Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231731.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_SRR6231731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:51:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,850,674
Mapped reads	1,994,267 / 69.96%
Unmapped reads	856,407 / 30.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,892 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	874,662 / 30.68%
Duplication rate	12.29%
Clipped reads	652,820 / 22.9%

2.2. ACGT Content

Number/percentage of A's	24,938,196 / 18.07%
Number/percentage of C's	18,143,029 / 13.15%
Number/percentage of T's	26,633,382 / 19.3%
Number/percentage of G's	68,237,440 / 49.46%
Number/percentage of N's	26,510 / 0.02%
GC Percentage	62.6%

2.3. Coverage

Mean	0.0446

Standard Deviation	97.9544

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Mismatches and indels

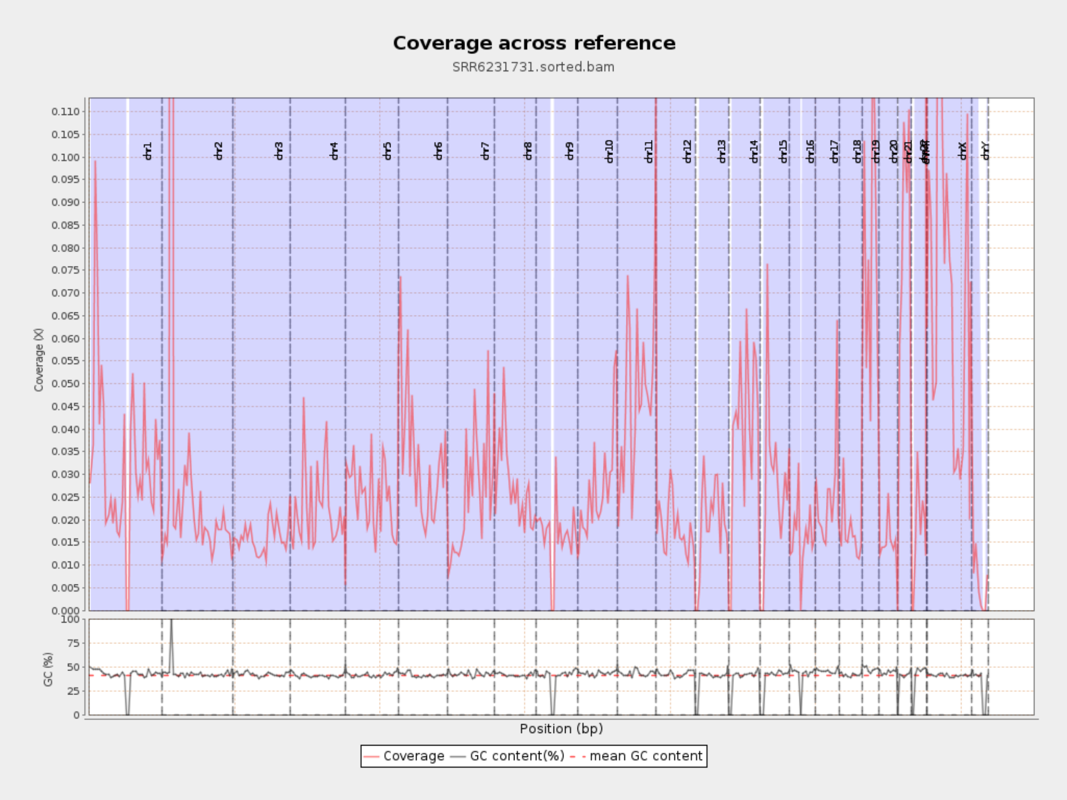
General error rate	0.53%
Mismatches	714,450
Insertions	7,738
Mapped reads with at least one insertion	0.38%
Deletions	20,450
Mapped reads with at least one deletion	1.02%
Homopolymer indels	44.87%

2.6. Chromosome stats

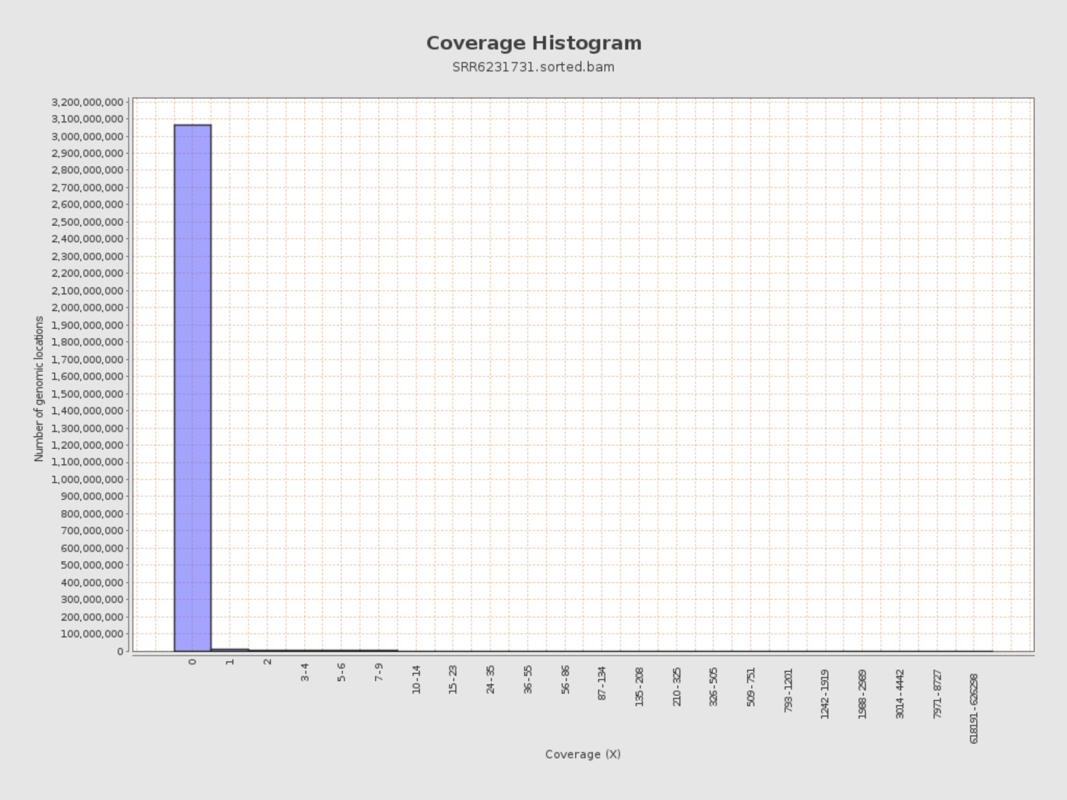
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8263237	0.0332	0.5894
chr2	243199373	53066284	0.2182	349.4759
chr3	198022430	3182440	0.0161	0.308
chr4	191154276	4313878	0.0226	0.3523
chr5	180915260	4542601	0.0251	0.3771
chr6	171115067	5720049	0.0334	0.4863
chr7	159138663	4024162	0.0253	0.4783

chr8	146364022	4001724	0.0273	0.468
chr9	141213431	2315506	0.0164	0.328
chr10	135534747	3638565	0.0268	0.4091
chr11	135006516	6402103	0.0474	0.6345
chr12	133851895	2426524	0.0181	0.3495
chr13	115169878	2203360	0.0191	0.3487
chr14	107349540	4213102	0.0392	0.5667
chr15	102531392	2812323	0.0274	0.4141
chr16	90354753	1471208	0.0163	0.3289
chr17	81195210	2116270	0.0261	0.3987
chr18	78077248	1331431	0.0171	0.5446
chr19	59128983	4600463	0.0778	0.7431
chr20	63025520	974580	0.0155	0.3083
chr21	48129895	3589459	0.0746	0.7034
chr22	51304566	875102	0.0171	0.3142
chrMT	16571	54369	3.281	4.8077
chrX	155270560	11457677	0.0738	0.6762
chrY	59373566	415440	0.007	0.1828

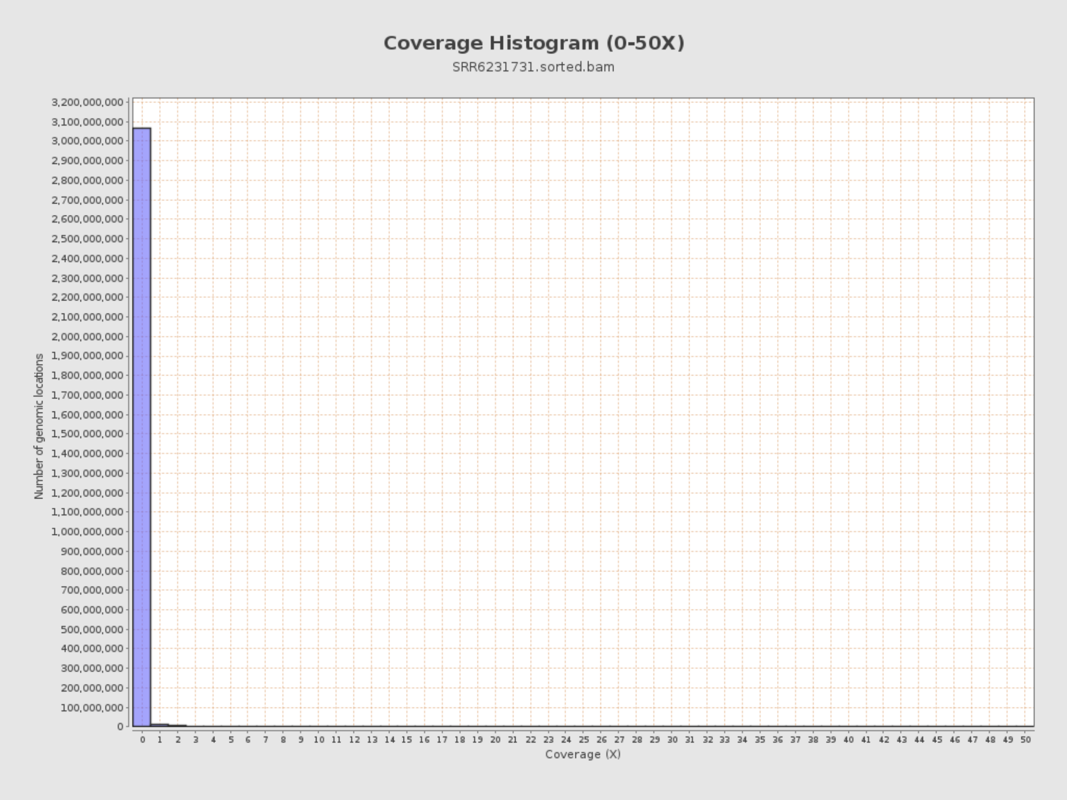
3. Results : Coverage across reference



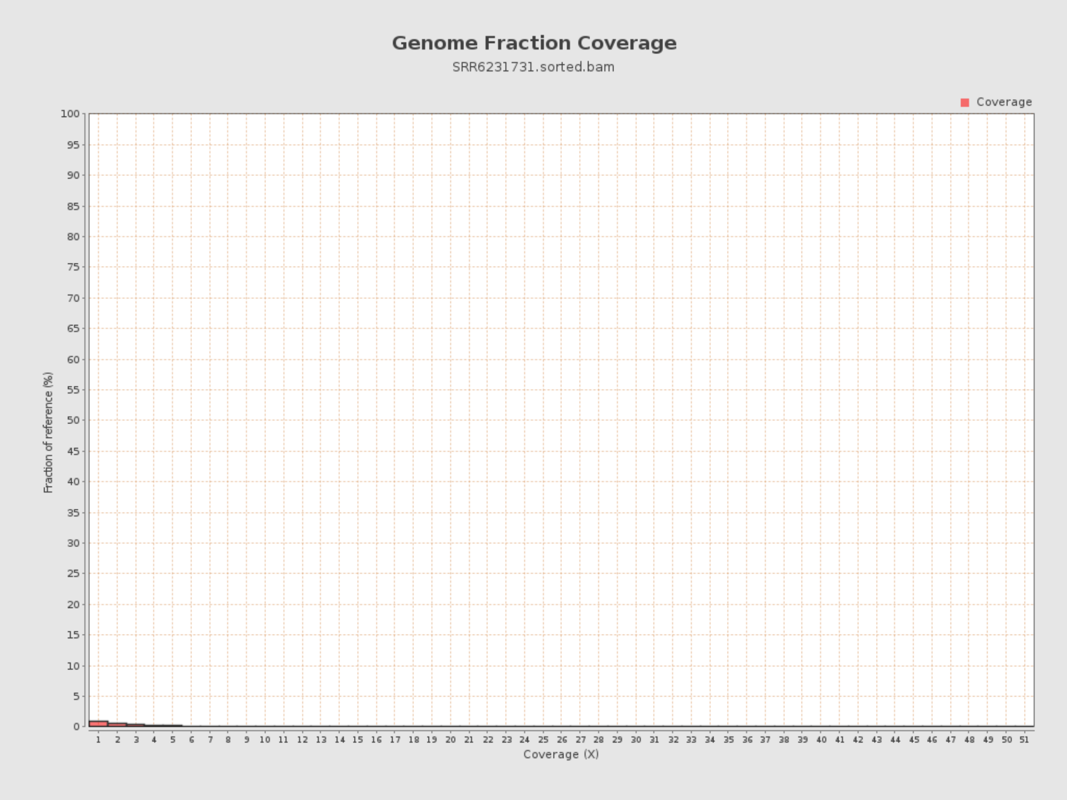
4. Results : Coverage Histogram



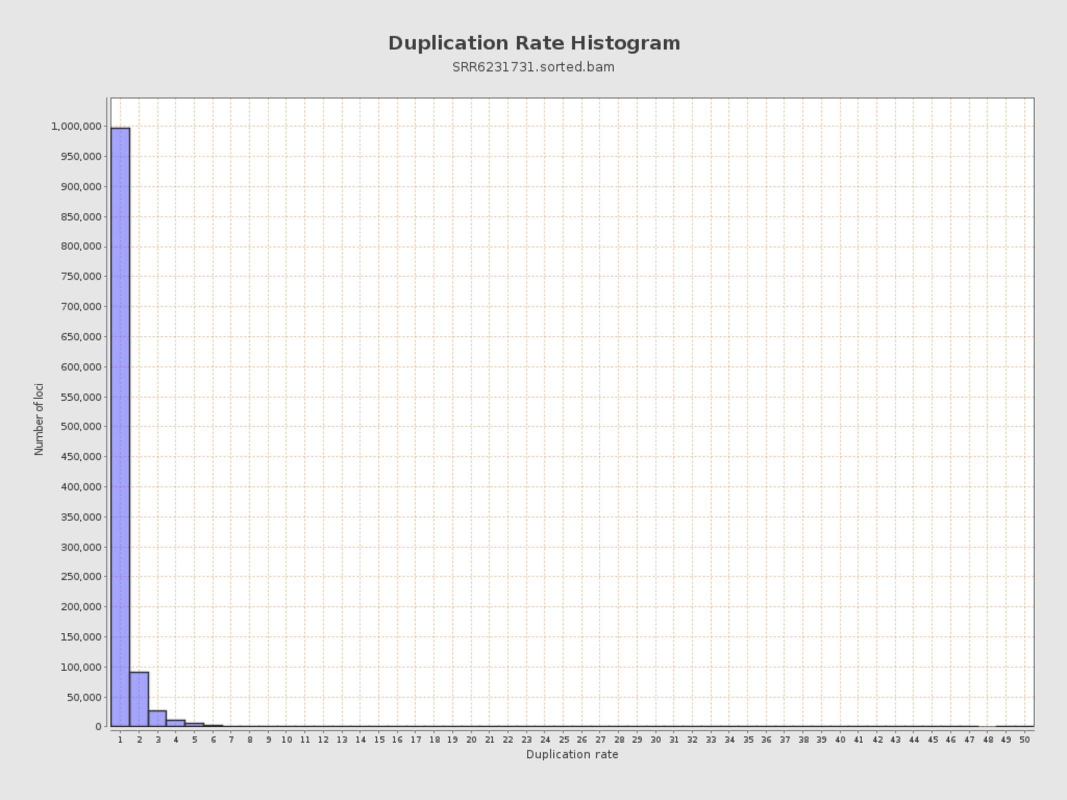
5. Results : Coverage Histogram (0-50X)



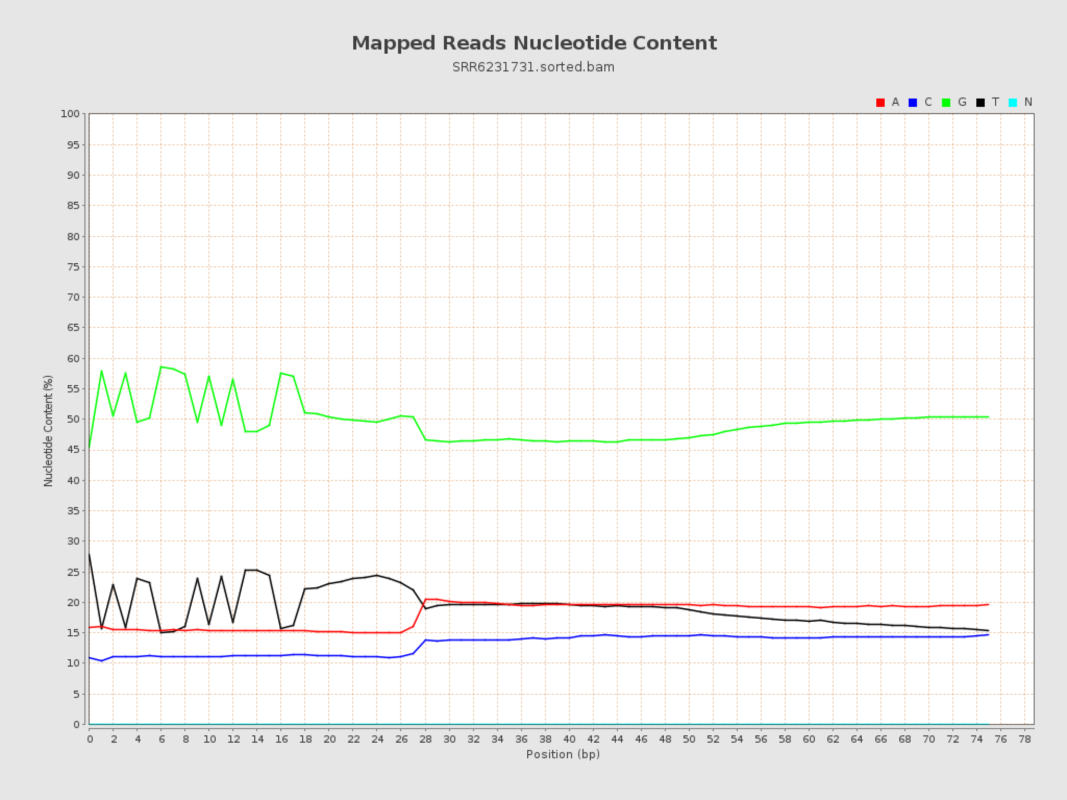
6. Results : Genome Fraction Coverage



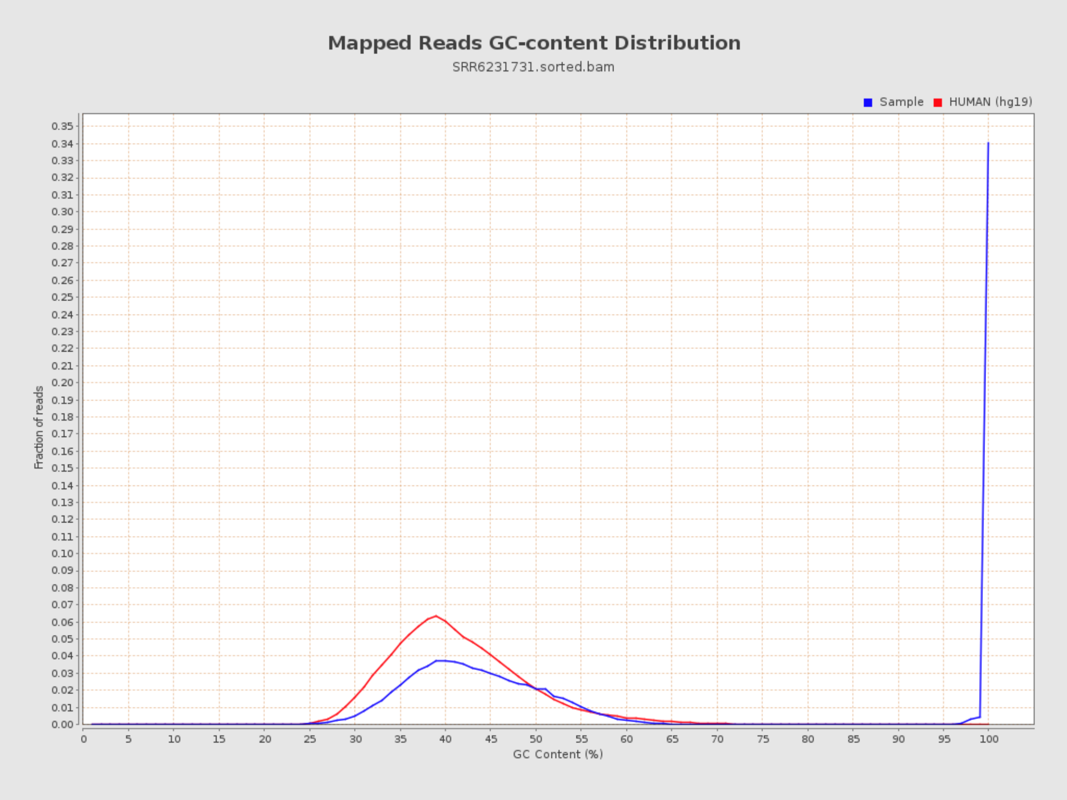
7. Results : Duplication Rate Histogram



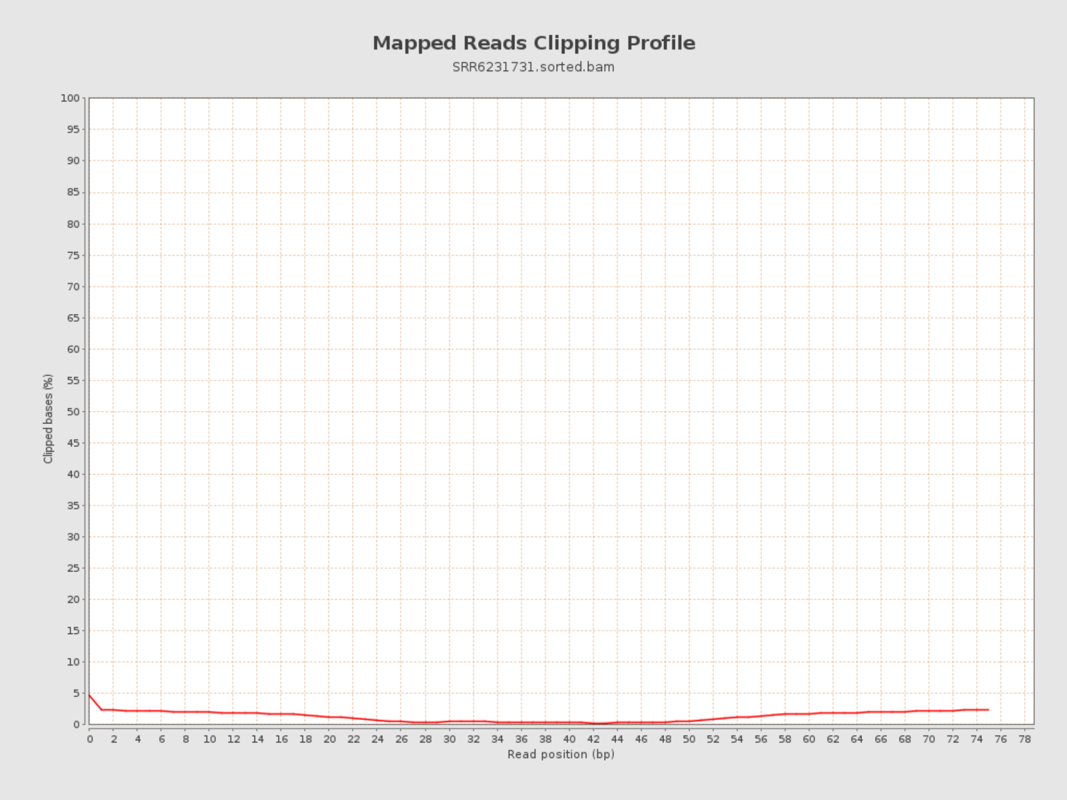
8. Results : Mapped Reads Nucleotide Content



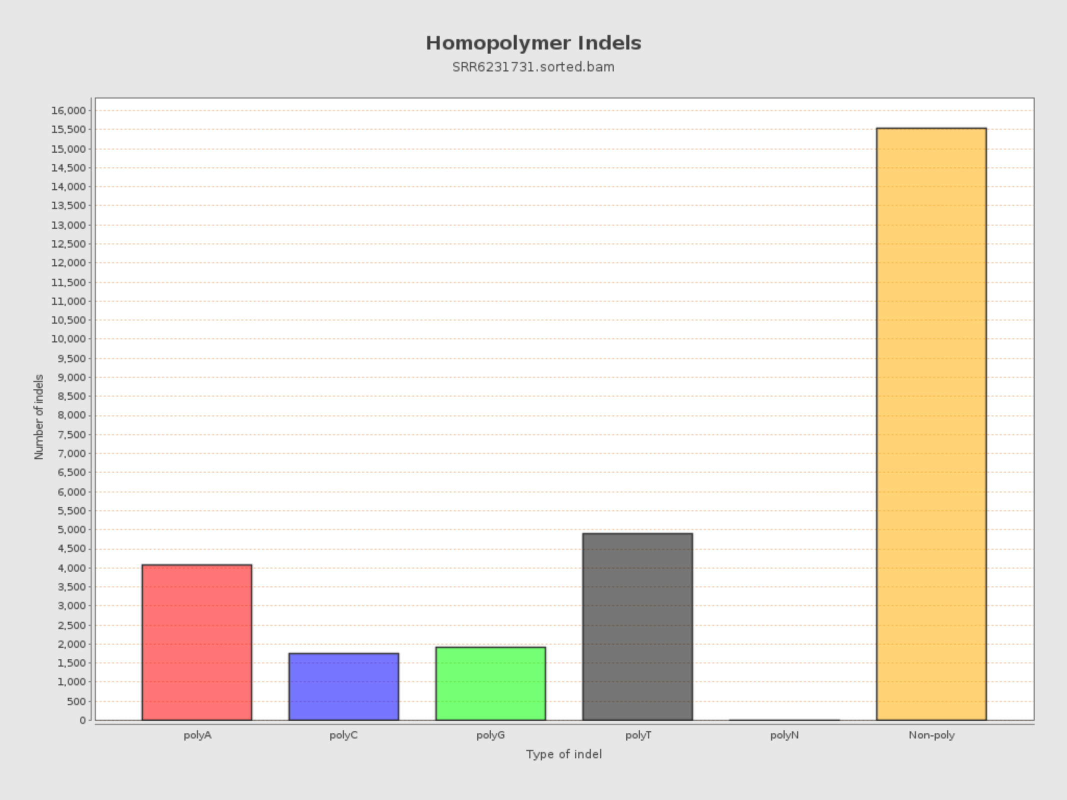
9. Results : Mapped Reads GC-content Distribution



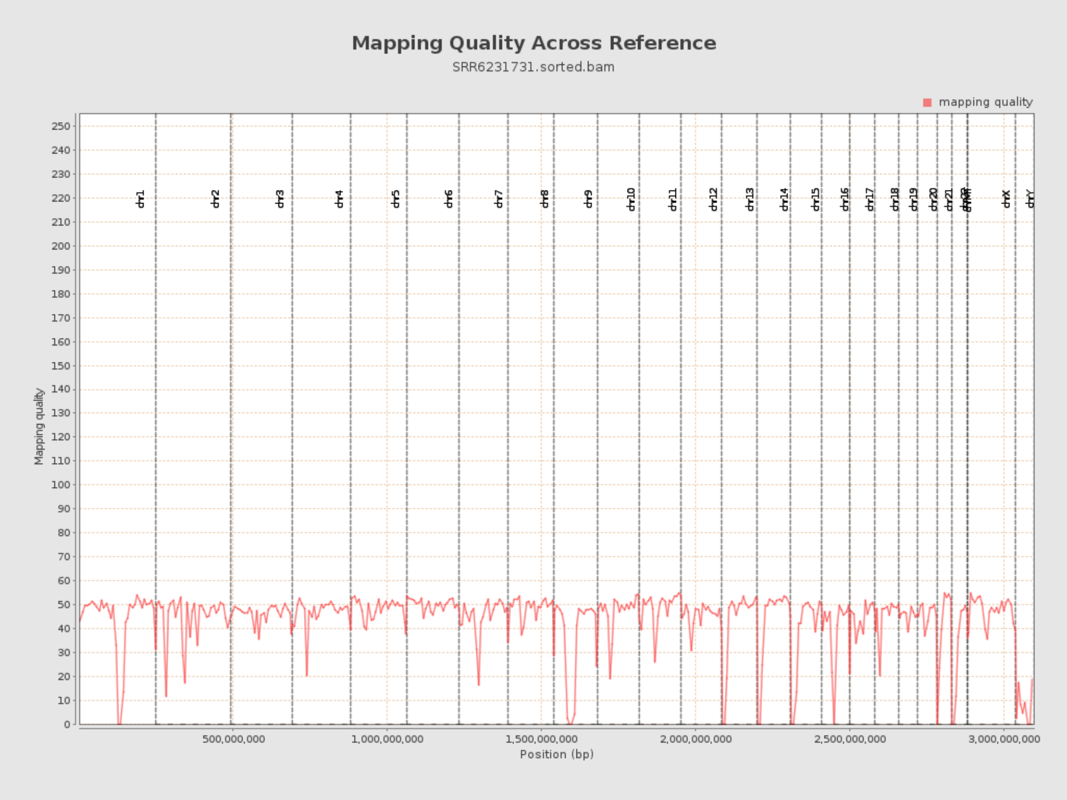
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram