Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:17:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083751.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_SRR3083751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:17:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,173,120
Mapped reads	1,800,776 / 82.87%
Unmapped reads	372,344 / 17.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,582 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	54,860 / 2.52%
Duplication rate	2.57%
Clipped reads	1,248,882 / 57.47%

2.2. ACGT Content

Number/percentage of A's	32,296,782 / 29.75%
Number/percentage of C's	20,865,520 / 19.22%
Number/percentage of T's	32,090,388 / 29.56%
Number/percentage of G's	23,311,721 / 21.47%
Number/percentage of N's	6,337 / 0.01%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.2833

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

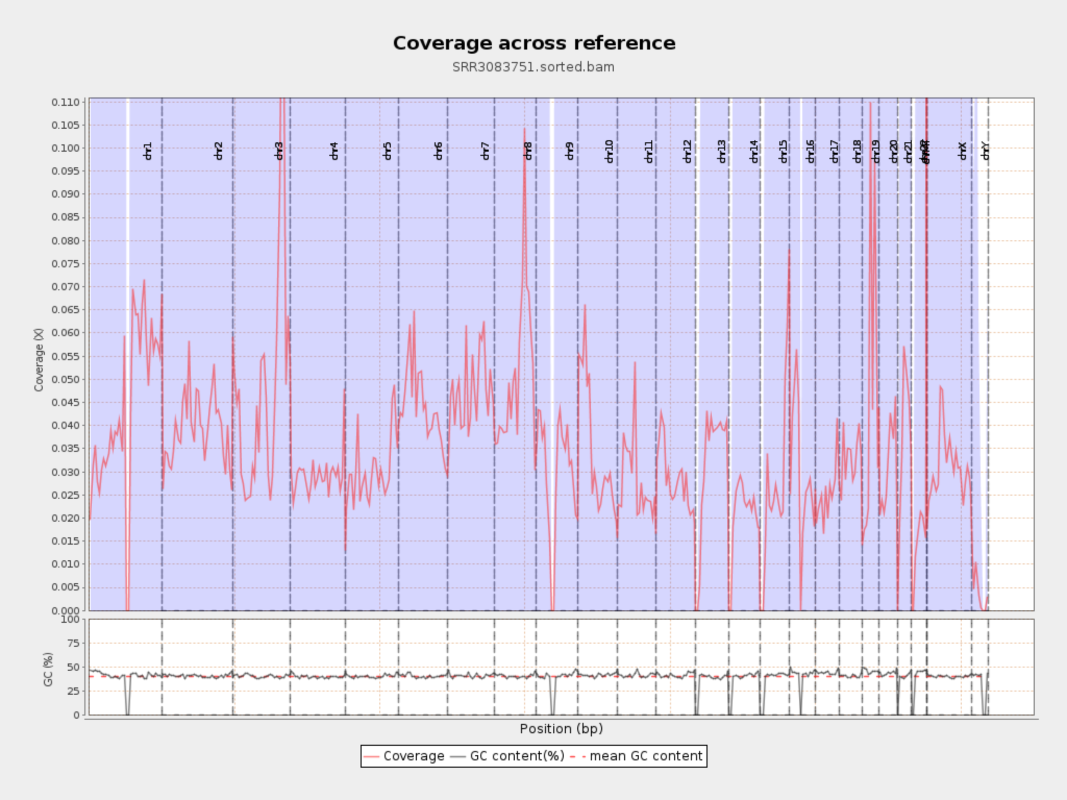
General error rate	0.84%
Mismatches	894,588
Insertions	7,610
Mapped reads with at least one insertion	0.42%
Deletions	21,111
Mapped reads with at least one deletion	1.16%
Homopolymer indels	46.03%

2.6. Chromosome stats

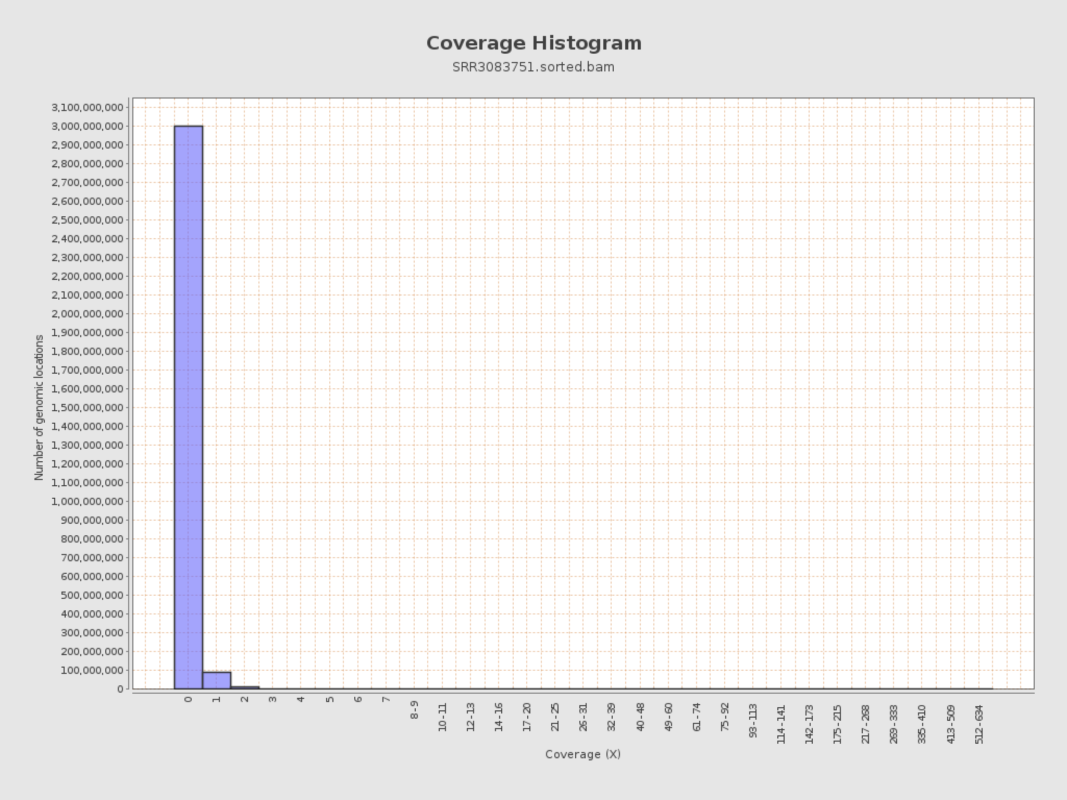
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10837295	0.0435	0.5616
chr2	243199373	9598296	0.0395	0.2561
chr3	198022430	9688809	0.0489	0.2447
chr4	191154276	5599026	0.0293	0.19
chr5	180915260	5472956	0.0303	0.1905
chr6	171115067	7538389	0.0441	0.2631
chr7	159138663	7606017	0.0478	0.4057

chr8	146364022	7539247	0.0515	0.3731
chr9	141213431	4228083	0.0299	0.2106
chr10	135534747	4801606	0.0354	0.2527
chr11	135006516	3765496	0.0279	0.1978
chr12	133851895	3832854	0.0286	0.1855
chr13	115169878	3577964	0.0311	0.192
chr14	107349540	2207193	0.0206	0.1577
chr15	102531392	2693431	0.0263	0.1784
chr16	90354753	2709002	0.03	0.1938
chr17	81195210	2077301	0.0256	0.1775
chr18	78077248	2563612	0.0328	0.3129
chr19	59128983	2758833	0.0467	0.4015
chr20	63025520	1975968	0.0314	0.1955
chr21	48129895	1753272	0.0364	0.2107
chr22	51304566	701773	0.0137	0.1271
chrMT	16571	5641	0.3404	0.6709
chrX	155270560	4847237	0.0312	0.1977
chrY	59373566	224335	0.0038	0.079

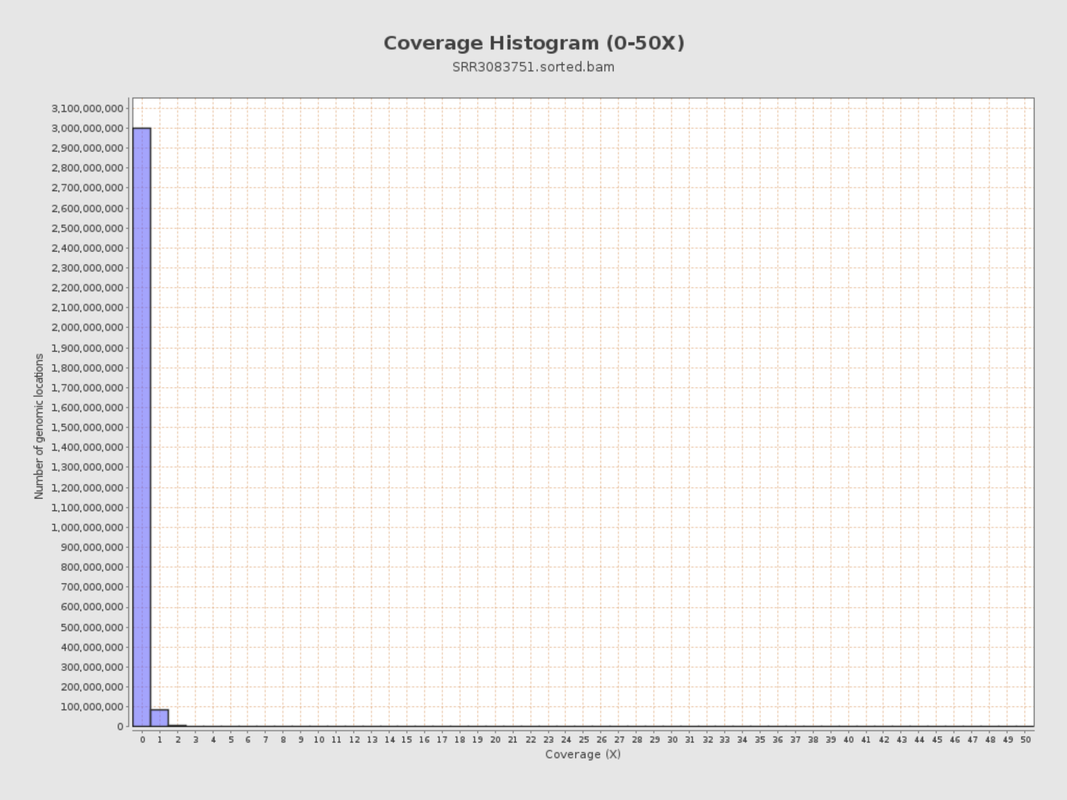
3. Results : Coverage across reference



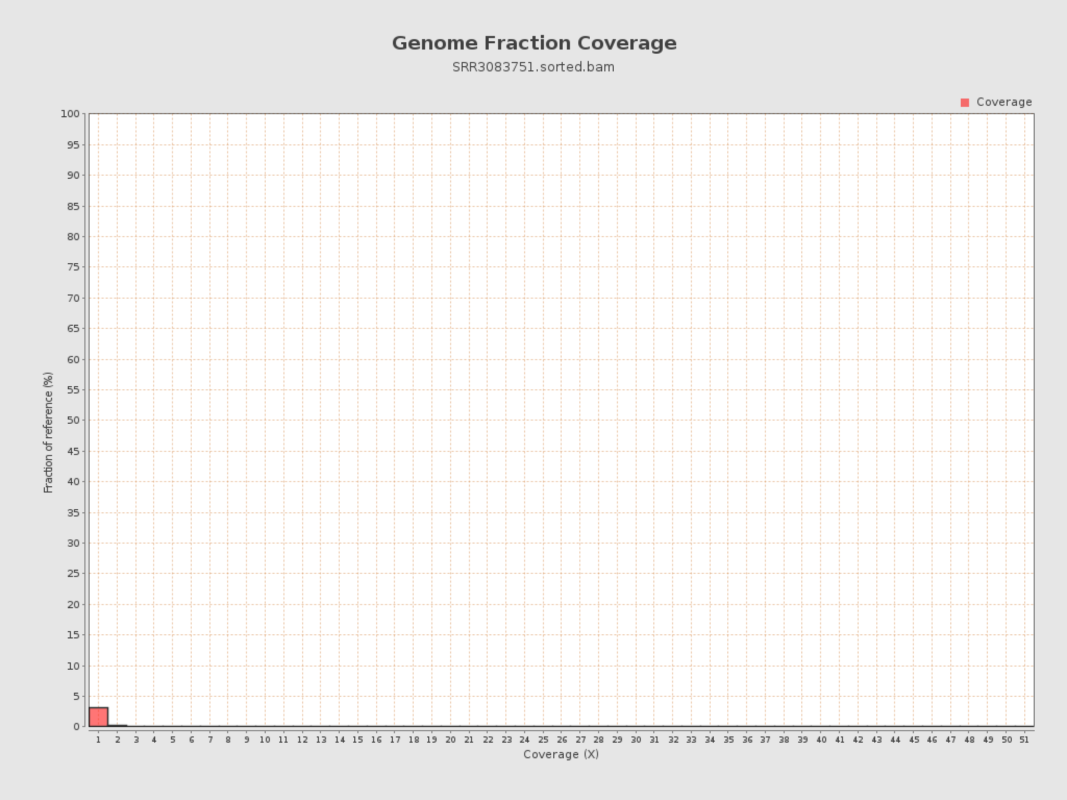
4. Results : Coverage Histogram



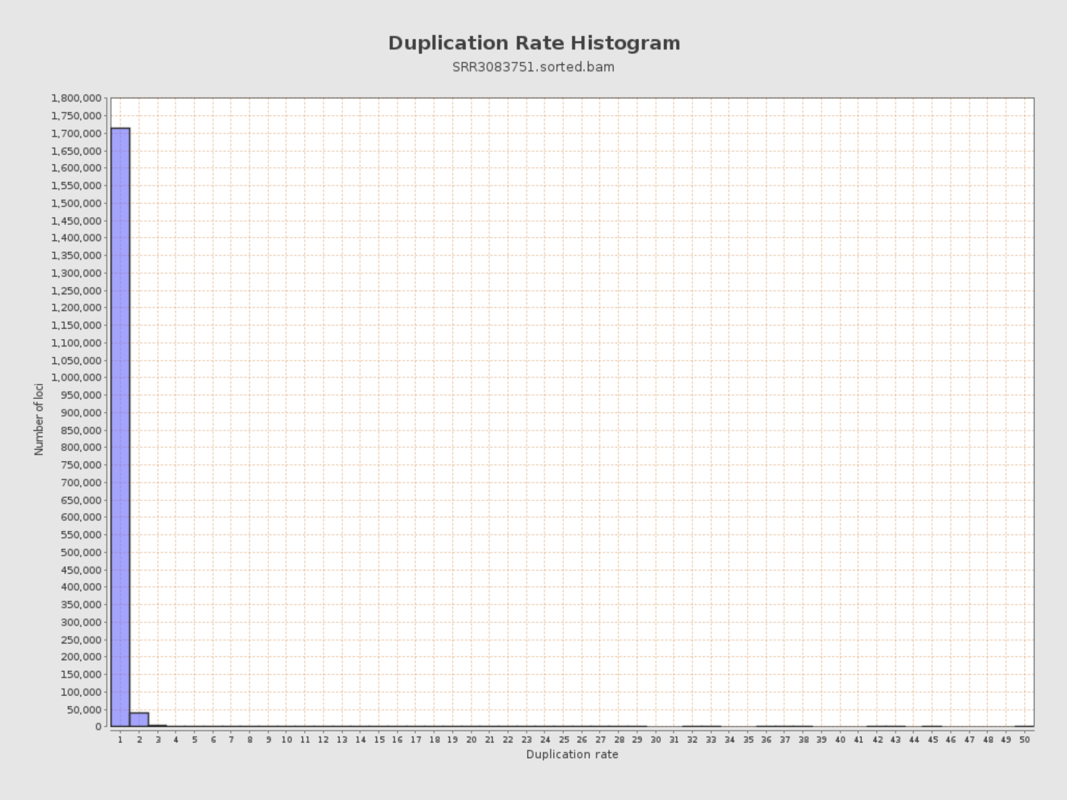
5. Results : Coverage Histogram (0-50X)



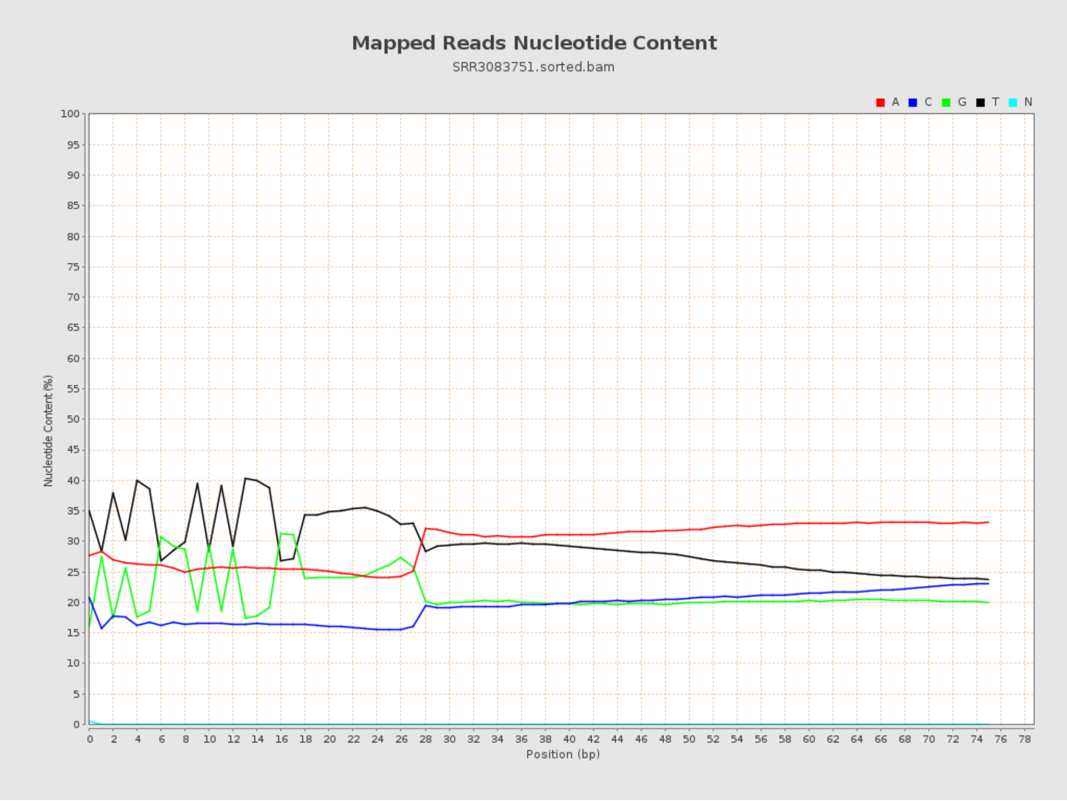
6. Results : Genome Fraction Coverage



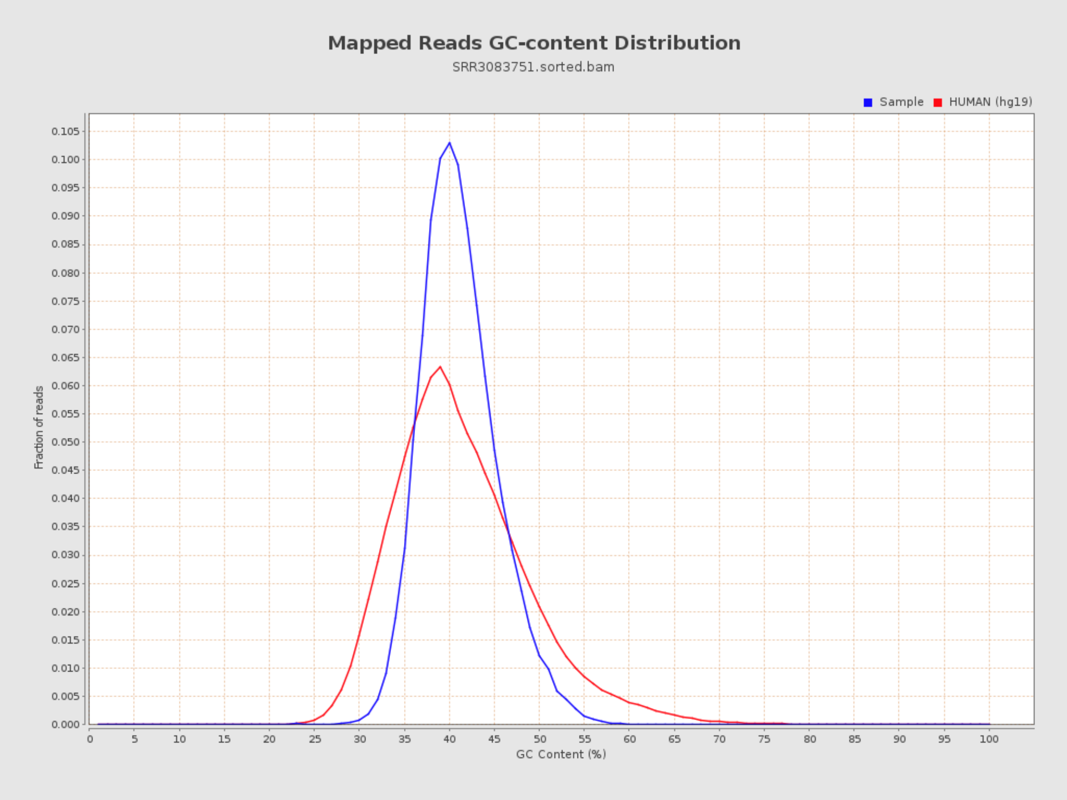
7. Results : Duplication Rate Histogram



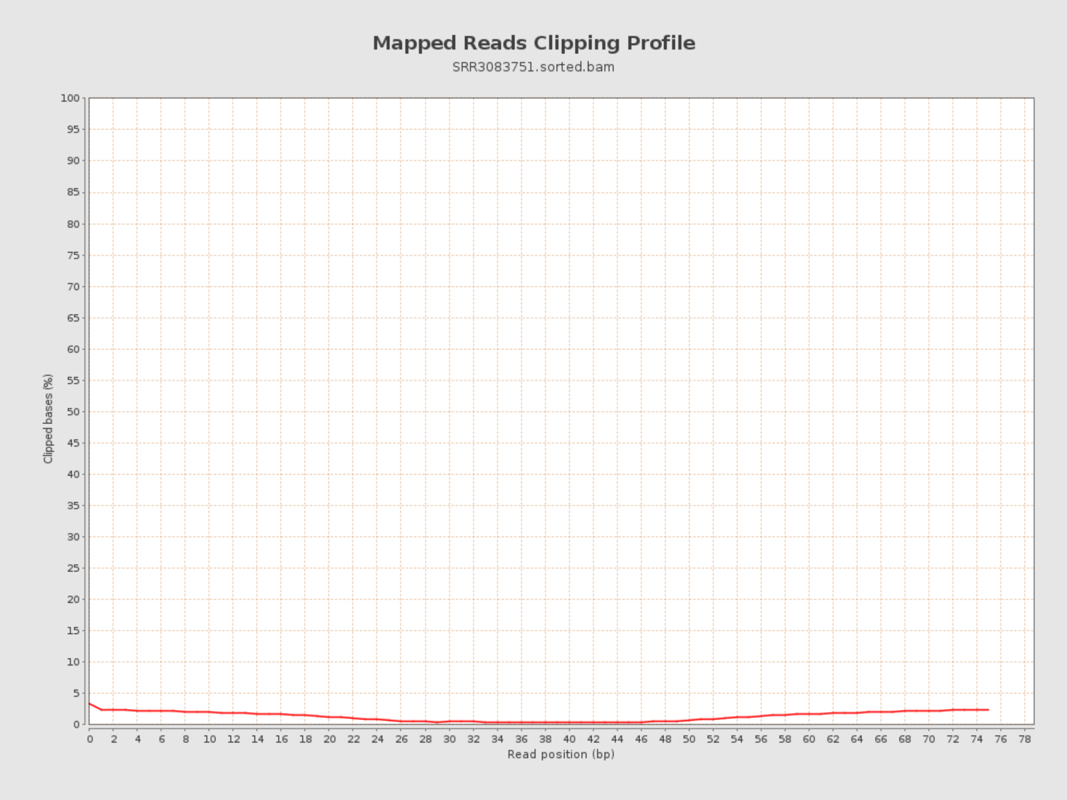
8. Results : Mapped Reads Nucleotide Content



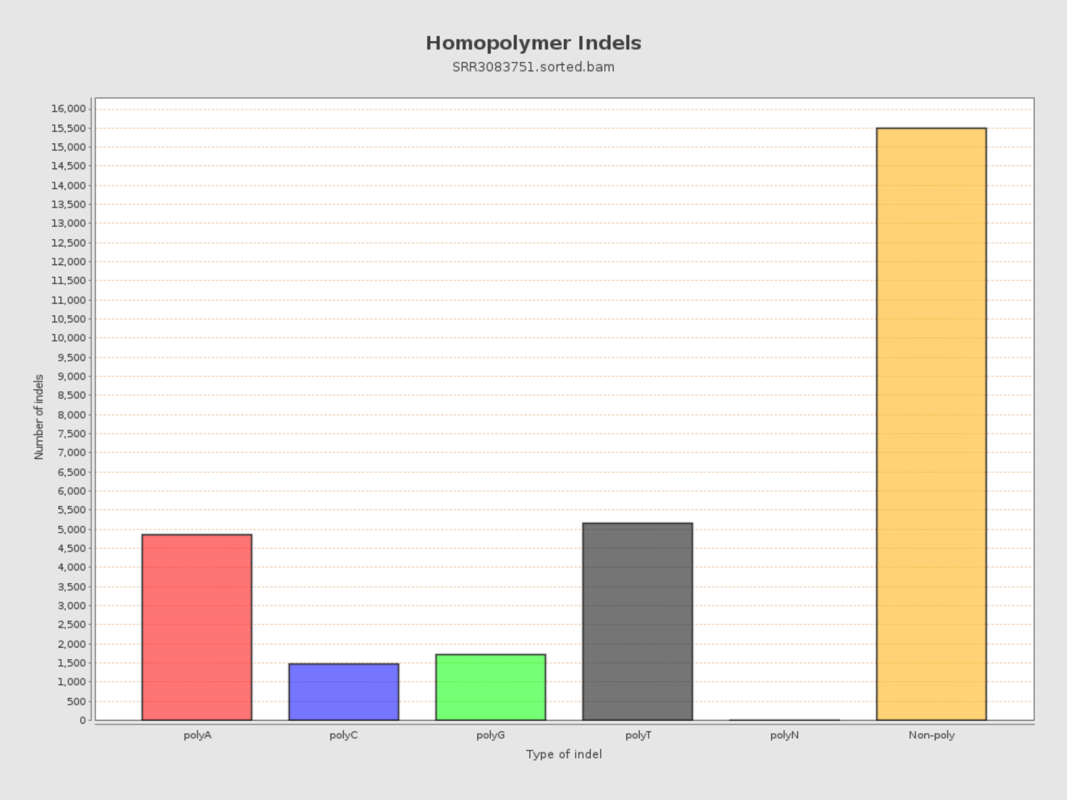
9. Results : Mapped Reads GC-content Distribution



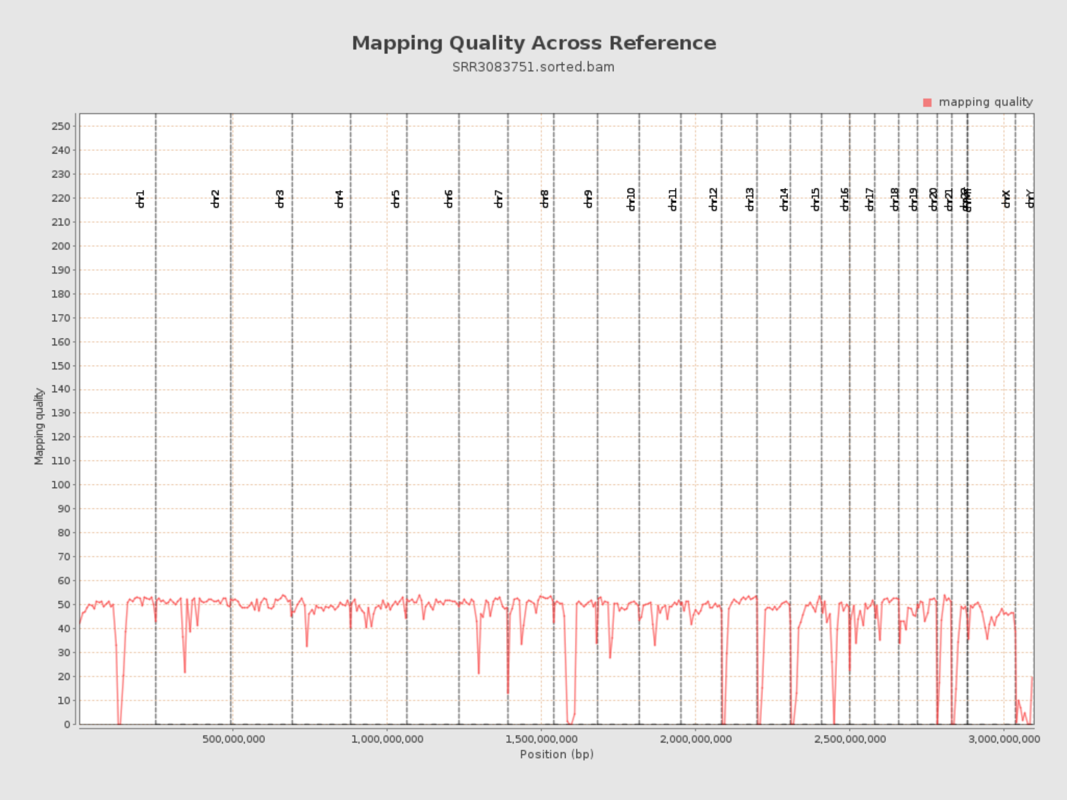
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram