Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:55:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004153.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_SRR6004153 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,371,862
Mapped reads	2,146,950 / 90.52%
Unmapped reads	224,912 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,617 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	57,288 / 2.42%
Duplication rate	1.67%
Clipped reads	1,082,950 / 45.66%

2.2. ACGT Content

Number/percentage of A's	37,943,515 / 27.07%
Number/percentage of C's	27,688,723 / 19.75%
Number/percentage of T's	41,321,688 / 29.48%
Number/percentage of G's	33,179,944 / 23.67%
Number/percentage of N's	27,204 / 0.02%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0453

Standard Deviation	0.3961

2.4. Mapping Quality

Mean Mapping Quality	42.08

2.5. Mismatches and indels

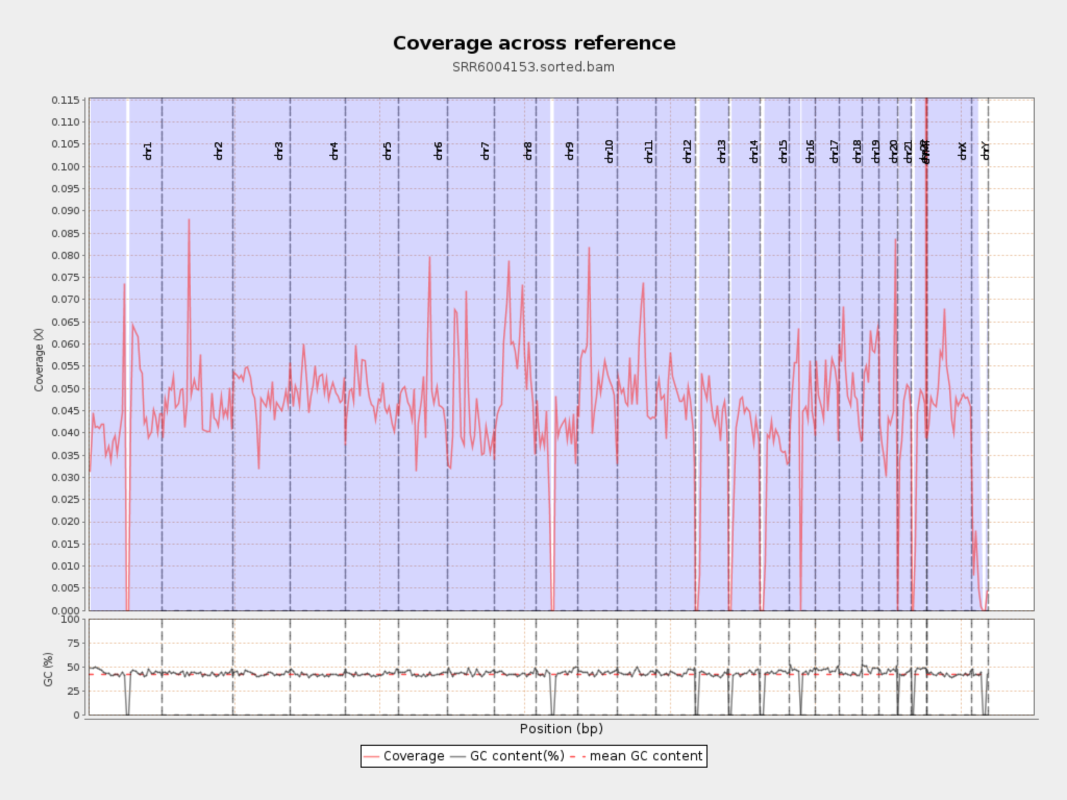
General error rate	0.84%
Mismatches	1,154,823
Insertions	11,311
Mapped reads with at least one insertion	0.52%
Deletions	36,264
Mapped reads with at least one deletion	1.67%
Homopolymer indels	44.55%

2.6. Chromosome stats

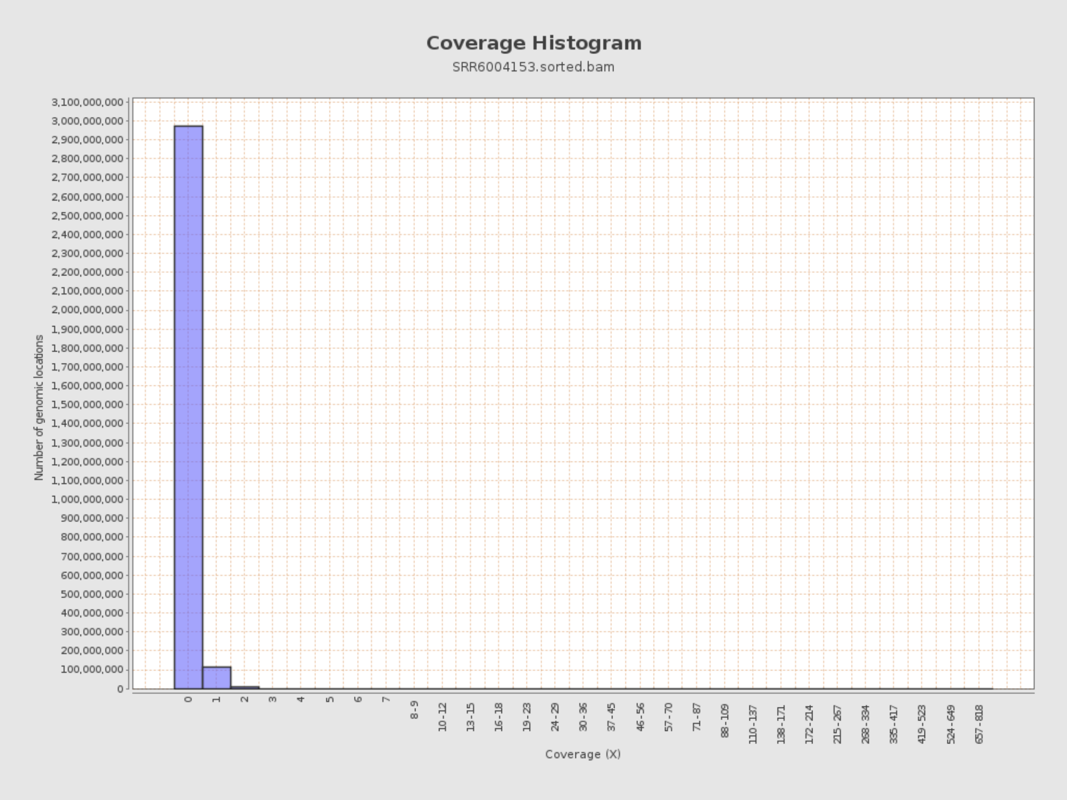
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10420134	0.0418	0.7015
chr2	243199373	11586214	0.0476	0.5327
chr3	198022430	9569136	0.0483	0.2389
chr4	191154276	9612658	0.0503	0.2578
chr5	180915260	8700389	0.0481	0.2416
chr6	171115067	8205737	0.048	0.2768
chr7	159138663	7036717	0.0442	0.5081

chr8	146364022	8139371	0.0556	0.4115
chr9	141213431	4990268	0.0353	0.37
chr10	135534747	7148340	0.0527	0.403
chr11	135006516	6935488	0.0514	0.3932
chr12	133851895	6431223	0.048	0.2424
chr13	115169878	4427593	0.0384	0.2105
chr14	107349540	3884729	0.0362	0.2547
chr15	102531392	3117974	0.0304	0.2085
chr16	90354753	4097079	0.0453	0.2855
chr17	81195210	4073369	0.0502	0.2793
chr18	78077248	3991796	0.0511	0.7152
chr19	59128983	3359138	0.0568	0.5325
chr20	63025520	2841339	0.0451	0.2442
chr21	48129895	1924693	0.04	0.2422
chr22	51304566	1654784	0.0323	0.193
chrMT	16571	108973	6.5761	4.8854
chrX	155270560	7589121	0.0489	0.2843
chrY	59373566	376177	0.0063	0.1323

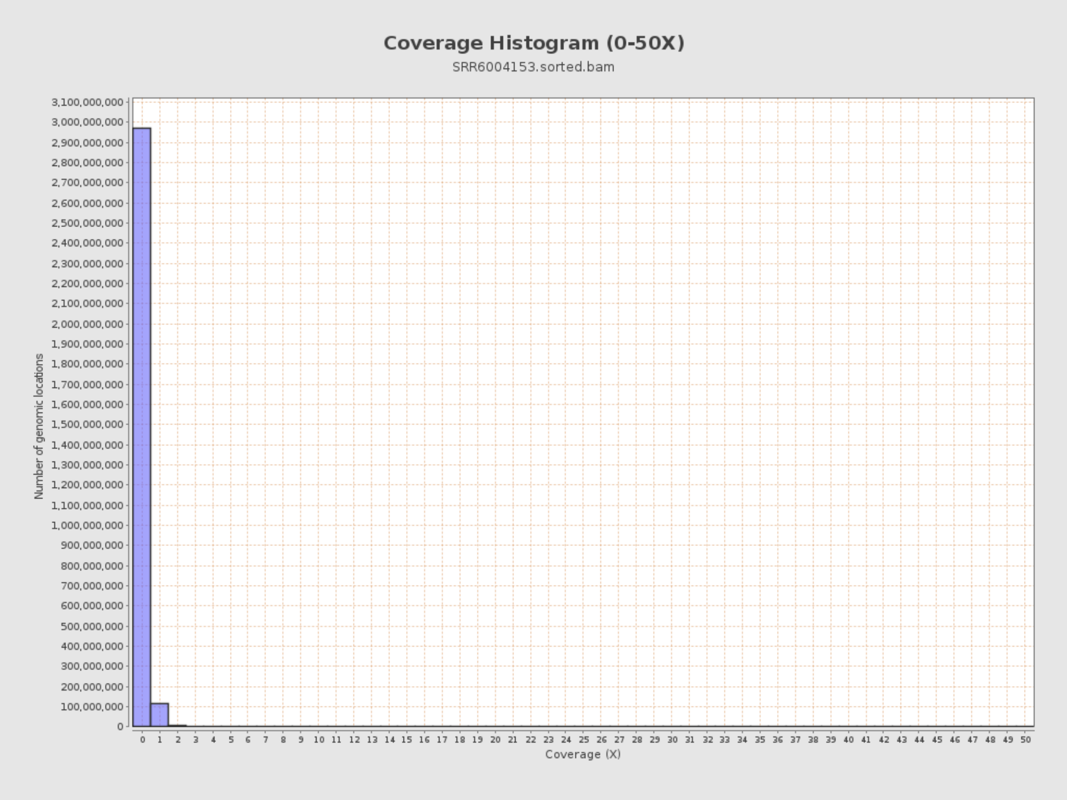
3. Results : Coverage across reference



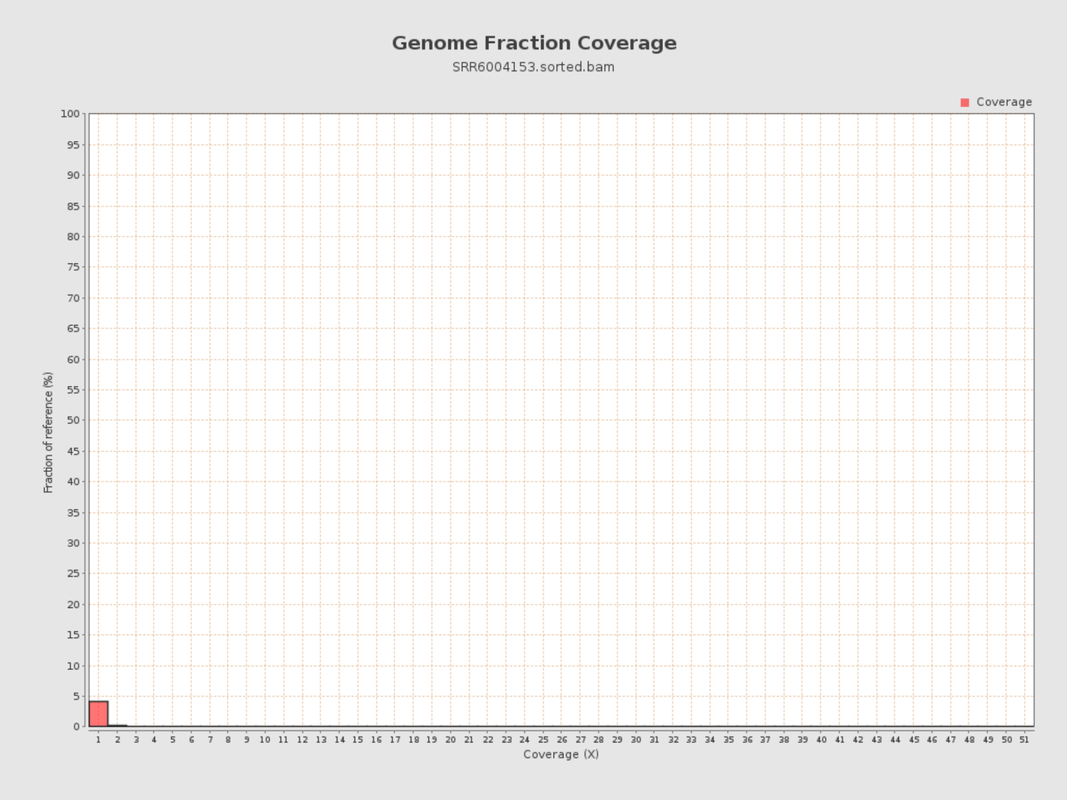
4. Results : Coverage Histogram



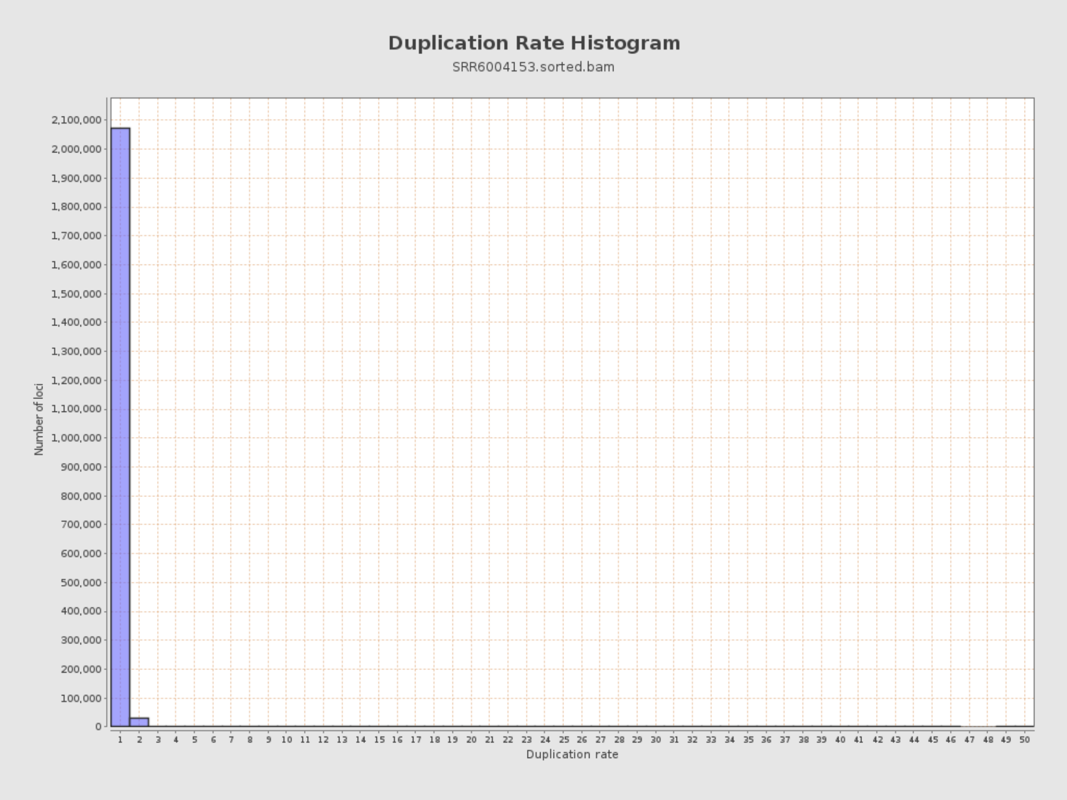
5. Results : Coverage Histogram (0-50X)



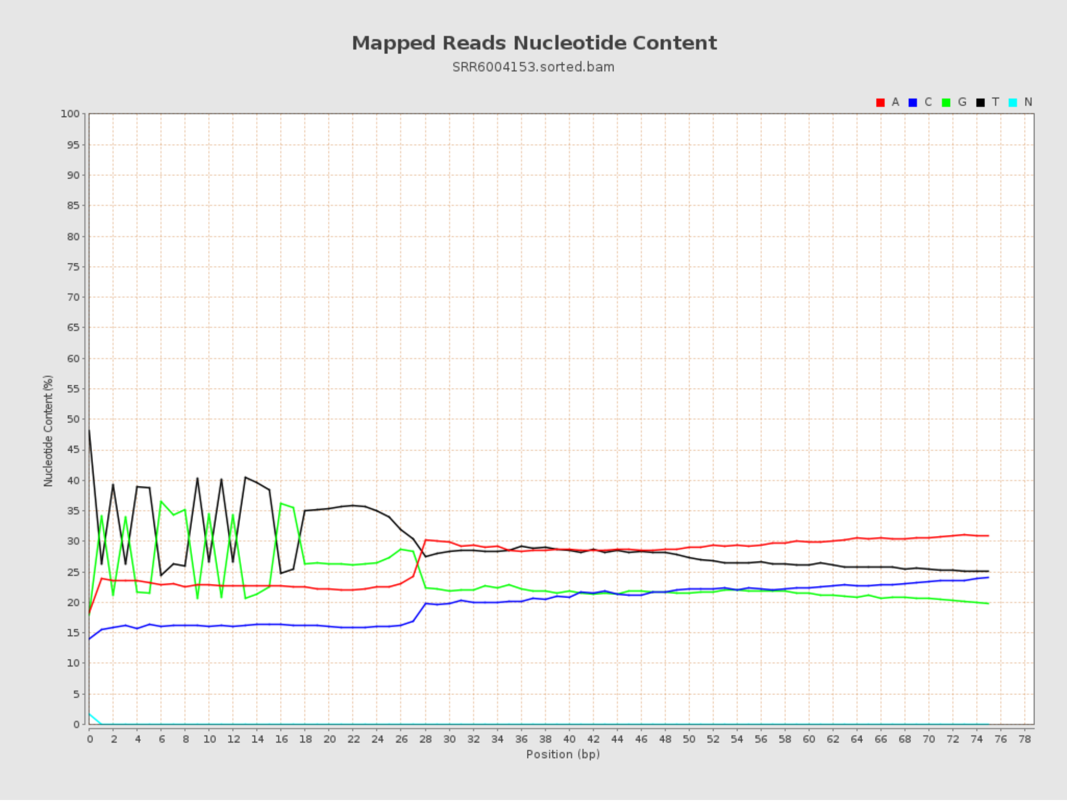
6. Results : Genome Fraction Coverage



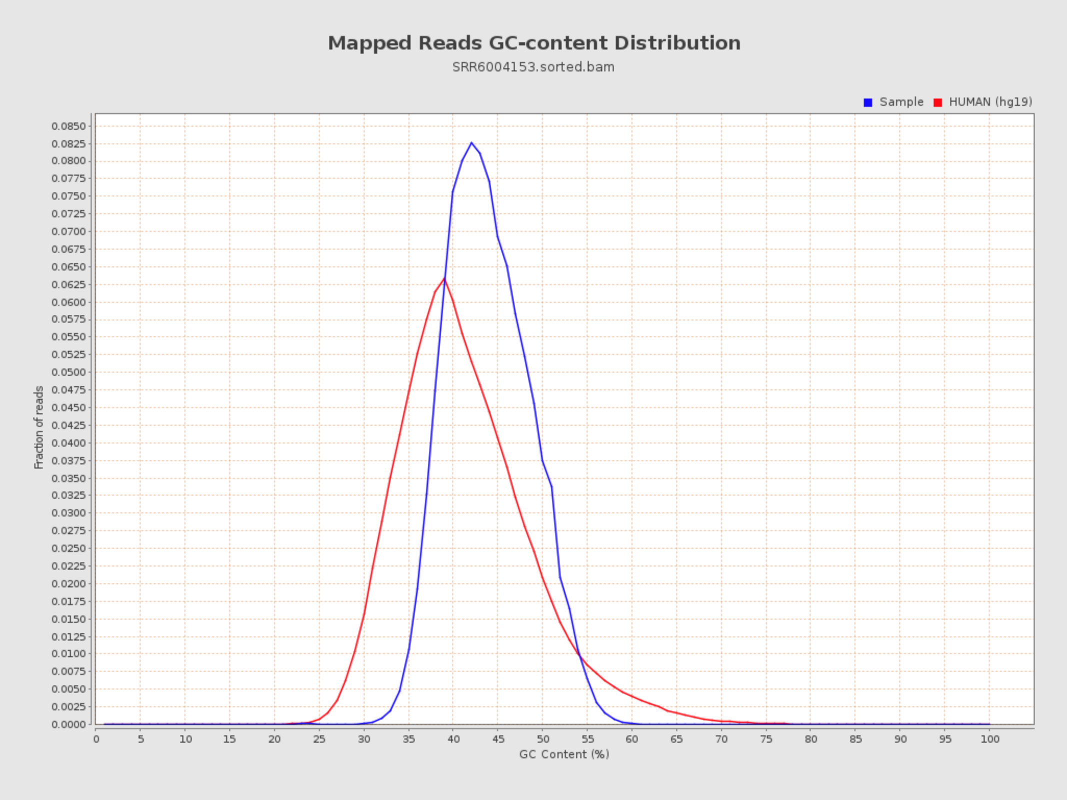
7. Results : Duplication Rate Histogram



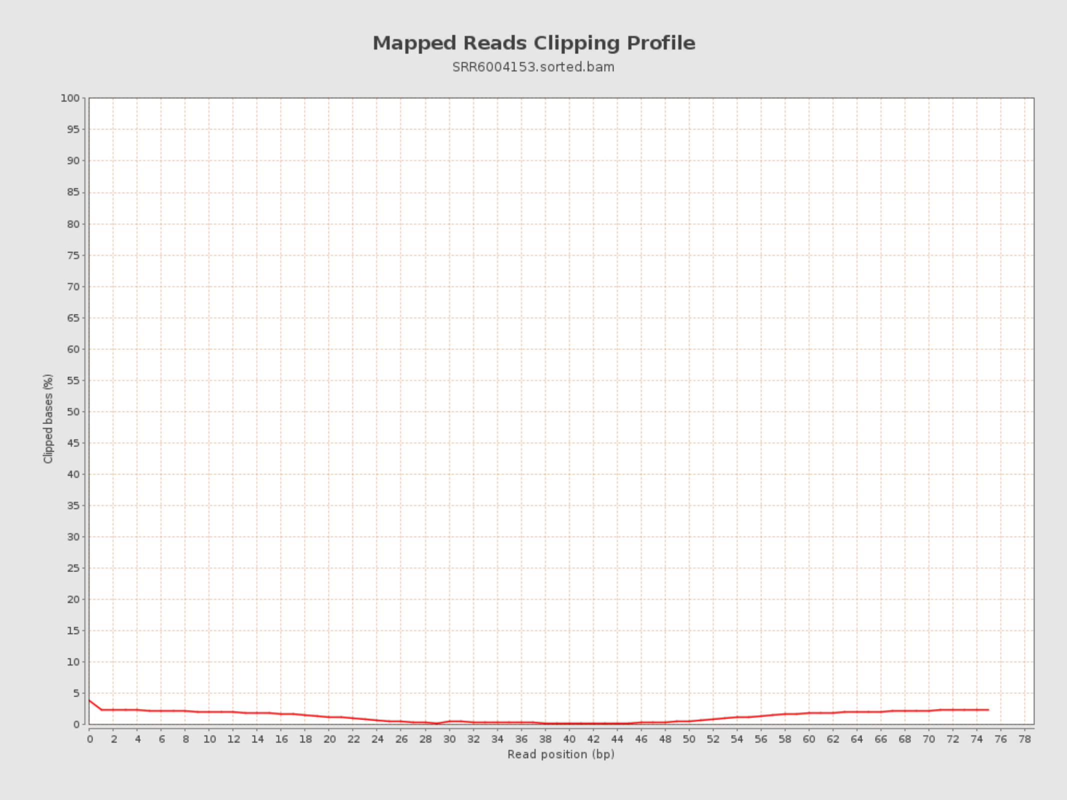
8. Results : Mapped Reads Nucleotide Content



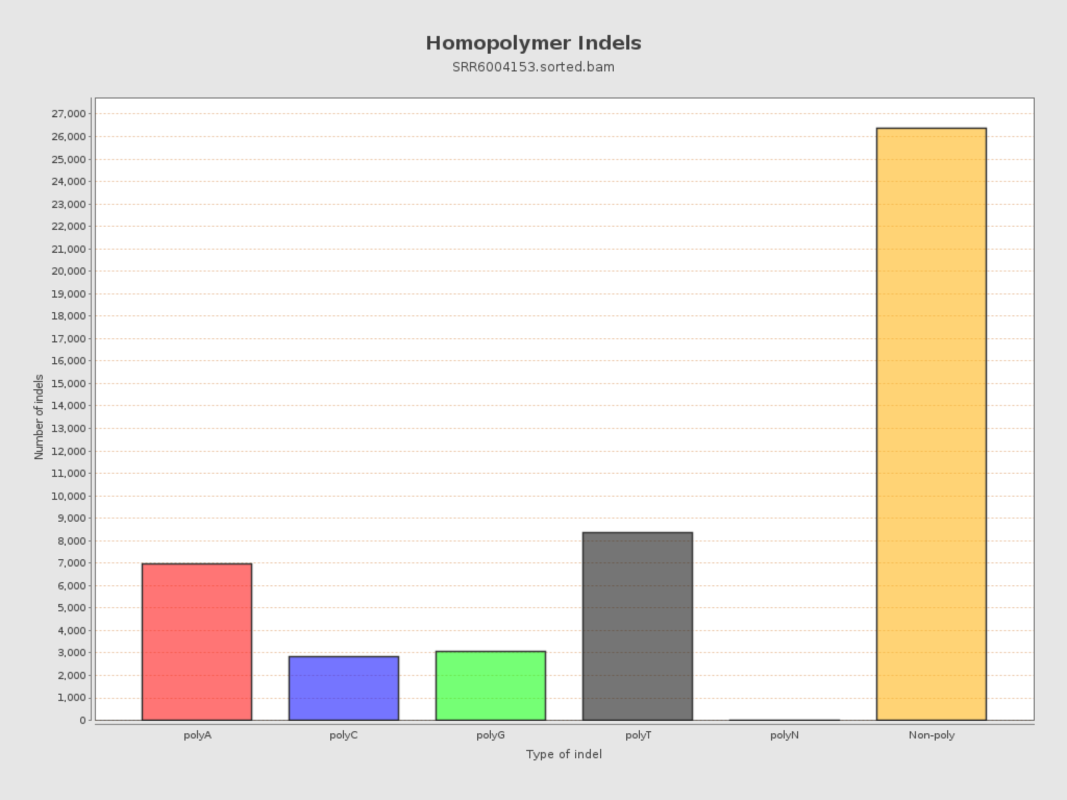
9. Results : Mapped Reads GC-content Distribution



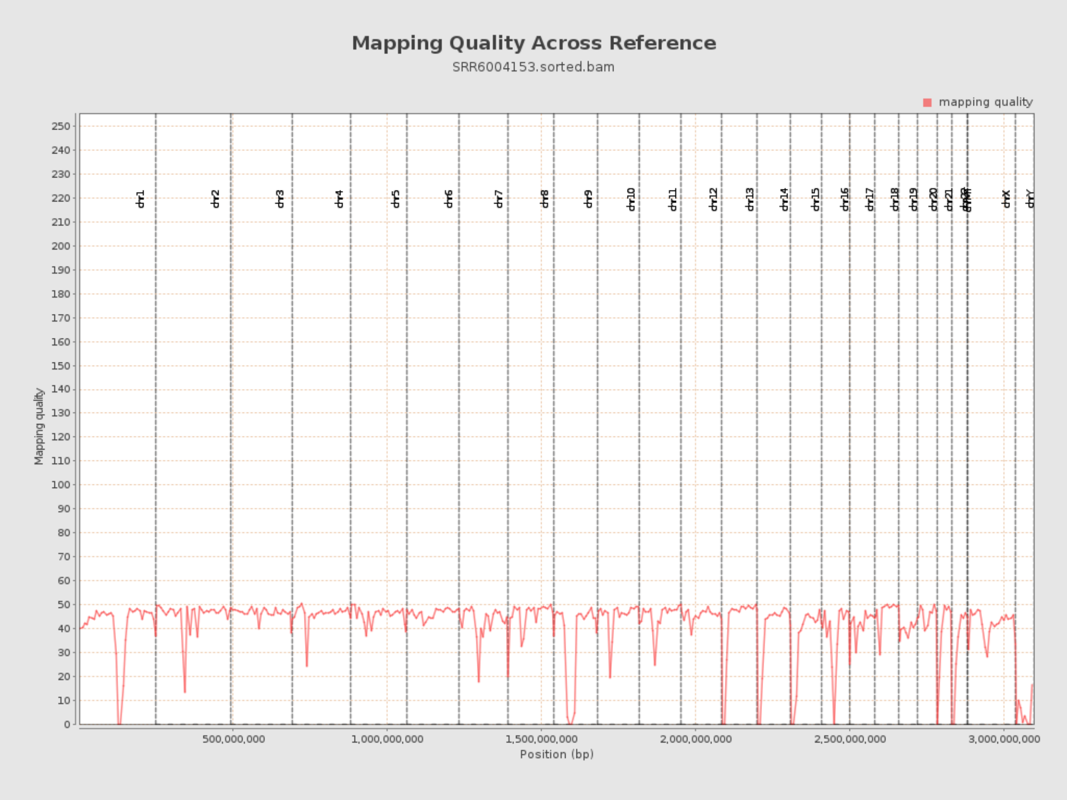
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram