Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083657.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_SRR3083657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083657.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:30:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,527,871
Mapped reads	1,255,608 / 82.18%
Unmapped reads	272,263 / 17.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,475 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	33,106 / 2.17%
Duplication rate	1.87%
Clipped reads	762,506 / 49.91%

2.2. ACGT Content

Number/percentage of A's	23,586,325 / 30%
Number/percentage of C's	15,047,909 / 19.14%
Number/percentage of T's	22,924,992 / 29.15%
Number/percentage of G's	17,068,887 / 21.71%
Number/percentage of N's	5,096 / 0.01%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.3385

2.4. Mapping Quality

Mean Mapping Quality	42.7

2.5. Mismatches and indels

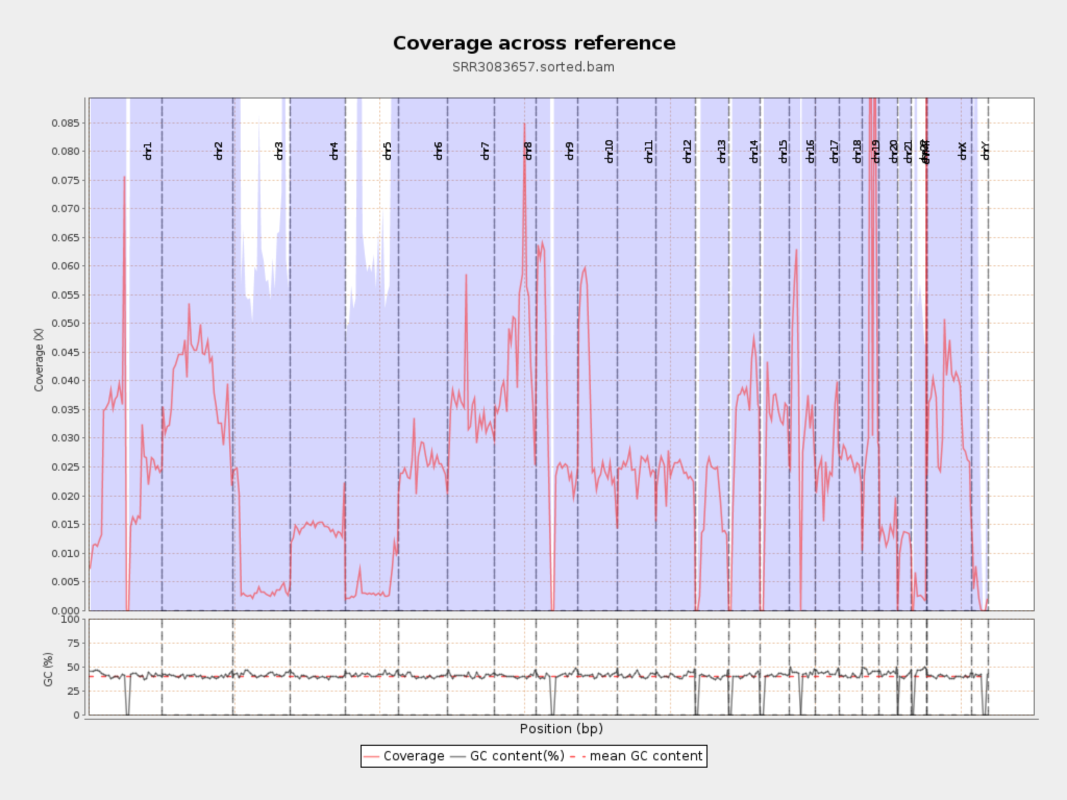
General error rate	0.86%
Mismatches	670,657
Insertions	5,781
Mapped reads with at least one insertion	0.46%
Deletions	17,029
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.71%

2.6. Chromosome stats

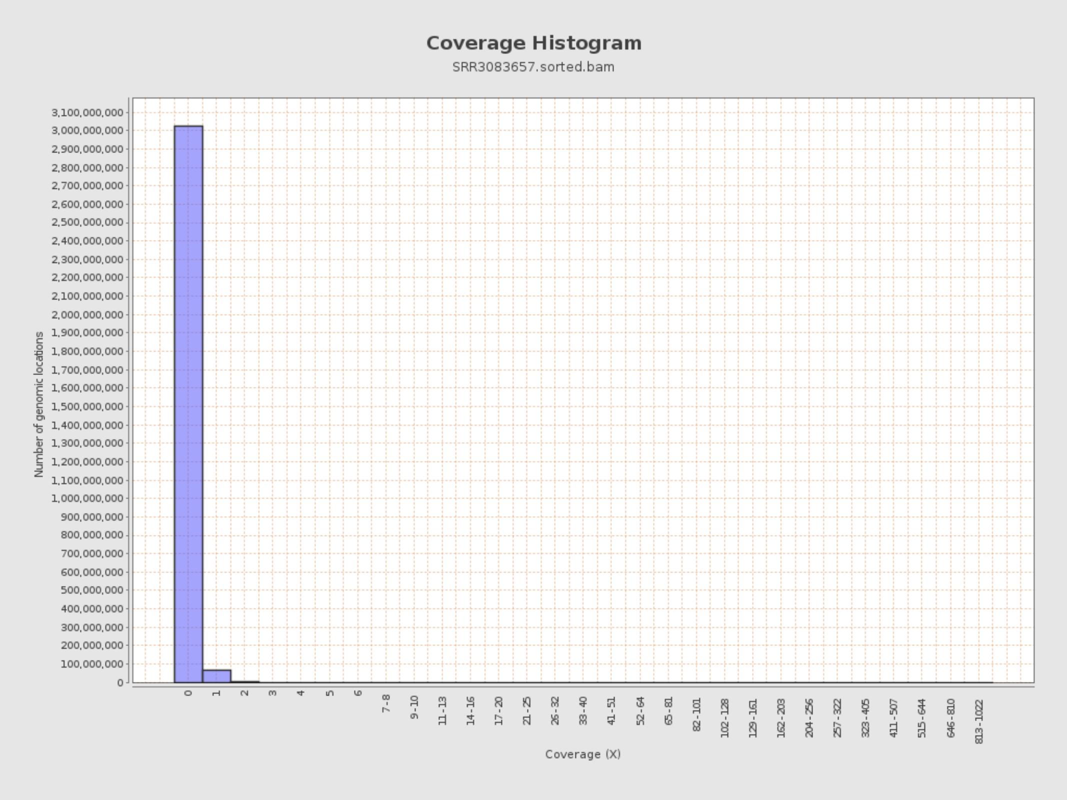
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6113410	0.0245	0.9138
chr2	243199373	9754083	0.0401	0.2552
chr3	198022430	1143458	0.0058	0.084
chr4	191154276	2784027	0.0146	0.128
chr5	180915260	717893	0.004	0.0724
chr6	171115067	4362038	0.0255	0.1873
chr7	159138663	5575784	0.035	0.4403

chr8	146364022	6711282	0.0459	0.2662
chr9	141213431	4334769	0.0307	0.2163
chr10	135534747	4578441	0.0338	0.238
chr11	135006516	3336783	0.0247	0.2082
chr12	133851895	3229214	0.0241	0.1647
chr13	115169878	1884910	0.0164	0.1345
chr14	107349540	3519125	0.0328	0.1939
chr15	102531392	2992539	0.0292	0.1806
chr16	90354753	3248115	0.0359	0.2107
chr17	81195210	2105119	0.0259	0.1797
chr18	78077248	2043383	0.0262	0.3646
chr19	59128983	3050646	0.0516	0.5549
chr20	63025520	881748	0.014	0.1267
chr21	48129895	539854	0.0112	0.1132
chr22	51304566	127422	0.0025	0.0719
chrMT	16571	3304	0.1994	0.5052
chrX	155270560	5442655	0.0351	0.2097
chrY	59373566	180718	0.003	0.0691

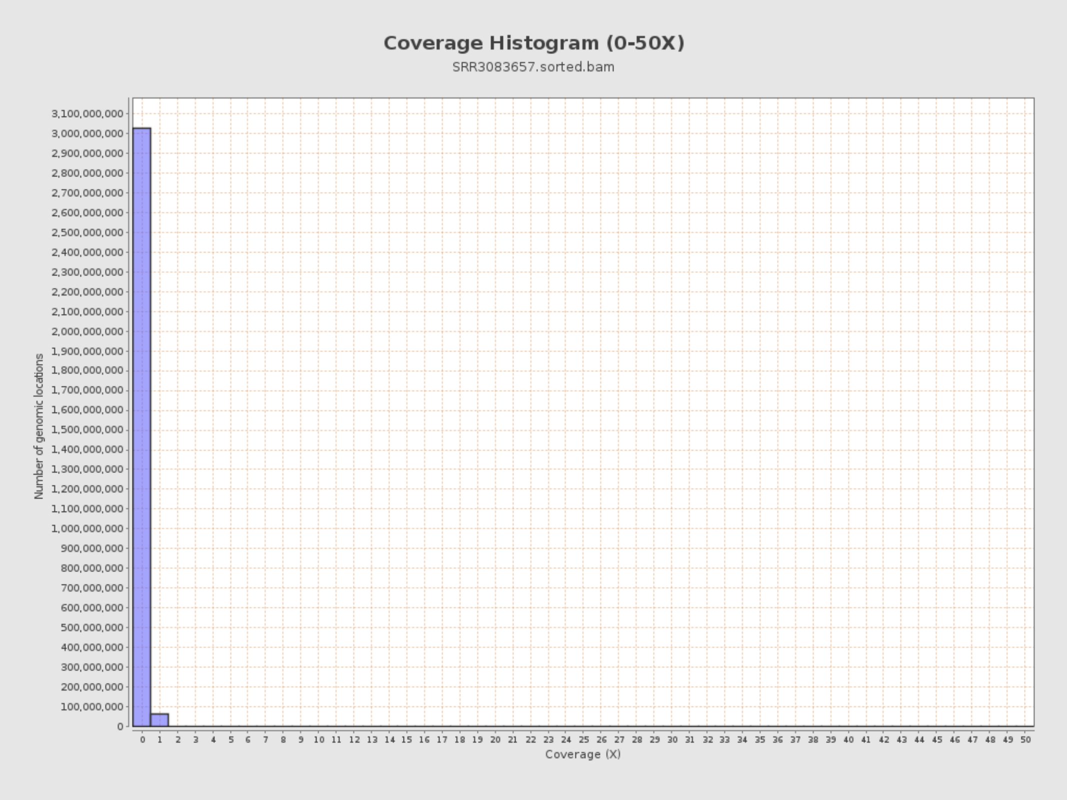
3. Results : Coverage across reference



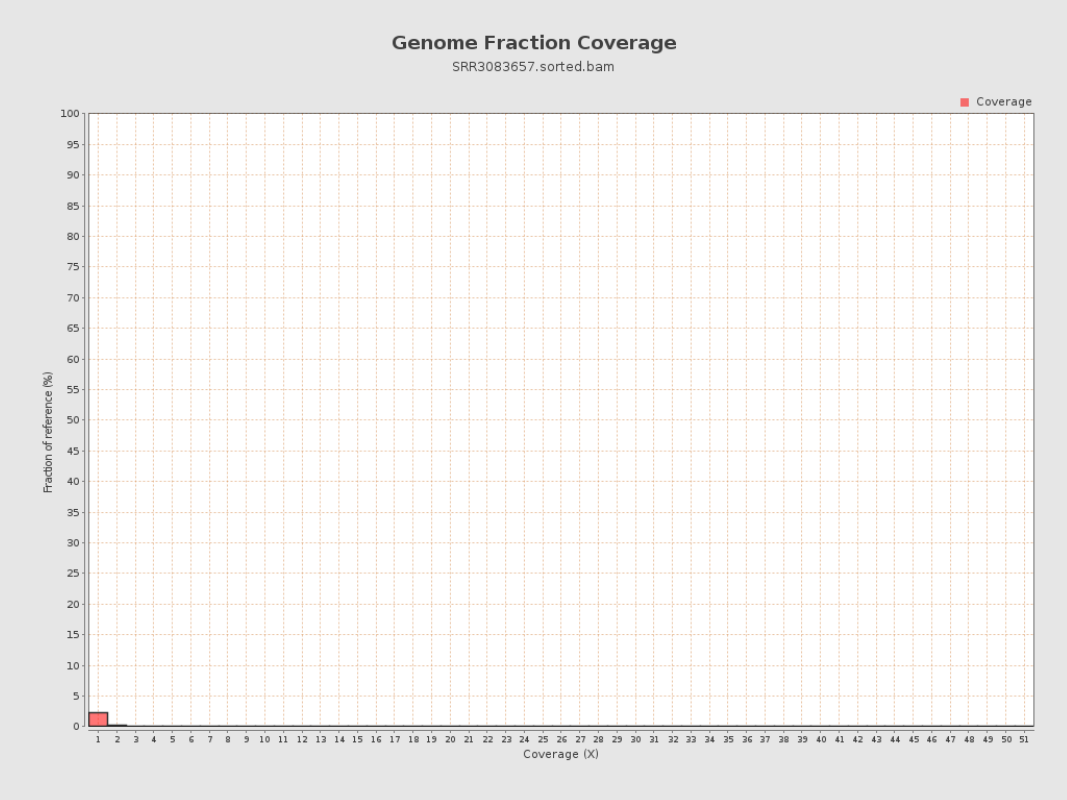
4. Results : Coverage Histogram



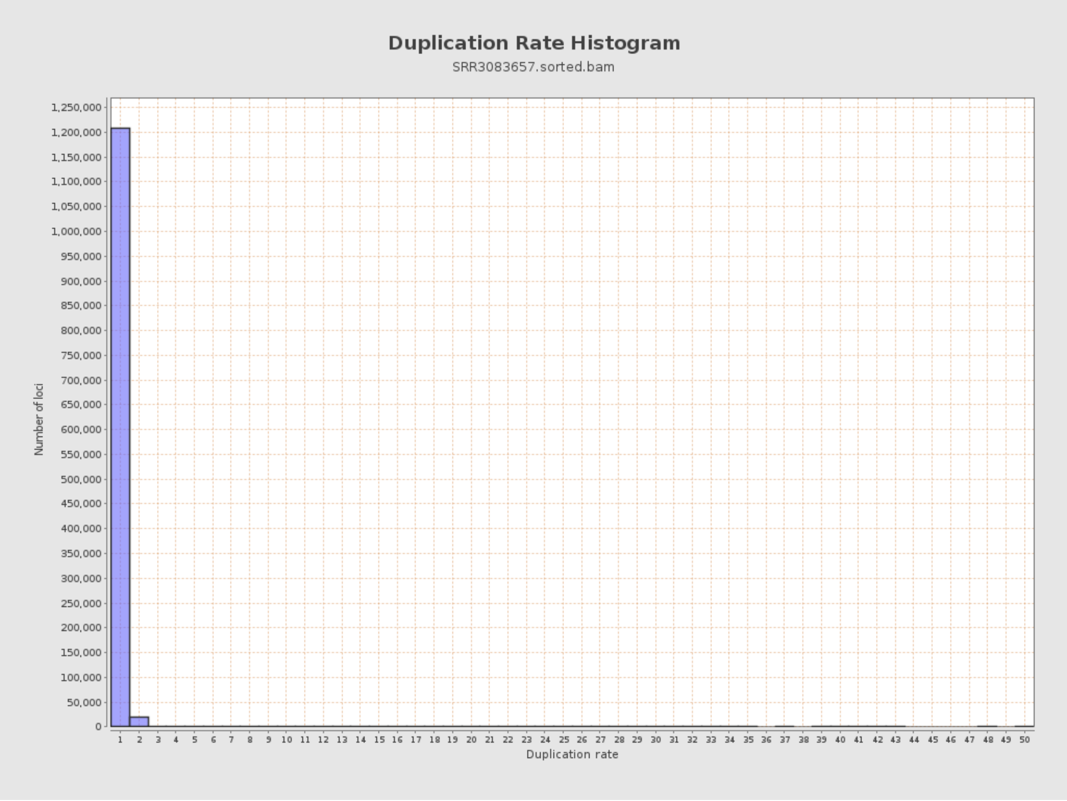
5. Results : Coverage Histogram (0-50X)



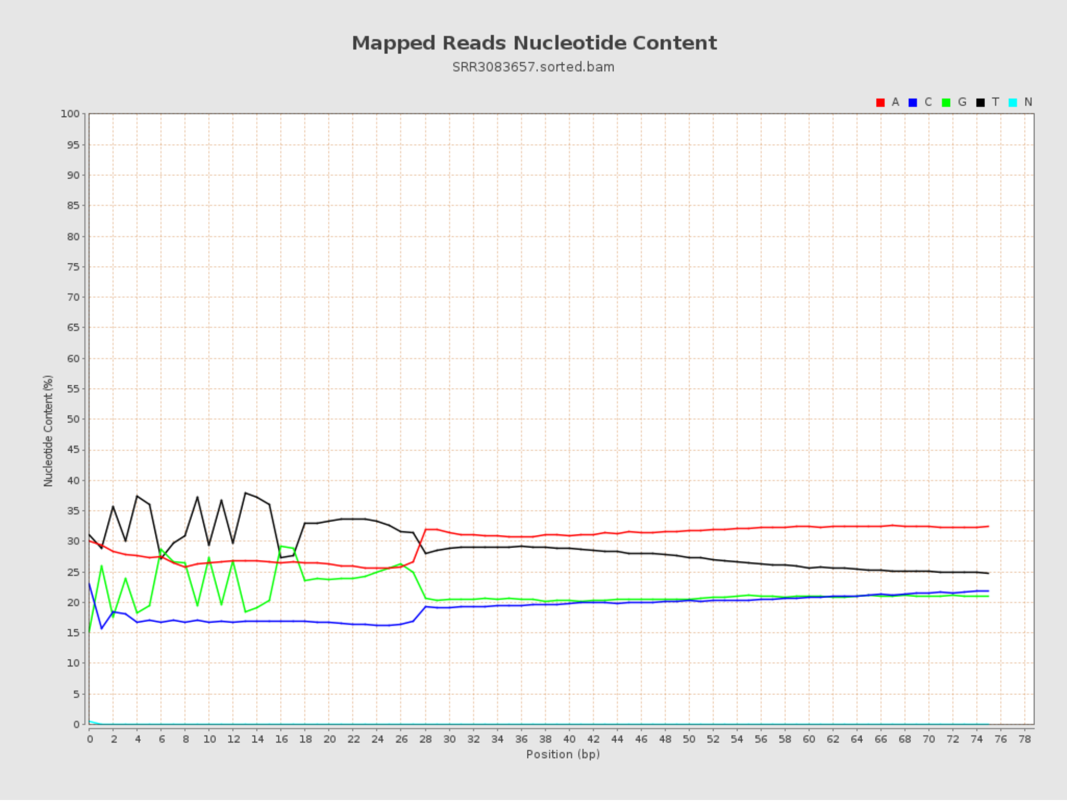
6. Results : Genome Fraction Coverage



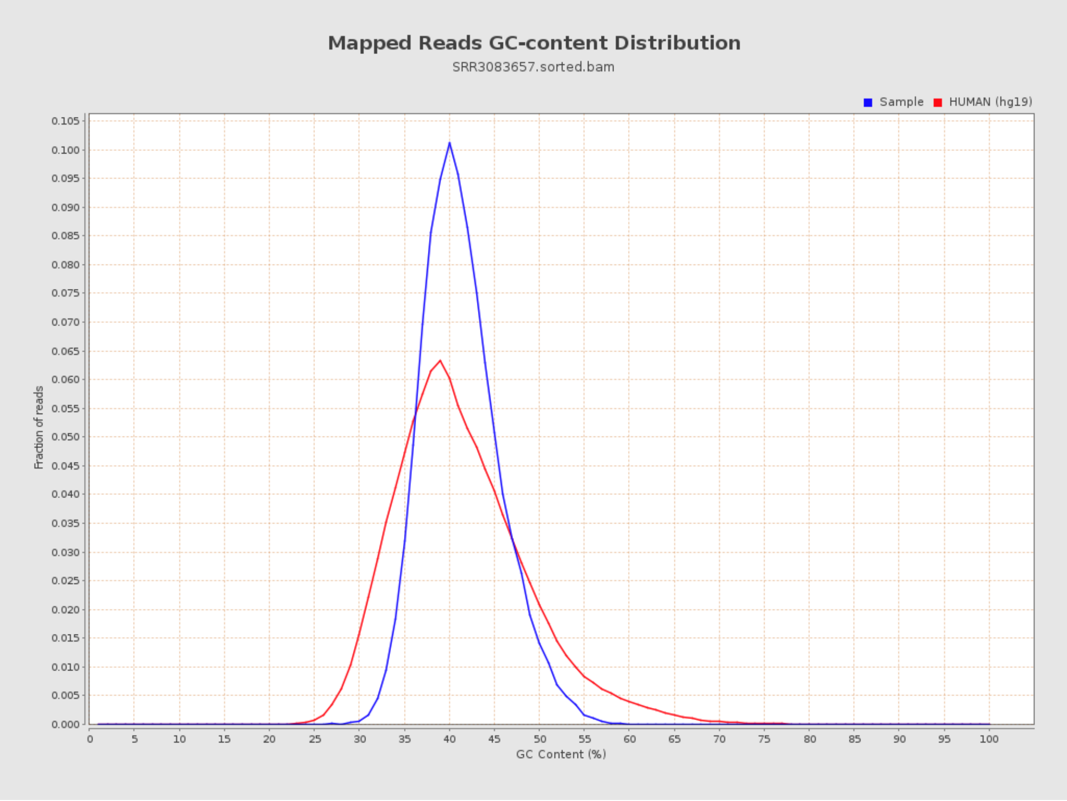
7. Results : Duplication Rate Histogram



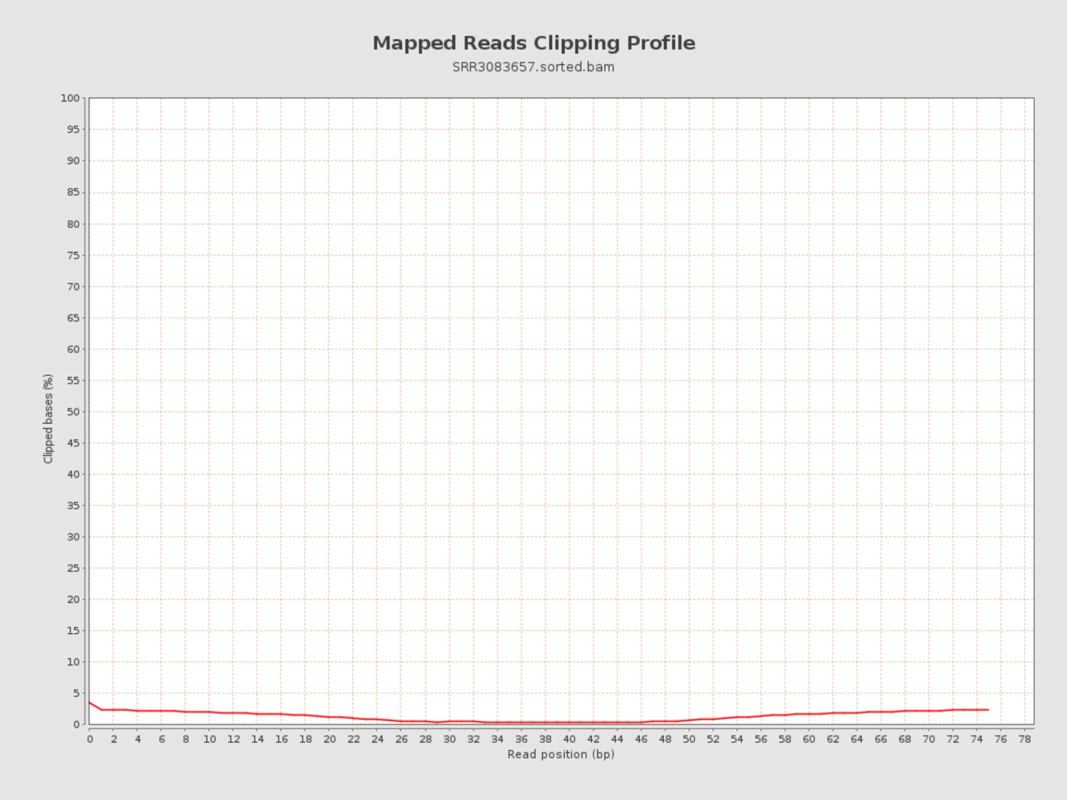
8. Results : Mapped Reads Nucleotide Content



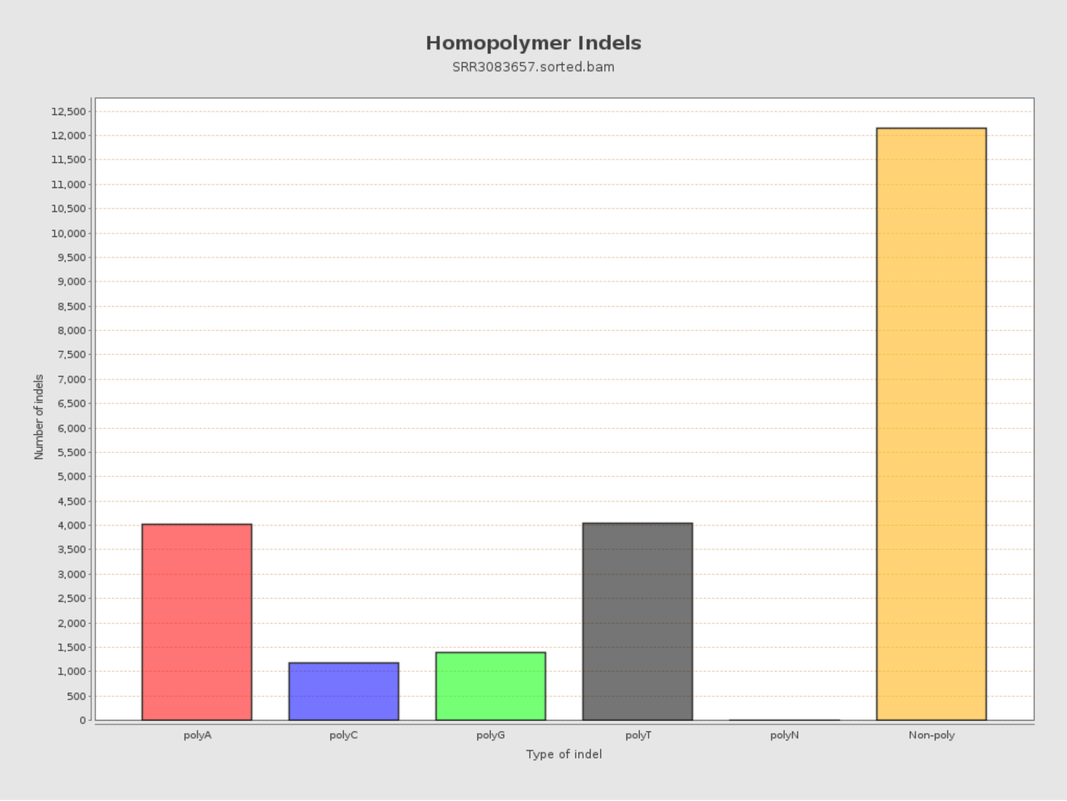
9. Results : Mapped Reads GC-content Distribution



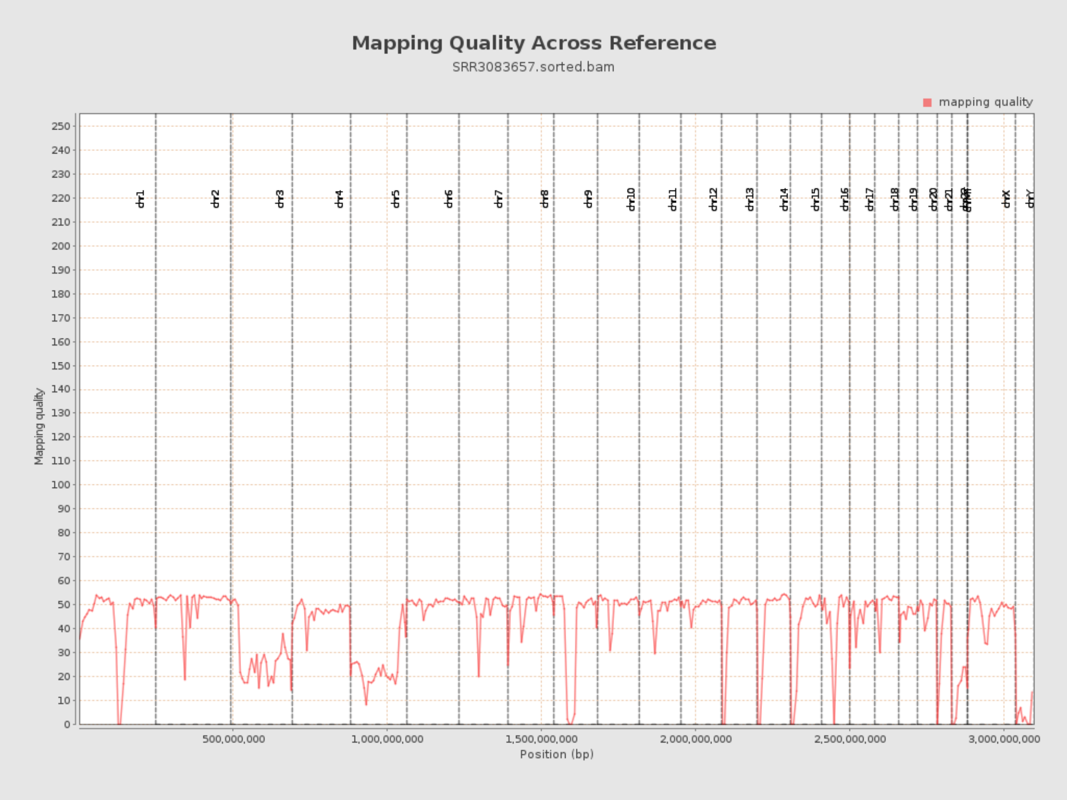
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram