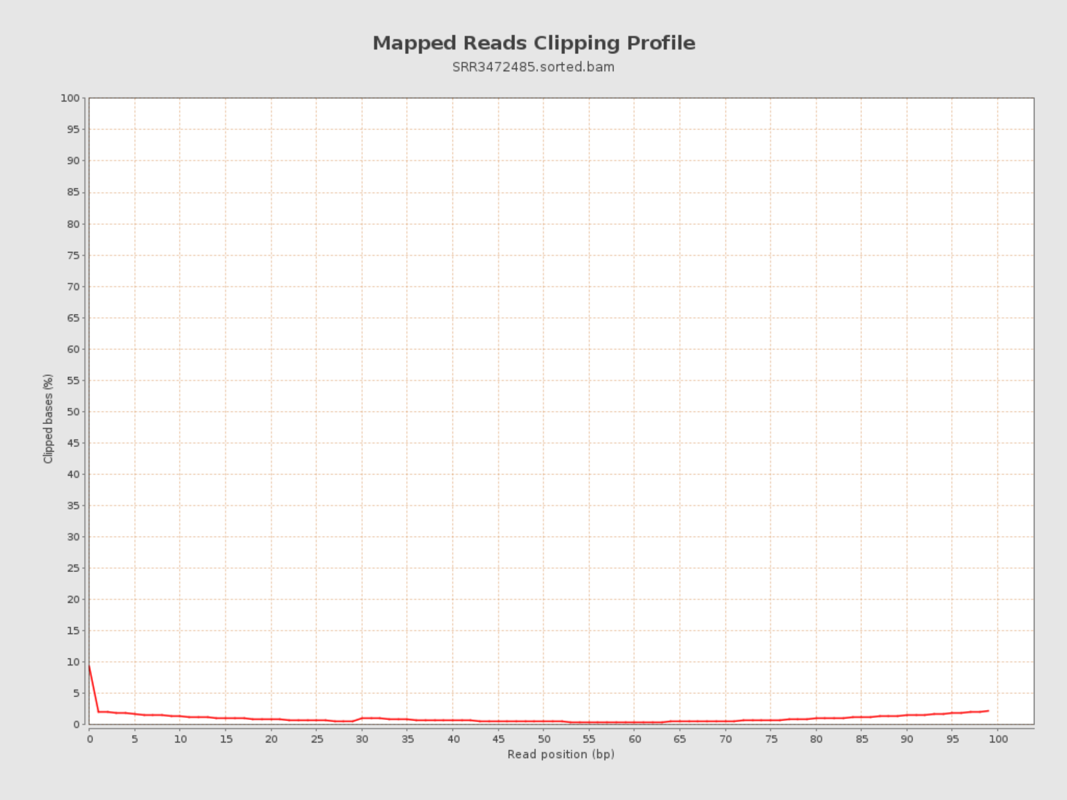
8. Results : Mapped Reads Nucleotide Content



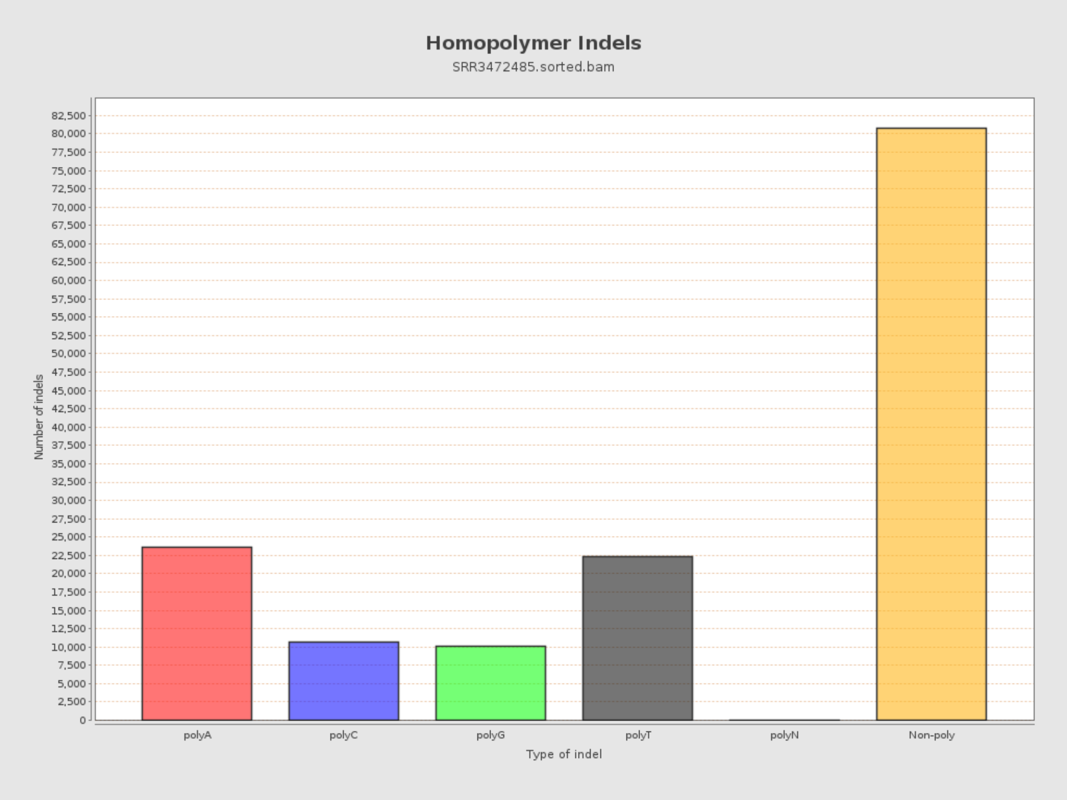
9. Results : Mapped Reads GC-content Distribution



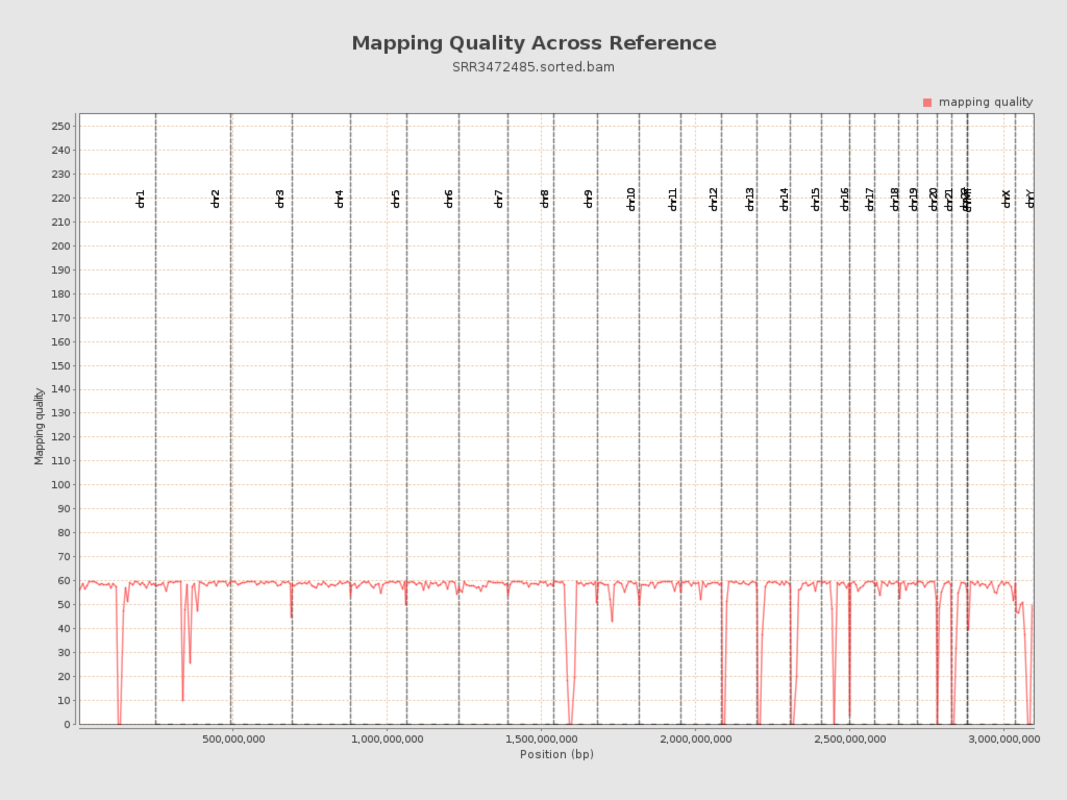
10. Results : Mapped Reads Clipping Profile



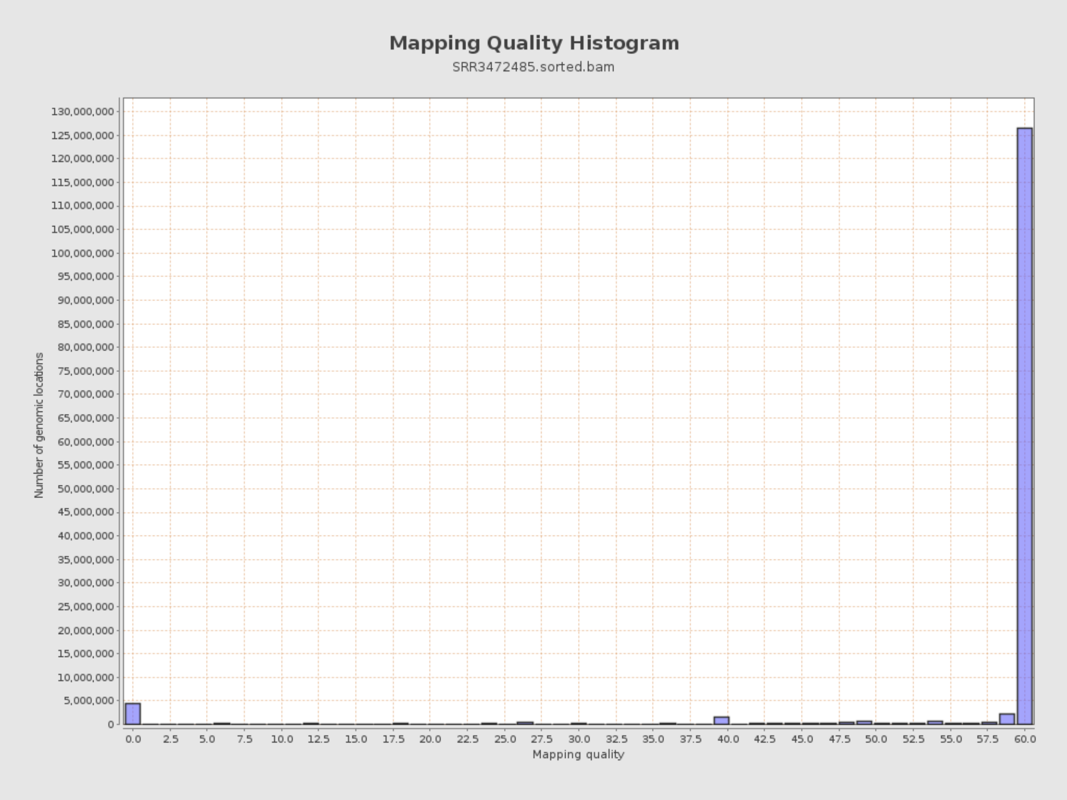
11. Results : Homopolymer Indels



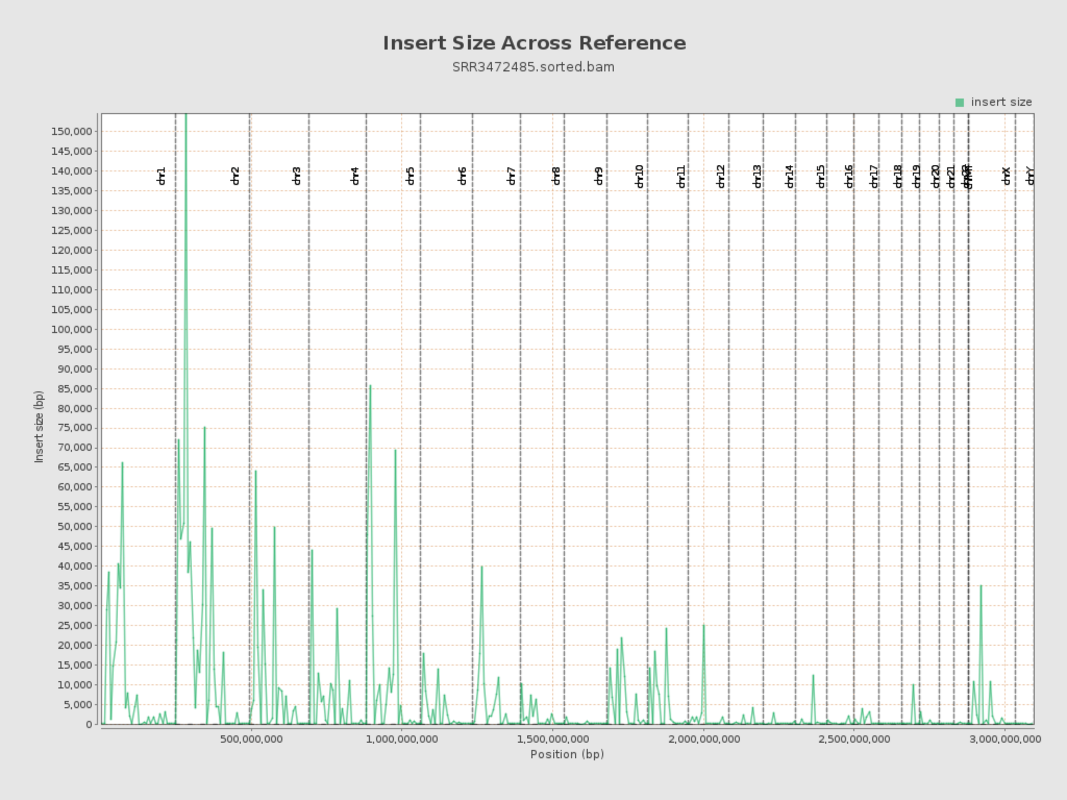
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram