Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:39:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013242.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_SRR6013242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:39:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,962,442
Mapped reads	1,683,983 / 85.81%
Unmapped reads	278,459 / 14.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,011 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	169,623 / 8.64%
Duplication rate	8.25%
Clipped reads	967,527 / 49.3%

2.2. ACGT Content

Number/percentage of A's	30,272,509 / 28.16%
Number/percentage of C's	18,911,204 / 17.59%
Number/percentage of T's	35,205,044 / 32.75%
Number/percentage of G's	23,084,958 / 21.48%
Number/percentage of N's	22,046 / 0.02%
GC Percentage	39.07%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.3645

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Mismatches and indels

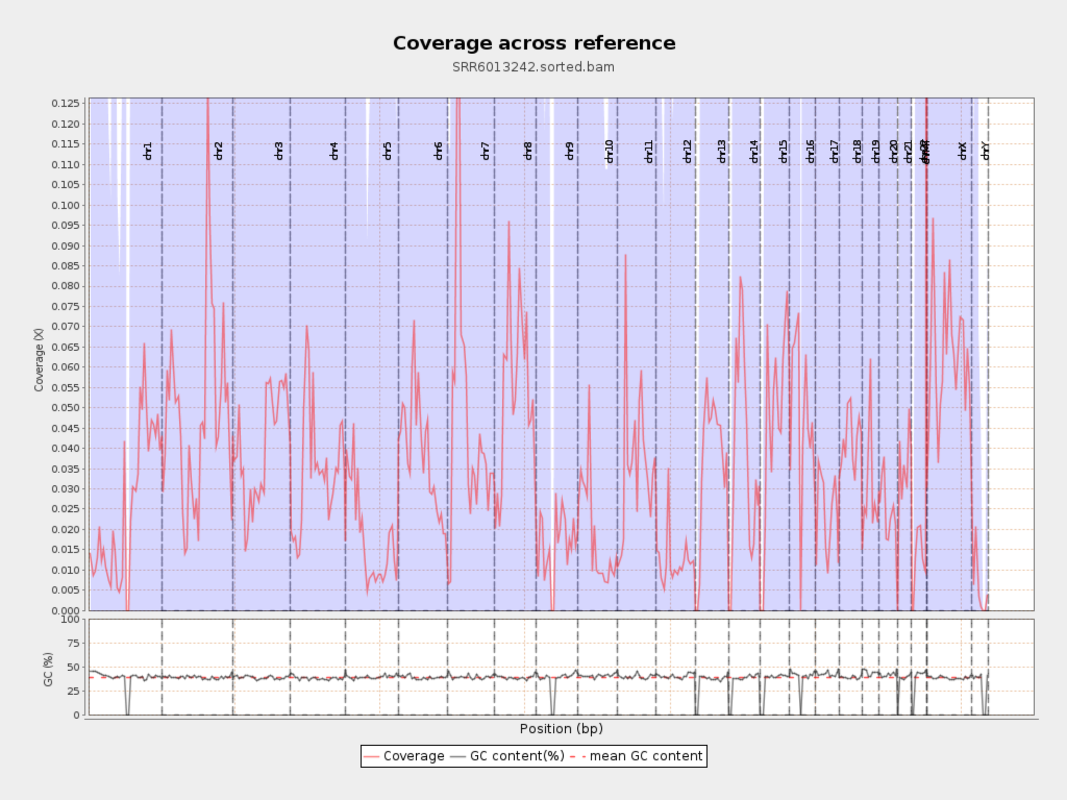
General error rate	0.98%
Mismatches	1,040,239
Insertions	7,679
Mapped reads with at least one insertion	0.45%
Deletions	51,660
Mapped reads with at least one deletion	3.01%
Homopolymer indels	42.92%

2.6. Chromosome stats

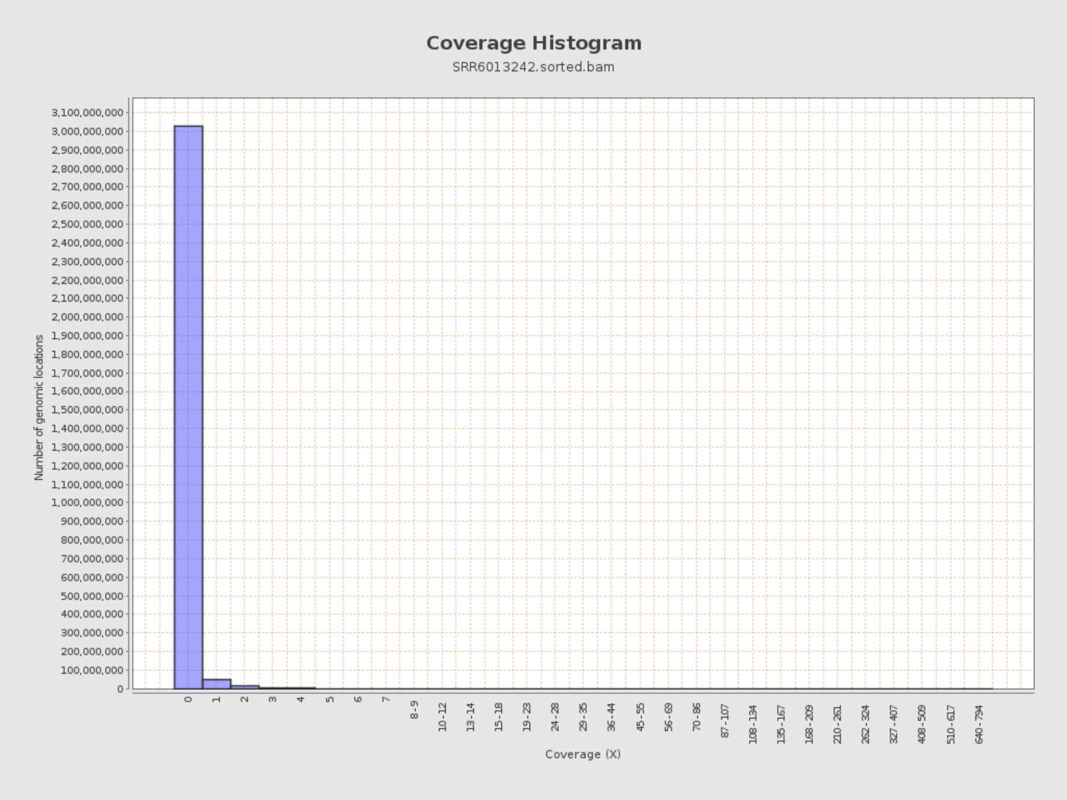
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6360192	0.0255	0.5396
chr2	243199373	11843398	0.0487	0.4281
chr3	198022430	8036749	0.0406	0.289
chr4	191154276	6611759	0.0346	0.2735
chr5	180915260	3180287	0.0176	0.1893
chr6	171115067	6576632	0.0384	0.4037
chr7	159138663	7692654	0.0483	0.4967

chr8	146364022	7831254	0.0535	0.5715
chr9	141213431	2253227	0.016	0.2507
chr10	135534747	2521238	0.0186	0.2865
chr11	135006516	4884002	0.0362	0.3016
chr12	133851895	1662587	0.0124	0.1559
chr13	115169878	4184072	0.0363	0.2755
chr14	107349540	4062706	0.0378	0.2848
chr15	102531392	4759766	0.0464	0.3059
chr16	90354753	4367149	0.0483	0.3207
chr17	81195210	1894827	0.0233	0.2315
chr18	78077248	3269971	0.0419	0.5324
chr19	59128983	1826247	0.0309	0.4152
chr20	63025520	1545848	0.0245	0.2249
chr21	48129895	1628888	0.0338	0.2844
chr22	51304566	621004	0.0121	0.1497
chrMT	16571	9896	0.5972	1.0761
chrX	155270560	9599007	0.0618	0.3773
chrY	59373566	362338	0.0061	0.1997

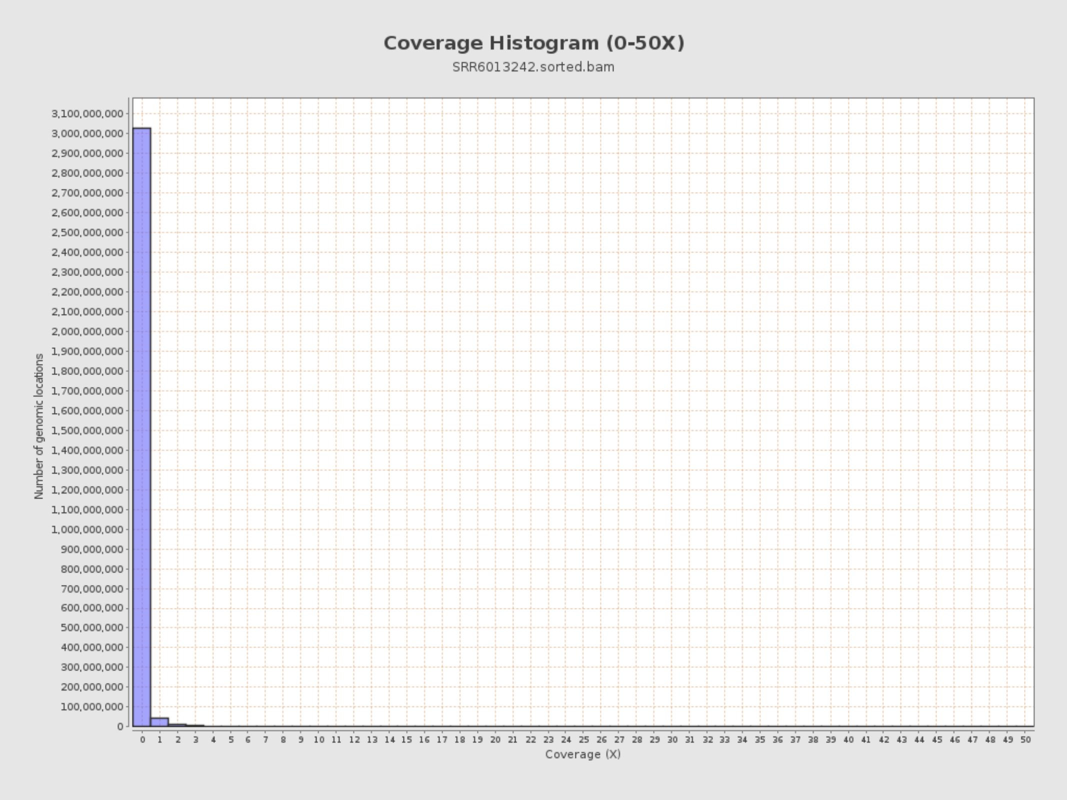
3. Results : Coverage across reference



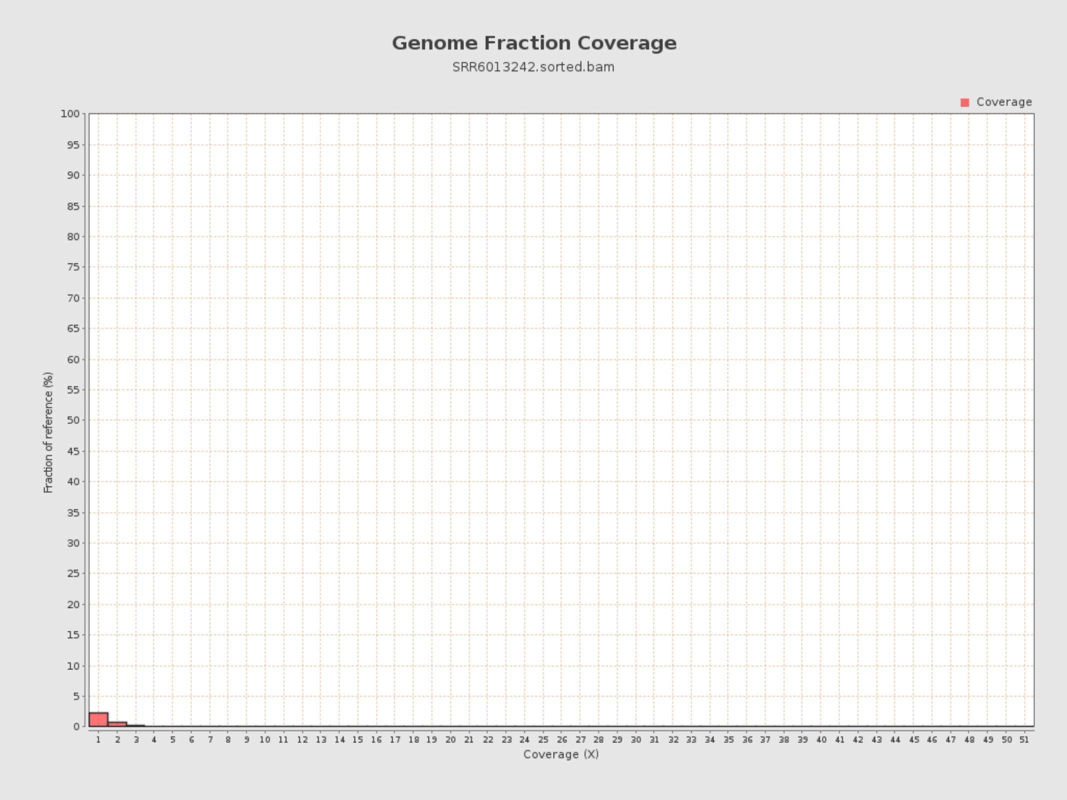
4. Results : Coverage Histogram



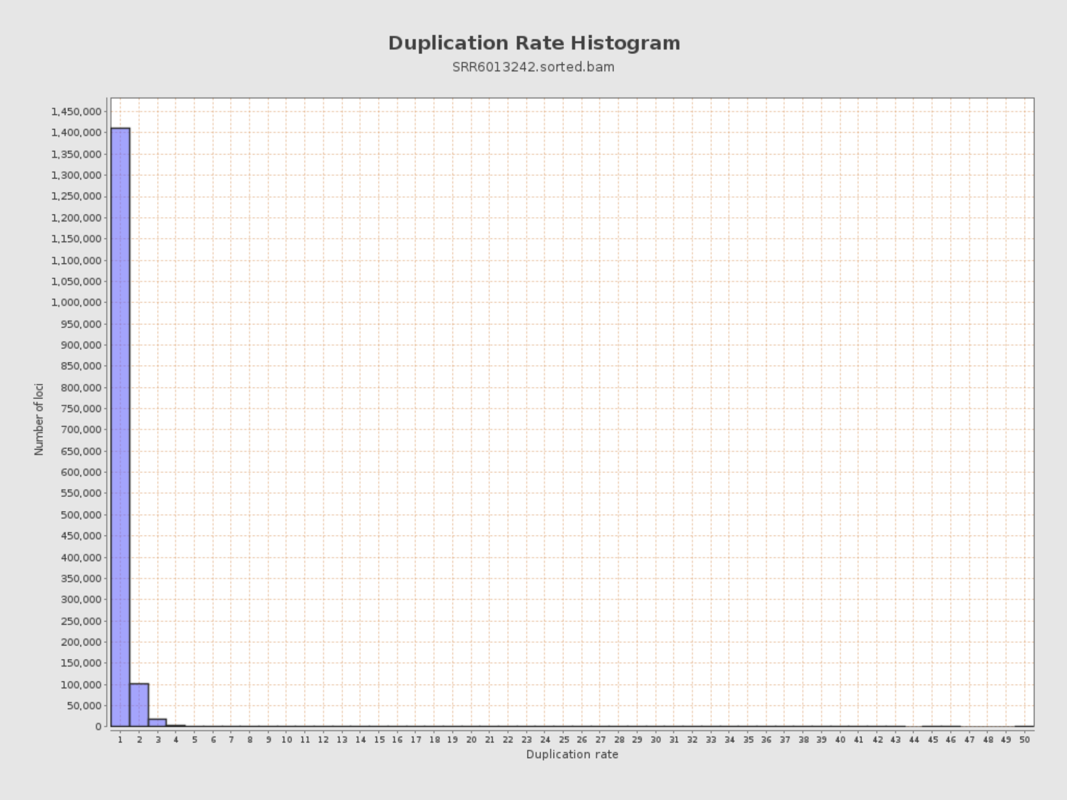
5. Results : Coverage Histogram (0-50X)



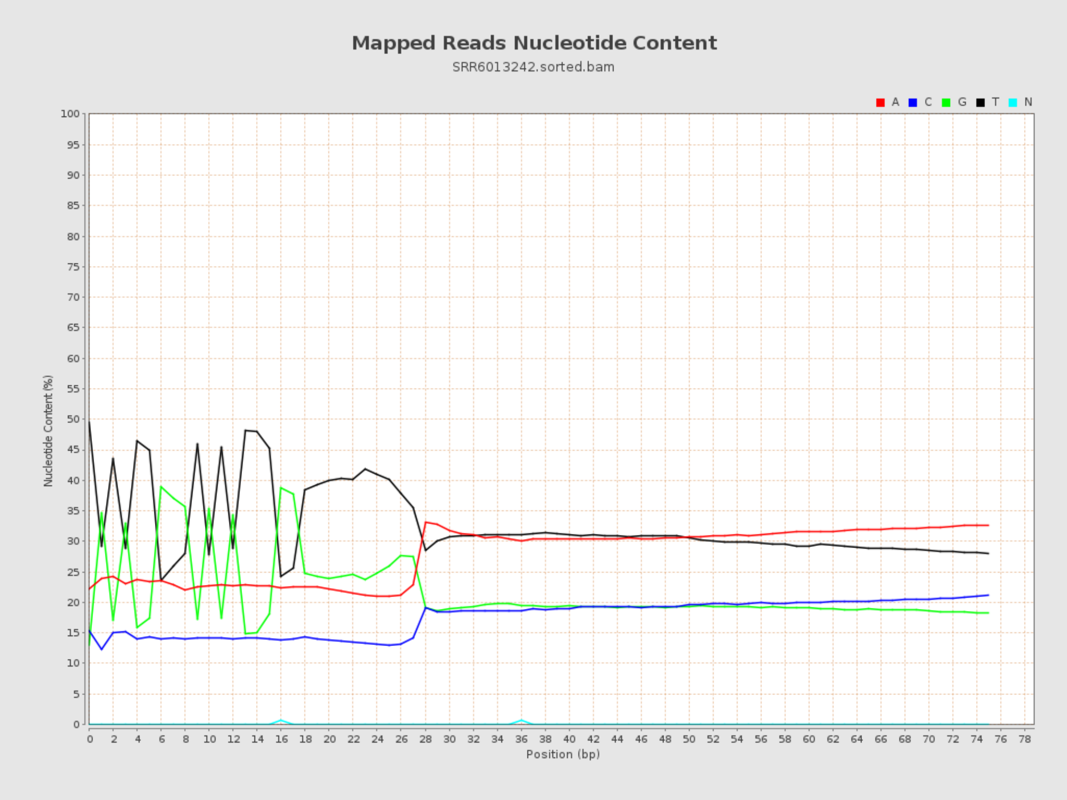
6. Results : Genome Fraction Coverage



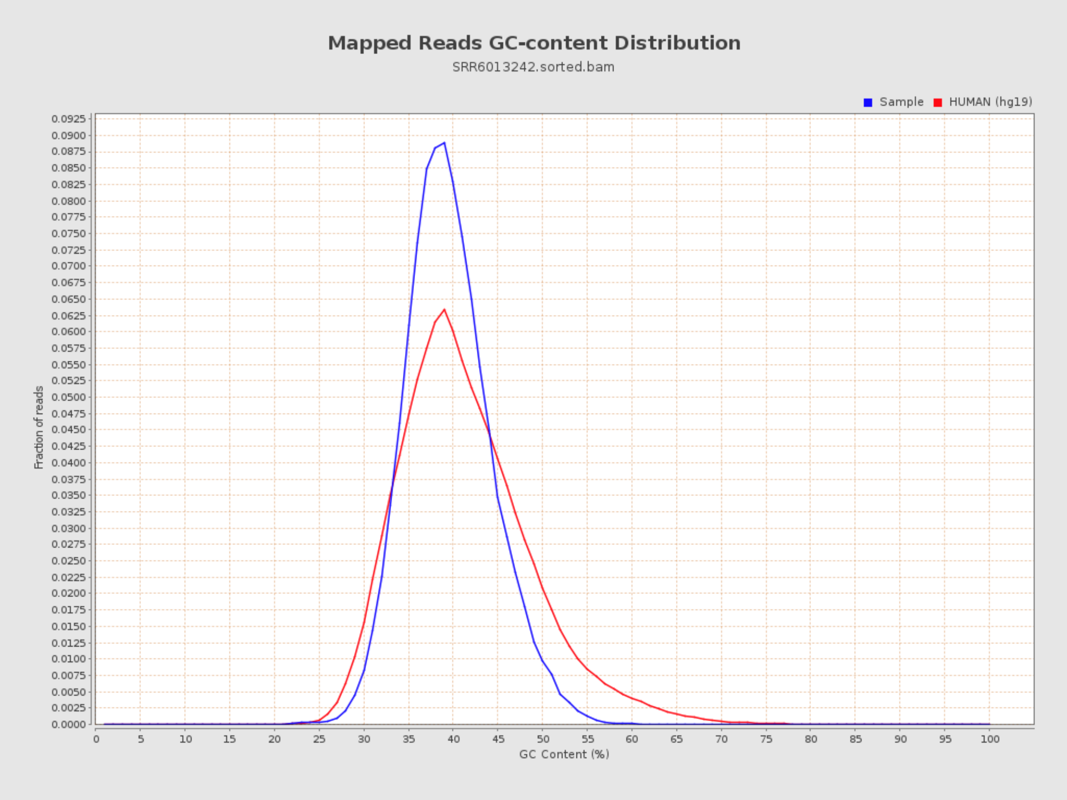
7. Results : Duplication Rate Histogram



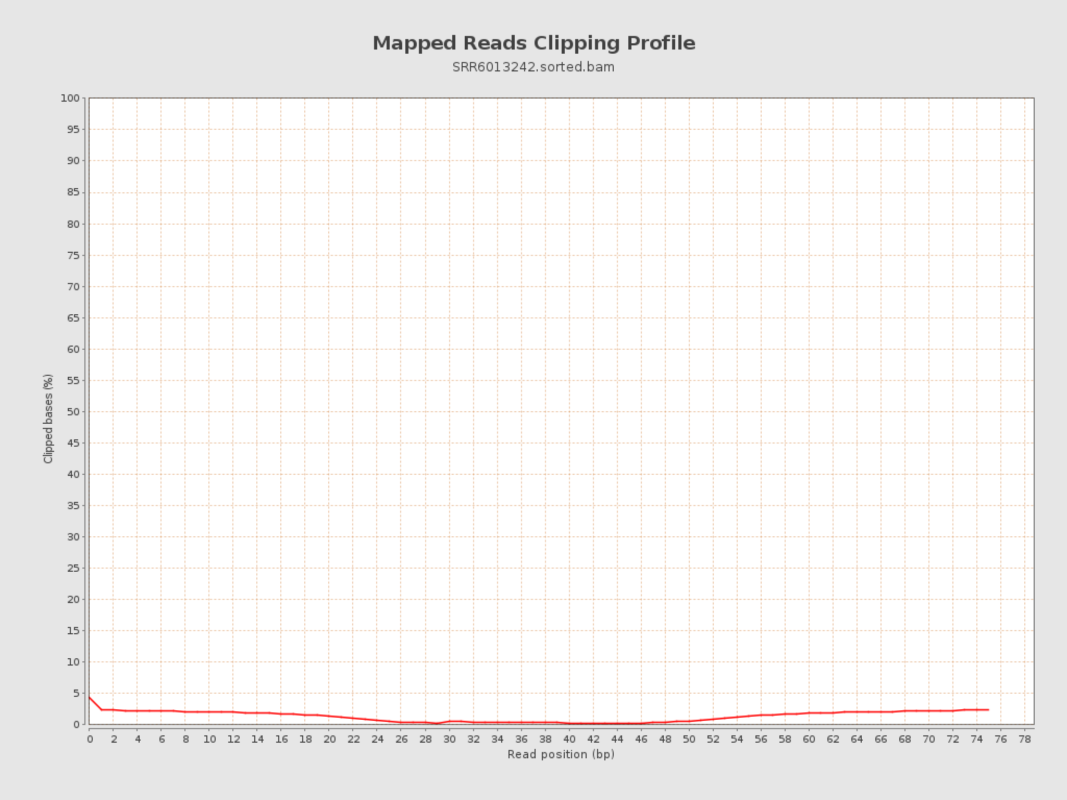
8. Results : Mapped Reads Nucleotide Content



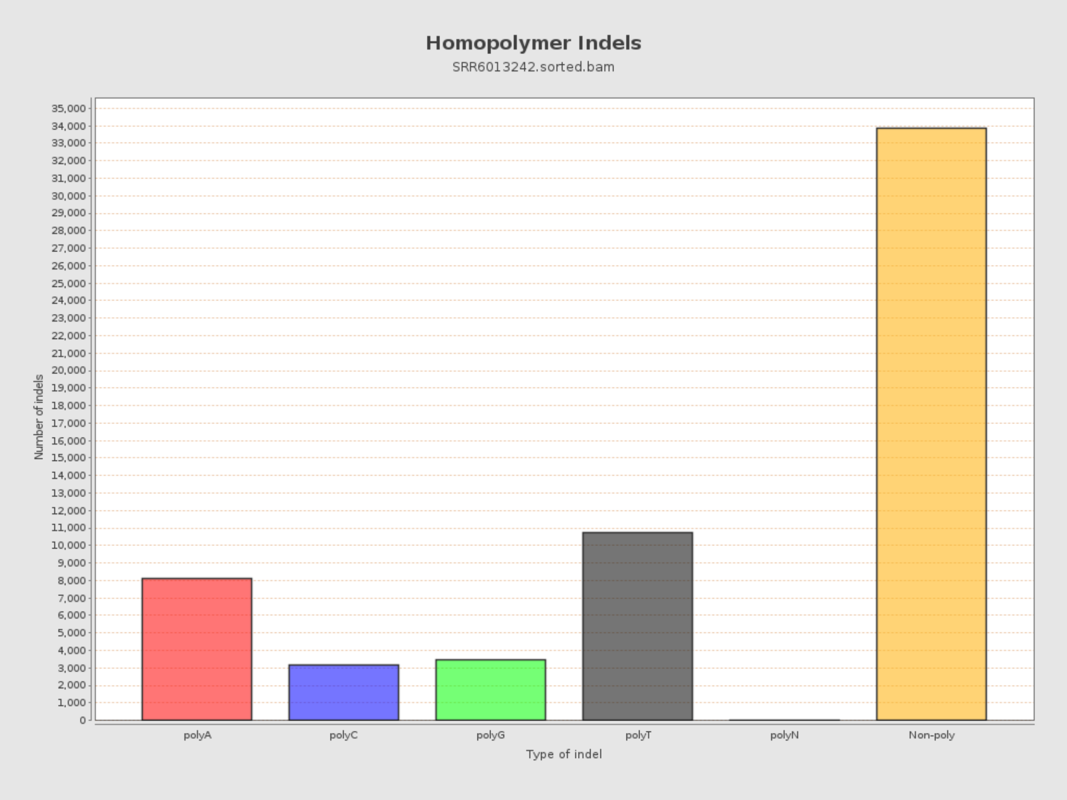
9. Results : Mapped Reads GC-content Distribution



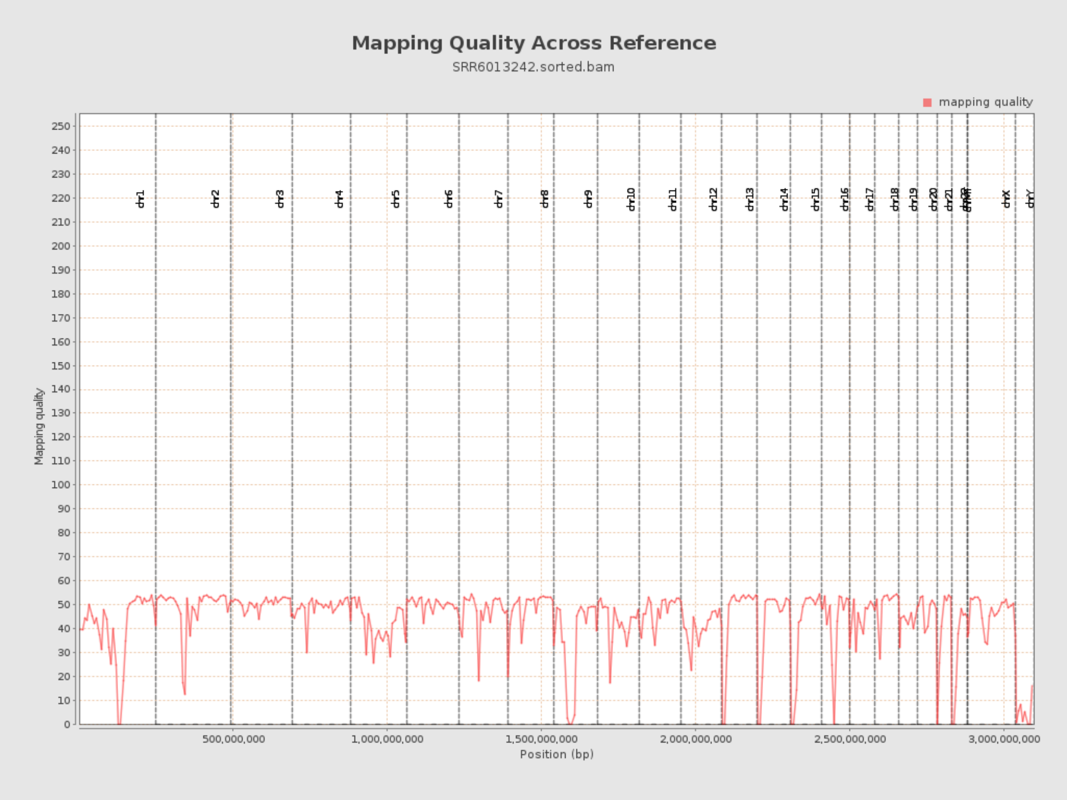
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram