Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:49:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081112.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_SRR3081112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:49:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,821,357
Mapped reads	2,562,295 / 90.82%
Unmapped reads	259,062 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,962 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	128,755 / 4.56%
Duplication rate	3.57%
Clipped reads	1,138,159 / 40.34%

2.2. ACGT Content

Number/percentage of A's	46,170,735 / 26.96%
Number/percentage of C's	33,271,771 / 19.43%
Number/percentage of T's	52,072,418 / 30.41%
Number/percentage of G's	39,714,418 / 23.19%
Number/percentage of N's	1,854 / 0%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0553

Standard Deviation	0.5471

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

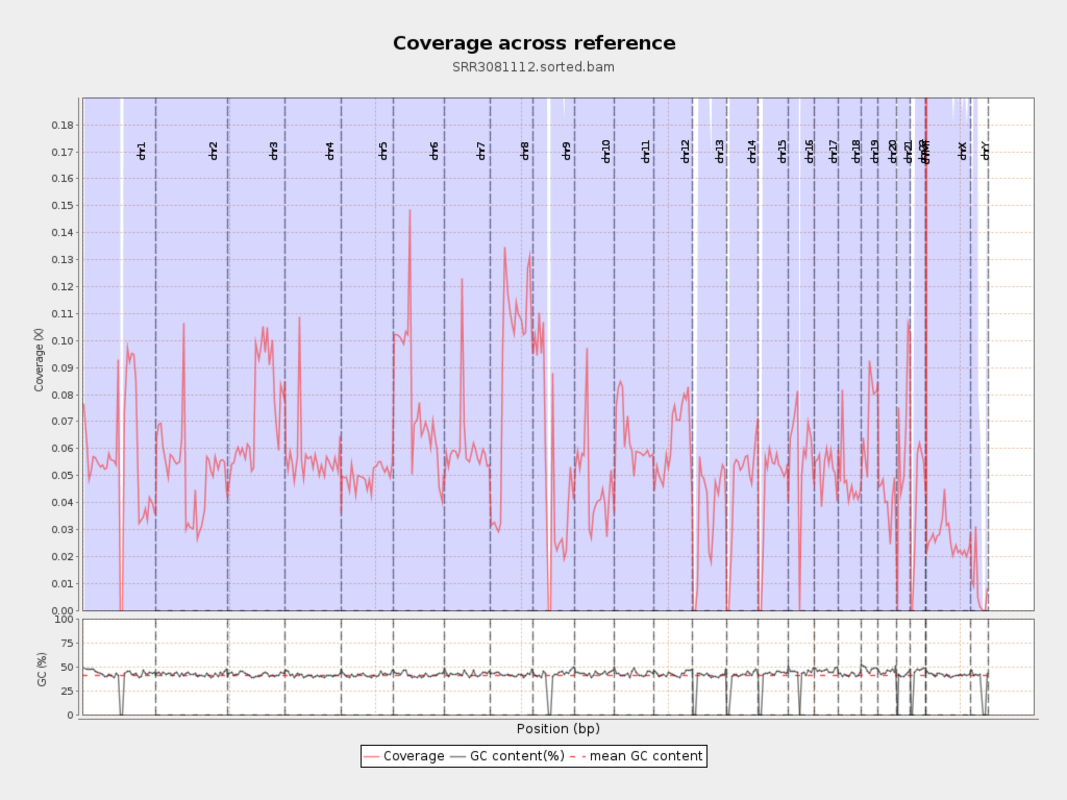
General error rate	0.92%
Mismatches	1,548,855
Insertions	13,519
Mapped reads with at least one insertion	0.52%
Deletions	38,170
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.03%

2.6. Chromosome stats

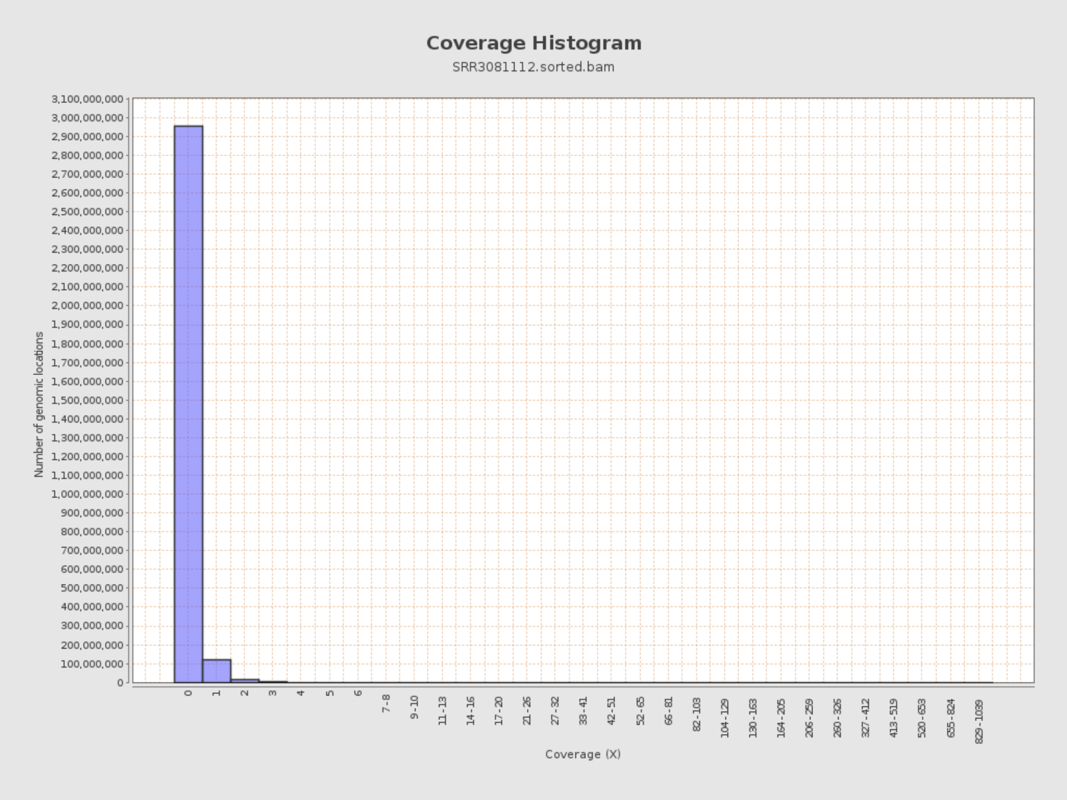
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13711312	0.055	0.8601
chr2	243199373	12497001	0.0514	0.5802
chr3	198022430	14421495	0.0728	0.3137
chr4	191154276	10870355	0.0569	0.3518
chr5	180915260	9082855	0.0502	0.2627
chr6	171115067	13359838	0.0781	0.6339
chr7	159138663	9672047	0.0608	0.9084

chr8	146364022	13234065	0.0904	0.5155
chr9	141213431	7325192	0.0519	0.634
chr10	135534747	6328212	0.0467	0.4821
chr11	135006516	8609694	0.0638	0.5129
chr12	133851895	8449342	0.0631	0.3195
chr13	115169878	4153641	0.0361	0.2158
chr14	107349540	4949069	0.0461	0.3696
chr15	102531392	4559827	0.0445	0.2674
chr16	90354753	5121299	0.0567	0.3906
chr17	81195210	4321441	0.0532	0.3121
chr18	78077248	3820249	0.0489	1.2369
chr19	59128983	4264779	0.0721	0.6709
chr20	63025520	2633665	0.0418	0.2719
chr21	48129895	3151358	0.0655	0.4142
chr22	51304566	2033213	0.0396	0.2282
chrMT	16571	149924	9.0474	5.359
chrX	155270560	4099019	0.0264	0.2735
chrY	59373566	481747	0.0081	0.2438

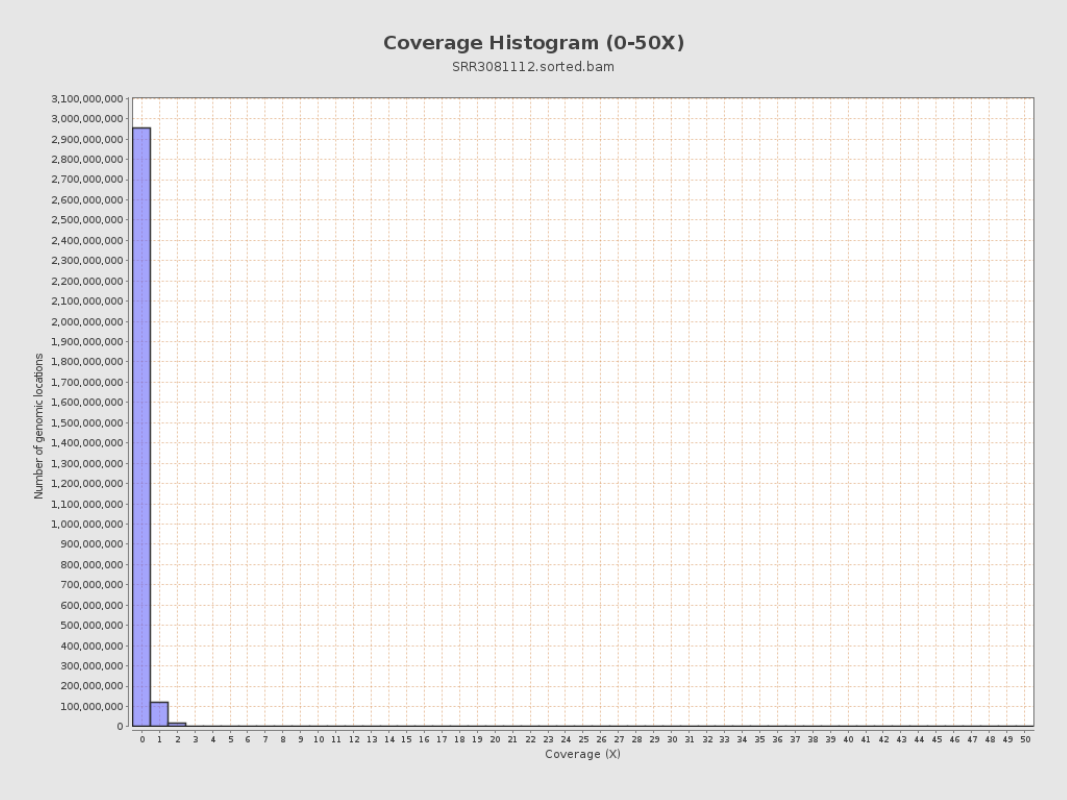
3. Results : Coverage across reference



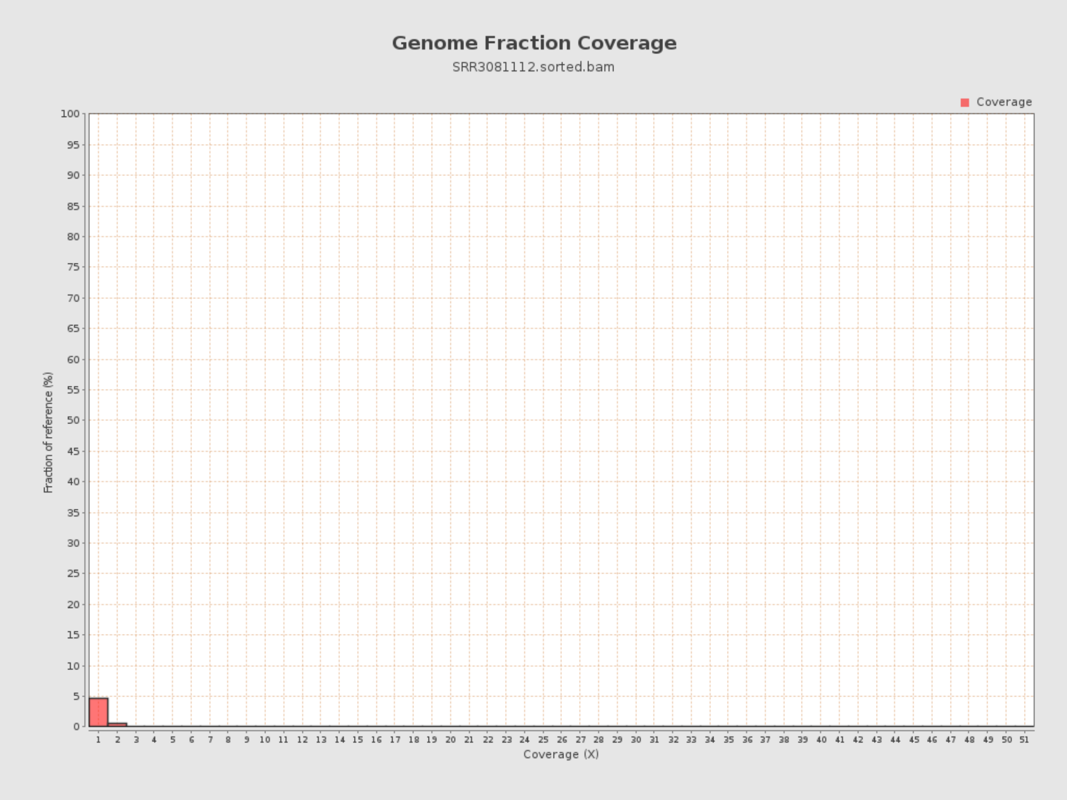
4. Results : Coverage Histogram



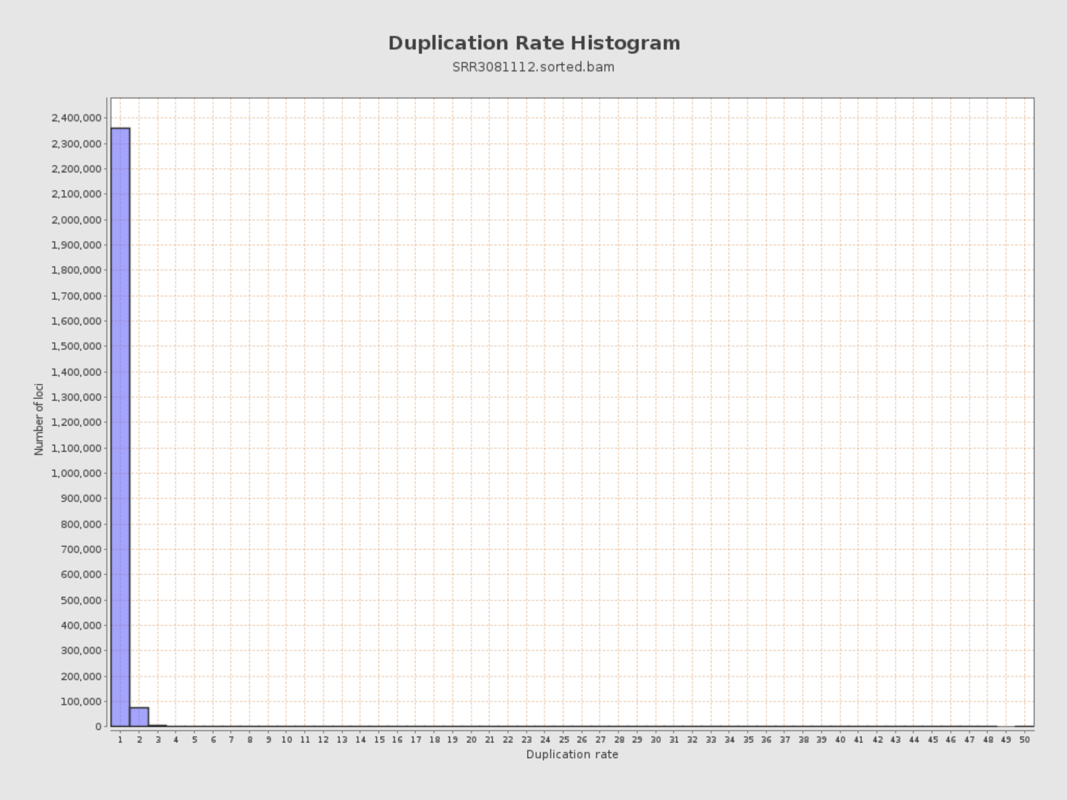
5. Results : Coverage Histogram (0-50X)



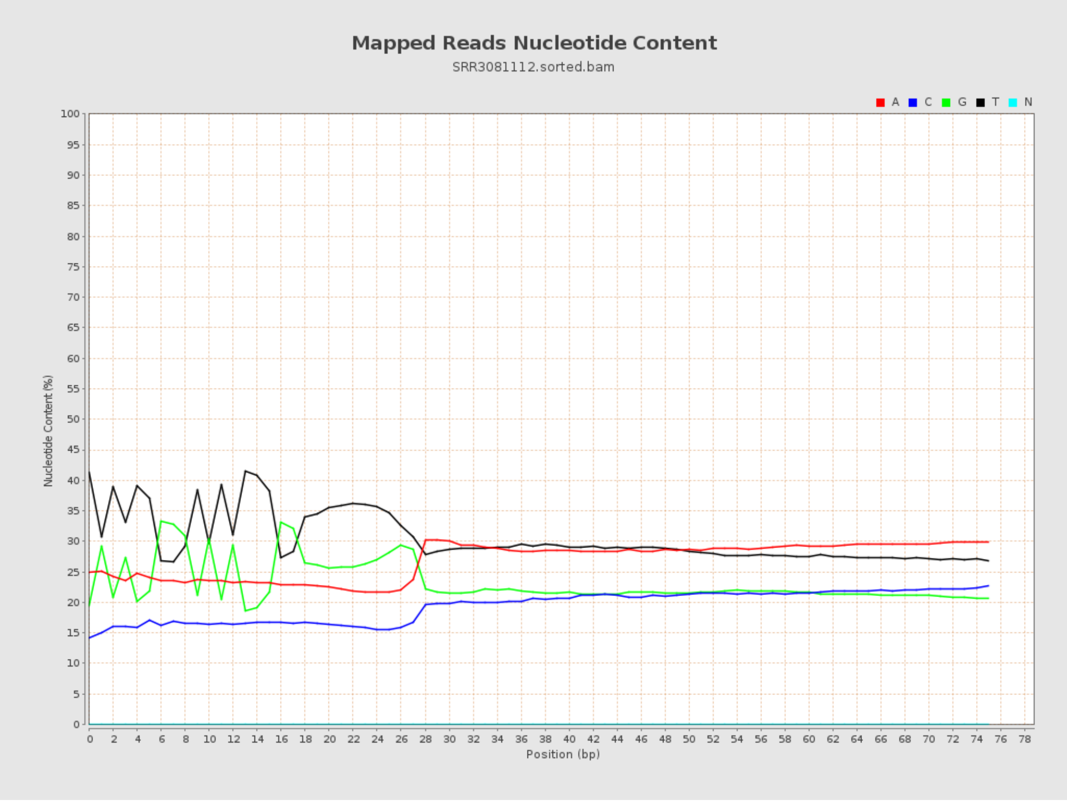
6. Results : Genome Fraction Coverage



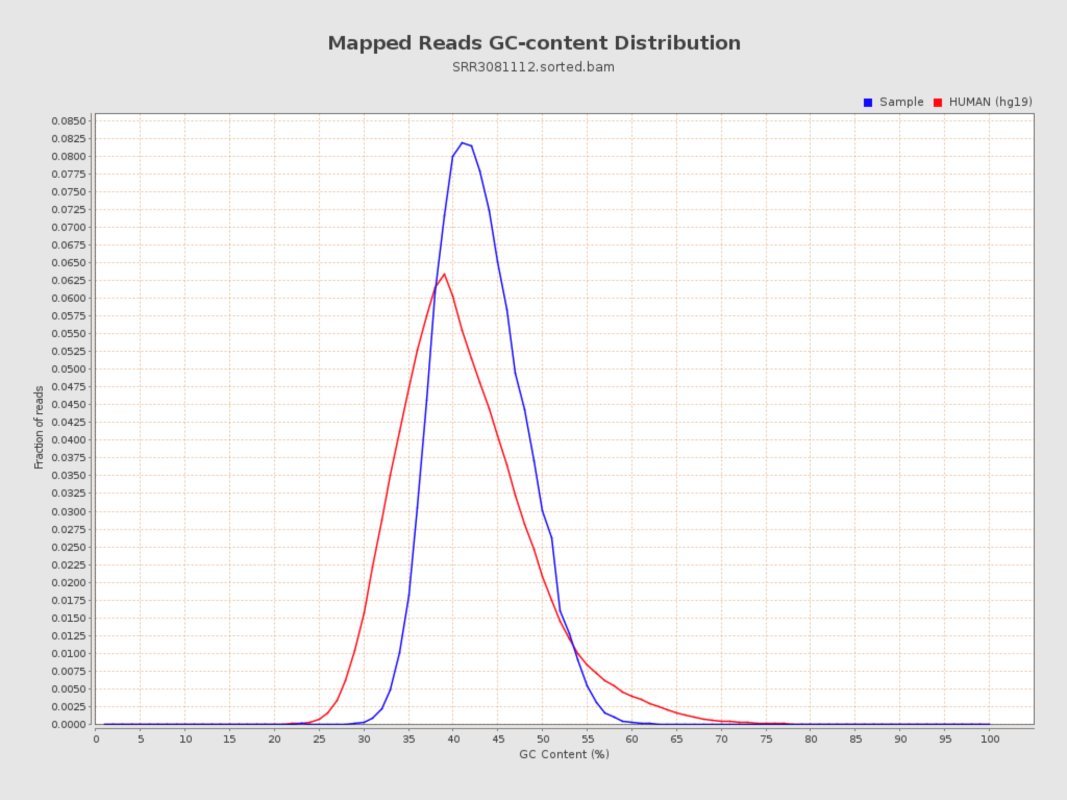
7. Results : Duplication Rate Histogram



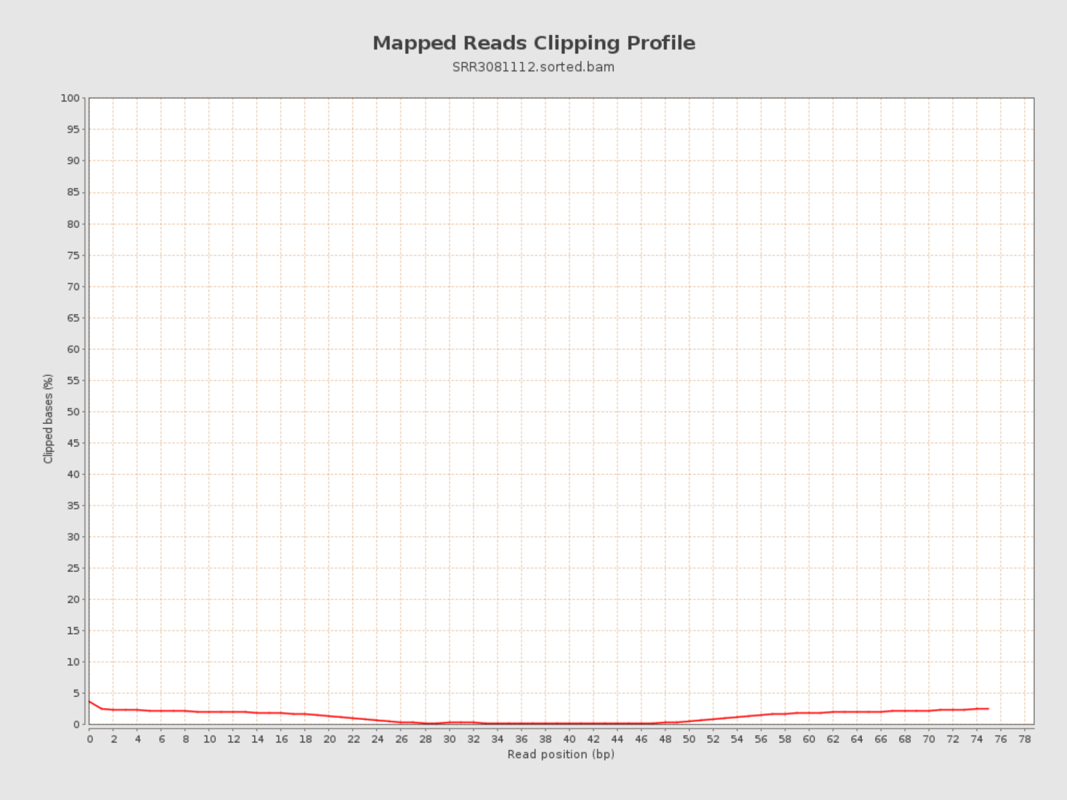
8. Results : Mapped Reads Nucleotide Content



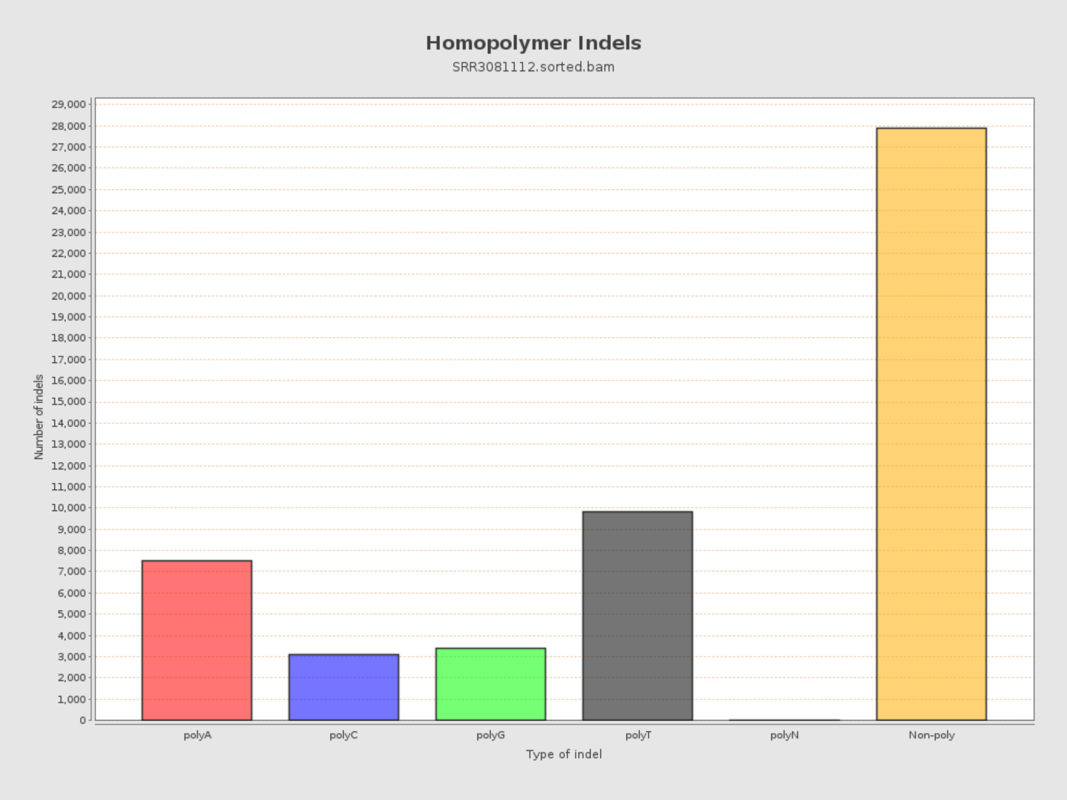
9. Results : Mapped Reads GC-content Distribution



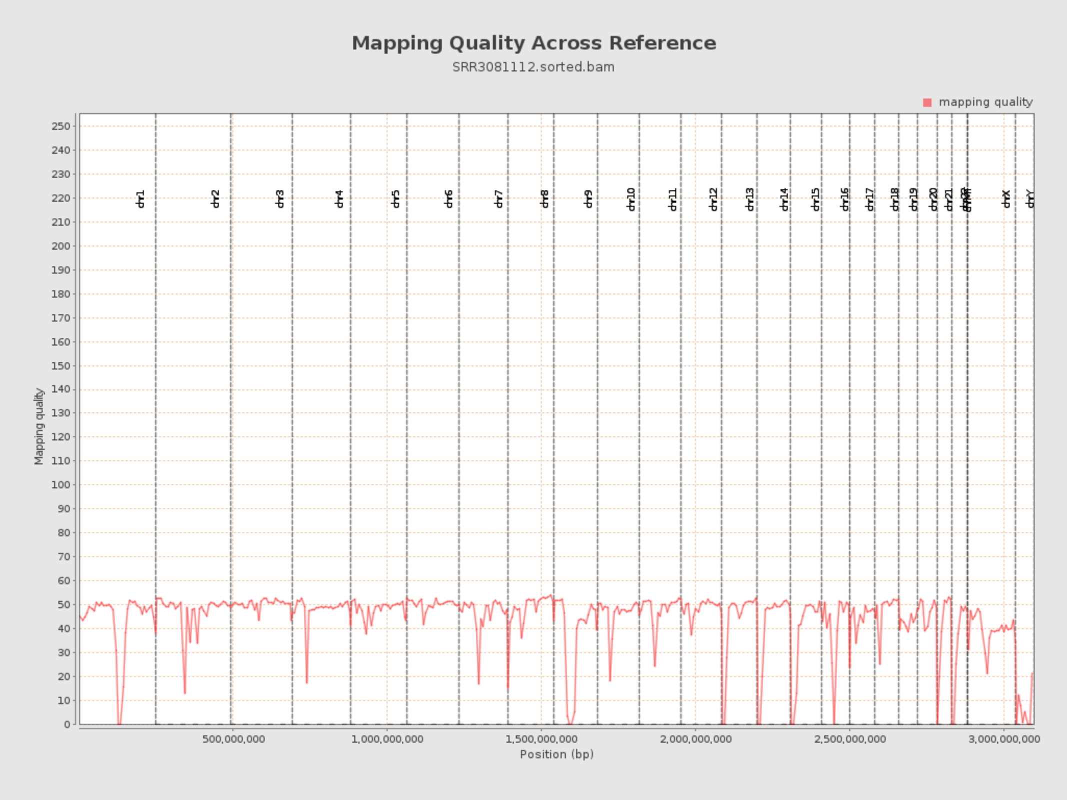
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram