Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:50:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013246.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_SRR6013246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:50:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,393,560
Mapped reads	1,059,885 / 76.06%
Unmapped reads	333,675 / 23.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,732 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	127,385 / 9.14%
Duplication rate	9.85%
Clipped reads	670,429 / 48.11%

2.2. ACGT Content

Number/percentage of A's	18,426,700 / 27.97%
Number/percentage of C's	11,121,962 / 16.88%
Number/percentage of T's	22,146,492 / 33.62%
Number/percentage of G's	14,168,124 / 21.51%
Number/percentage of N's	13,780 / 0.02%
GC Percentage	38.39%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.2994

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

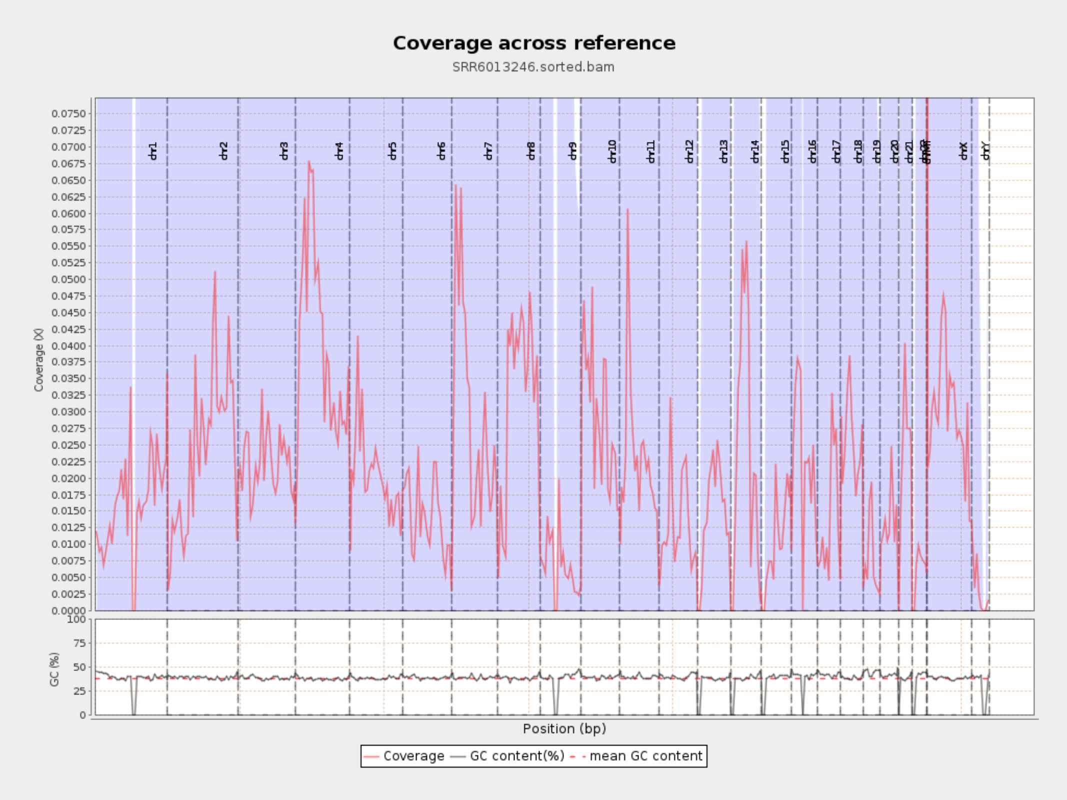
General error rate	1.09%
Mismatches	713,564
Insertions	4,665
Mapped reads with at least one insertion	0.44%
Deletions	43,896
Mapped reads with at least one deletion	4.05%
Homopolymer indels	41.92%

2.6. Chromosome stats

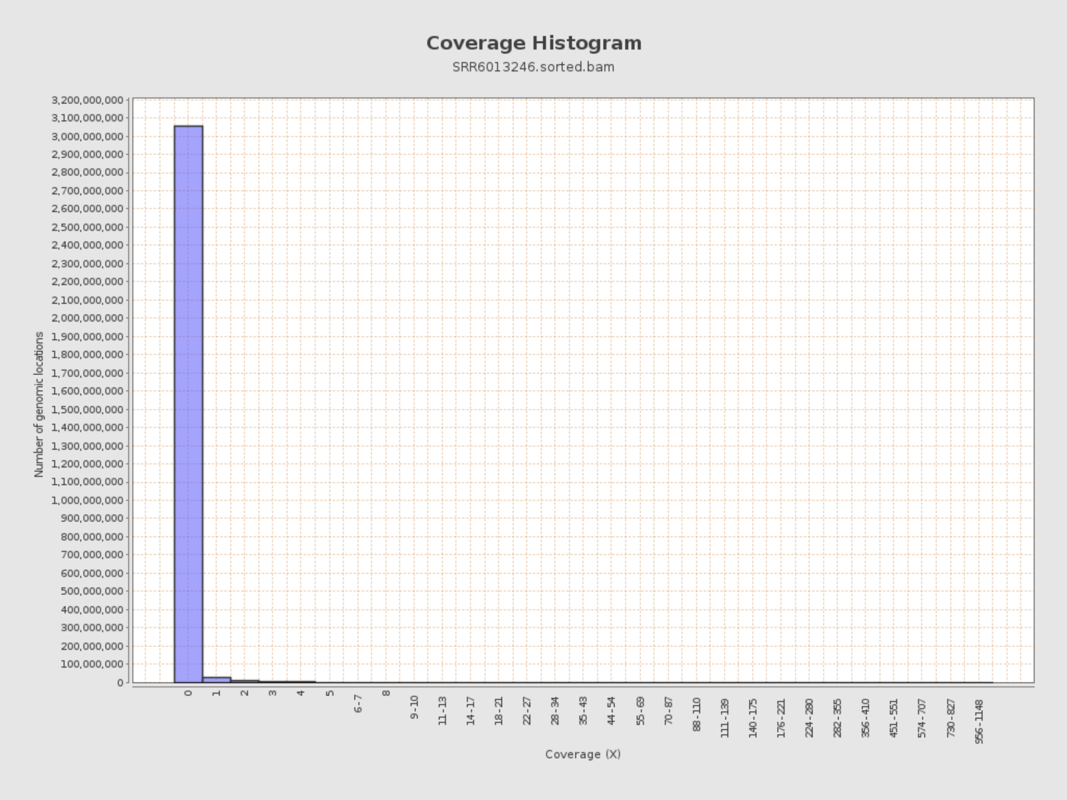
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4017860	0.0161	0.4301
chr2	243199373	5913136	0.0243	0.3047
chr3	198022430	4419362	0.0223	0.2224
chr4	191154276	7696740	0.0403	0.3054
chr5	180915260	3741122	0.0207	0.2121
chr6	171115067	2453000	0.0143	0.2078
chr7	159138663	4766016	0.0299	0.321

chr8	146364022	4813665	0.0329	0.6784
chr9	141213431	956249	0.0068	0.1589
chr10	135534747	3990283	0.0294	0.312
chr11	135006516	3120457	0.0231	0.2338
chr12	133851895	1790301	0.0134	0.1693
chr13	115169878	1702833	0.0148	0.1822
chr14	107349540	2673945	0.0249	0.2427
chr15	102531392	1081662	0.0105	0.1467
chr16	90354753	2013047	0.0223	0.225
chr17	81195210	1122283	0.0138	0.1756
chr18	78077248	2003003	0.0257	0.3761
chr19	59128983	475673	0.008	0.3342
chr20	63025520	841293	0.0133	0.1714
chr21	48129895	1183601	0.0246	0.2319
chr22	51304566	321360	0.0063	0.1079
chrMT	16571	39272	2.3699	2.3625
chrX	155270560	4637212	0.0299	0.2659
chrY	59373566	180455	0.003	0.0795

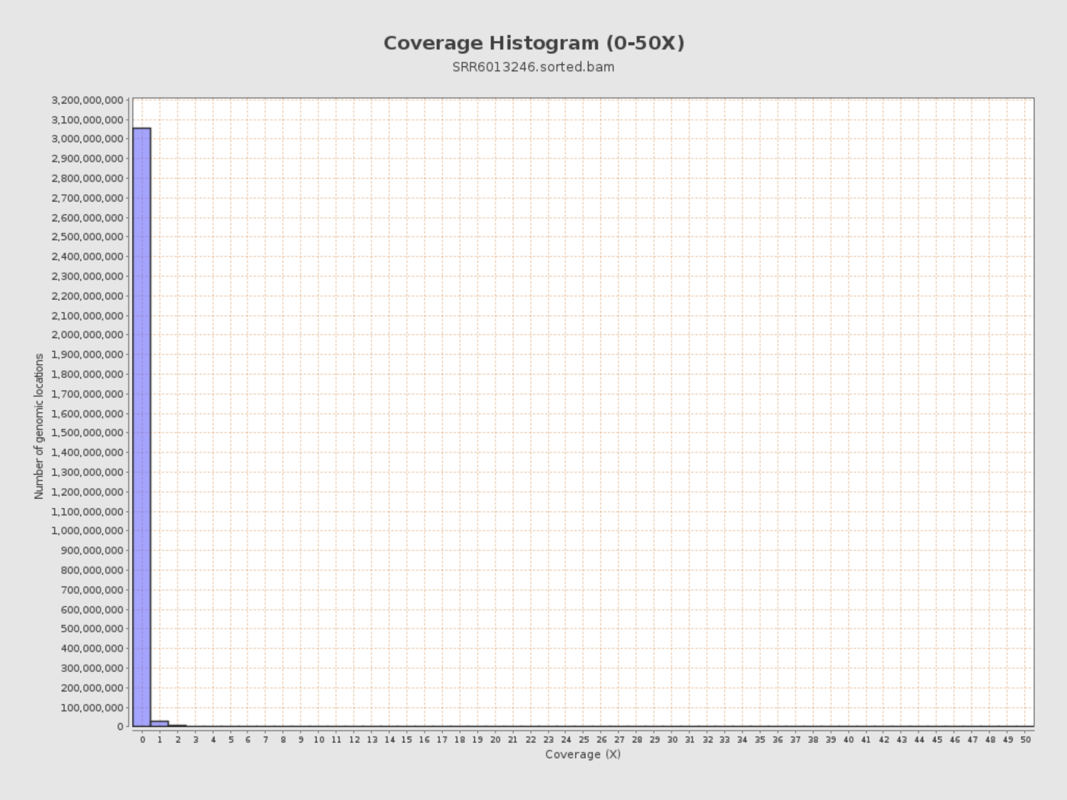
3. Results : Coverage across reference



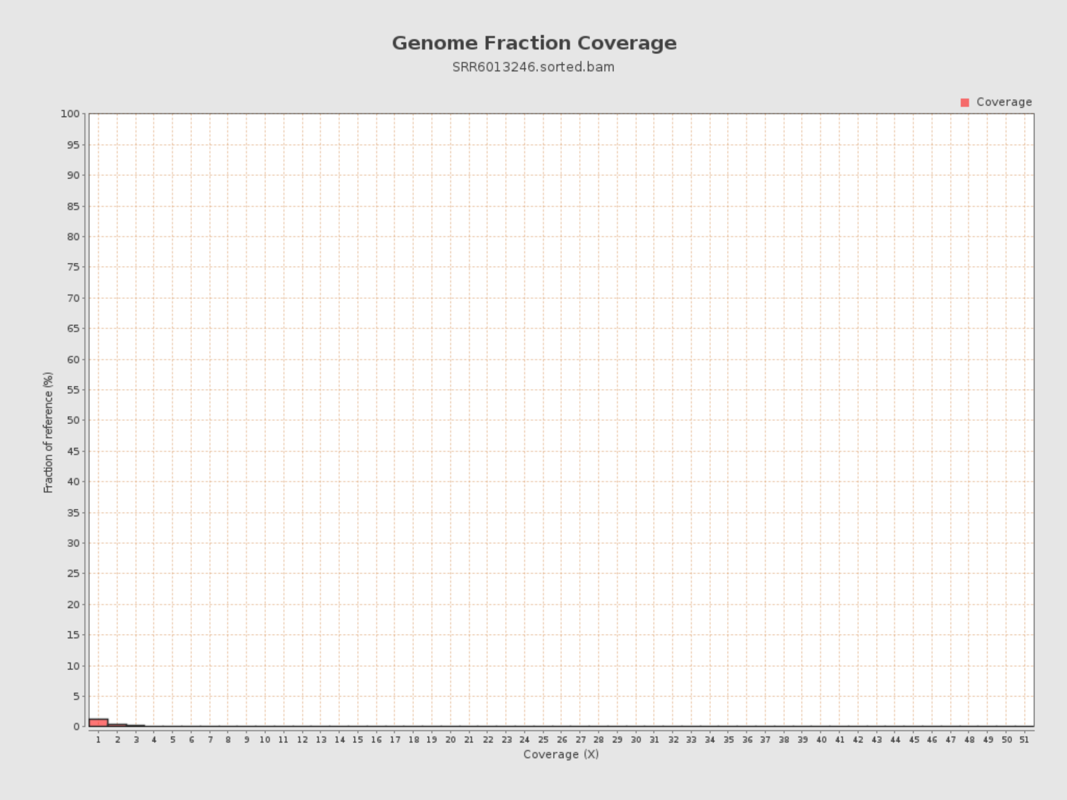
4. Results : Coverage Histogram



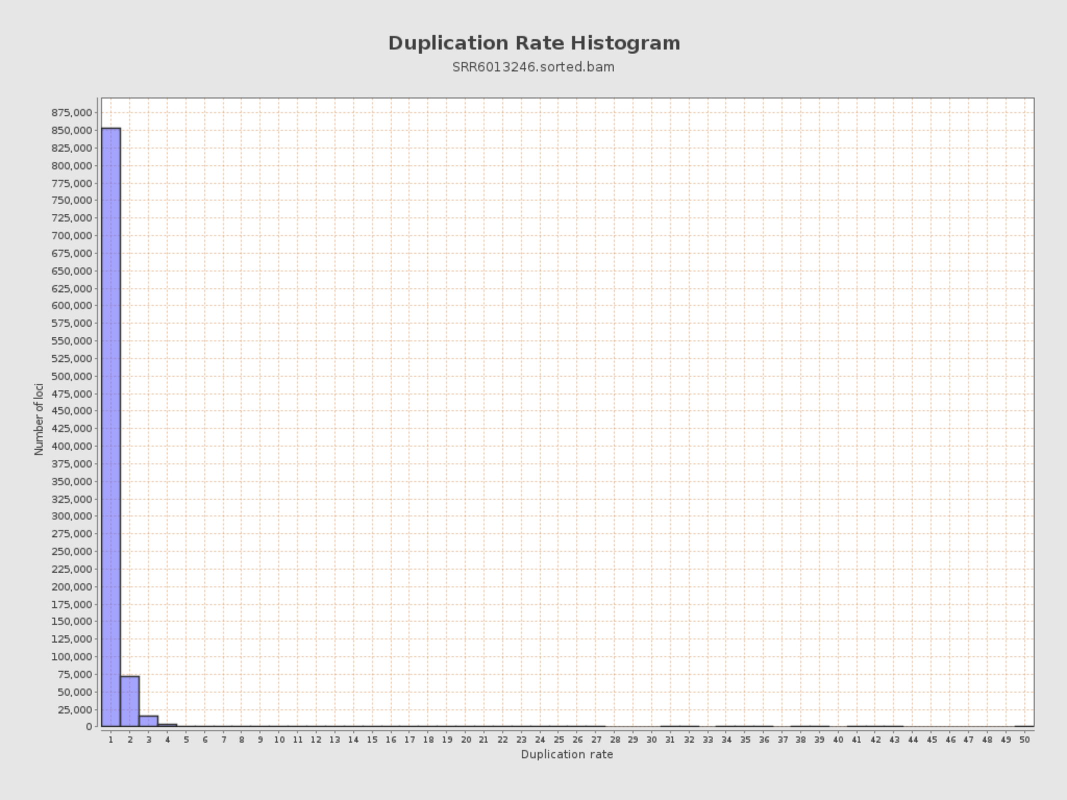
5. Results : Coverage Histogram (0-50X)



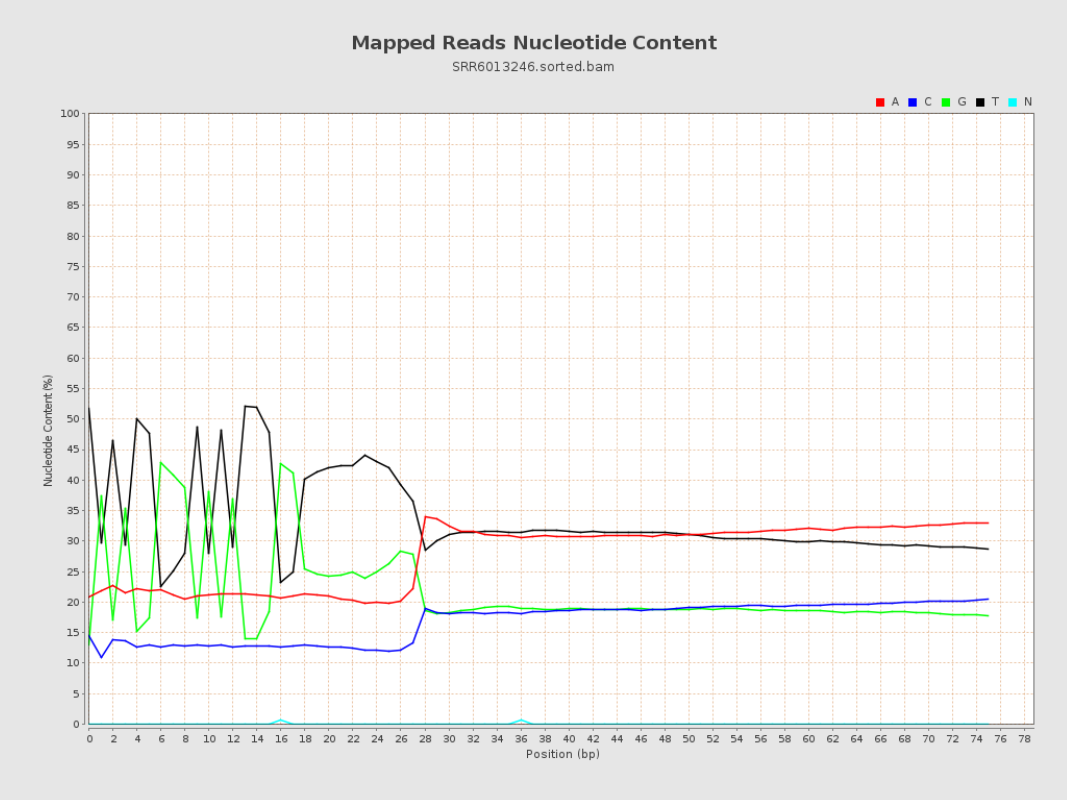
6. Results : Genome Fraction Coverage



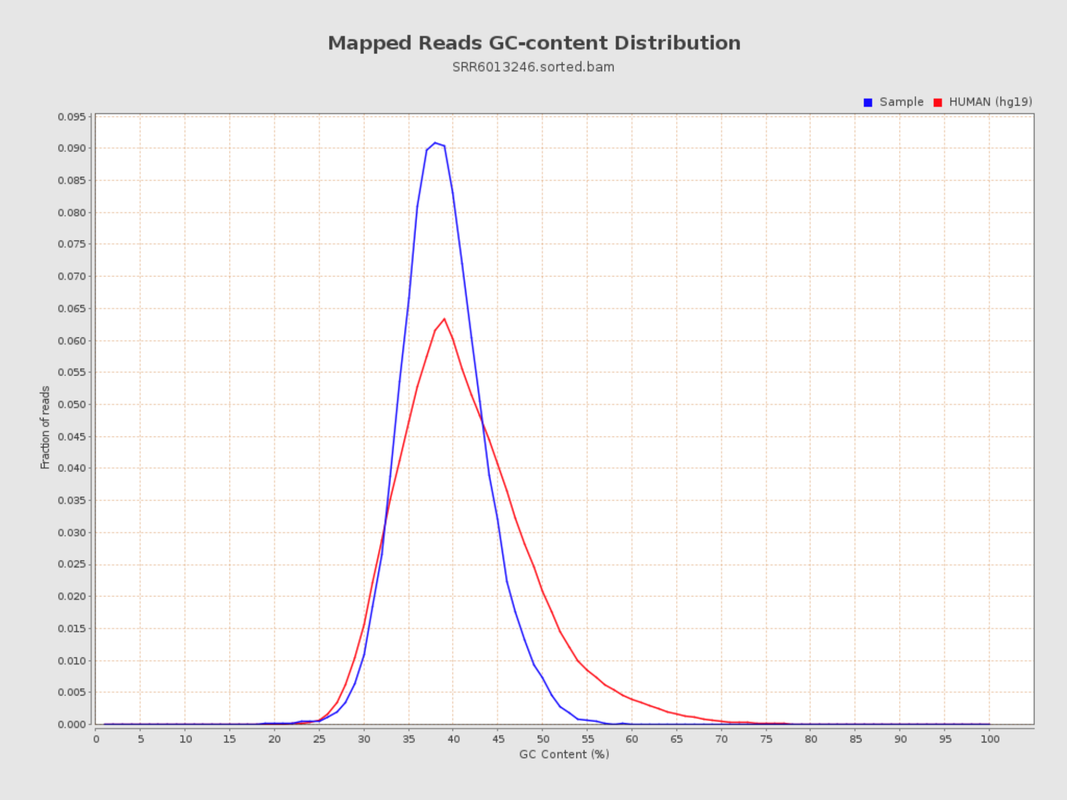
7. Results : Duplication Rate Histogram



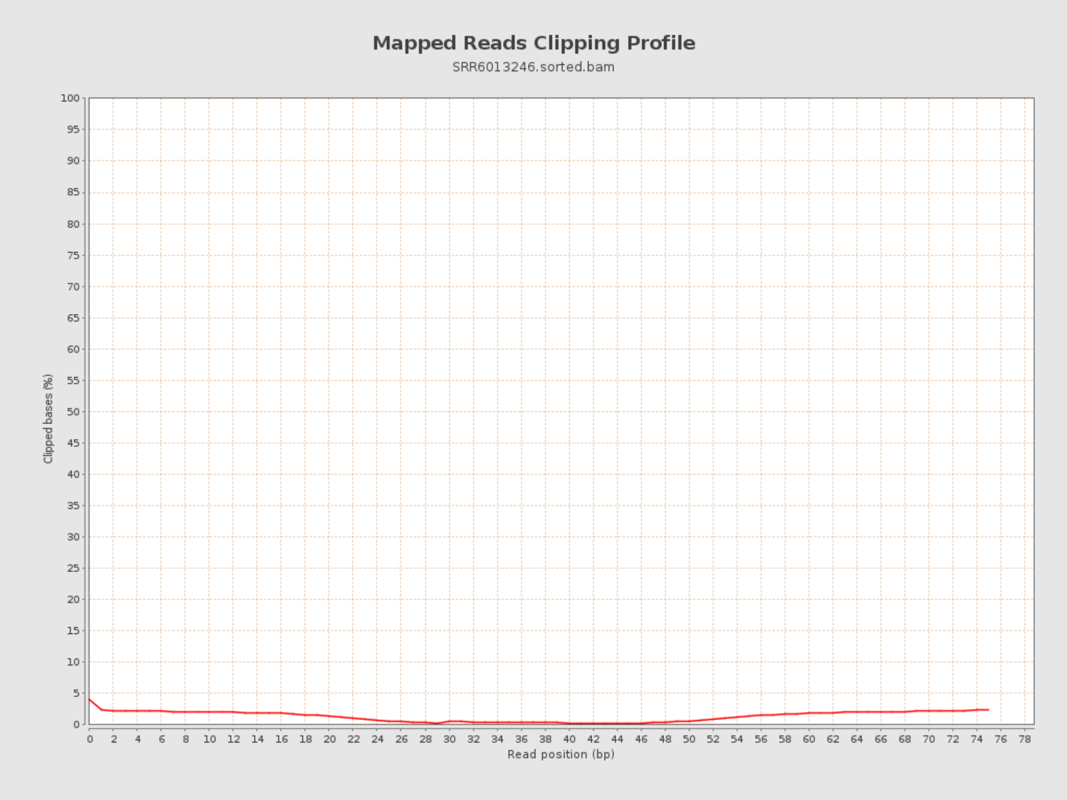
8. Results : Mapped Reads Nucleotide Content



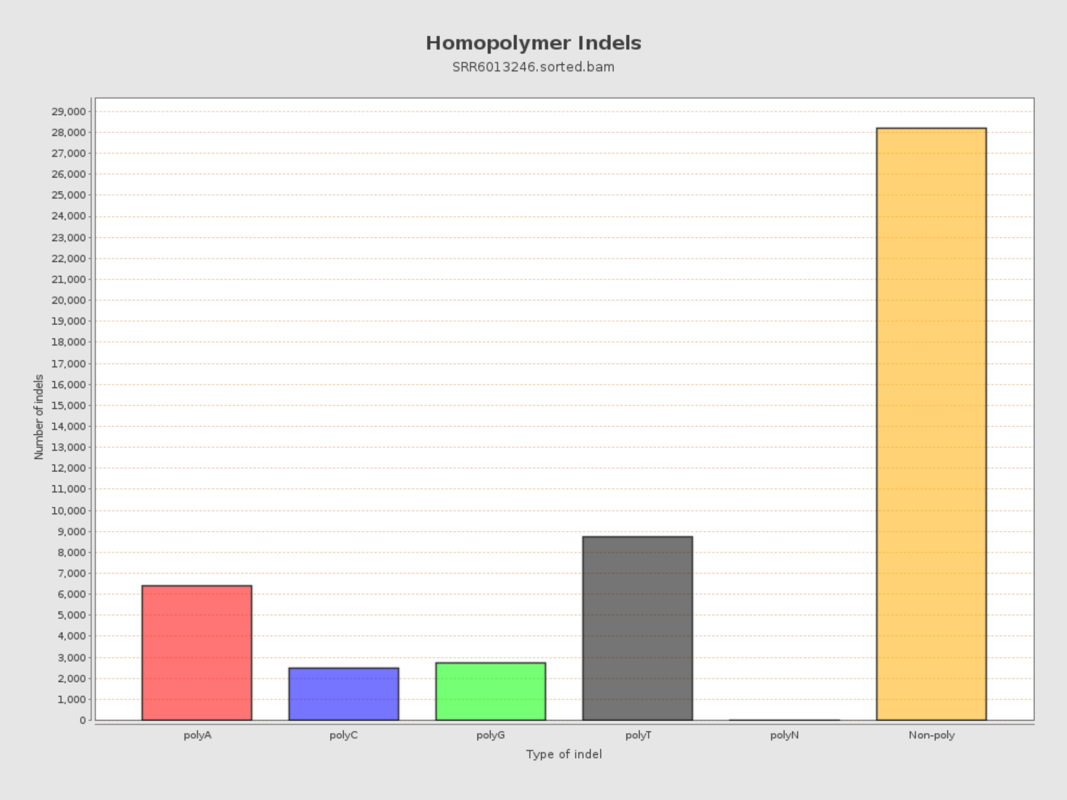
9. Results : Mapped Reads GC-content Distribution



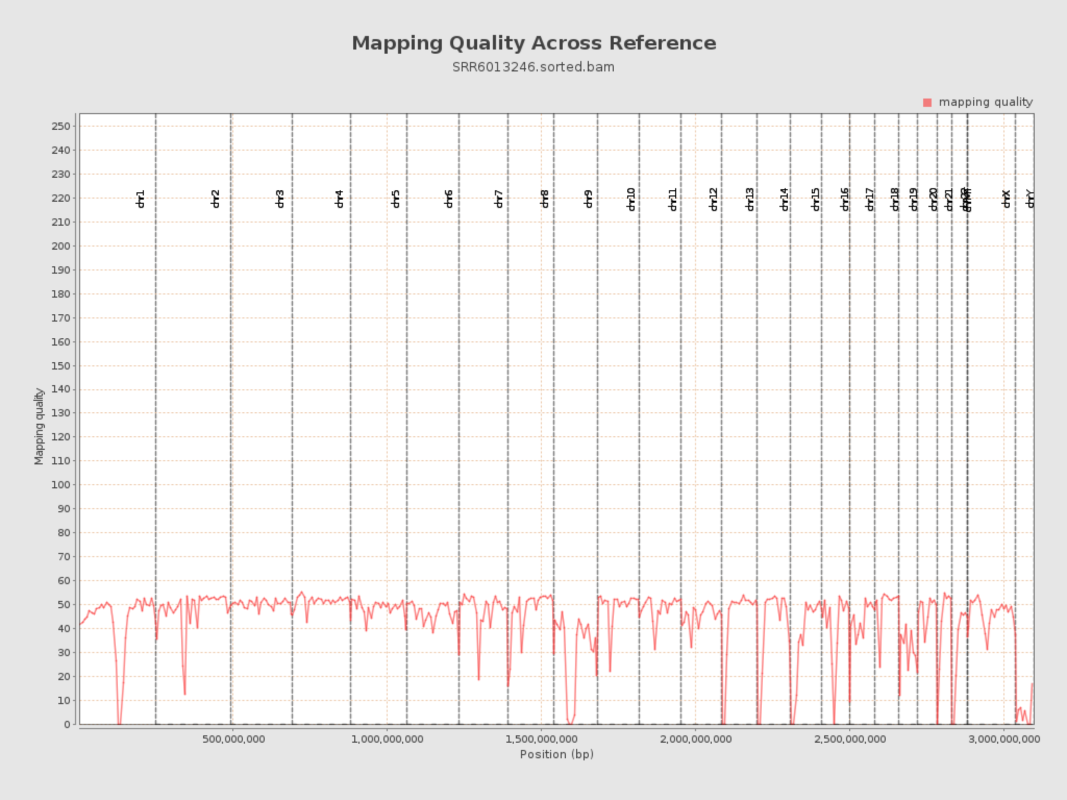
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram