Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:05:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081114.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_SRR3081114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:05:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,033,894
Mapped reads	2,806,118 / 92.49%
Unmapped reads	227,776 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,443 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	140,131 / 4.62%
Duplication rate	4.08%
Clipped reads	1,145,696 / 37.76%

2.2. ACGT Content

Number/percentage of A's	52,498,379 / 27.62%
Number/percentage of C's	37,031,260 / 19.48%
Number/percentage of T's	58,068,586 / 30.55%
Number/percentage of G's	42,503,340 / 22.36%
Number/percentage of N's	2,043 / 0%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0614

Standard Deviation	0.4352

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

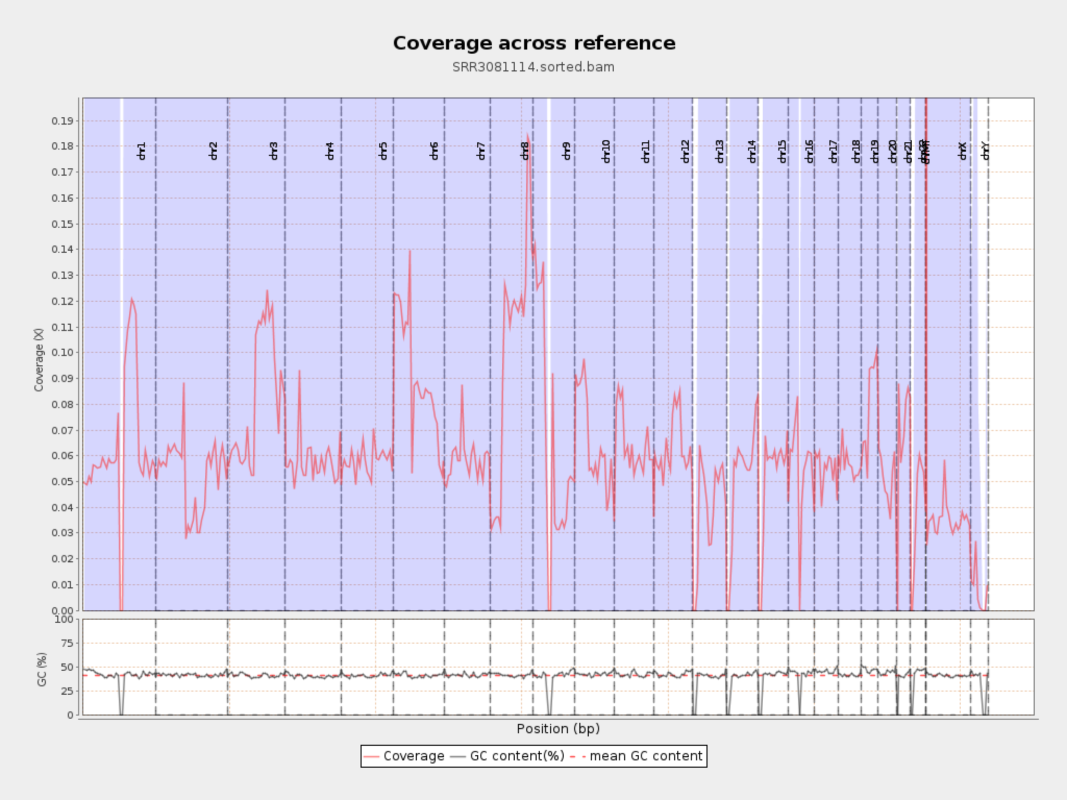
General error rate	0.88%
Mismatches	1,644,724
Insertions	13,785
Mapped reads with at least one insertion	0.49%
Deletions	38,801
Mapped reads with at least one deletion	1.37%
Homopolymer indels	47.2%

2.6. Chromosome stats

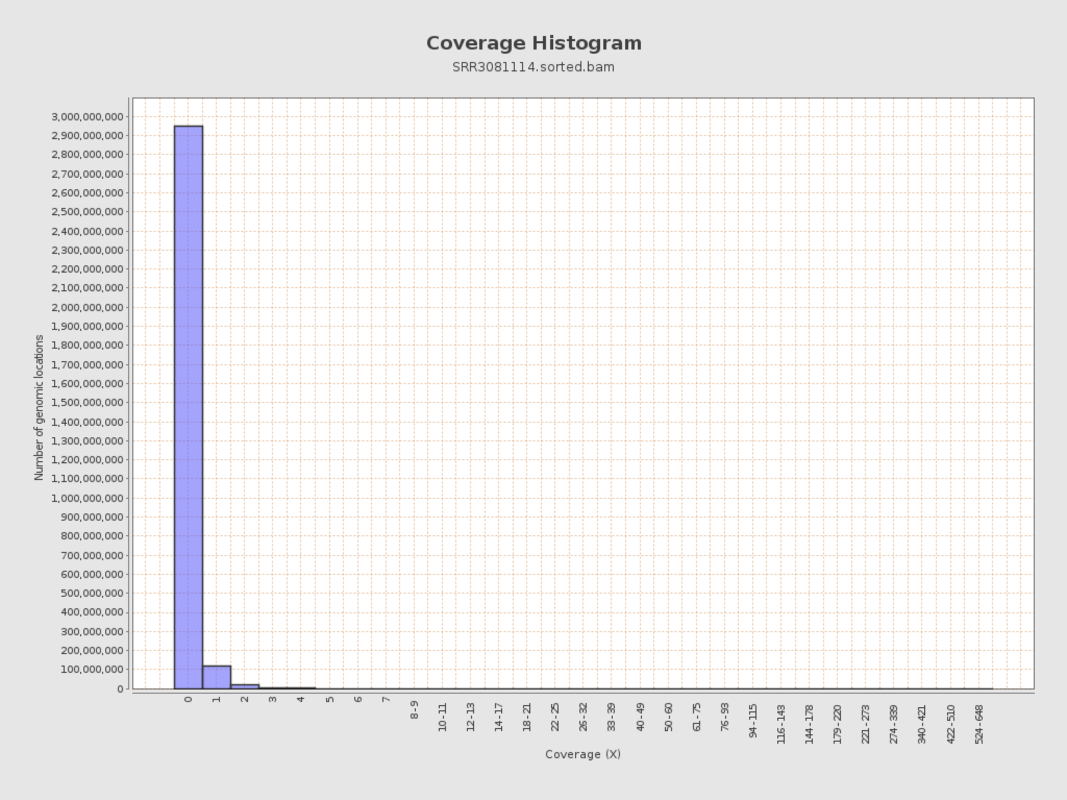
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15756364	0.0632	0.5698
chr2	243199373	12849719	0.0528	0.4656
chr3	198022430	16228801	0.082	0.353
chr4	191154276	11098035	0.0581	0.3255
chr5	180915260	10536908	0.0582	0.2959
chr6	171115067	15592068	0.0911	0.5346
chr7	159138663	9342403	0.0587	0.5228

chr8	146364022	15012269	0.1026	0.4936
chr9	141213431	9282845	0.0657	0.5345
chr10	135534747	8899293	0.0657	0.3995
chr11	135006516	8706378	0.0645	0.412
chr12	133851895	8462994	0.0632	0.3297
chr13	115169878	4555764	0.0396	0.244
chr14	107349540	5437077	0.0506	0.36
chr15	102531392	5075599	0.0495	0.2776
chr16	90354753	4859236	0.0538	0.3543
chr17	81195210	4510477	0.0556	0.3051
chr18	78077248	4429628	0.0567	0.8734
chr19	59128983	4722480	0.0799	0.5152
chr20	63025520	3242339	0.0514	0.3034
chr21	48129895	3353820	0.0697	0.4249
chr22	51304566	1941792	0.0378	0.2378
chrMT	16571	351267	21.1977	13.215
chrX	155270560	5465247	0.0352	0.2642
chrY	59373566	460900	0.0078	0.1898

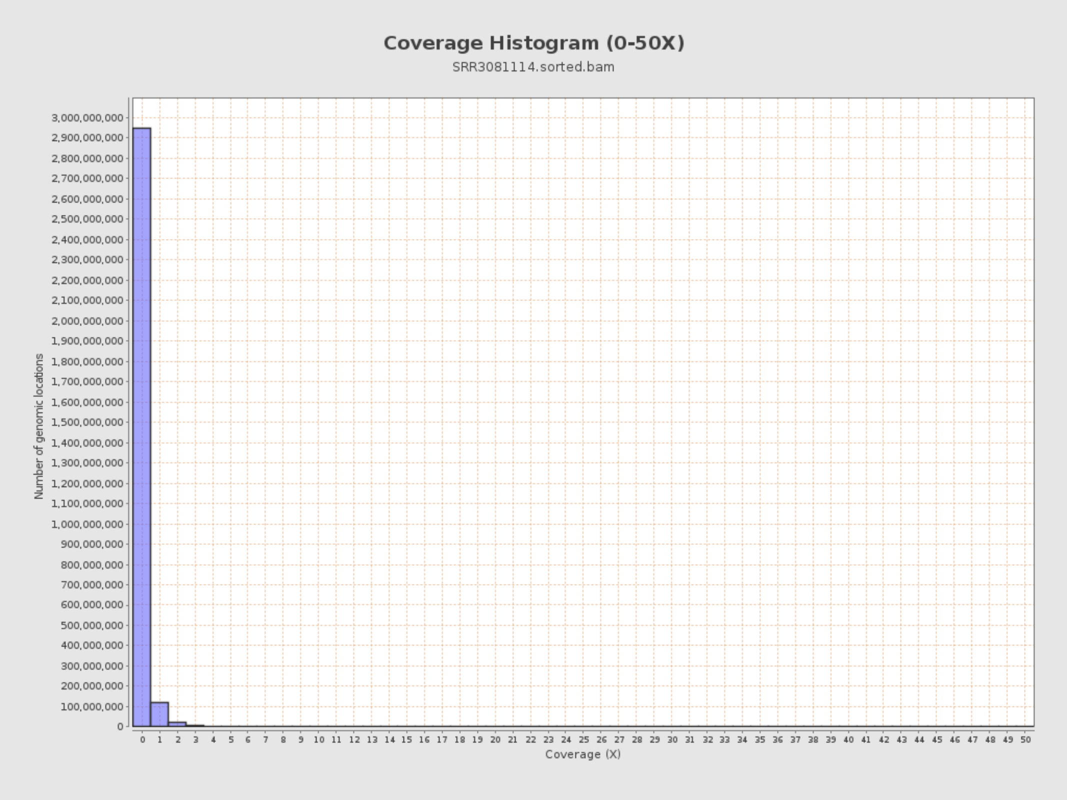
3. Results : Coverage across reference



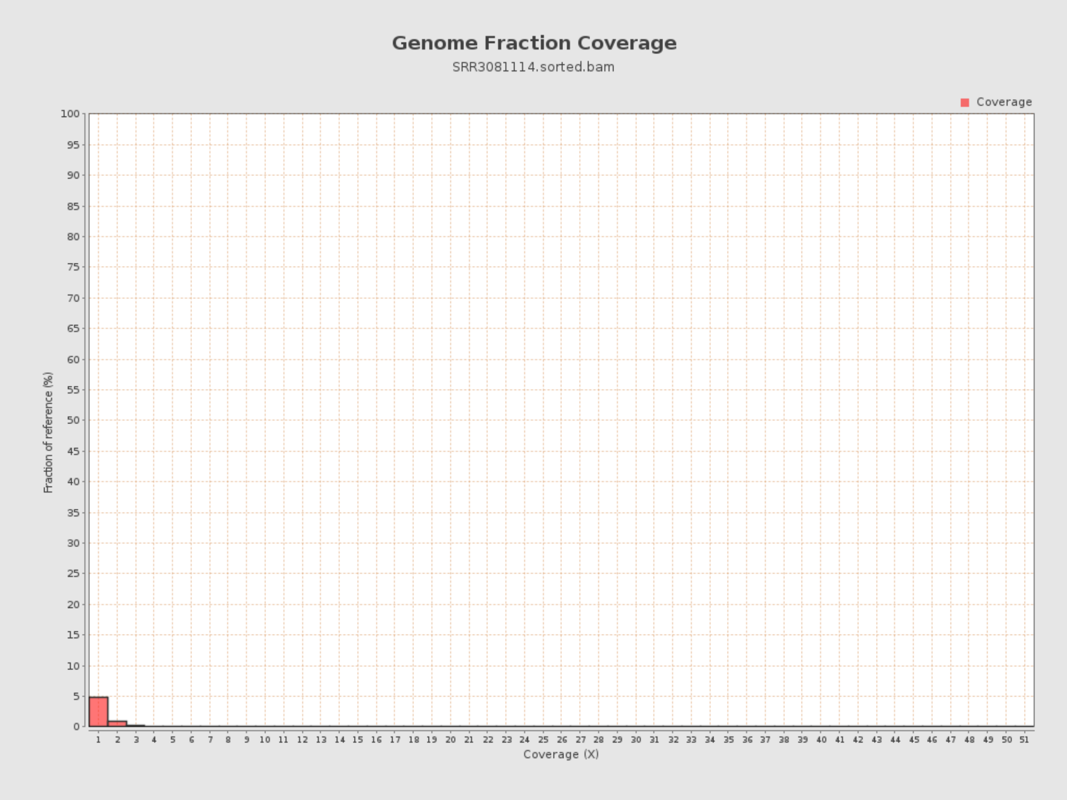
4. Results : Coverage Histogram



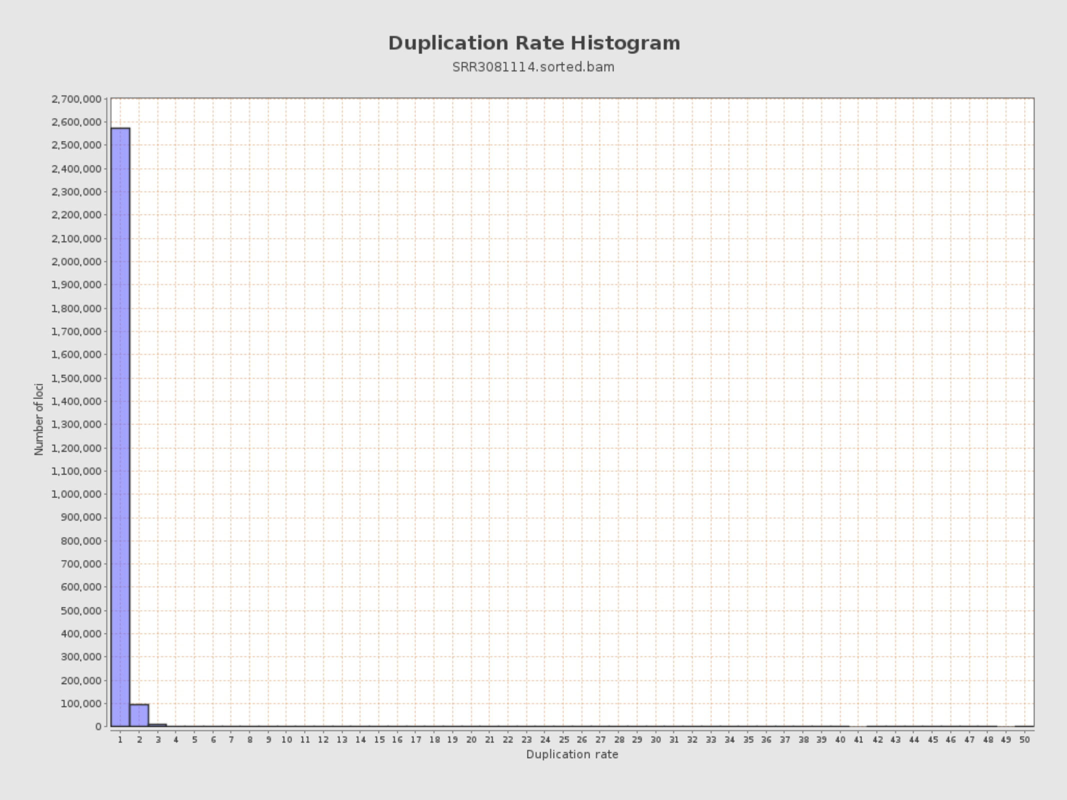
5. Results : Coverage Histogram (0-50X)



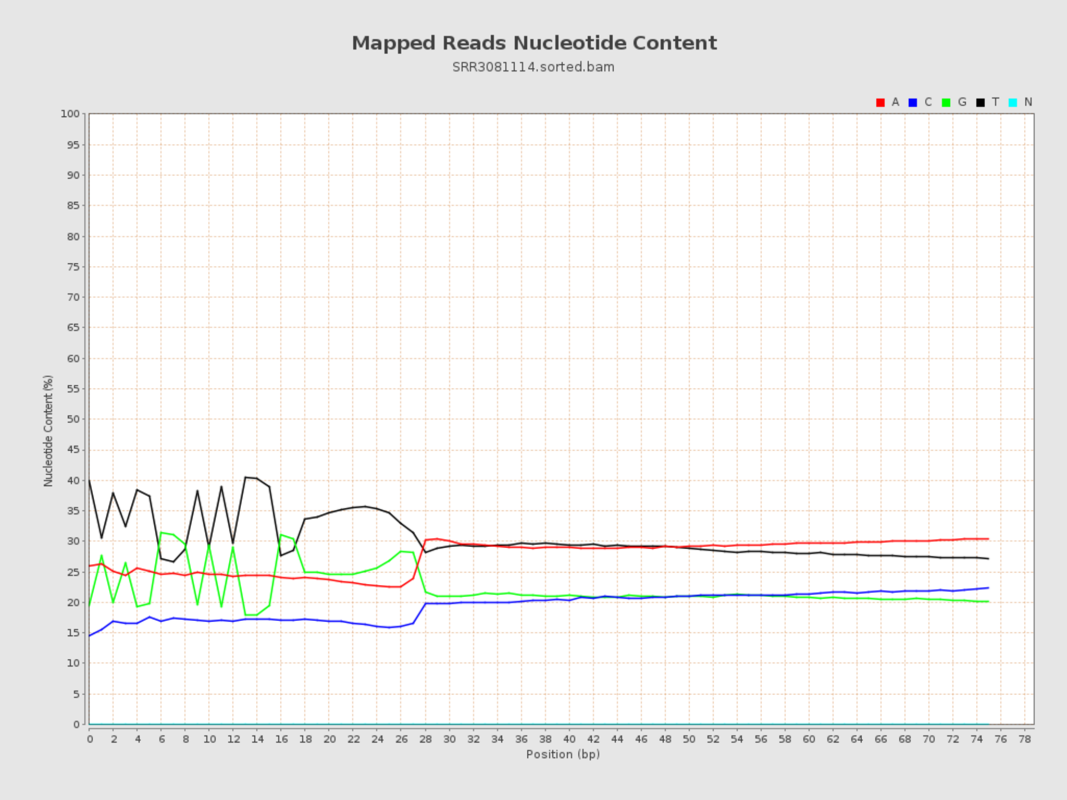
6. Results : Genome Fraction Coverage



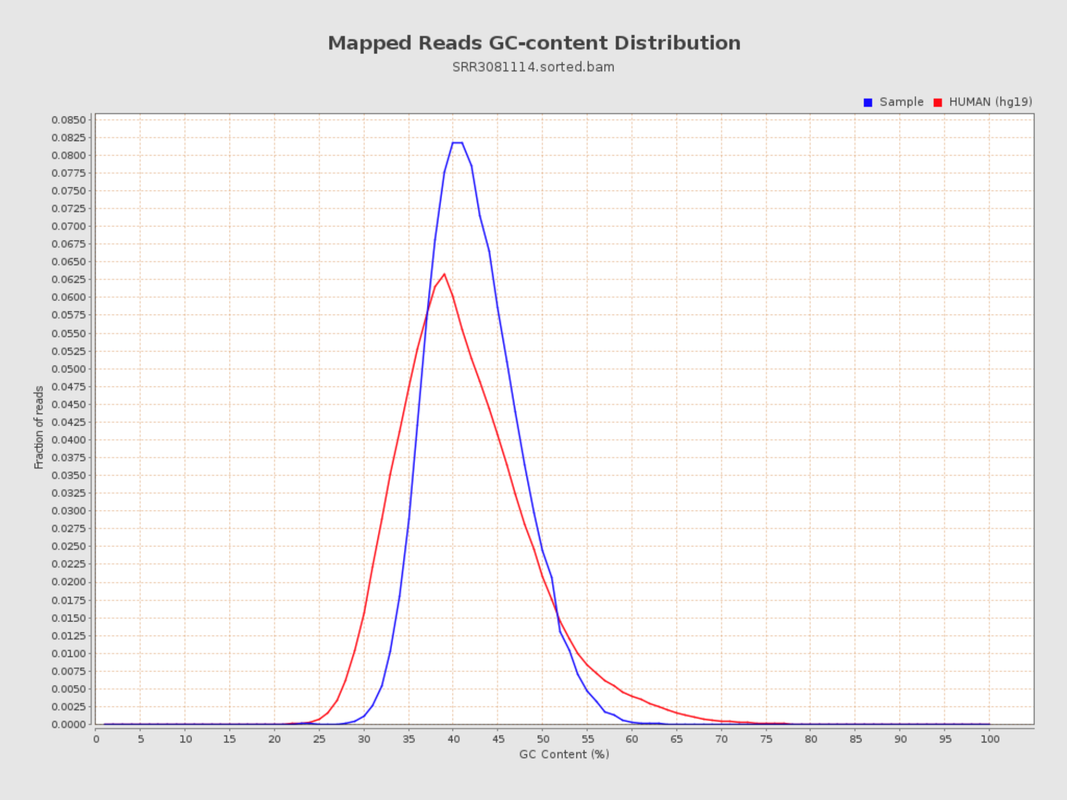
7. Results : Duplication Rate Histogram



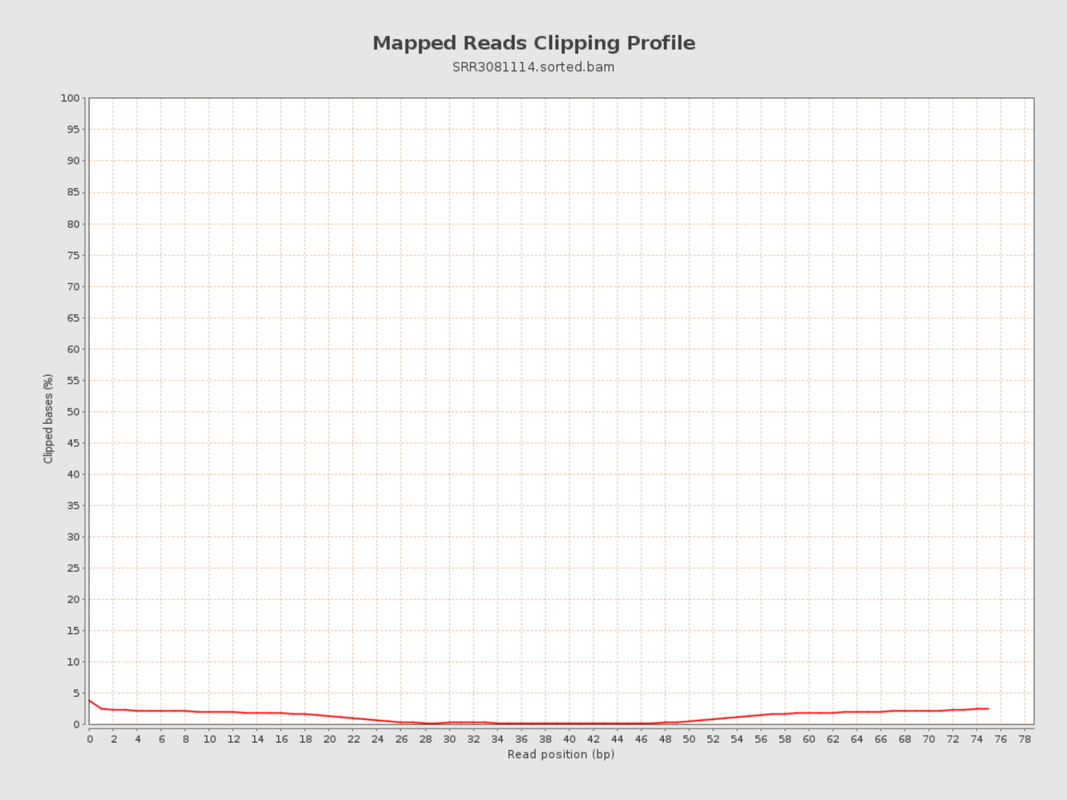
8. Results : Mapped Reads Nucleotide Content



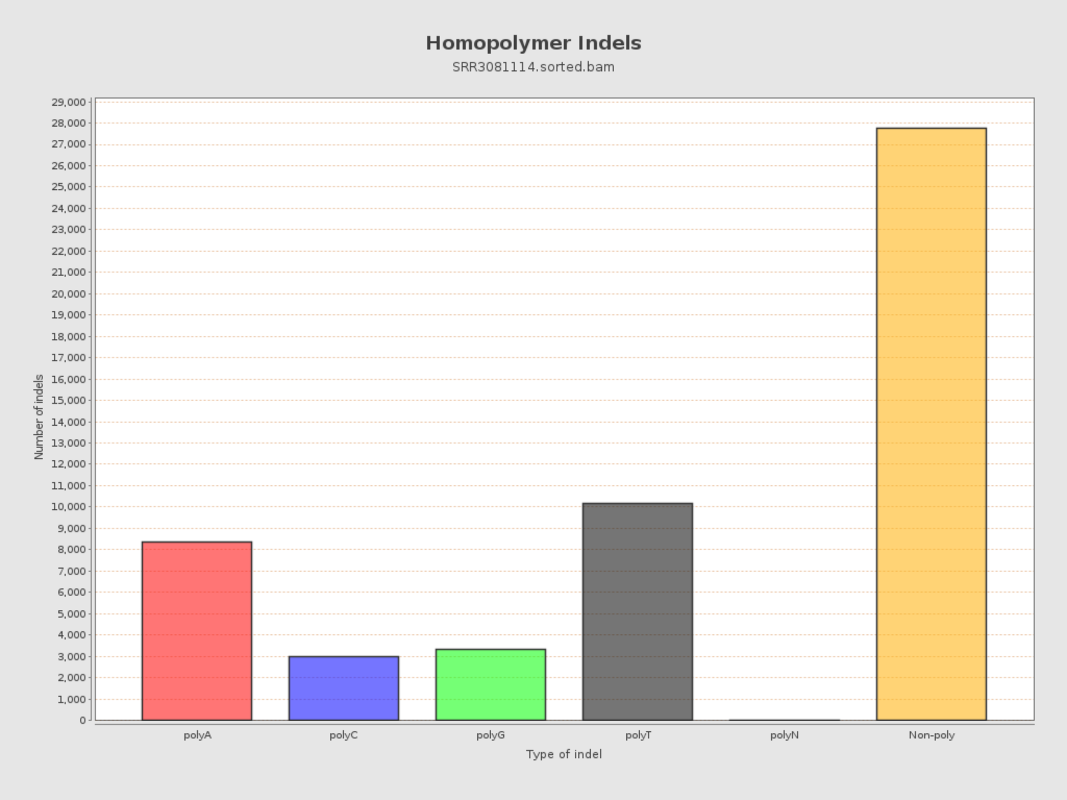
9. Results : Mapped Reads GC-content Distribution



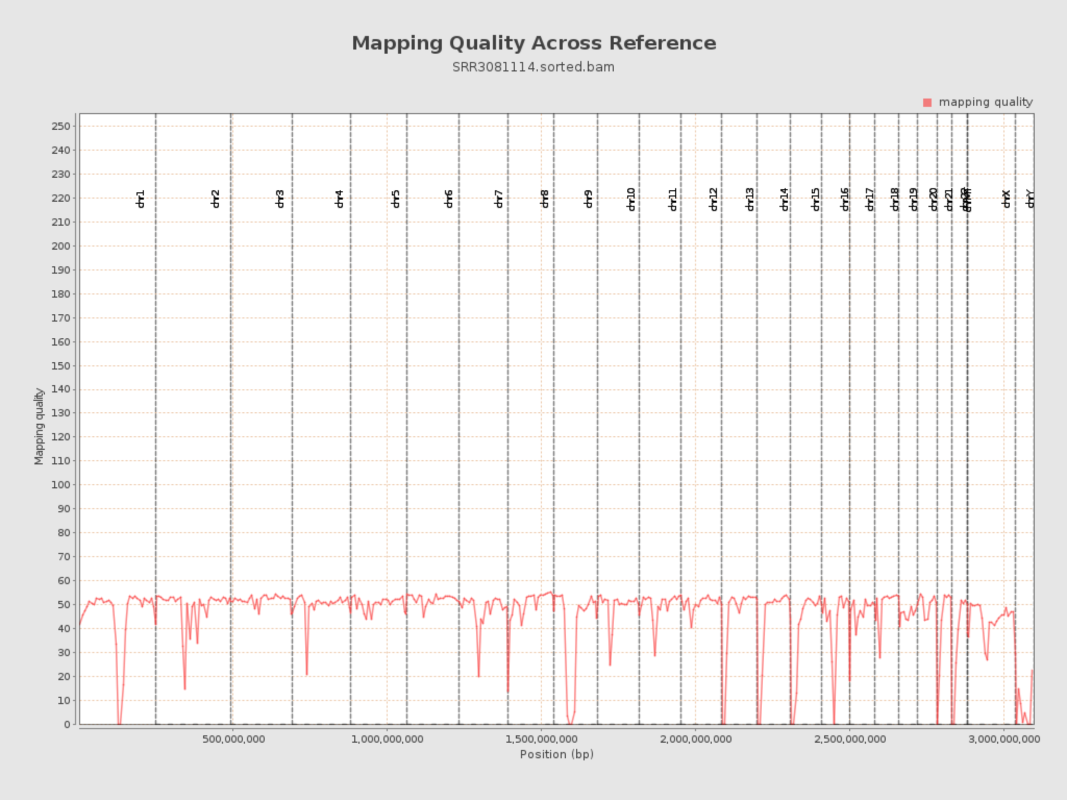
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram