Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:34:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230364.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_SRR6230364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230364.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:34:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,491,366
Mapped reads	1,289,327 / 86.45%
Unmapped reads	202,039 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,456 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	104,646 / 7.02%
Duplication rate	6.3%
Clipped reads	500,739 / 33.58%

2.2. ACGT Content

Number/percentage of A's	25,997,250 / 29.51%
Number/percentage of C's	16,301,262 / 18.51%
Number/percentage of T's	28,049,056 / 31.84%
Number/percentage of G's	17,695,124 / 20.09%
Number/percentage of N's	40,236 / 0.05%
GC Percentage	38.6%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.4372

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

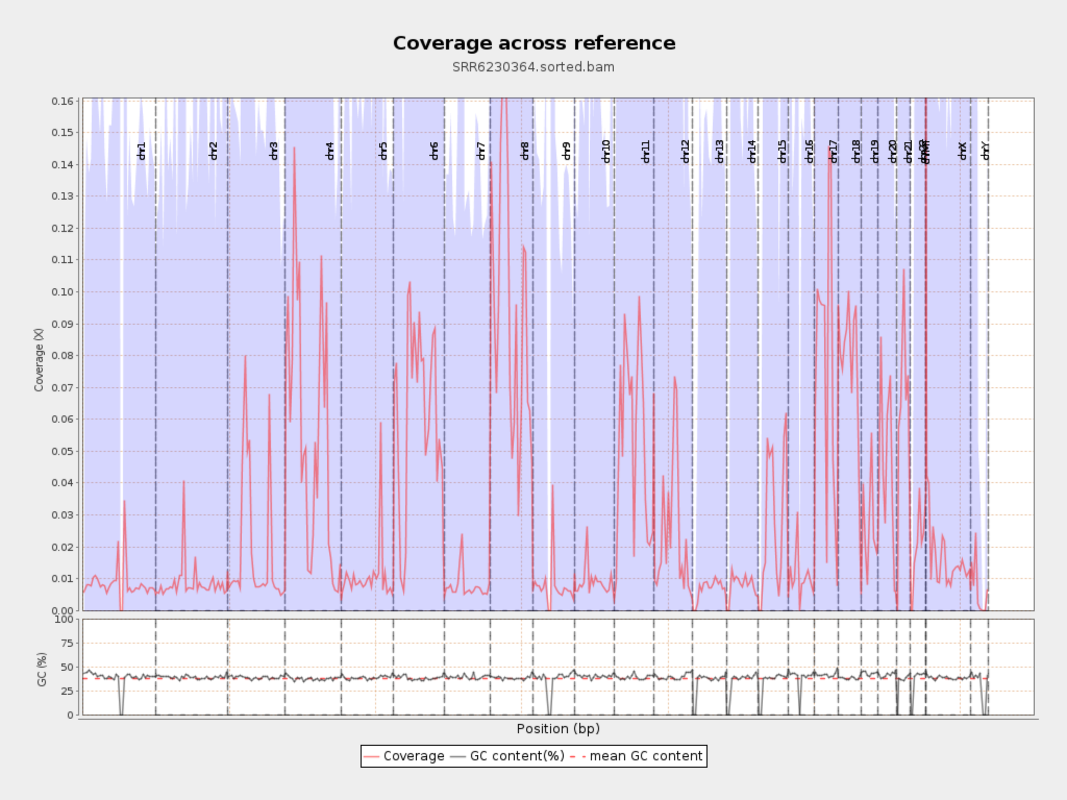
General error rate	0.92%
Mismatches	796,835
Insertions	8,241
Mapped reads with at least one insertion	0.63%
Deletions	25,939
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.7%

2.6. Chromosome stats

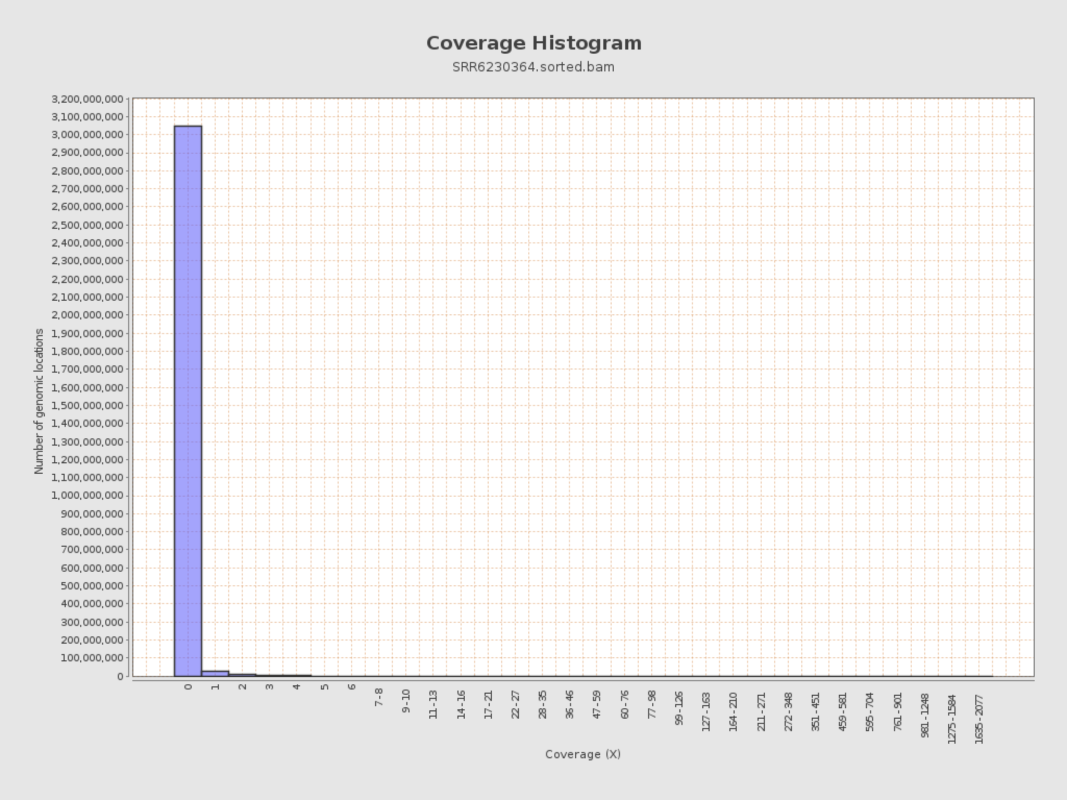
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2087764	0.0084	0.2782
chr2	243199373	2124792	0.0087	0.294
chr3	198022430	3647686	0.0184	0.2282
chr4	191154276	10406116	0.0544	0.4058
chr5	180915260	1974042	0.0109	0.174
chr6	171115067	10790649	0.0631	0.4619
chr7	159138663	1247691	0.0078	0.2187

chr8	146364022	13922005	0.0951	1.4089
chr9	141213431	1110765	0.0079	0.2787
chr10	135534747	1212877	0.0089	0.1892
chr11	135006516	7155963	0.053	0.4539
chr12	133851895	3204993	0.0239	0.2604
chr13	115169878	775080	0.0067	0.1338
chr14	107349540	847922	0.0079	0.1614
chr15	102531392	2828463	0.0276	0.2758
chr16	90354753	925583	0.0102	0.2074
chr17	81195210	6448848	0.0794	0.5175
chr18	78077248	6186568	0.0792	0.7257
chr19	59128983	1569343	0.0265	0.2968
chr20	63025520	2797260	0.0444	0.3483
chr21	48129895	2962142	0.0615	0.4228
chr22	51304566	1004288	0.0196	0.2222
chrMT	16571	3537	0.2134	0.6633
chrX	155270560	2491627	0.016	0.2404
chrY	59373566	399806	0.0067	0.1896

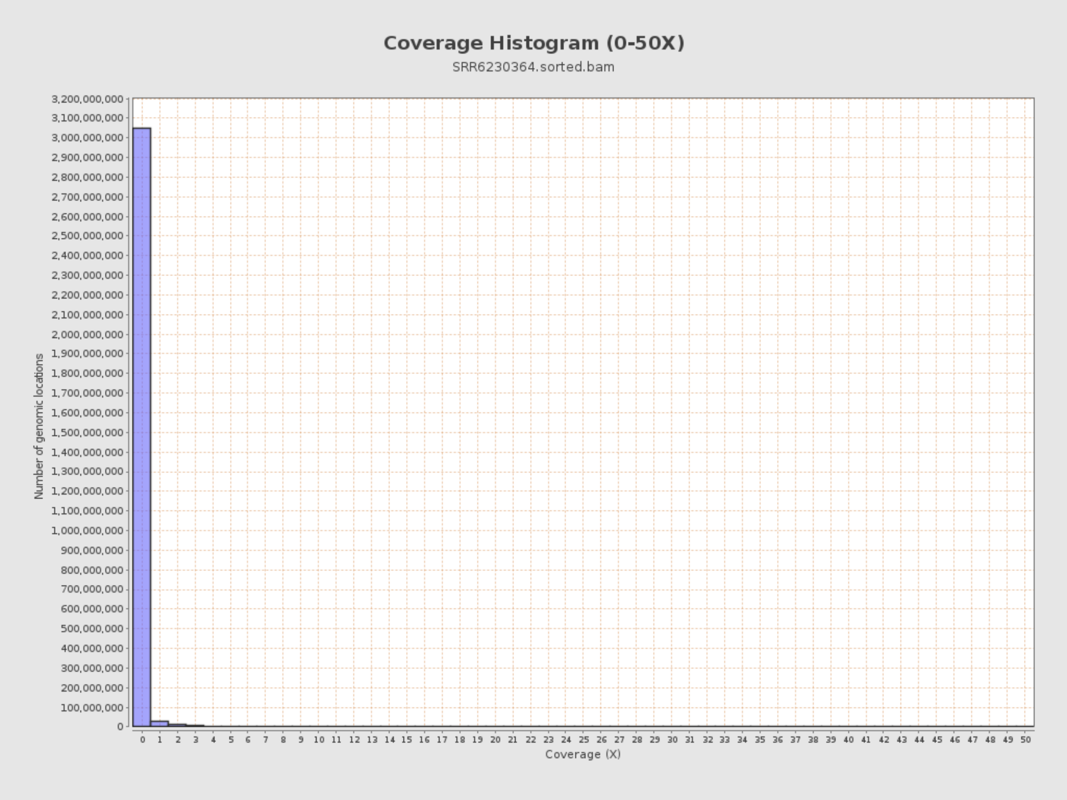
3. Results : Coverage across reference



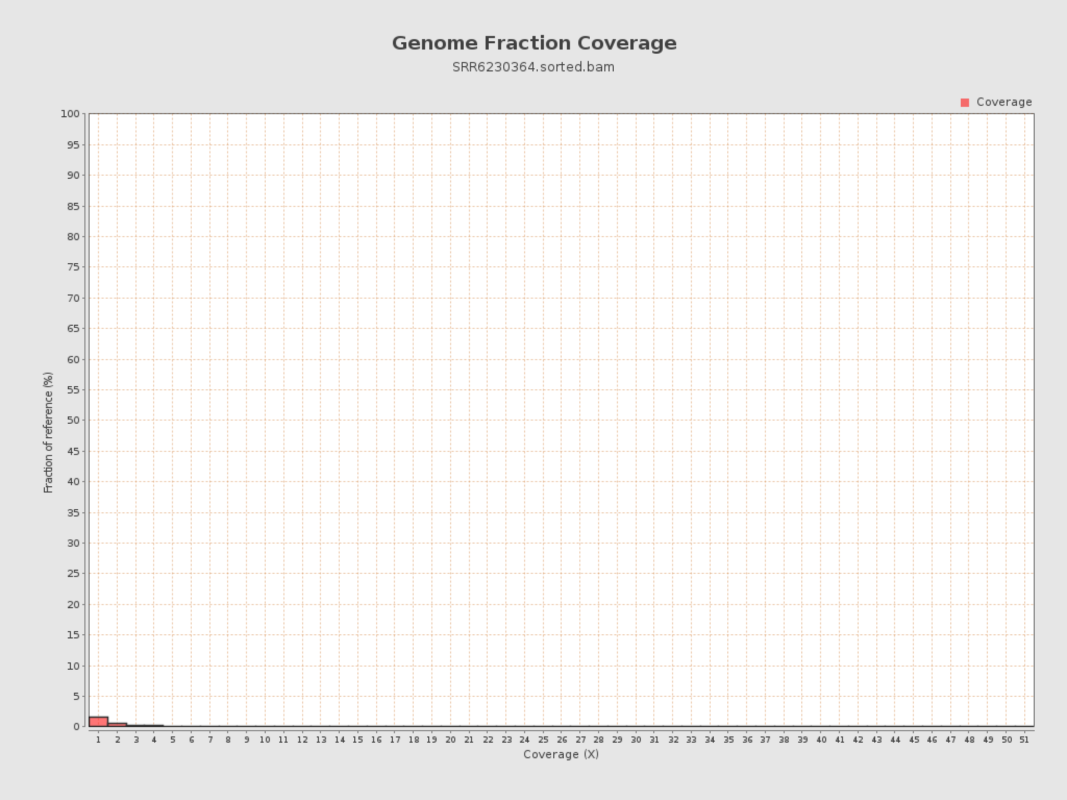
4. Results : Coverage Histogram



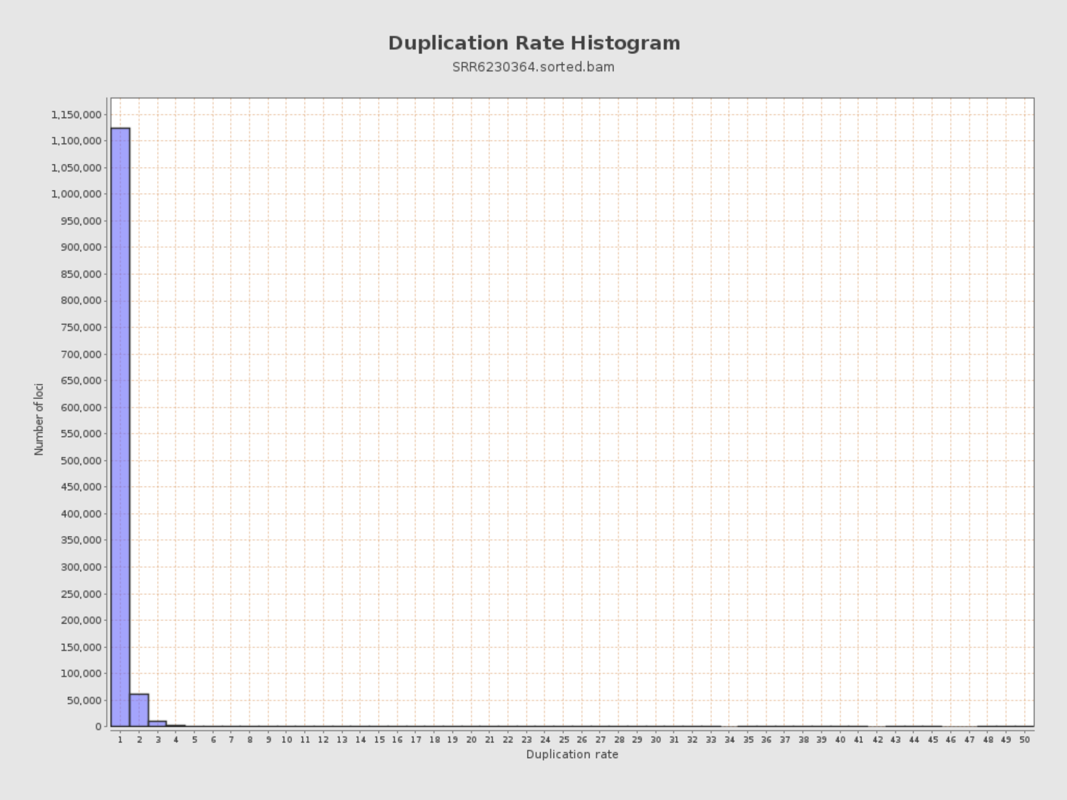
5. Results : Coverage Histogram (0-50X)



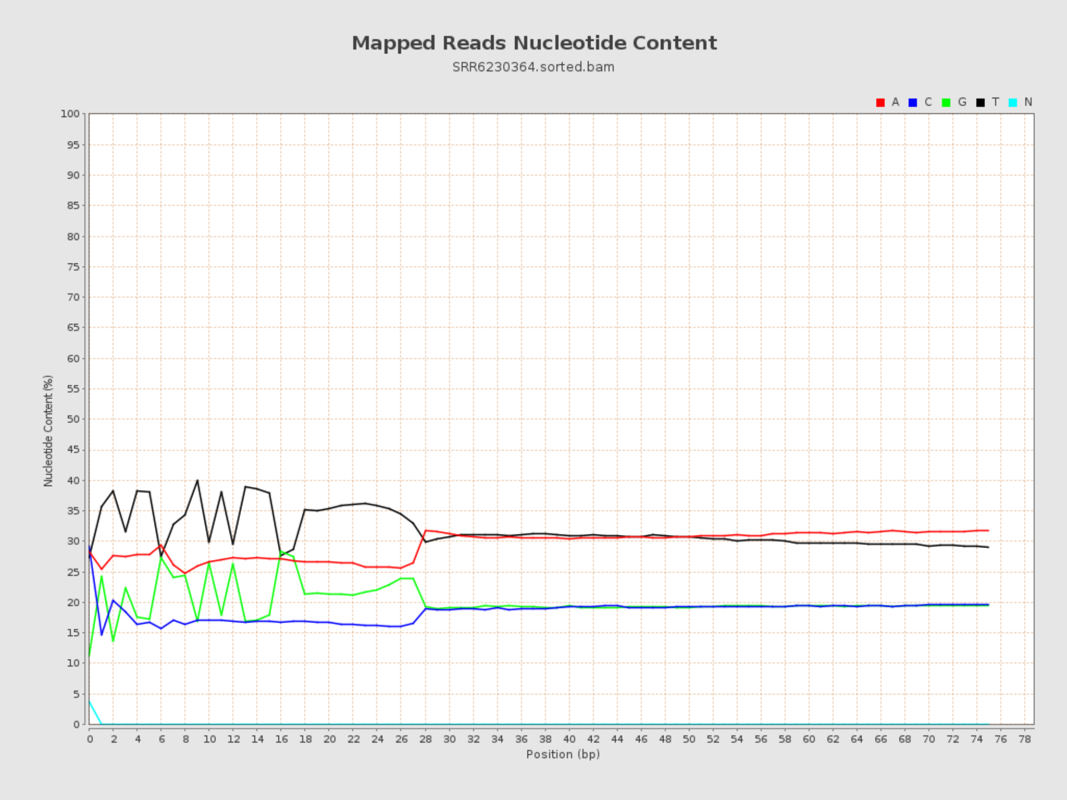
6. Results : Genome Fraction Coverage



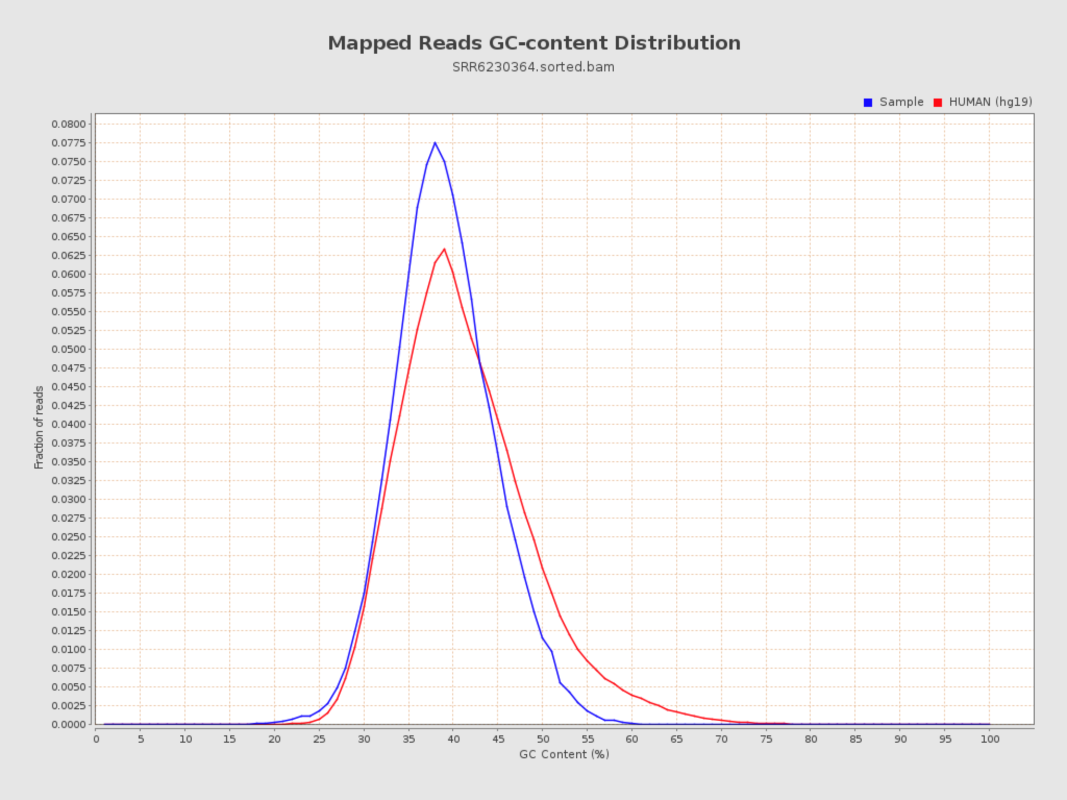
7. Results : Duplication Rate Histogram



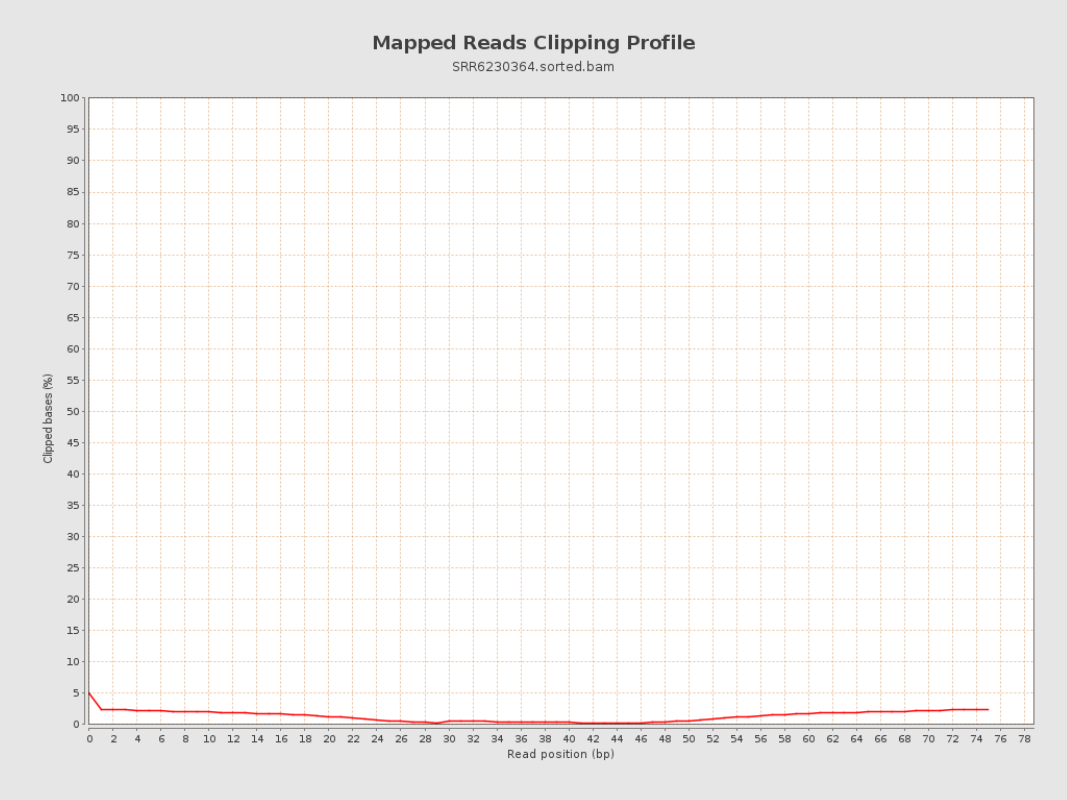
8. Results : Mapped Reads Nucleotide Content



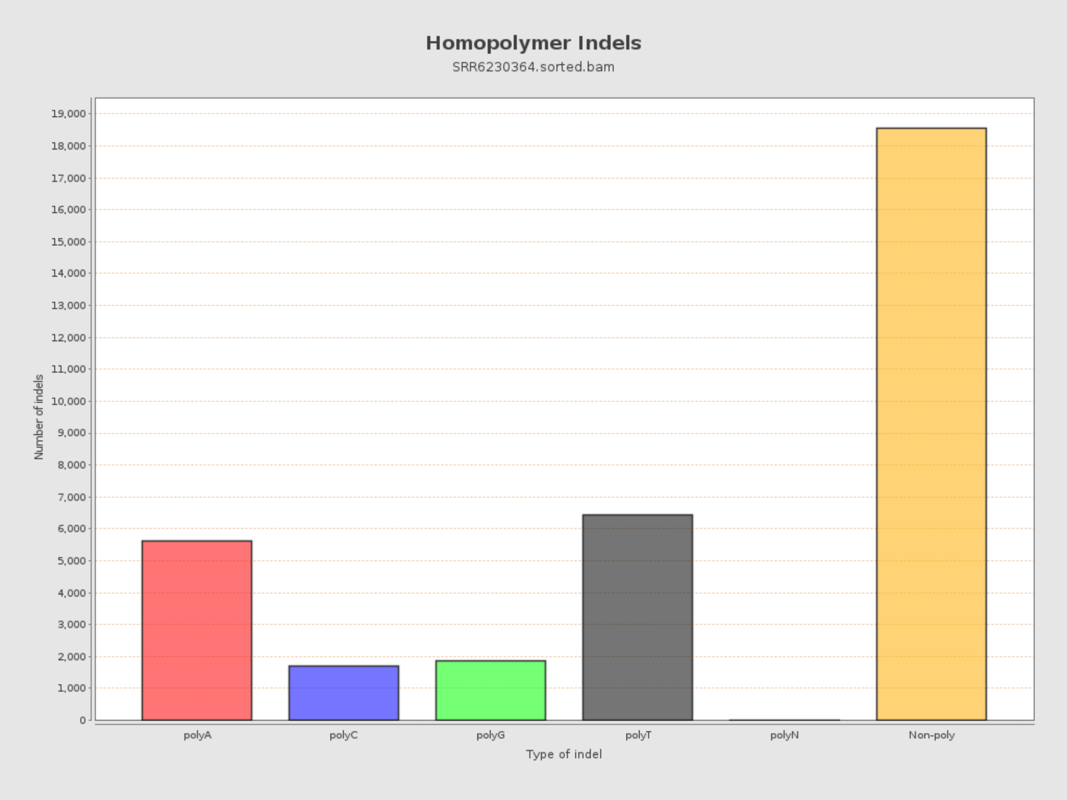
9. Results : Mapped Reads GC-content Distribution



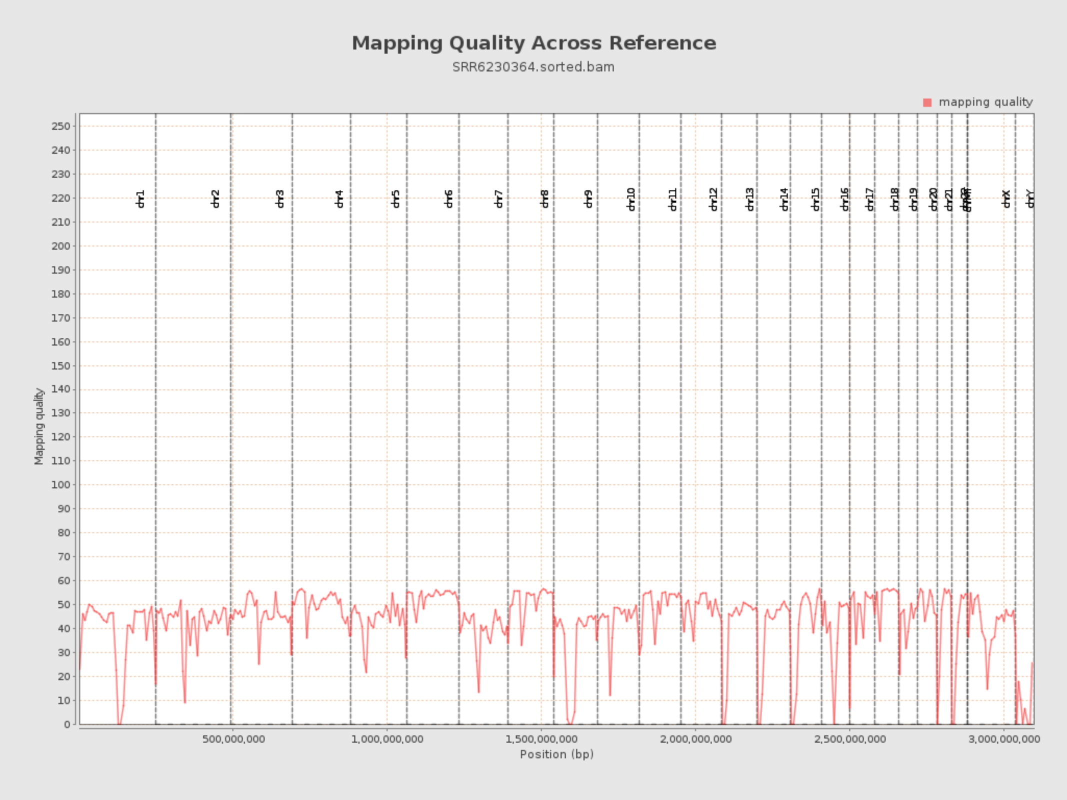
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram