Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:55:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472486.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_SRR3472486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472486_1.fastq.gz SRR3472486_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:55:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,934,302
Mapped reads	17,748,460 / 98.96%
Unmapped reads	185,842 / 1.04%
Mapped paired reads	17,748,460 / 98.96%
Mapped reads, first in pair	8,898,622 / 49.62%
Mapped reads, second in pair	8,849,838 / 49.35%
Mapped reads, both in pair	17,651,930 / 98.43%
Mapped reads, singletons	96,530 / 0.54%
Secondary alignments	0
Supplementary alignments	73,889 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	11,721,037 / 65.36%
Duplication rate	46.28%
Clipped reads	1,447,618 / 8.07%

2.2. ACGT Content

Number/percentage of A's	467,956,227 / 26.77%
Number/percentage of C's	409,199,789 / 23.4%
Number/percentage of T's	465,650,025 / 26.63%
Number/percentage of G's	405,284,456 / 23.18%
Number/percentage of N's	273,799 / 0.02%

GC Percentage	46.59%

2.3. Coverage

Mean	0.5648
Standard Deviation	23.6796

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	29,688.73
Standard Deviation	1,690,879.7
P25/Median/P75	167 / 230 / 308

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,079,178
Insertions	93,371
Mapped reads with at least one insertion	0.52%
Deletions	78,294
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.31%

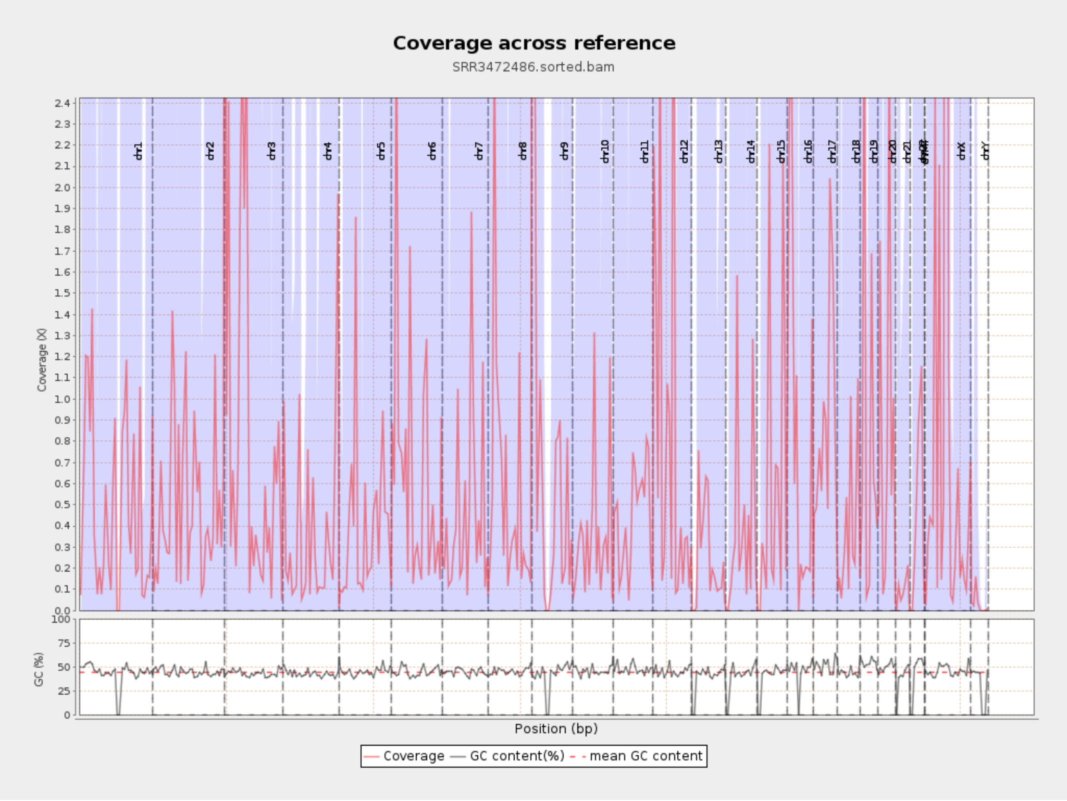
2.7. Chromosome stats

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

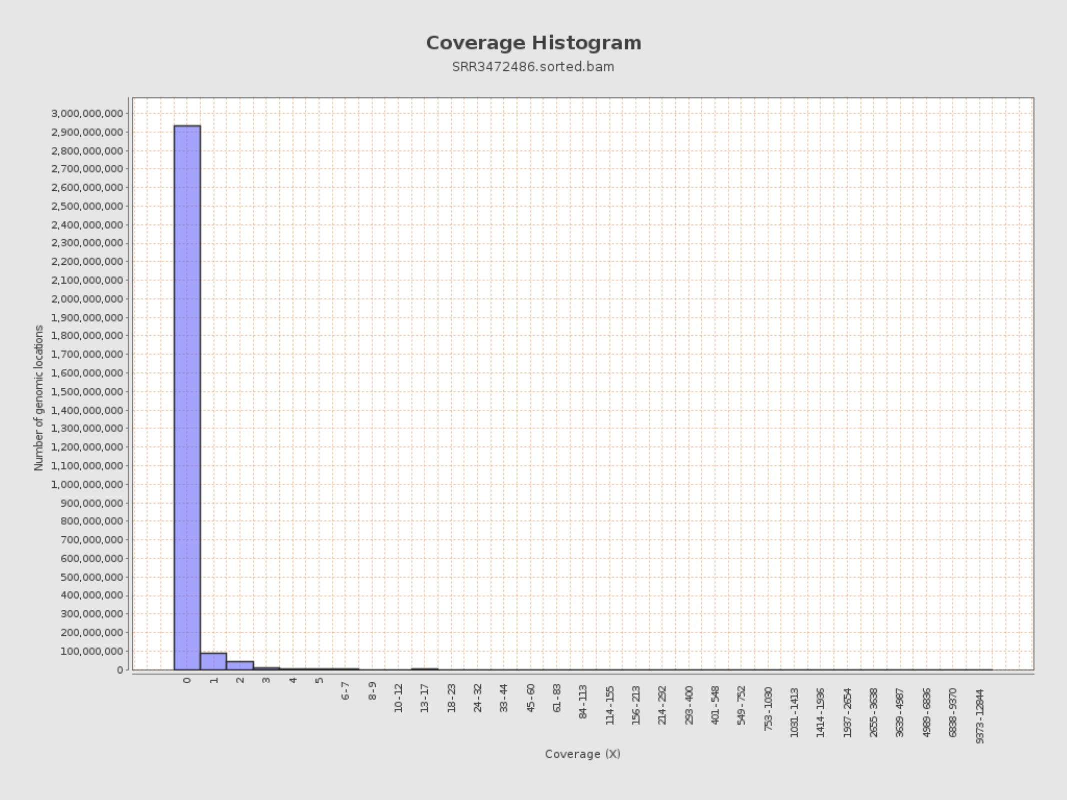
		bases	coverage	deviation
chr1	249250621	121911601	0.4891	15.4689
chr2	243199373	119015108	0.4894	15.3337
chr3	198022430	170680849	0.8619	22.4034
chr4	191154276	68059572	0.356	12.2105
chr5	180915260	72663824	0.4016	13.1439
chr6	171115067	110817274	0.6476	21.7119
chr7	159138663	73794852	0.4637	13.992
chr8	146364022	84431633	0.5769	19.8897
chr9	141213431	95669750	0.6775	20.4395
chr10	135534747	50159884	0.3701	17.2515
chr11	135006516	60000326	0.4444	14.7478
chr12	133851895	119180836	0.8904	45.0706
chr13	115169878	28722561	0.2494	9.5723
chr14	107349540	40930903	0.3813	19.339
chr15	102531392	61493743	0.5998	23.6416
chr16	90354753	75241430	0.8327	27.1366
chr17	81195210	71660854	0.8826	26.702
chr18	78077248	31658195	0.4055	15.0663
chr19	59128983	52420210	0.8865	36.6357
chr20	63025520	56956316	0.9037	41.3751
chr21	48129895	4675512	0.0971	3.9553
chr22	51304566	22598118	0.4405	14.1877
chrMT	16571	2347	0.1416	0.5654
chrX	155270560	153820151	0.9907	53.2778

chrY	59373566	1990781	0.0335	1.5997

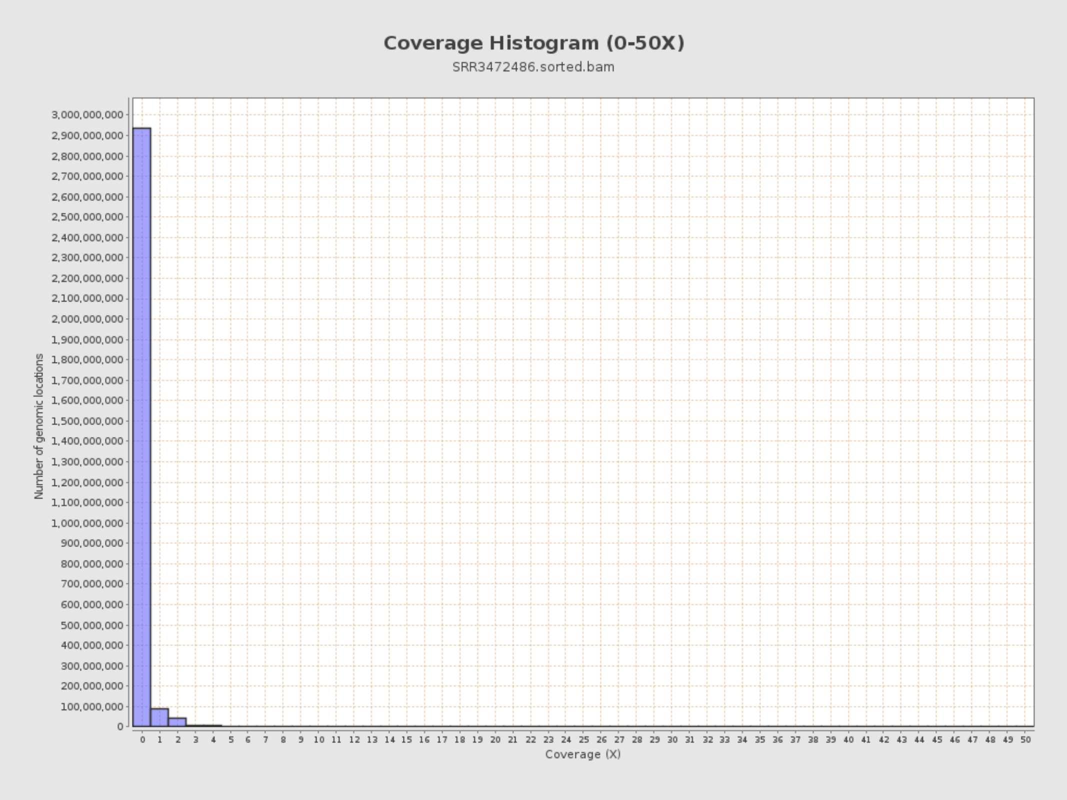
3. Results : Coverage across reference



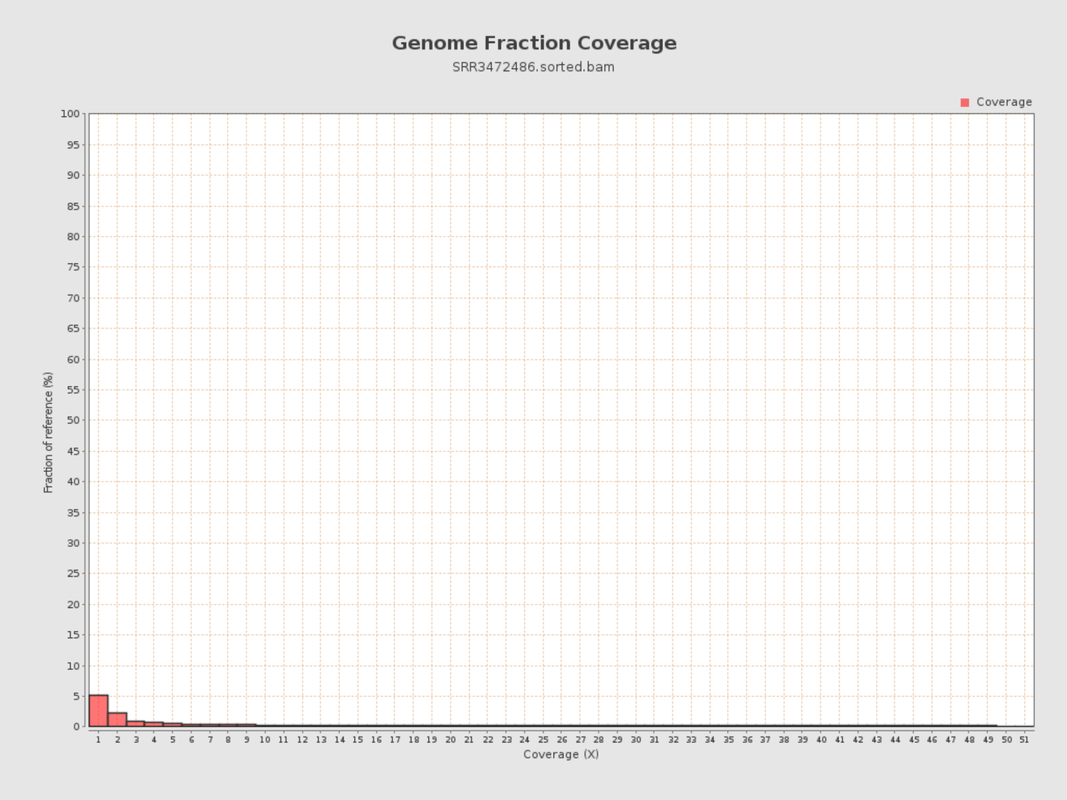
4. Results : Coverage Histogram



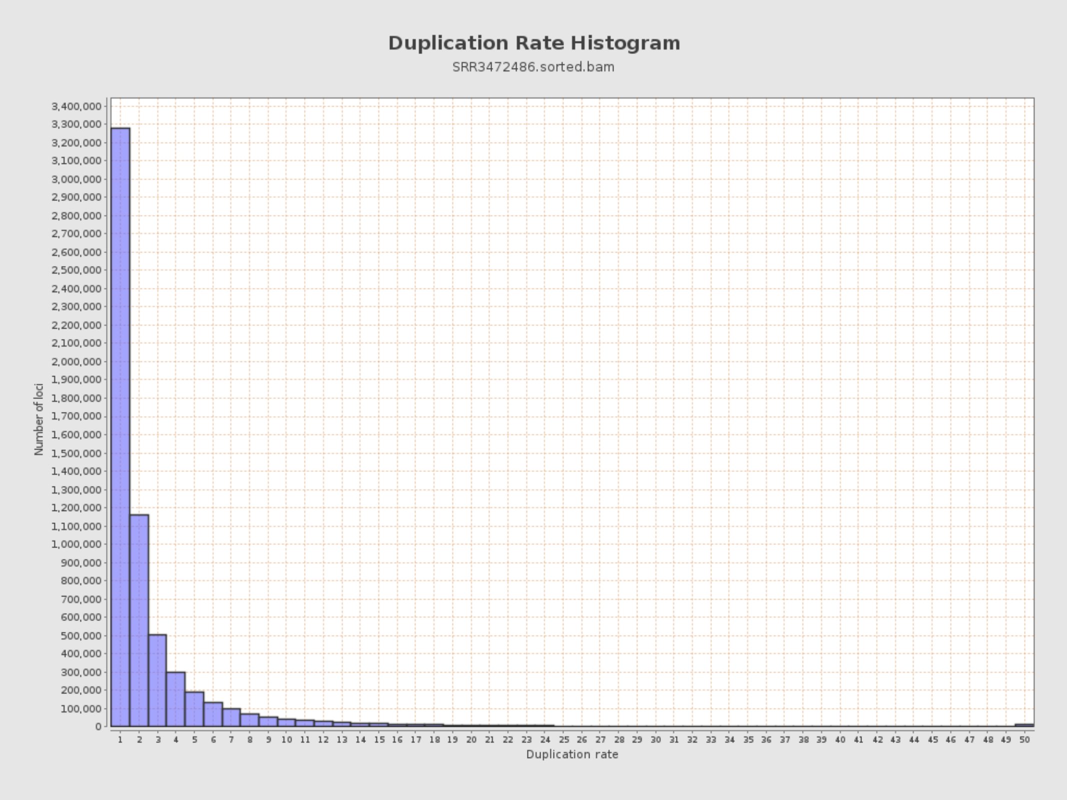
5. Results : Coverage Histogram (0-50X)



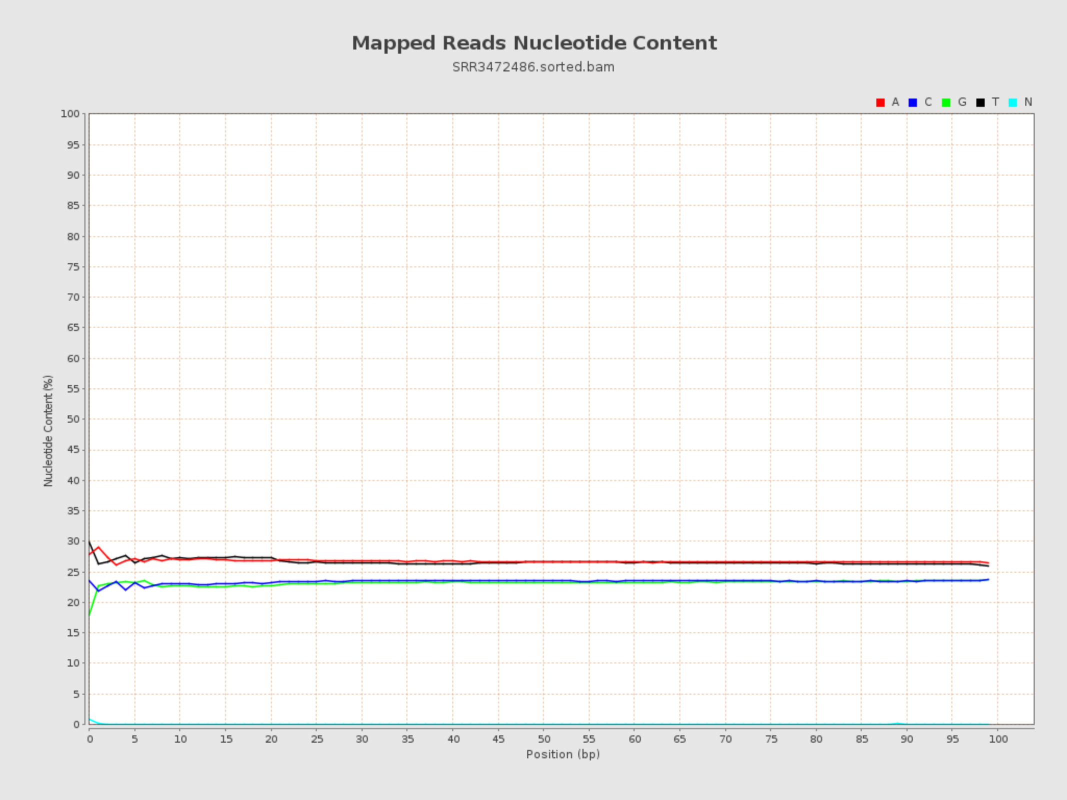
6. Results : Genome Fraction Coverage



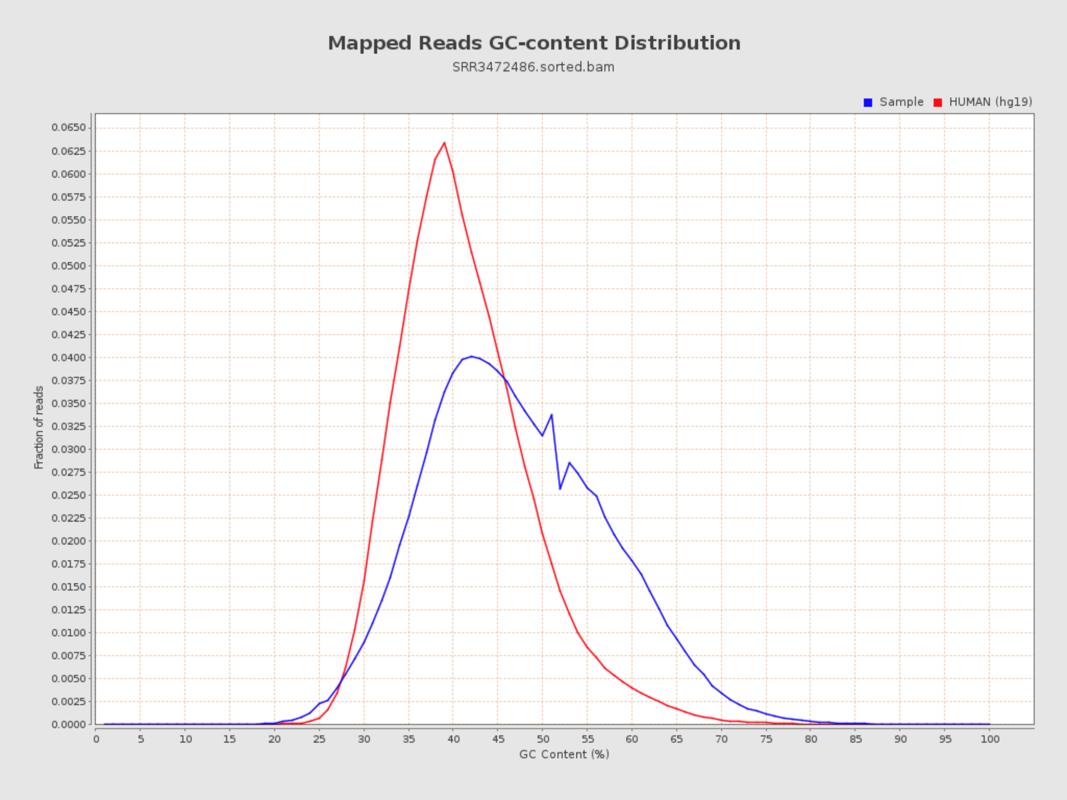
7. Results : Duplication Rate Histogram



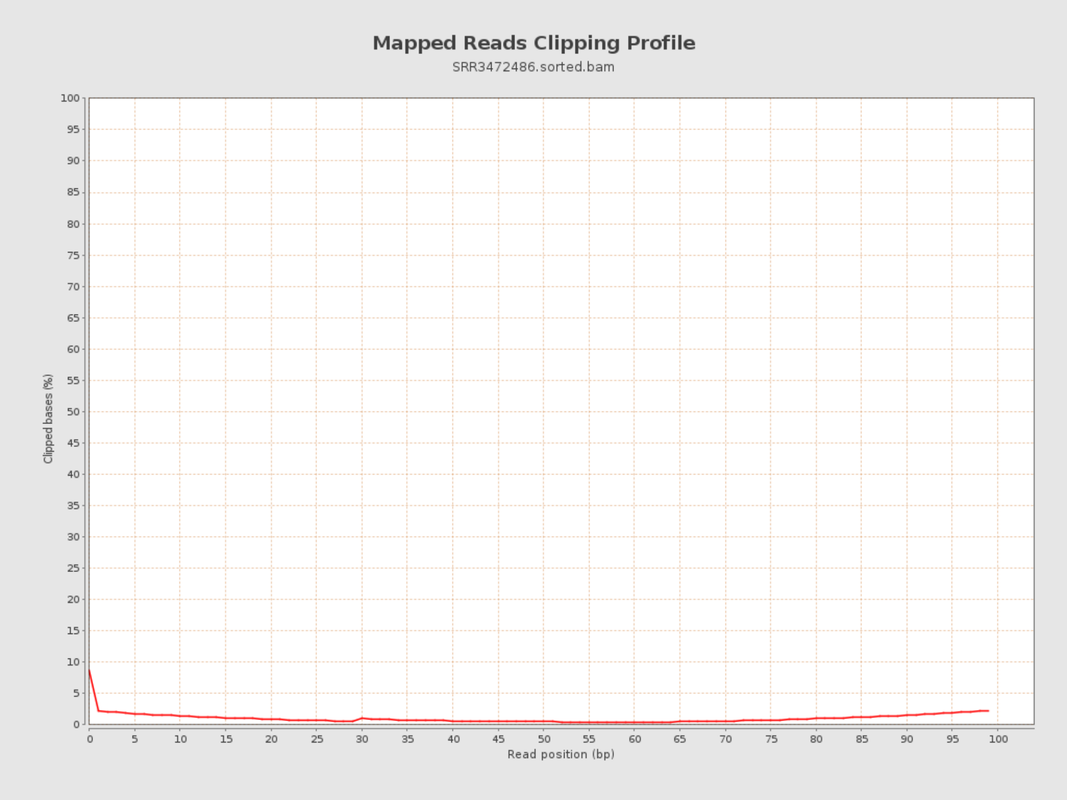
8. Results : Mapped Reads Nucleotide Content



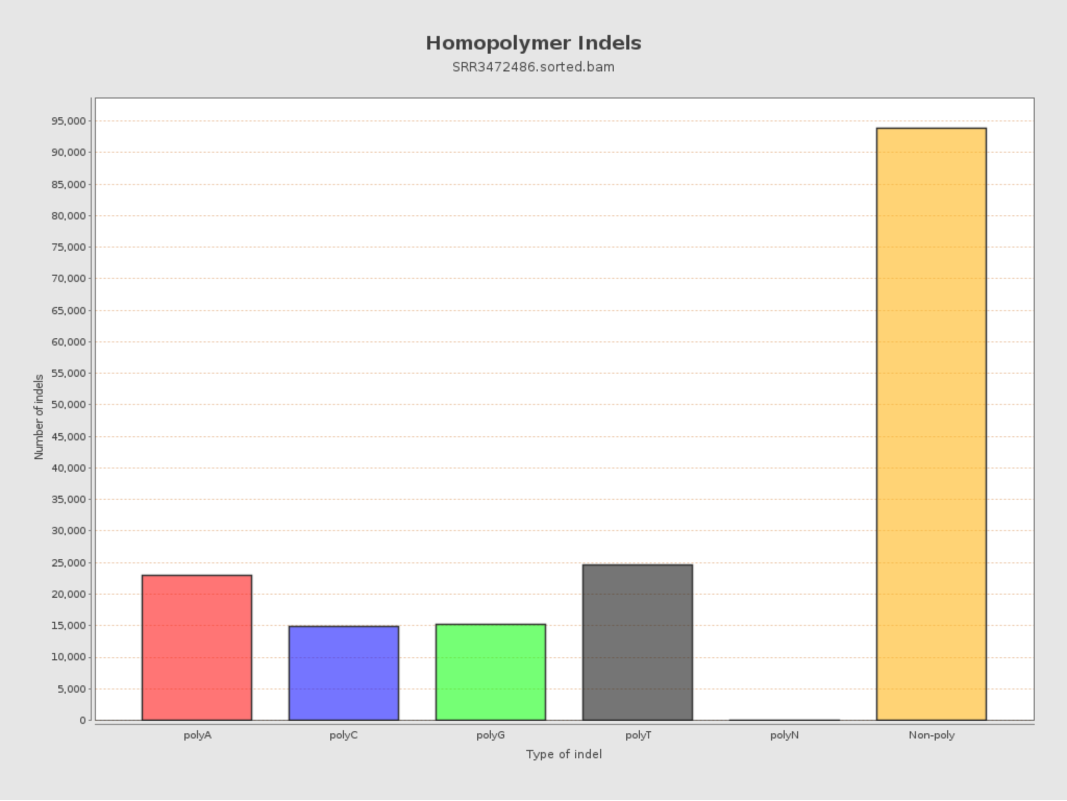
9. Results : Mapped Reads GC-content Distribution



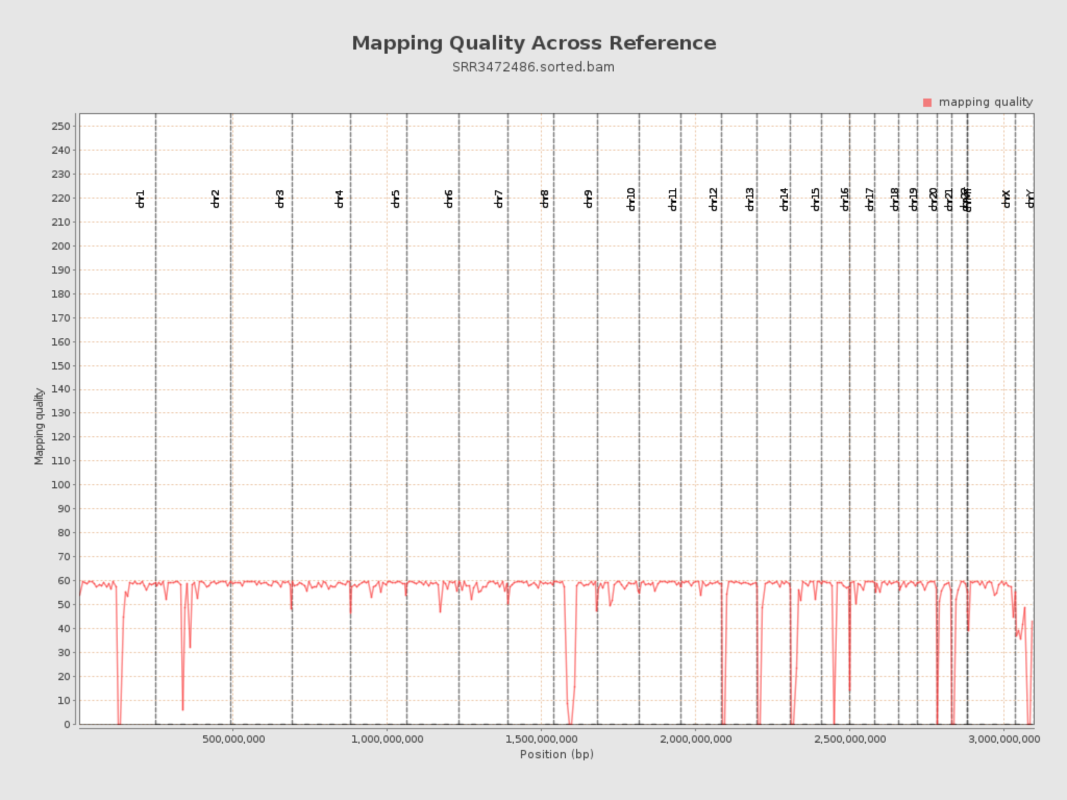
10. Results : Mapped Reads Clipping Profile



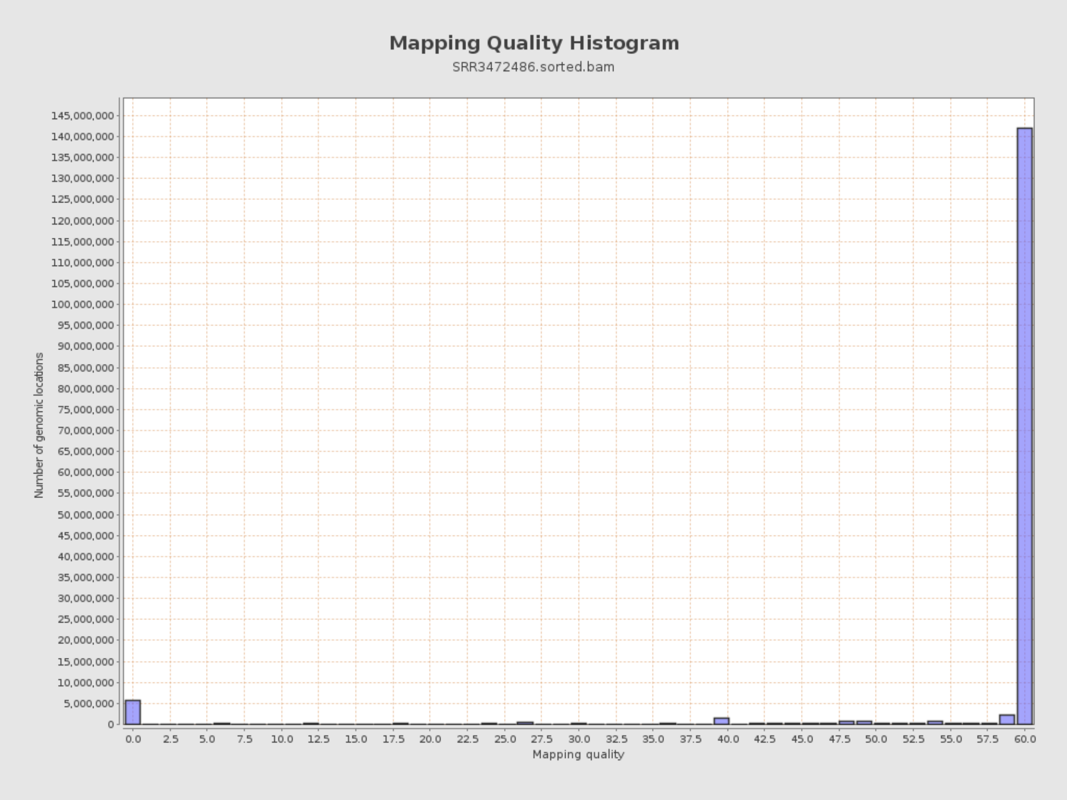
11. Results : Homopolymer Indels



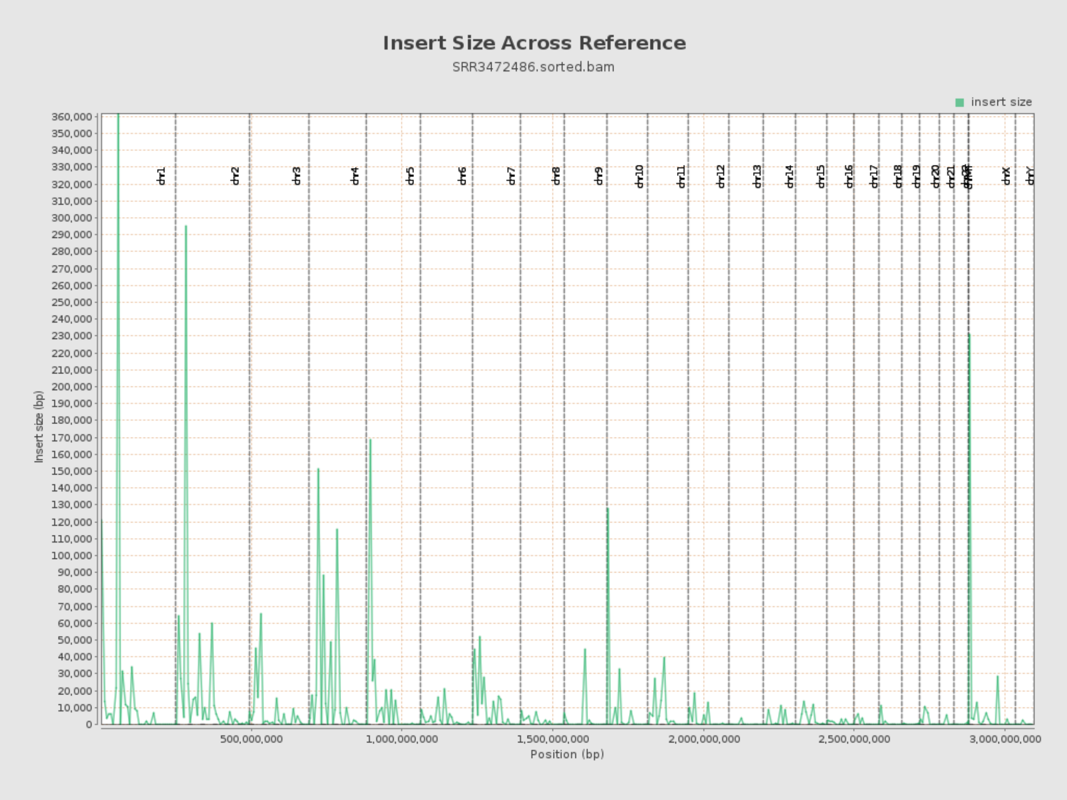
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram