Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004128.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_SRR6004128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004128.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:30:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,296,544
Mapped reads	2,419,198 / 73.39%
Unmapped reads	877,346 / 26.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,688 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	339,326 / 10.29%
Duplication rate	10.22%
Clipped reads	1,158,583 / 35.15%

2.2. ACGT Content

Number/percentage of A's	43,353,022 / 27.18%
Number/percentage of C's	29,429,501 / 18.45%
Number/percentage of T's	51,525,116 / 32.3%
Number/percentage of G's	35,181,841 / 22.06%
Number/percentage of N's	21,087 / 0.01%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.5409

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

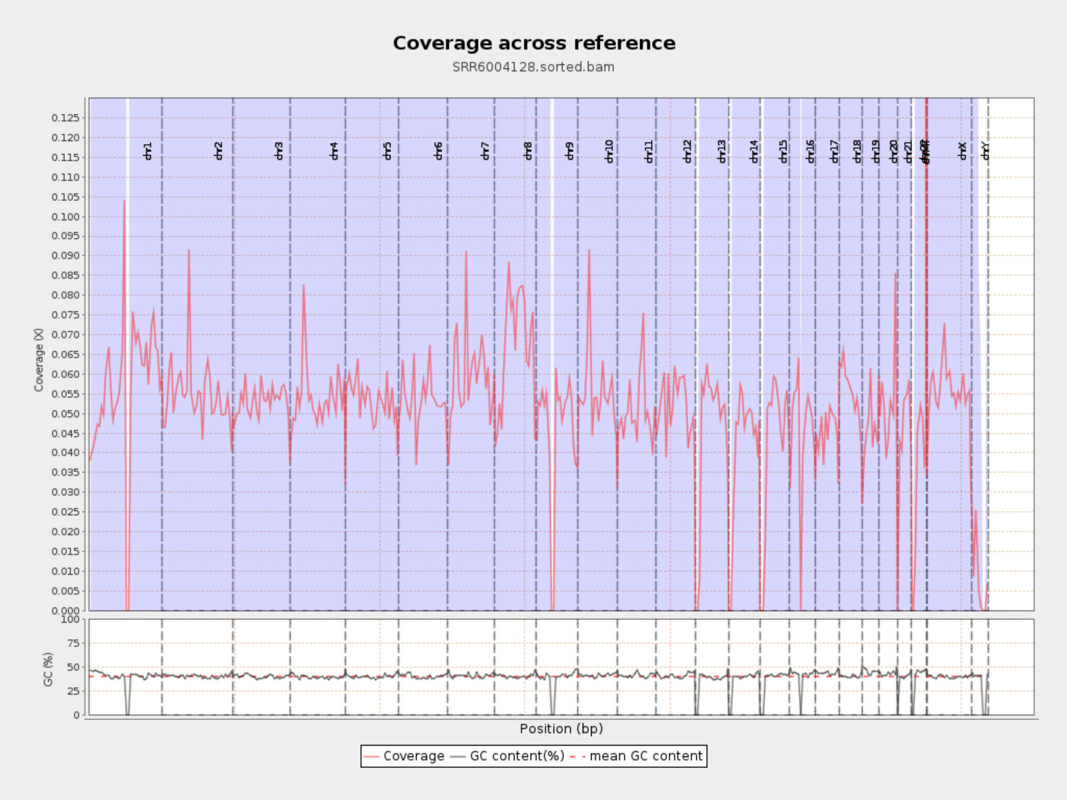
General error rate	1.02%
Mismatches	1,599,700
Insertions	13,410
Mapped reads with at least one insertion	0.55%
Deletions	47,634
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.35%

2.6. Chromosome stats

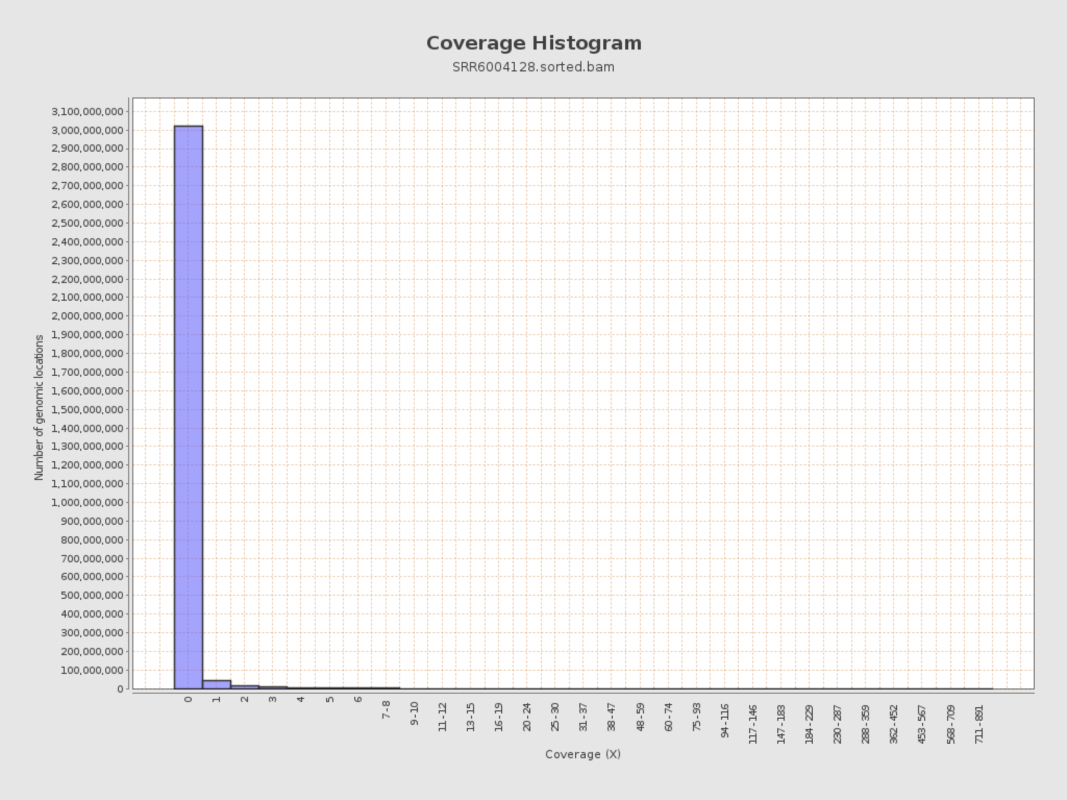
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14054670	0.0564	0.8707
chr2	243199373	13360277	0.0549	0.5982
chr3	198022430	10538539	0.0532	0.4378
chr4	191154276	10391759	0.0544	0.4549
chr5	180915260	9724506	0.0538	0.4392
chr6	171115067	9175740	0.0536	0.4722
chr7	159138663	9536151	0.0599	0.69

chr8	146364022	9830980	0.0672	0.6225
chr9	141213431	6453195	0.0457	0.5018
chr10	135534747	7584454	0.056	0.5431
chr11	135006516	6870923	0.0509	0.4844
chr12	133851895	6983870	0.0522	0.4306
chr13	115169878	5162023	0.0448	0.4059
chr14	107349540	4352656	0.0405	0.3883
chr15	102531392	4283479	0.0418	0.3836
chr16	90354753	4136810	0.0458	0.4235
chr17	81195210	3684835	0.0454	0.4179
chr18	78077248	4379969	0.0561	0.7964
chr19	59128983	2720870	0.046	0.6004
chr20	63025520	3376329	0.0536	0.4432
chr21	48129895	2134161	0.0443	0.4074
chr22	51304566	1609101	0.0314	0.3335
chrMT	16571	119138	7.1895	6.3389
chrX	155270560	8654155	0.0557	0.4598
chrY	59373566	470034	0.0079	0.1995

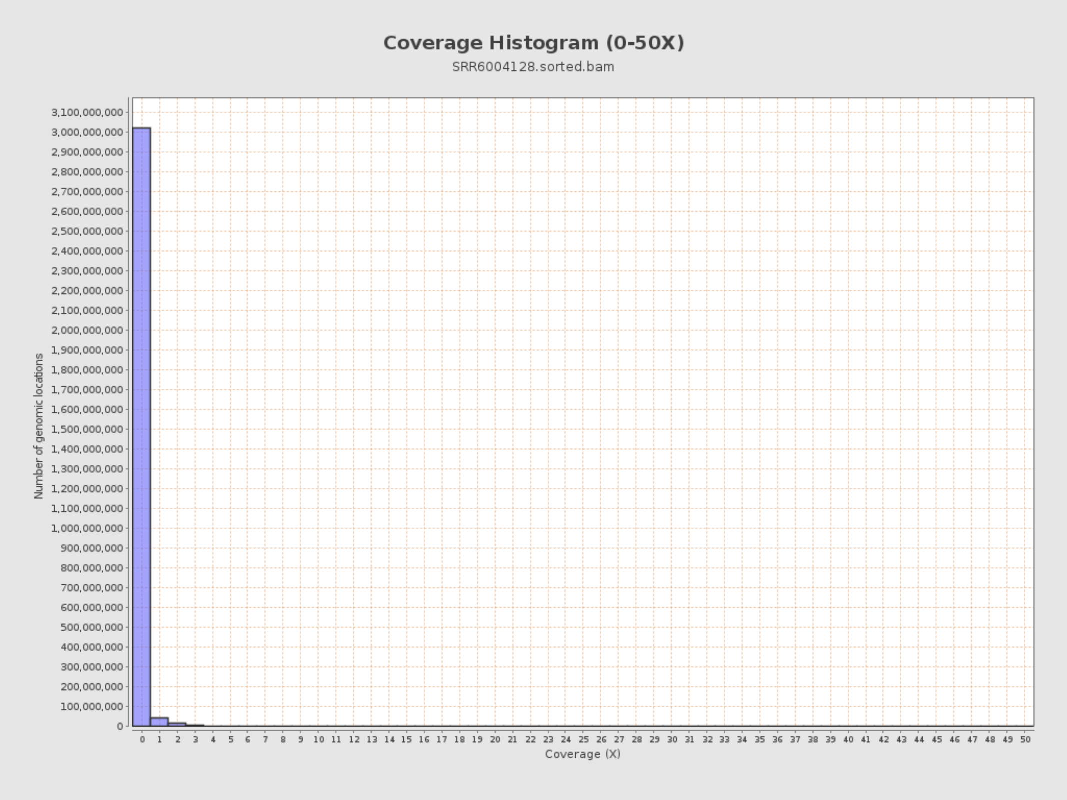
3. Results : Coverage across reference



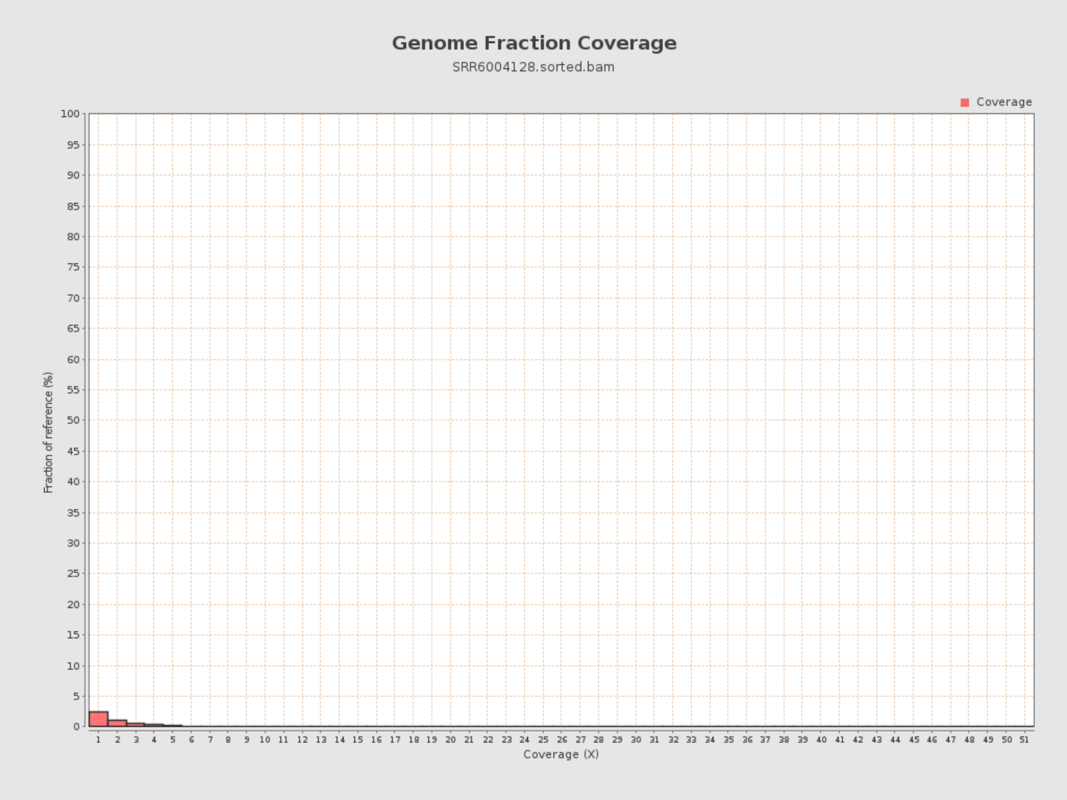
4. Results : Coverage Histogram



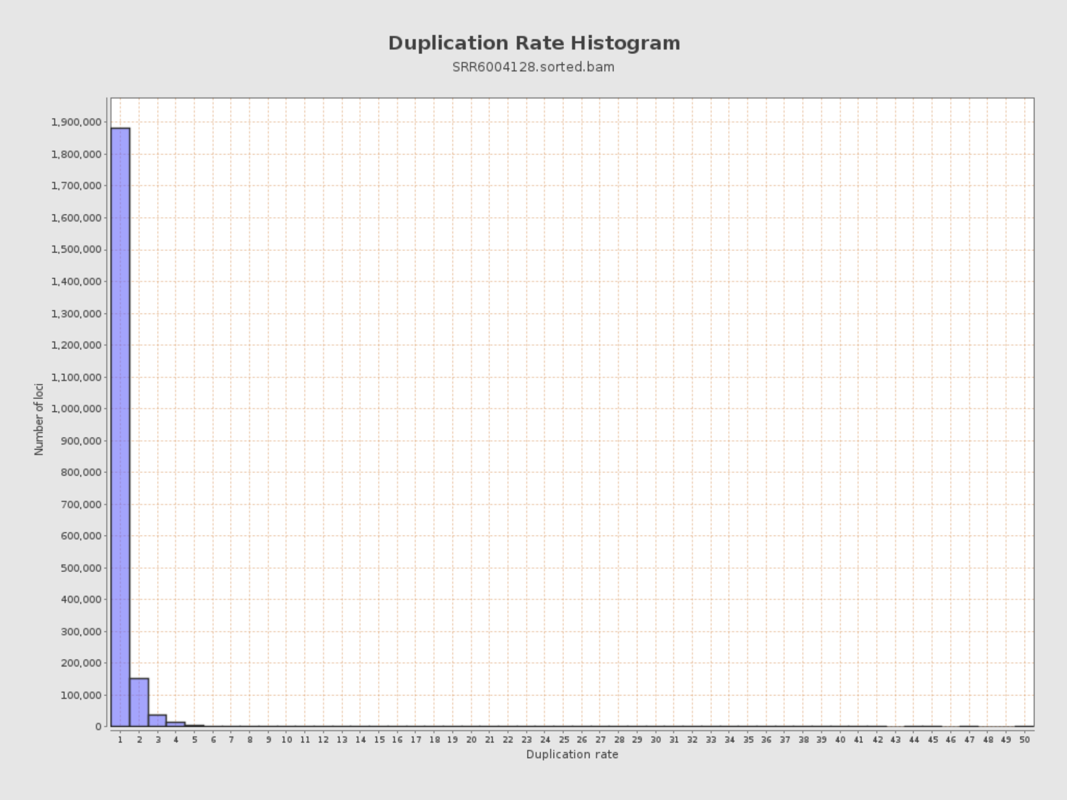
5. Results : Coverage Histogram (0-50X)



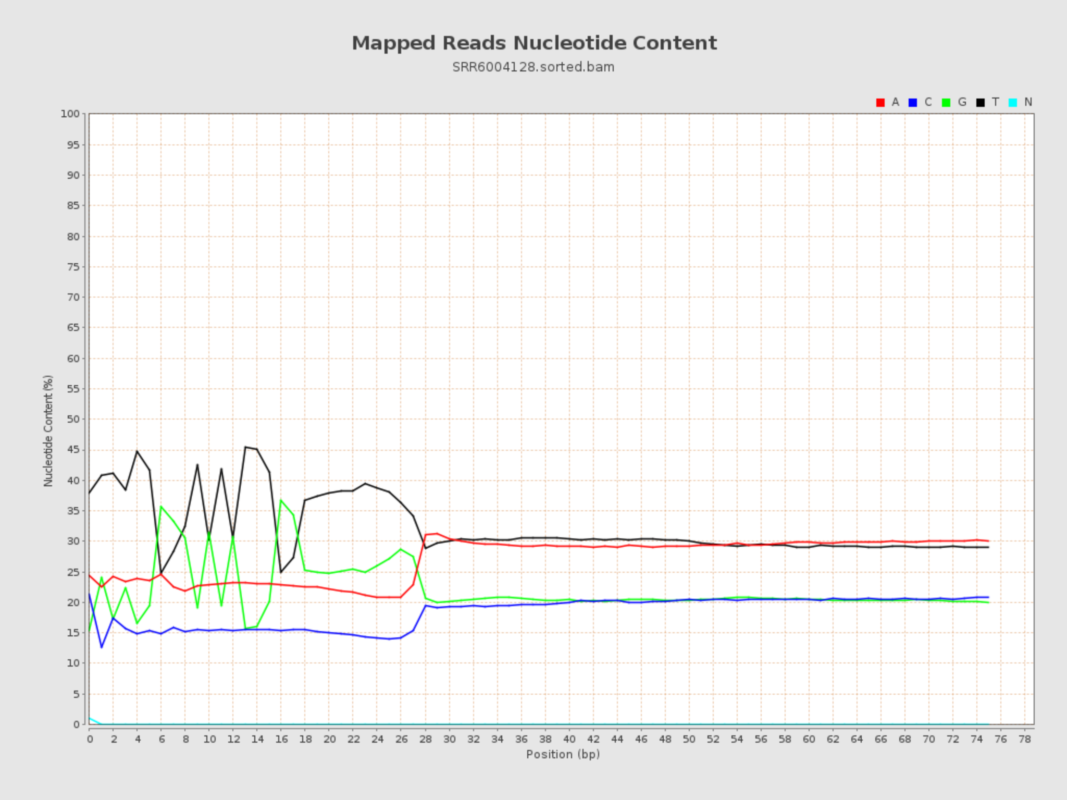
6. Results : Genome Fraction Coverage



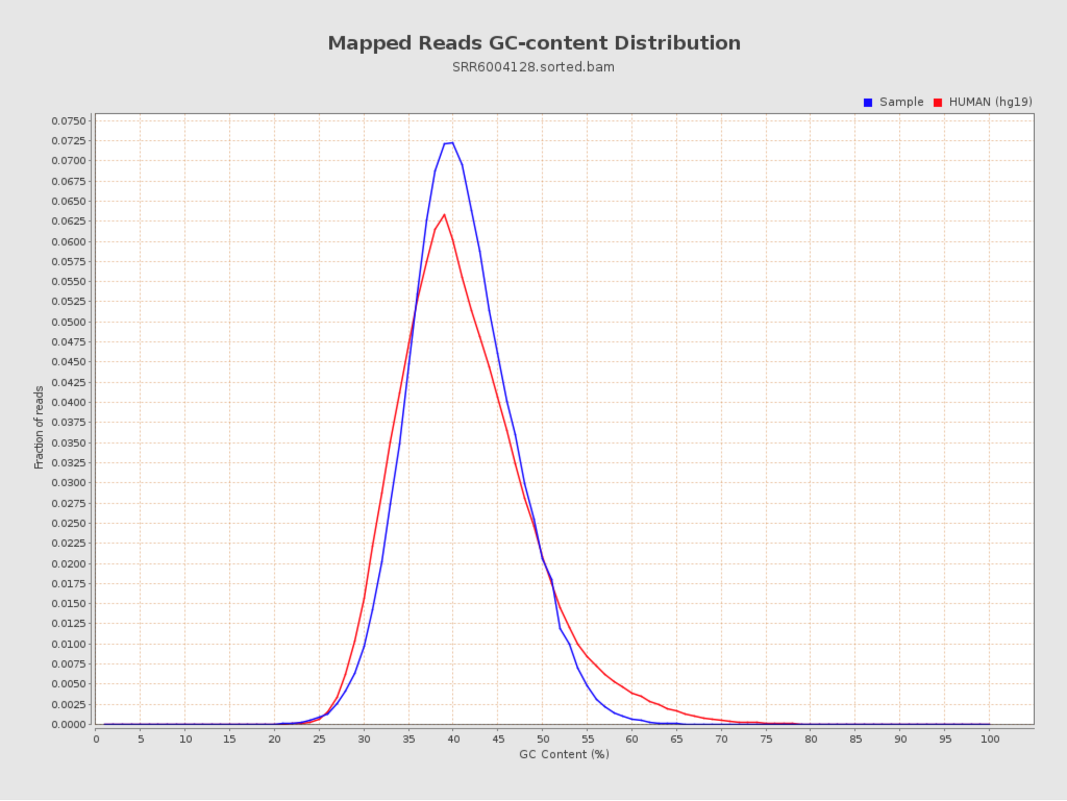
7. Results : Duplication Rate Histogram



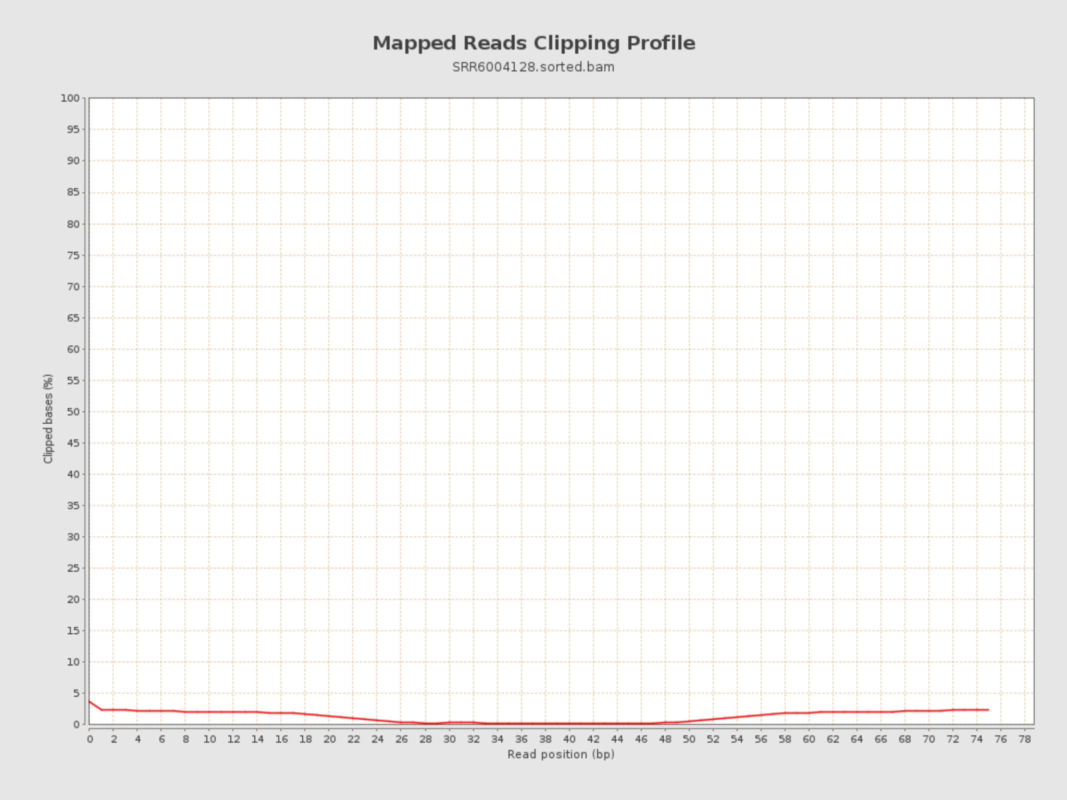
8. Results : Mapped Reads Nucleotide Content



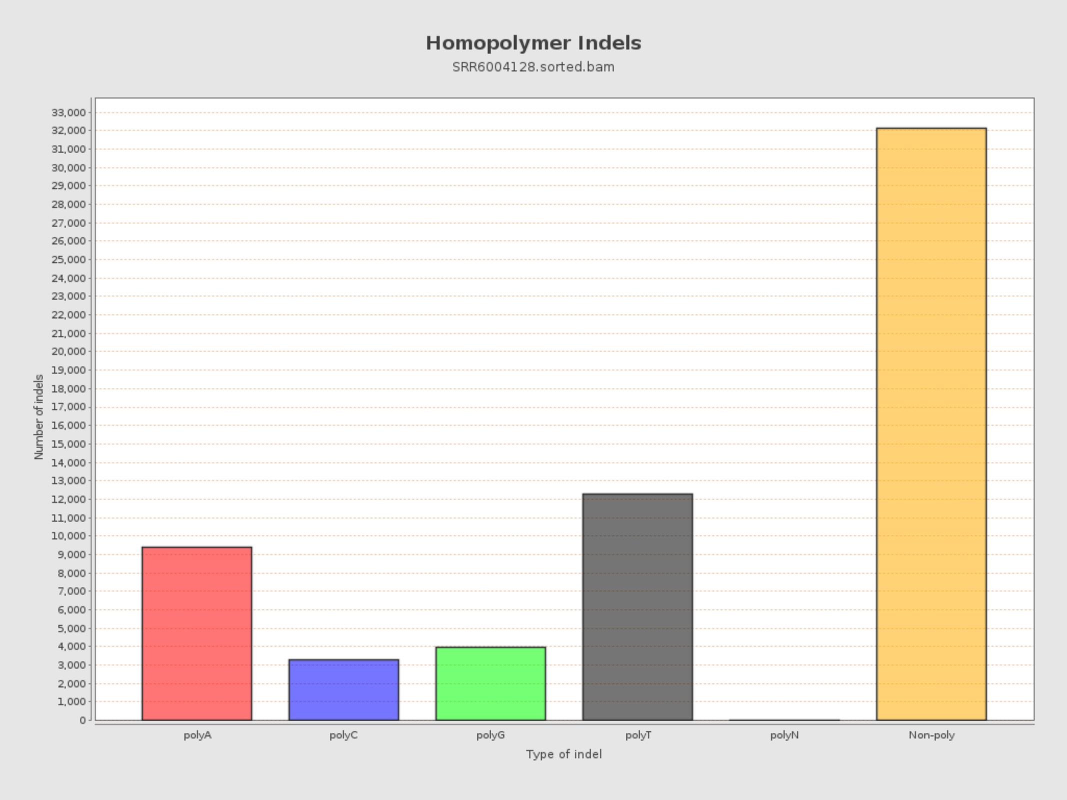
9. Results : Mapped Reads GC-content Distribution



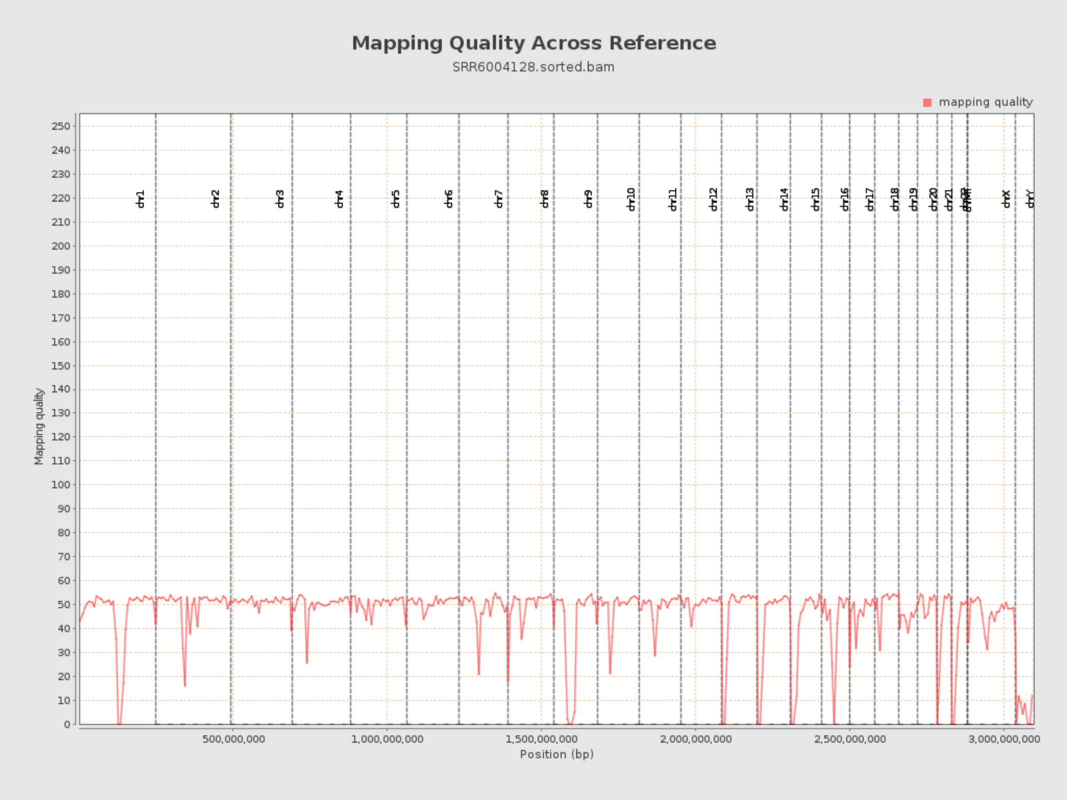
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram