Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:16:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234138.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_SRR6234138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:16:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,011,542
Mapped reads	1,146,673 / 57%
Unmapped reads	864,869 / 43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,361 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	193,966 / 9.64%
Duplication rate	12.41%
Clipped reads	691,338 / 34.37%

2.2. ACGT Content

Number/percentage of A's	19,429,016 / 27.19%
Number/percentage of C's	11,559,669 / 16.17%
Number/percentage of T's	24,693,348 / 34.55%
Number/percentage of G's	15,770,607 / 22.07%
Number/percentage of N's	13,700 / 0.02%
GC Percentage	38.24%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.3696

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

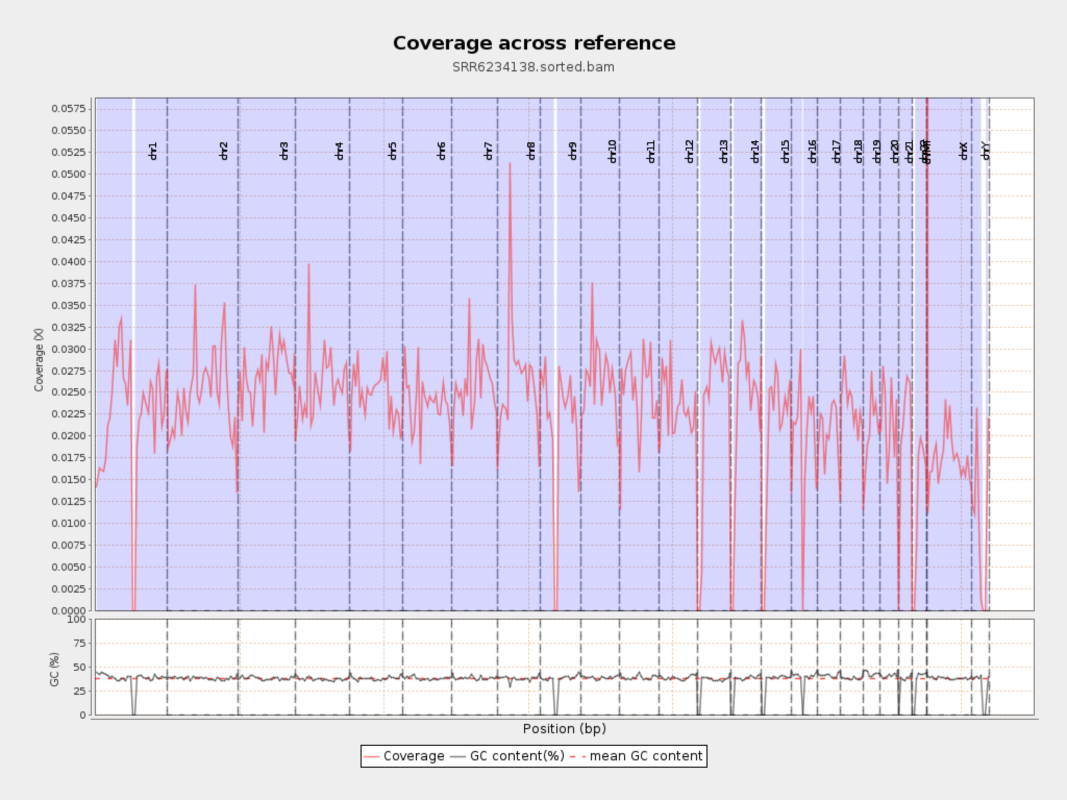
General error rate	0.93%
Mismatches	651,313
Insertions	6,343
Mapped reads with at least one insertion	0.55%
Deletions	24,162
Mapped reads with at least one deletion	2.08%
Homopolymer indels	44.26%

2.6. Chromosome stats

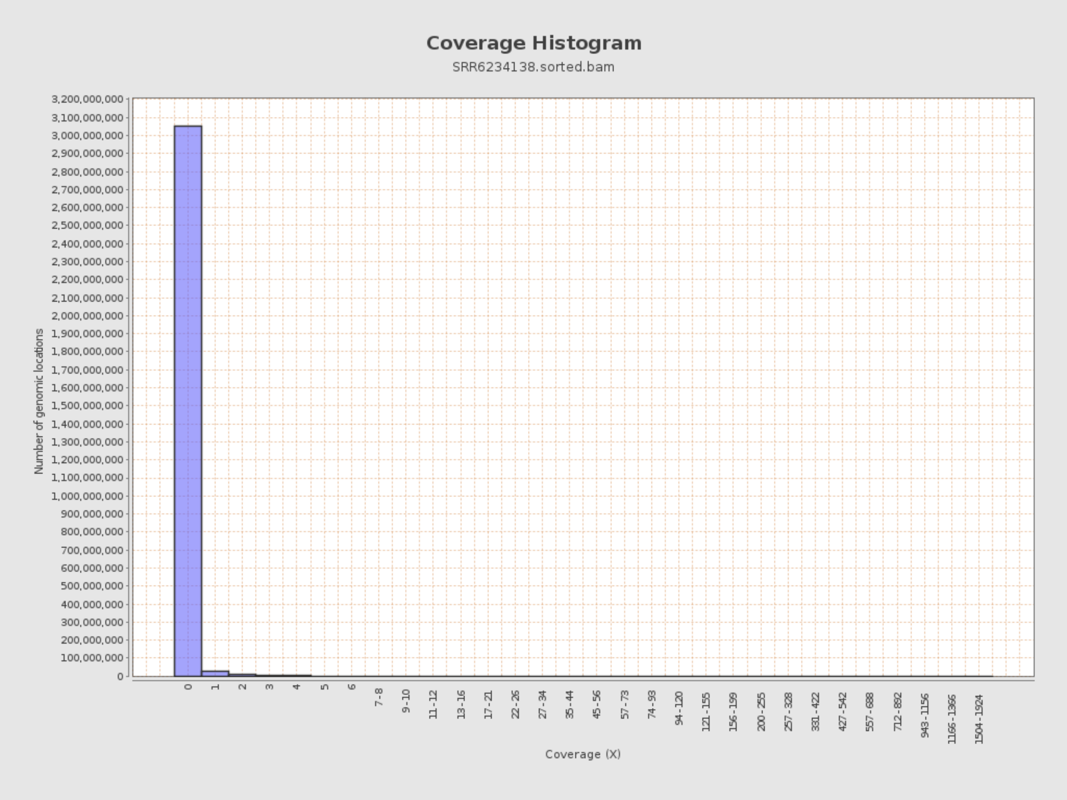
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5538198	0.0222	0.3252
chr2	243199373	6019180	0.0247	0.3793
chr3	198022430	5381404	0.0272	0.2662
chr4	191154276	4914000	0.0257	0.2759
chr5	180915260	4500409	0.0249	0.2527
chr6	171115067	4088037	0.0239	0.2689
chr7	159138663	4122940	0.0259	0.3089

chr8	146364022	3915135	0.0267	1.1427
chr9	141213431	2990202	0.0212	0.2649
chr10	135534747	3572480	0.0264	0.2876
chr11	135006516	3405825	0.0252	0.2912
chr12	133851895	3146949	0.0235	0.2458
chr13	115169878	2640466	0.0229	0.2547
chr14	107349540	2425356	0.0226	0.2454
chr15	102531392	2049897	0.02	0.224
chr16	90354753	1747014	0.0193	0.2188
chr17	81195210	1651996	0.0203	0.2227
chr18	78077248	1857977	0.0238	0.428
chr19	59128983	1227448	0.0208	0.2502
chr20	63025520	1348566	0.0214	0.2309
chr21	48129895	1004121	0.0209	0.235
chr22	51304566	641169	0.0125	0.1669
chrMT	16571	16477	0.9943	1.5865
chrX	155270560	2718158	0.0175	0.2134
chrY	59373566	585221	0.0099	0.1886

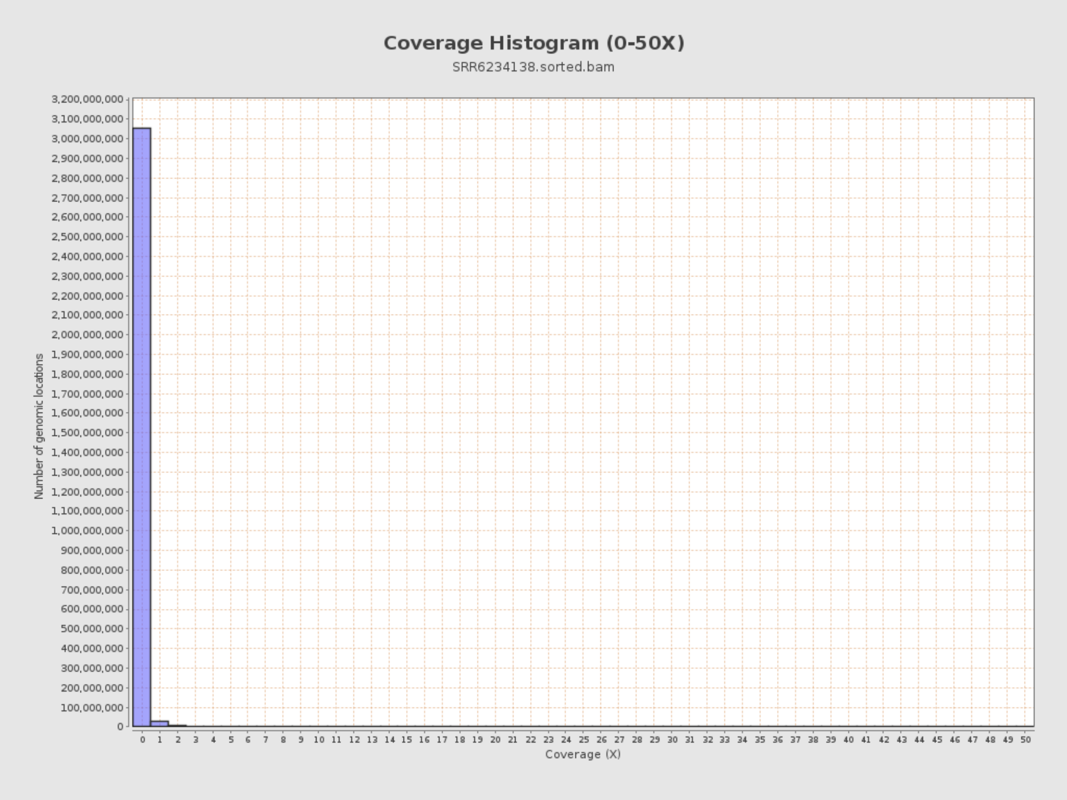
3. Results : Coverage across reference



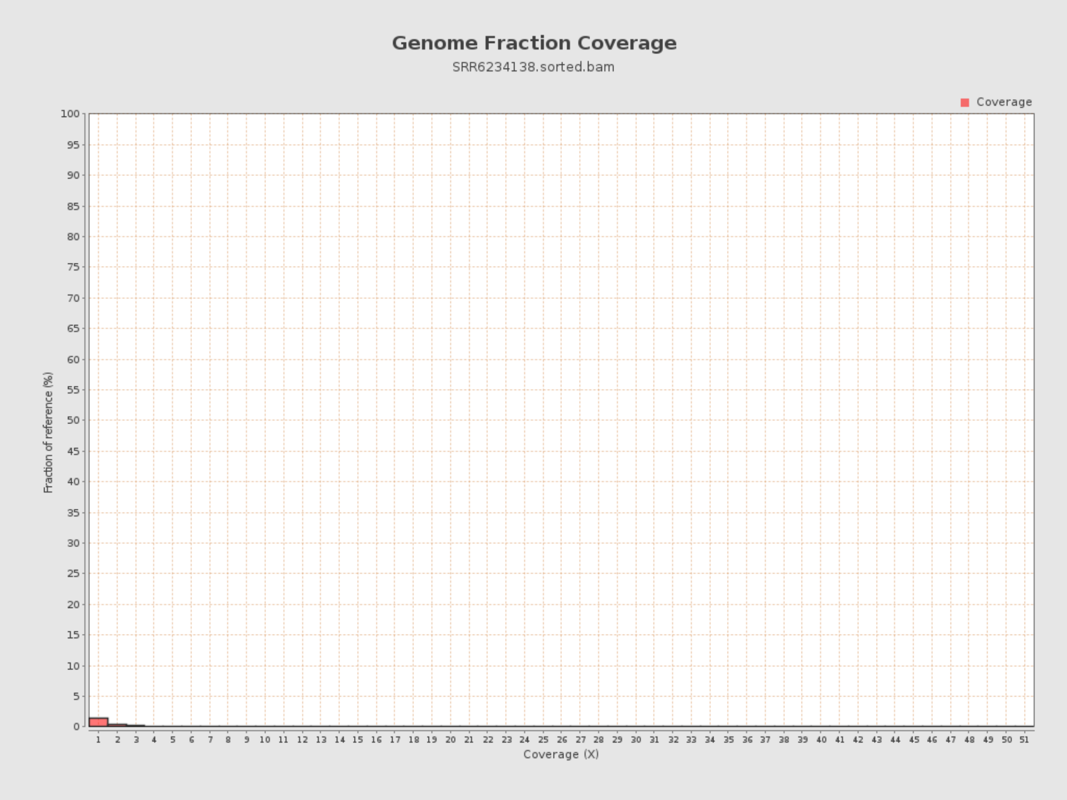
4. Results : Coverage Histogram



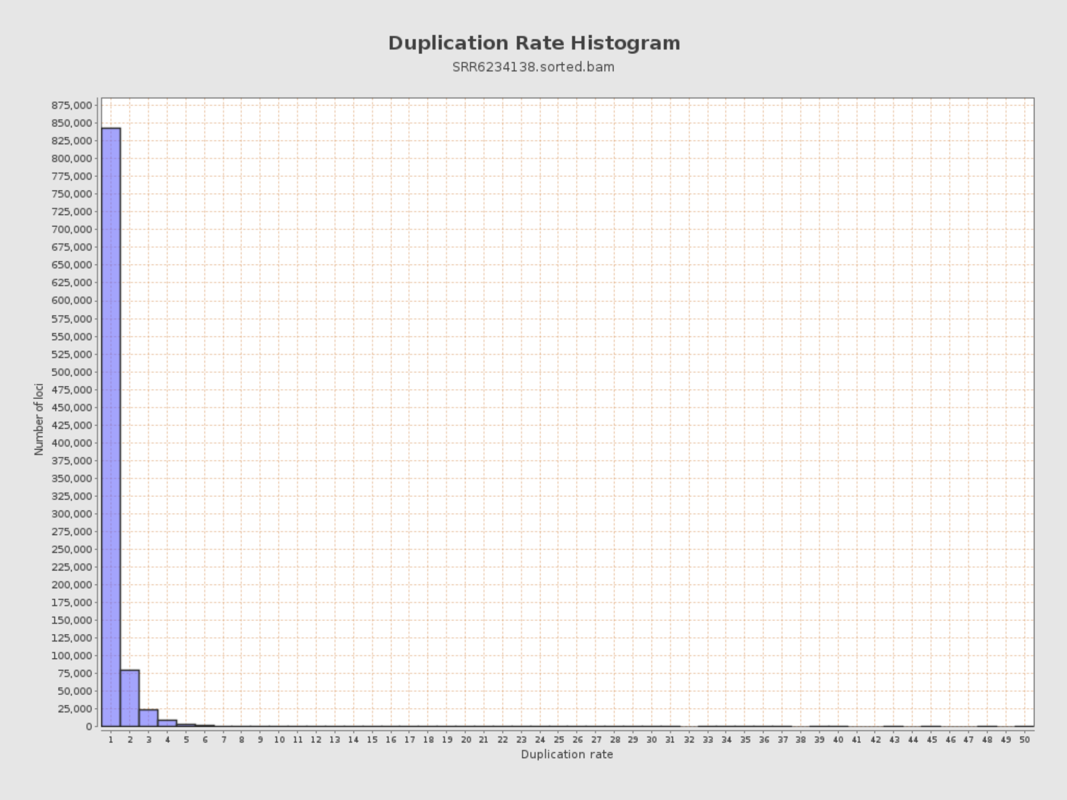
5. Results : Coverage Histogram (0-50X)



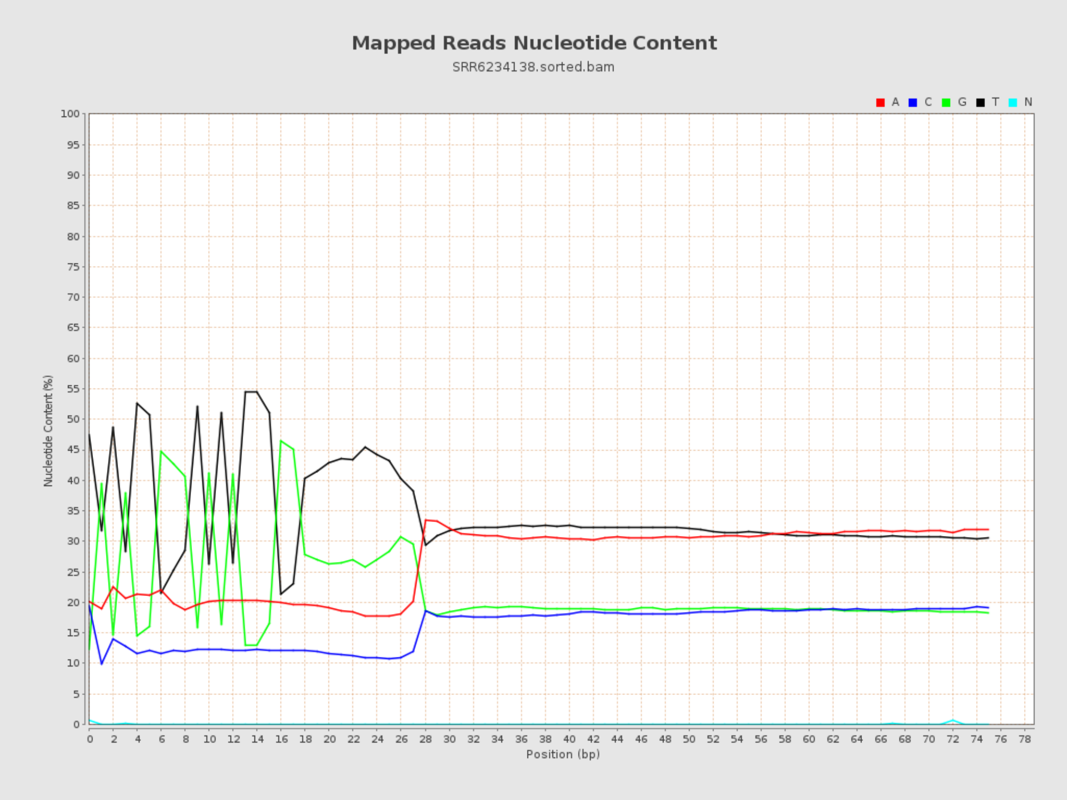
6. Results : Genome Fraction Coverage



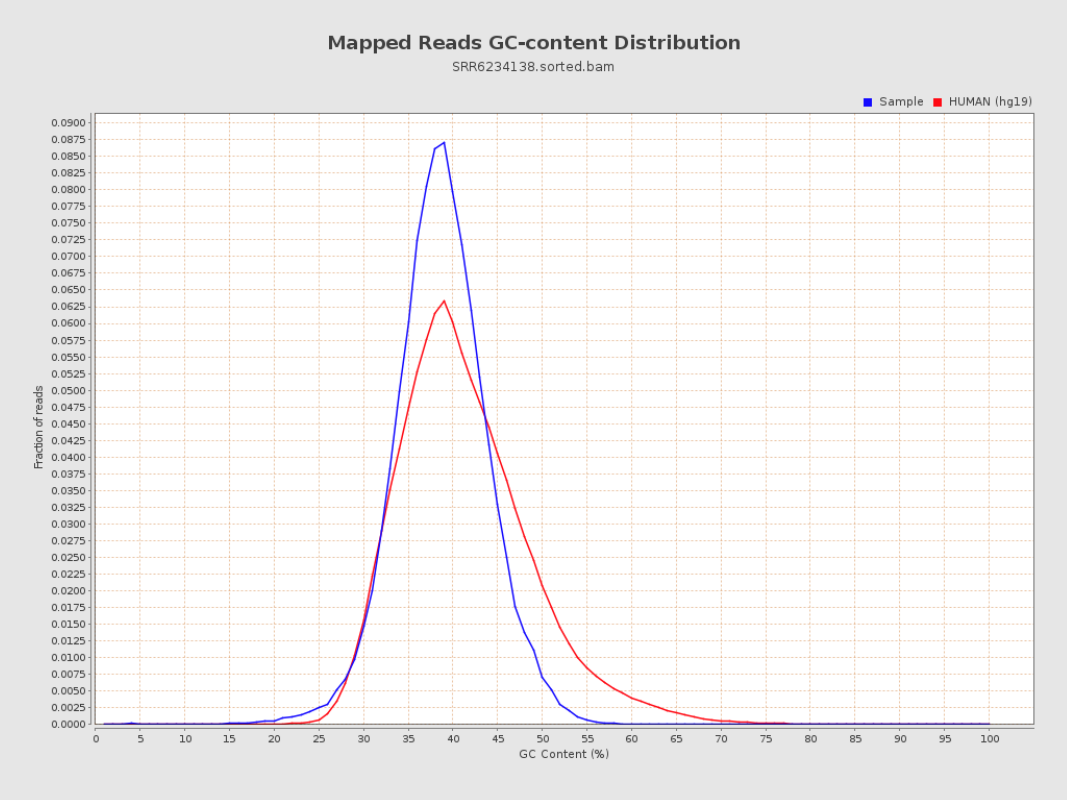
7. Results : Duplication Rate Histogram



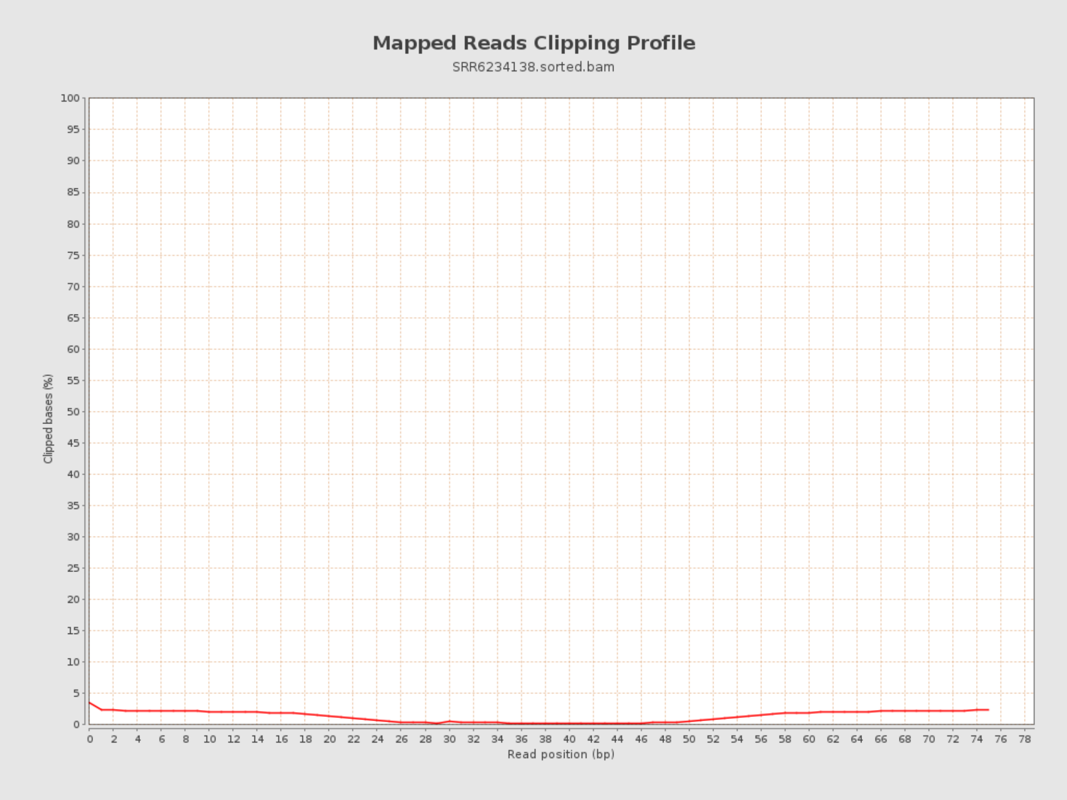
8. Results : Mapped Reads Nucleotide Content



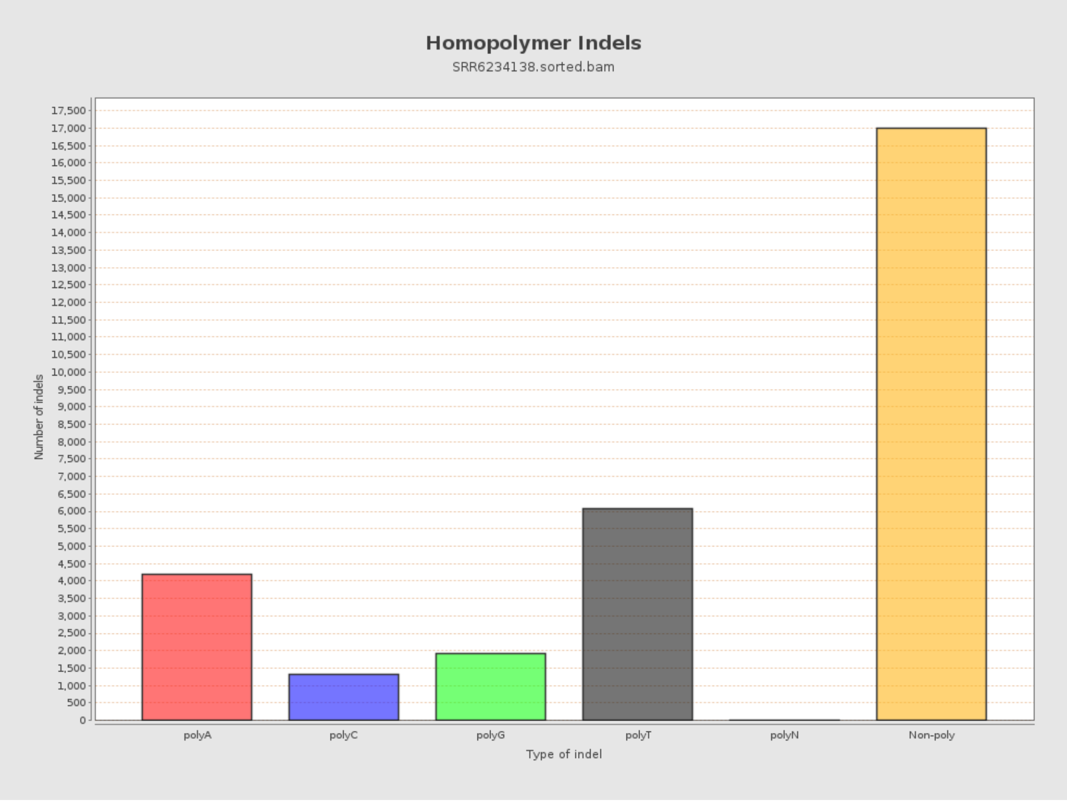
9. Results : Mapped Reads GC-content Distribution



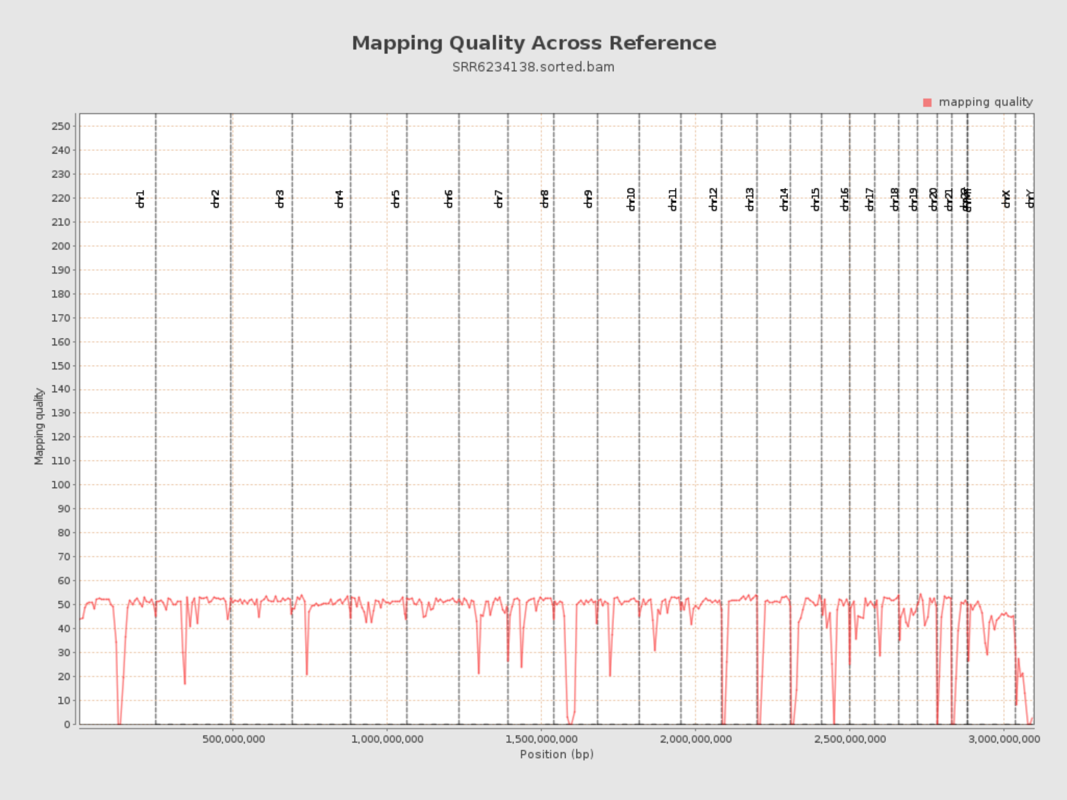
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram