Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:49:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212689.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_SRR3212689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212689.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:49:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,058,752
Mapped reads	2,582,162 / 84.42%
Unmapped reads	476,590 / 15.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,023 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	95,755 / 3.13%
Duplication rate	3.04%
Clipped reads	1,113,336 / 36.4%

2.2. ACGT Content

Number/percentage of A's	47,752,213 / 27.67%
Number/percentage of C's	30,514,370 / 17.68%
Number/percentage of T's	56,849,629 / 32.94%
Number/percentage of G's	37,430,202 / 21.69%
Number/percentage of N's	47,634 / 0.03%
GC Percentage	39.37%

2.3. Coverage

Mean	0.0558

Standard Deviation	0.3789

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

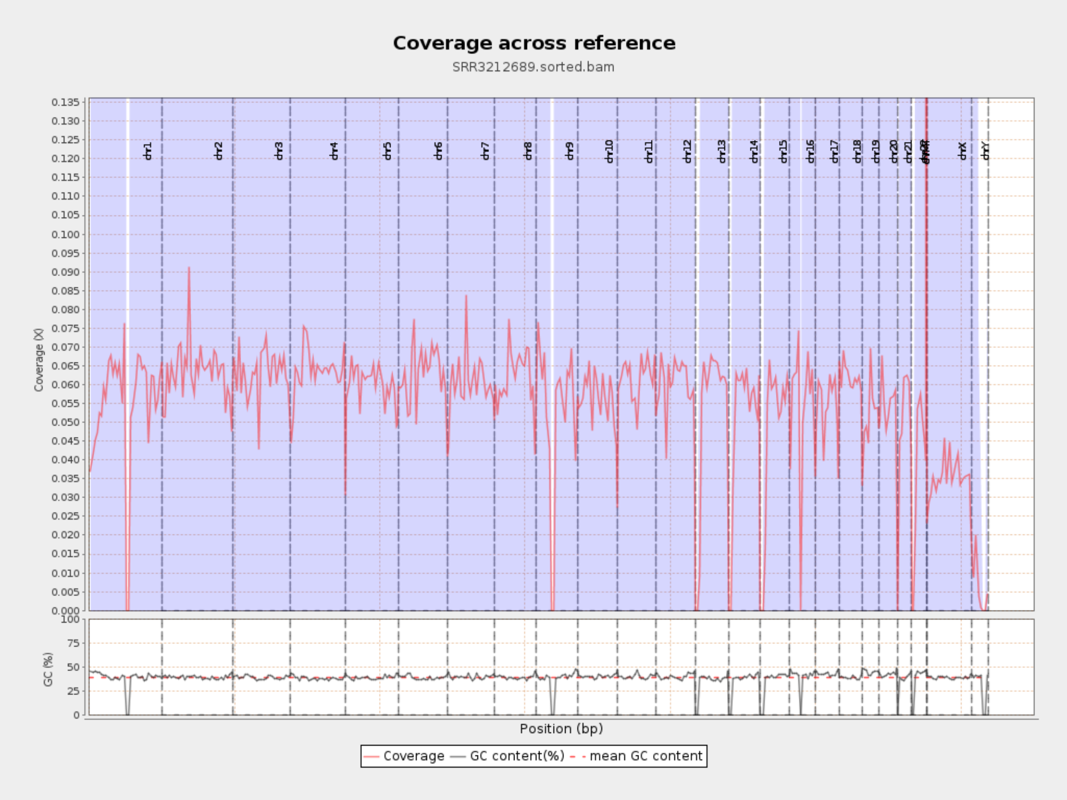
General error rate	0.99%
Mismatches	1,684,748
Insertions	15,184
Mapped reads with at least one insertion	0.58%
Deletions	40,462
Mapped reads with at least one deletion	1.55%
Homopolymer indels	49.61%

2.6. Chromosome stats

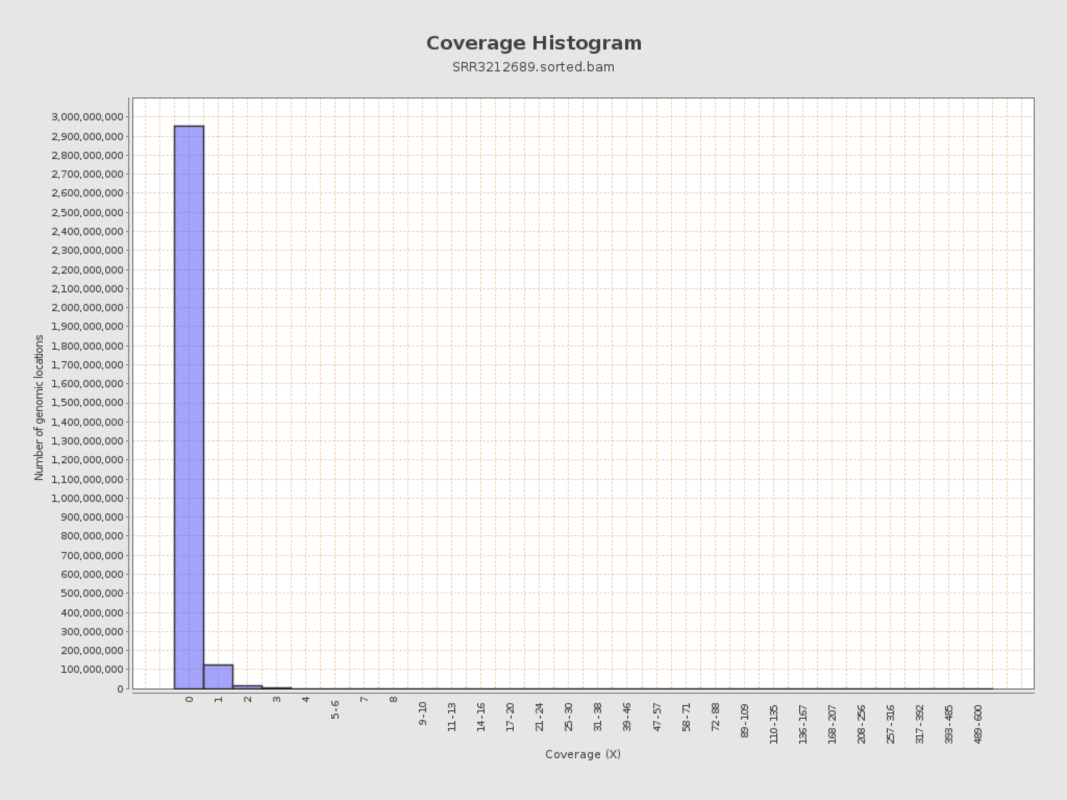
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13640165	0.0547	0.5798
chr2	243199373	15431646	0.0635	0.4313
chr3	198022430	12504117	0.0631	0.2878
chr4	191154276	12169488	0.0637	0.3056
chr5	180915260	10919488	0.0604	0.2816
chr6	171115067	10782181	0.063	0.3391
chr7	159138663	9745495	0.0612	0.5672

chr8	146364022	9086286	0.0621	0.4112
chr9	141213431	7447661	0.0527	0.3824
chr10	135534747	7720317	0.057	0.3333
chr11	135006516	8264656	0.0612	0.3596
chr12	133851895	8058274	0.0602	0.2833
chr13	115169878	6011115	0.0522	0.2617
chr14	107349540	5316740	0.0495	0.2756
chr15	102531392	4817750	0.047	0.2481
chr16	90354753	4910467	0.0543	0.2971
chr17	81195210	4370043	0.0538	0.305
chr18	78077248	4851174	0.0621	0.6763
chr19	59128983	3094558	0.0523	0.4542
chr20	63025520	3444385	0.0547	0.2801
chr21	48129895	2354556	0.0489	0.2725
chr22	51304566	1836550	0.0358	0.2156
chrMT	16571	41084	2.4793	2.5874
chrX	155270560	5494641	0.0354	0.2365
chrY	59373566	347134	0.0058	0.1568

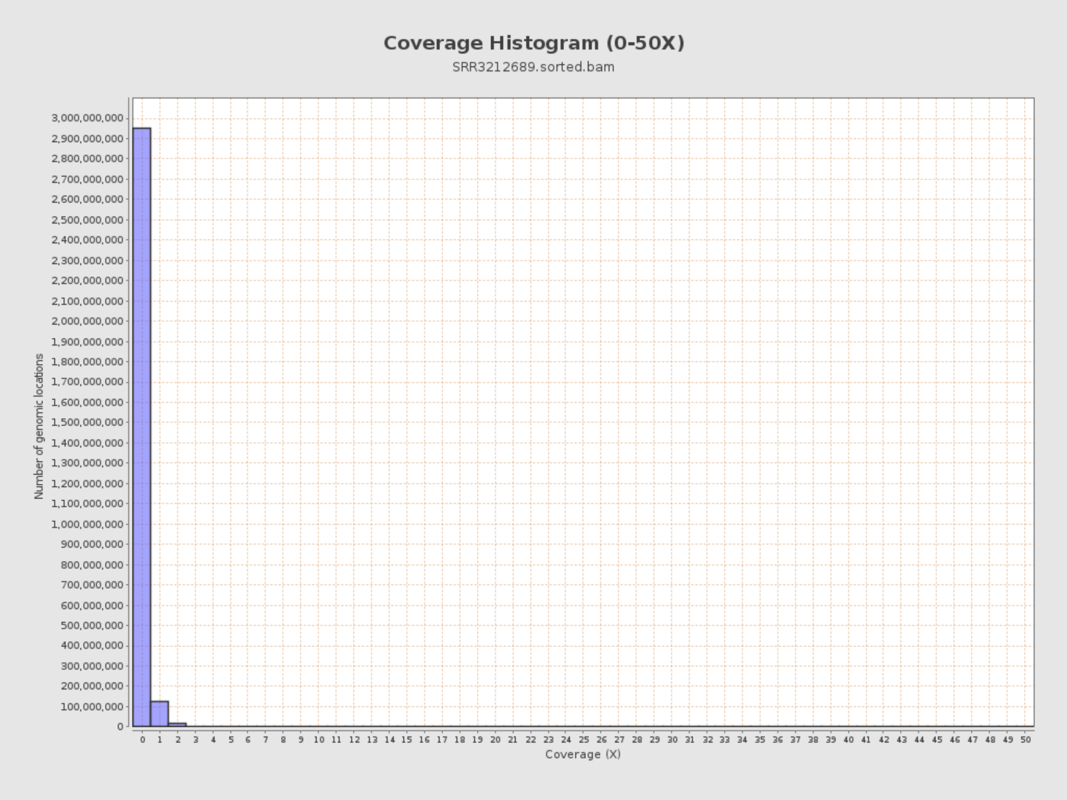
3. Results : Coverage across reference



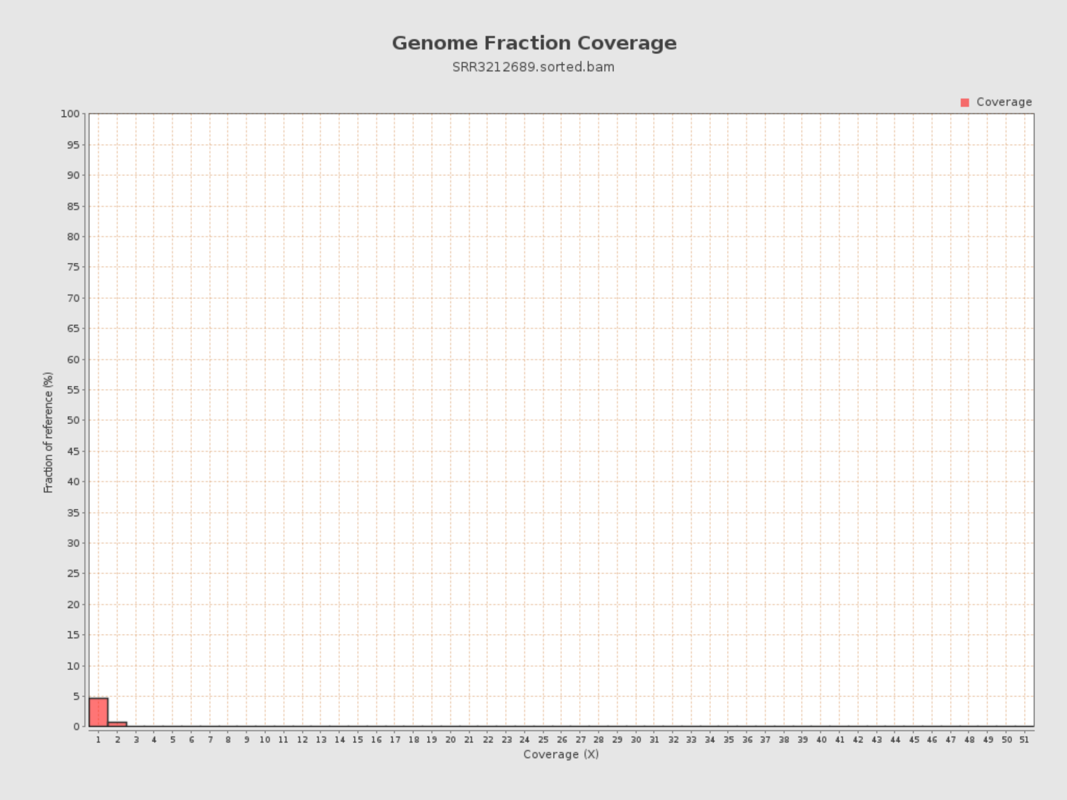
4. Results : Coverage Histogram



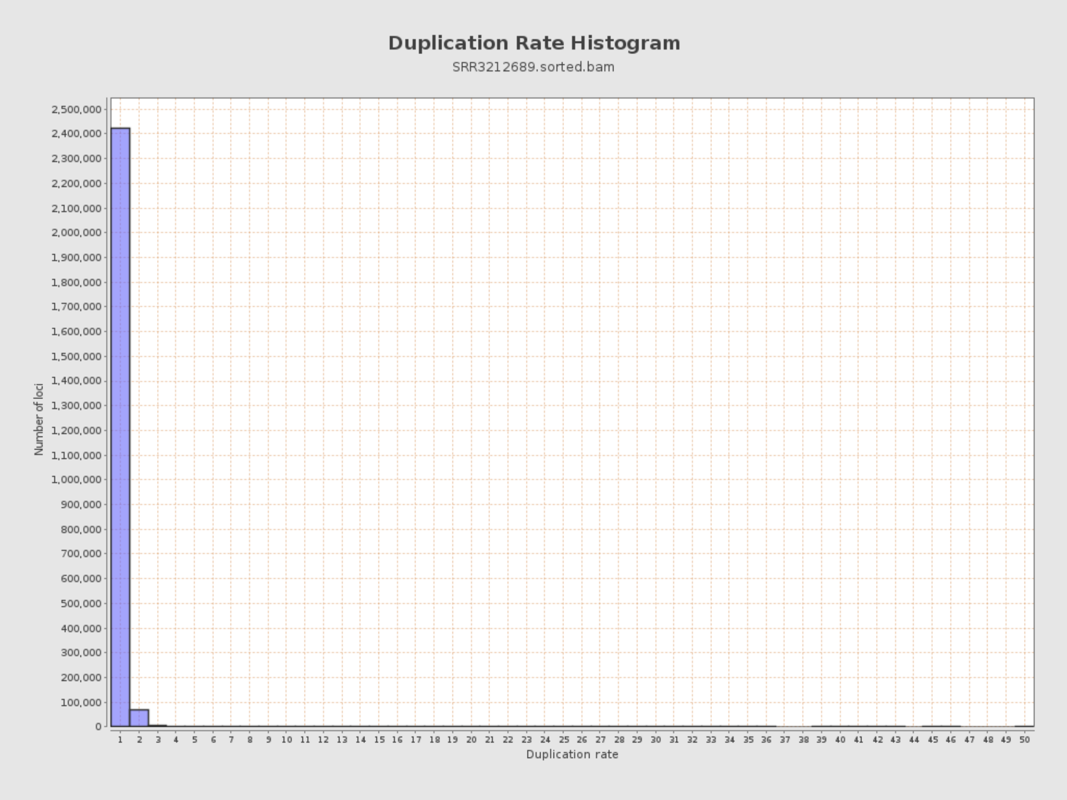
5. Results : Coverage Histogram (0-50X)



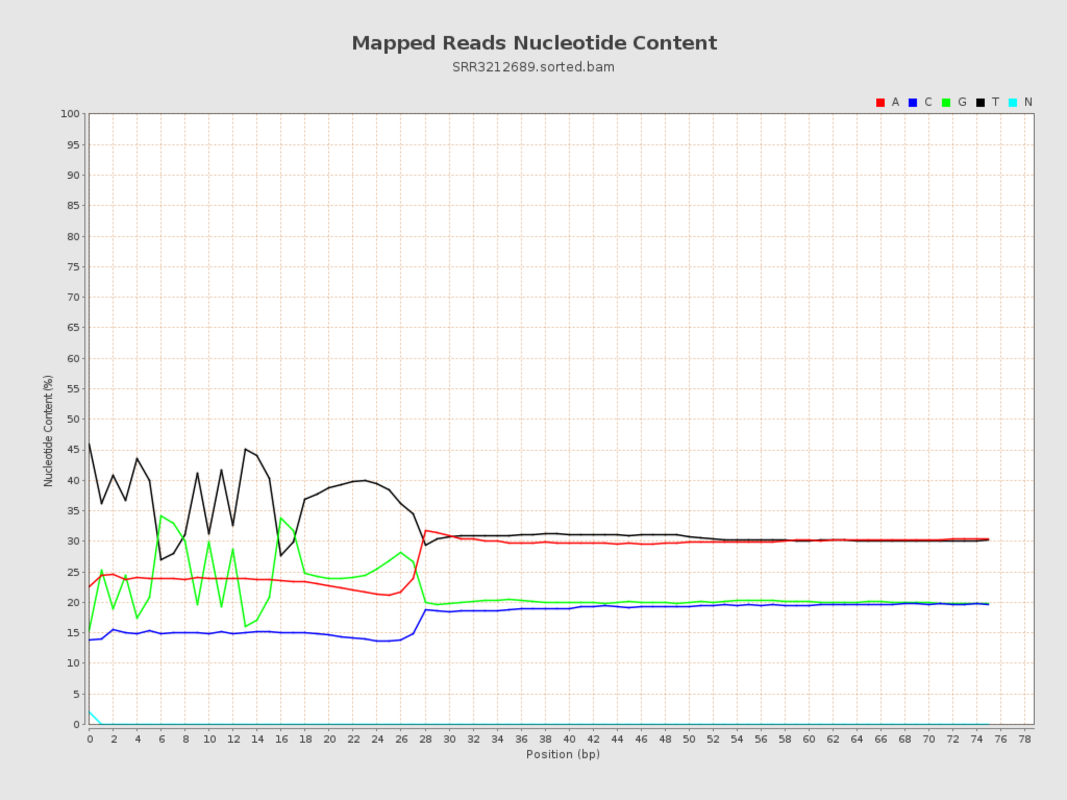
6. Results : Genome Fraction Coverage



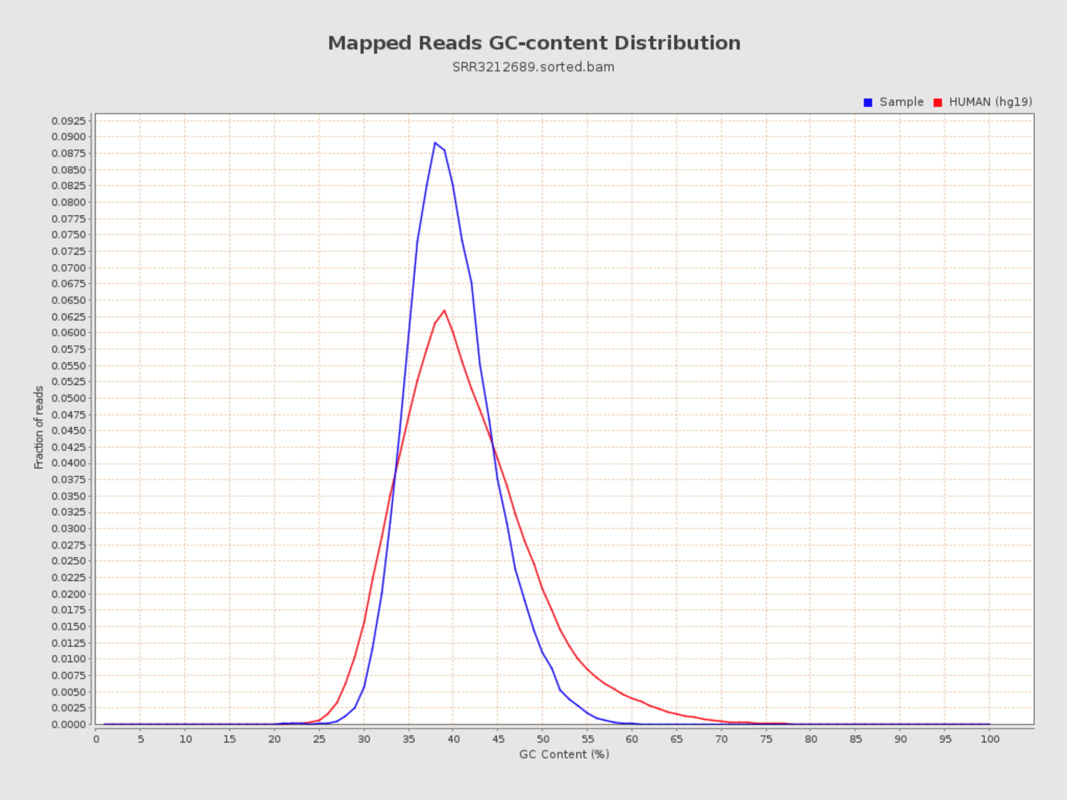
7. Results : Duplication Rate Histogram



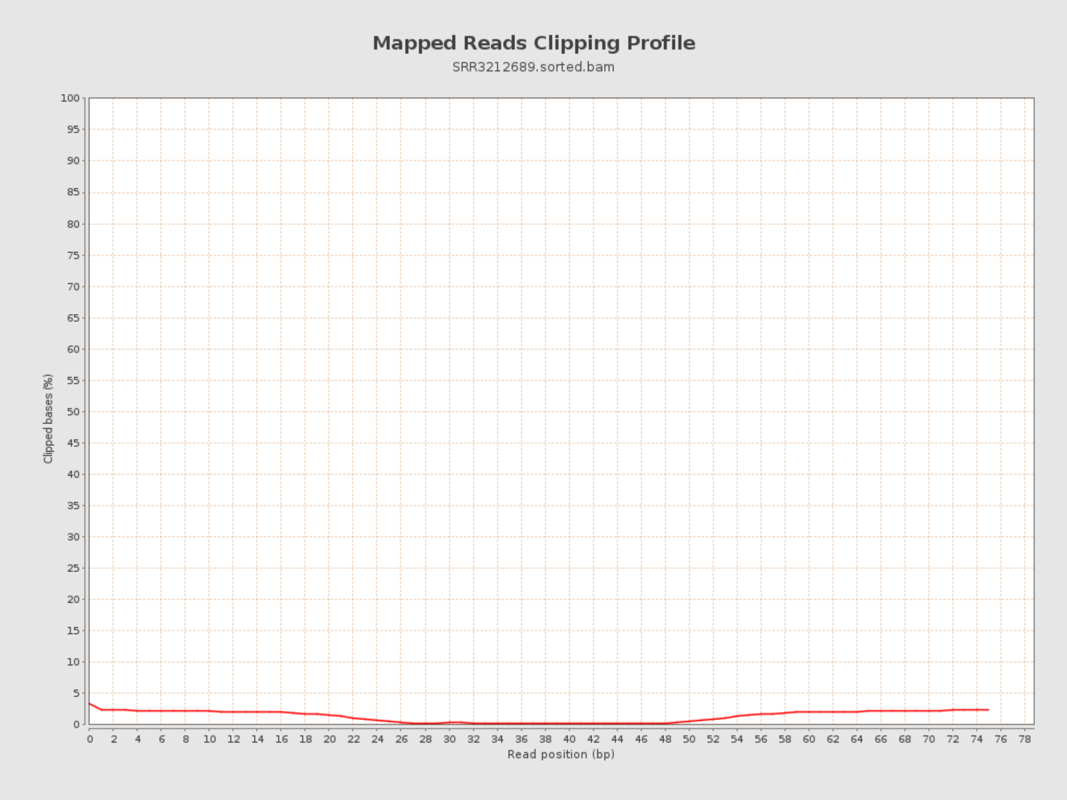
8. Results : Mapped Reads Nucleotide Content



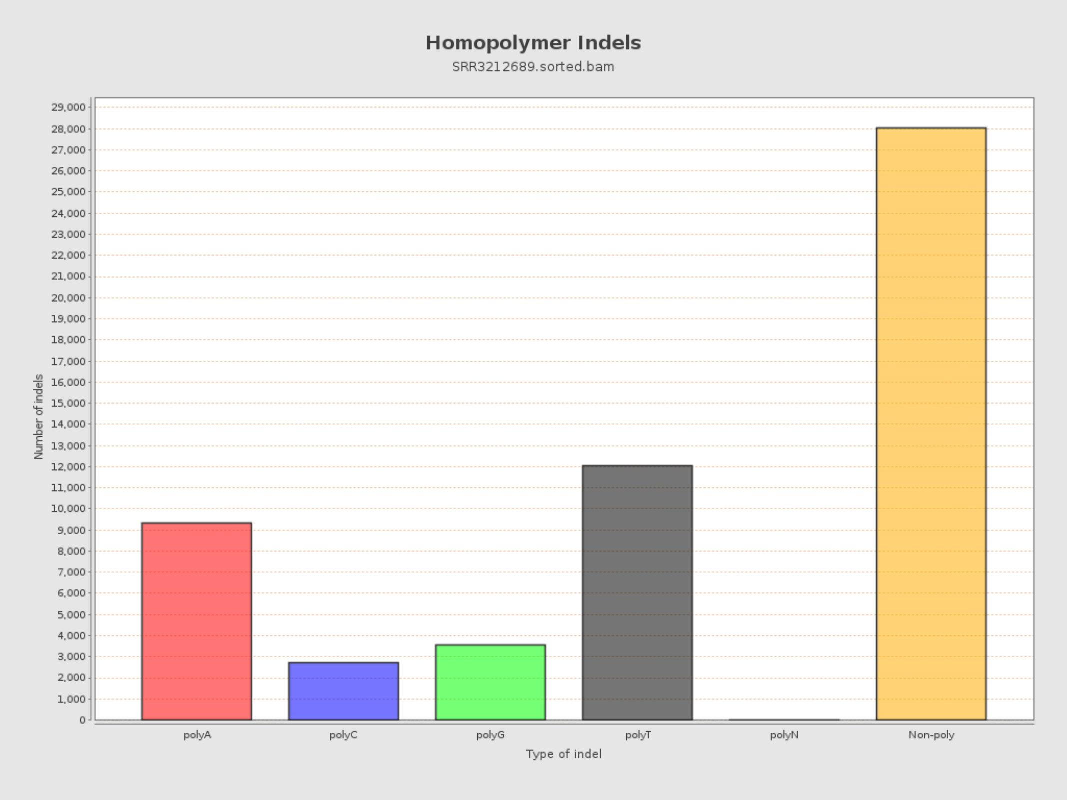
9. Results : Mapped Reads GC-content Distribution



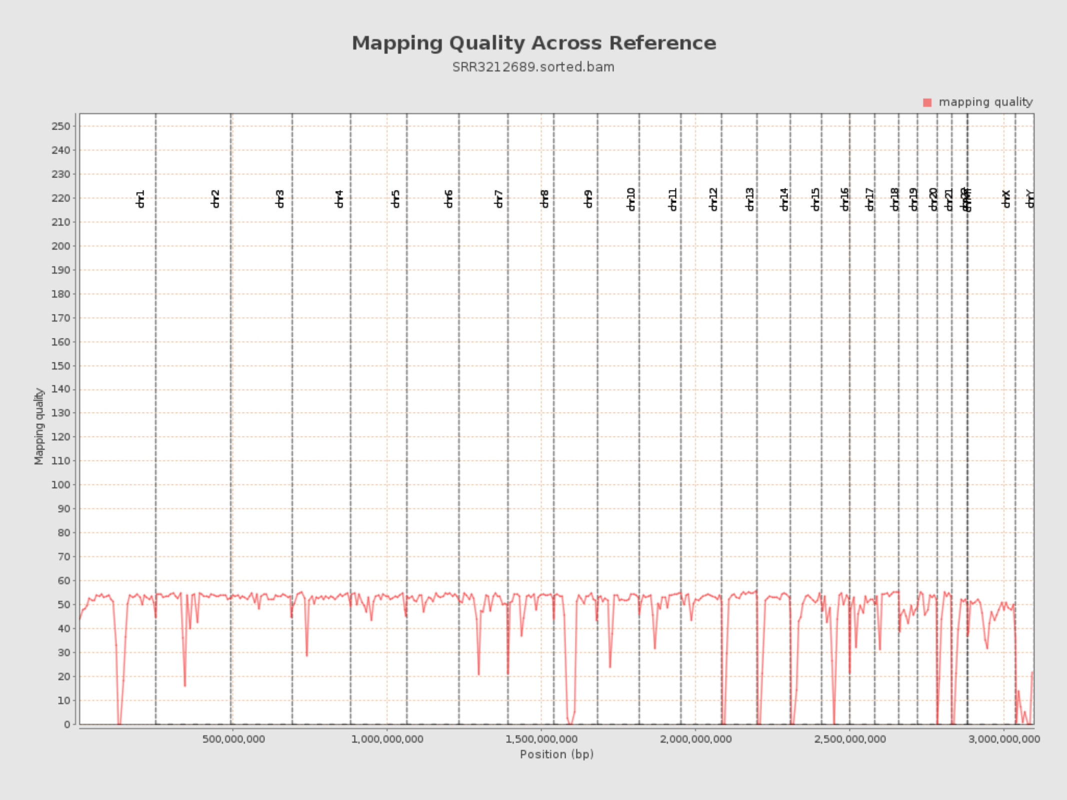
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram