Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008832.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_SRR6008832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:25:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,533,904
Mapped reads	1,386,527 / 90.39%
Unmapped reads	147,377 / 9.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,175 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	50,274 / 3.28%
Duplication rate	2.74%
Clipped reads	664,703 / 43.33%

2.2. ACGT Content

Number/percentage of A's	24,833,385 / 27.42%
Number/percentage of C's	16,697,665 / 18.44%
Number/percentage of T's	28,647,417 / 31.63%
Number/percentage of G's	20,269,188 / 22.38%
Number/percentage of N's	117,009 / 0.13%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.2976

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

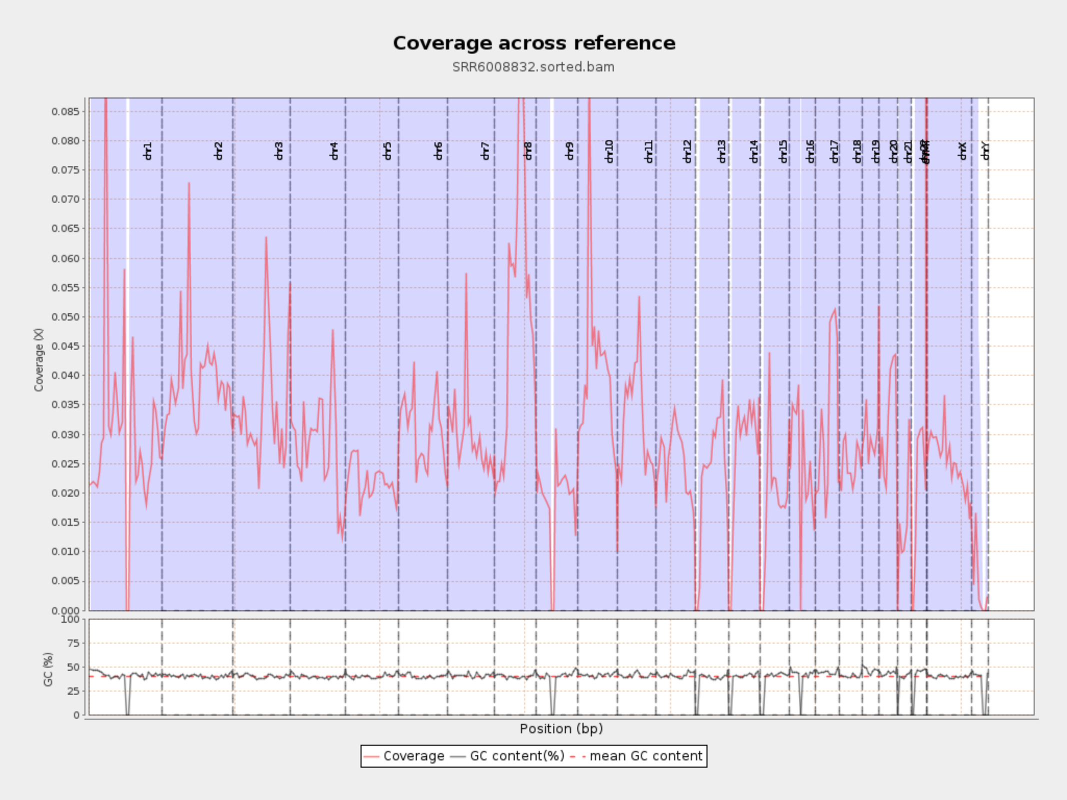
General error rate	0.82%
Mismatches	730,652
Insertions	6,360
Mapped reads with at least one insertion	0.45%
Deletions	25,905
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.94%

2.6. Chromosome stats

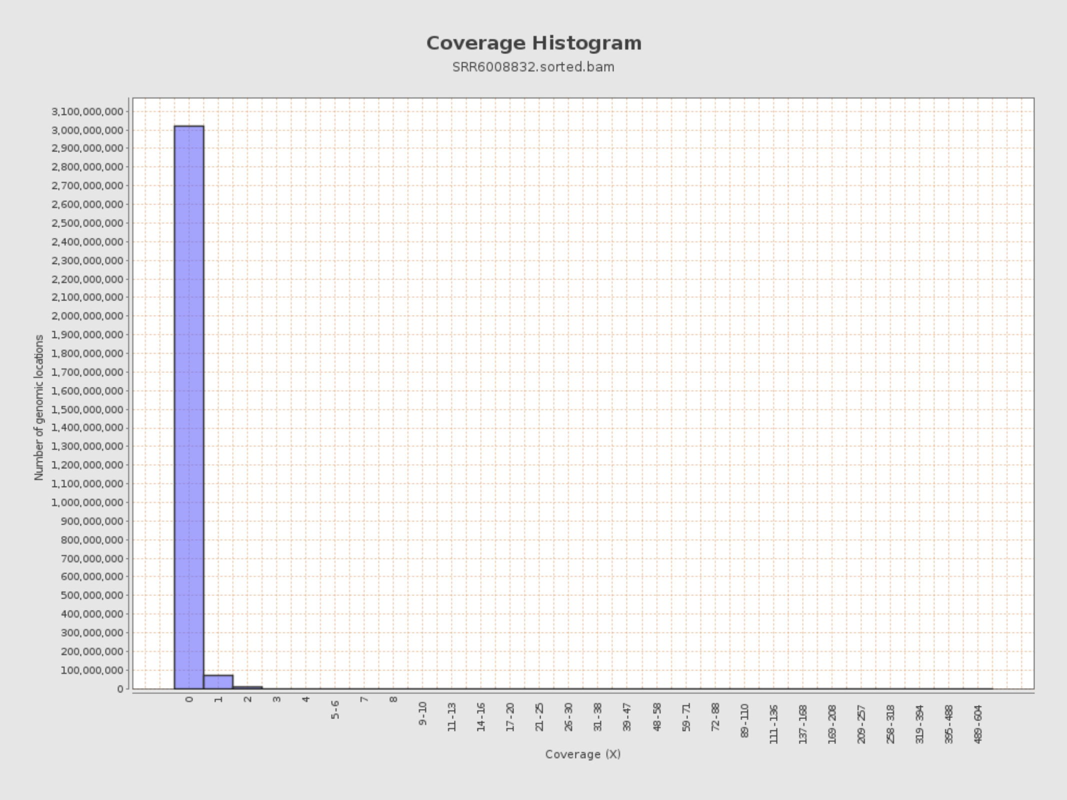
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7424936	0.0298	0.5385
chr2	243199373	9589116	0.0394	0.3334
chr3	198022430	6799570	0.0343	0.2206
chr4	191154276	5295518	0.0277	0.1999
chr5	180915260	4001852	0.0221	0.1669
chr6	171115067	5236701	0.0306	0.2169
chr7	159138663	4775129	0.03	0.376

chr8	146364022	7421897	0.0507	0.3982
chr9	141213431	2632833	0.0186	0.2183
chr10	135534747	5603324	0.0413	0.4574
chr11	135006516	4372724	0.0324	0.2632
chr12	133851895	3399816	0.0254	0.1799
chr13	115169878	2633597	0.0229	0.1684
chr14	107349540	2848416	0.0265	0.1886
chr15	102531392	1901150	0.0185	0.1532
chr16	90354753	2228041	0.0247	0.2343
chr17	81195210	2699072	0.0332	0.2439
chr18	78077248	1944335	0.0249	0.3793
chr19	59128983	1783133	0.0302	0.3399
chr20	63025520	2039344	0.0324	0.2052
chr21	48129895	750774	0.0156	0.1542
chr22	51304566	1014169	0.0198	0.1558
chrMT	16571	20558	1.2406	1.5114
chrX	155270560	3942543	0.0254	0.1953
chrY	59373566	252279	0.0042	0.1572

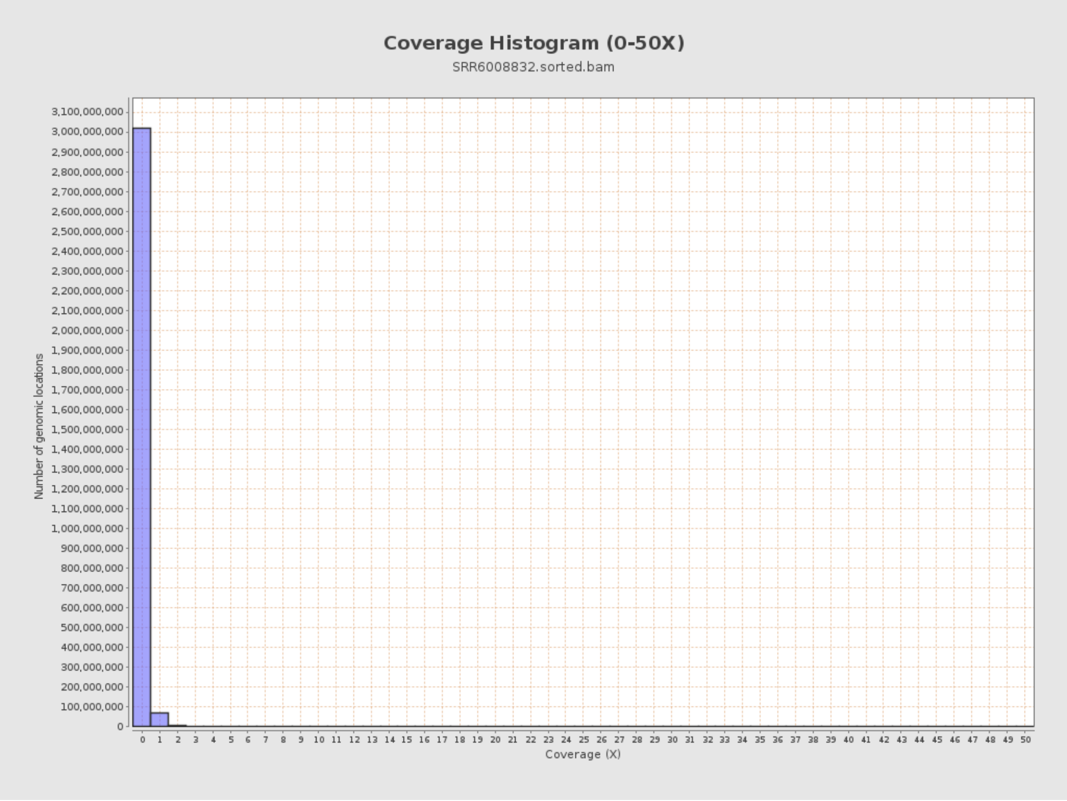
3. Results : Coverage across reference



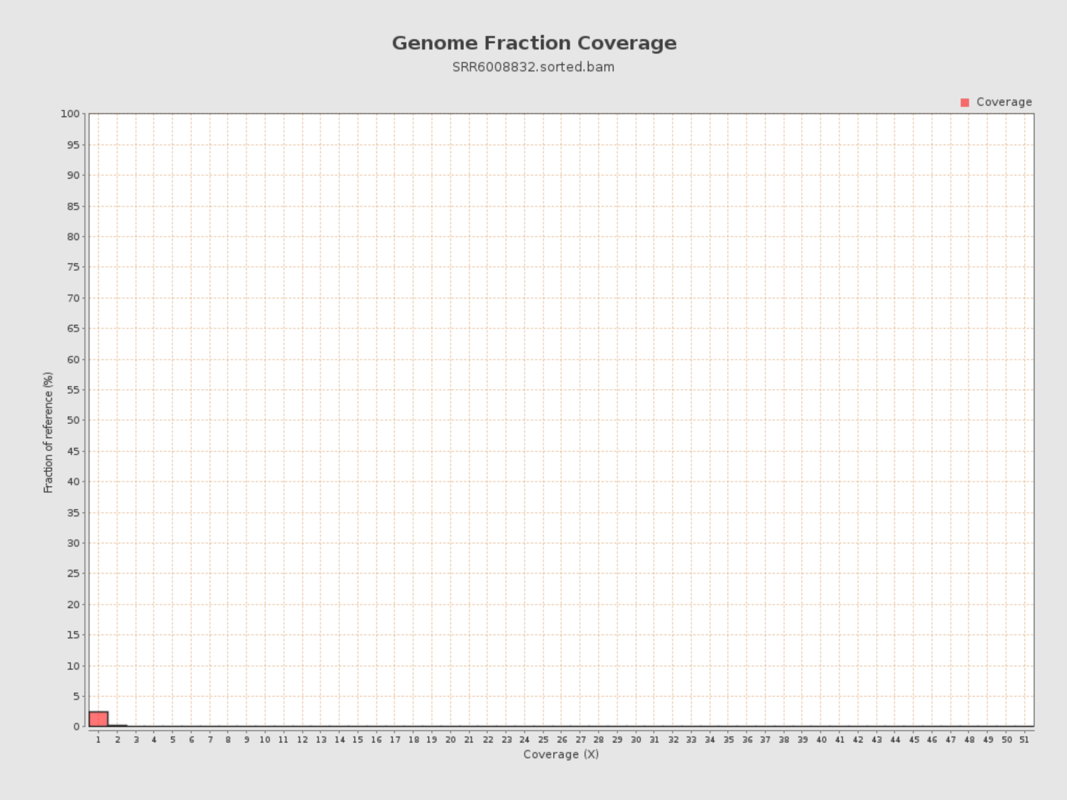
4. Results : Coverage Histogram



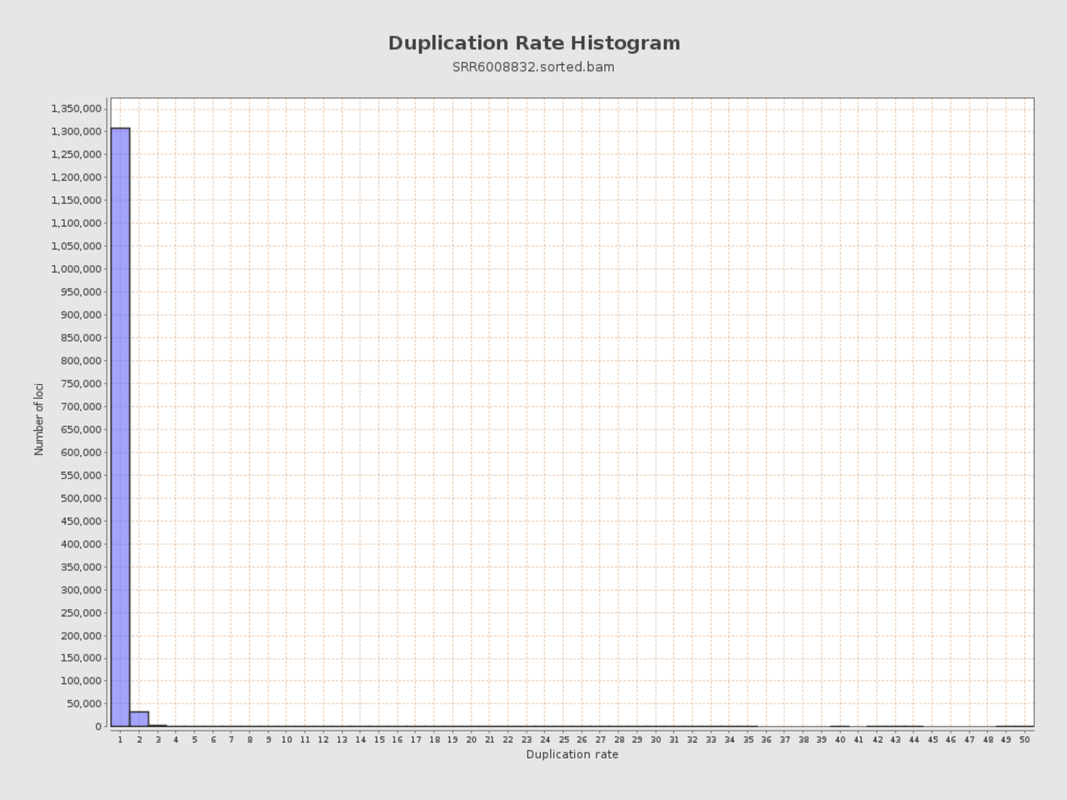
5. Results : Coverage Histogram (0-50X)



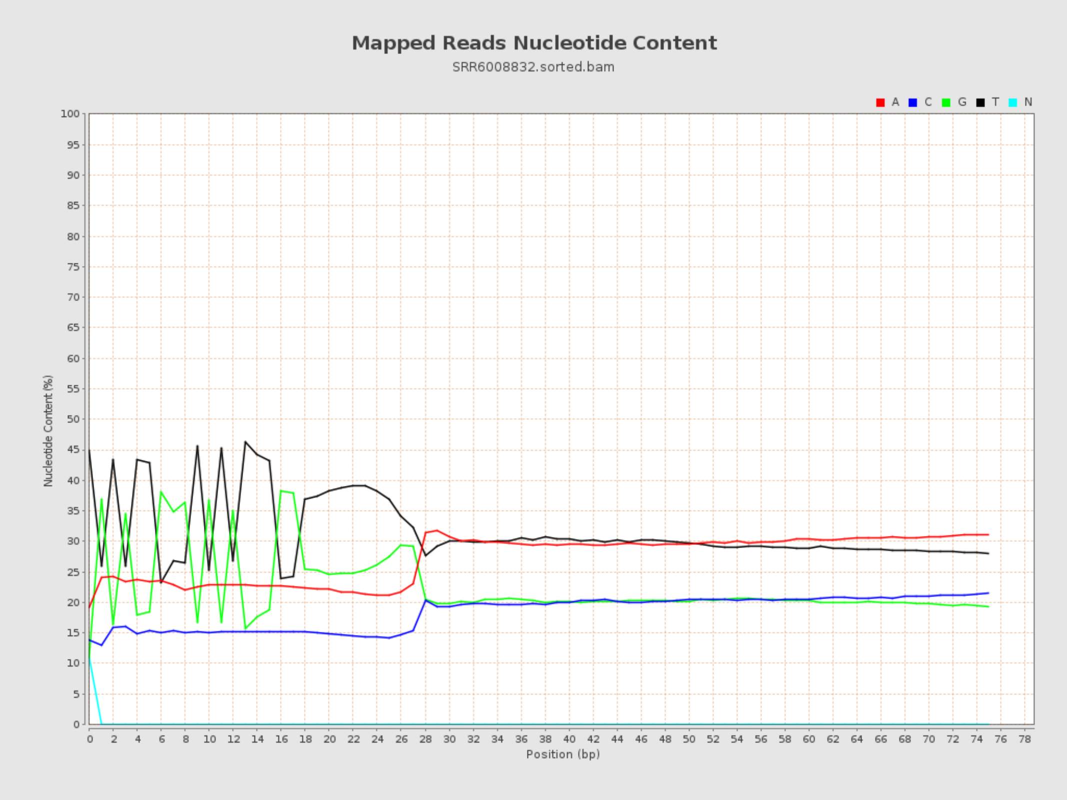
6. Results : Genome Fraction Coverage



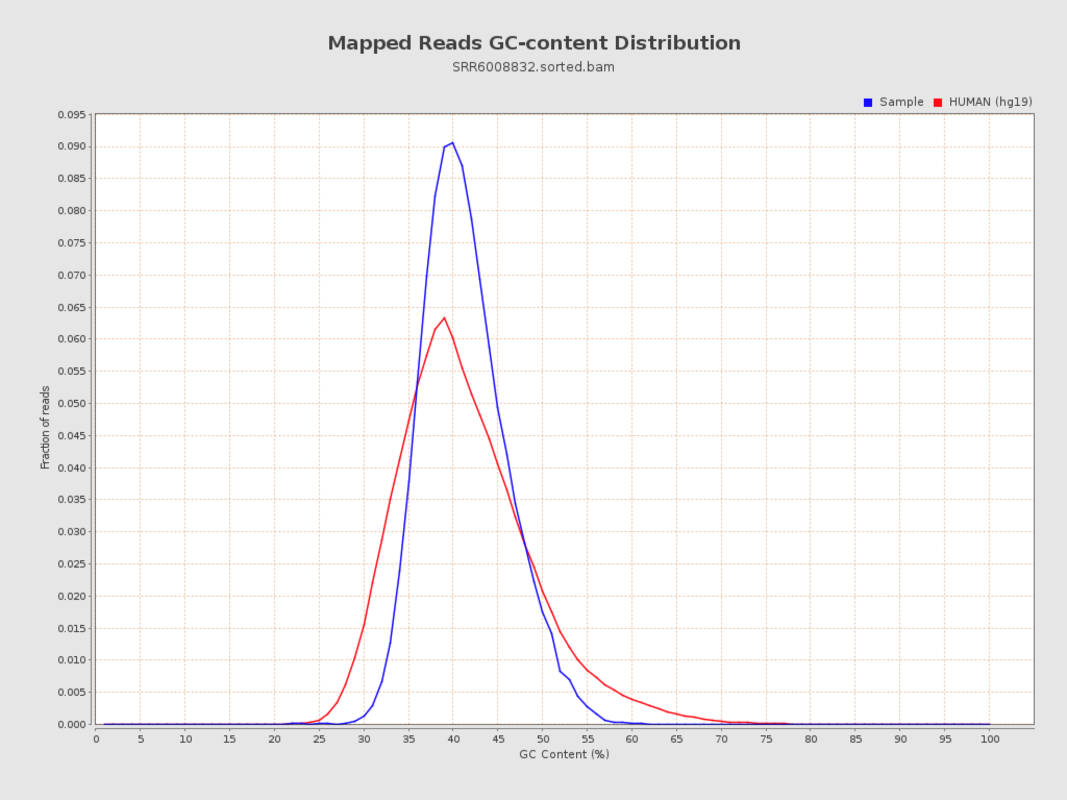
7. Results : Duplication Rate Histogram



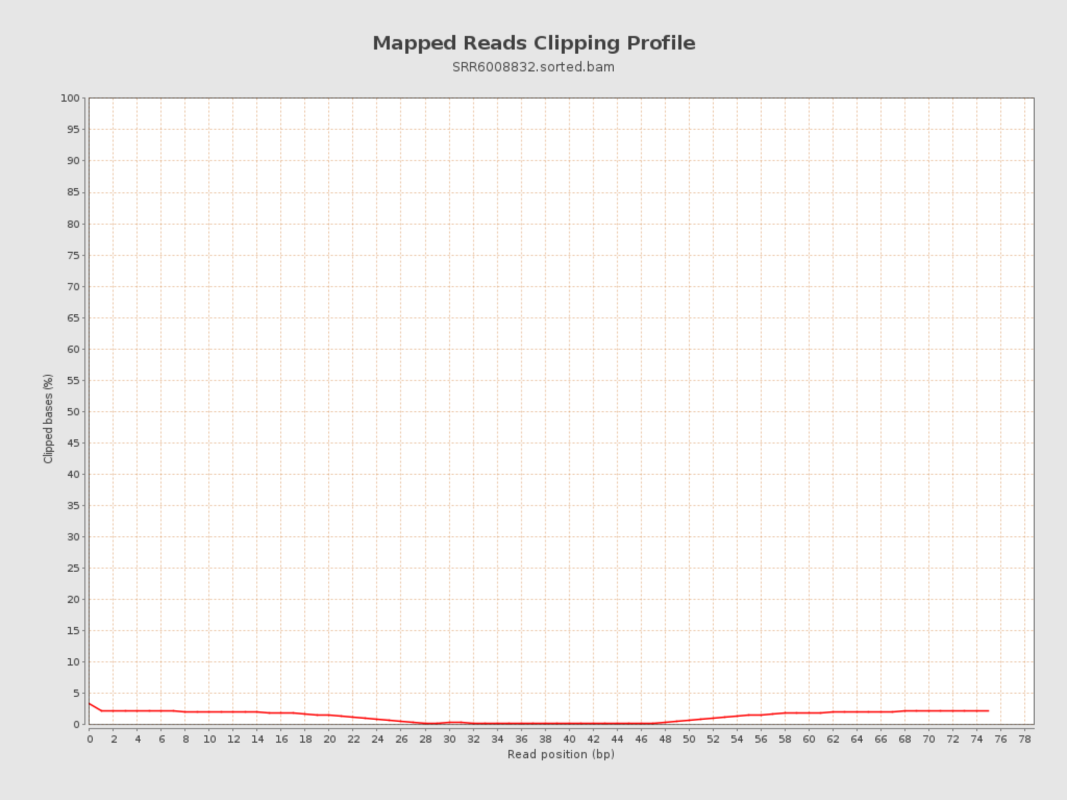
8. Results : Mapped Reads Nucleotide Content



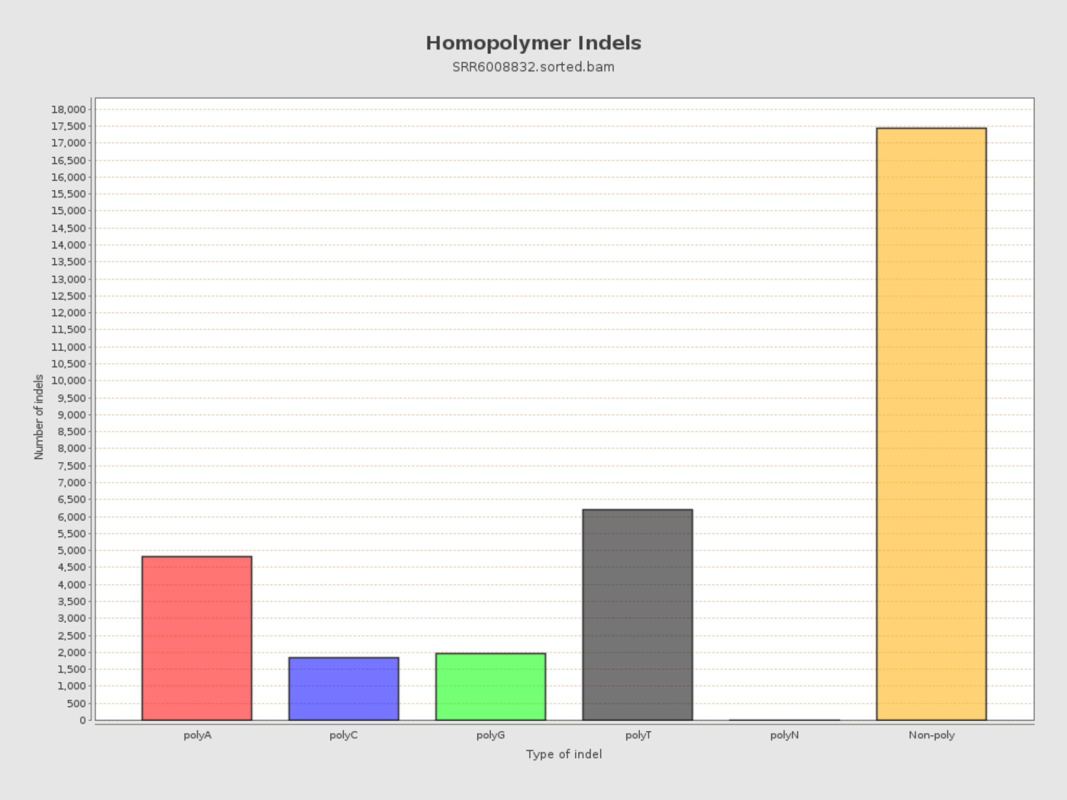
9. Results : Mapped Reads GC-content Distribution



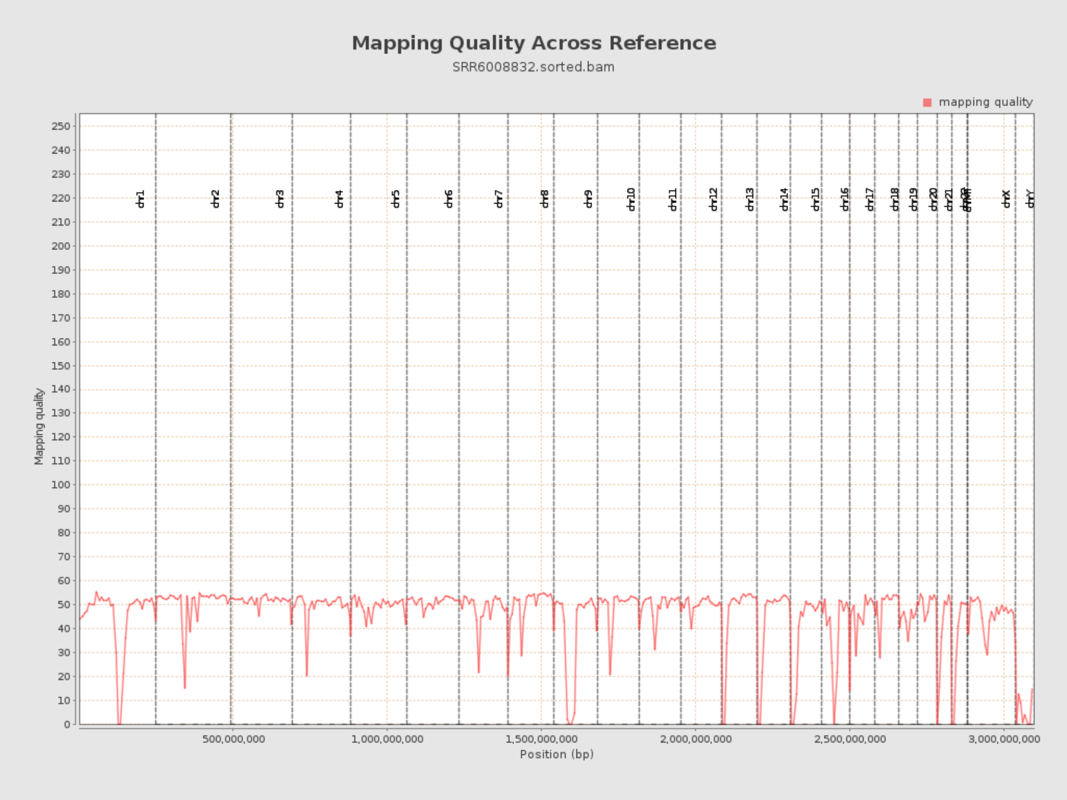
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram