Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 09:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472688.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_SRR3472688 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472688_1.fastq.gz SRR3472688_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 09:07:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472688.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,882,150
Mapped reads	13,757,578 / 99.1%
Unmapped reads	124,572 / 0.9%
Mapped paired reads	13,757,578 / 99.1%
Mapped reads, first in pair	6,919,370 / 49.84%
Mapped reads, second in pair	6,838,208 / 49.26%
Mapped reads, both in pair	13,669,108 / 98.47%
Mapped reads, singletons	88,470 / 0.64%
Secondary alignments	0
Supplementary alignments	21,935 / 0.16%
Read min/max/mean length	30 / 101 / 99.62
Duplicated reads (estimated)	7,120,364 / 51.29%
Duplication rate	45.63%
Clipped reads	650,563 / 4.69%

2.2. ACGT Content

Number/percentage of A's	369,850,893 / 27.25%
Number/percentage of C's	308,756,533 / 22.75%
Number/percentage of T's	376,552,329 / 27.74%
Number/percentage of G's	301,990,703 / 22.25%
Number/percentage of N's	300,948 / 0.02%

GC Percentage	44.99%

2.3. Coverage

Mean	0.4386
Standard Deviation	9.1522

2.4. Mapping Quality

Mean Mapping Quality	54.77

2.5. Insert size

Mean	20,651.91
Standard Deviation	1,474,470.02
P25/Median/P75	171 / 234 / 312

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	6,159,373
Insertions	63,065
Mapped reads with at least one insertion	0.45%
Deletions	77,279
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.47%

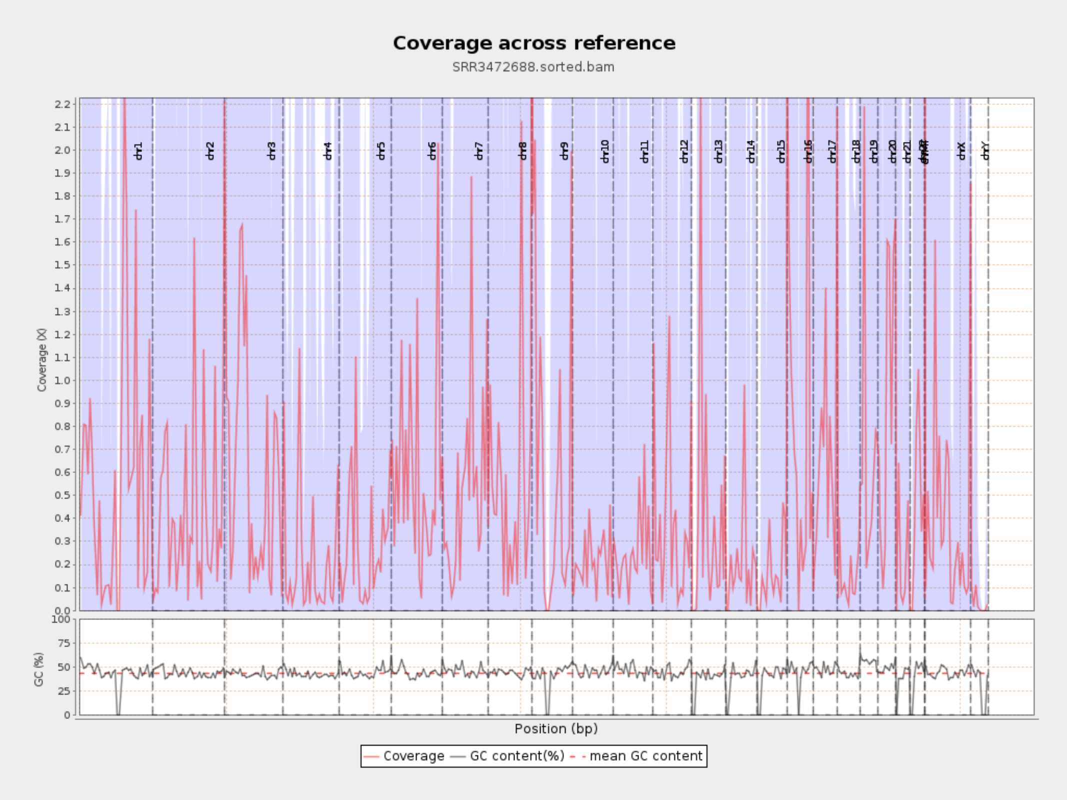
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

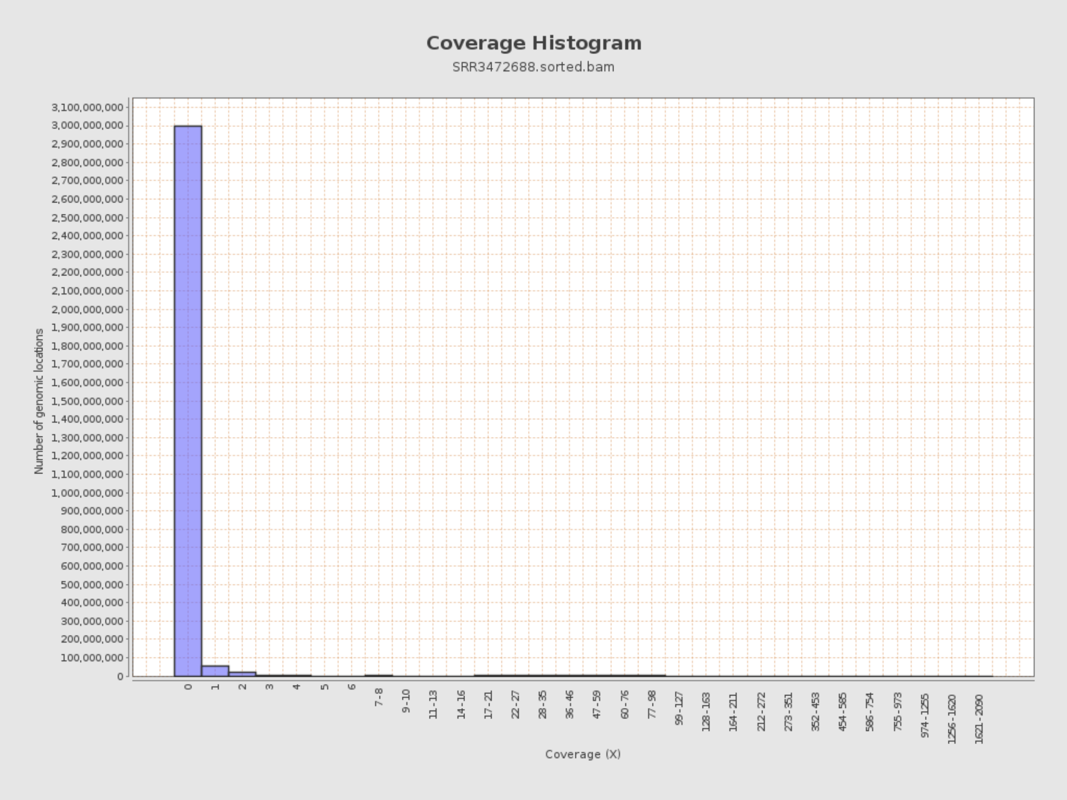
		bases	coverage	deviation
chr1	249250621	144826234	0.581	10.8197
chr2	243199373	101373554	0.4168	9.2415
chr3	198022430	125555156	0.634	10.2764
chr4	191154276	39135652	0.2047	5.5956
chr5	180915260	52610451	0.2908	6.5019
chr6	171115067	100595915	0.5879	10.014
chr7	159138663	86155149	0.5414	11.2026
chr8	146364022	79035294	0.54	9.9752
chr9	141213431	92067437	0.652	11.218
chr10	135534747	28551349	0.2107	5.0871
chr11	135006516	33883364	0.251	5.2983
chr12	133851895	51304122	0.3833	6.6349
chr13	115169878	44953342	0.3903	10.744
chr14	107349540	20898766	0.1947	4.4233
chr15	102531392	16648610	0.1624	3.67
chr16	90354753	79933601	0.8847	16.8928
chr17	81195210	54857852	0.6756	10.4775
chr18	78077248	11790953	0.151	3.3259
chr19	59128983	41760390	0.7063	9.7251
chr20	63025520	57287353	0.909	17.5383
chr21	48129895	10796207	0.2243	9.1802
chr22	51304566	23144905	0.4511	9.6128
chrMT	16571	49763	3.003	2.1515
chrX	155270560	58584084	0.3773	6.1417

chrY	59373566	1846264	0.0311	0.9828

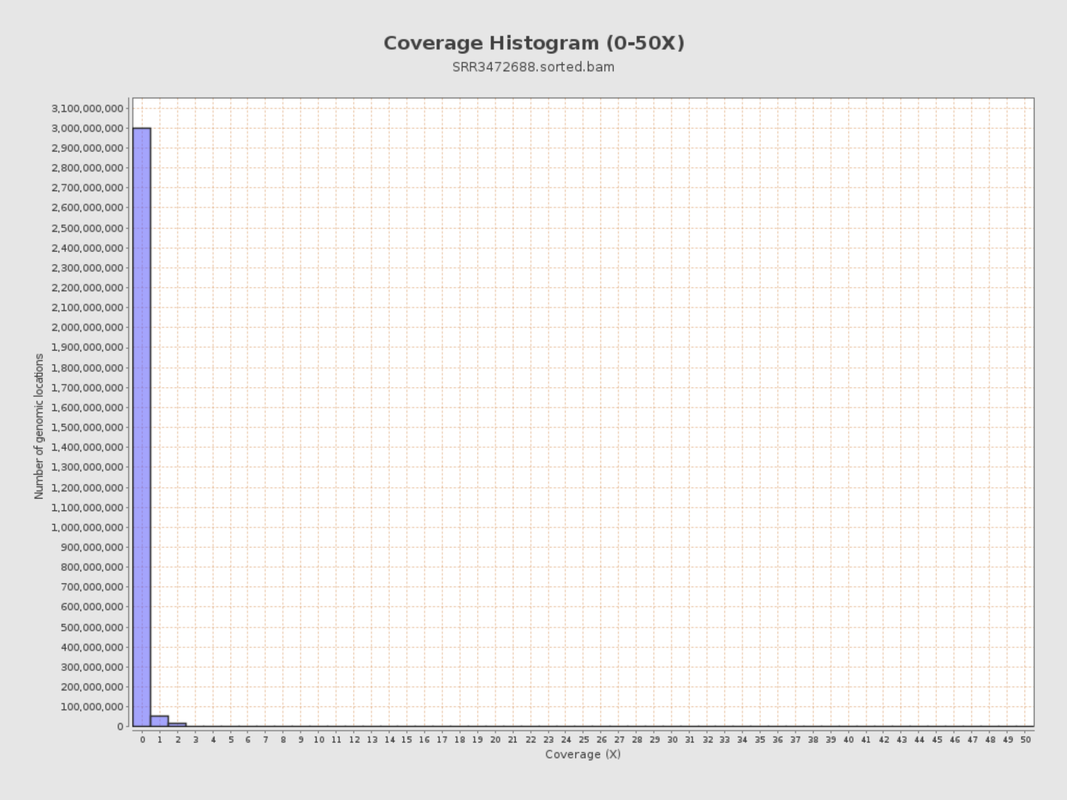
3. Results : Coverage across reference



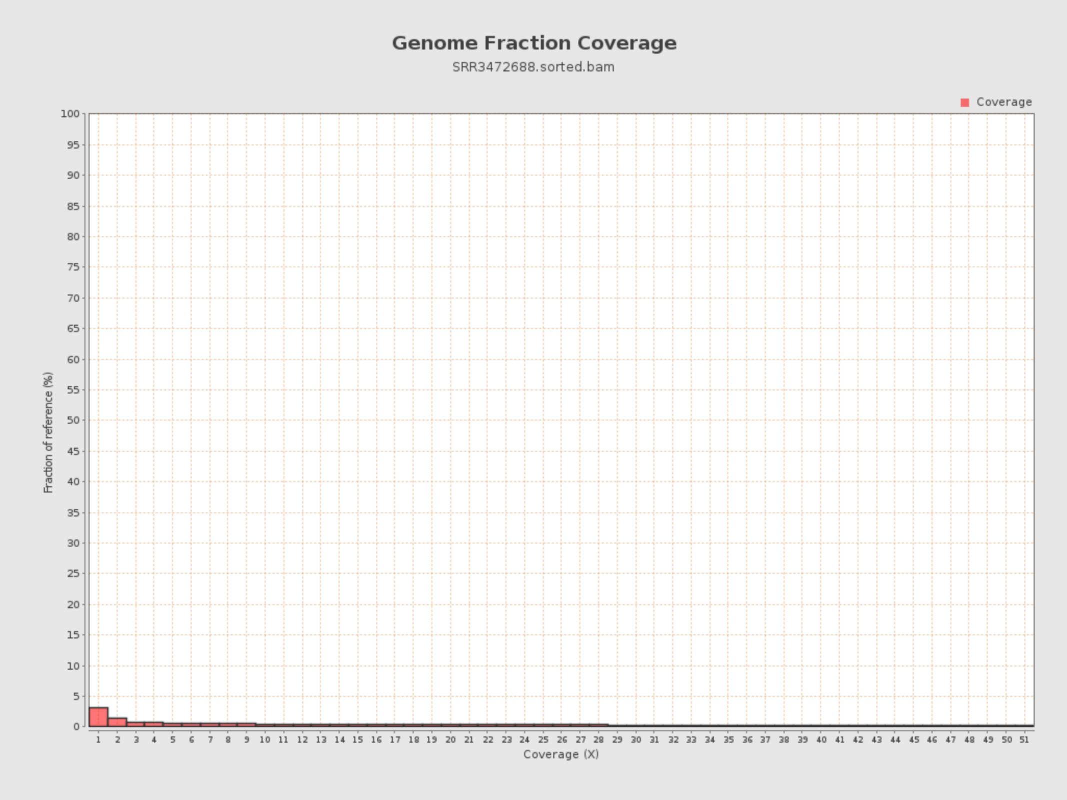
4. Results : Coverage Histogram



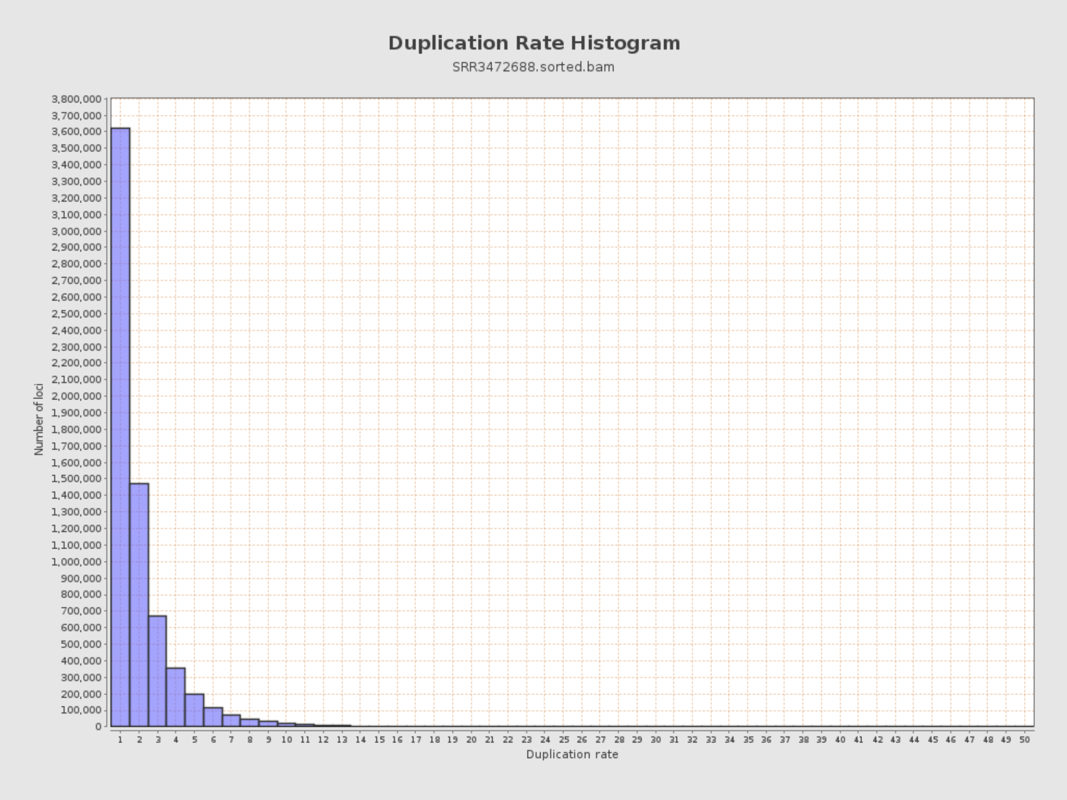
5. Results : Coverage Histogram (0-50X)



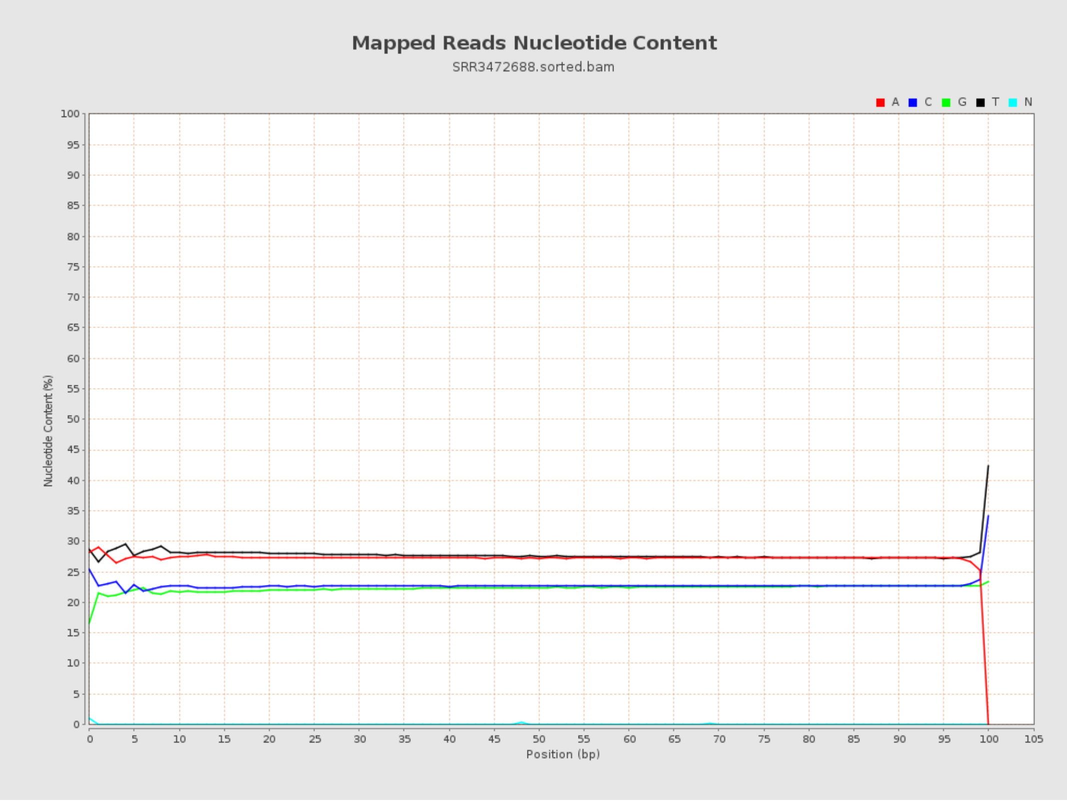
6. Results : Genome Fraction Coverage



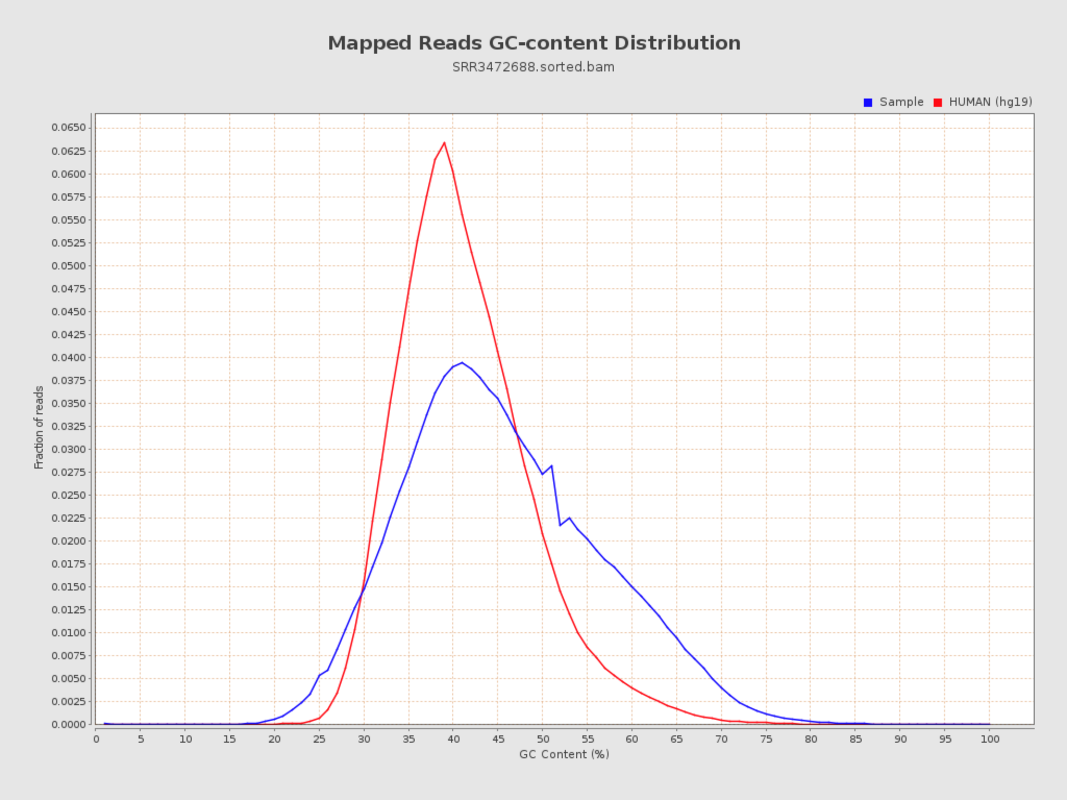
7. Results : Duplication Rate Histogram



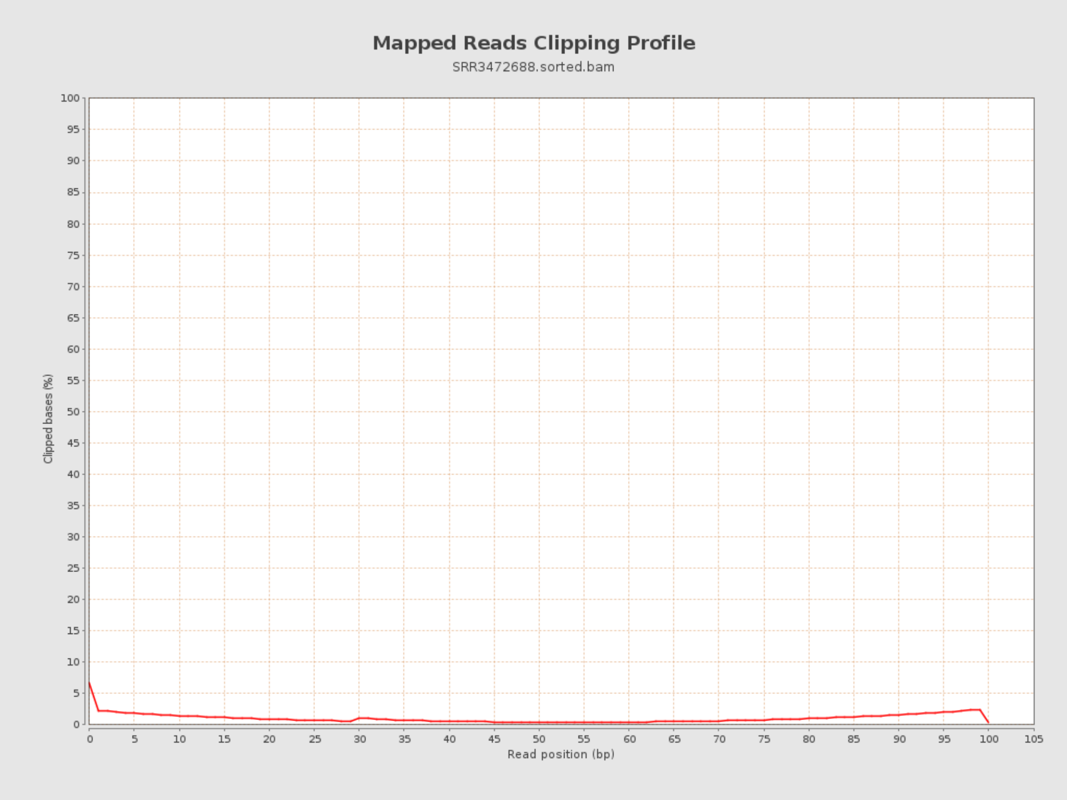
8. Results : Mapped Reads Nucleotide Content



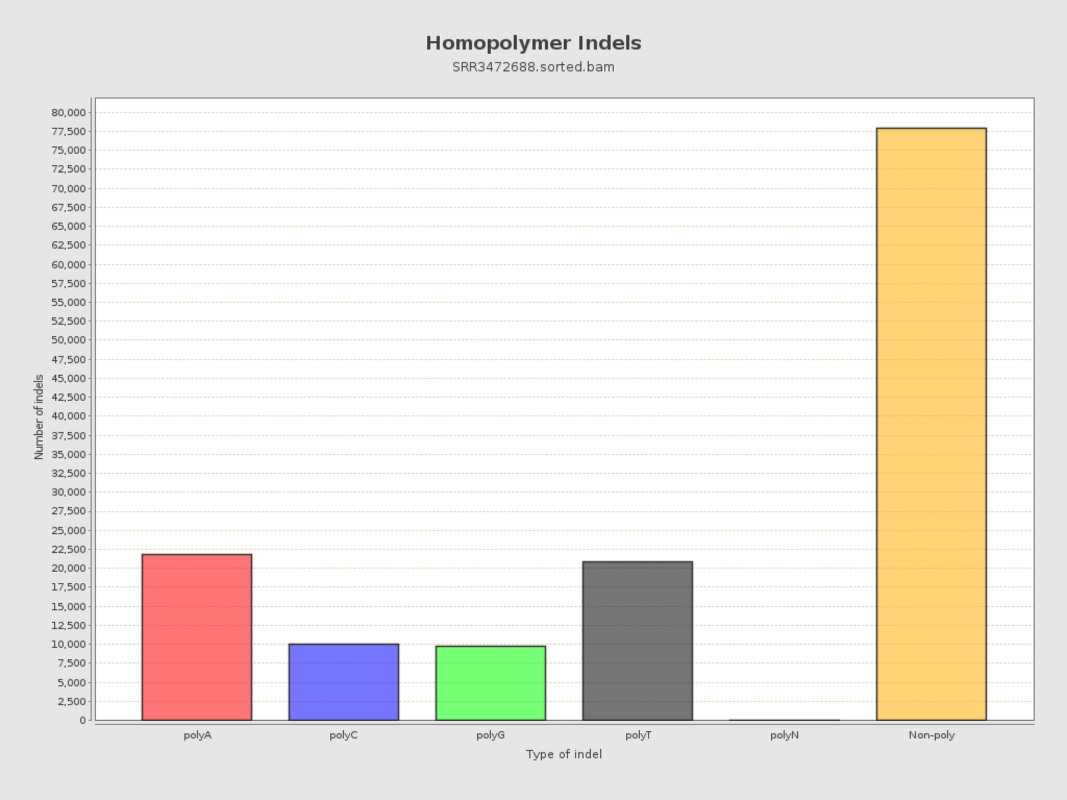
9. Results : Mapped Reads GC-content Distribution



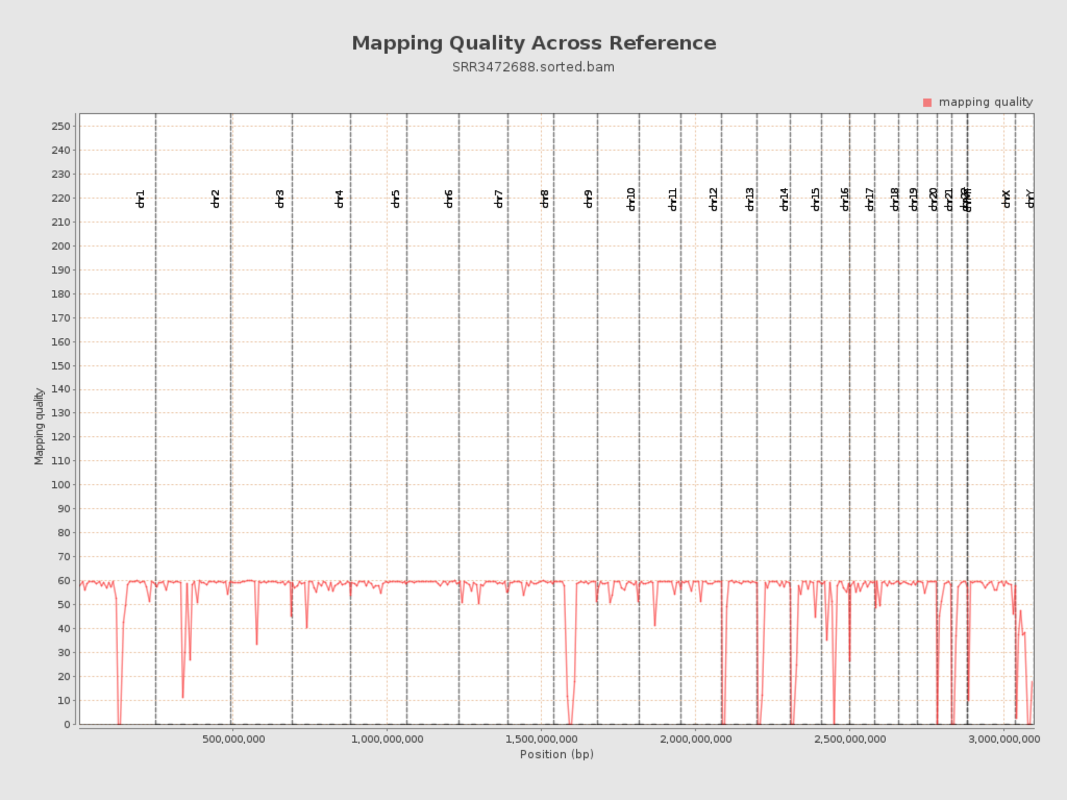
10. Results : Mapped Reads Clipping Profile



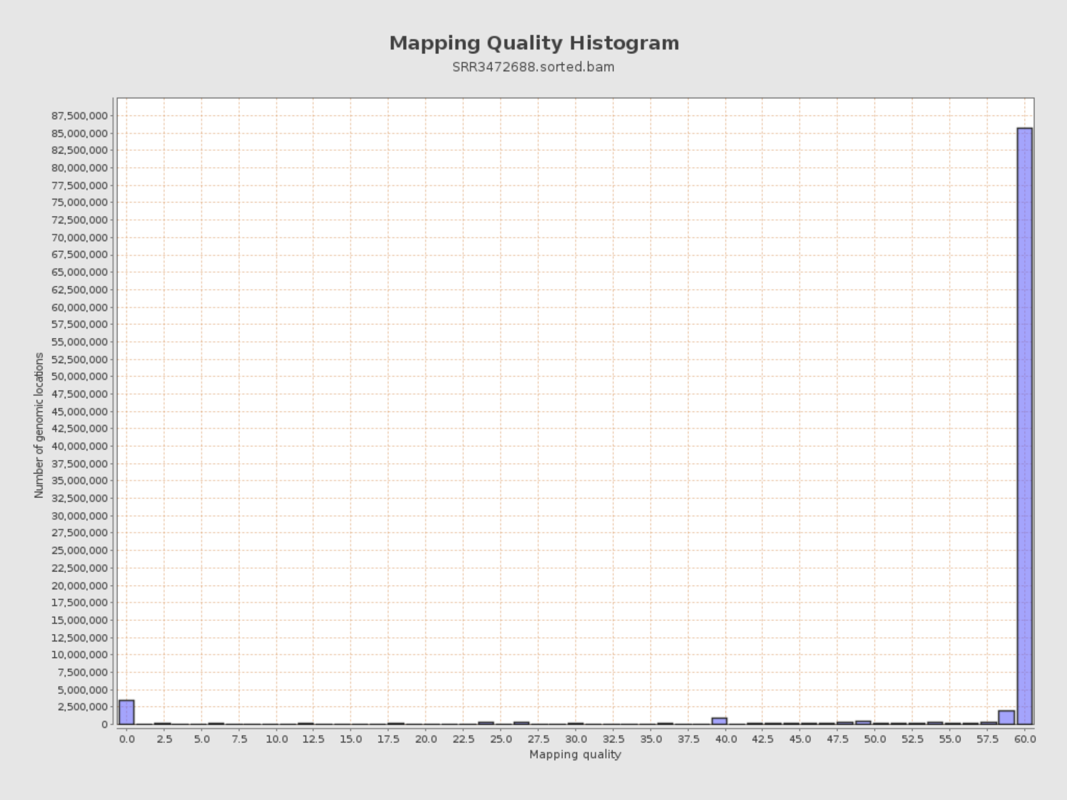
11. Results : Homopolymer Indels



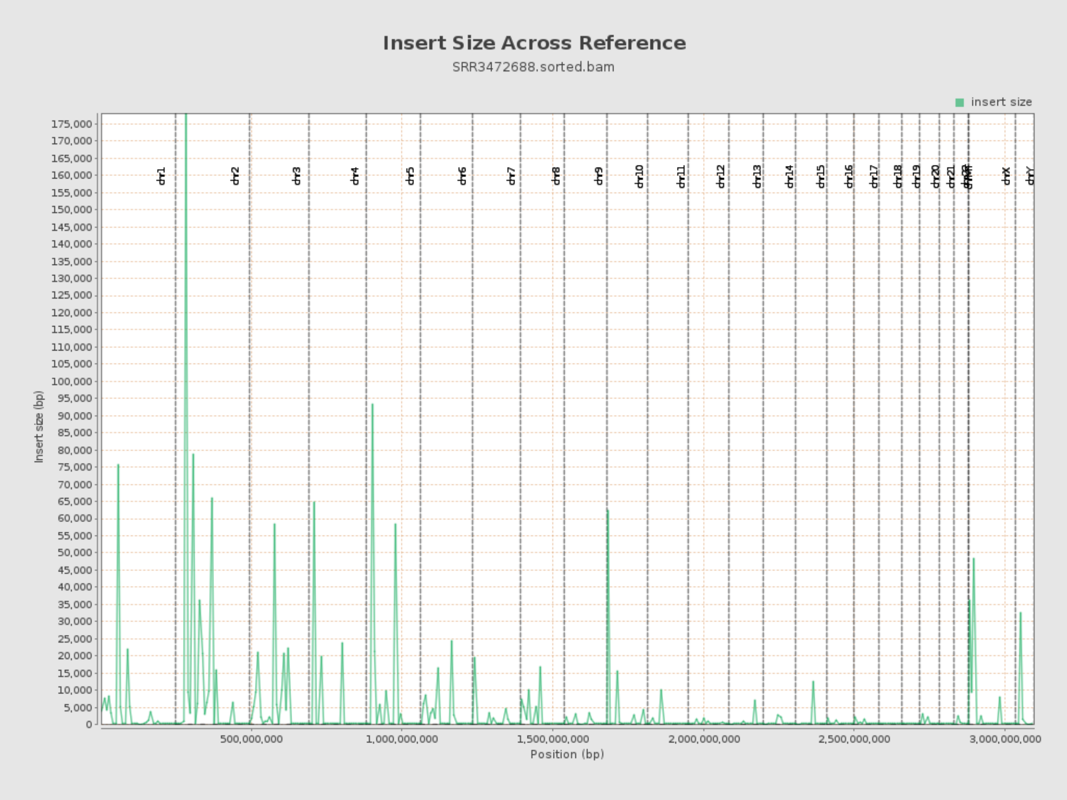
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram