Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:44:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004013.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_SRR6004013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:44:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,397,072
Mapped reads	2,076,308 / 86.62%
Unmapped reads	320,764 / 13.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,944 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	127,043 / 5.3%
Duplication rate	4.92%
Clipped reads	982,371 / 40.98%

2.2. ACGT Content

Number/percentage of A's	37,915,909 / 27.49%
Number/percentage of C's	26,242,290 / 19.02%
Number/percentage of T's	42,910,717 / 31.11%
Number/percentage of G's	30,846,878 / 22.36%
Number/percentage of N's	23,069 / 0.02%
GC Percentage	41.39%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.3924

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

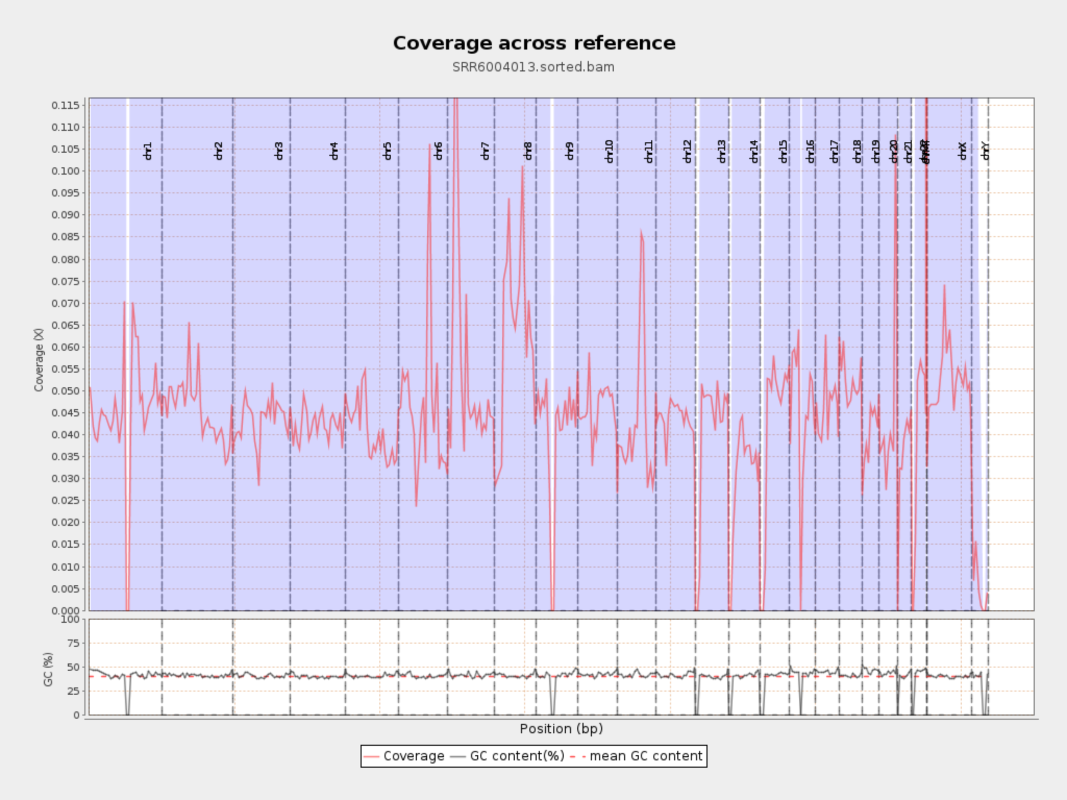
General error rate	0.9%
Mismatches	1,226,720
Insertions	9,947
Mapped reads with at least one insertion	0.48%
Deletions	33,944
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.83%

2.6. Chromosome stats

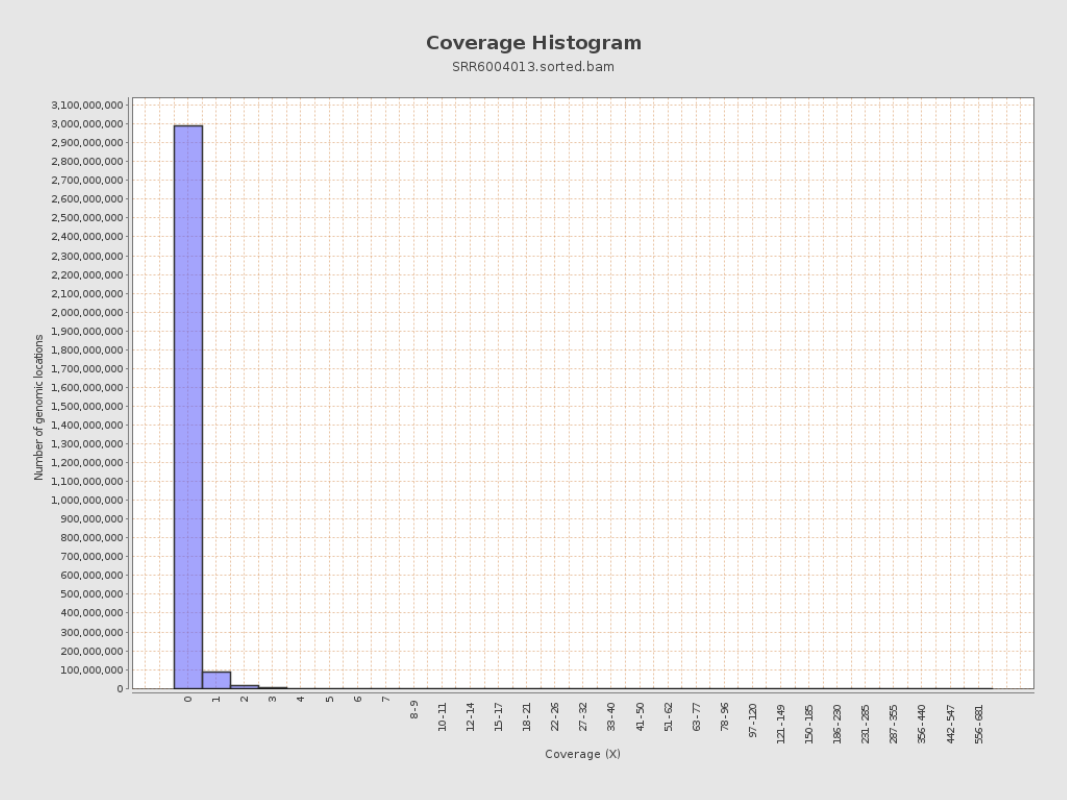
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11183019	0.0449	0.6493
chr2	243199373	11157875	0.0459	0.4309
chr3	198022430	8553210	0.0432	0.2544
chr4	191154276	8047040	0.0421	0.2621
chr5	180915260	7349849	0.0406	0.2483
chr6	171115067	8009634	0.0468	0.2822
chr7	159138663	8928170	0.0561	0.5227

chr8	146364022	9139604	0.0624	0.5249
chr9	141213431	5638747	0.0399	0.3336
chr10	135534747	6244661	0.0461	0.3514
chr11	135006516	5818744	0.0431	0.3277
chr12	133851895	5856383	0.0438	0.2583
chr13	115169878	4551827	0.0395	0.2544
chr14	107349540	3256246	0.0303	0.2355
chr15	102531392	4254069	0.0415	0.2476
chr16	90354753	4099908	0.0454	0.2791
chr17	81195210	3779829	0.0466	0.2824
chr18	78077248	4097131	0.0525	0.6381
chr19	59128983	2383076	0.0403	0.4843
chr20	63025520	2993072	0.0475	0.2806
chr21	48129895	1681381	0.0349	0.2387
chr22	51304566	1891249	0.0369	0.232
chrMT	16571	603724	36.4326	22.597
chrX	155270560	8143793	0.0524	0.3136
chrY	59373566	335597	0.0057	0.1142

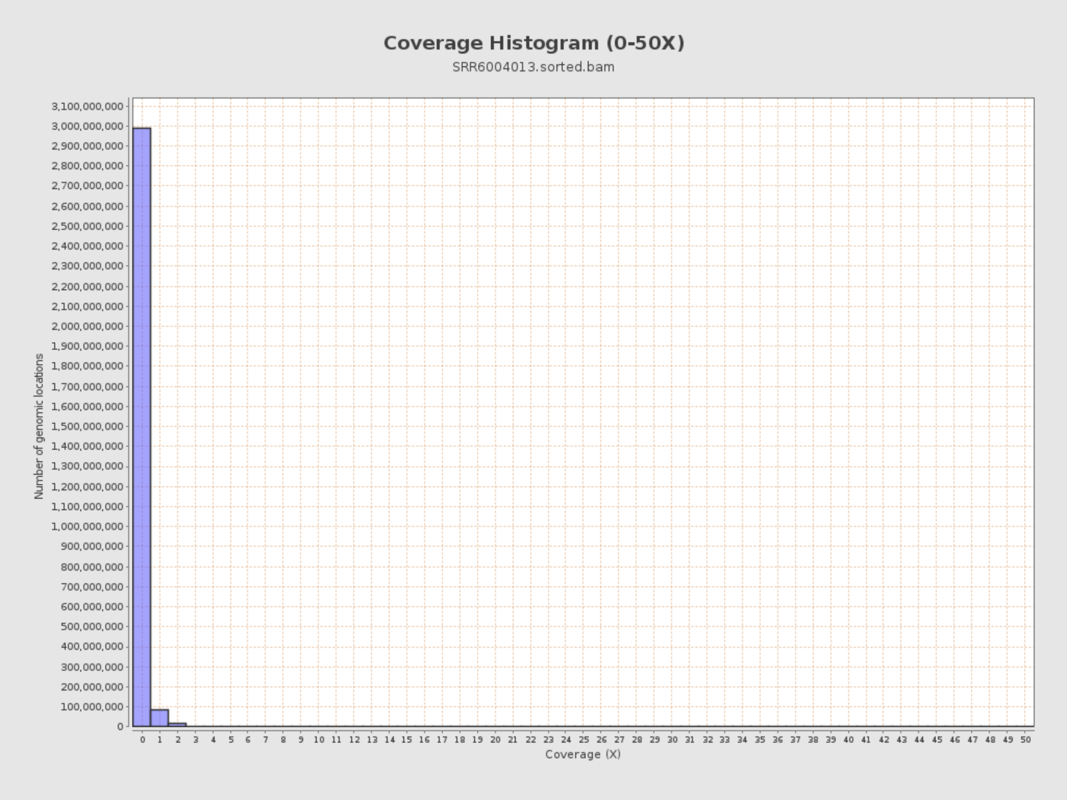
3. Results : Coverage across reference



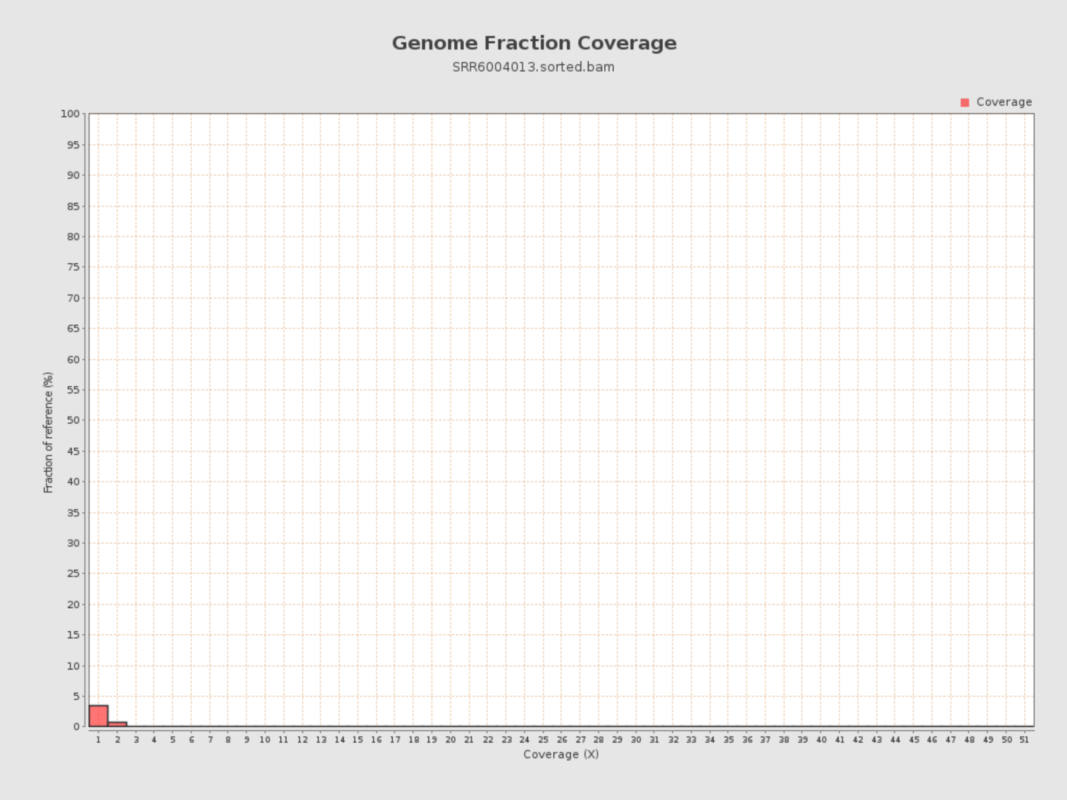
4. Results : Coverage Histogram



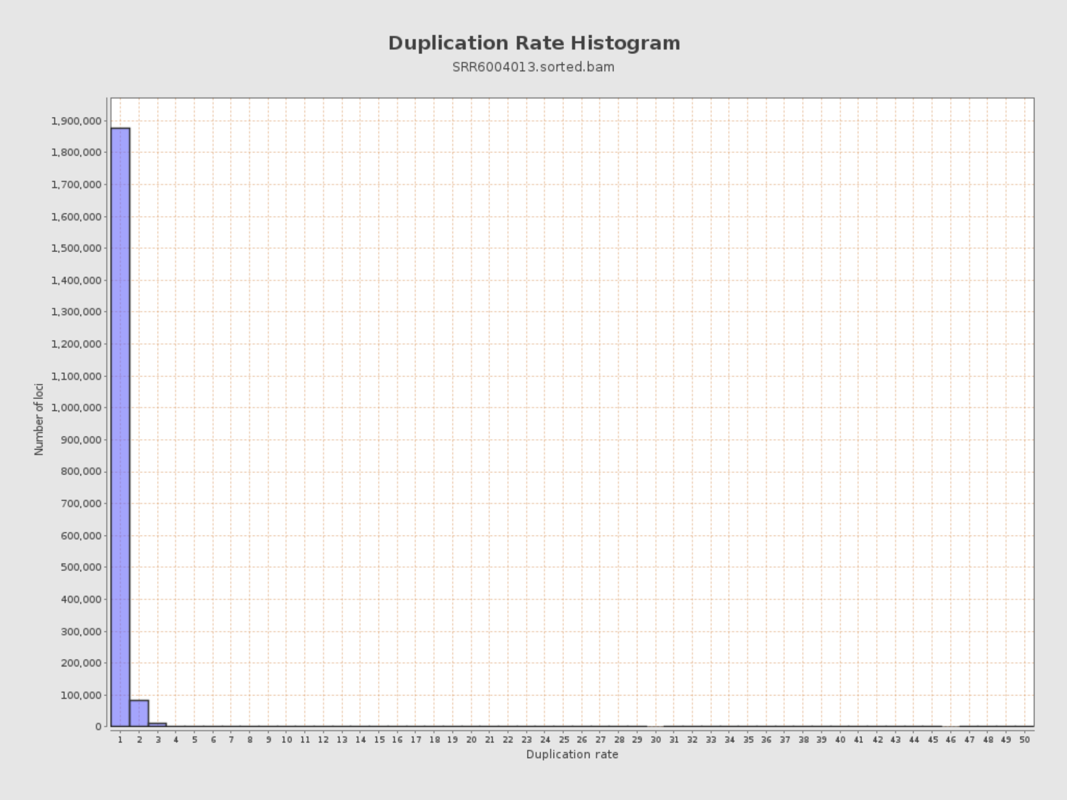
5. Results : Coverage Histogram (0-50X)



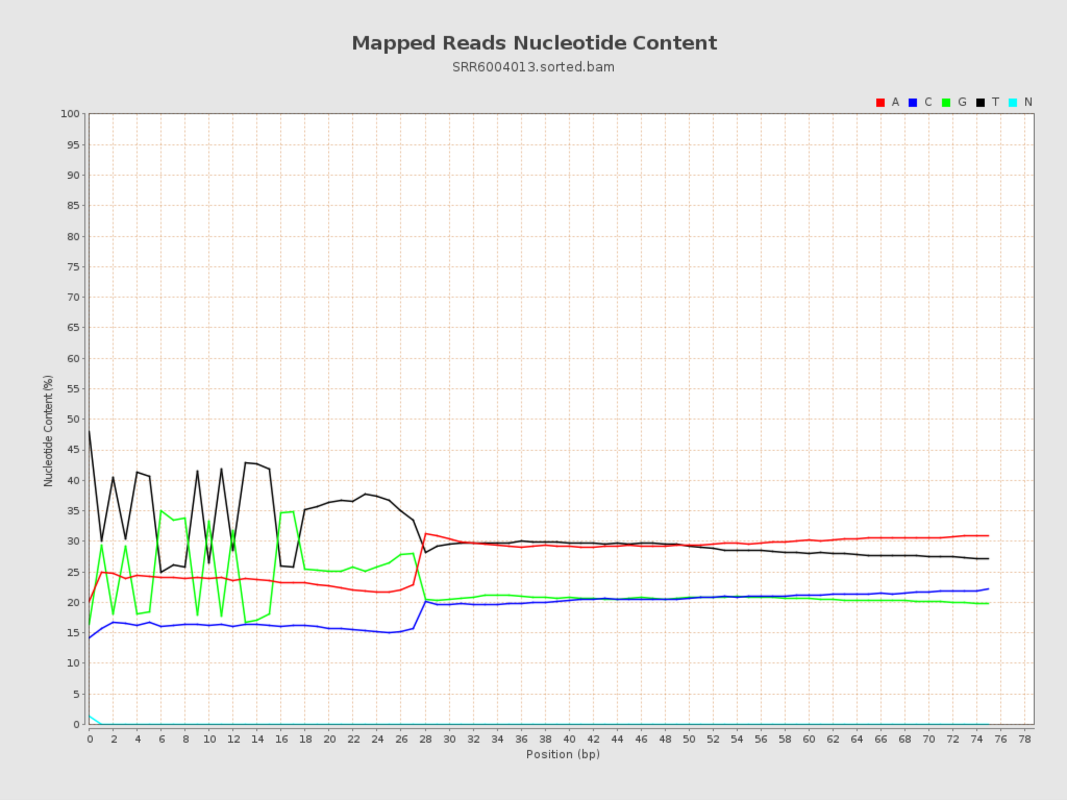
6. Results : Genome Fraction Coverage



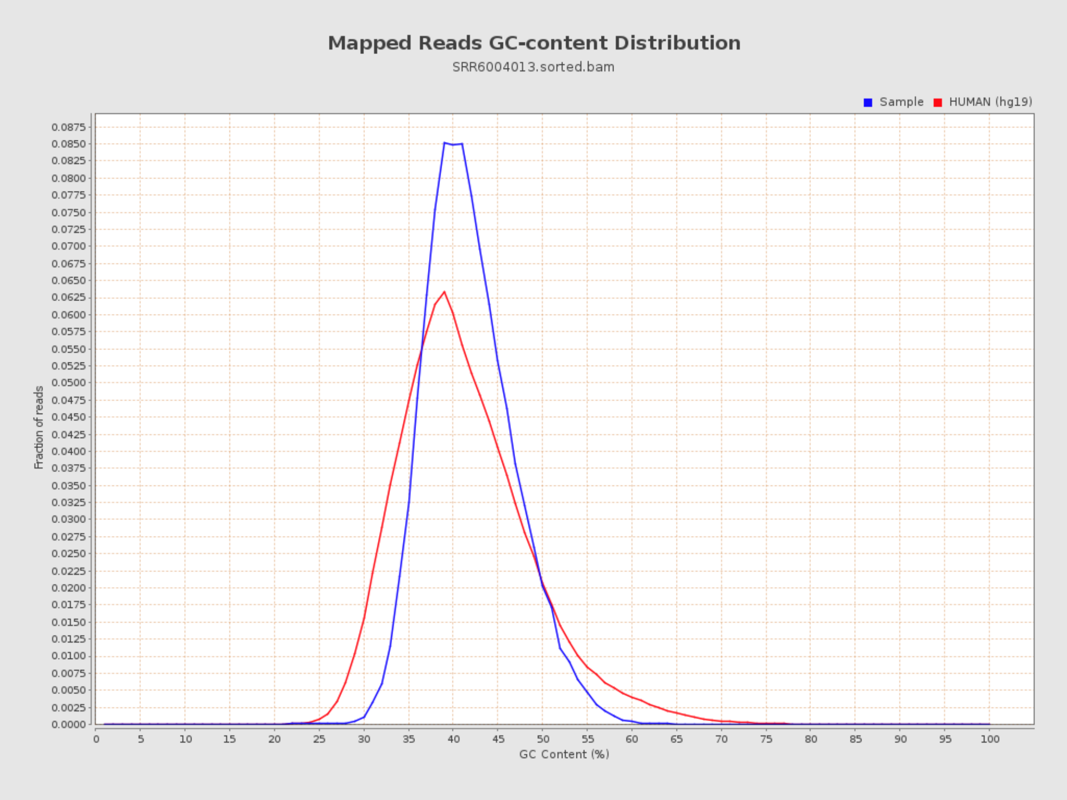
7. Results : Duplication Rate Histogram



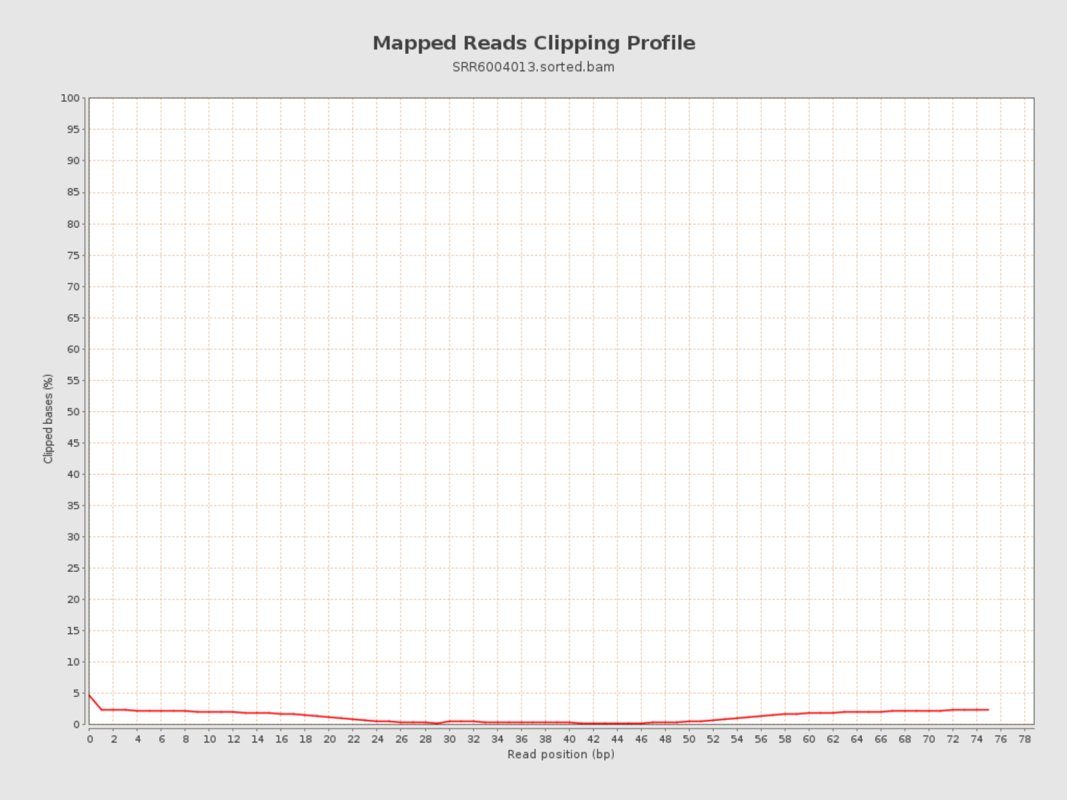
8. Results : Mapped Reads Nucleotide Content



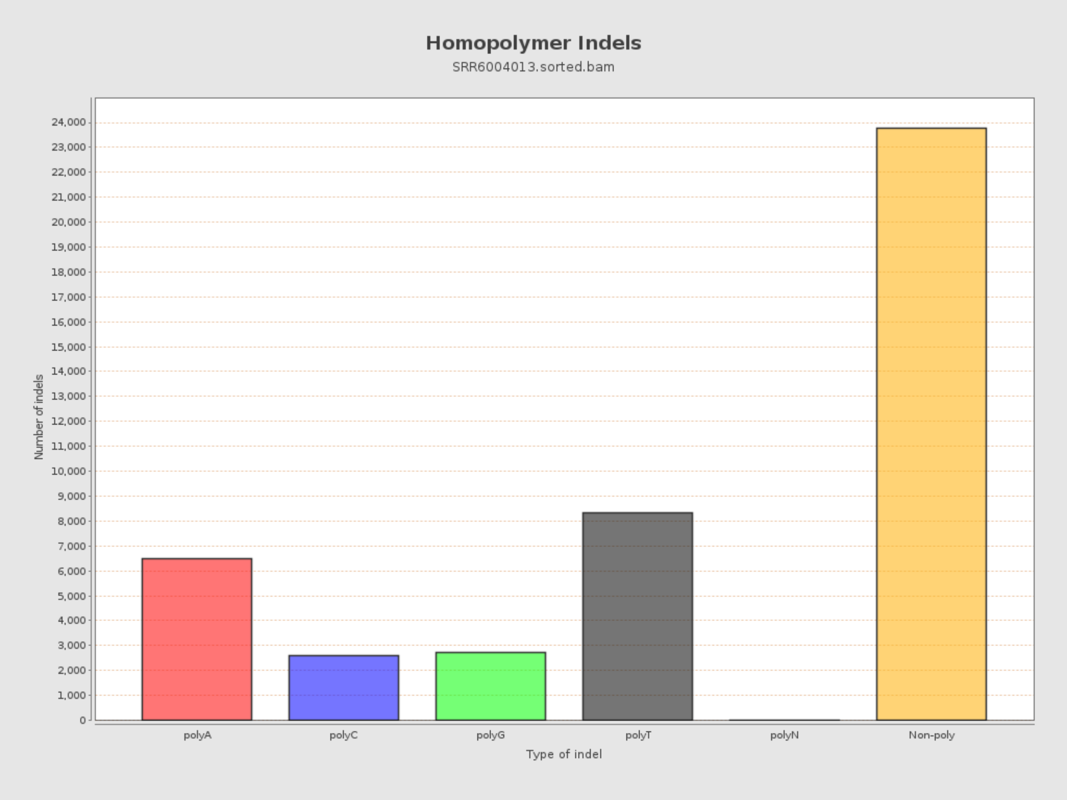
9. Results : Mapped Reads GC-content Distribution



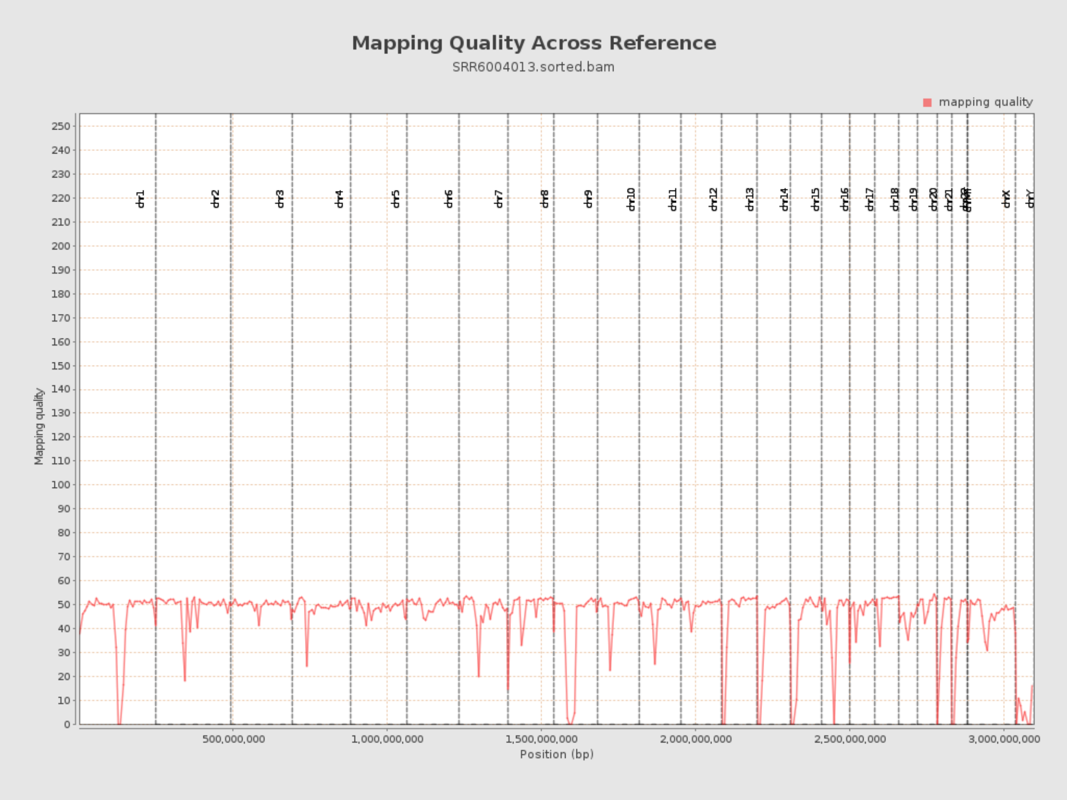
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram