Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:12:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004077.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_SRR6004077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004077.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:12:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,333,375
Mapped reads	2,087,019 / 89.44%
Unmapped reads	246,356 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,557 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	72,365 / 3.1%
Duplication rate	2.73%
Clipped reads	950,771 / 40.75%

2.2. ACGT Content

Number/percentage of A's	38,311,142 / 27.55%
Number/percentage of C's	26,344,512 / 18.94%
Number/percentage of T's	42,855,157 / 30.81%
Number/percentage of G's	31,544,716 / 22.68%
Number/percentage of N's	24,861 / 0.02%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0449

Standard Deviation	0.3595

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

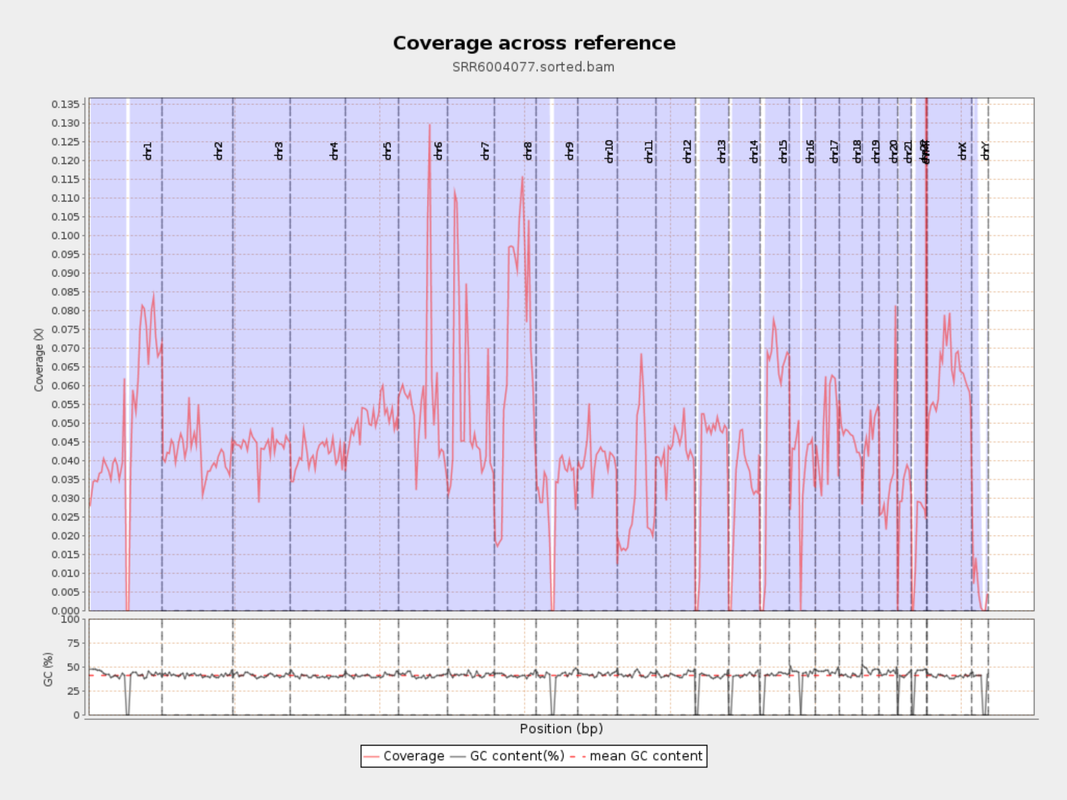
General error rate	0.86%
Mismatches	1,172,698
Insertions	9,823
Mapped reads with at least one insertion	0.47%
Deletions	33,015
Mapped reads with at least one deletion	1.57%
Homopolymer indels	46.51%

2.6. Chromosome stats

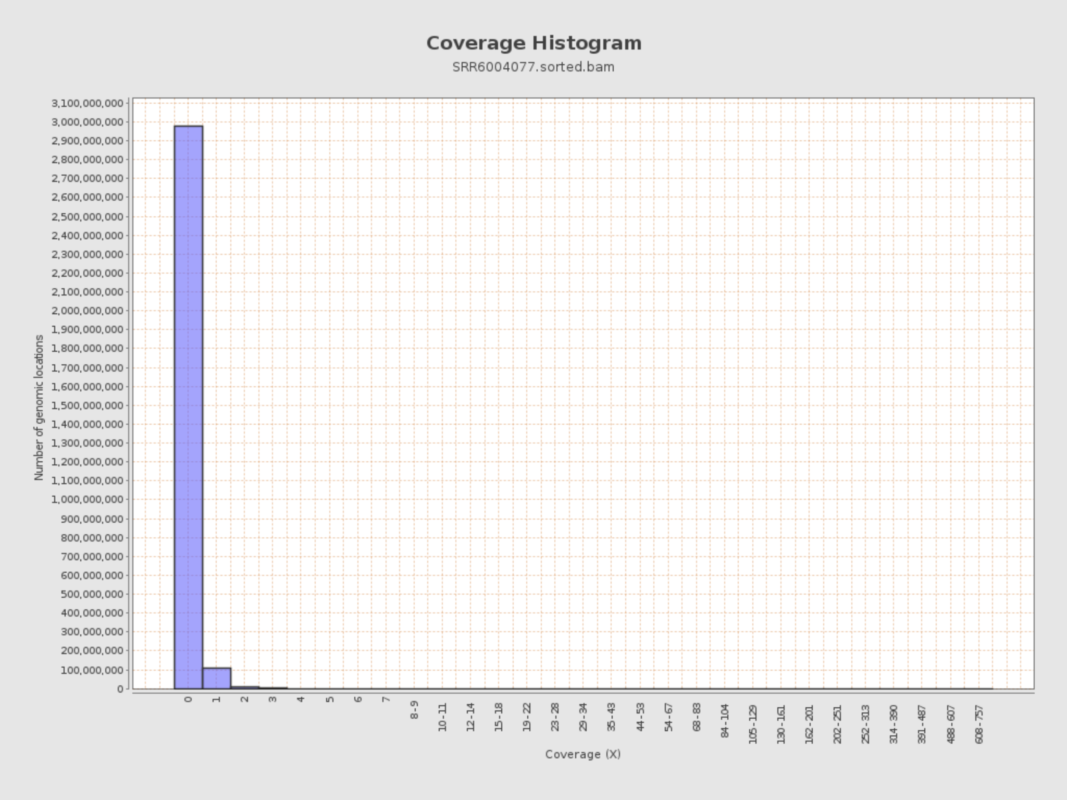
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12291118	0.0493	0.6165
chr2	243199373	10199015	0.0419	0.4132
chr3	198022430	8720385	0.044	0.2333
chr4	191154276	7894601	0.0413	0.2404
chr5	180915260	9161803	0.0506	0.2533
chr6	171115067	9783787	0.0572	0.2992
chr7	159138663	8740121	0.0549	0.6659

chr8	146364022	10310307	0.0704	0.4194
chr9	141213431	4319489	0.0306	0.271
chr10	135534747	5557801	0.041	0.2914
chr11	135006516	4145388	0.0307	0.2345
chr12	133851895	5735974	0.0429	0.2326
chr13	115169878	4710670	0.0409	0.2384
chr14	107349540	3417020	0.0318	0.2138
chr15	102531392	5527632	0.0539	0.2693
chr16	90354753	3411122	0.0378	0.2303
chr17	81195210	3993208	0.0492	0.2643
chr18	78077248	3606367	0.0462	0.4785
chr19	59128983	2778603	0.047	0.4742
chr20	63025520	2318951	0.0368	0.2227
chr21	48129895	1469010	0.0305	0.2058
chr22	51304566	1000924	0.0195	0.1527
chrMT	16571	28779	1.7367	1.8969
chrX	155270560	9673120	0.0623	0.3013
chrY	59373566	342572	0.0058	0.1096

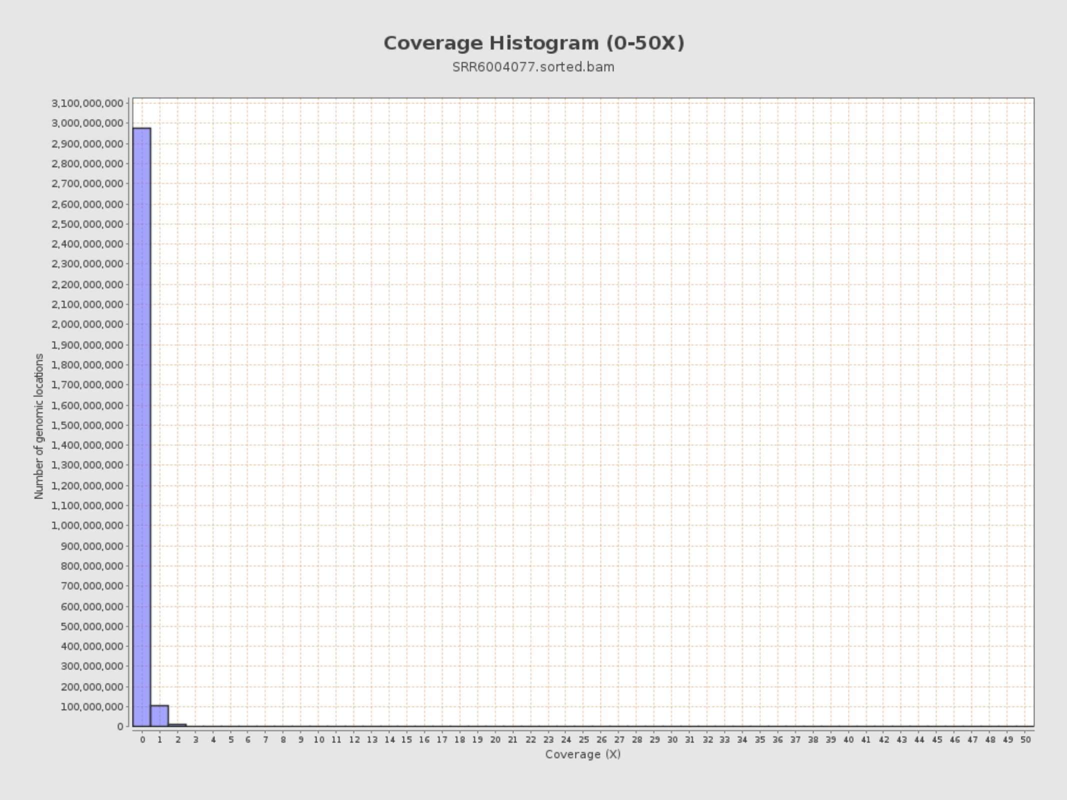
3. Results : Coverage across reference



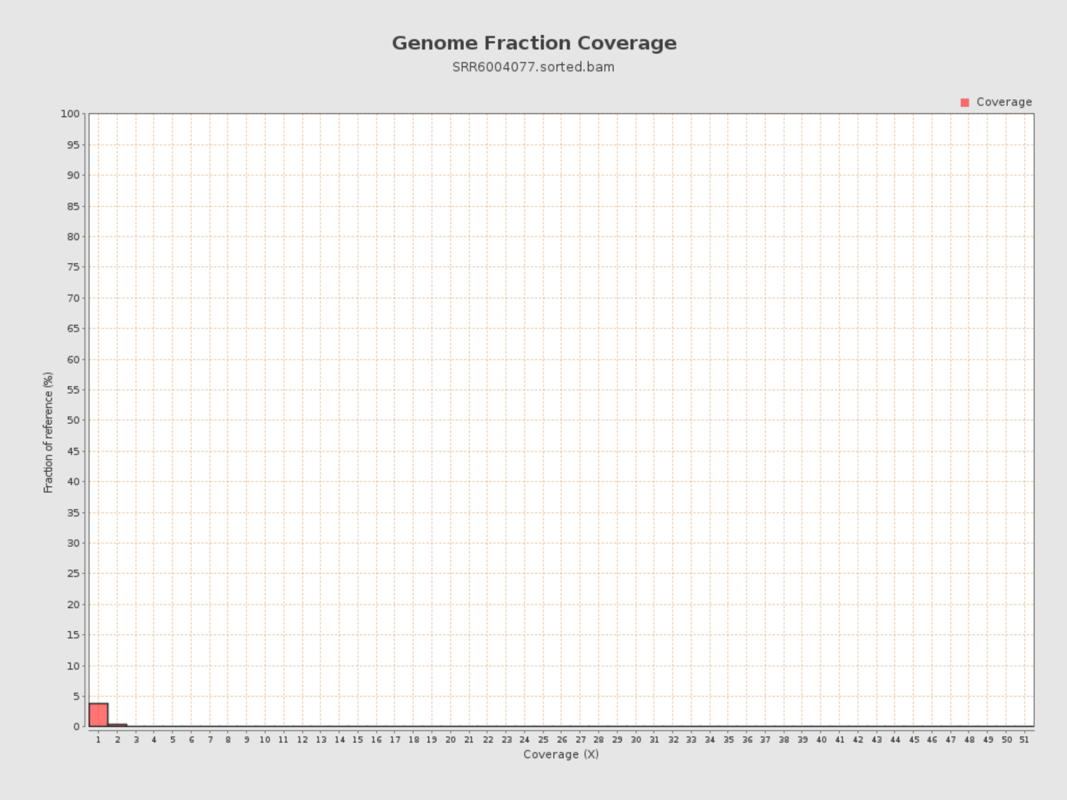
4. Results : Coverage Histogram



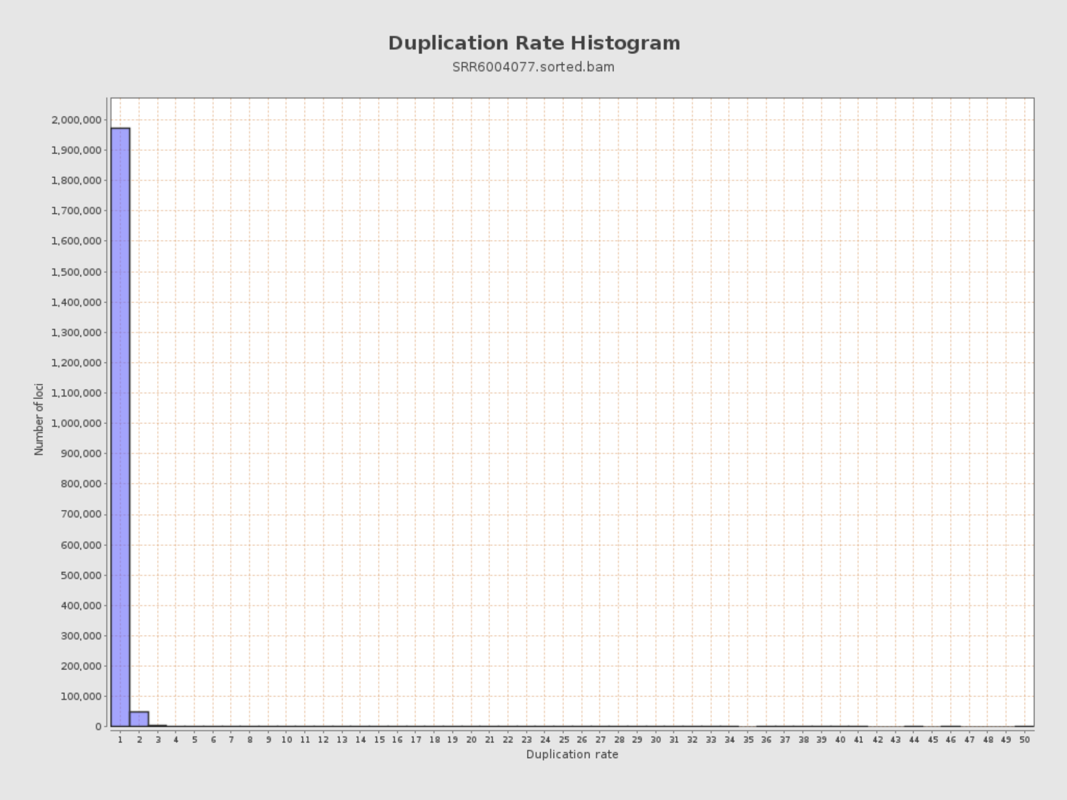
5. Results : Coverage Histogram (0-50X)



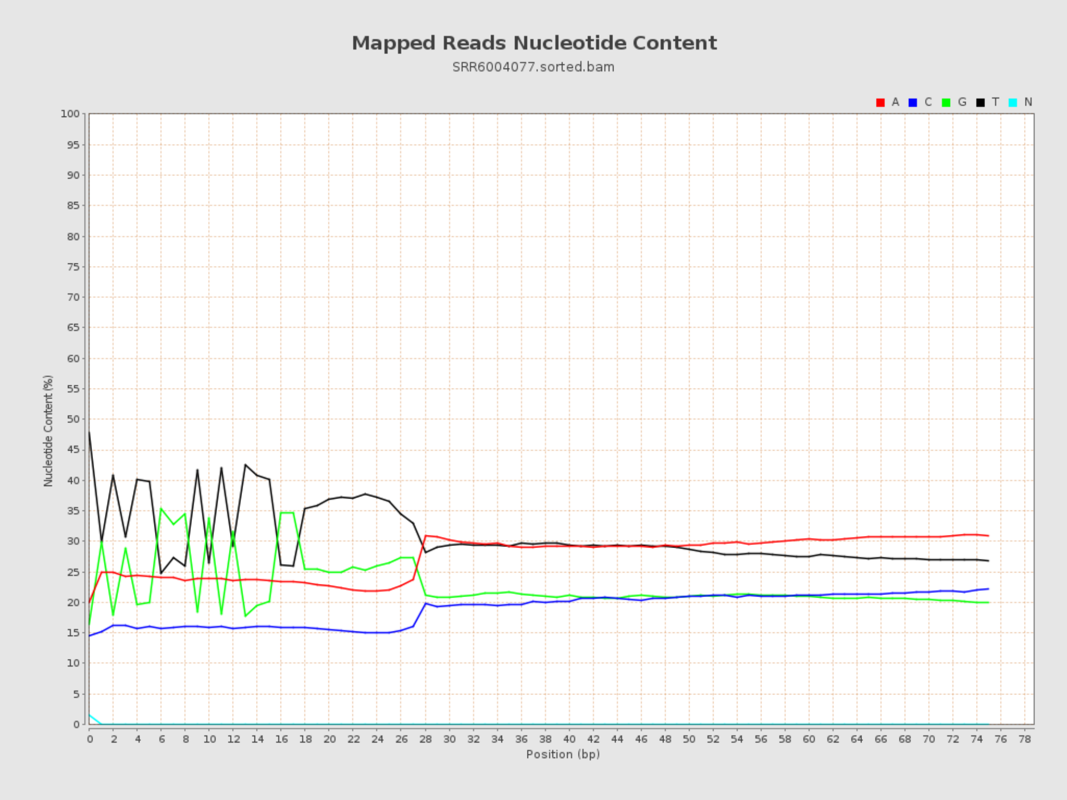
6. Results : Genome Fraction Coverage



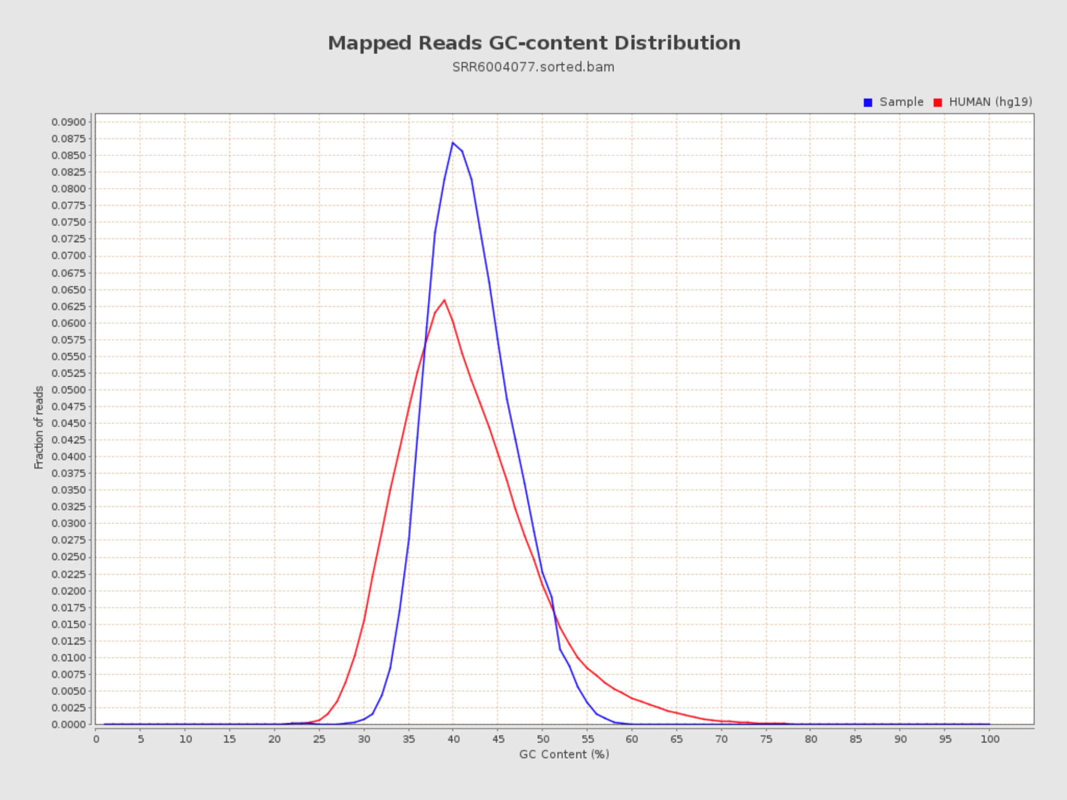
7. Results : Duplication Rate Histogram



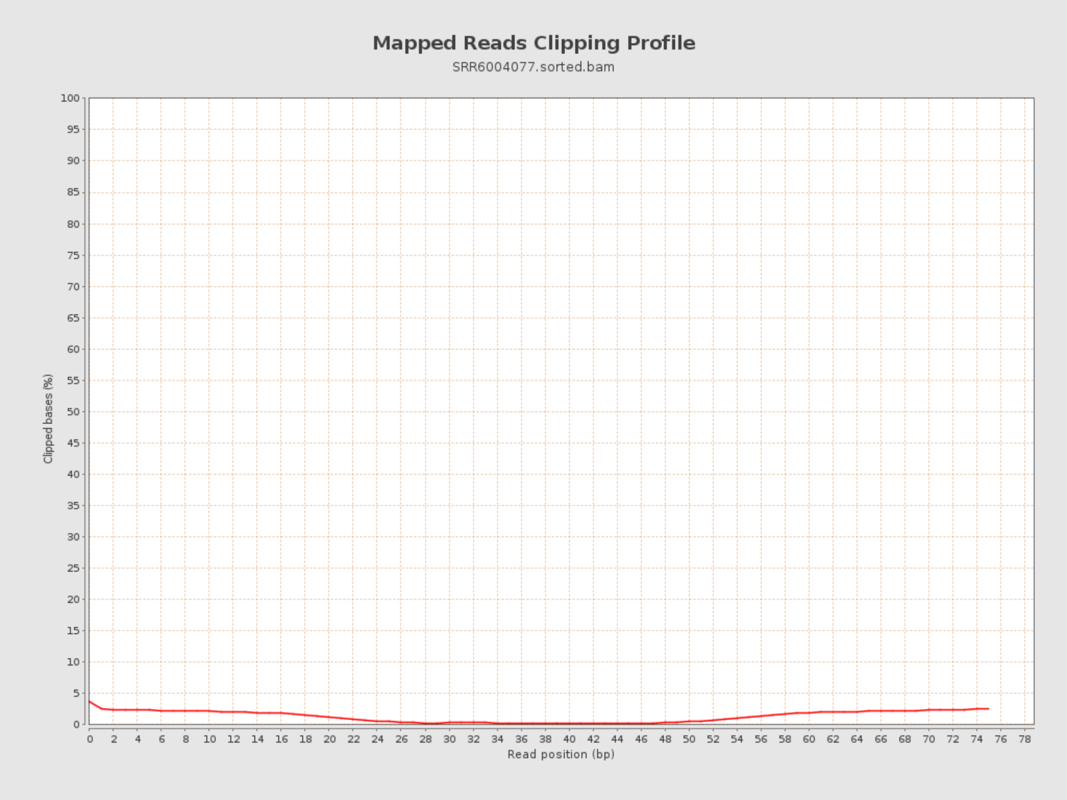
8. Results : Mapped Reads Nucleotide Content



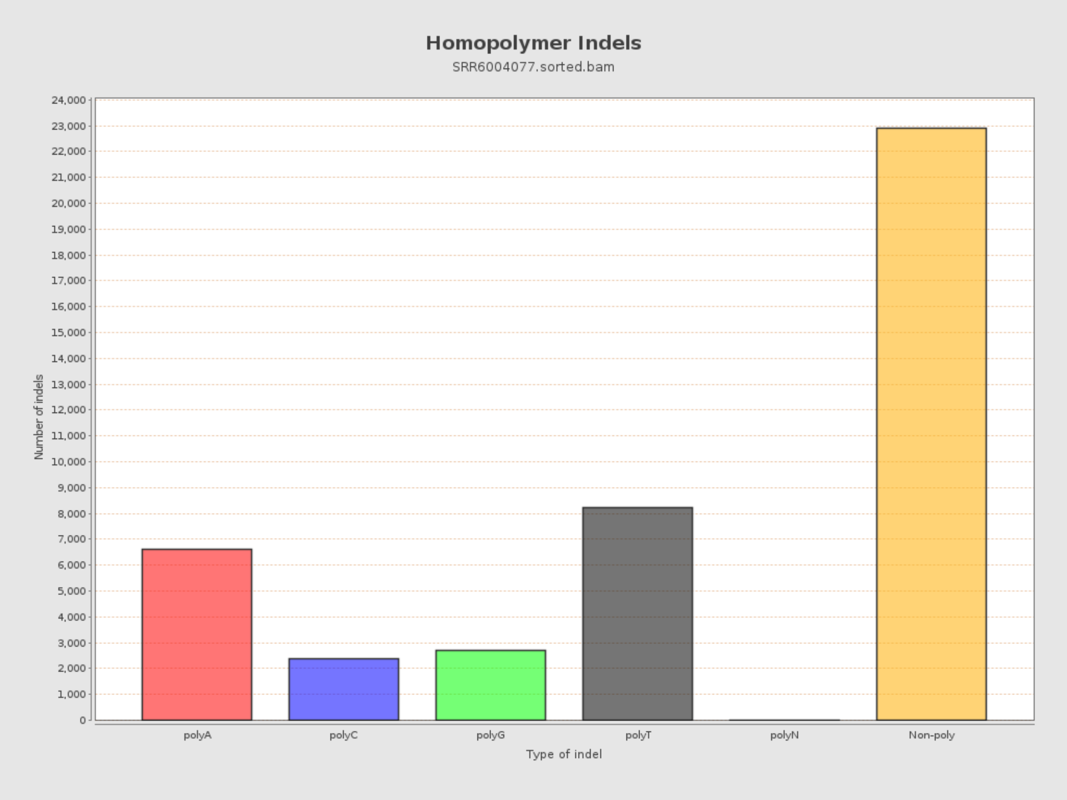
9. Results : Mapped Reads GC-content Distribution



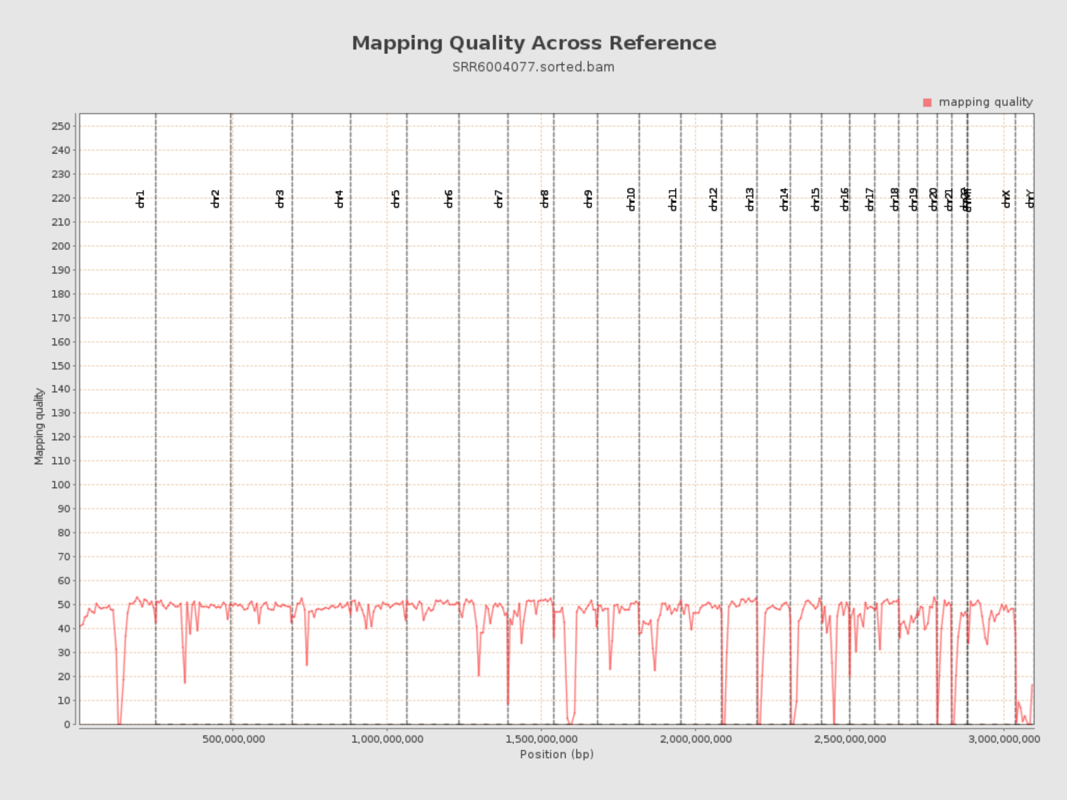
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram