Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:10:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004123.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_SRR6004123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:10:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,179,821
Mapped reads	2,457,075 / 77.27%
Unmapped reads	722,746 / 22.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,216 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	123,858 / 3.9%
Duplication rate	3.89%
Clipped reads	1,314,745 / 41.35%

2.2. ACGT Content

Number/percentage of A's	43,342,501 / 27.26%
Number/percentage of C's	27,732,304 / 17.44%
Number/percentage of T's	52,153,978 / 32.8%
Number/percentage of G's	35,754,561 / 22.49%
Number/percentage of N's	16,339 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0514

Standard Deviation	0.4686

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

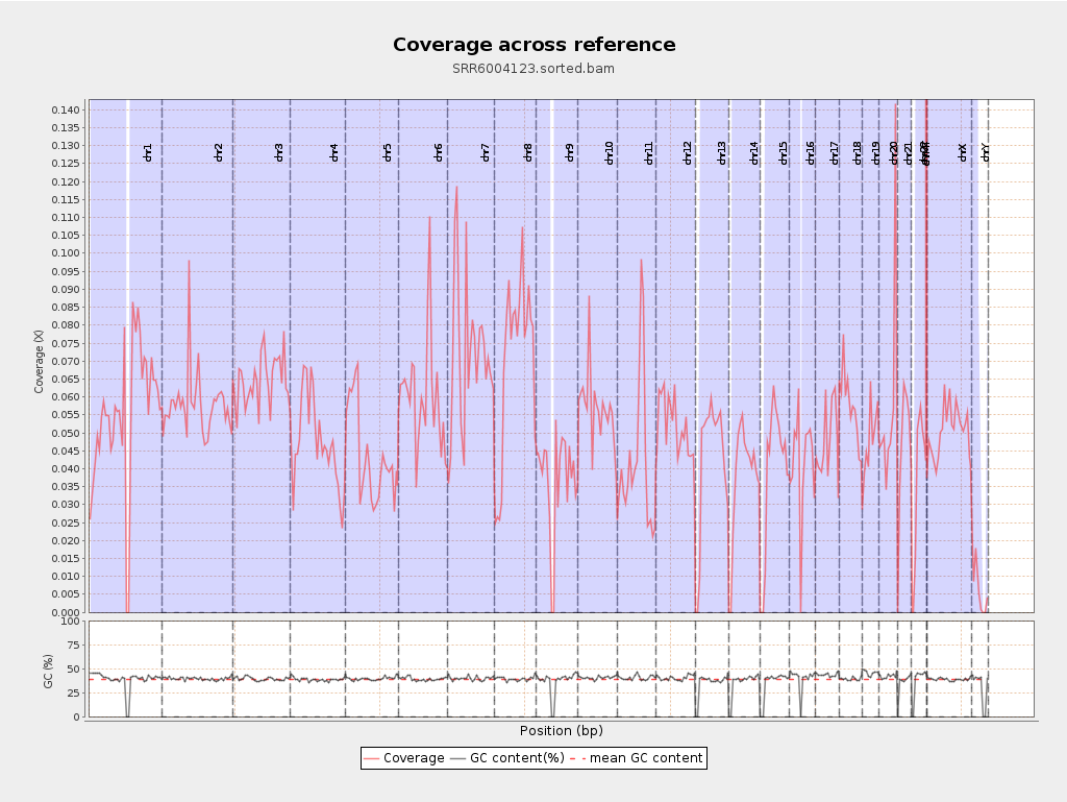
General error rate	1.06%
Mismatches	1,655,463
Insertions	14,806
Mapped reads with at least one insertion	0.6%
Deletions	50,137
Mapped reads with at least one deletion	2.02%
Homopolymer indels	47.32%

2.6. Chromosome stats

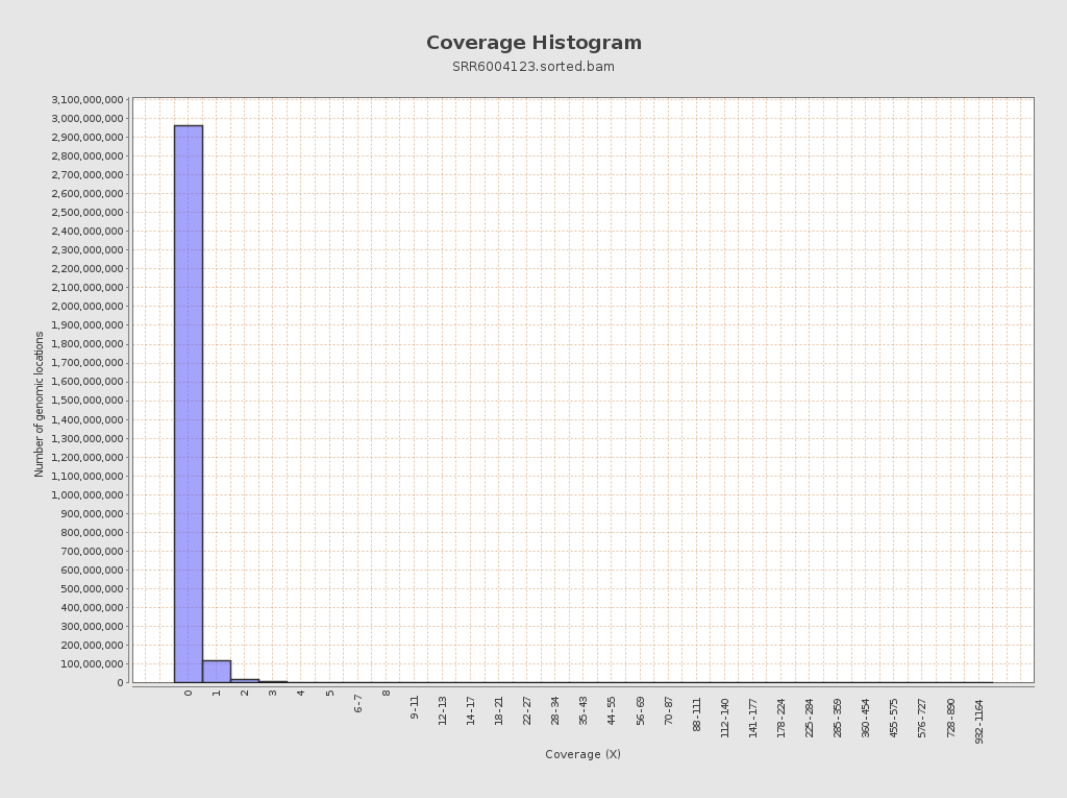
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13769944	0.0552	0.7588
chr2	243199373	14073375	0.0579	0.6142
chr3	198022430	12791192	0.0646	0.2954
chr4	191154276	8989537	0.047	0.2638
chr5	180915260	7897880	0.0437	0.244
chr6	171115067	10283844	0.0601	0.3319
chr7	159138663	11604294	0.0729	0.761

chr8	146364022	10206059	0.0697	0.7823
chr9	141213431	5139506	0.0364	0.4071
chr10	135534747	7709048	0.0569	0.4371
chr11	135006516	5708007	0.0423	0.3141
chr12	133851895	6924831	0.0517	0.2708
chr13	115169878	4834043	0.042	0.2372
chr14	107349540	4046778	0.0377	0.2728
chr15	102531392	4047274	0.0395	0.2342
chr16	90354753	3769420	0.0417	0.2754
chr17	81195210	3884485	0.0478	0.2707
chr18	78077248	4508091	0.0577	0.8257
chr19	59128983	2852822	0.0482	0.5247
chr20	63025520	3744614	0.0594	0.3039
chr21	48129895	2226400	0.0463	0.2688
chr22	51304566	1793396	0.035	0.2126
chrMT	16571	57561	3.4736	3.2385
chrX	155270560	7841308	0.0505	0.305
chrY	59373566	377756	0.0064	0.1297

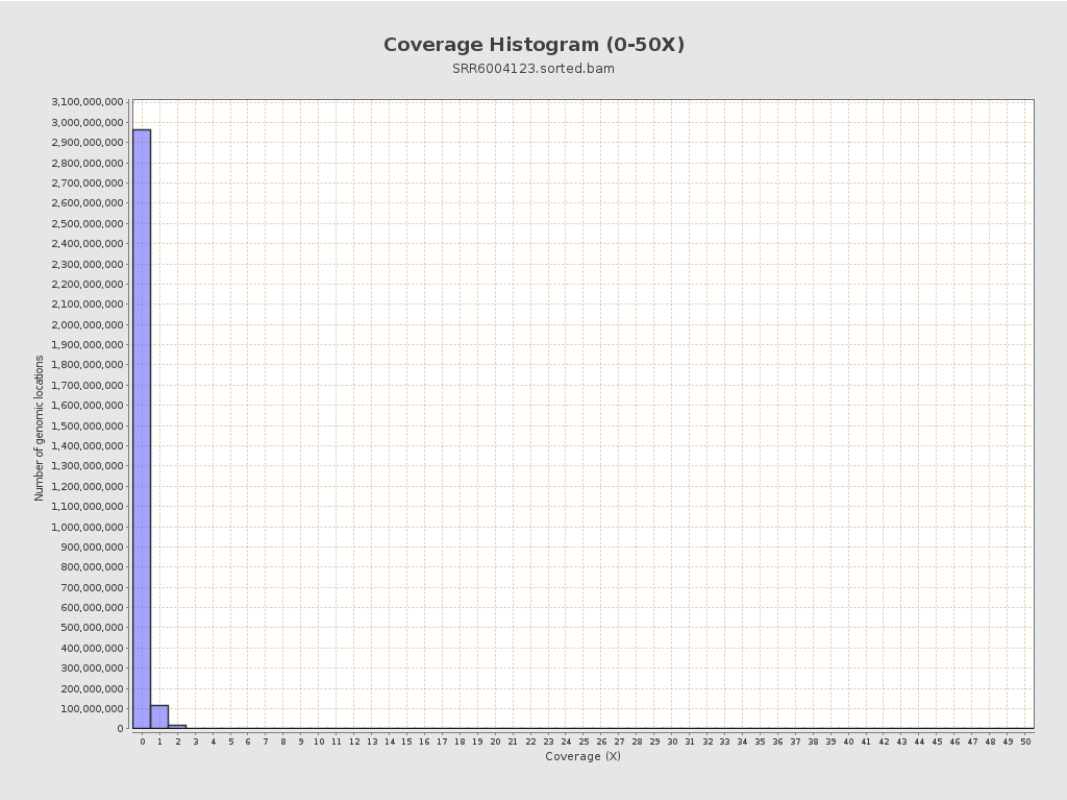
3. Results : Coverage across reference



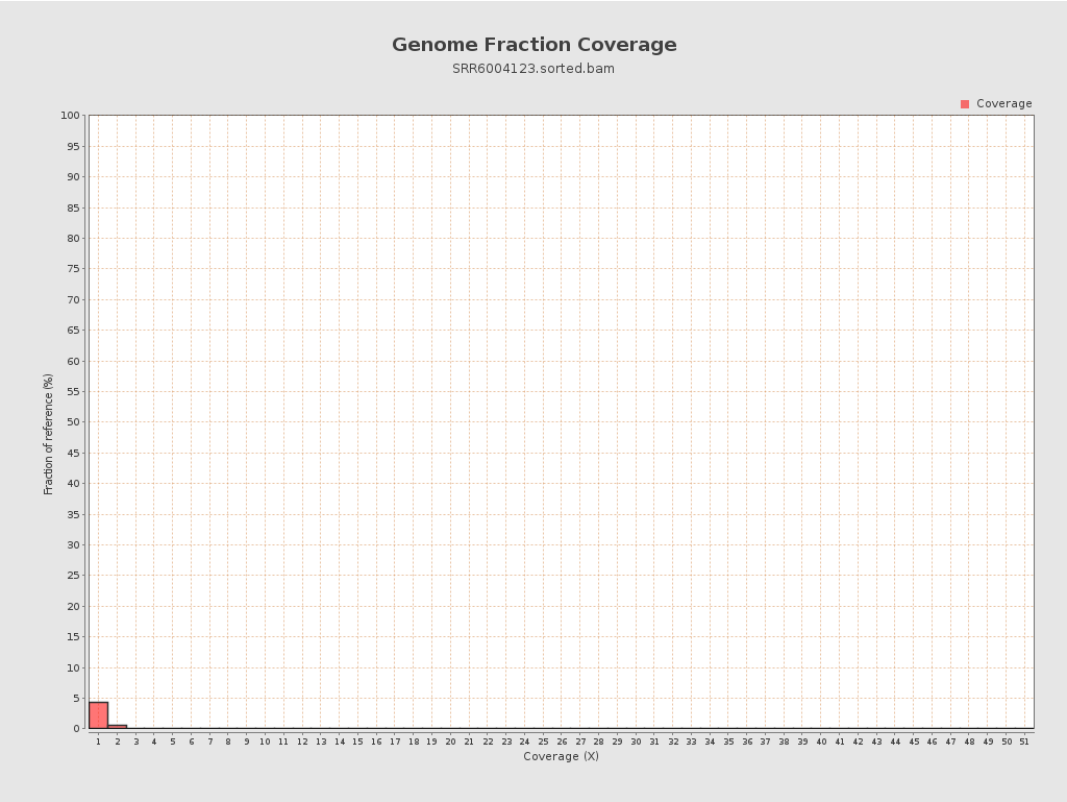
4. Results : Coverage Histogram



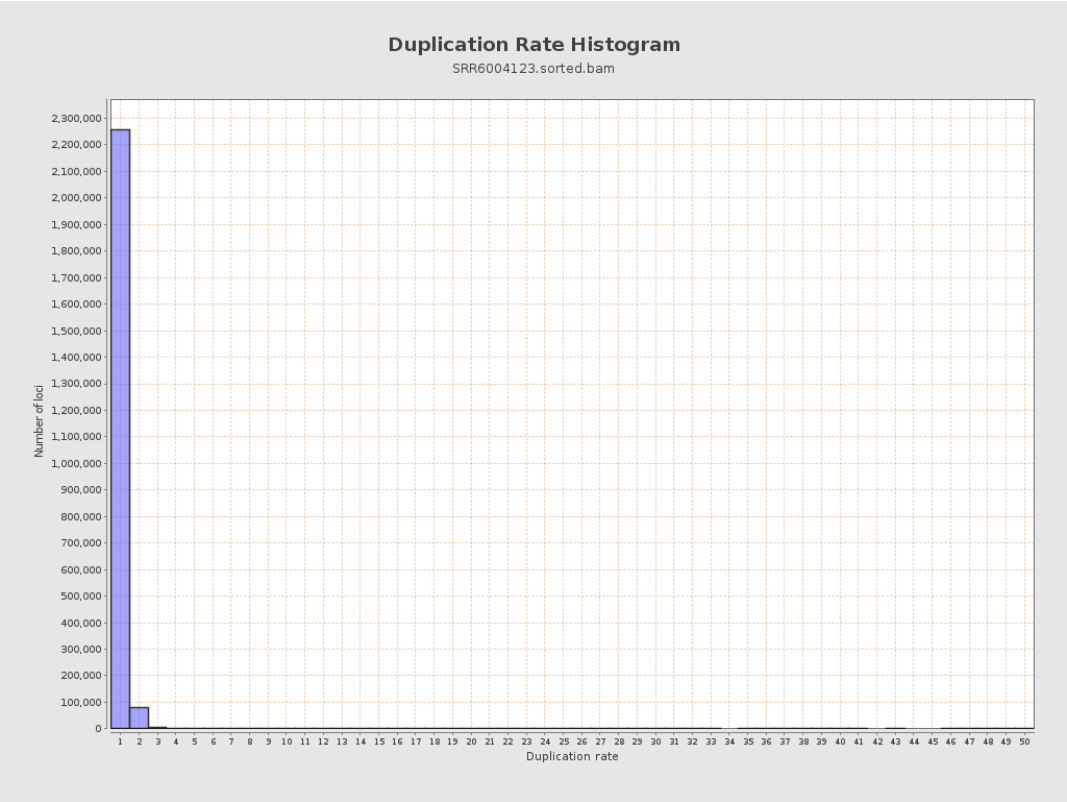
5. Results : Coverage Histogram (0-50X)



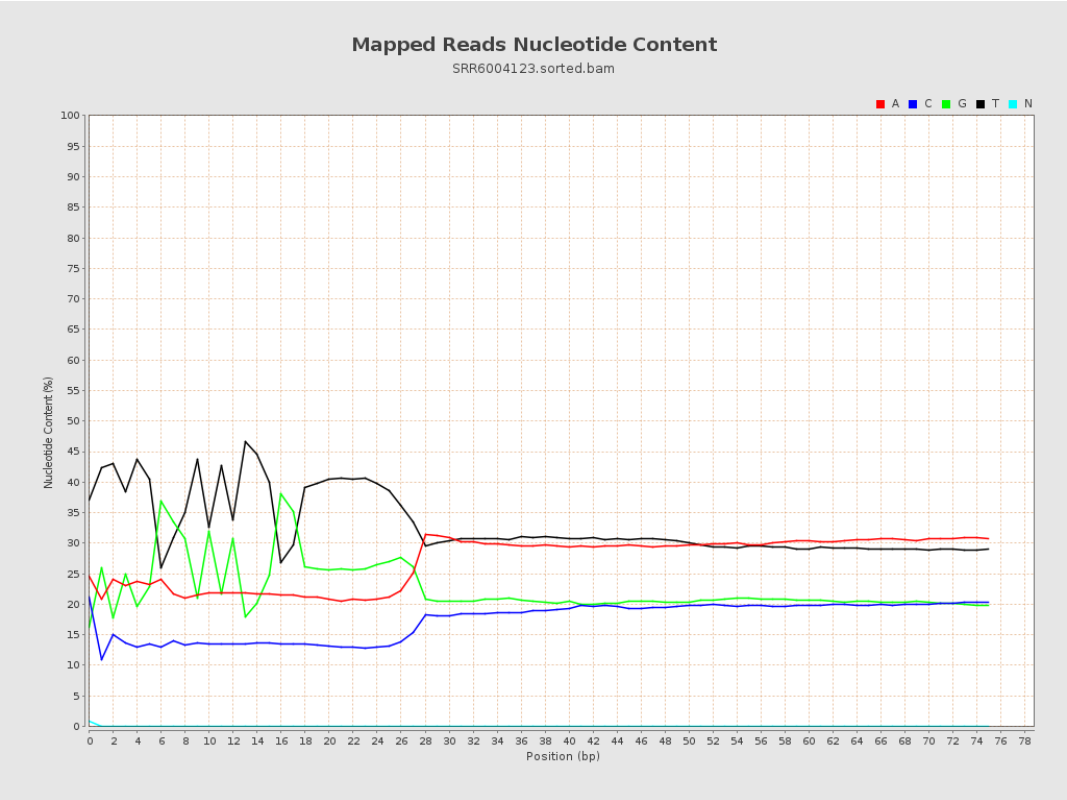
6. Results : Genome Fraction Coverage



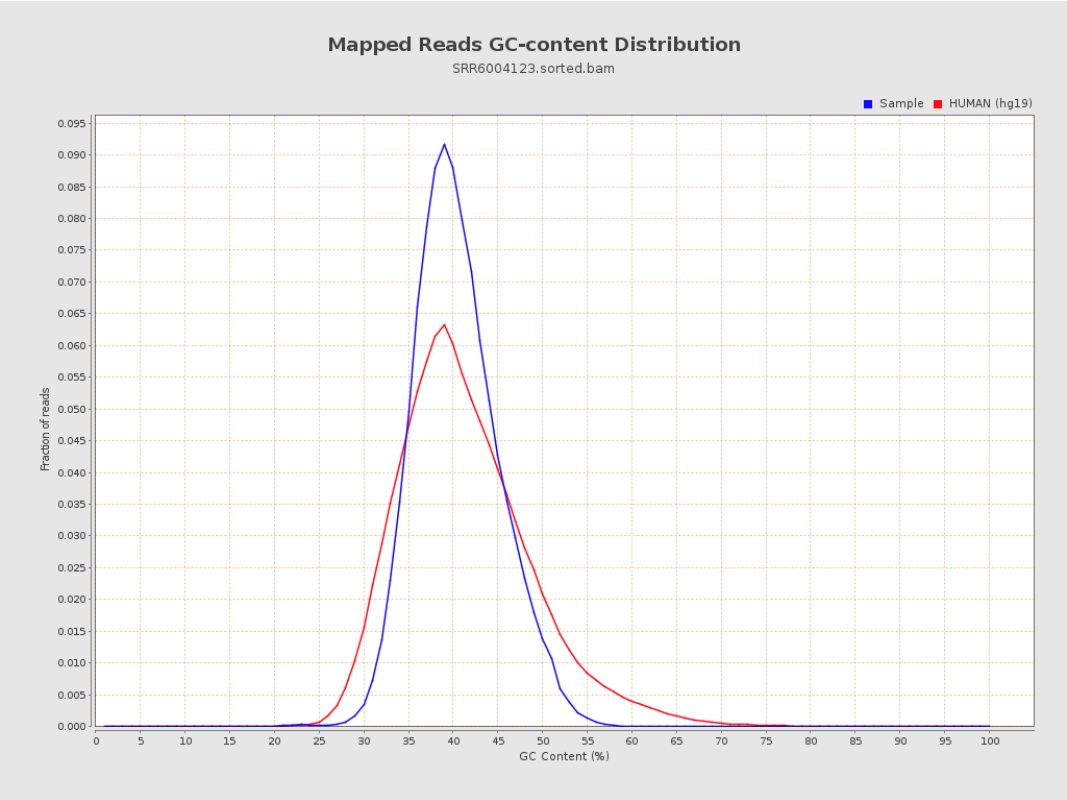
7. Results : Duplication Rate Histogram



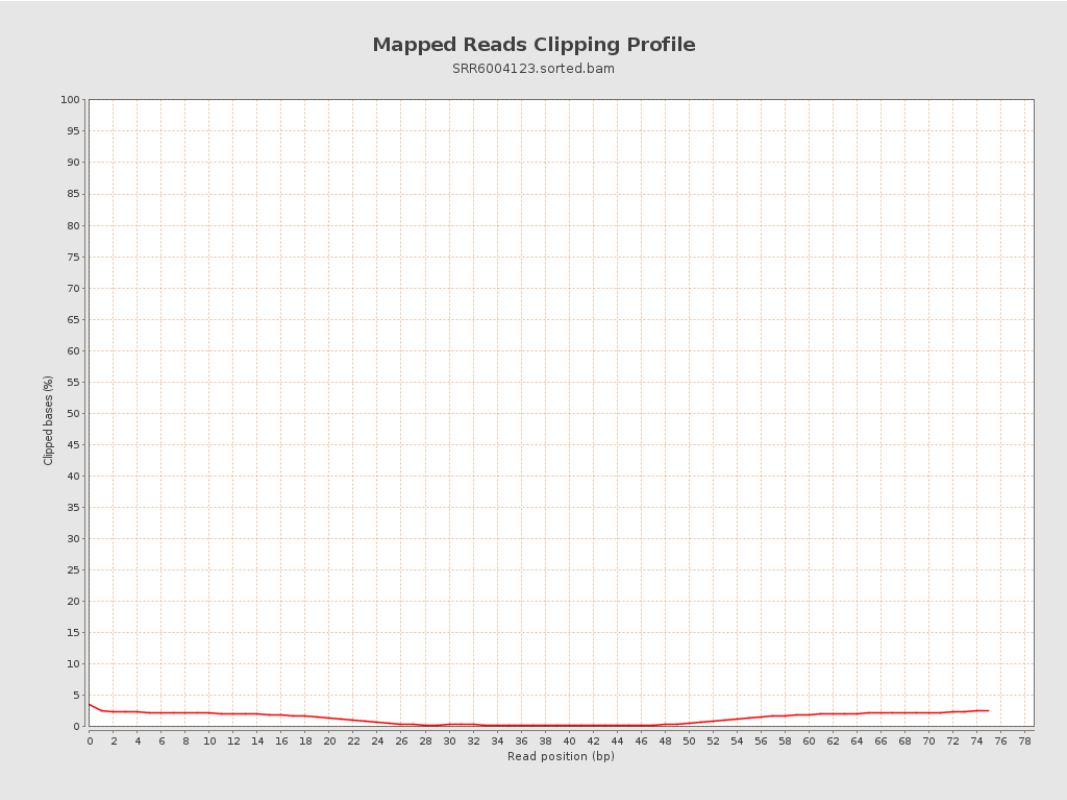
8. Results : Mapped Reads Nucleotide Content



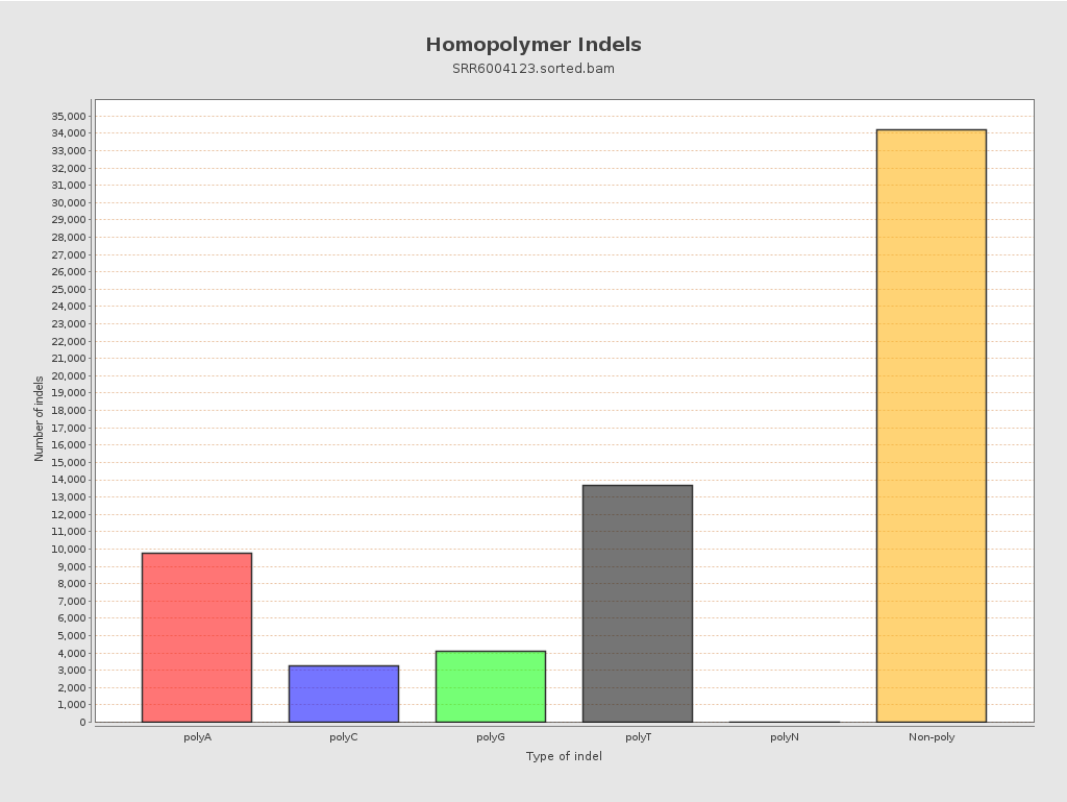
9. Results : Mapped Reads GC-content Distribution



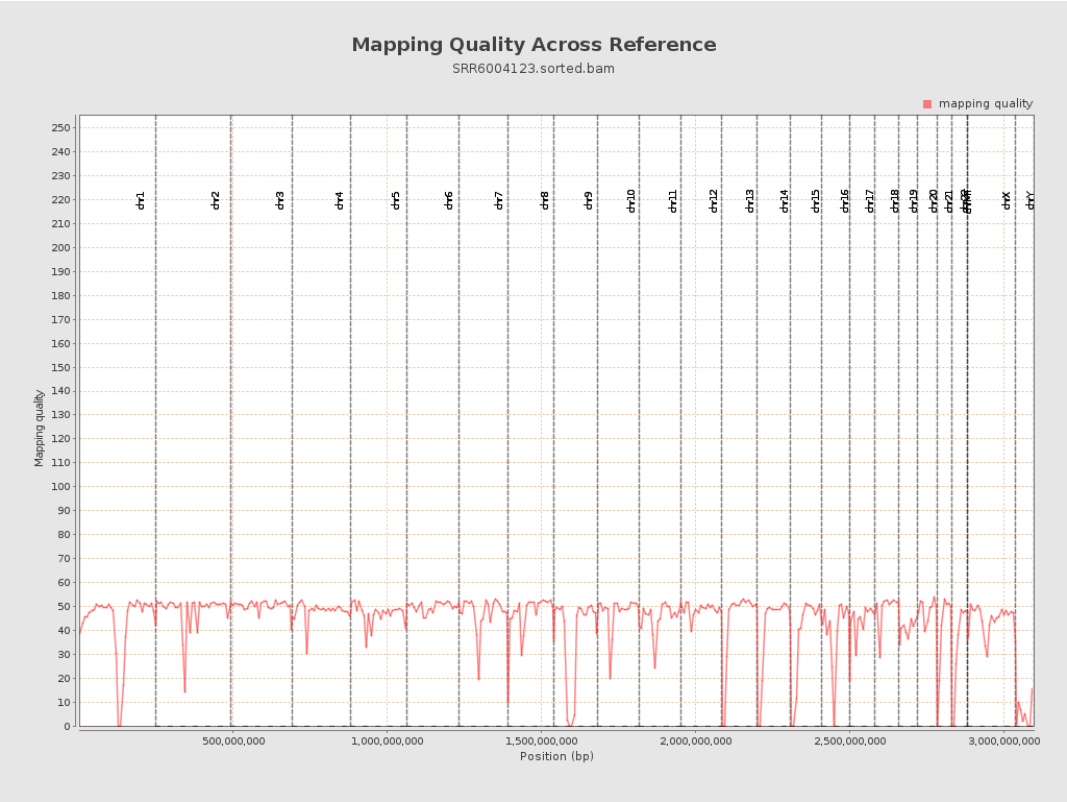
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram