Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:53:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004016.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_SRR6004016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:53:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,585,084
Mapped reads	2,256,828 / 87.3%
Unmapped reads	328,256 / 12.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,839 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	115,451 / 4.47%
Duplication rate	4.27%
Clipped reads	1,107,459 / 42.84%

2.2. ACGT Content

Number/percentage of A's	40,812,965 / 27.46%
Number/percentage of C's	28,080,680 / 18.9%
Number/percentage of T's	46,386,874 / 31.21%
Number/percentage of G's	33,301,585 / 22.41%
Number/percentage of N's	25,009 / 0.02%
GC Percentage	41.31%

2.3. Coverage

Mean	0.048

Standard Deviation	0.3668

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

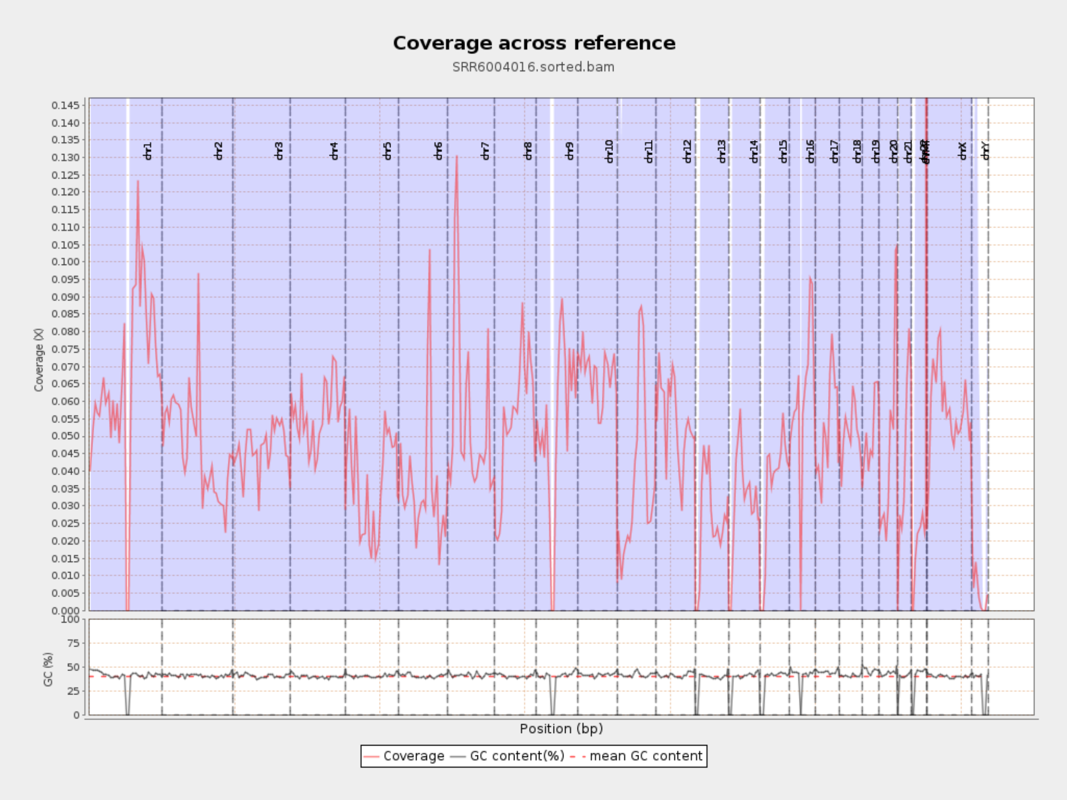
General error rate	0.88%
Mismatches	1,297,098
Insertions	10,319
Mapped reads with at least one insertion	0.45%
Deletions	34,901
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.51%

2.6. Chromosome stats

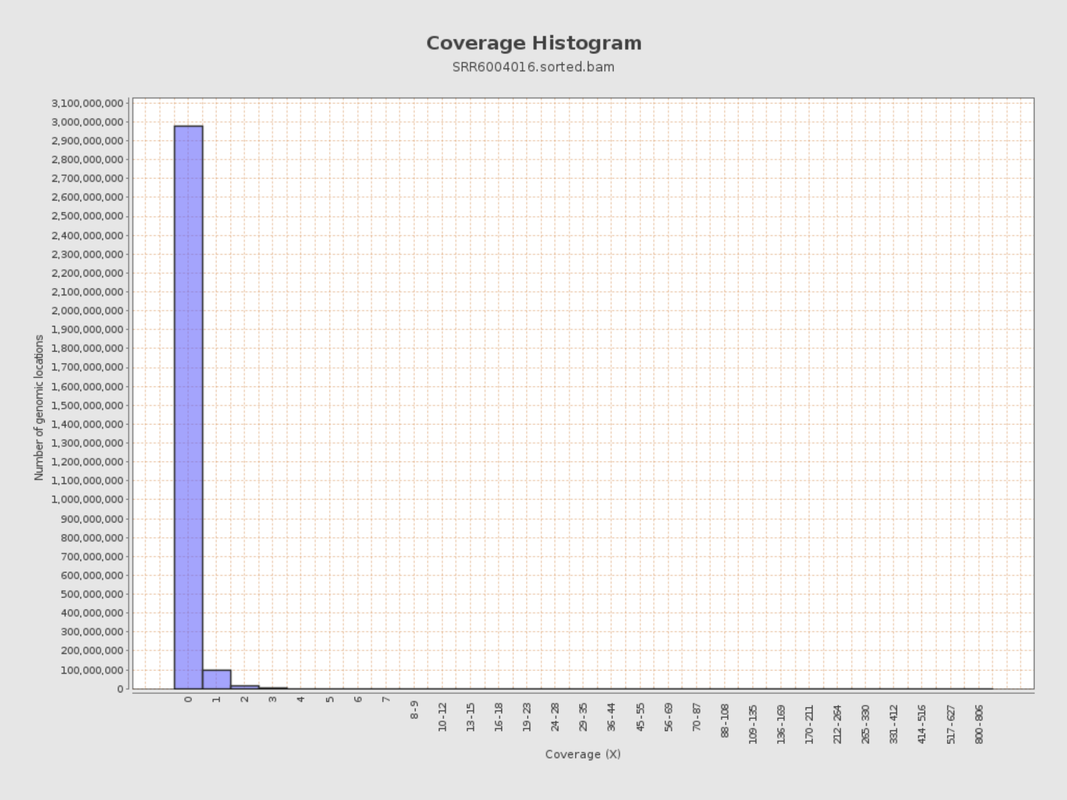
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16631211	0.0667	0.6529
chr2	243199373	11487844	0.0472	0.4415
chr3	198022430	9196976	0.0464	0.2543
chr4	191154276	10796007	0.0565	0.2915
chr5	180915260	6644600	0.0367	0.2268
chr6	171115067	6142178	0.0359	0.2462
chr7	159138663	9010575	0.0566	0.4791

chr8	146364022	7900818	0.054	0.4502
chr9	141213431	7494324	0.0531	0.343
chr10	135534747	9155183	0.0675	0.3774
chr11	135006516	5079934	0.0376	0.2788
chr12	133851895	7266530	0.0543	0.282
chr13	115169878	2891386	0.0251	0.2034
chr14	107349540	3361028	0.0313	0.2258
chr15	102531392	3584373	0.035	0.2279
chr16	90354753	5528873	0.0612	0.3064
chr17	81195210	4283997	0.0528	0.2828
chr18	78077248	4008012	0.0513	0.5393
chr19	59128983	2981936	0.0504	0.4625
chr20	63025520	2919629	0.0463	0.2639
chr21	48129895	2114738	0.0439	0.2617
chr22	51304566	912061	0.0178	0.1549
chrMT	16571	78864	4.7592	4.0022
chrX	155270560	8888529	0.0572	0.303
chrY	59373566	307954	0.0052	0.1021

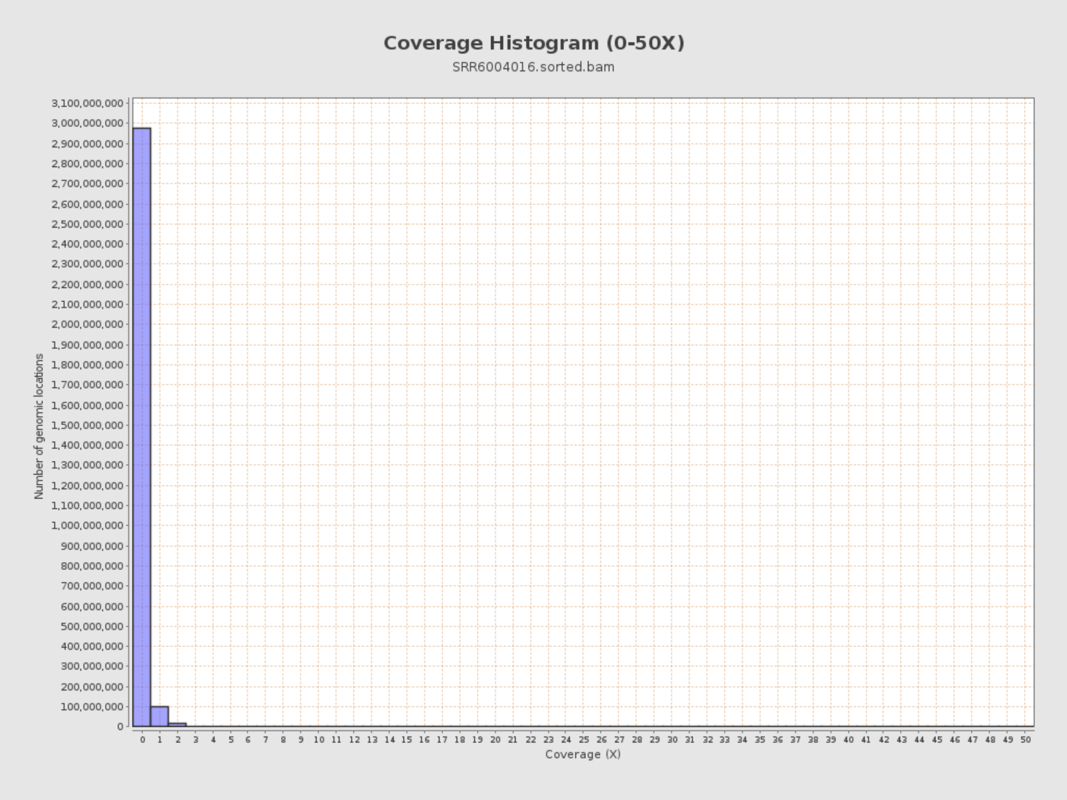
3. Results : Coverage across reference



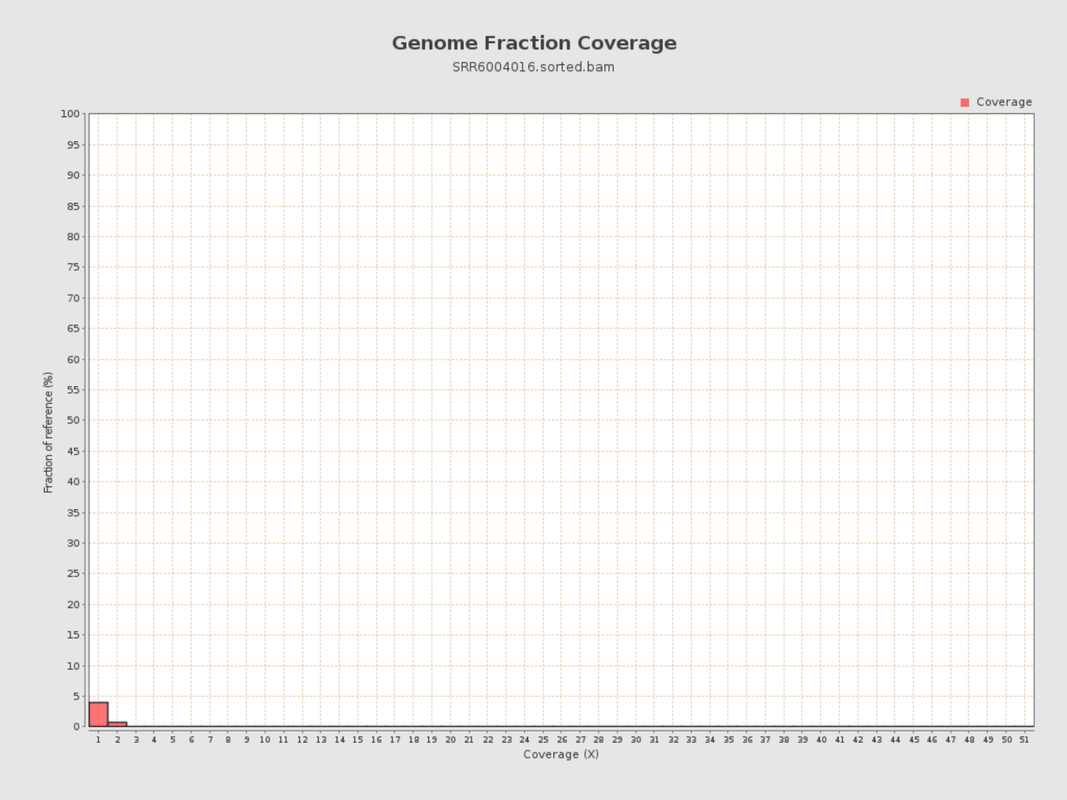
4. Results : Coverage Histogram



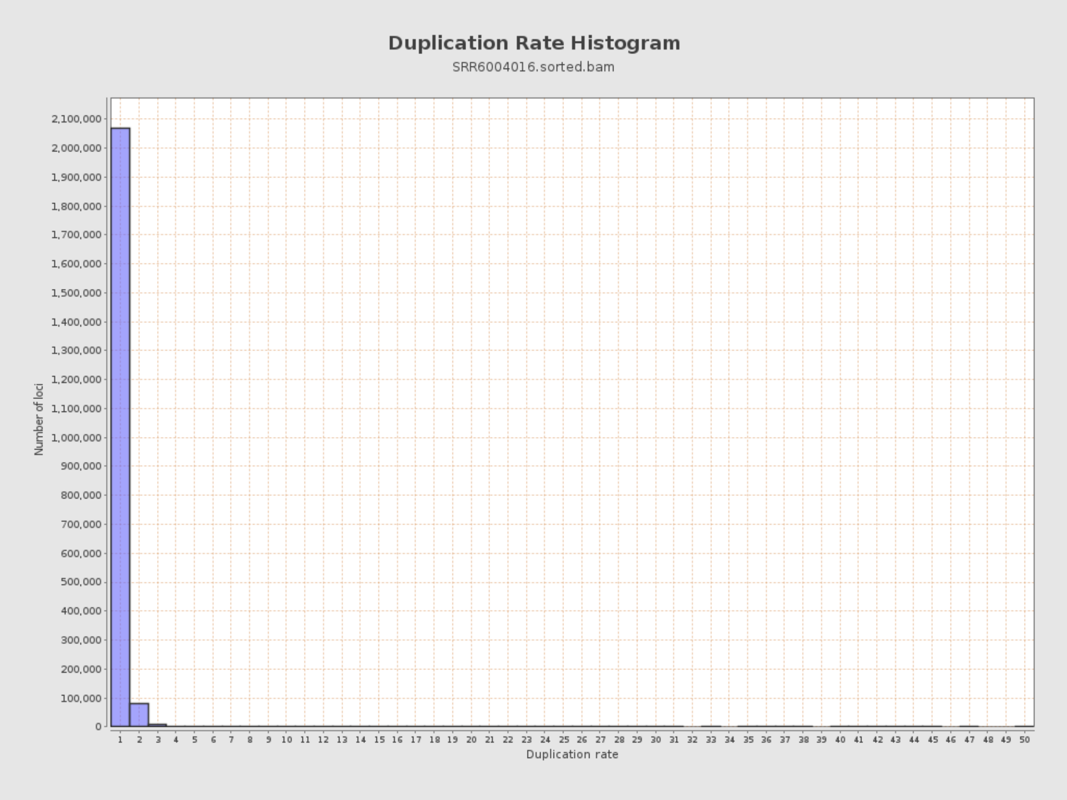
5. Results : Coverage Histogram (0-50X)



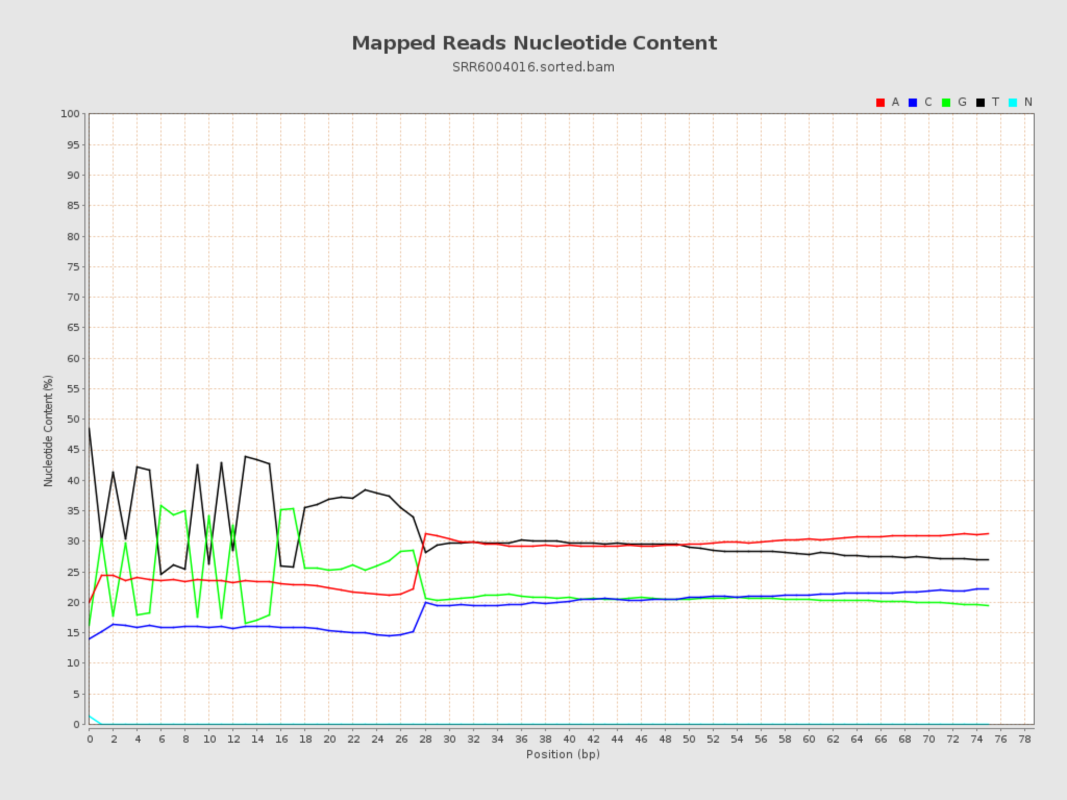
6. Results : Genome Fraction Coverage



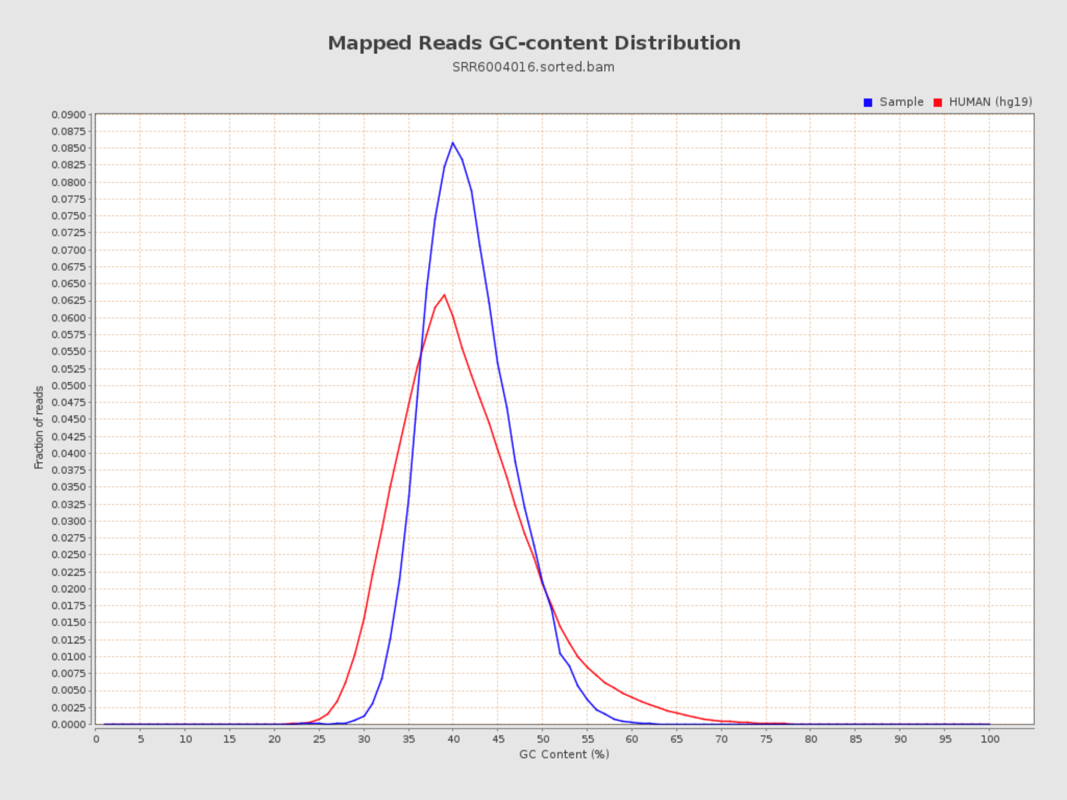
7. Results : Duplication Rate Histogram



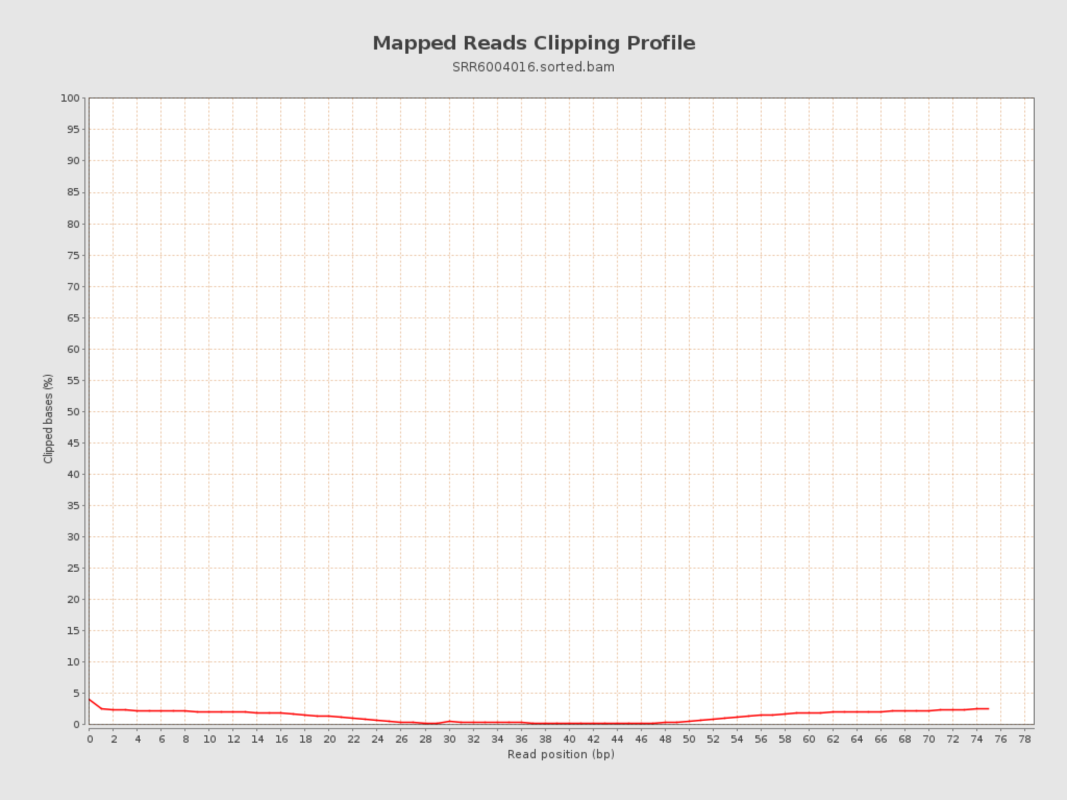
8. Results : Mapped Reads Nucleotide Content



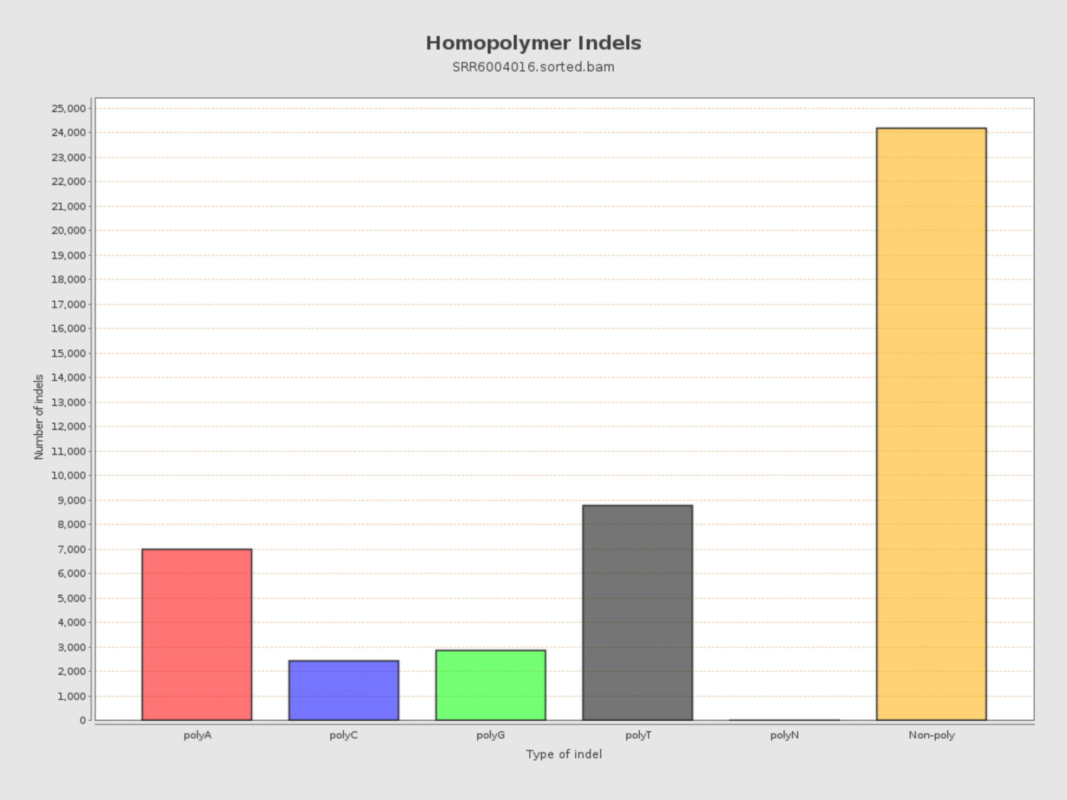
9. Results : Mapped Reads GC-content Distribution



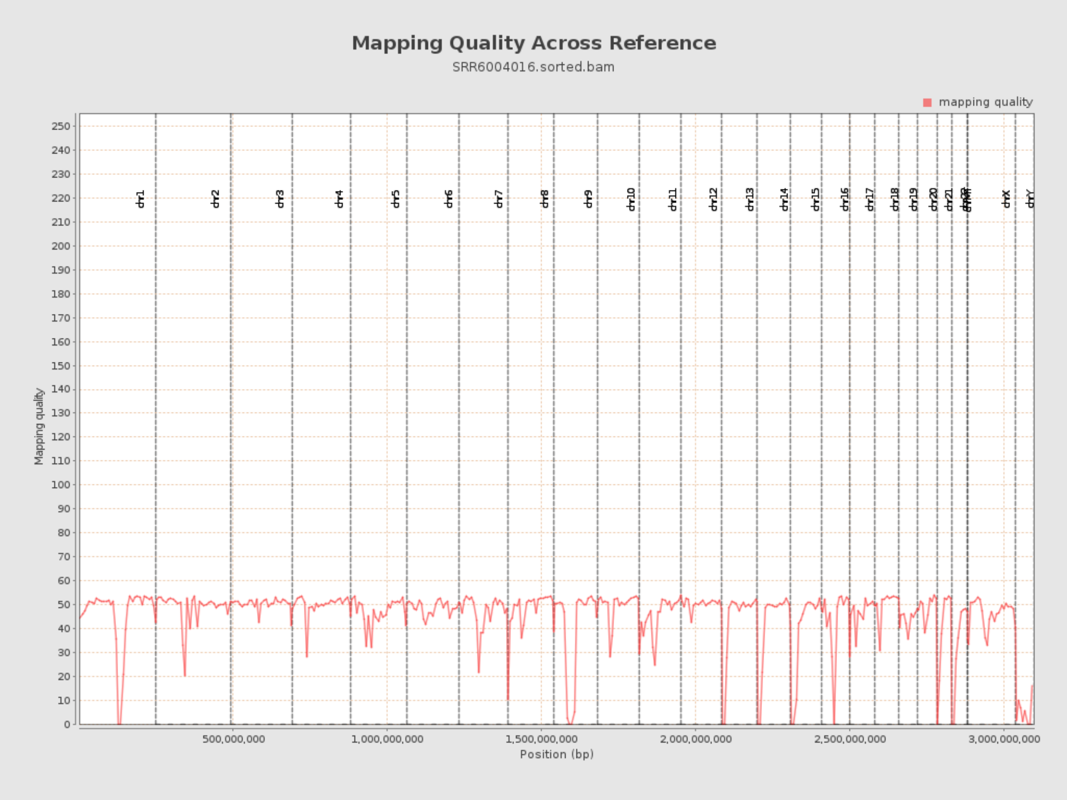
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram