Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 07:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472684.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_SRR3472684 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472684_1.fastq.gz SRR3472684_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 07:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472684.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,830,184
Mapped reads	16,692,652 / 99.18%
Unmapped reads	137,532 / 0.82%
Mapped paired reads	16,692,652 / 99.18%
Mapped reads, first in pair	8,364,457 / 49.7%
Mapped reads, second in pair	8,328,195 / 49.48%
Mapped reads, both in pair	16,601,918 / 98.64%
Mapped reads, singletons	90,734 / 0.54%
Secondary alignments	0
Supplementary alignments	91,752 / 0.55%
Read min/max/mean length	30 / 101 / 99.8
Duplicated reads (estimated)	11,148,472 / 66.24%
Duplication rate	49.18%
Clipped reads	1,288,766 / 7.66%

2.2. ACGT Content

Number/percentage of A's	438,740,902 / 26.74%
Number/percentage of C's	384,534,544 / 23.44%
Number/percentage of T's	436,640,674 / 26.61%
Number/percentage of G's	380,370,563 / 23.18%
Number/percentage of N's	310,124 / 0.02%

GC Percentage	46.62%

2.3. Coverage

Mean	0.53
Standard Deviation	19.7205

2.4. Mapping Quality

Mean Mapping Quality	54.79

2.5. Insert size

Mean	23,610.98
Standard Deviation	1,507,648.46
P25/Median/P75	158 / 219 / 291

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,348,884
Insertions	107,597
Mapped reads with at least one insertion	0.64%
Deletions	88,787
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.76%

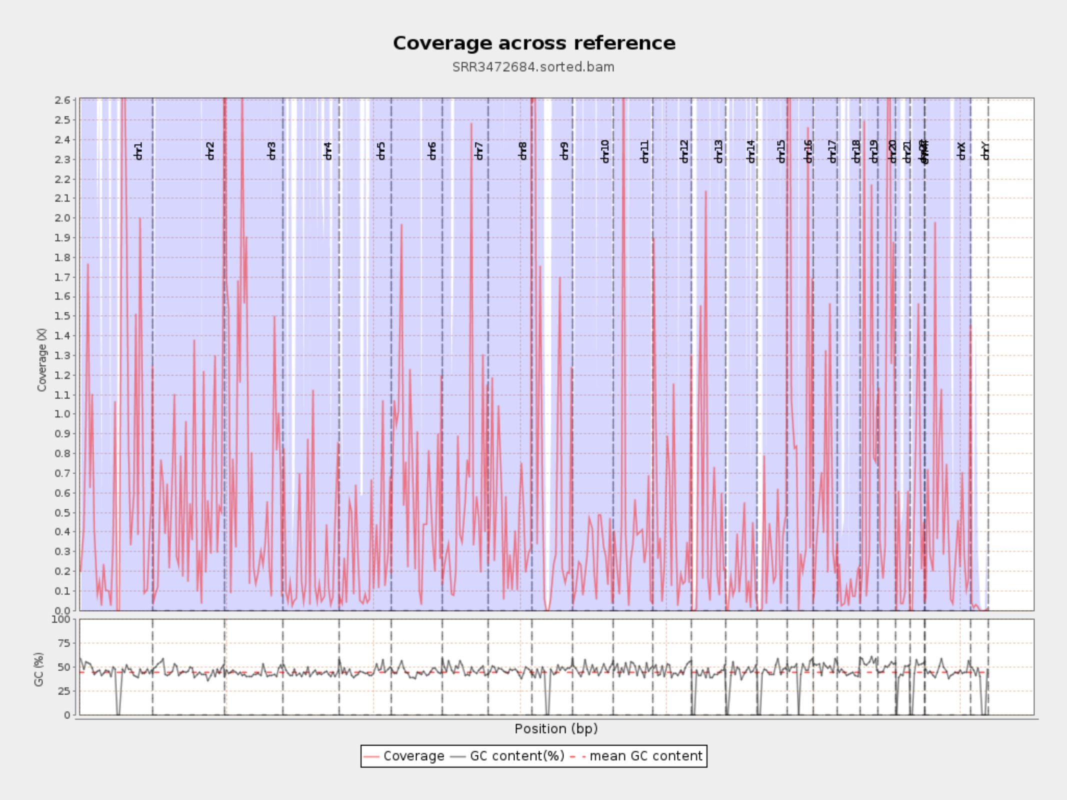
2.7. Chromosome stats

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

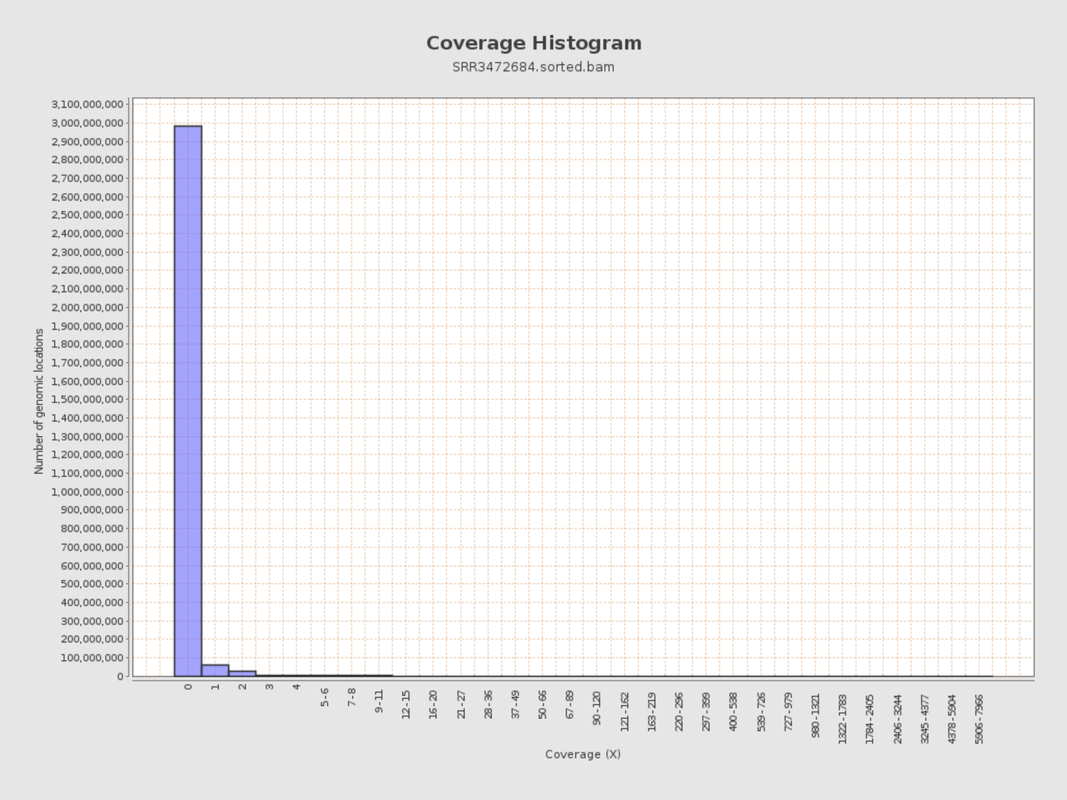
		bases	coverage	deviation
chr1	249250621	181543849	0.7284	22.7418
chr2	243199373	131117032	0.5391	21.3522
chr3	198022430	170352366	0.8603	23.996
chr4	191154276	49582173	0.2594	14.069
chr5	180915260	52562852	0.2905	12.2807
chr6	171115067	112702563	0.6586	20.5492
chr7	159138663	91243795	0.5734	18.7818
chr8	146364022	64830720	0.4429	13.7482
chr9	141213431	110369212	0.7816	21.8402
chr10	135534747	34692685	0.256	11.1358
chr11	135006516	63587016	0.471	28.0194
chr12	133851895	65129843	0.4866	18.8543
chr13	115169878	57216444	0.4968	19.1048
chr14	107349540	18234795	0.1699	6.6965
chr15	102531392	27834071	0.2715	16.6358
chr16	90354753	102440759	1.1338	30.4267
chr17	81195210	45237360	0.5571	18.0727
chr18	78077248	8718889	0.1117	3.9794
chr19	59128983	54619836	0.9237	31.5271
chr20	63025520	82335137	1.3064	35.1108
chr21	48129895	11391765	0.2367	12.1844
chr22	51304566	29113051	0.5675	21.4155
chrMT	16571	4721	0.2849	0.7263
chrX	155270560	75179933	0.4842	15.4708

chrY	59373566	774193	0.013	0.7457

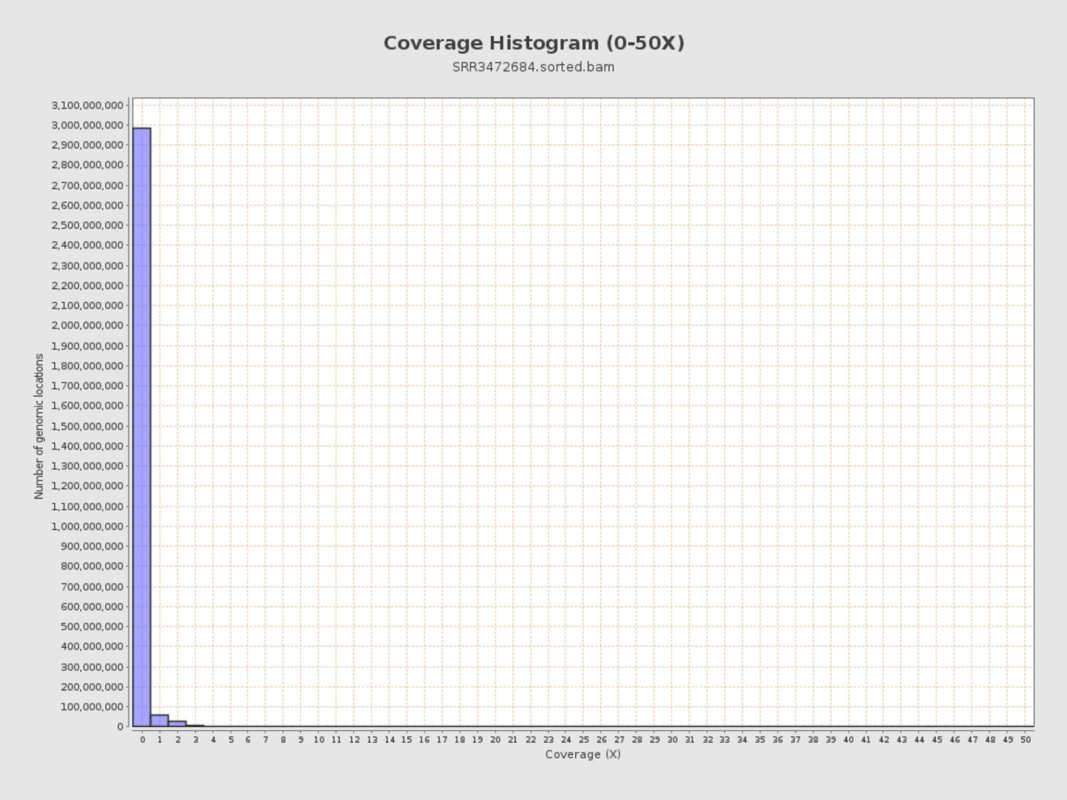
3. Results : Coverage across reference



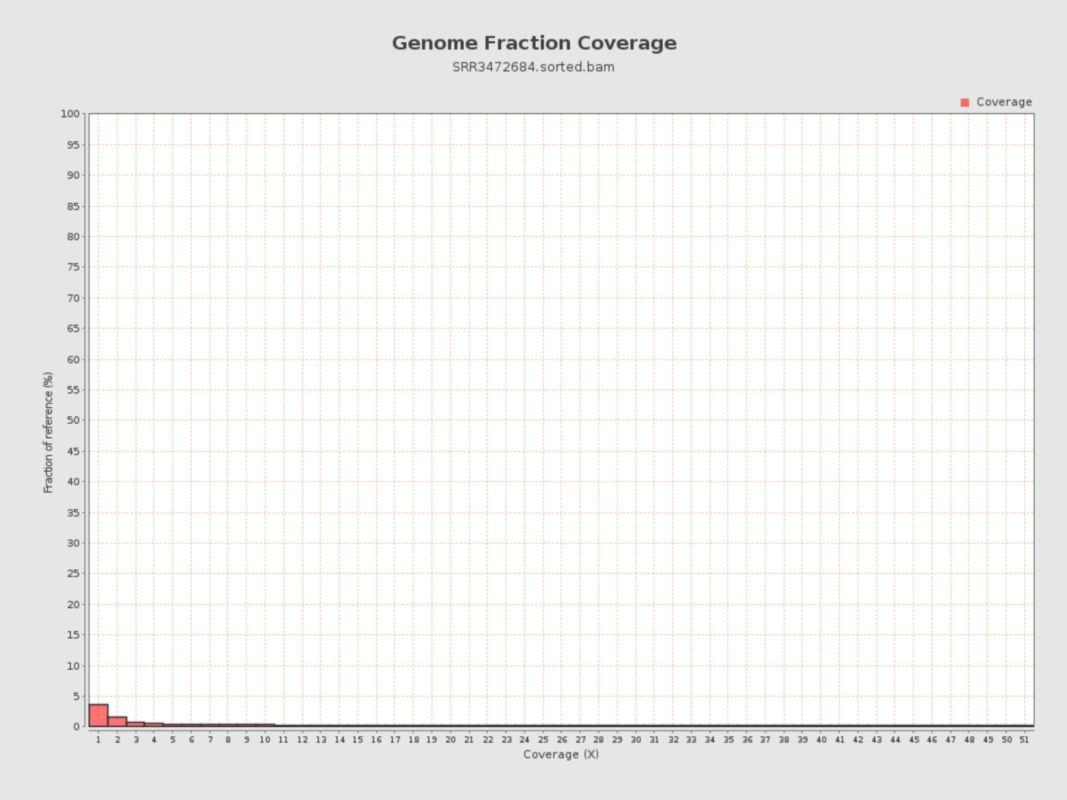
4. Results : Coverage Histogram



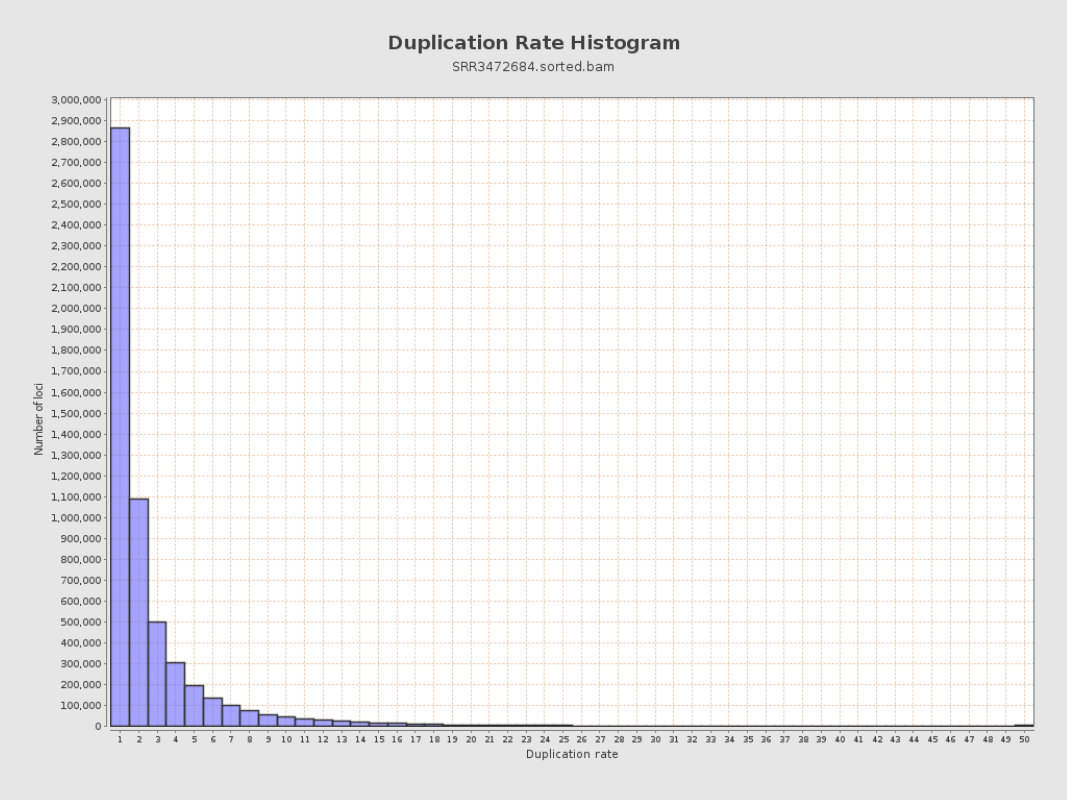
5. Results : Coverage Histogram (0-50X)



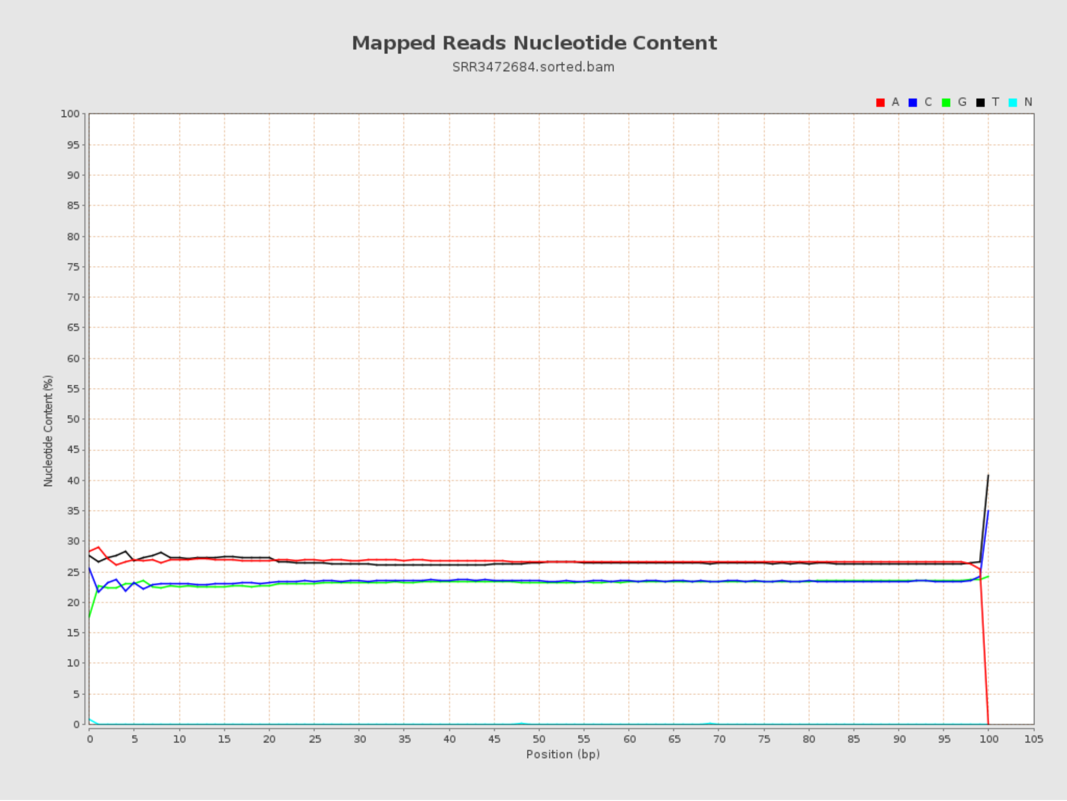
6. Results : Genome Fraction Coverage



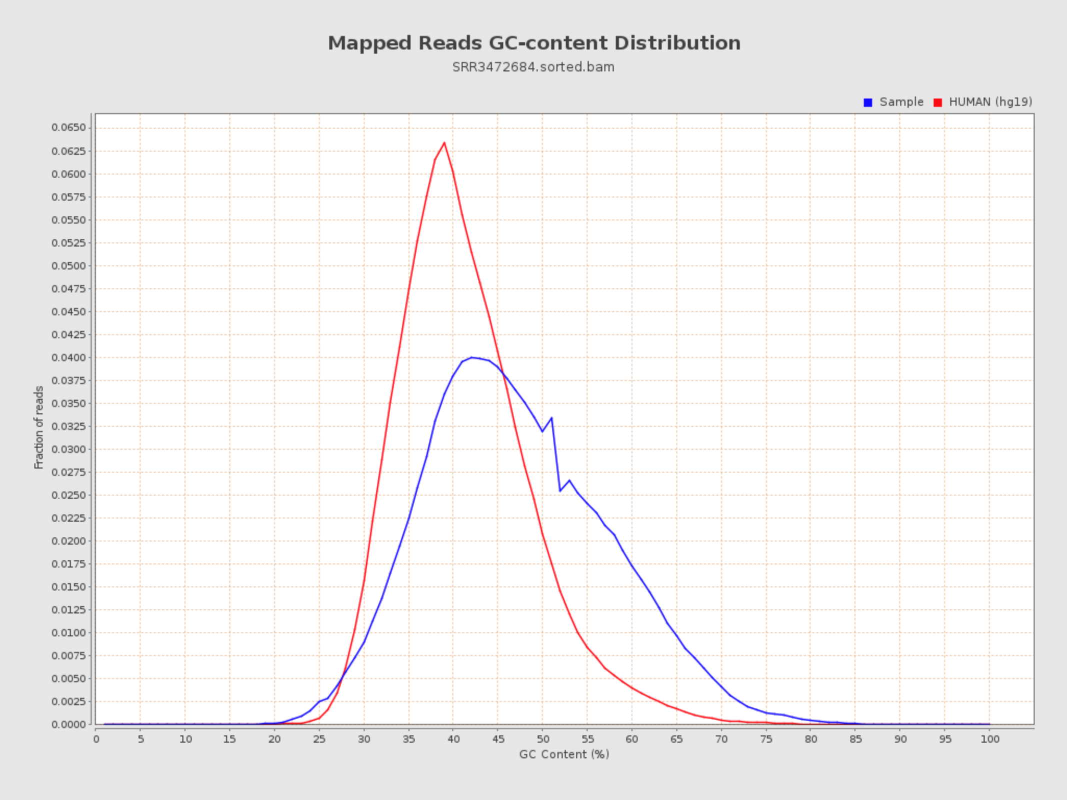
7. Results : Duplication Rate Histogram



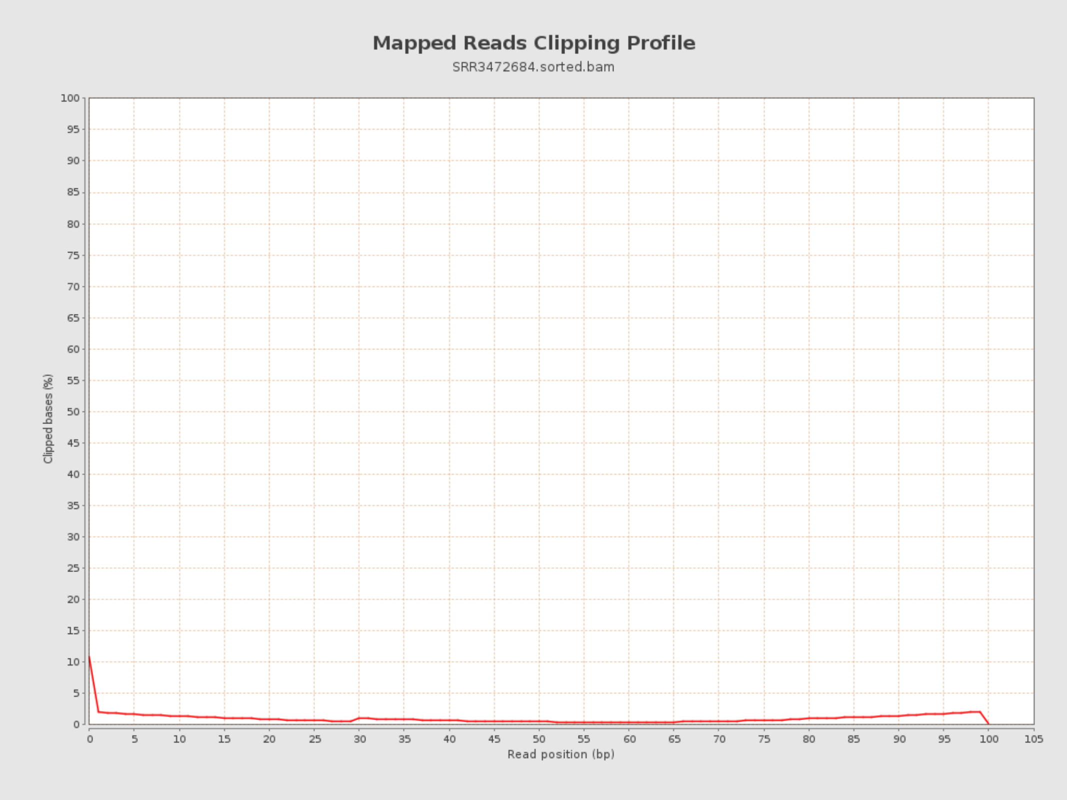
8. Results : Mapped Reads Nucleotide Content



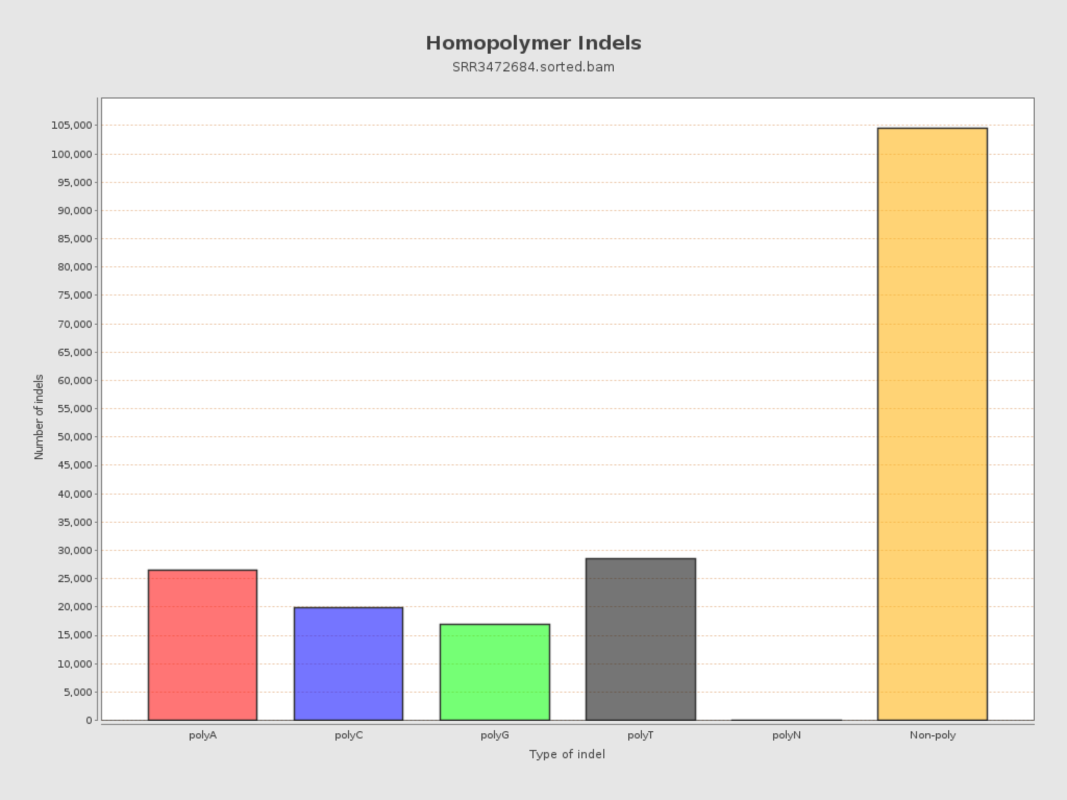
9. Results : Mapped Reads GC-content Distribution



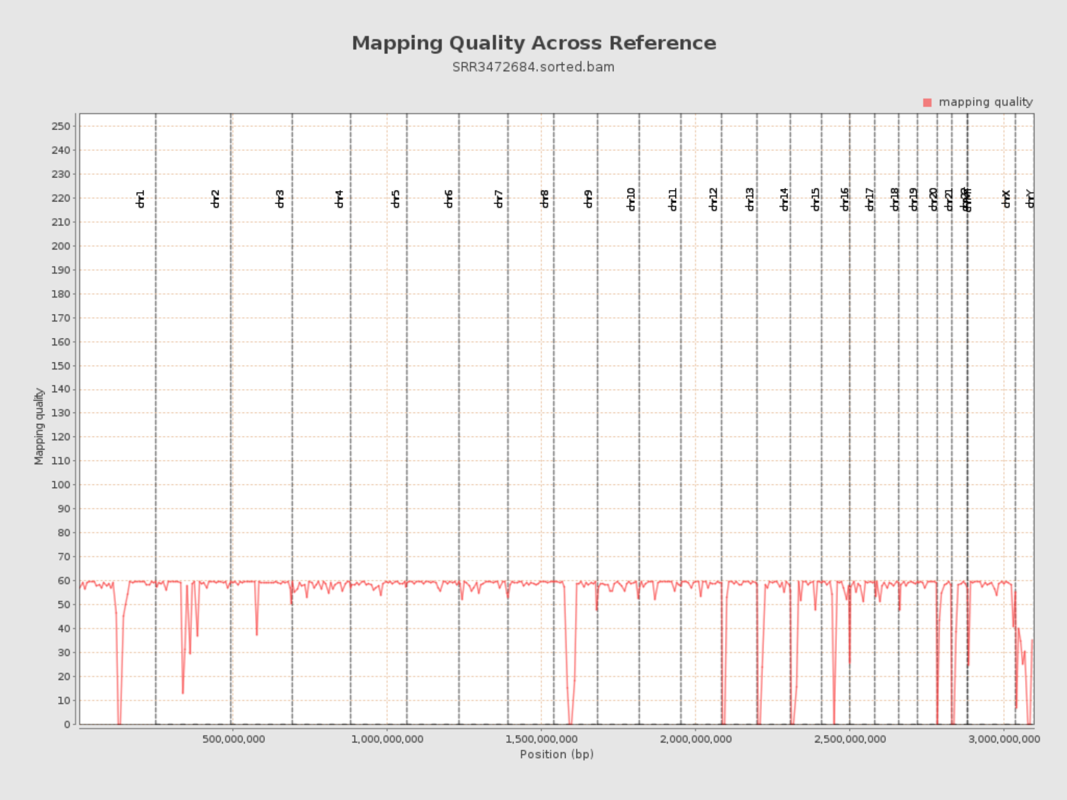
10. Results : Mapped Reads Clipping Profile



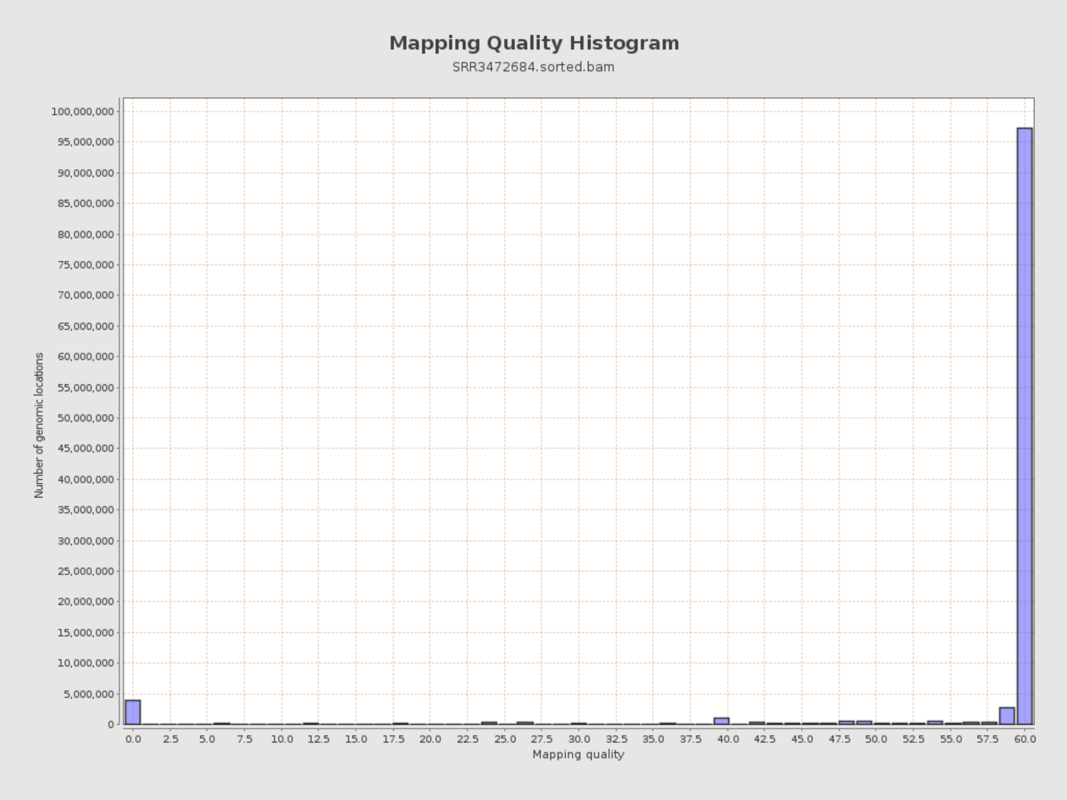
11. Results : Homopolymer Indels



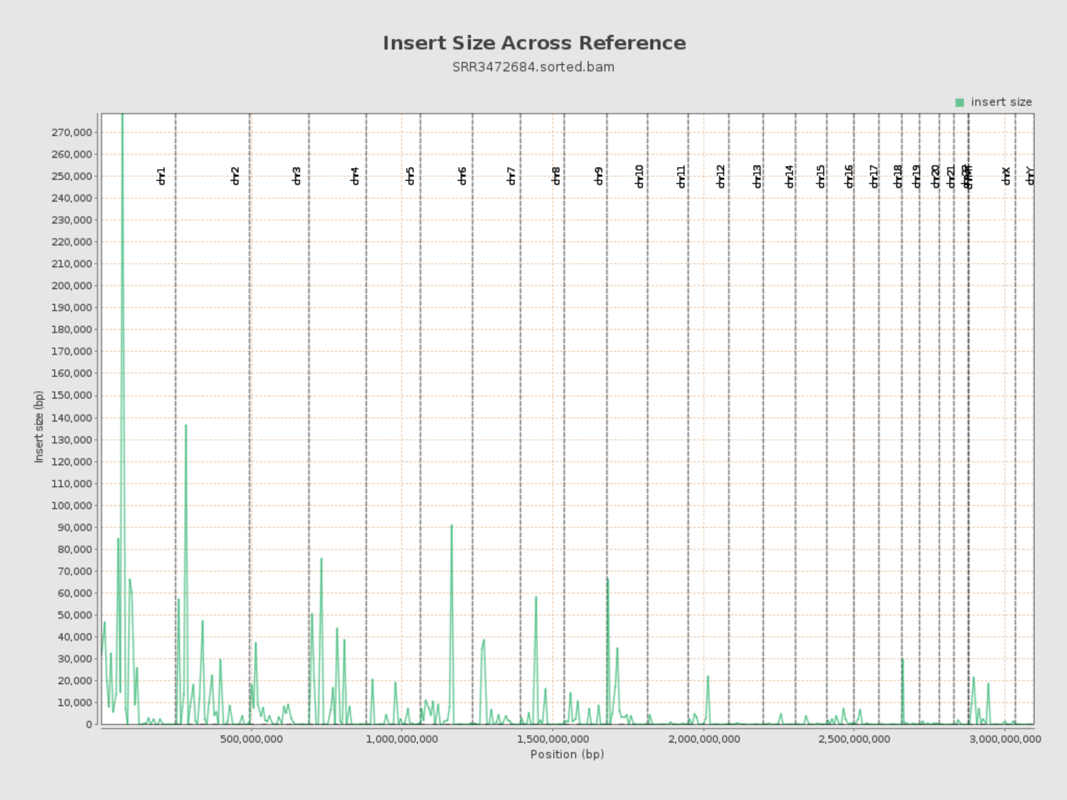
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram