Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:09:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083650.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_SRR3083650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:09:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,541,932
Mapped reads	1,143,485 / 74.16%
Unmapped reads	398,447 / 25.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,683 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	24,086 / 1.56%
Duplication rate	1.61%
Clipped reads	611,262 / 39.64%

2.2. ACGT Content

Number/percentage of A's	22,367,564 / 30.49%
Number/percentage of C's	13,714,962 / 18.69%
Number/percentage of T's	21,144,987 / 28.82%
Number/percentage of G's	16,137,139 / 21.99%
Number/percentage of N's	4,342 / 0.01%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2372

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

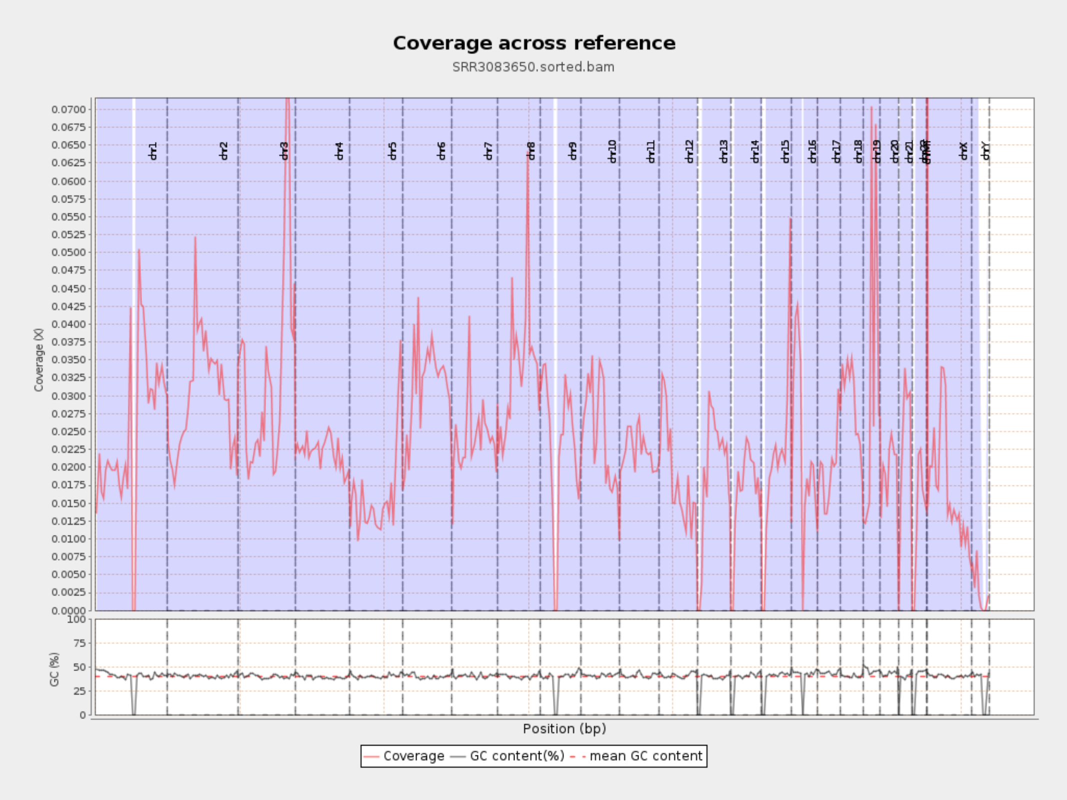
General error rate	0.95%
Mismatches	688,812
Insertions	5,543
Mapped reads with at least one insertion	0.48%
Deletions	15,575
Mapped reads with at least one deletion	1.35%
Homopolymer indels	45.37%

2.6. Chromosome stats

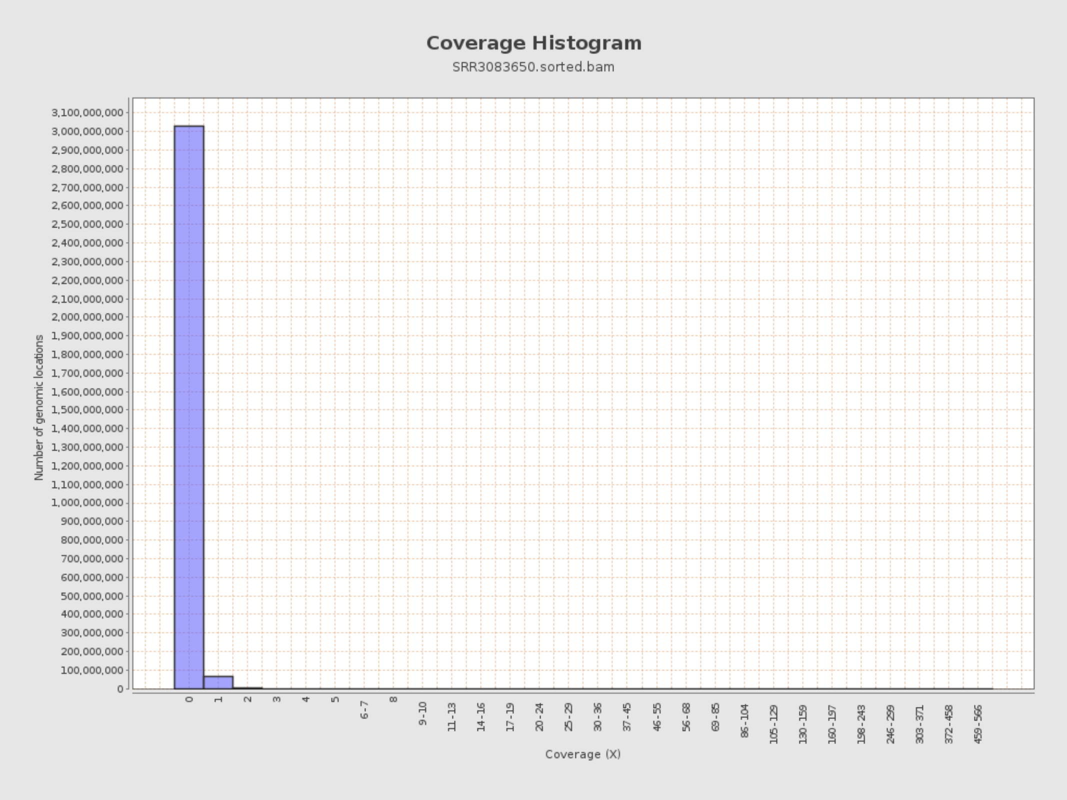
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6245688	0.0251	0.507
chr2	243199373	7273197	0.0299	0.2358
chr3	198022430	6480218	0.0327	0.1893
chr4	191154276	4230097	0.0221	0.1564
chr5	180915260	2951518	0.0163	0.1333
chr6	171115067	5358102	0.0313	0.2111
chr7	159138663	3854187	0.0242	0.2701

chr8	146364022	4989736	0.0341	0.2943
chr9	141213431	3273245	0.0232	0.1826
chr10	135534747	3369473	0.0249	0.2095
chr11	135006516	3009331	0.0223	0.1736
chr12	133851895	2530289	0.0189	0.1451
chr13	115169878	2239578	0.0194	0.1448
chr14	107349540	1748781	0.0163	0.1345
chr15	102531392	2133144	0.0208	0.1509
chr16	90354753	2029893	0.0225	0.1612
chr17	81195210	1609817	0.0198	0.1517
chr18	78077248	2315013	0.0297	0.3151
chr19	59128983	1891903	0.032	0.332
chr20	63025520	1228557	0.0195	0.1467
chr21	48129895	1116537	0.0232	0.1605
chr22	51304566	690674	0.0135	0.1205
chrMT	16571	18219	1.0995	1.2274
chrX	155270560	2648880	0.0171	0.1448
chrY	59373566	157549	0.0027	0.0669

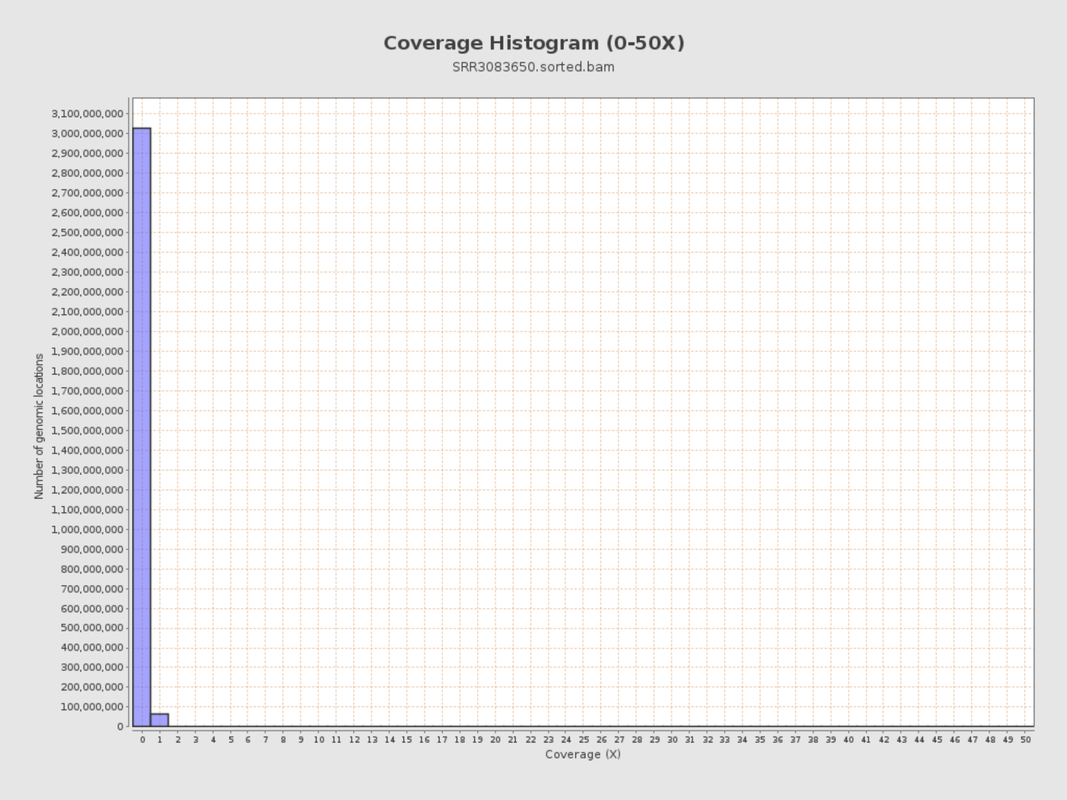
3. Results : Coverage across reference



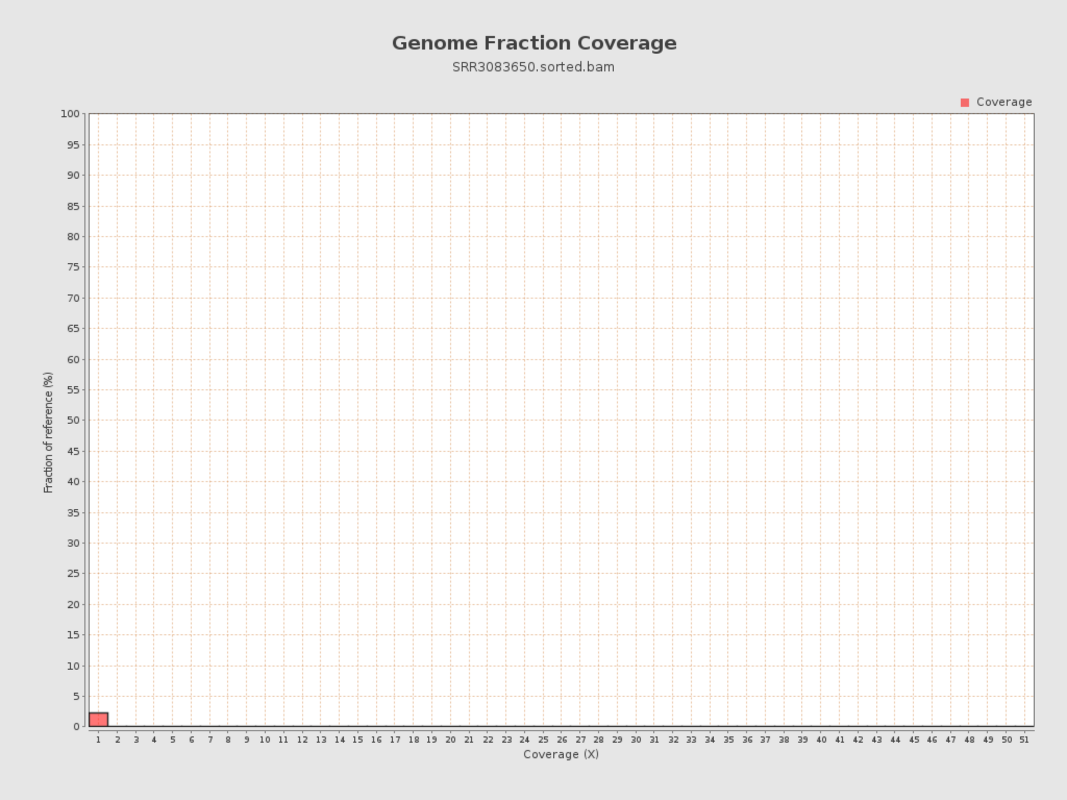
4. Results : Coverage Histogram



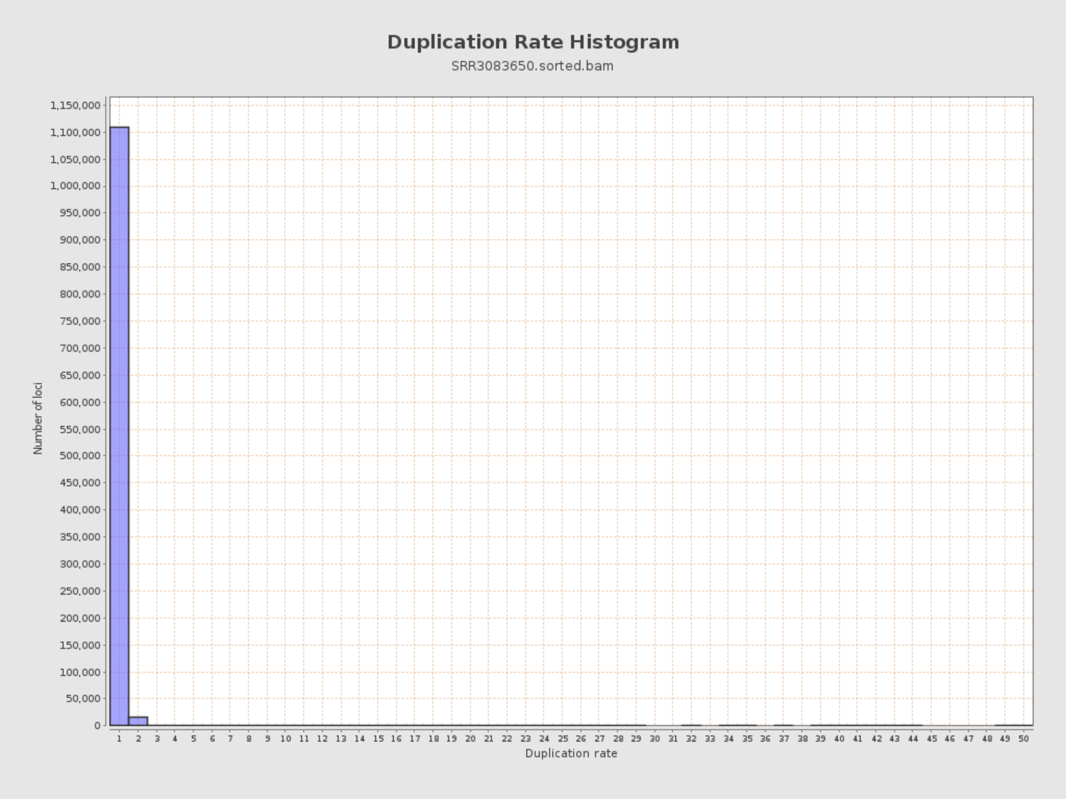
5. Results : Coverage Histogram (0-50X)



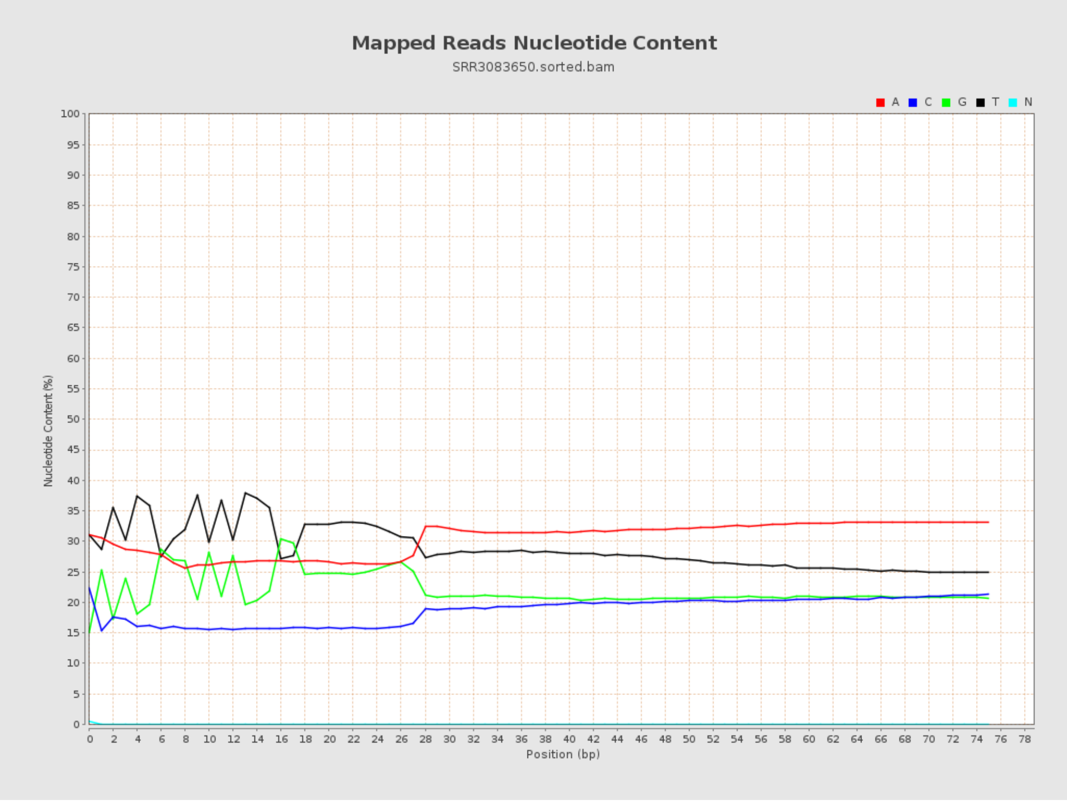
6. Results : Genome Fraction Coverage



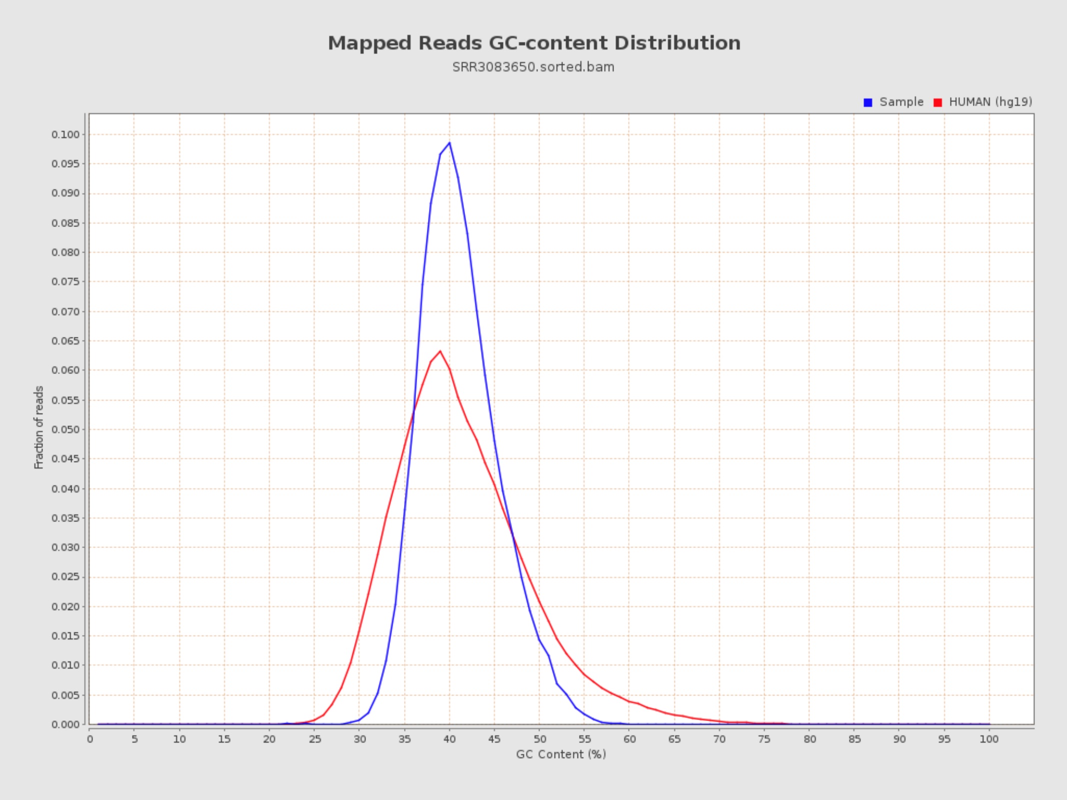
7. Results : Duplication Rate Histogram



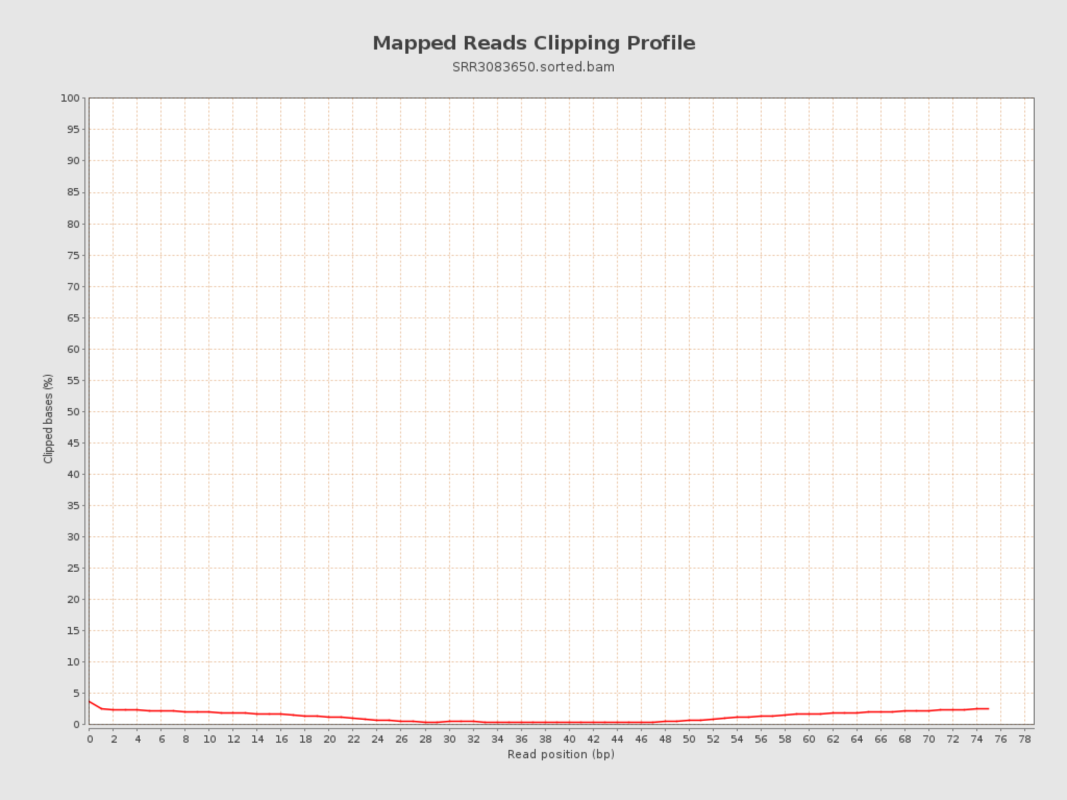
8. Results : Mapped Reads Nucleotide Content



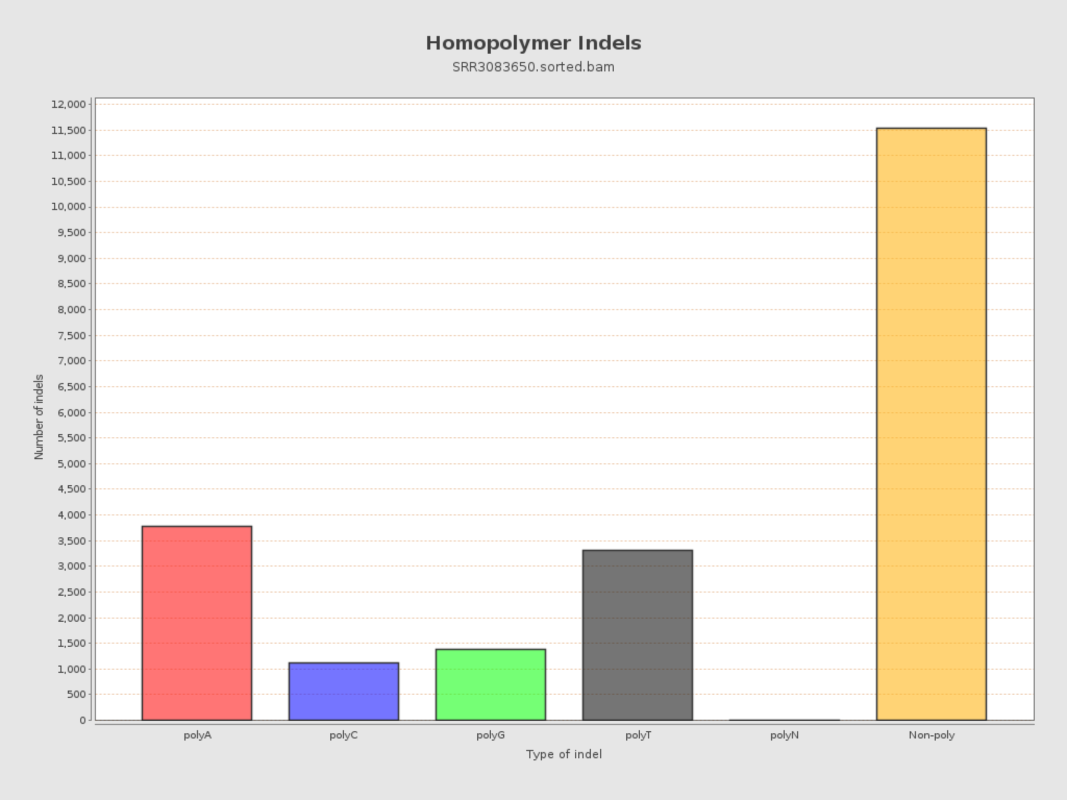
9. Results : Mapped Reads GC-content Distribution



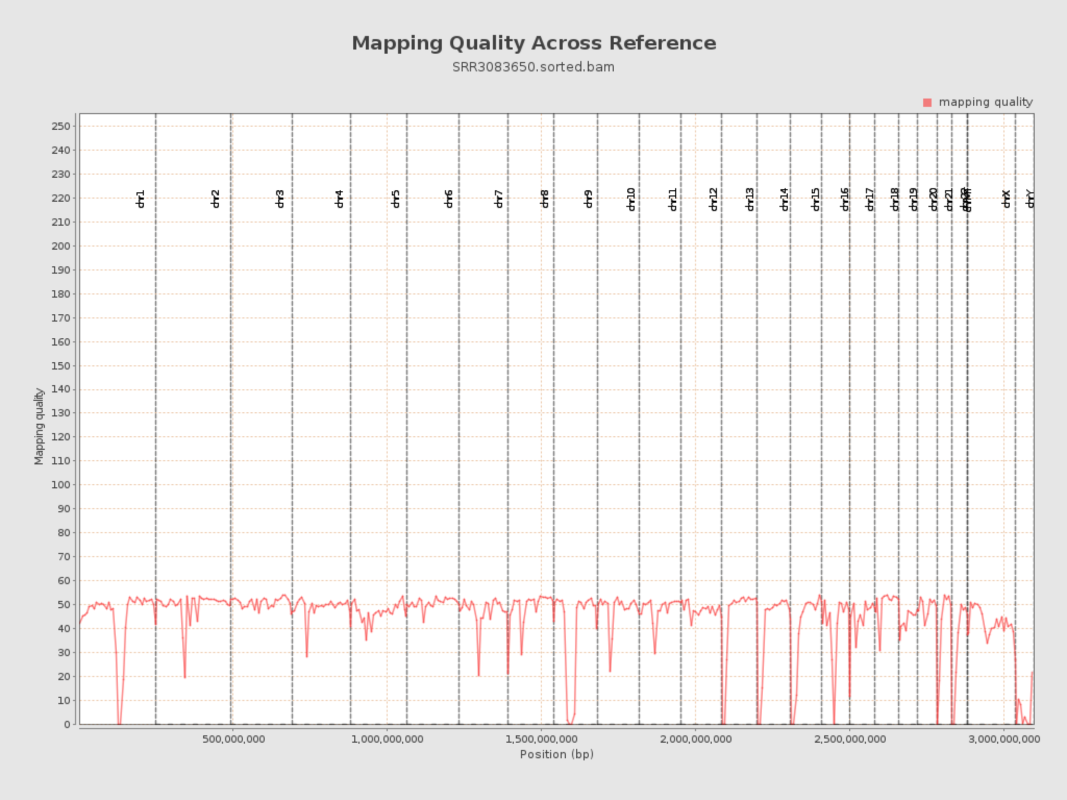
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram