Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:27:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081057.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_SRR3081057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:27:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,476,340
Mapped reads	2,232,026 / 90.13%
Unmapped reads	244,314 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,678 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	110,671 / 4.47%
Duplication rate	3.99%
Clipped reads	985,439 / 39.79%

2.2. ACGT Content

Number/percentage of A's	41,535,023 / 27.72%
Number/percentage of C's	28,434,413 / 18.98%
Number/percentage of T's	46,736,191 / 31.19%
Number/percentage of G's	33,116,746 / 22.1%
Number/percentage of N's	1,610 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.3907

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

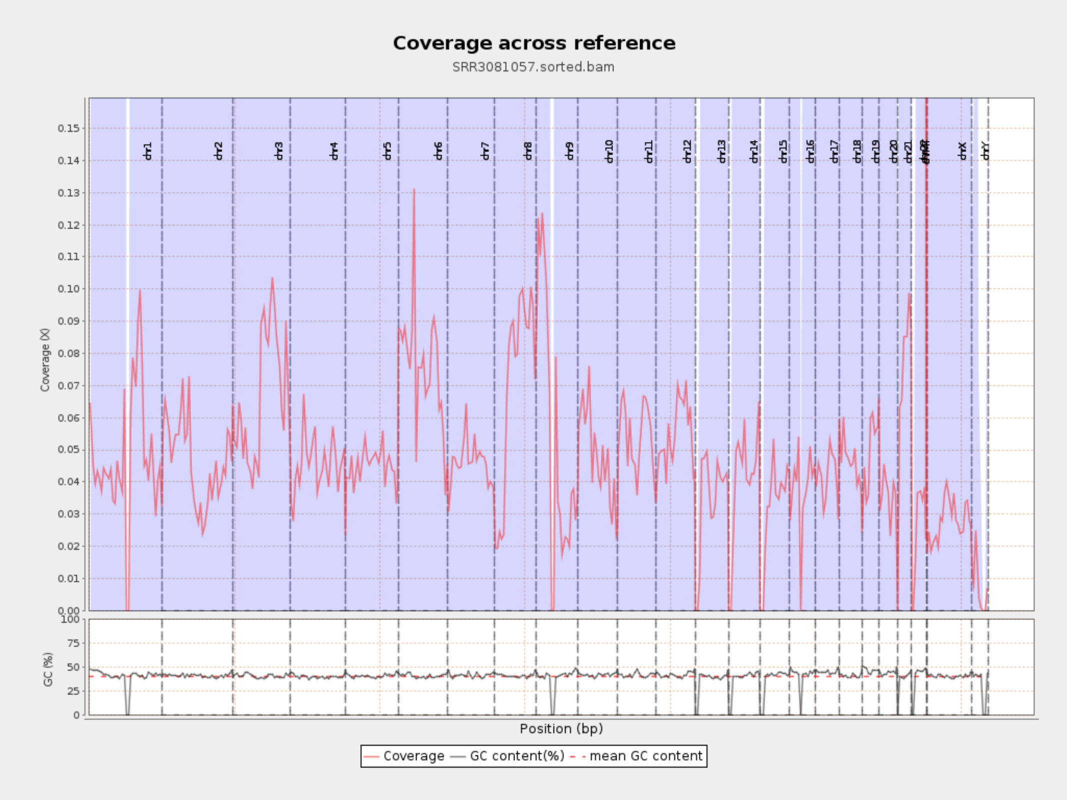
General error rate	0.92%
Mismatches	1,356,108
Insertions	11,828
Mapped reads with at least one insertion	0.52%
Deletions	32,984
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.48%

2.6. Chromosome stats

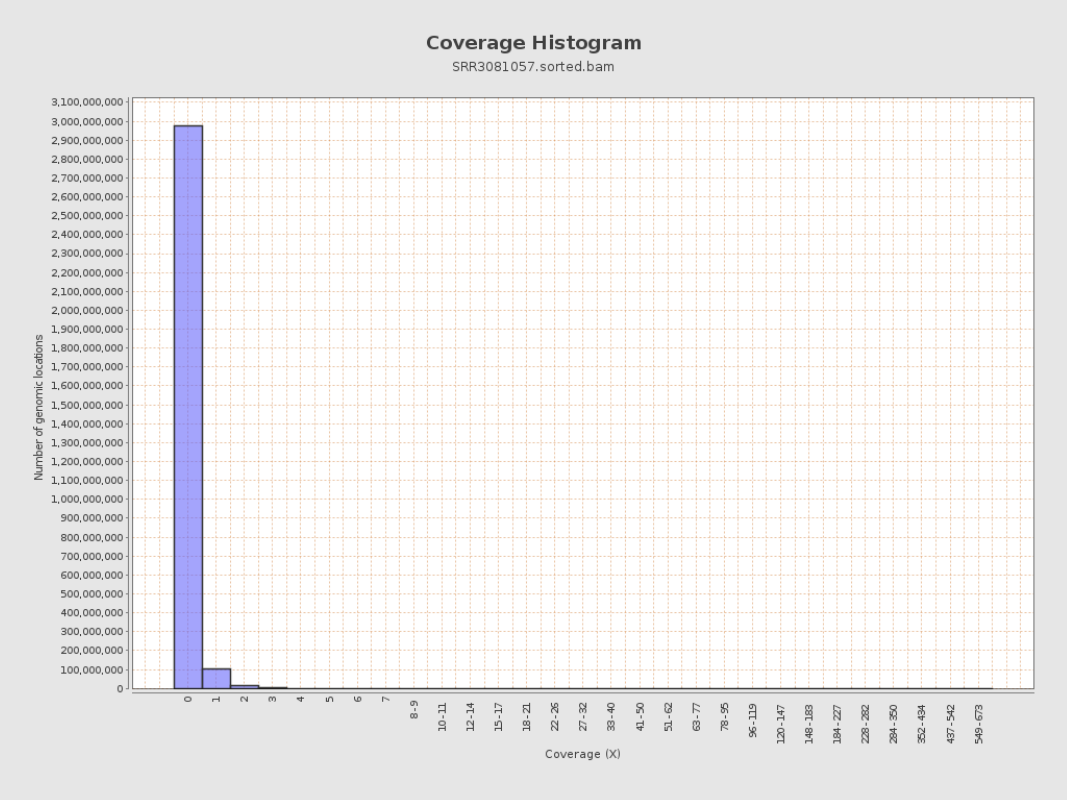
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11852037	0.0476	0.5716
chr2	243199373	11335172	0.0466	0.4384
chr3	198022430	13255313	0.0669	0.305
chr4	191154276	8708641	0.0456	0.2745
chr5	180915260	8137737	0.045	0.2488
chr6	171115067	12968364	0.0758	0.4895
chr7	159138663	7359073	0.0462	0.3743

chr8	146364022	10251205	0.07	0.4609
chr9	141213431	7601947	0.0538	0.4553
chr10	135534747	6663937	0.0492	0.3878
chr11	135006516	7225708	0.0535	0.3419
chr12	133851895	7354216	0.0549	0.289
chr13	115169878	3913813	0.034	0.2161
chr14	107349540	4301776	0.0401	0.2994
chr15	102531392	3303530	0.0322	0.2116
chr16	90354753	3424973	0.0379	0.2824
chr17	81195210	3366315	0.0415	0.2536
chr18	78077248	3680642	0.0471	0.7877
chr19	59128983	2904063	0.0491	0.4175
chr20	63025520	2246171	0.0356	0.2379
chr21	48129895	3509104	0.0729	0.3599
chr22	51304566	1296235	0.0253	0.185
chrMT	16571	471702	28.4655	13.3304
chrX	155270560	4349636	0.028	0.2312
chrY	59373566	396890	0.0067	0.1789

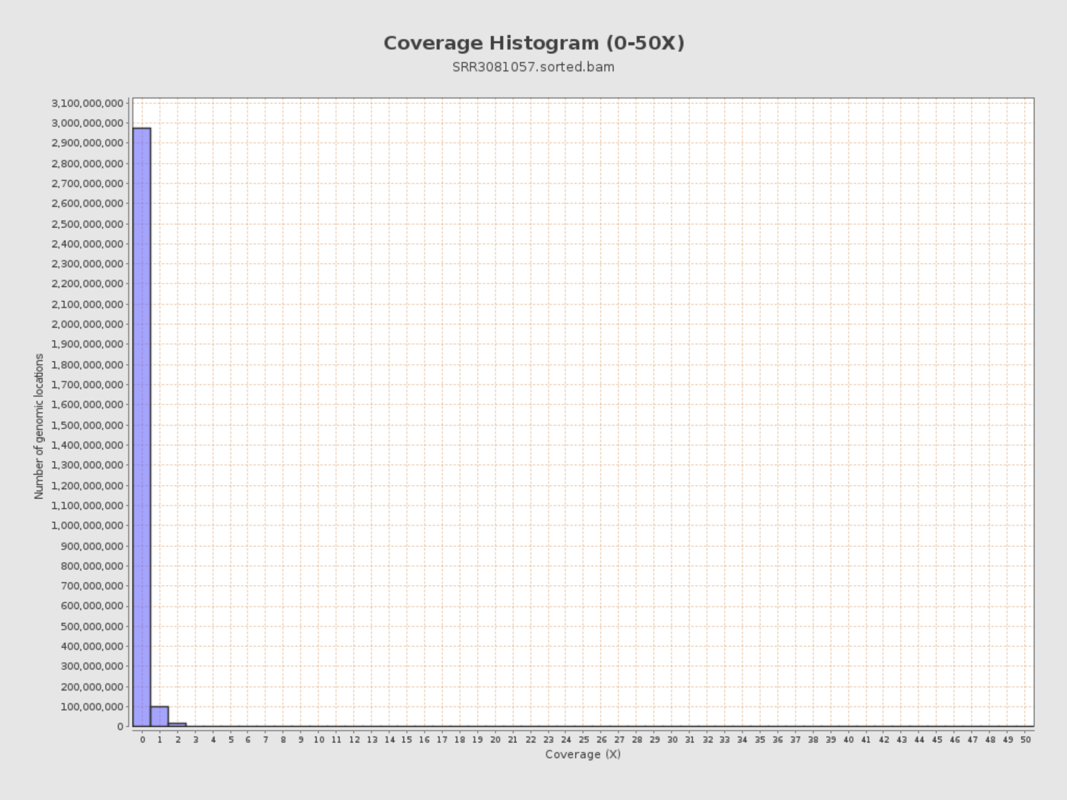
3. Results : Coverage across reference



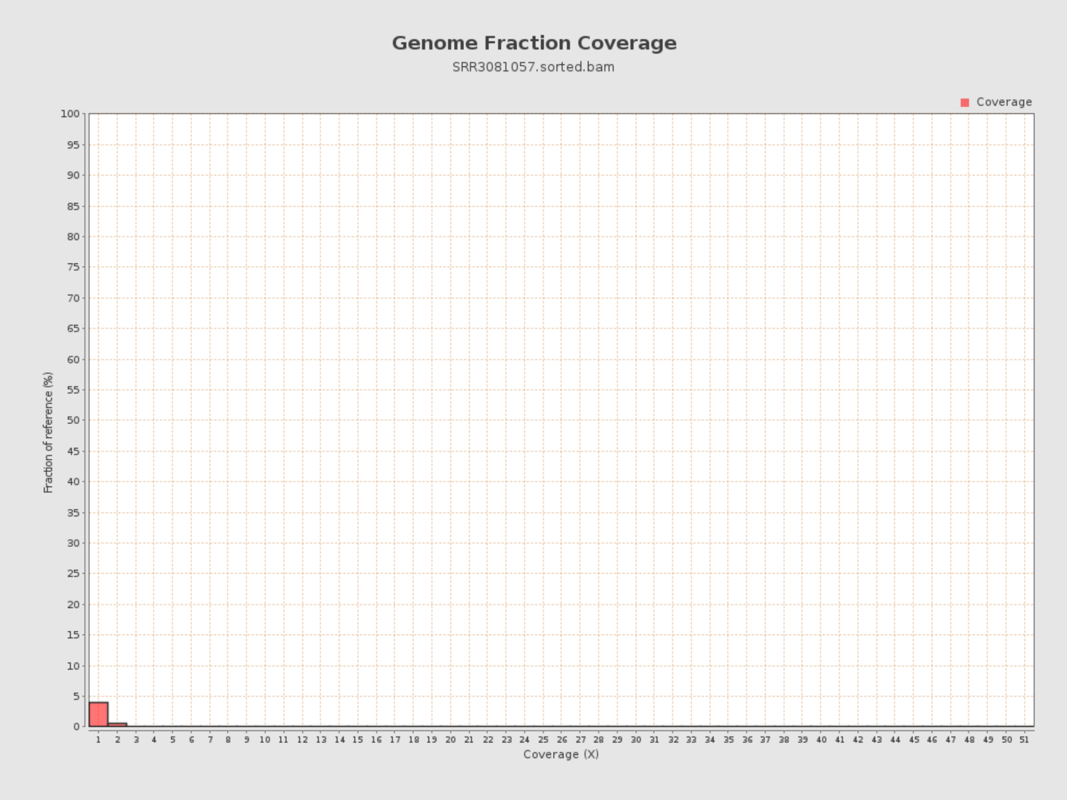
4. Results : Coverage Histogram



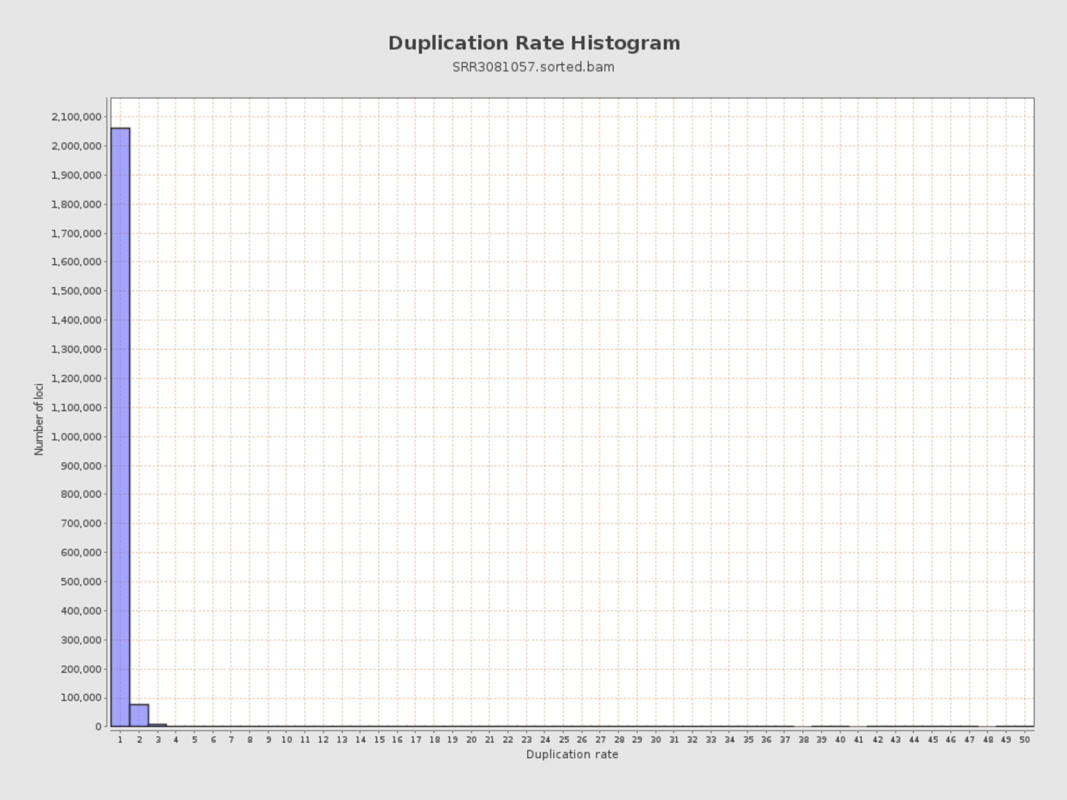
5. Results : Coverage Histogram (0-50X)



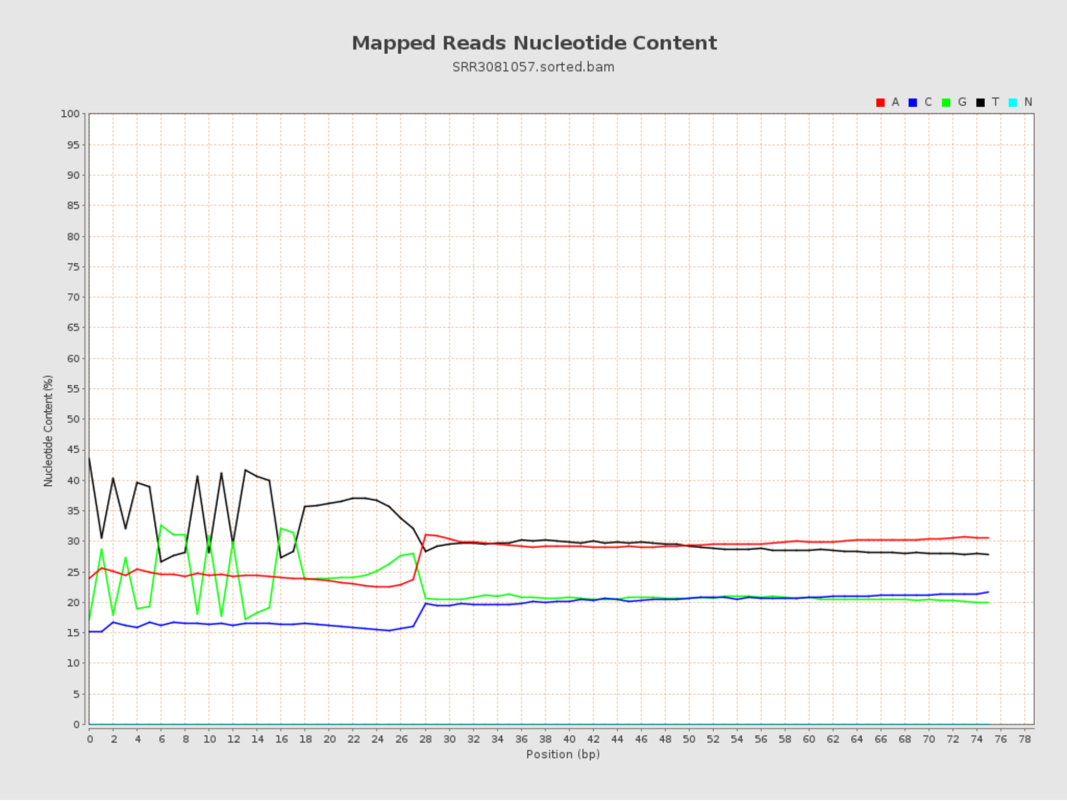
6. Results : Genome Fraction Coverage



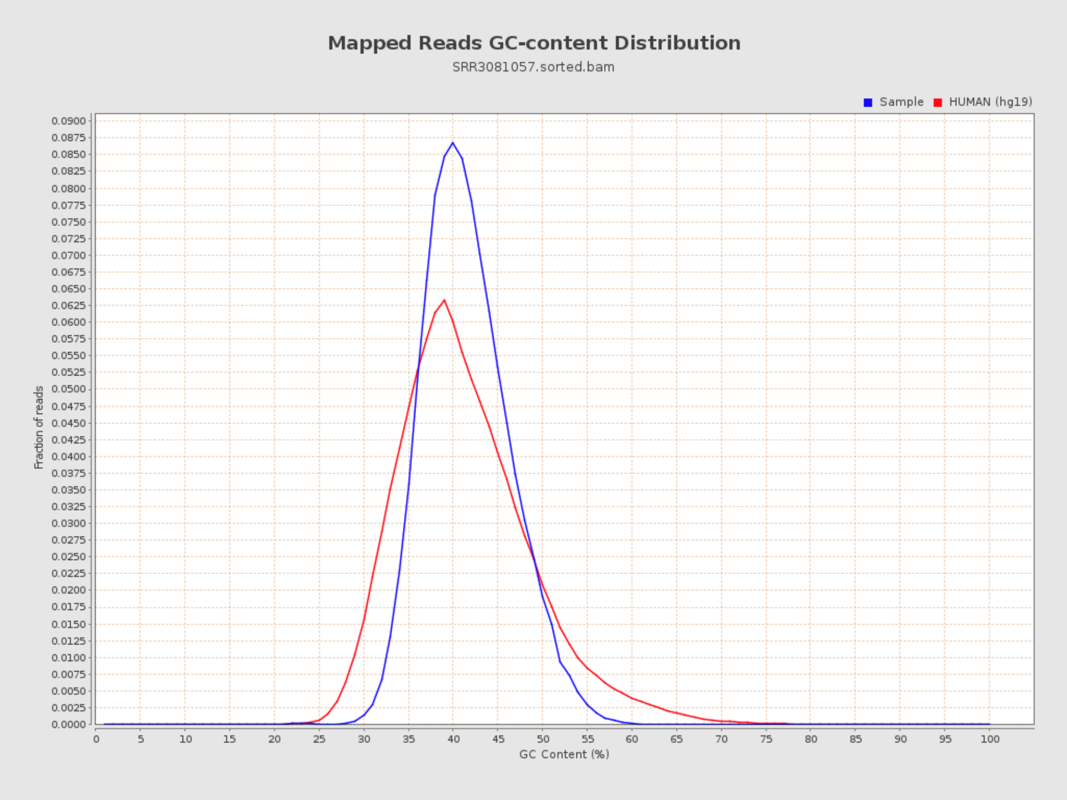
7. Results : Duplication Rate Histogram



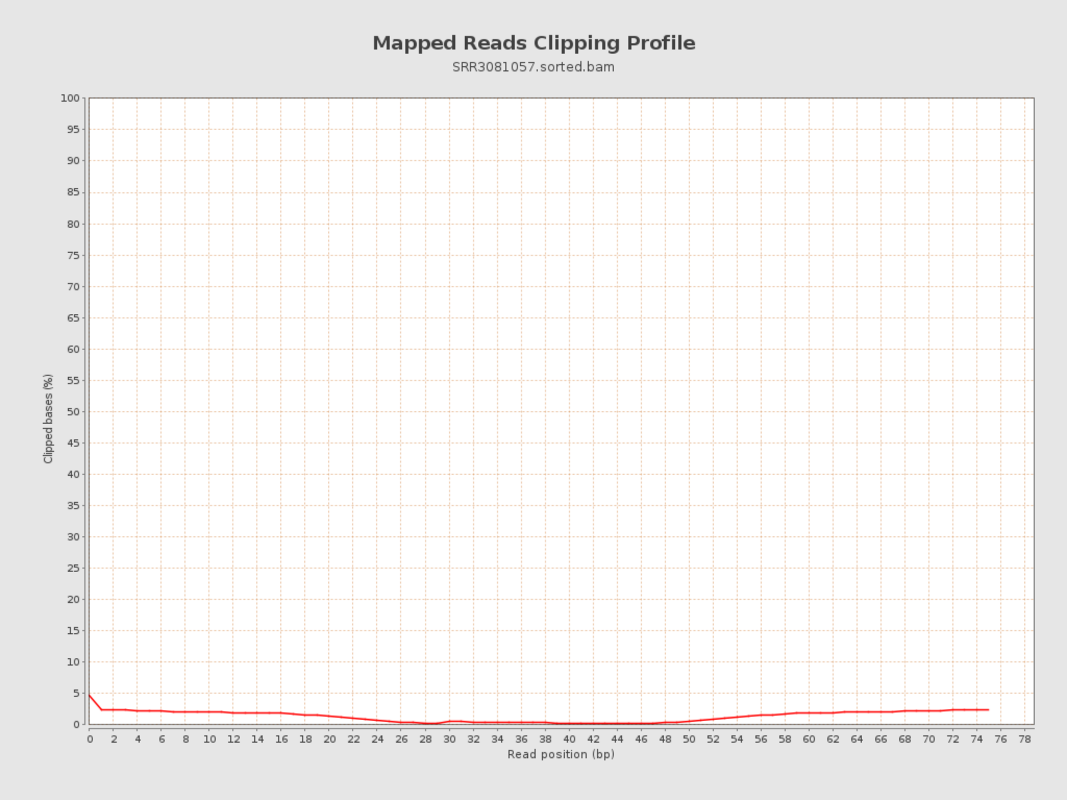
8. Results : Mapped Reads Nucleotide Content



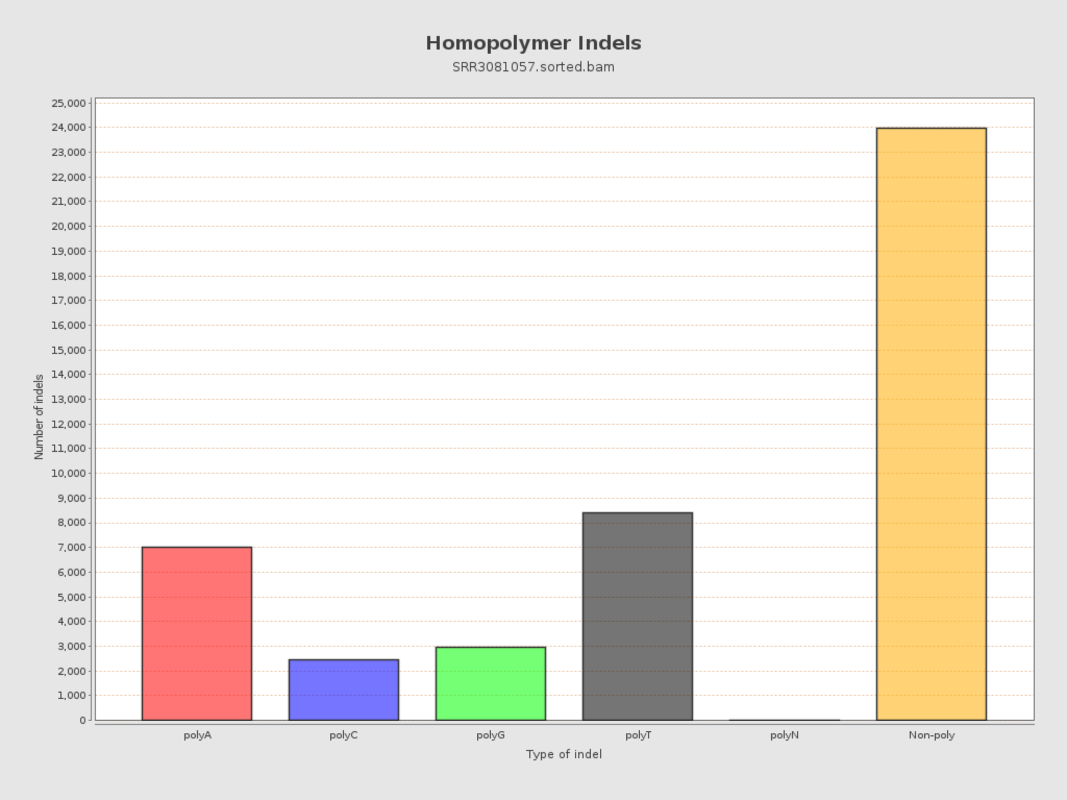
9. Results : Mapped Reads GC-content Distribution



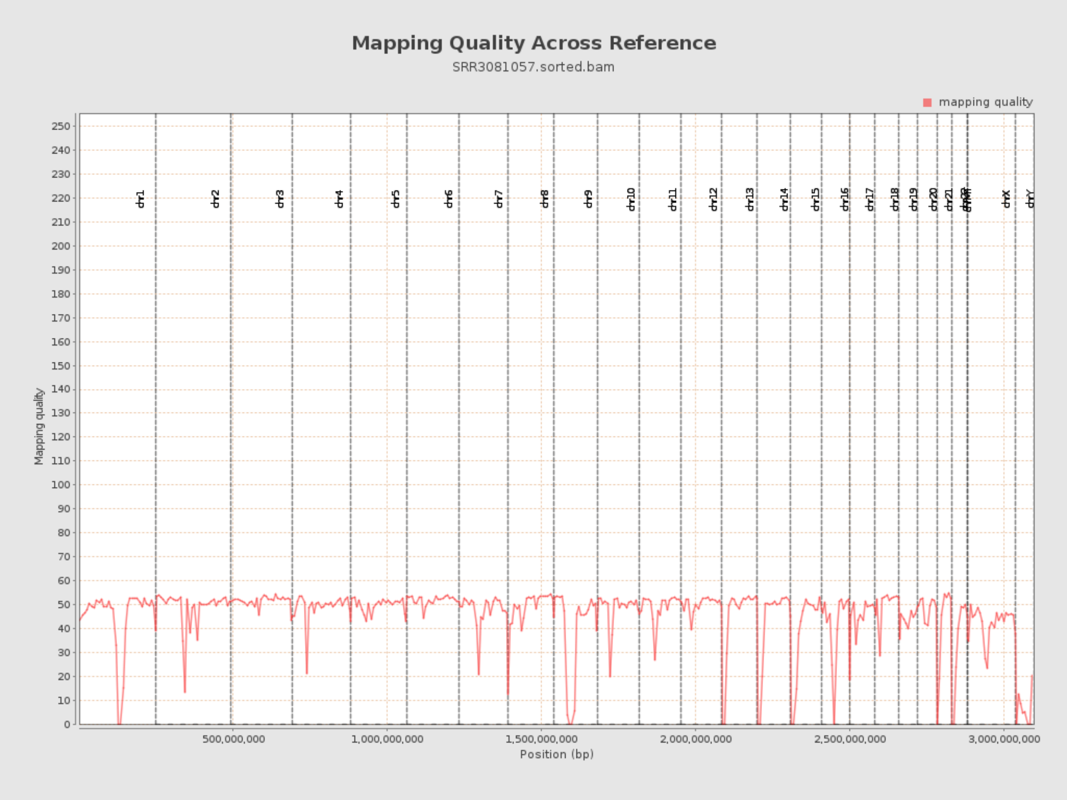
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram