Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:27:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083635.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_SRR3083635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:27:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,968,426
Mapped reads	2,382,459 / 80.26%
Unmapped reads	585,967 / 19.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,831 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	100,334 / 3.38%
Duplication rate	3.6%
Clipped reads	1,886,346 / 63.55%

2.2. ACGT Content

Number/percentage of A's	40,846,688 / 30.05%
Number/percentage of C's	27,577,649 / 20.29%
Number/percentage of T's	38,865,789 / 28.59%
Number/percentage of G's	28,626,214 / 21.06%
Number/percentage of N's	7,442 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.2985

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

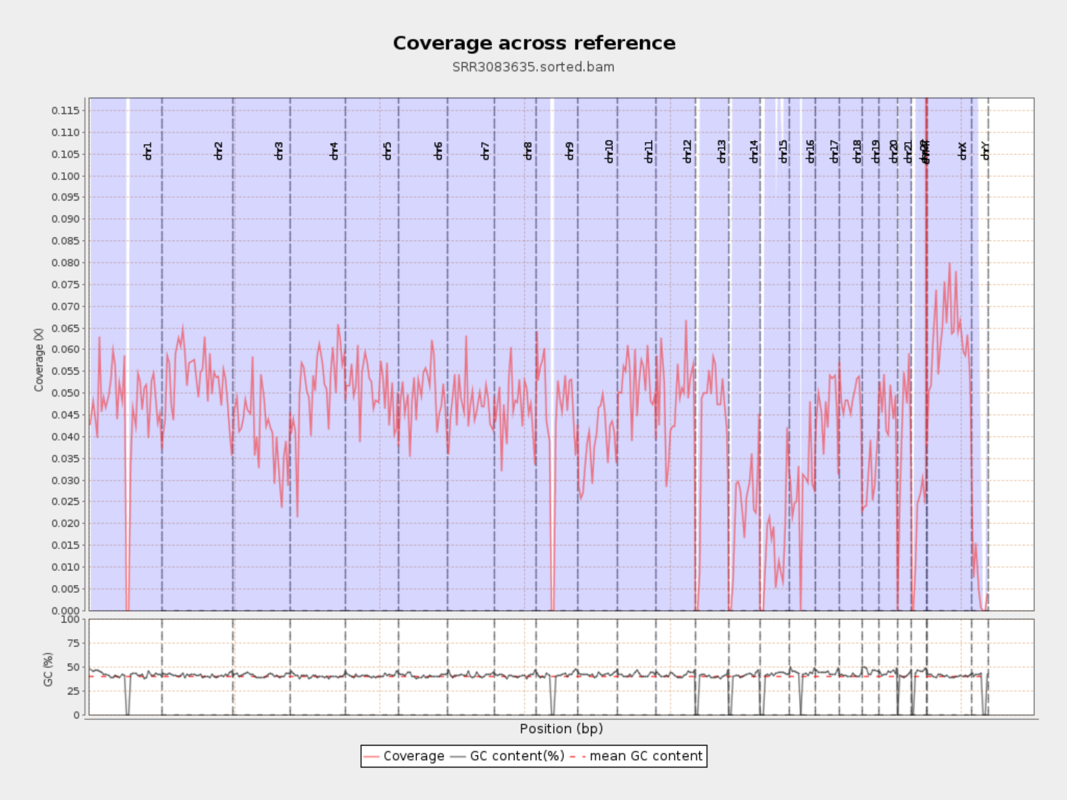
General error rate	0.81%
Mismatches	1,079,850
Insertions	8,769
Mapped reads with at least one insertion	0.37%
Deletions	25,119
Mapped reads with at least one deletion	1.05%
Homopolymer indels	45.46%

2.6. Chromosome stats

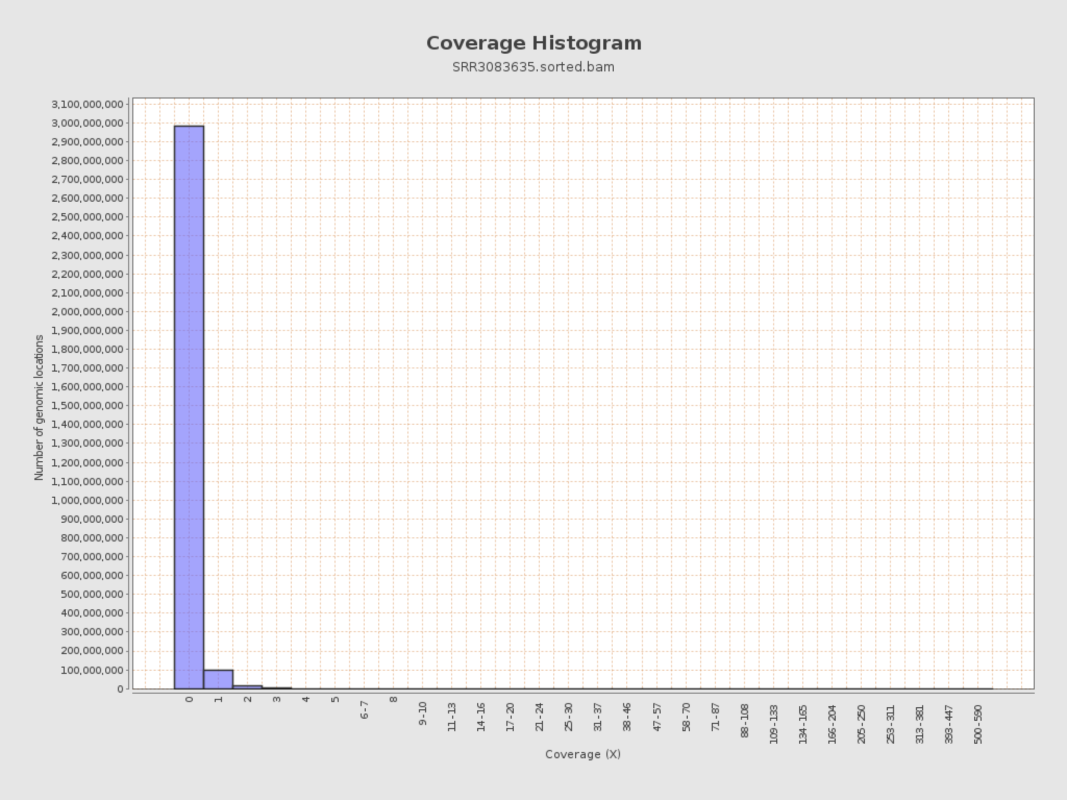
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11410355	0.0458	0.4374
chr2	243199373	12968058	0.0533	0.3091
chr3	198022430	8137750	0.0411	0.2324
chr4	191154276	9843095	0.0515	0.2701
chr5	180915260	9219254	0.051	0.2593
chr6	171115067	8445050	0.0494	0.2763
chr7	159138663	7595996	0.0477	0.4191

chr8	146364022	6822093	0.0466	0.4169
chr9	141213431	6172692	0.0437	0.2684
chr10	135534747	5188068	0.0383	0.2675
chr11	135006516	7066421	0.0523	0.2736
chr12	133851895	6558446	0.049	0.2581
chr13	115169878	4825504	0.0419	0.2355
chr14	107349540	2400032	0.0224	0.1854
chr15	102531392	1489776	0.0145	0.1412
chr16	90354753	2487007	0.0275	0.1964
chr17	81195210	3758962	0.0463	0.2535
chr18	78077248	3832647	0.0491	0.368
chr19	59128983	1823849	0.0308	0.3565
chr20	63025520	2924368	0.0464	0.2533
chr21	48129895	1910227	0.0397	0.2353
chr22	51304566	961262	0.0187	0.1542
chrMT	16571	47026	2.8378	2.2723
chrX	155270560	9740586	0.0627	0.3074
chrY	59373566	334206	0.0056	0.1049

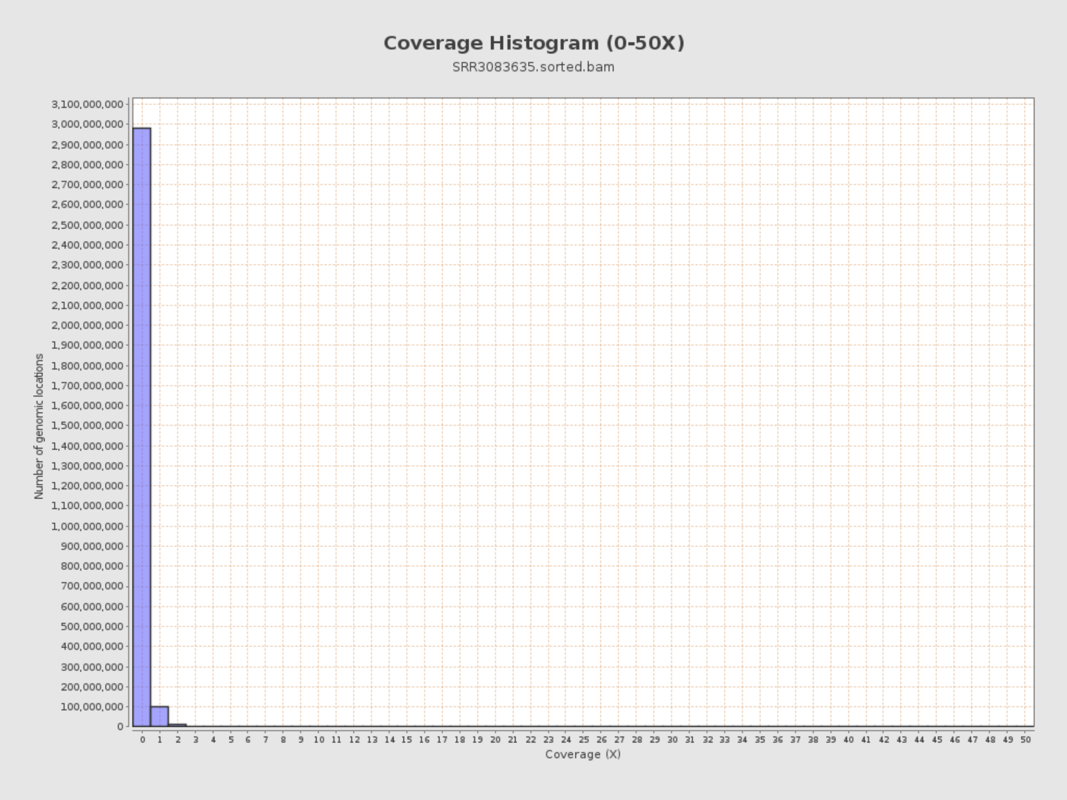
3. Results : Coverage across reference



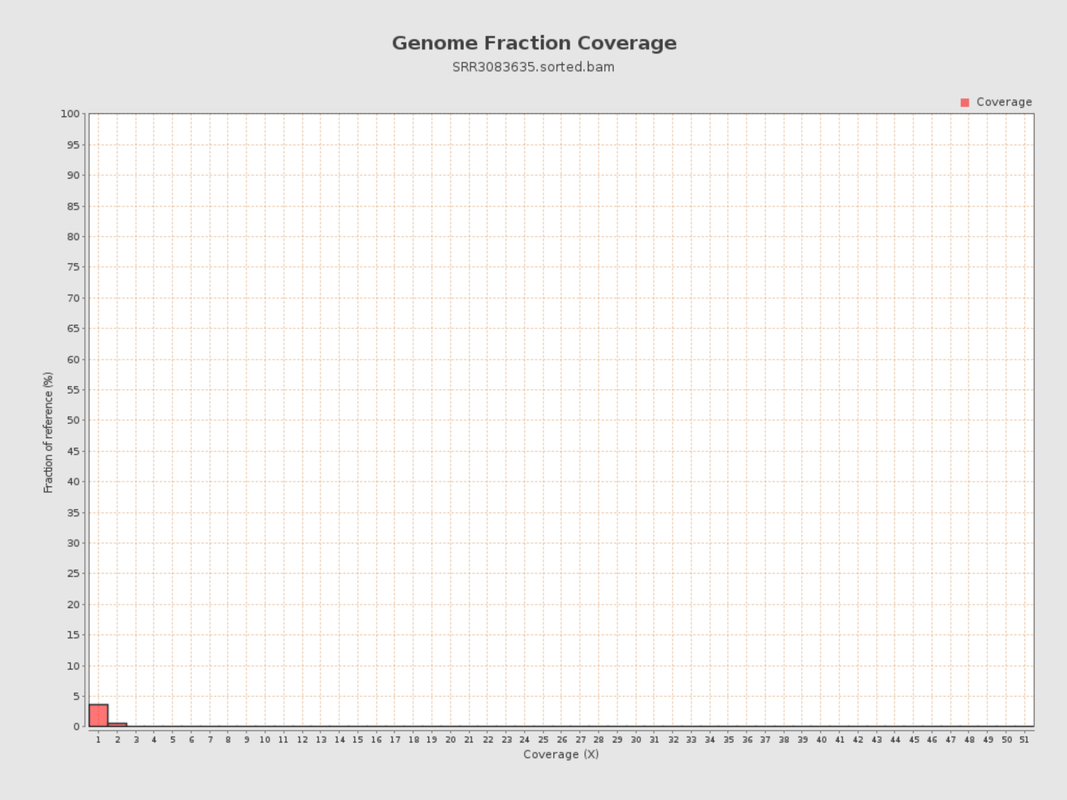
4. Results : Coverage Histogram



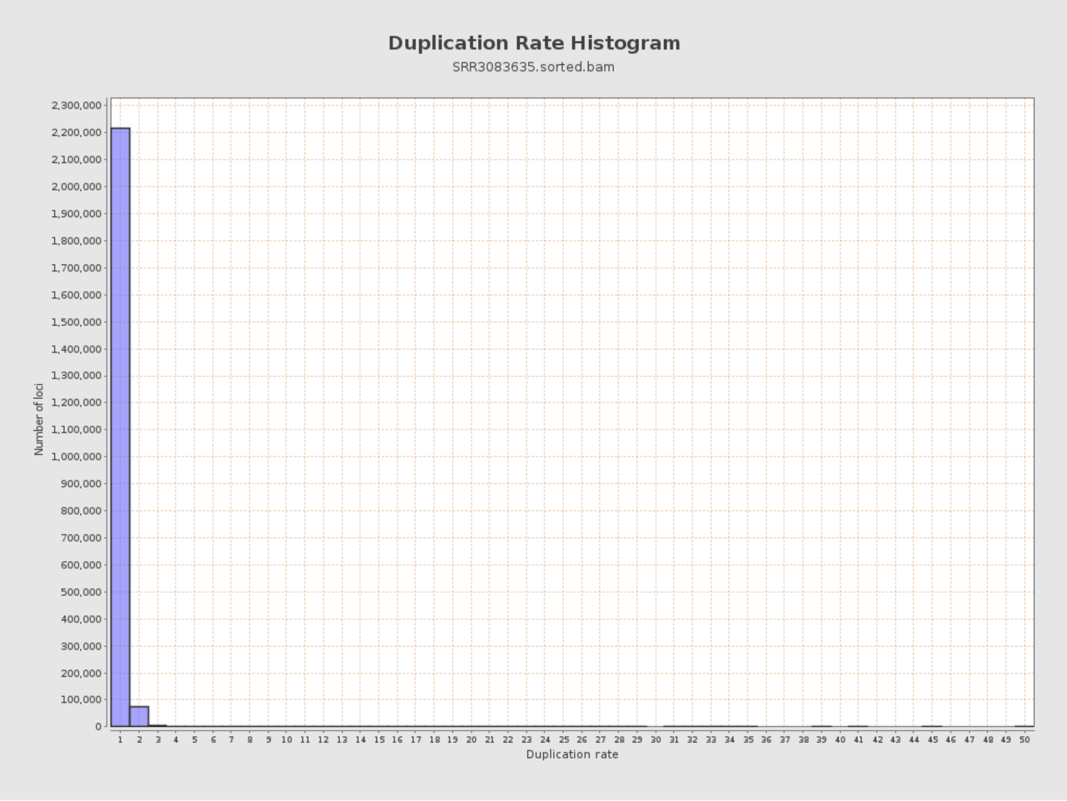
5. Results : Coverage Histogram (0-50X)



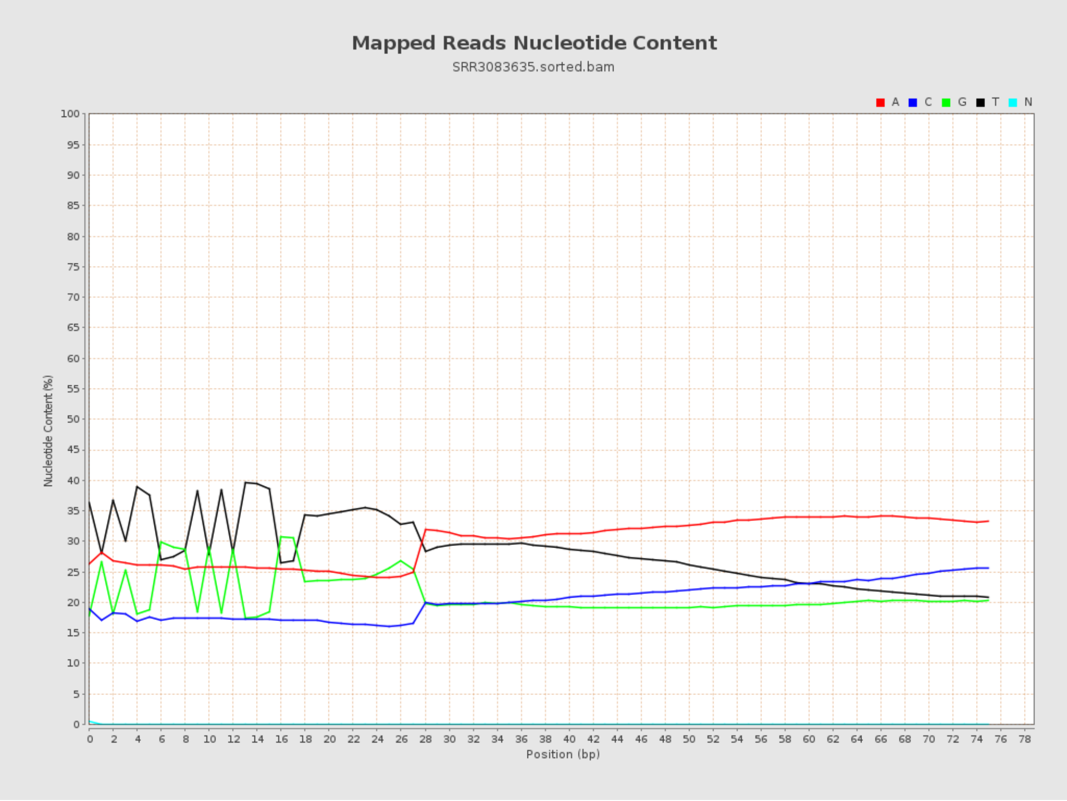
6. Results : Genome Fraction Coverage



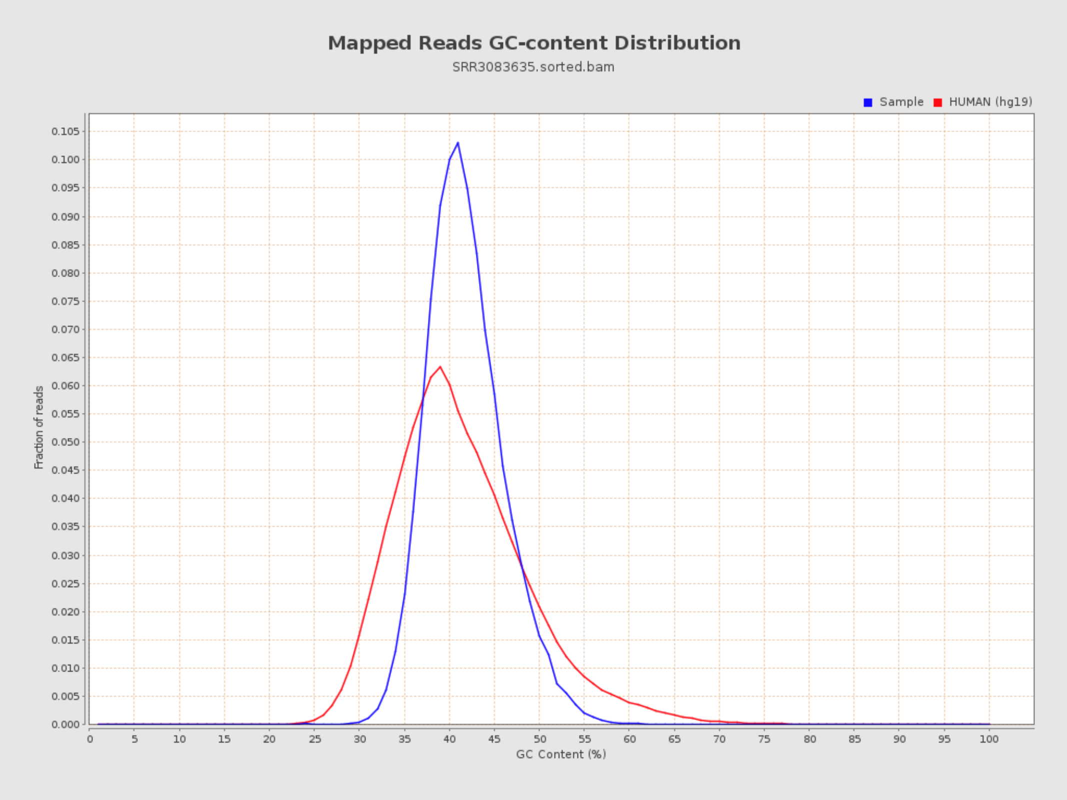
7. Results : Duplication Rate Histogram



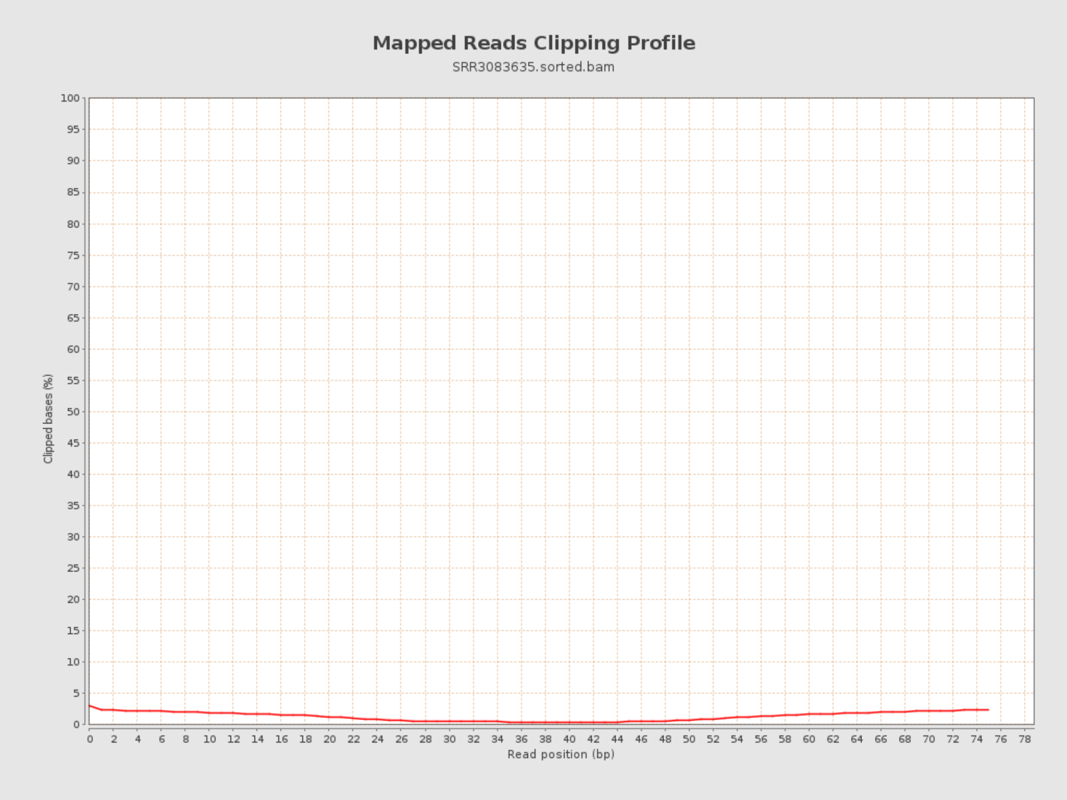
8. Results : Mapped Reads Nucleotide Content



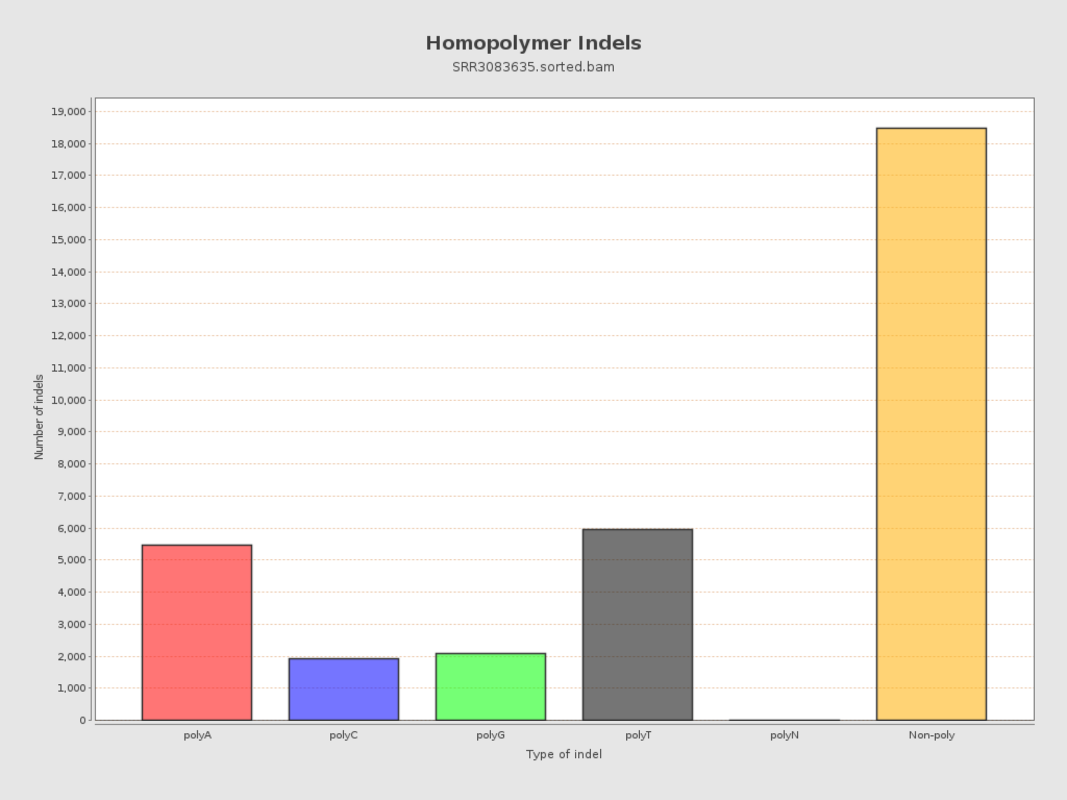
9. Results : Mapped Reads GC-content Distribution



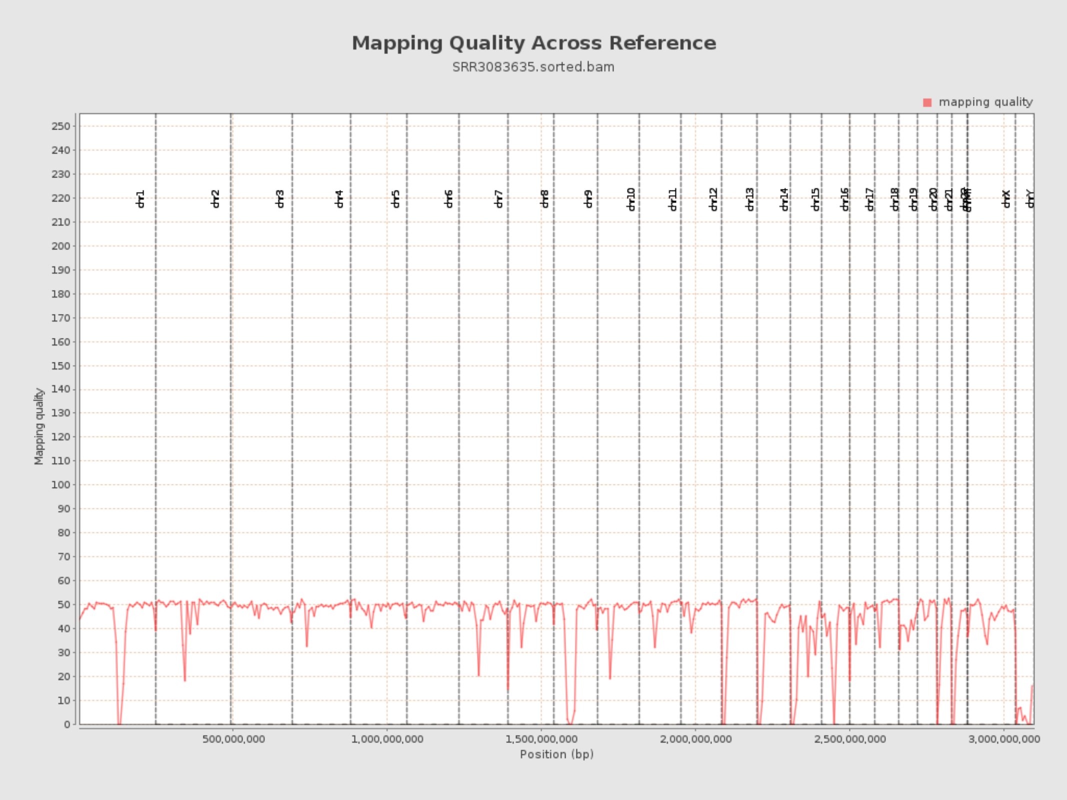
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram