Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:39:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083610.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_SRR3083610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:39:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,920,965
Mapped reads	1,730,532 / 90.09%
Unmapped reads	190,433 / 9.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,416 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	81,173 / 4.23%
Duplication rate	3.94%
Clipped reads	807,712 / 42.05%

2.2. ACGT Content

Number/percentage of A's	30,132,564 / 26.38%
Number/percentage of C's	21,592,158 / 18.9%
Number/percentage of T's	35,655,861 / 31.21%
Number/percentage of G's	26,860,247 / 23.51%
Number/percentage of N's	5,647 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0369

Standard Deviation	0.3053

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

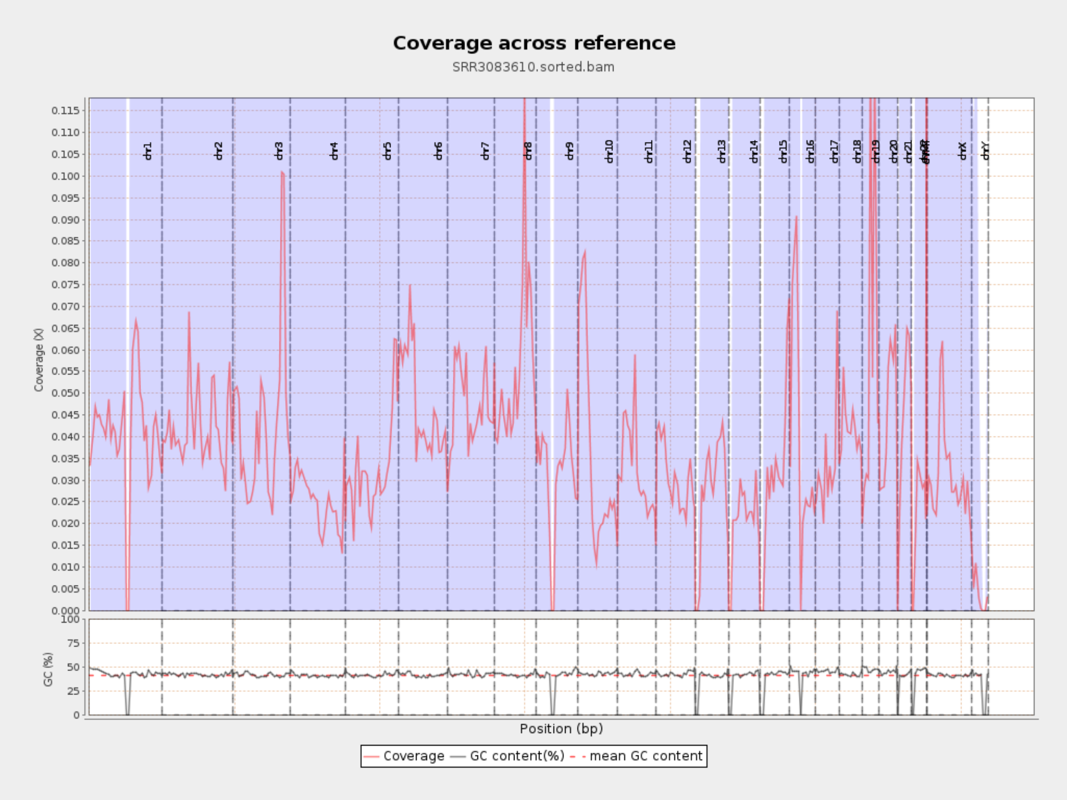
General error rate	0.71%
Mismatches	797,737
Insertions	8,423
Mapped reads with at least one insertion	0.48%
Deletions	25,799
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.82%

2.6. Chromosome stats

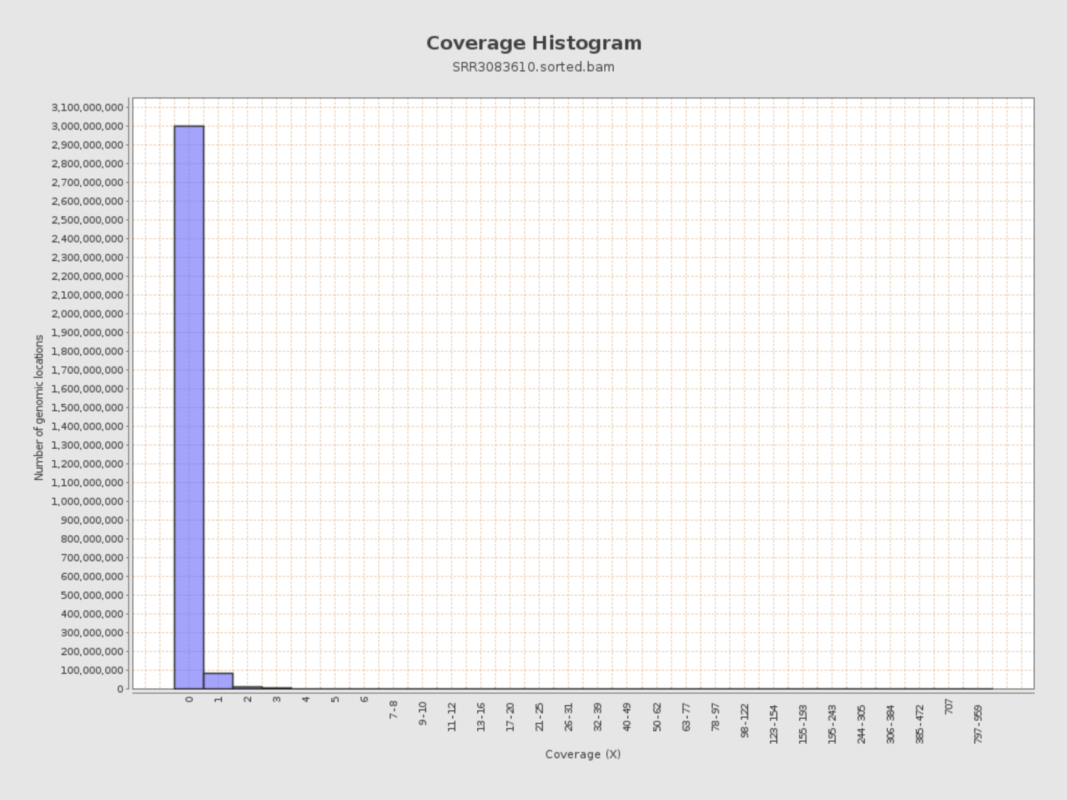
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10181105	0.0408	0.4488
chr2	243199373	10284972	0.0423	0.5008
chr3	198022430	8455111	0.0427	0.2413
chr4	191154276	4839310	0.0253	0.1891
chr5	180915260	5863653	0.0324	0.2106
chr6	171115067	8082677	0.0472	0.2947
chr7	159138663	7532106	0.0473	0.4338

chr8	146364022	8231659	0.0562	0.3176
chr9	141213431	4422794	0.0313	0.2518
chr10	135534747	4970606	0.0367	0.2518
chr11	135006516	4393143	0.0325	0.2516
chr12	133851895	4089709	0.0306	0.2033
chr13	115169878	3119208	0.0271	0.1913
chr14	107349540	2233837	0.0208	0.1699
chr15	102531392	3066681	0.0299	0.2113
chr16	90354753	3663513	0.0405	0.2433
chr17	81195210	2802772	0.0345	0.2206
chr18	78077248	3282954	0.042	0.4129
chr19	59128983	3579333	0.0605	0.3776
chr20	63025520	2892771	0.0459	0.2549
chr21	48129895	2095713	0.0435	0.2481
chr22	51304566	1112593	0.0217	0.1726
chrMT	16571	3874	0.2338	0.5775
chrX	155270560	4859127	0.0313	0.2189
chrY	59373566	228917	0.0039	0.0857

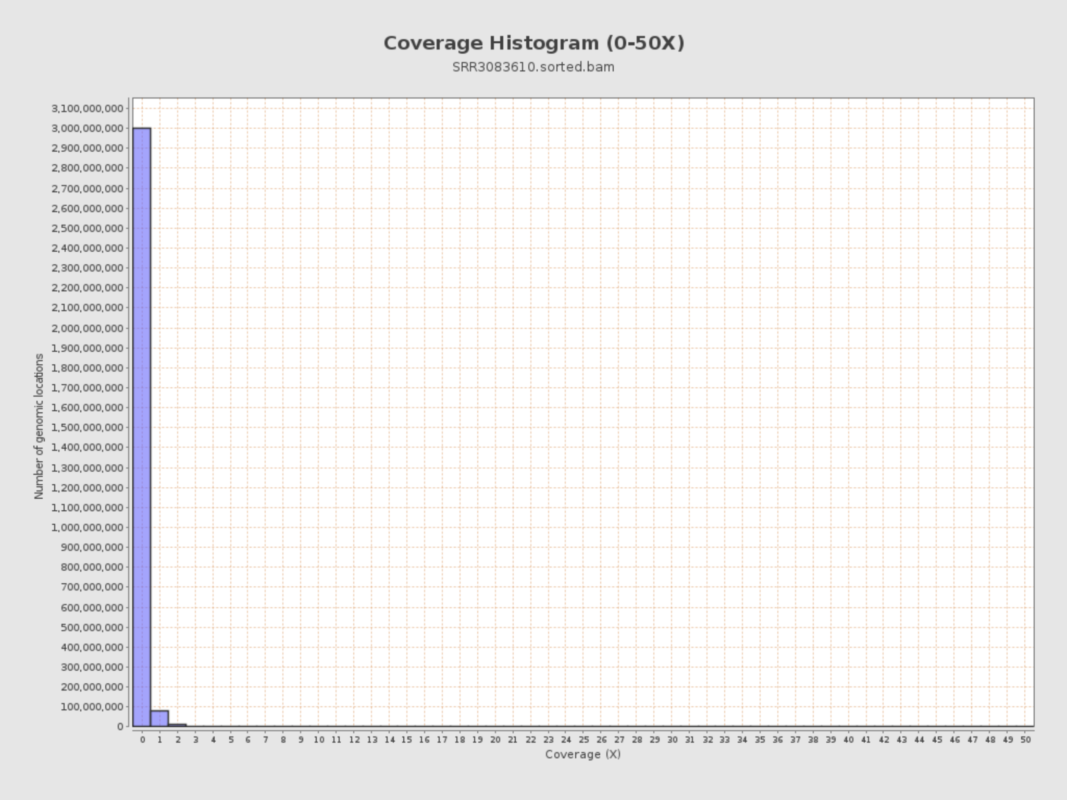
3. Results : Coverage across reference



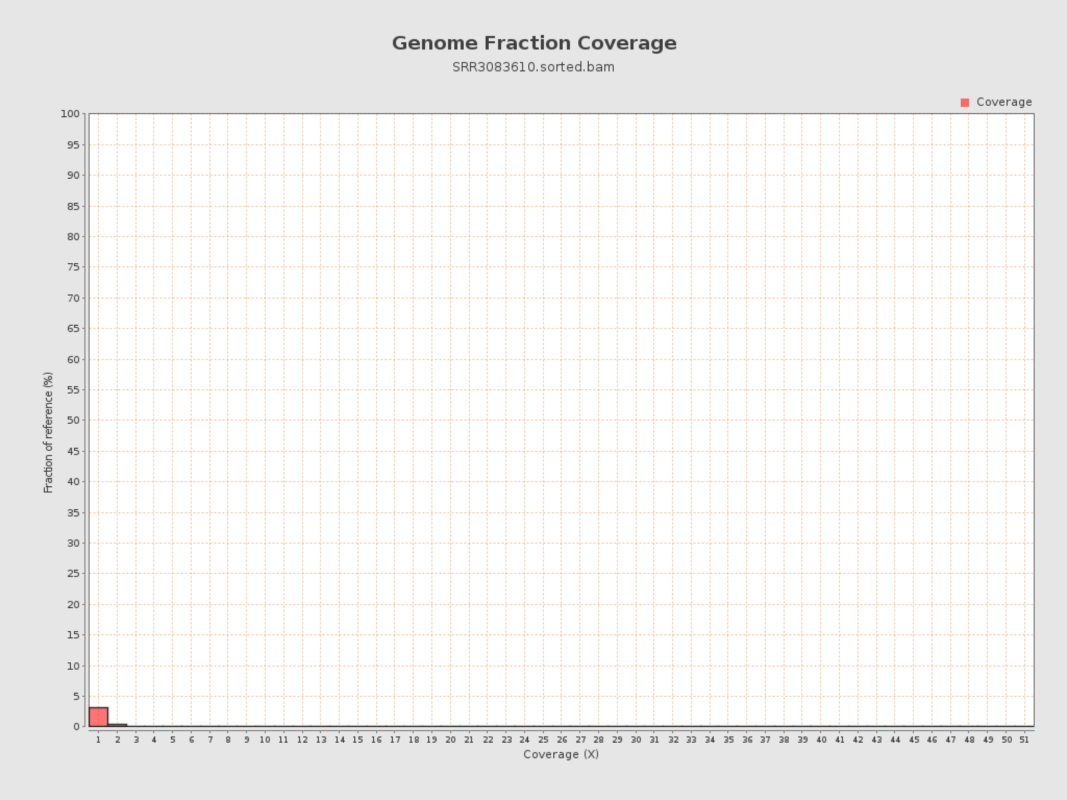
4. Results : Coverage Histogram



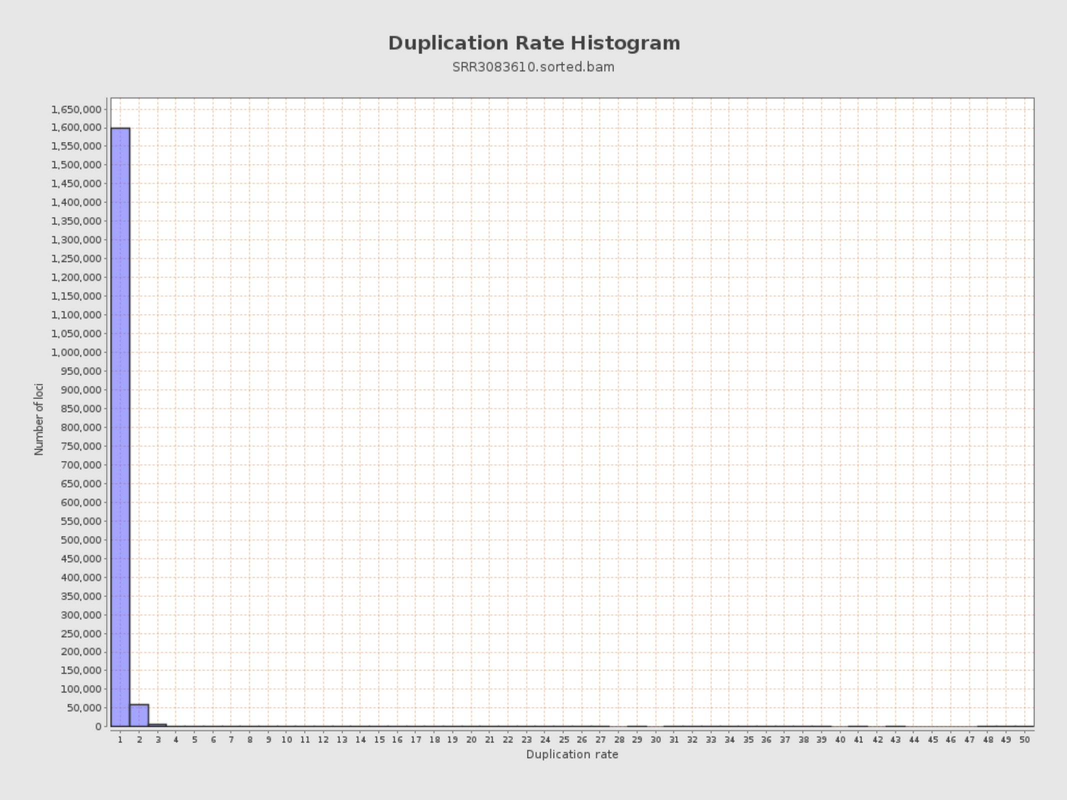
5. Results : Coverage Histogram (0-50X)



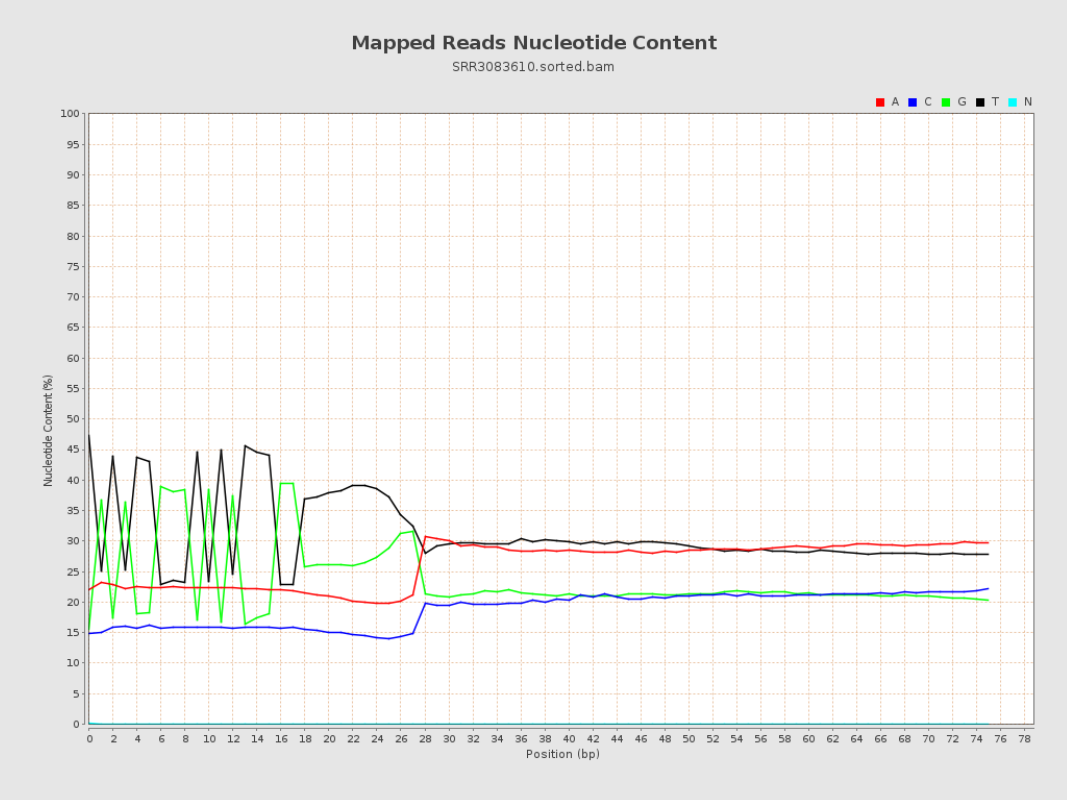
6. Results : Genome Fraction Coverage



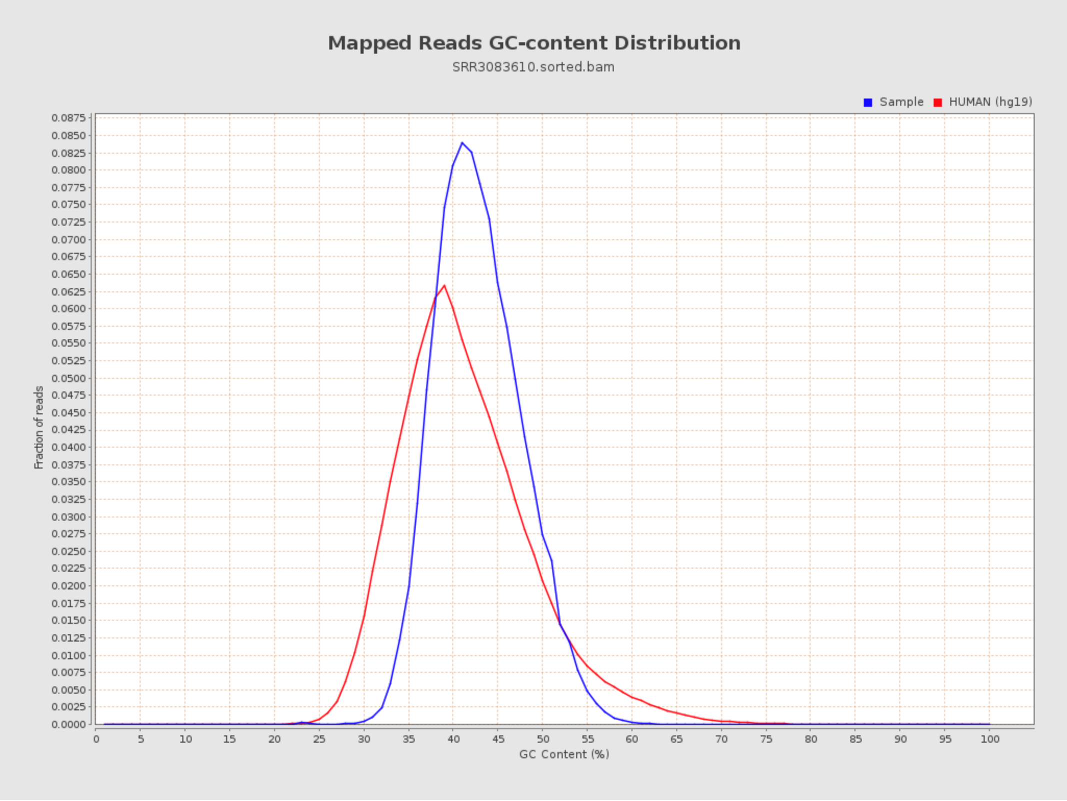
7. Results : Duplication Rate Histogram



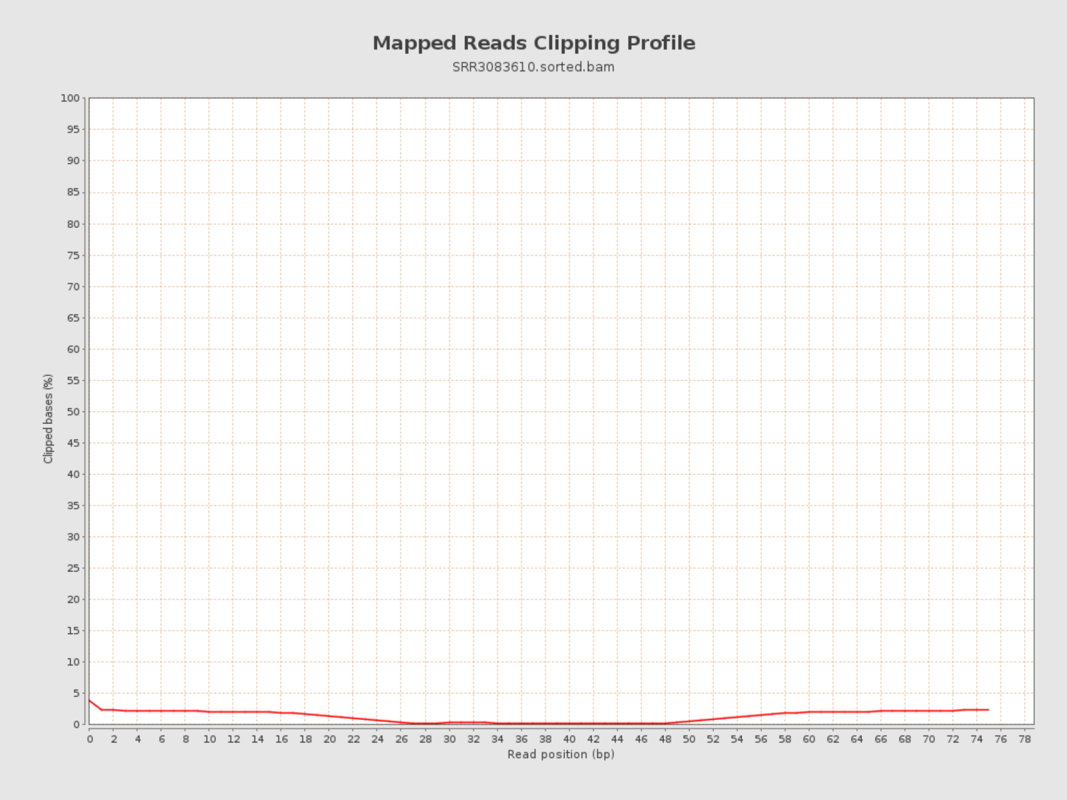
8. Results : Mapped Reads Nucleotide Content



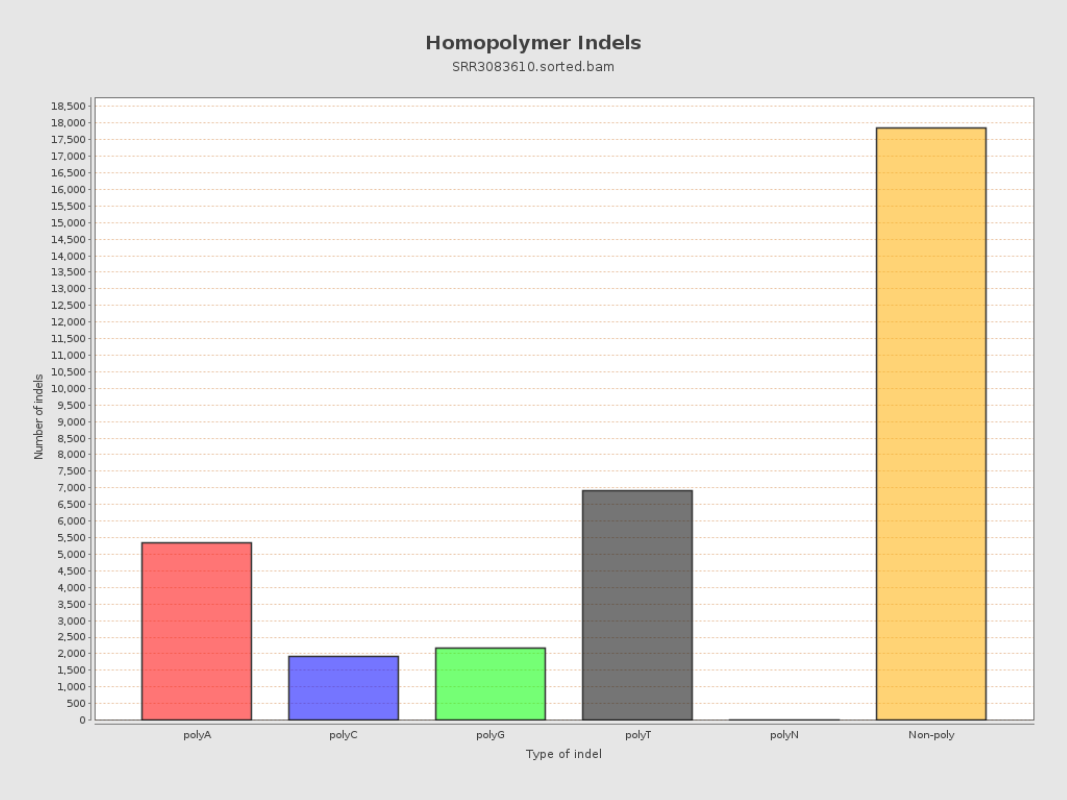
9. Results : Mapped Reads GC-content Distribution



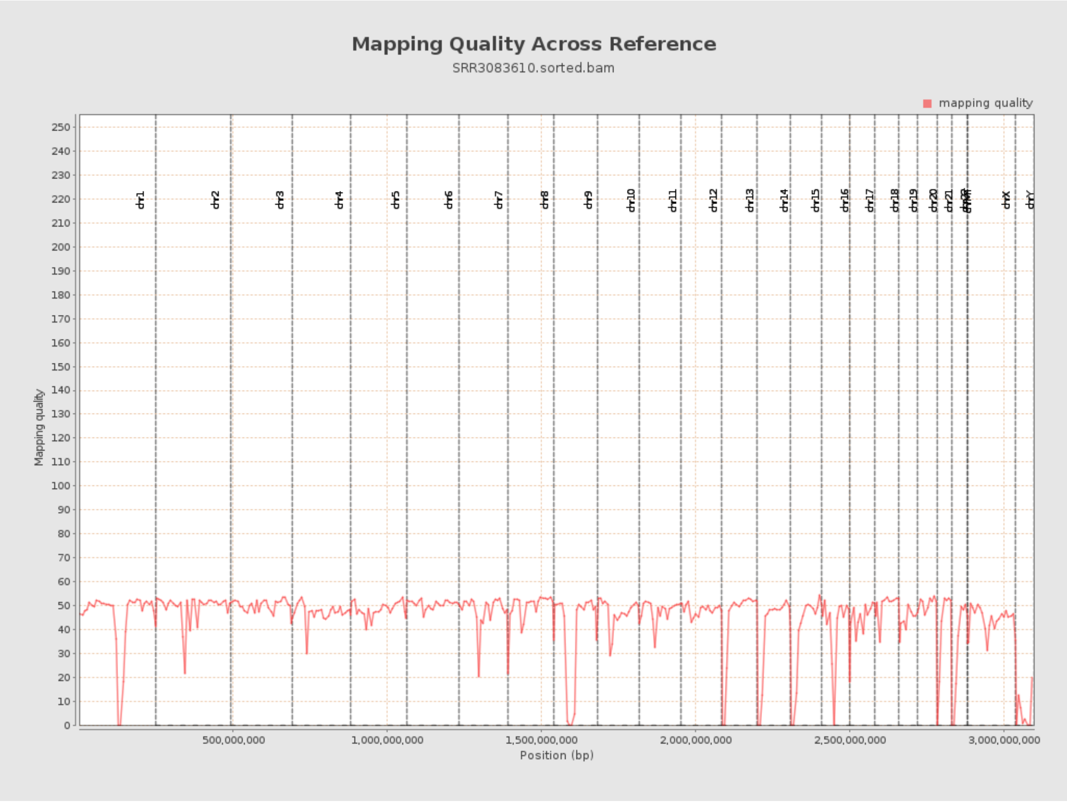
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram