Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:37:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004011.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_SRR6004011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:37:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,682,667
Mapped reads	1,542,701 / 91.68%
Unmapped reads	139,966 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,477 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	49,566 / 2.95%
Duplication rate	2.12%
Clipped reads	747,409 / 44.42%

2.2. ACGT Content

Number/percentage of A's	28,371,468 / 27.82%
Number/percentage of C's	19,233,485 / 18.86%
Number/percentage of T's	31,008,848 / 30.4%
Number/percentage of G's	23,359,256 / 22.9%
Number/percentage of N's	21,533 / 0.02%
GC Percentage	41.76%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3503

2.4. Mapping Quality

Mean Mapping Quality	42.76

2.5. Mismatches and indels

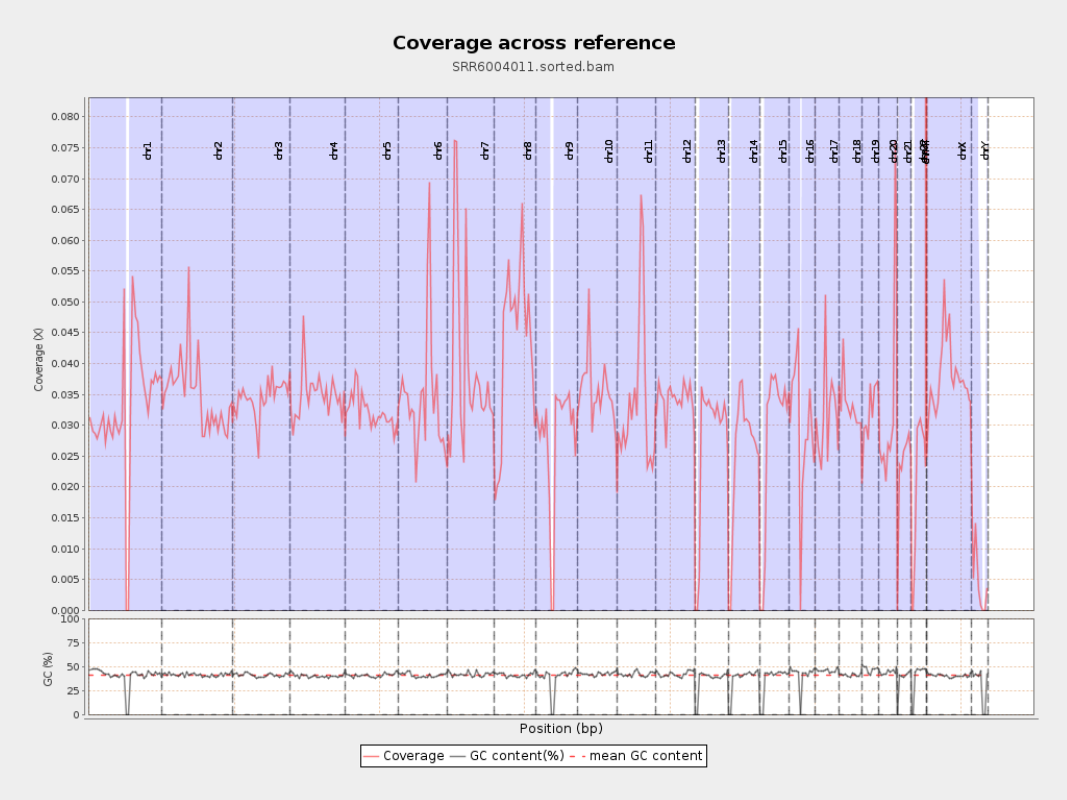
General error rate	0.81%
Mismatches	805,479
Insertions	8,313
Mapped reads with at least one insertion	0.53%
Deletions	25,336
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.6%

2.6. Chromosome stats

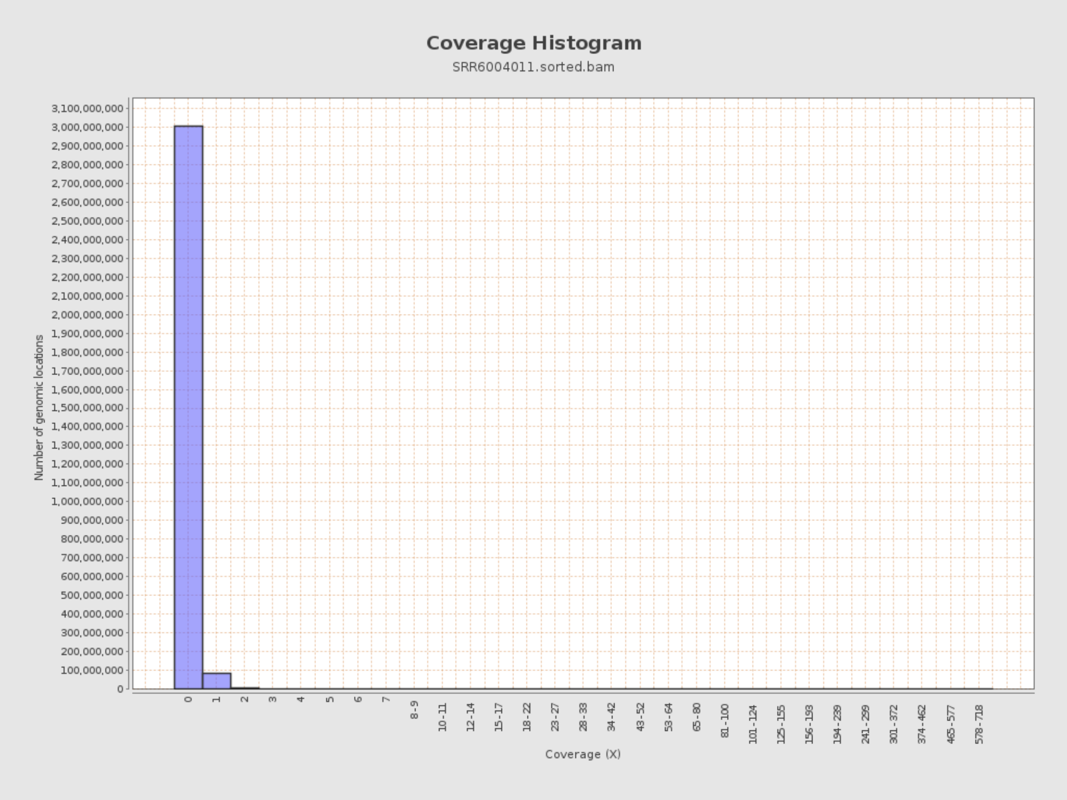
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8167040	0.0328	0.5487
chr2	243199373	8523228	0.035	0.3861
chr3	198022430	6815837	0.0344	0.2058
chr4	191154276	6644996	0.0348	0.2292
chr5	180915260	5820335	0.0322	0.2005
chr6	171115067	5906405	0.0345	0.2213
chr7	159138663	6343857	0.0399	0.5082

chr8	146364022	6268216	0.0428	0.4864
chr9	141213431	3894361	0.0276	0.2779
chr10	135534747	4842903	0.0357	0.2953
chr11	135006516	4587445	0.034	0.3509
chr12	133851895	4584417	0.0342	0.2074
chr13	115169878	3141883	0.0273	0.1842
chr14	107349540	2725688	0.0254	0.1974
chr15	102531392	2885598	0.0281	0.1904
chr16	90354753	2693718	0.0298	0.2164
chr17	81195210	2595577	0.032	0.2259
chr18	78077248	2608390	0.0334	0.5773
chr19	59128983	1900231	0.0321	0.4057
chr20	63025520	2128871	0.0338	0.2181
chr21	48129895	1115246	0.0232	0.1861
chr22	51304566	1034589	0.0202	0.1539
chrMT	16571	678818	40.9642	29.6011
chrX	155270560	5849181	0.0377	0.2372
chrY	59373566	281923	0.0047	0.1154

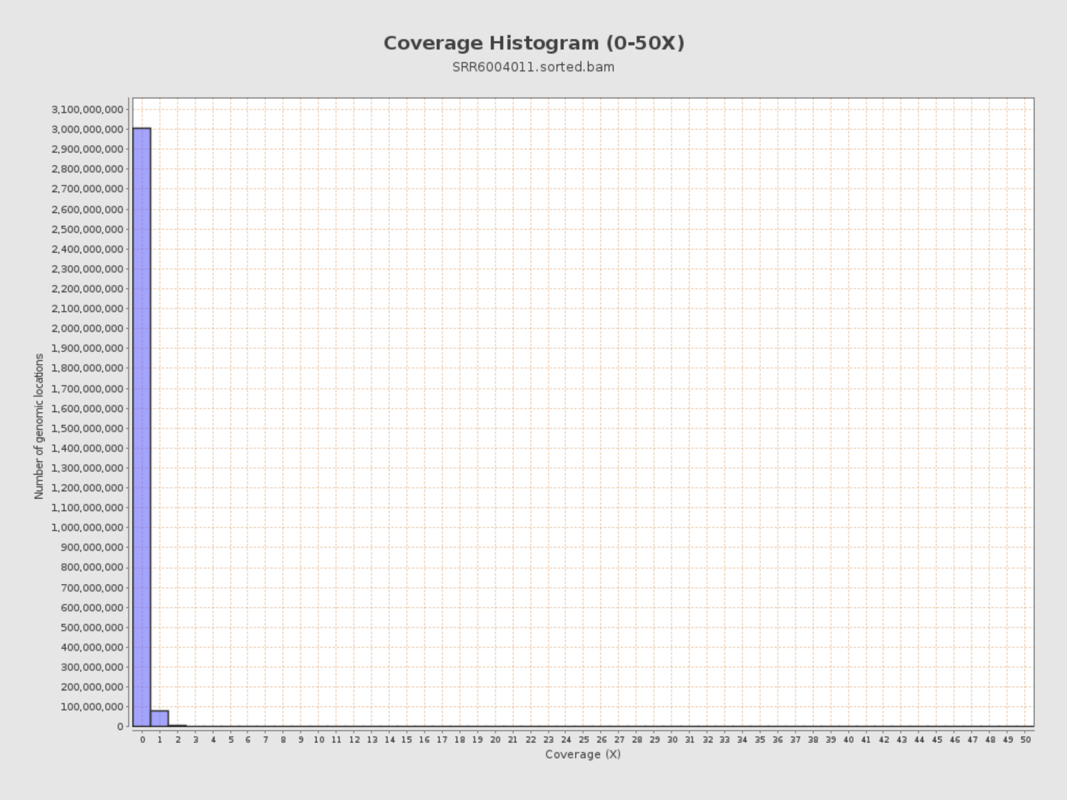
3. Results : Coverage across reference



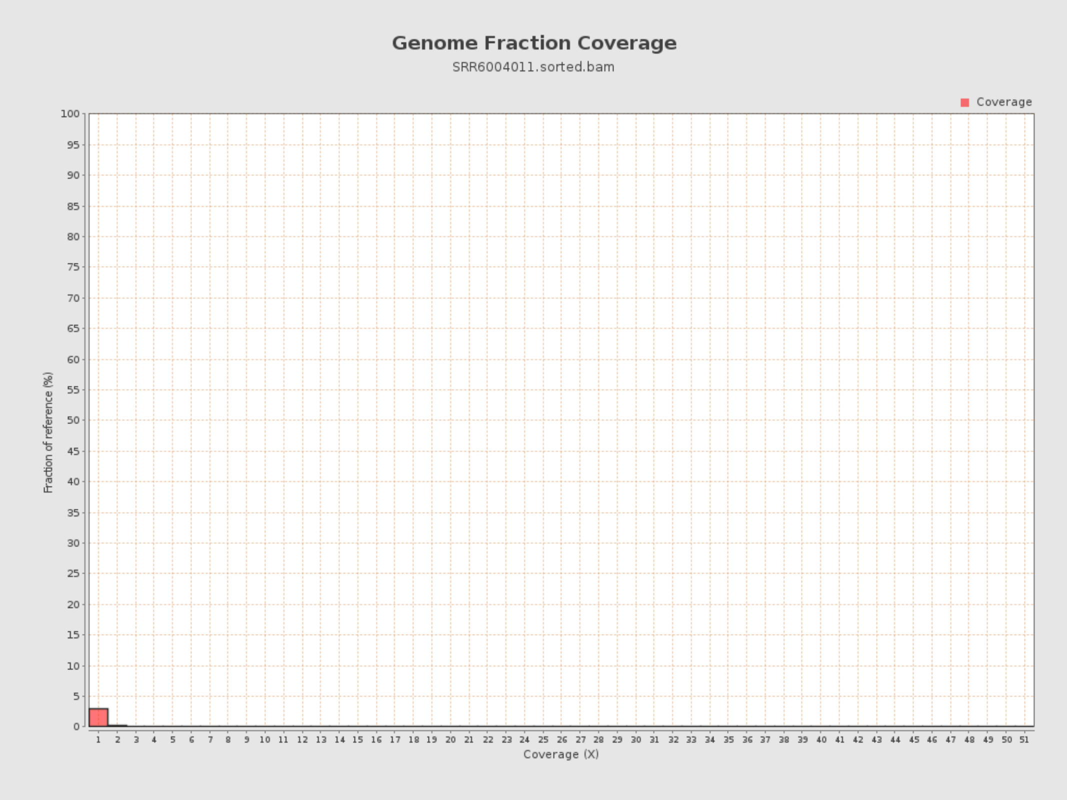
4. Results : Coverage Histogram



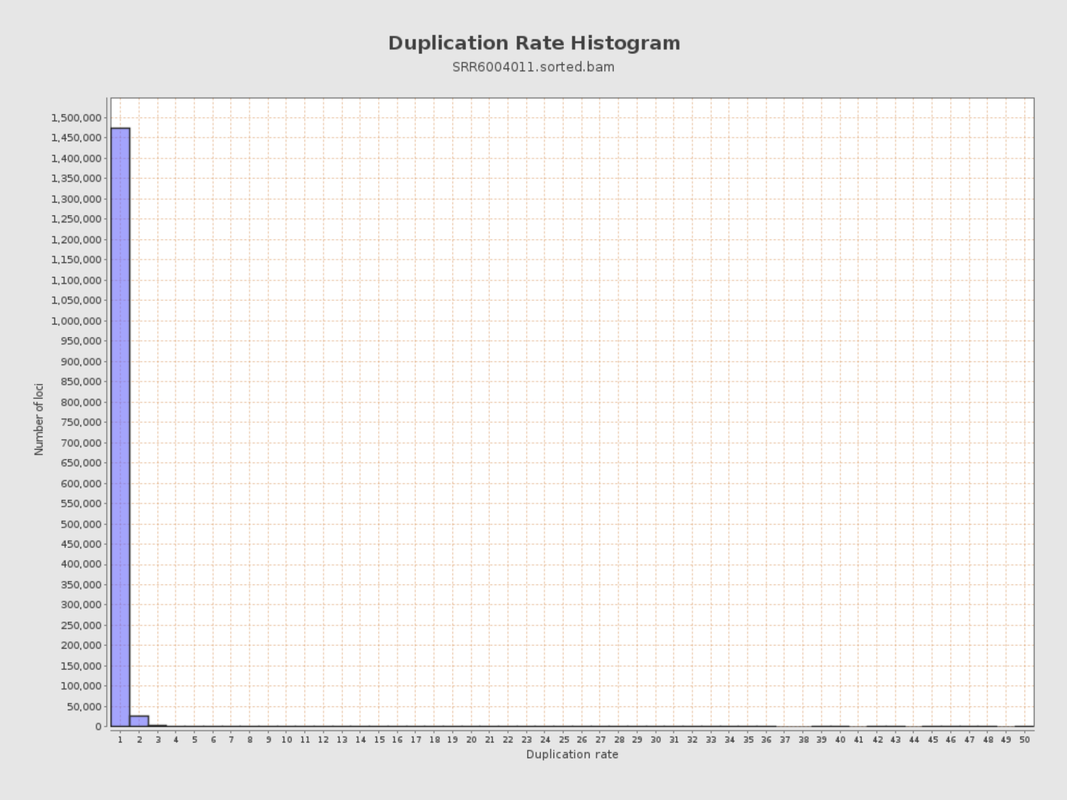
5. Results : Coverage Histogram (0-50X)



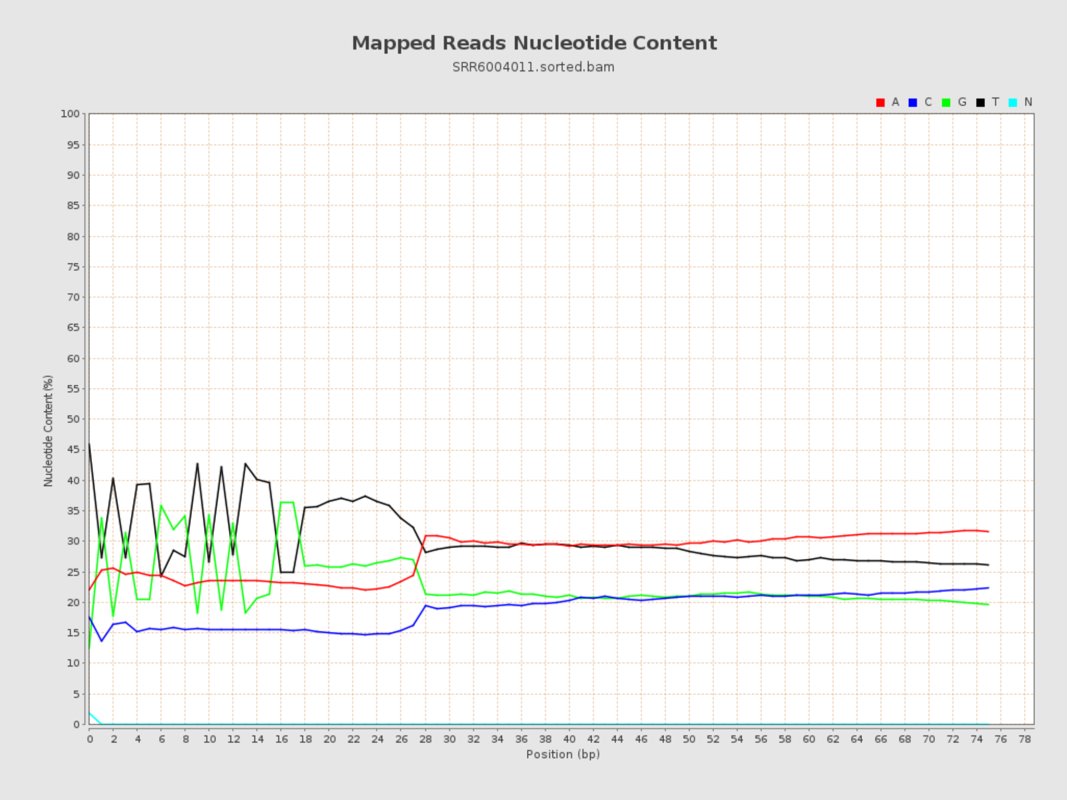
6. Results : Genome Fraction Coverage



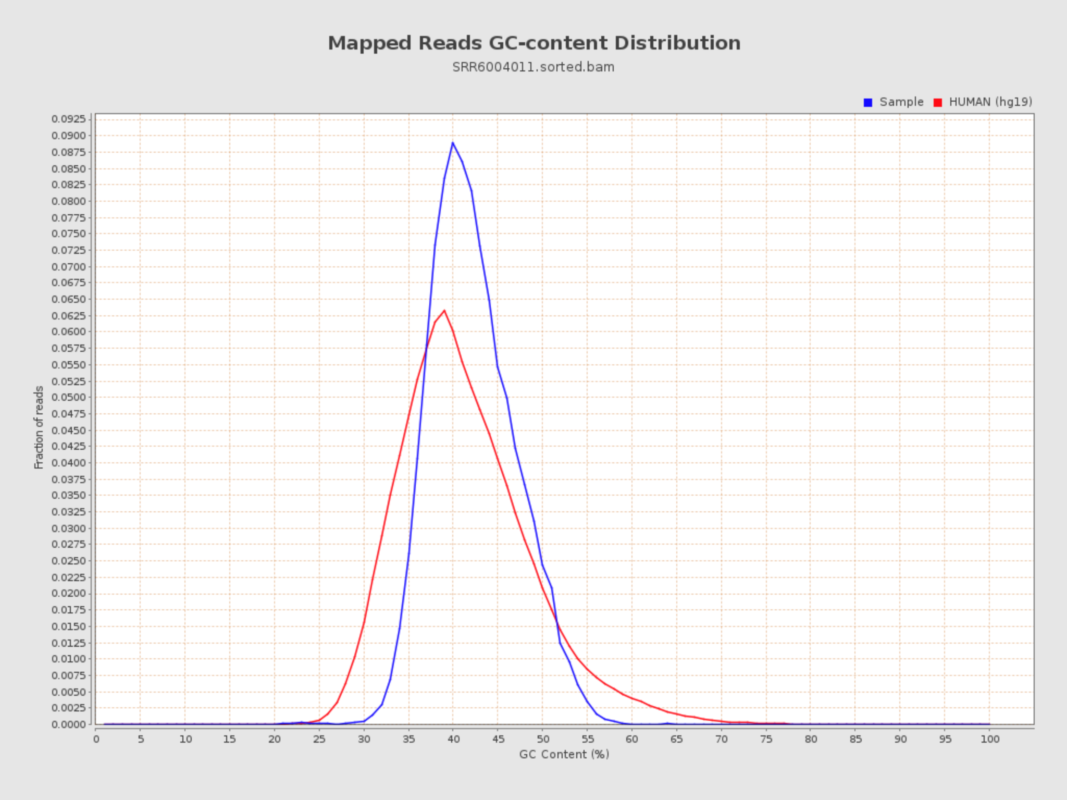
7. Results : Duplication Rate Histogram



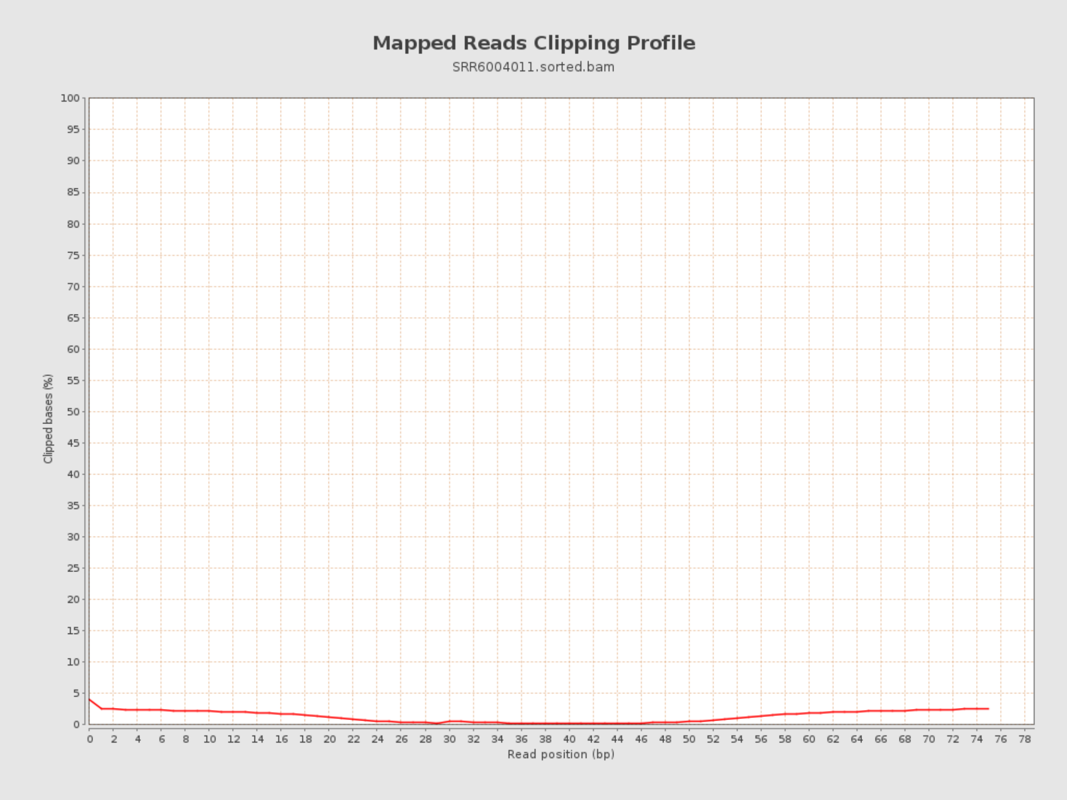
8. Results : Mapped Reads Nucleotide Content



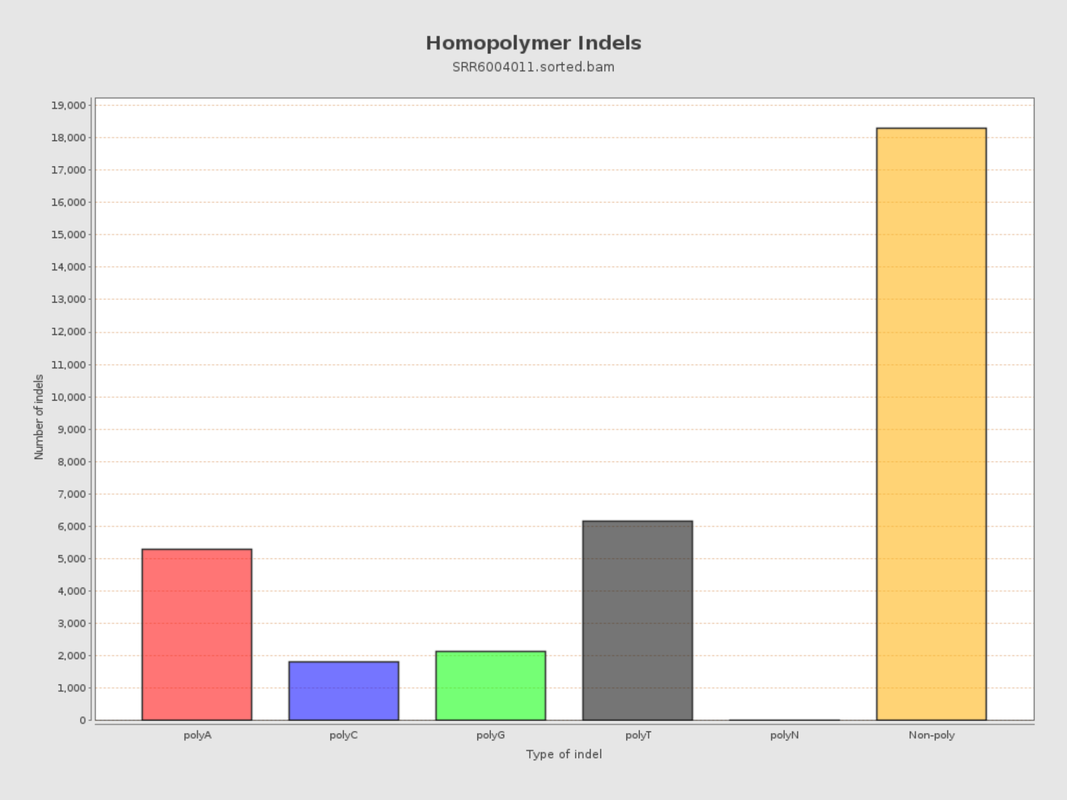
9. Results : Mapped Reads GC-content Distribution



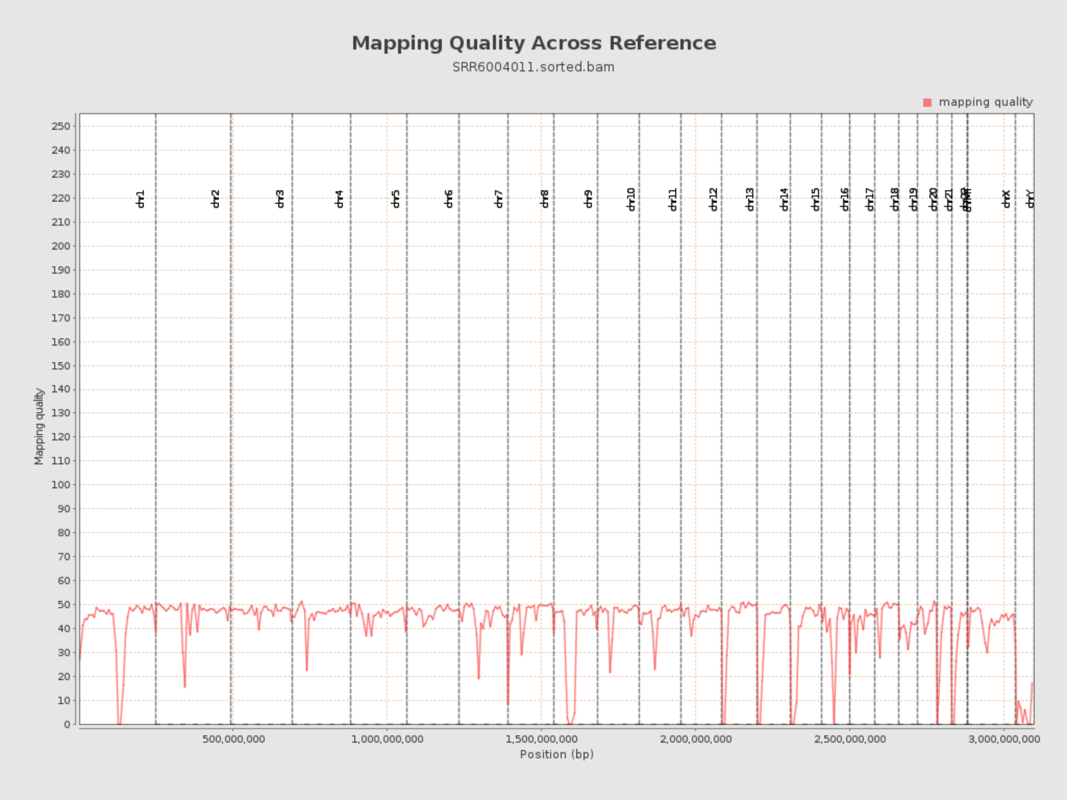
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram