Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:24:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081116.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_SRR3081116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:24:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,951,715
Mapped reads	3,621,888 / 91.65%
Unmapped reads	329,827 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,143 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	198,874 / 5.03%
Duplication rate	4.37%
Clipped reads	1,598,839 / 40.46%

2.2. ACGT Content

Number/percentage of A's	68,730,192 / 28.27%
Number/percentage of C's	46,878,645 / 19.28%
Number/percentage of T's	74,831,827 / 30.78%
Number/percentage of G's	52,642,802 / 21.66%
Number/percentage of N's	2,746 / 0%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0786

Standard Deviation	0.5463

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

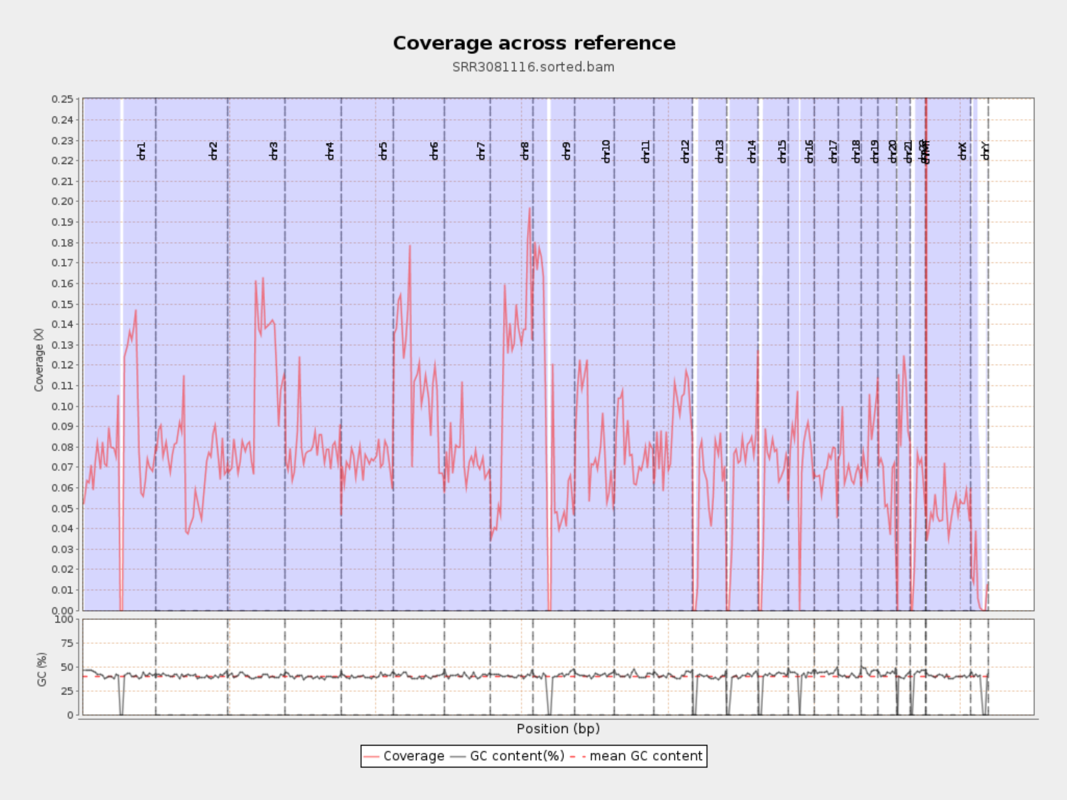
General error rate	0.89%
Mismatches	2,135,068
Insertions	17,860
Mapped reads with at least one insertion	0.49%
Deletions	50,697
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.16%

2.6. Chromosome stats

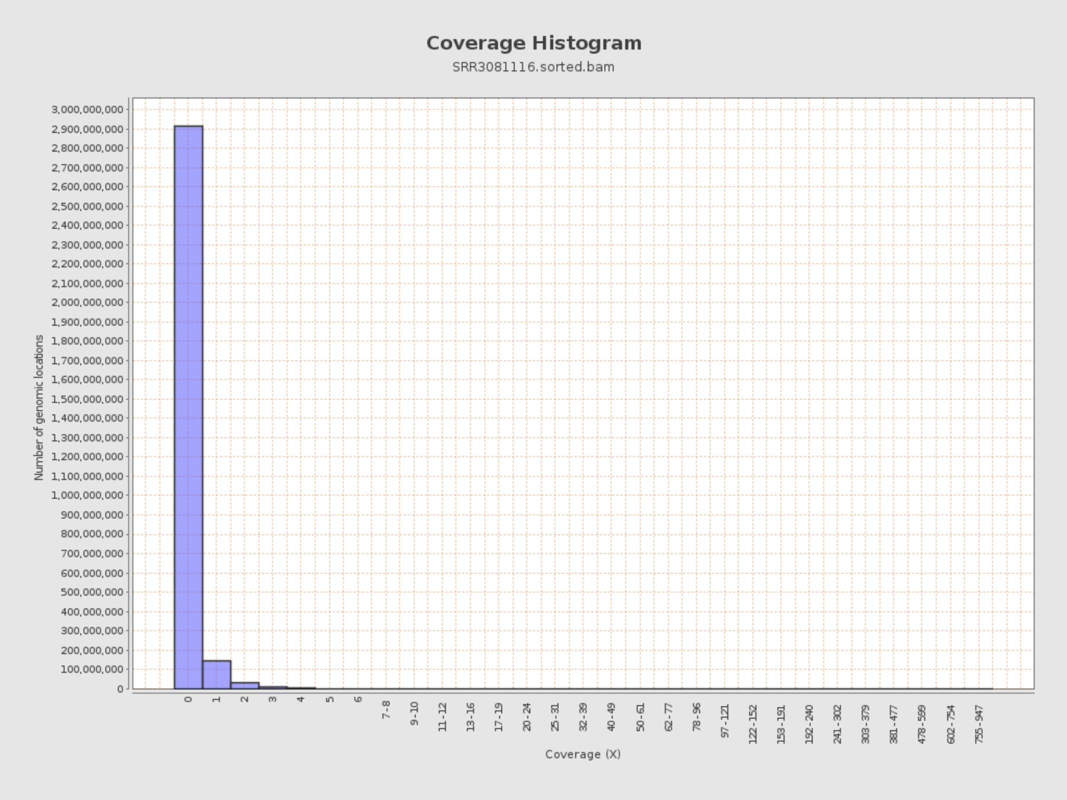
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19776515	0.0793	0.789
chr2	243199373	17371240	0.0714	0.5927
chr3	198022430	20745778	0.1048	0.4141
chr4	191154276	15226009	0.0797	0.4042
chr5	180915260	13224764	0.0731	0.3441
chr6	171115067	19749777	0.1154	0.6235
chr7	159138663	11829224	0.0743	0.5813

chr8	146364022	16980565	0.116	0.6595
chr9	141213431	12103452	0.0857	0.6827
chr10	135534747	11305894	0.0834	0.5395
chr11	135006516	10760132	0.0797	0.4904
chr12	133851895	12125161	0.0906	0.4038
chr13	115169878	6518761	0.0566	0.2962
chr14	107349540	7094163	0.0661	0.4428
chr15	102531392	6303266	0.0615	0.3207
chr16	90354753	6745373	0.0747	0.4423
chr17	81195210	5595393	0.0689	0.3497
chr18	78077248	5532135	0.0709	1.1763
chr19	59128983	5049199	0.0854	0.679
chr20	63025520	3795880	0.0602	0.3313
chr21	48129895	4434766	0.0921	0.4872
chr22	51304566	2436377	0.0475	0.2716
chrMT	16571	215591	13.0101	8.3851
chrX	155270560	7611324	0.049	0.3327
chrY	59373566	645260	0.0109	0.2594

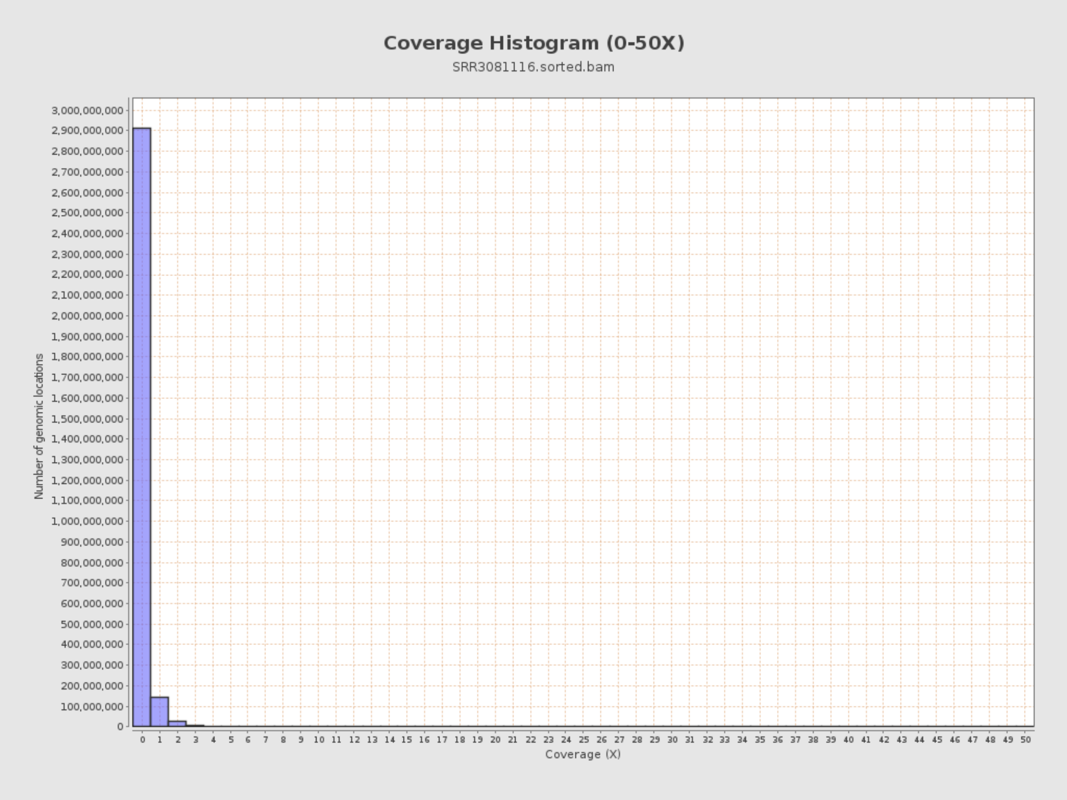
3. Results : Coverage across reference



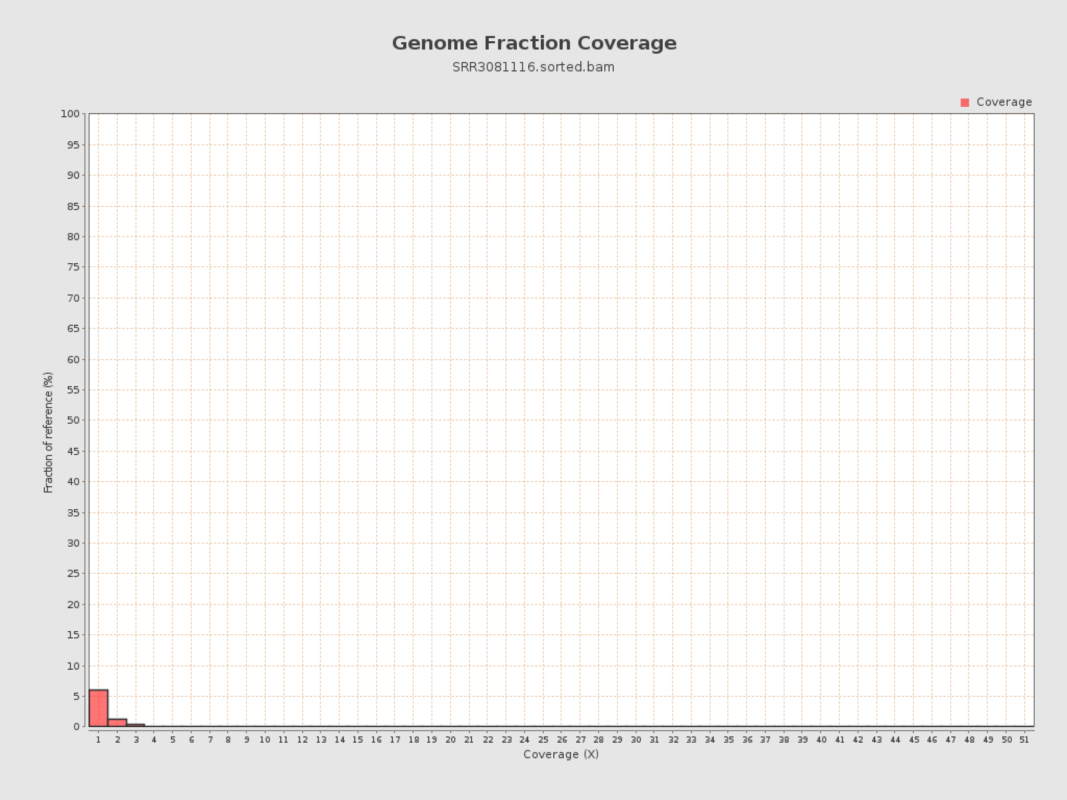
4. Results : Coverage Histogram



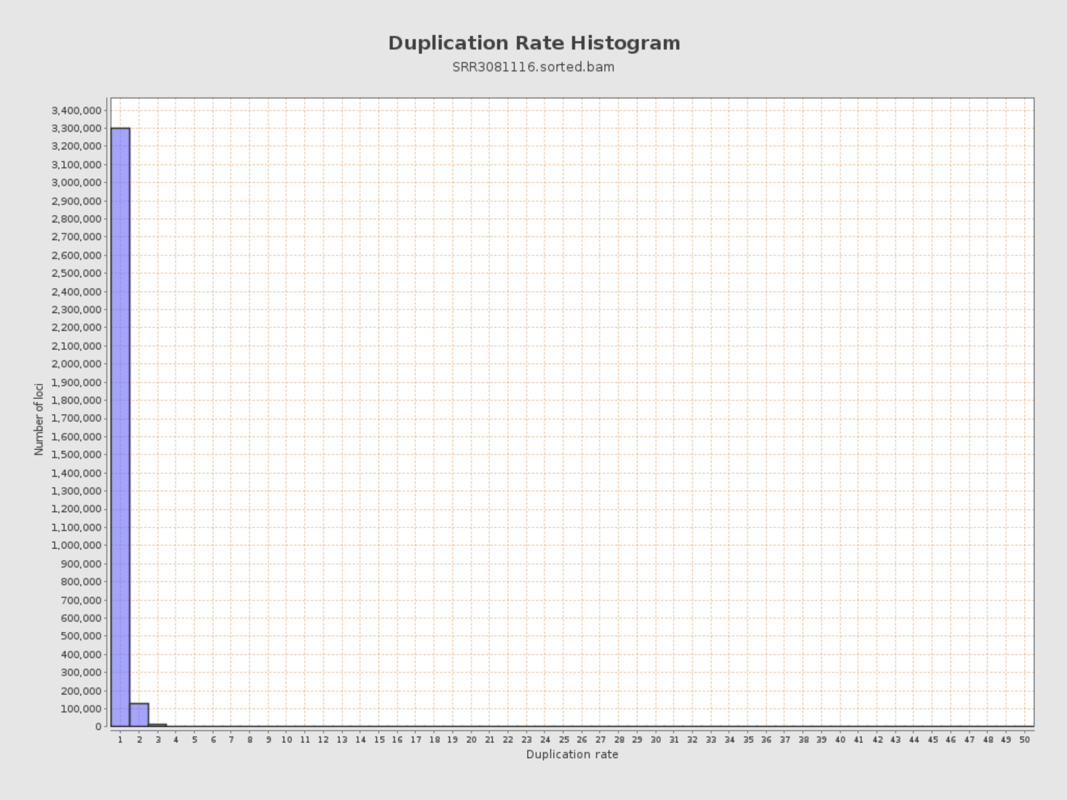
5. Results : Coverage Histogram (0-50X)



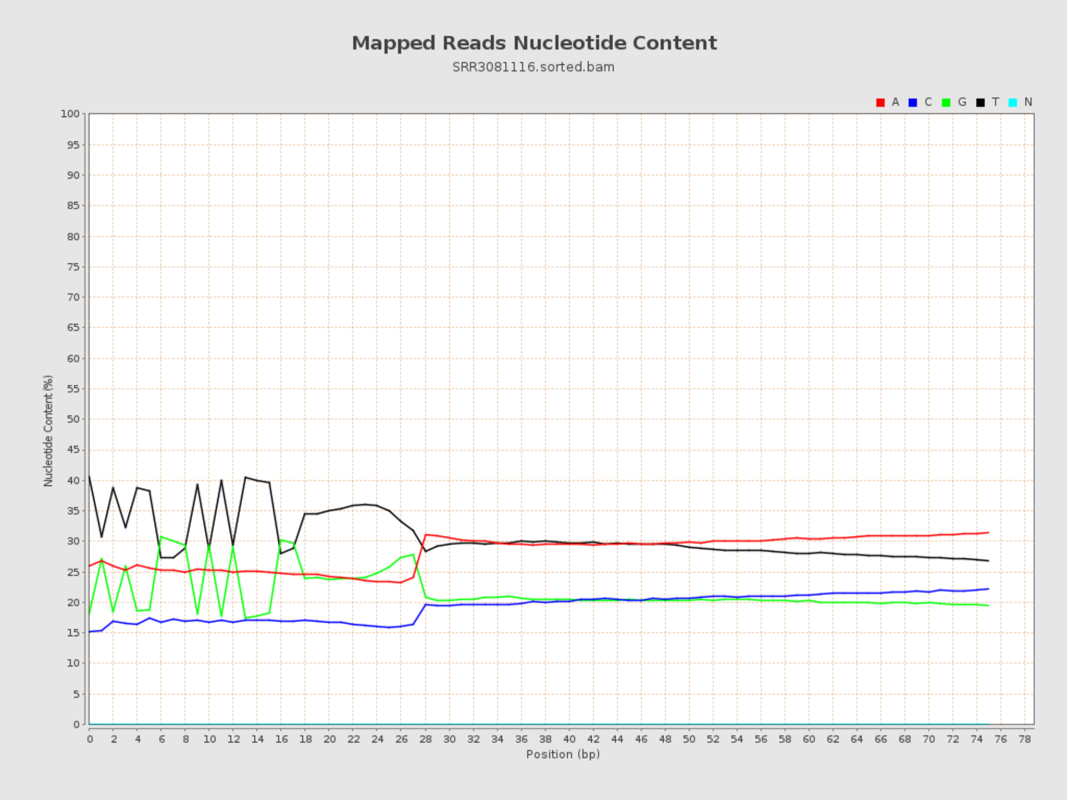
6. Results : Genome Fraction Coverage



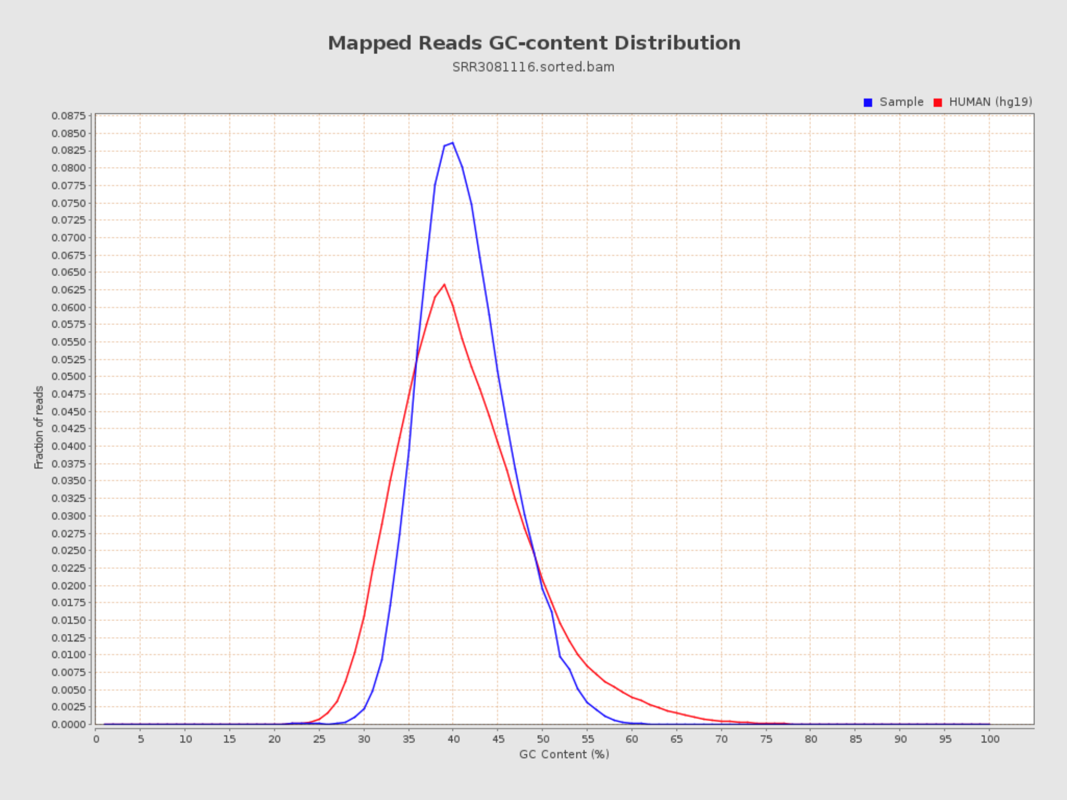
7. Results : Duplication Rate Histogram



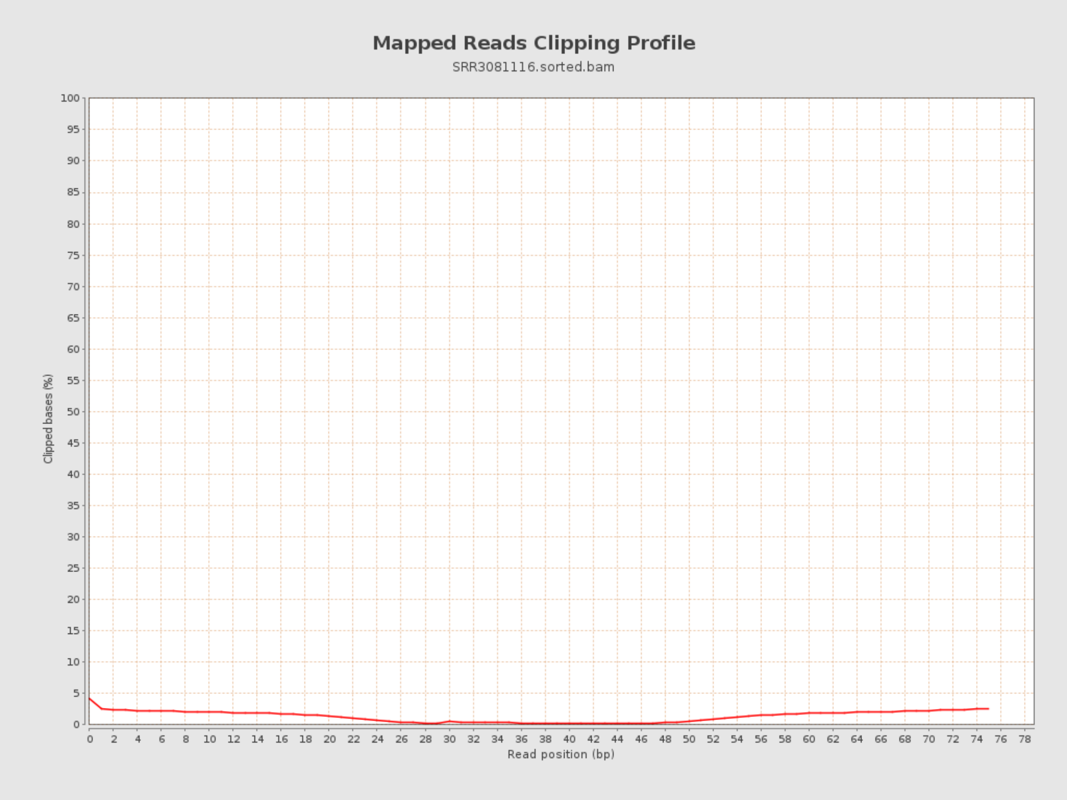
8. Results : Mapped Reads Nucleotide Content



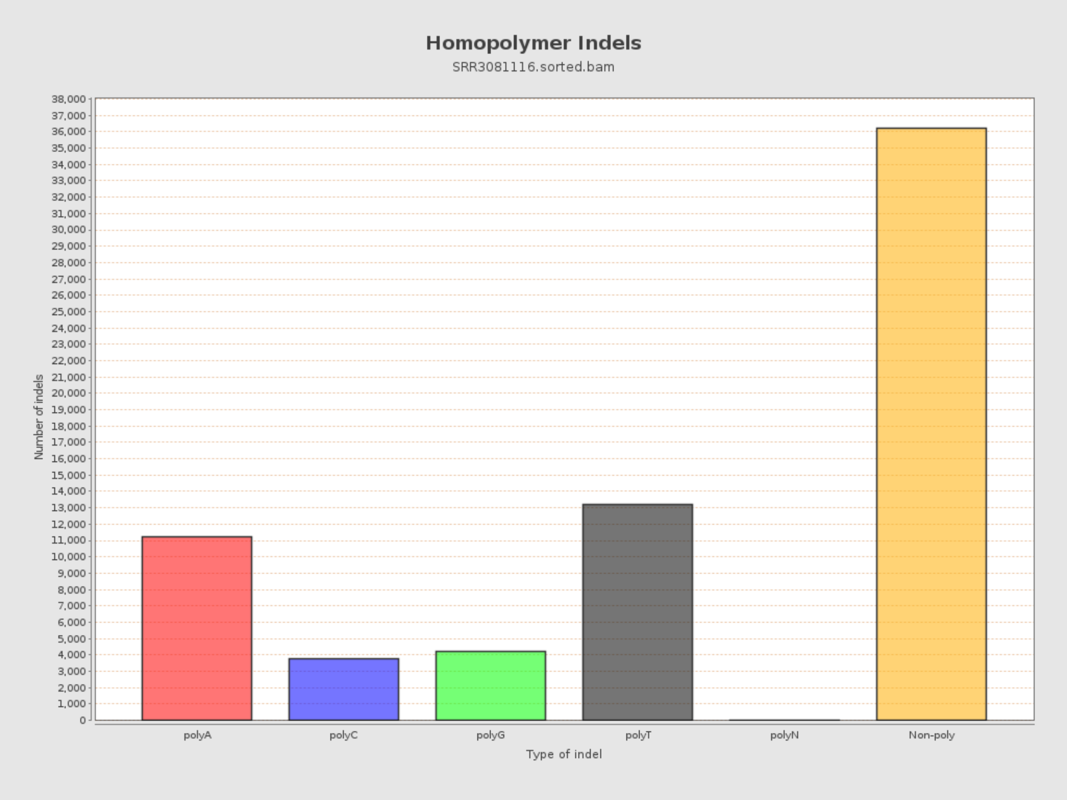
9. Results : Mapped Reads GC-content Distribution



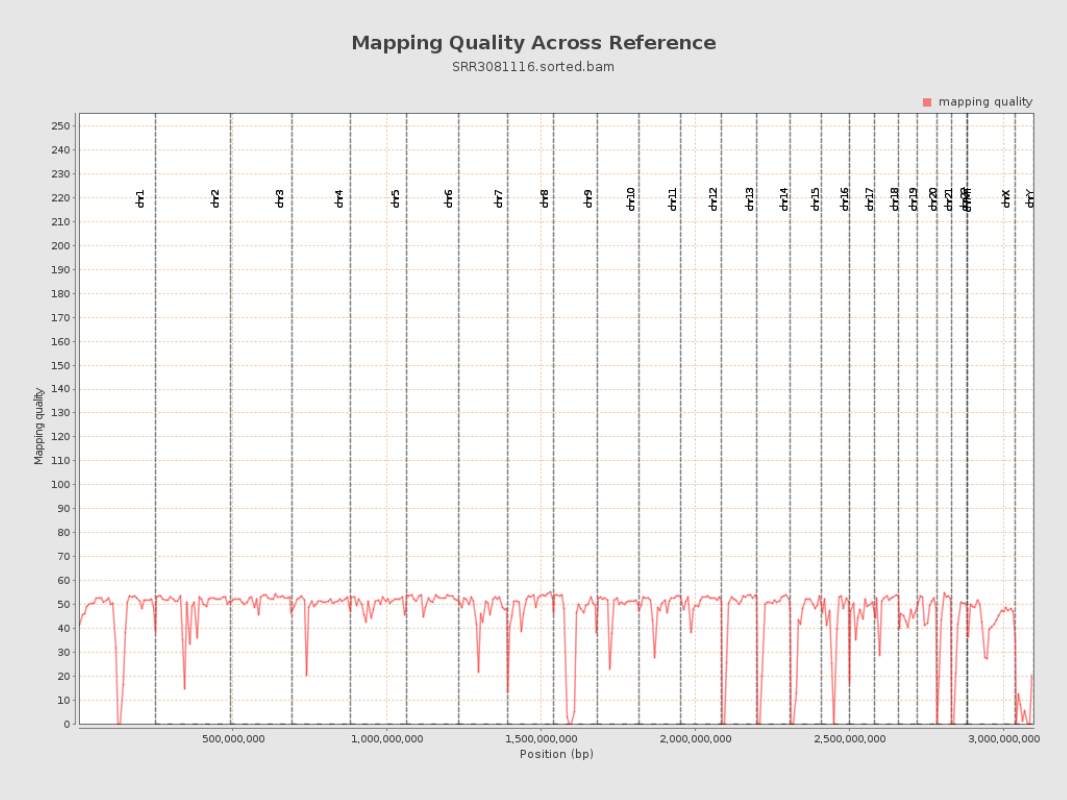
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram