Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:09:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240264.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_SRR6240264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:09:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,029,991
Mapped reads	1,308,275 / 64.45%
Unmapped reads	721,716 / 35.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,816 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	77,388 / 3.81%
Duplication rate	4.65%
Clipped reads	793,727 / 39.1%

2.2. ACGT Content

Number/percentage of A's	23,078,652 / 28.25%
Number/percentage of C's	14,213,172 / 17.4%
Number/percentage of T's	26,290,521 / 32.19%
Number/percentage of G's	18,077,847 / 22.13%
Number/percentage of N's	20,026 / 0.02%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2984

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

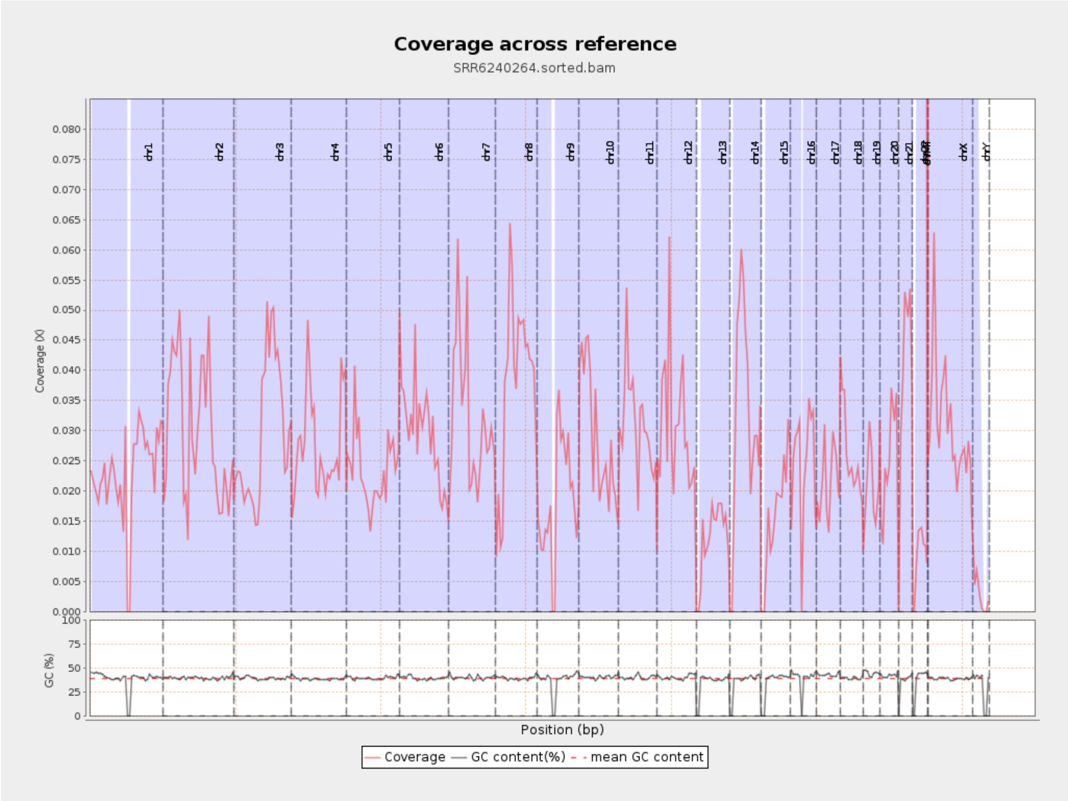
General error rate	0.93%
Mismatches	747,012
Insertions	6,417
Mapped reads with at least one insertion	0.48%
Deletions	26,971
Mapped reads with at least one deletion	2.02%
Homopolymer indels	48.76%

2.6. Chromosome stats

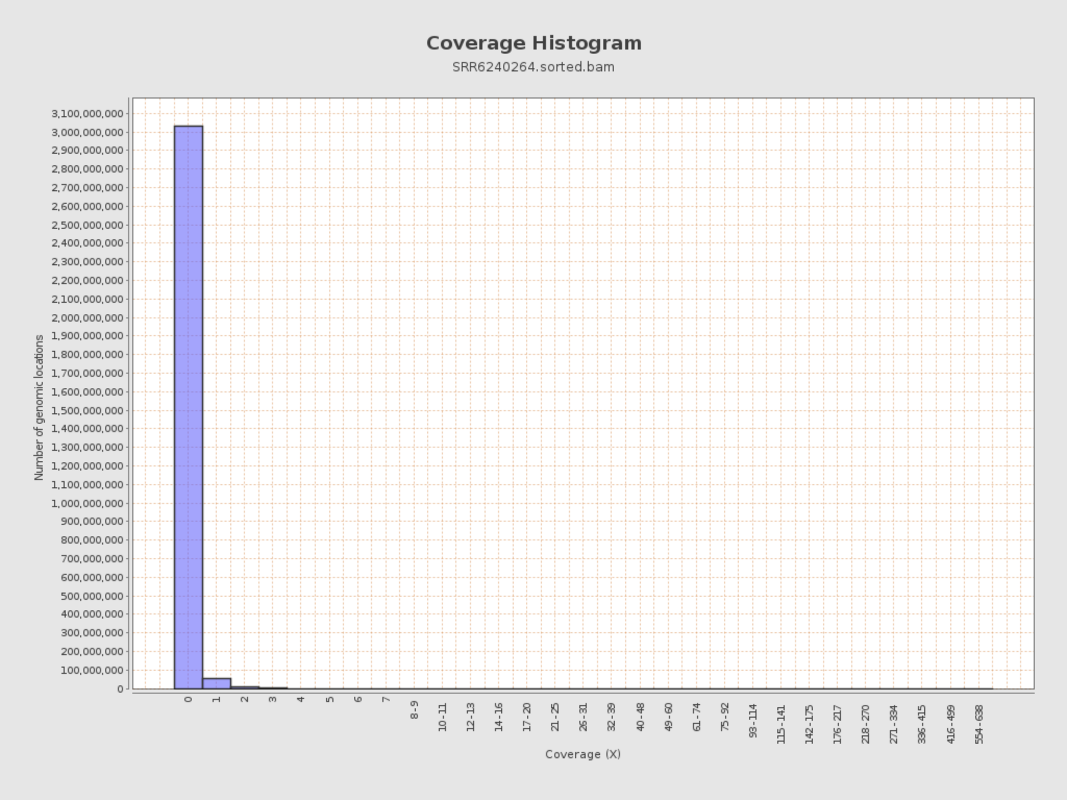
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5717943	0.0229	0.4029
chr2	243199373	7298008	0.03	0.3901
chr3	198022430	5814255	0.0294	0.2047
chr4	191154276	5288135	0.0277	0.2029
chr5	180915260	4230445	0.0234	0.2827
chr6	171115067	5118177	0.0299	0.2887
chr7	159138663	5189996	0.0326	0.4845

chr8	146364022	5524902	0.0377	0.4504
chr9	141213431	2599597	0.0184	0.2446
chr10	135534747	4000613	0.0295	0.2483
chr11	135006516	4171588	0.0309	0.3156
chr12	133851895	4086092	0.0305	0.212
chr13	115169878	1395912	0.0121	0.1304
chr14	107349540	3490013	0.0325	0.2223
chr15	102531392	1618103	0.0158	0.1605
chr16	90354753	2239982	0.0248	0.1931
chr17	81195210	1732260	0.0213	0.2013
chr18	78077248	2040555	0.0261	0.4131
chr19	59128983	1259254	0.0213	0.2974
chr20	63025520	1578017	0.025	0.1933
chr21	48129895	1902540	0.0395	0.2464
chr22	51304566	458830	0.0089	0.1078
chrMT	16571	18120	1.0935	1.6107
chrX	155270560	4783272	0.0308	0.2331
chrY	59373566	169969	0.0029	0.0685

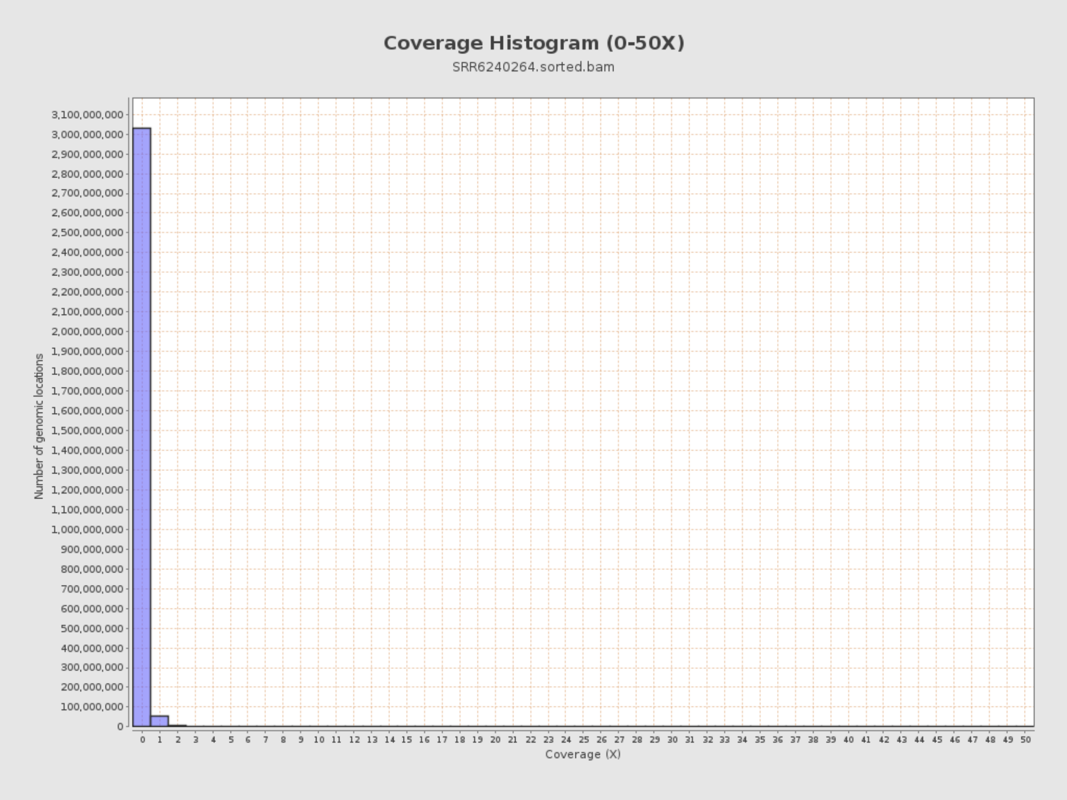
3. Results : Coverage across reference



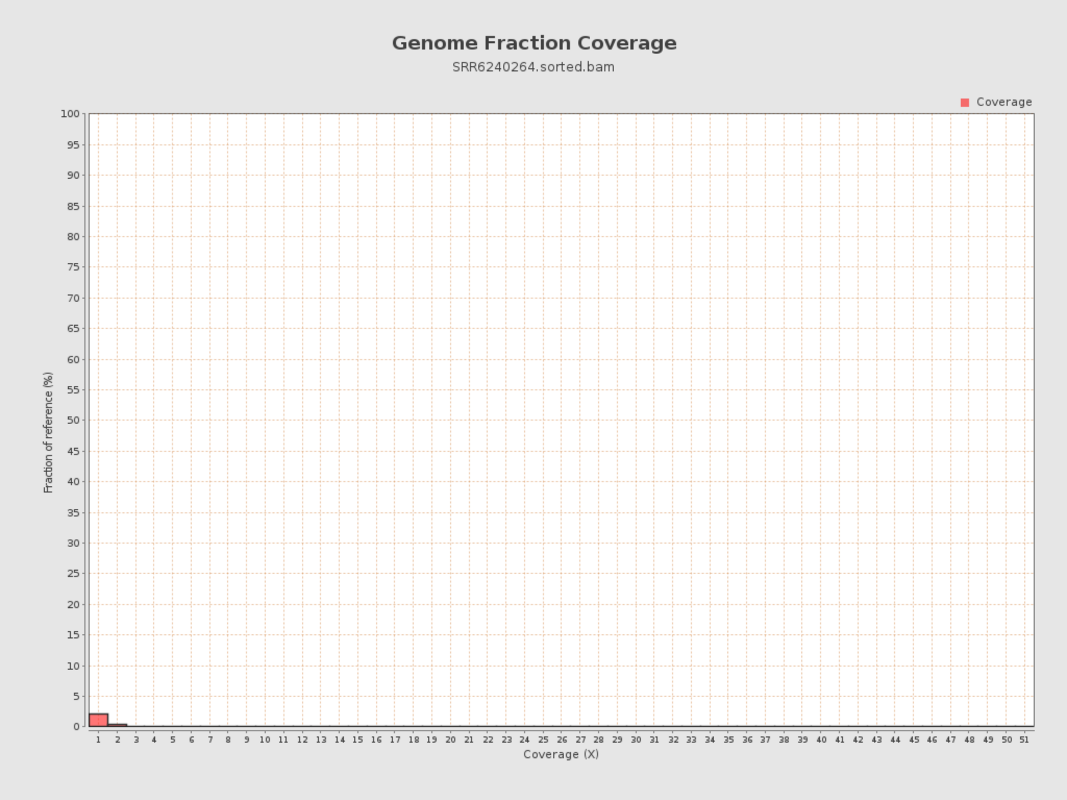
4. Results : Coverage Histogram



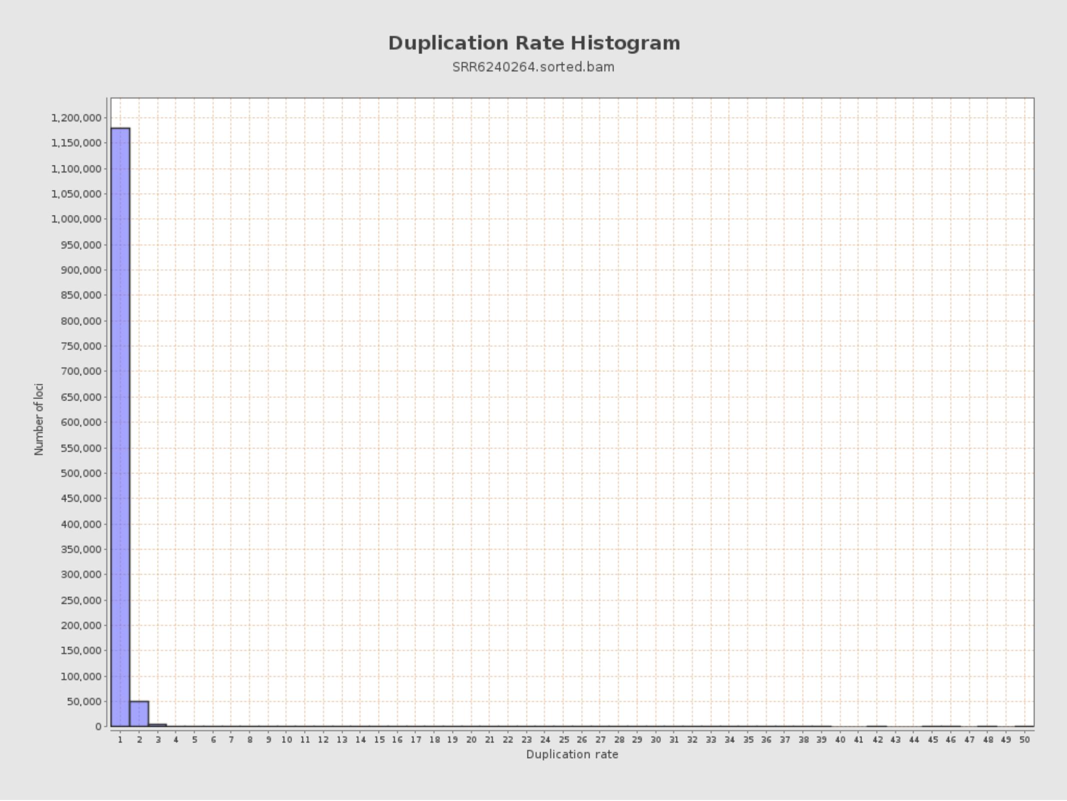
5. Results : Coverage Histogram (0-50X)



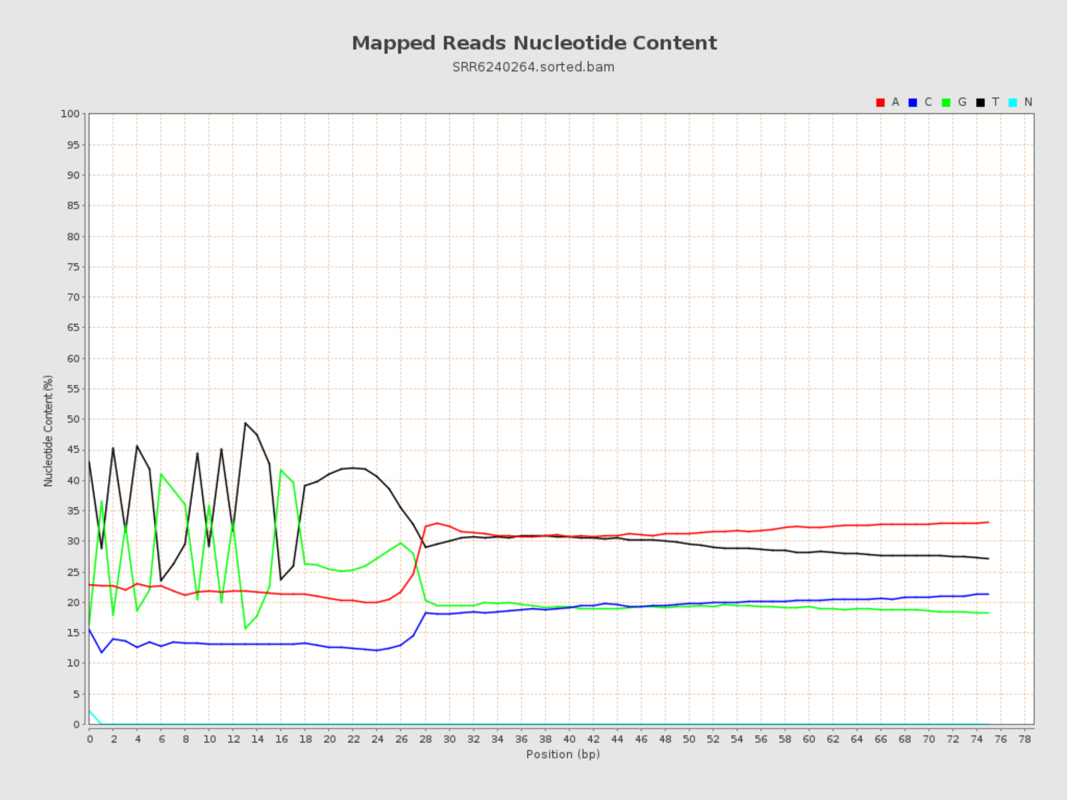
6. Results : Genome Fraction Coverage



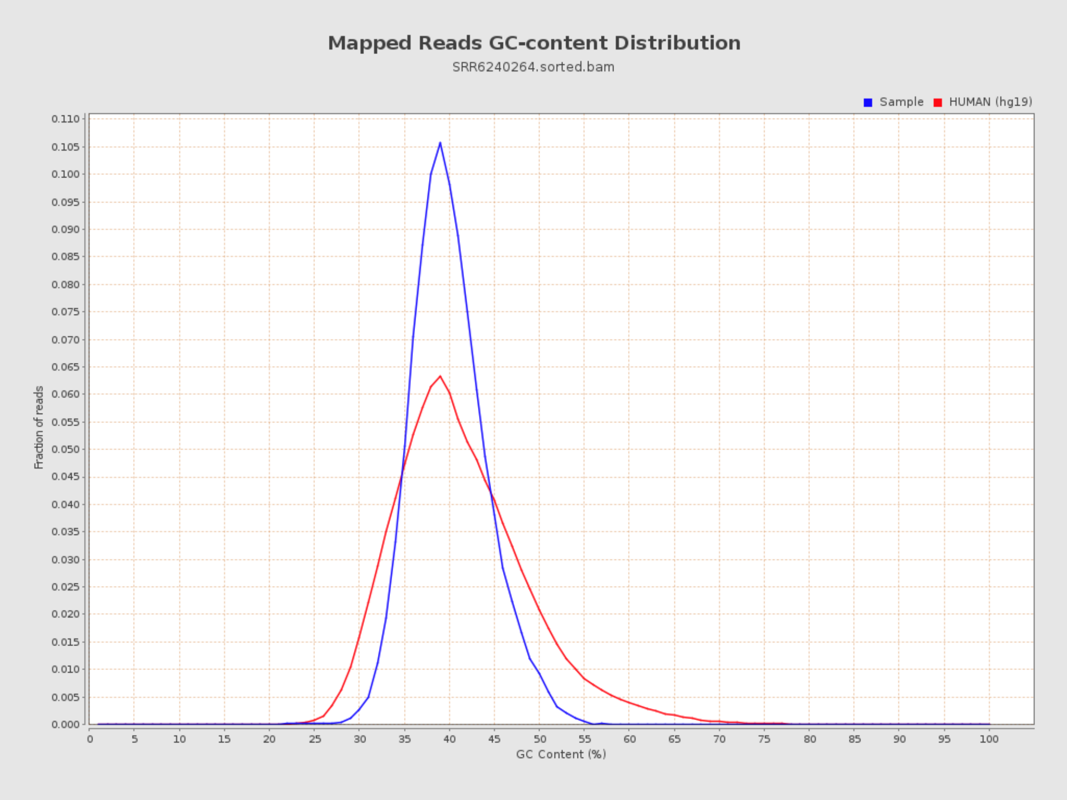
7. Results : Duplication Rate Histogram



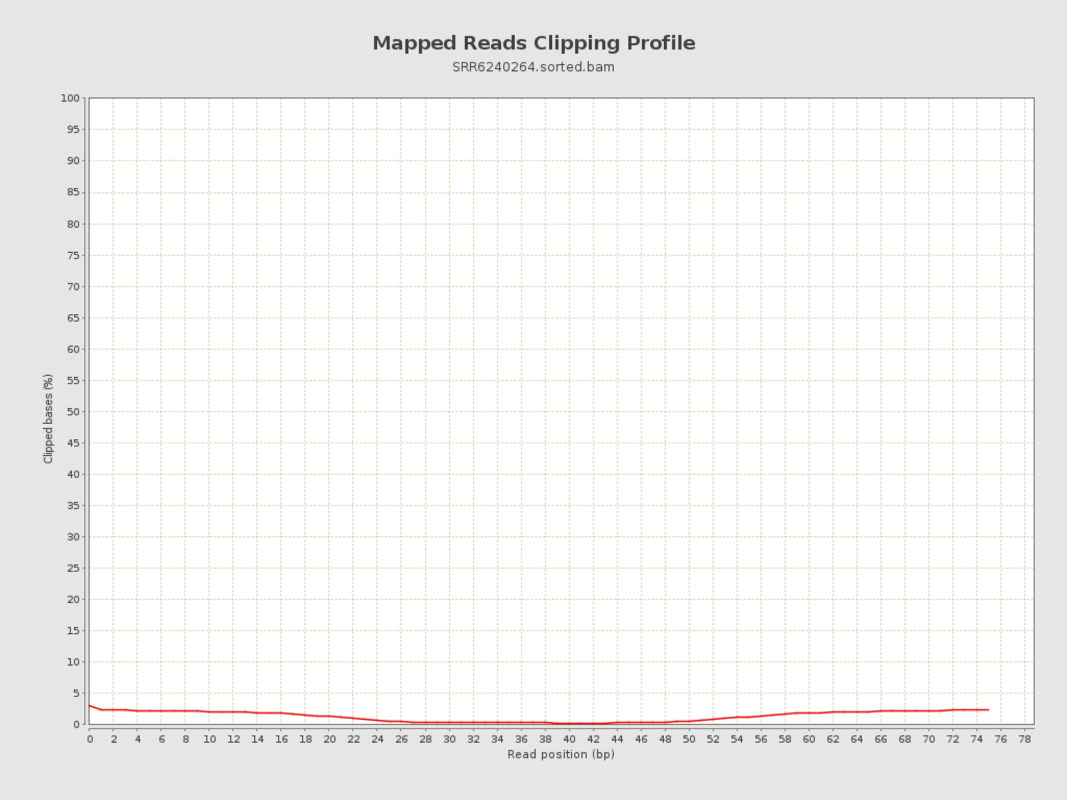
8. Results : Mapped Reads Nucleotide Content



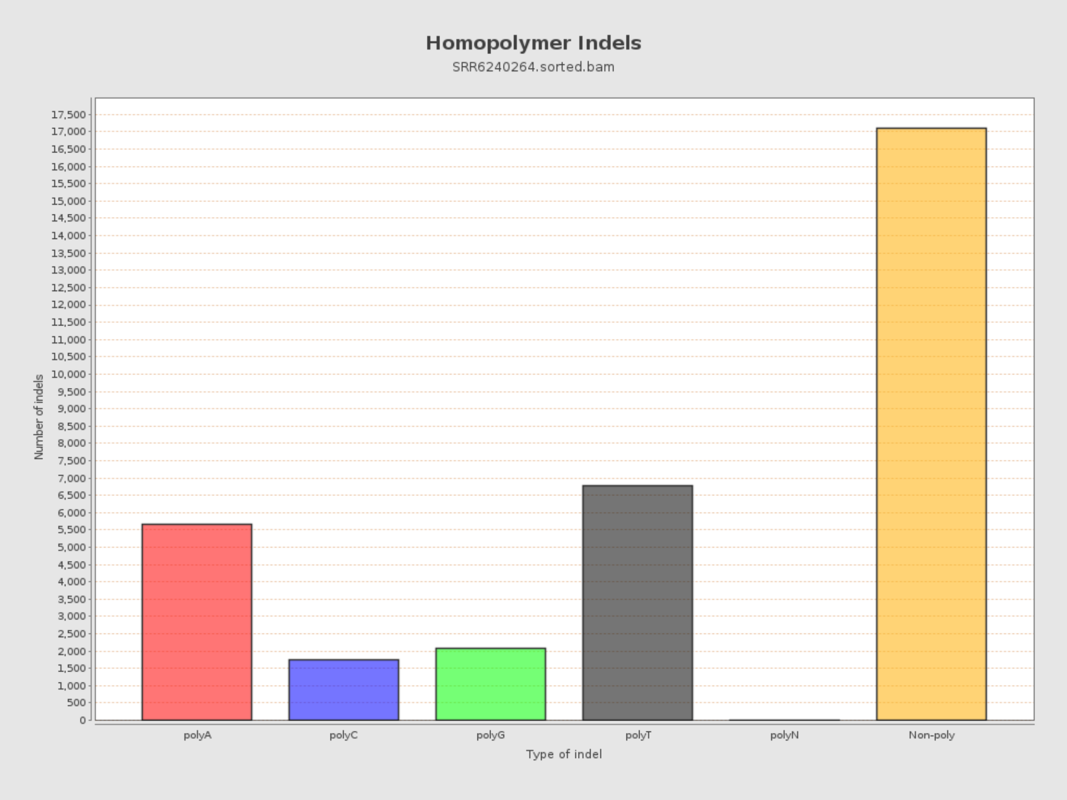
9. Results : Mapped Reads GC-content Distribution



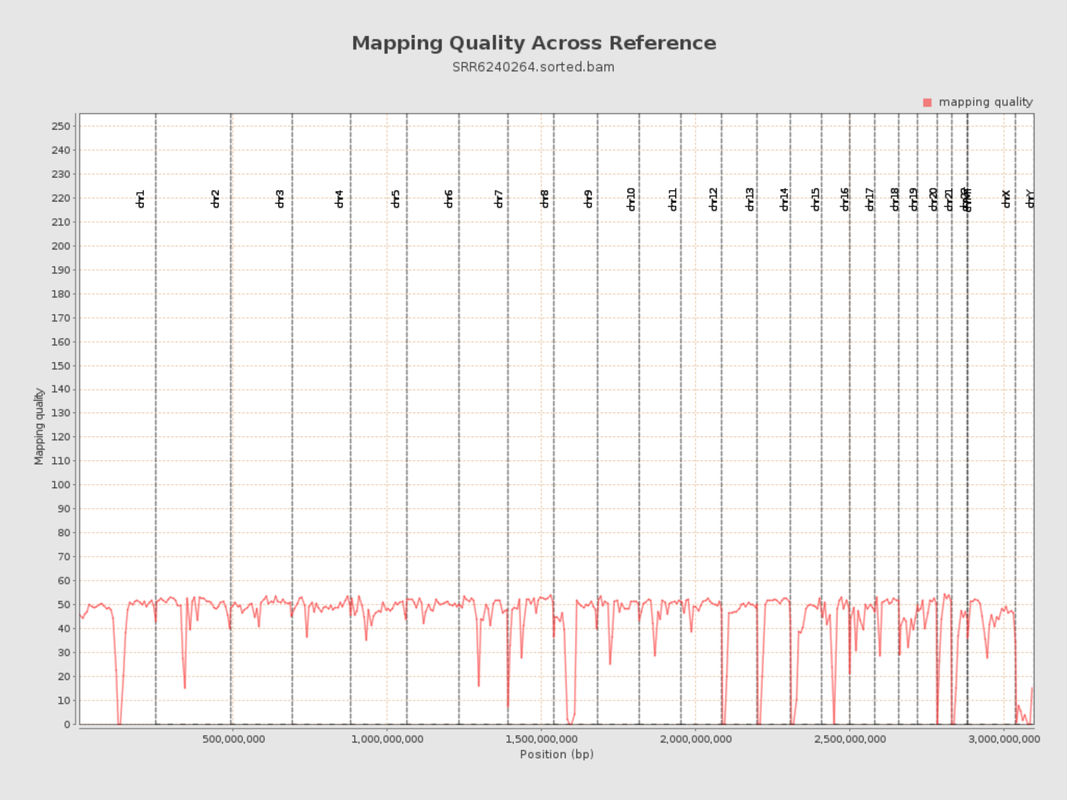
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram