Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:30:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004027.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_SRR6004027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:30:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,574,907
Mapped reads	2,276,901 / 88.43%
Unmapped reads	298,006 / 11.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,801 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	91,647 / 3.56%
Duplication rate	2.84%
Clipped reads	1,195,530 / 46.43%

2.2. ACGT Content

Number/percentage of A's	40,197,862 / 27.07%
Number/percentage of C's	27,473,695 / 18.5%
Number/percentage of T's	46,092,880 / 31.04%
Number/percentage of G's	34,715,481 / 23.38%
Number/percentage of N's	22,136 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.048

Standard Deviation	0.4708

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

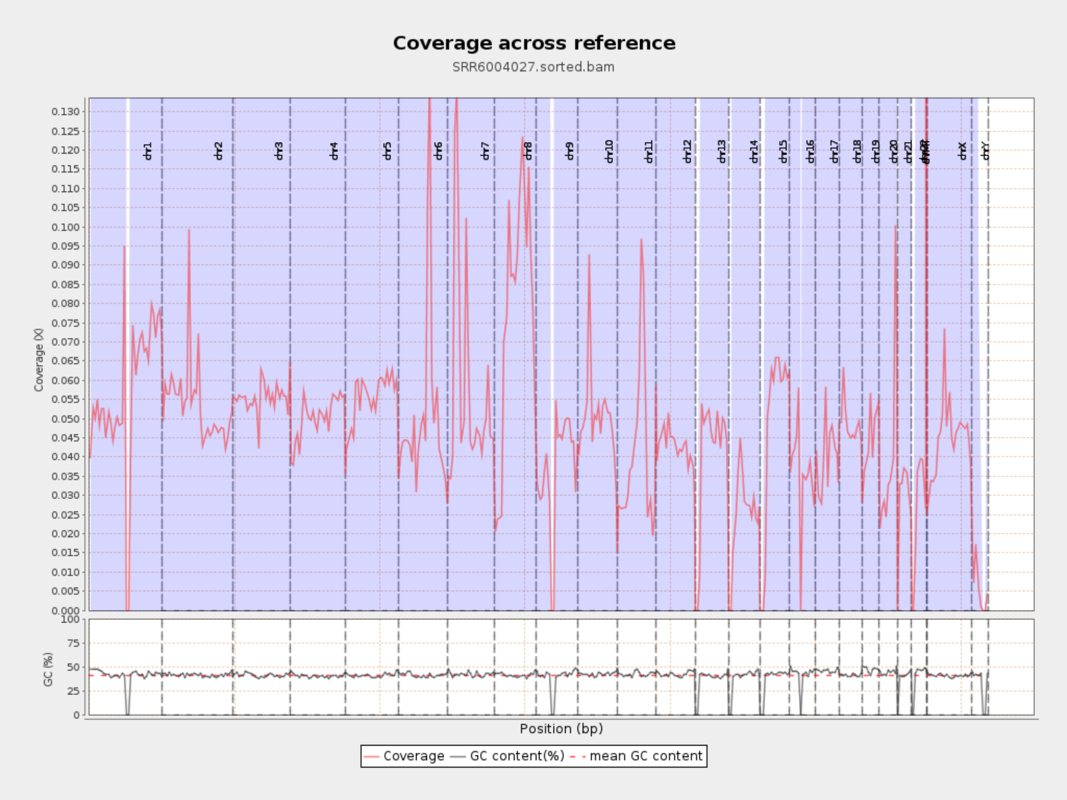
General error rate	0.93%
Mismatches	1,354,635
Insertions	11,869
Mapped reads with at least one insertion	0.52%
Deletions	39,627
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.35%

2.6. Chromosome stats

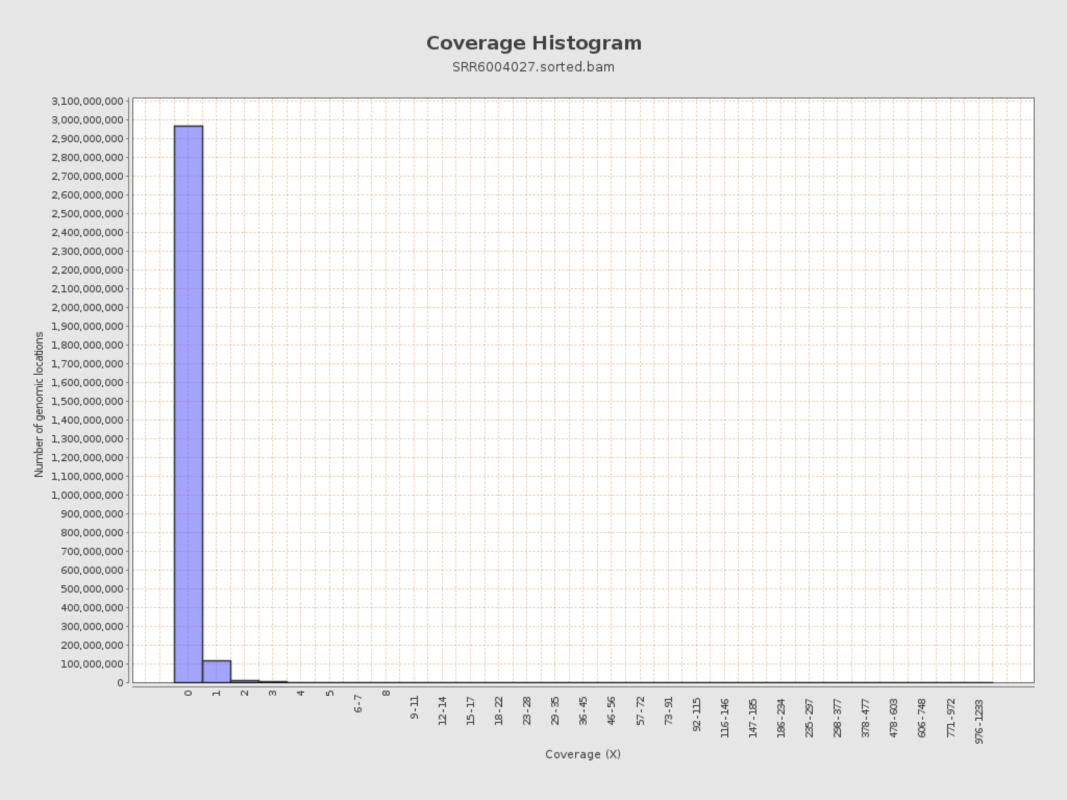
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14079275	0.0565	0.984
chr2	243199373	13080860	0.0538	0.5378
chr3	198022430	10940262	0.0552	0.2637
chr4	191154276	9593779	0.0502	0.2651
chr5	180915260	10077848	0.0557	0.2685
chr6	171115067	8740552	0.0511	0.2988
chr7	159138663	9462529	0.0595	0.7302

chr8	146364022	11379887	0.0778	0.5004
chr9	141213431	5147152	0.0364	0.4202
chr10	135534747	6905538	0.051	0.4311
chr11	135006516	5551397	0.0411	0.3311
chr12	133851895	5734374	0.0428	0.2447
chr13	115169878	4605569	0.04	0.2325
chr14	107349540	2690219	0.0251	0.2424
chr15	102531392	4936486	0.0481	0.2575
chr16	90354753	3205147	0.0355	0.2705
chr17	81195210	3279750	0.0404	0.2491
chr18	78077248	3828170	0.049	0.749
chr19	59128983	2645531	0.0447	0.6771
chr20	63025520	2592788	0.0411	0.2493
chr21	48129895	1429998	0.0297	0.2212
chr22	51304566	1295455	0.0253	0.1748
chrMT	16571	42469	2.5629	2.5643
chrX	155270560	6972550	0.0449	0.2912
chrY	59373566	349220	0.0059	0.1216

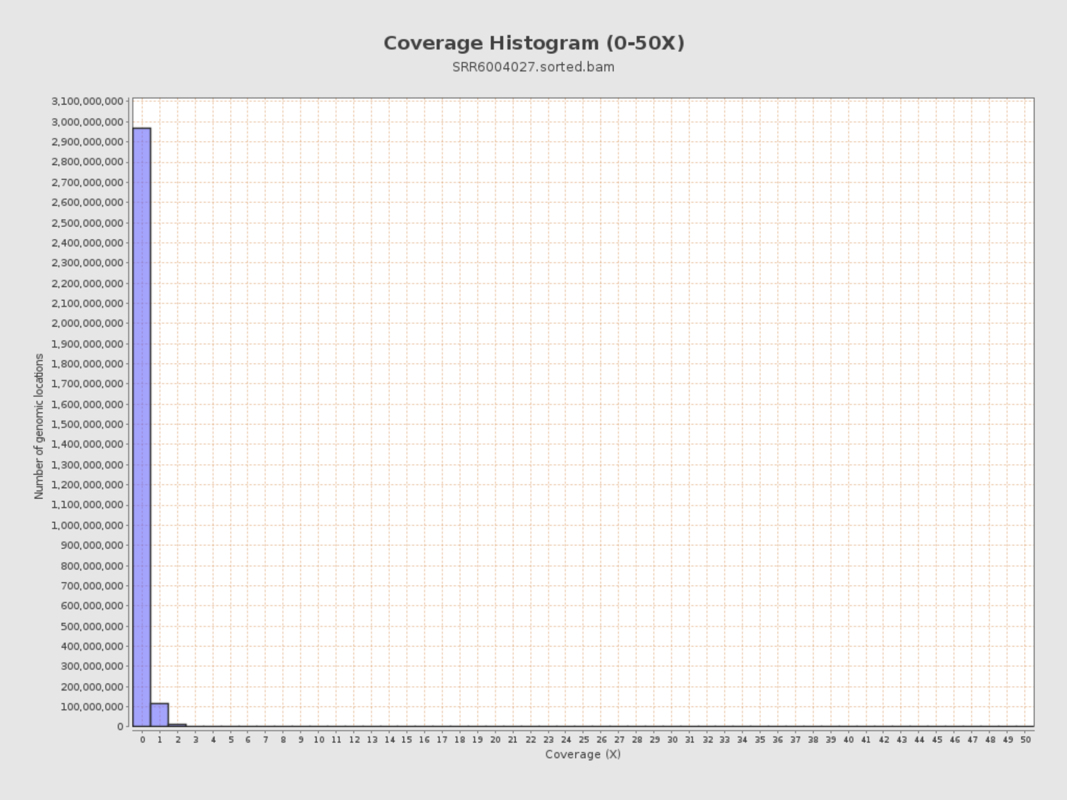
3. Results : Coverage across reference



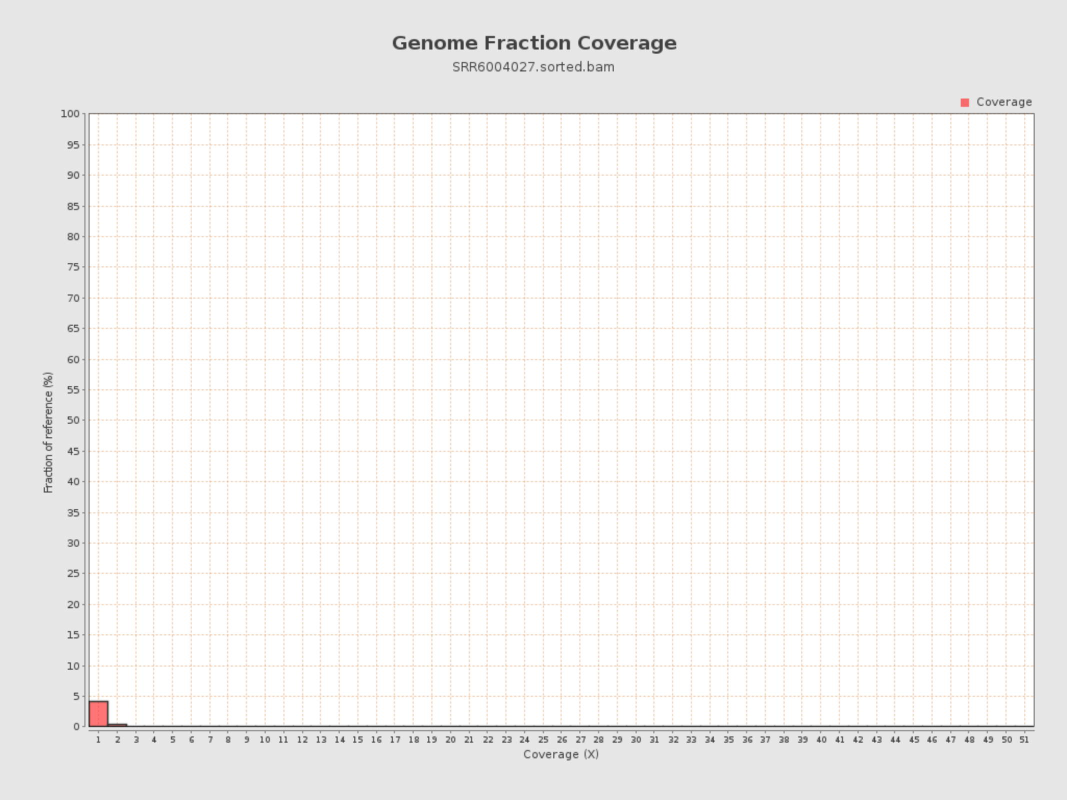
4. Results : Coverage Histogram



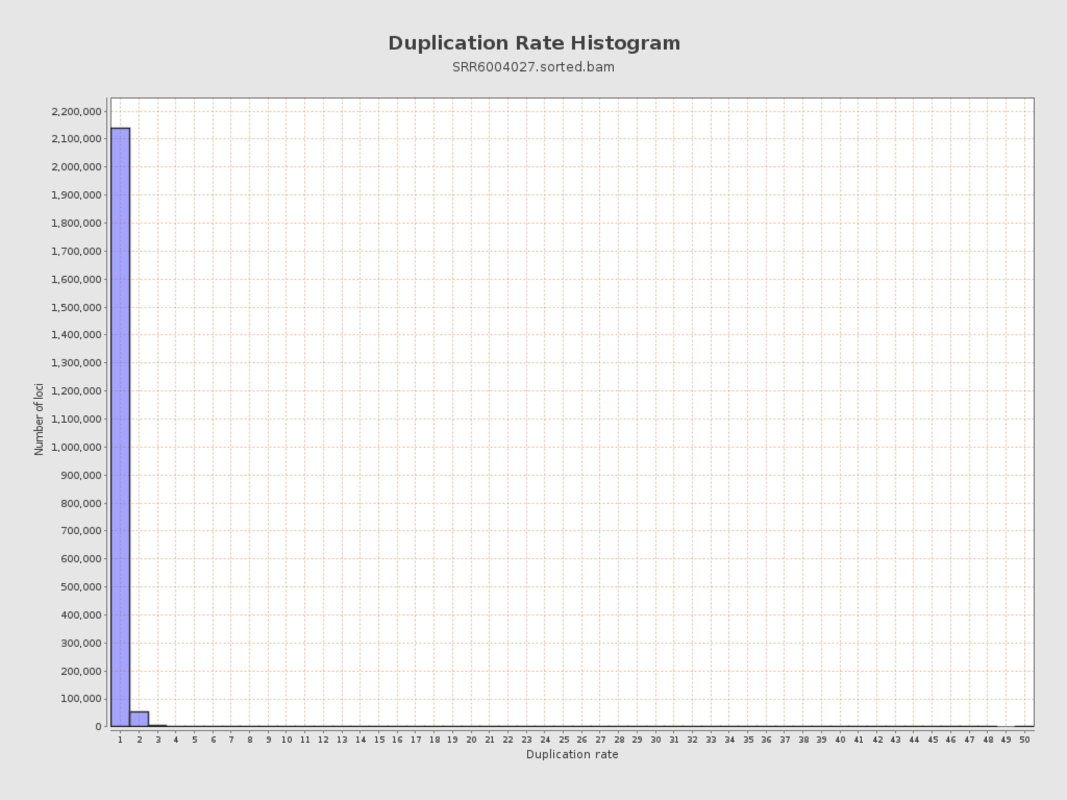
5. Results : Coverage Histogram (0-50X)



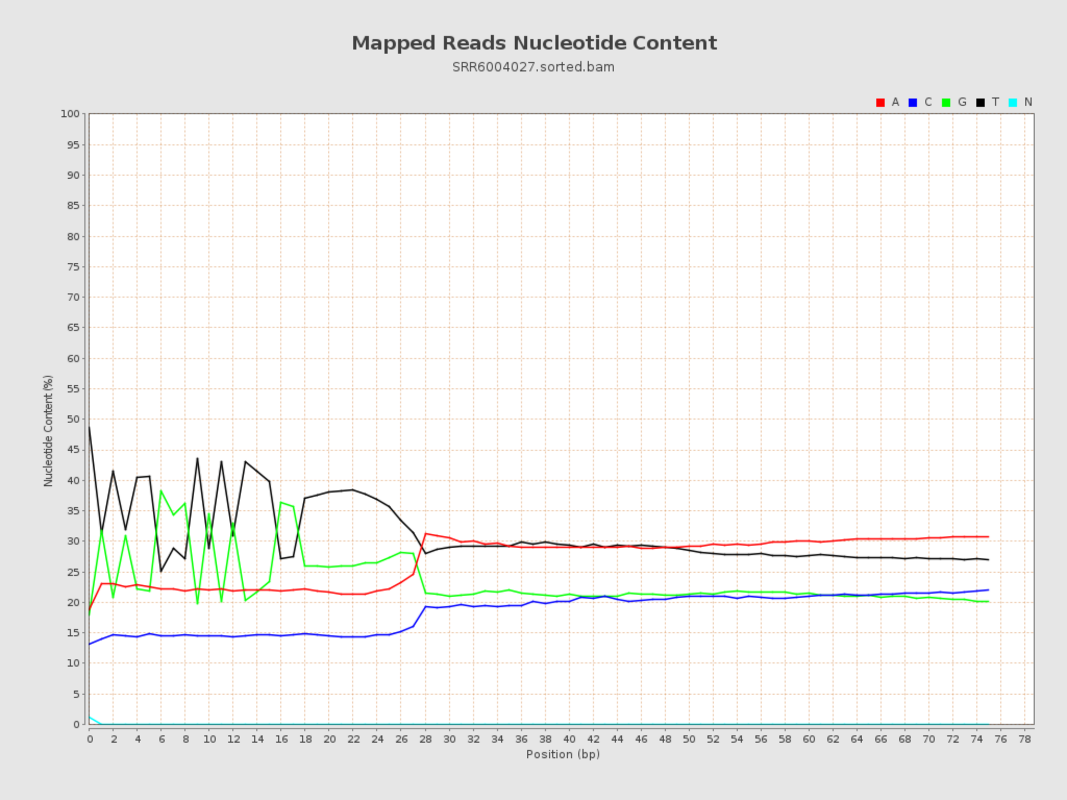
6. Results : Genome Fraction Coverage



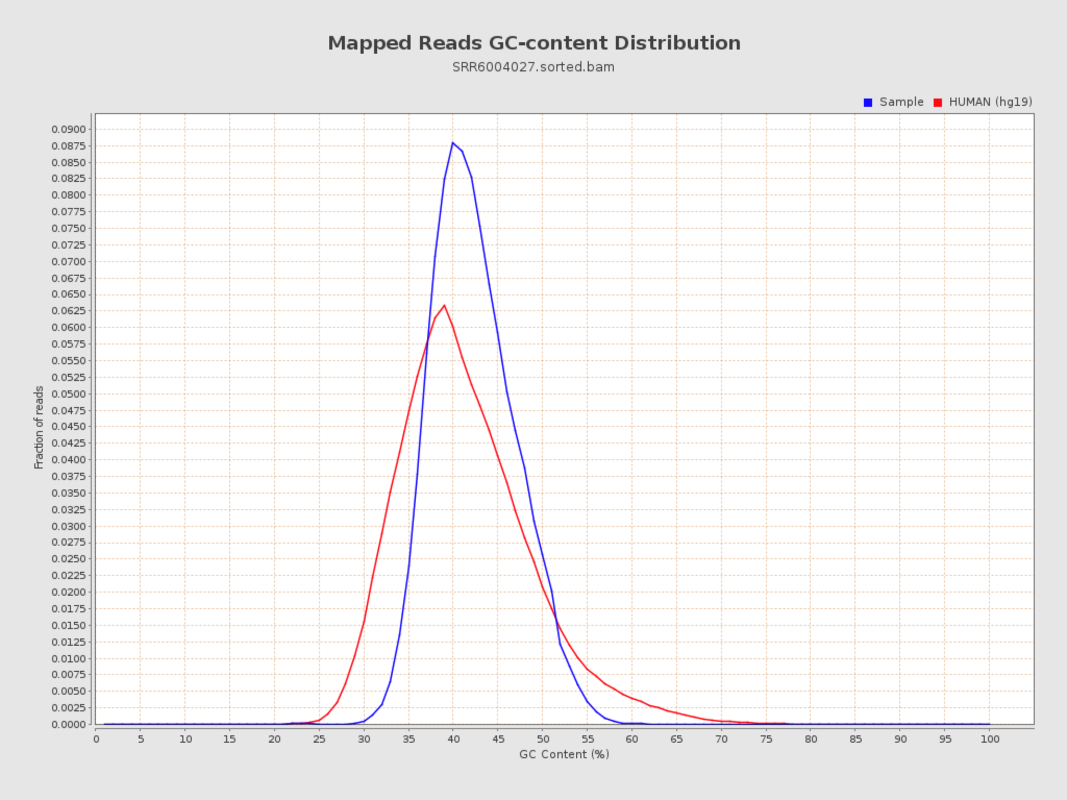
7. Results : Duplication Rate Histogram



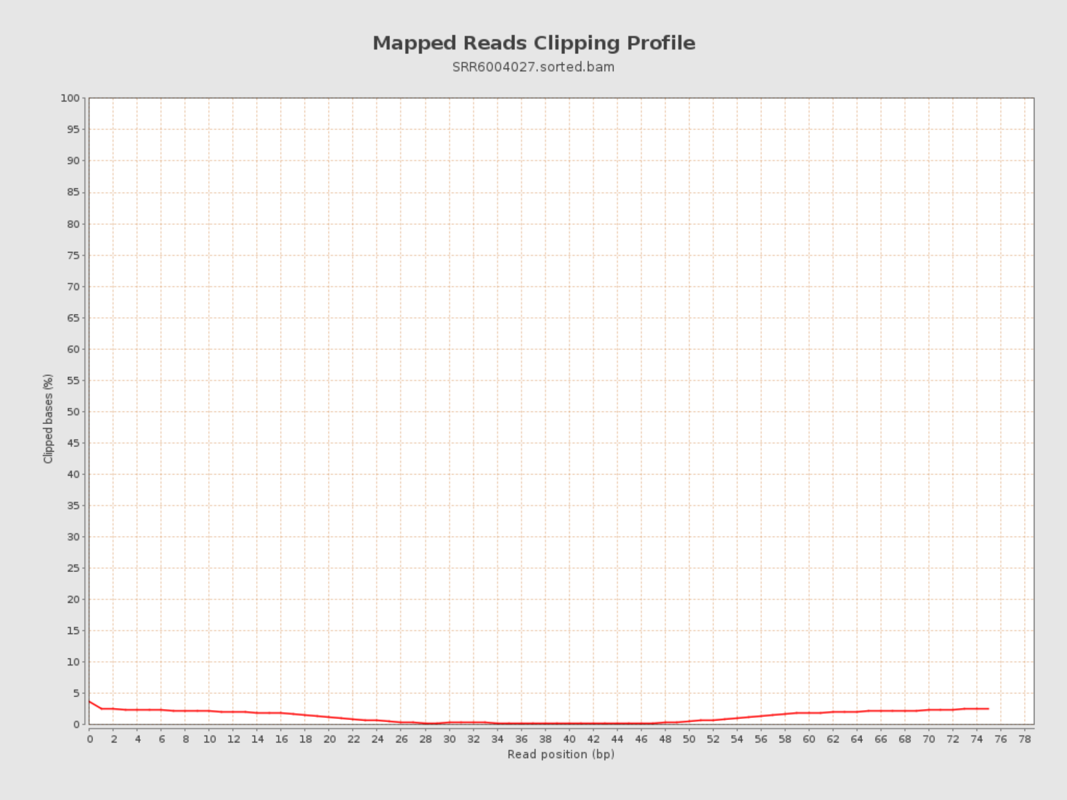
8. Results : Mapped Reads Nucleotide Content



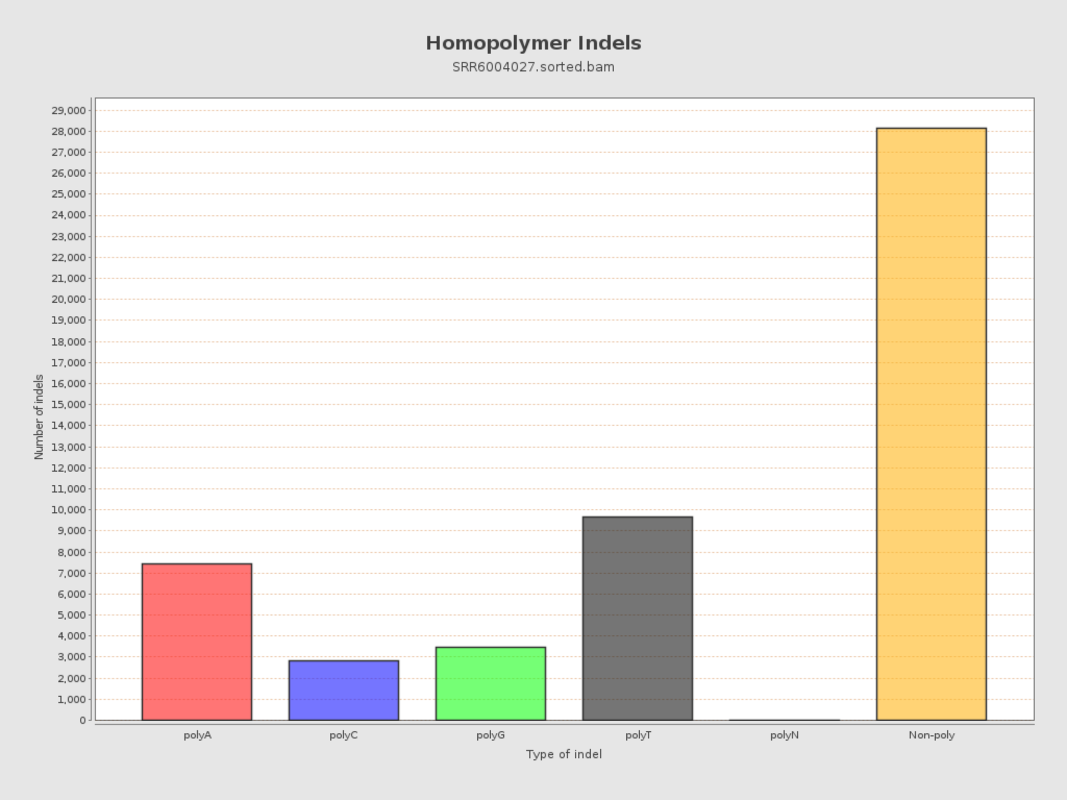
9. Results : Mapped Reads GC-content Distribution



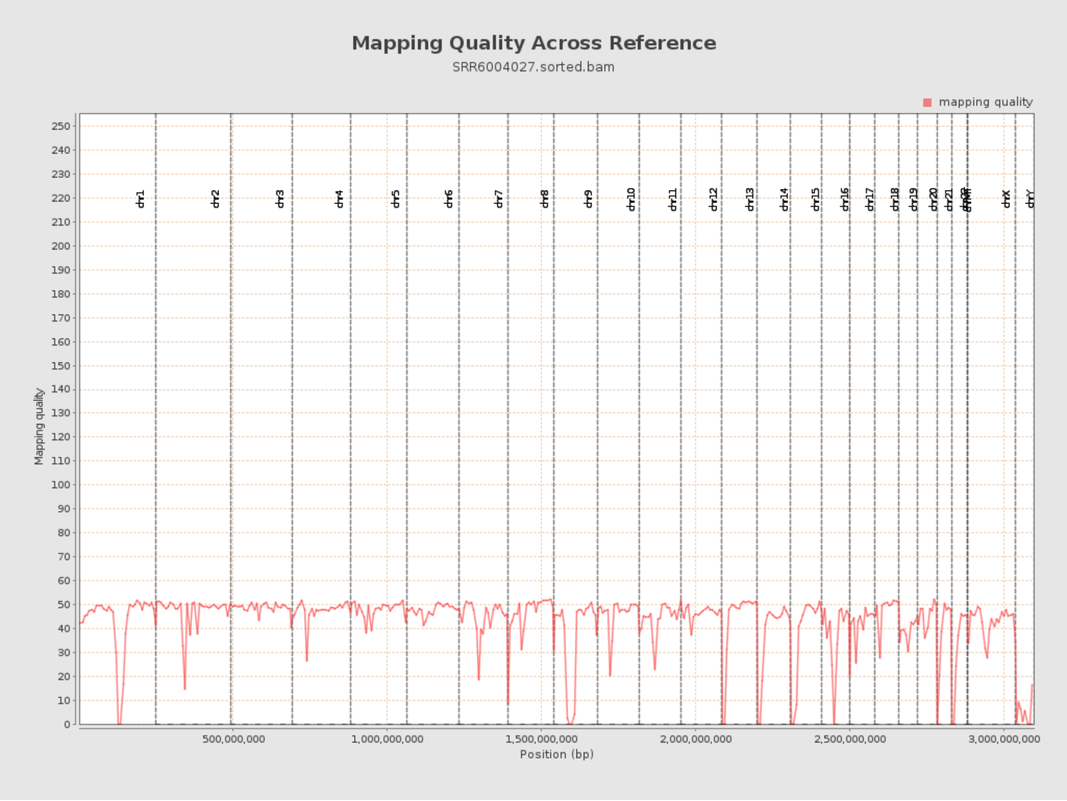
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram