Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:56:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008821.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_SRR6008821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	986,780
Mapped reads	712,642 / 72.22%
Unmapped reads	274,138 / 27.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,377 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,859 / 2.72%
Duplication rate	3.27%
Clipped reads	482,792 / 48.93%

2.2. ACGT Content

Number/percentage of A's	12,428,009 / 28.51%
Number/percentage of C's	8,092,554 / 18.57%
Number/percentage of T's	13,082,153 / 30.01%
Number/percentage of G's	9,971,919 / 22.88%
Number/percentage of N's	15,011 / 0.03%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1662

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

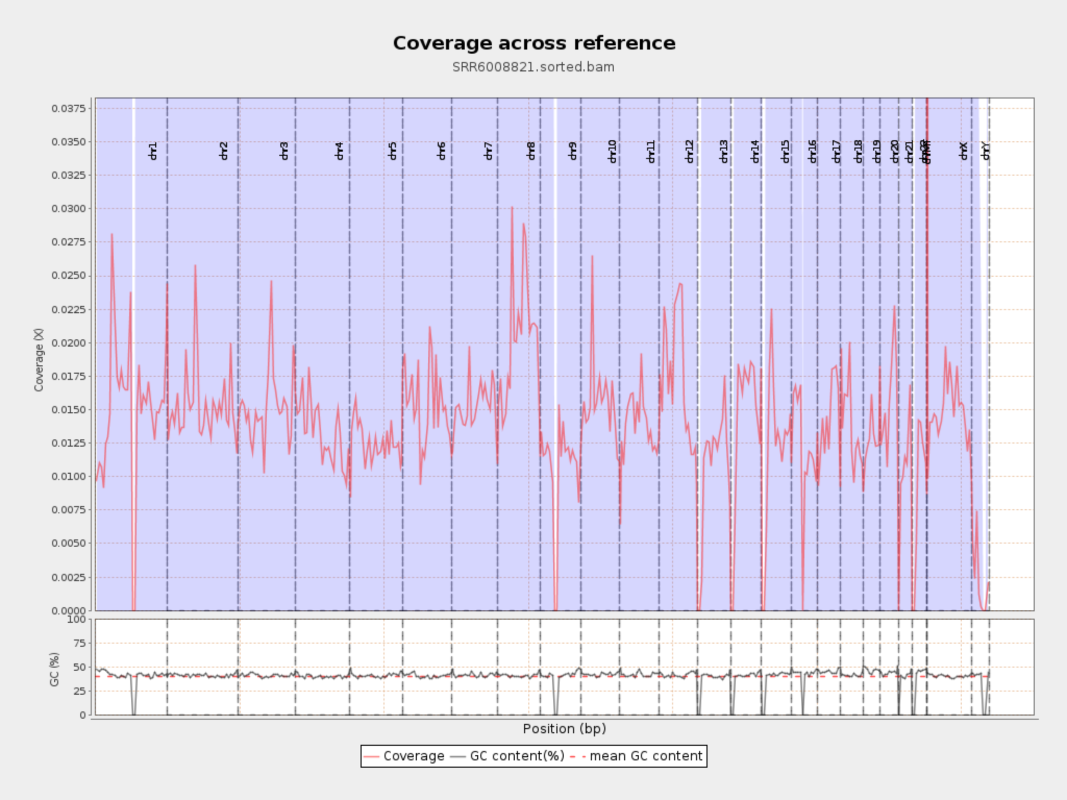
General error rate	1.09%
Mismatches	469,701
Insertions	3,447
Mapped reads with at least one insertion	0.48%
Deletions	14,875
Mapped reads with at least one deletion	2.06%
Homopolymer indels	47.88%

2.6. Chromosome stats

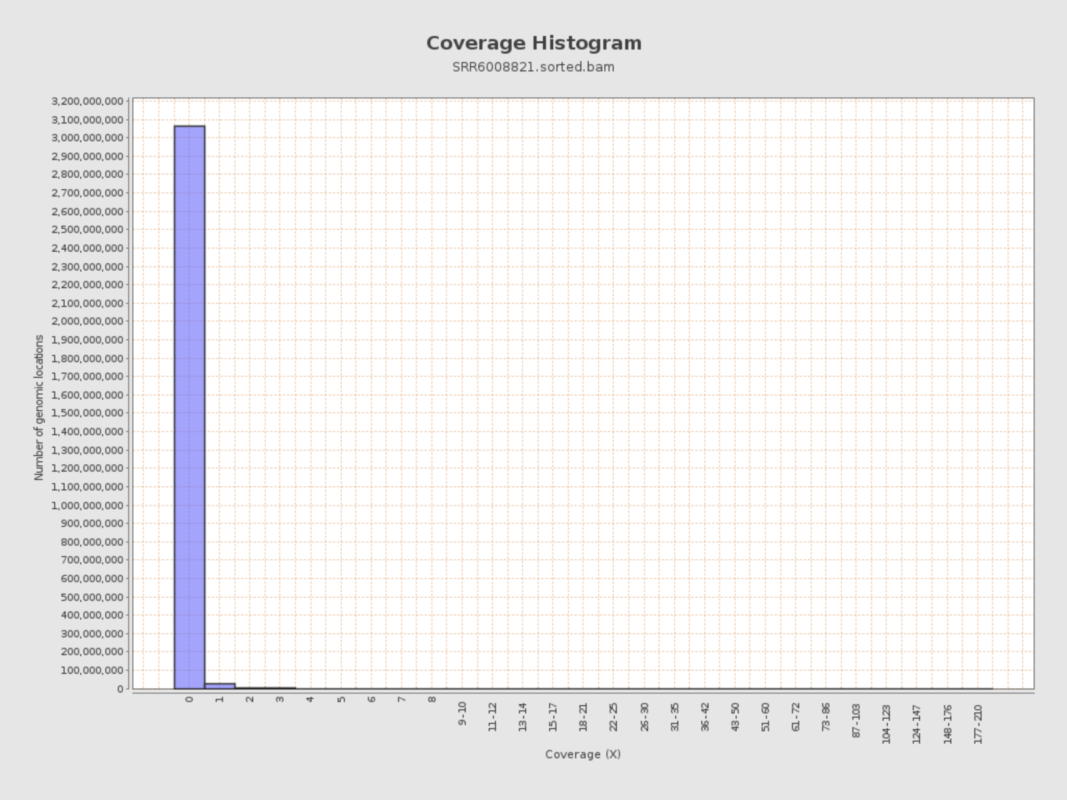
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3722177	0.0149	0.2192
chr2	243199373	3726600	0.0153	0.1797
chr3	198022430	3007274	0.0152	0.154
chr4	191154276	2547367	0.0133	0.1467
chr5	180915260	2284277	0.0126	0.1402
chr6	171115067	2647008	0.0155	0.1638
chr7	159138663	2437941	0.0153	0.1859

chr8	146364022	3002359	0.0205	0.2049
chr9	141213431	1489223	0.0105	0.1459
chr10	135534747	2114262	0.0156	0.1804
chr11	135006516	1874801	0.0139	0.1601
chr12	133851895	2338033	0.0175	0.1709
chr13	115169878	1214012	0.0105	0.1287
chr14	107349540	1488429	0.0139	0.149
chr15	102531392	1225830	0.012	0.1362
chr16	90354753	1068851	0.0118	0.1378
chr17	81195210	1156418	0.0142	0.1533
chr18	78077248	1079715	0.0138	0.2186
chr19	59128983	762713	0.0129	0.1621
chr20	63025520	986397	0.0157	0.1575
chr21	48129895	509257	0.0106	0.1324
chr22	51304566	460024	0.009	0.1157
chrMT	16571	19212	1.1594	1.321
chrX	155270560	2319700	0.0149	0.1557
chrY	59373566	131370	0.0022	0.0708

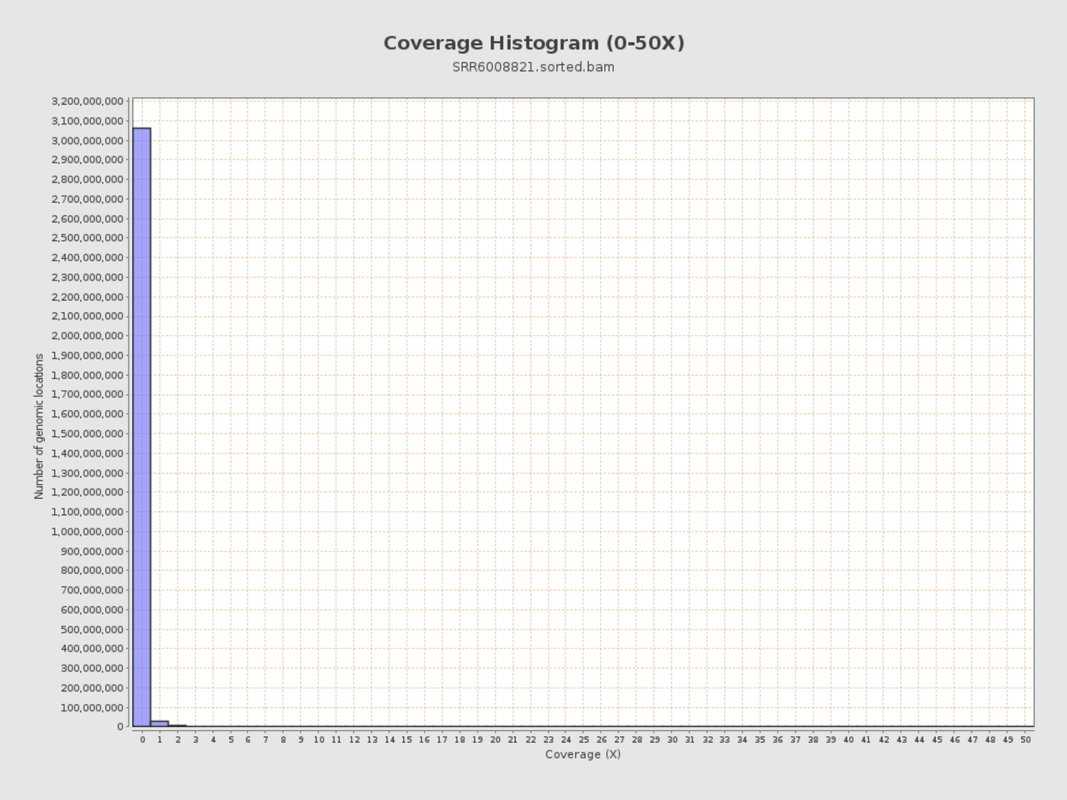
3. Results : Coverage across reference



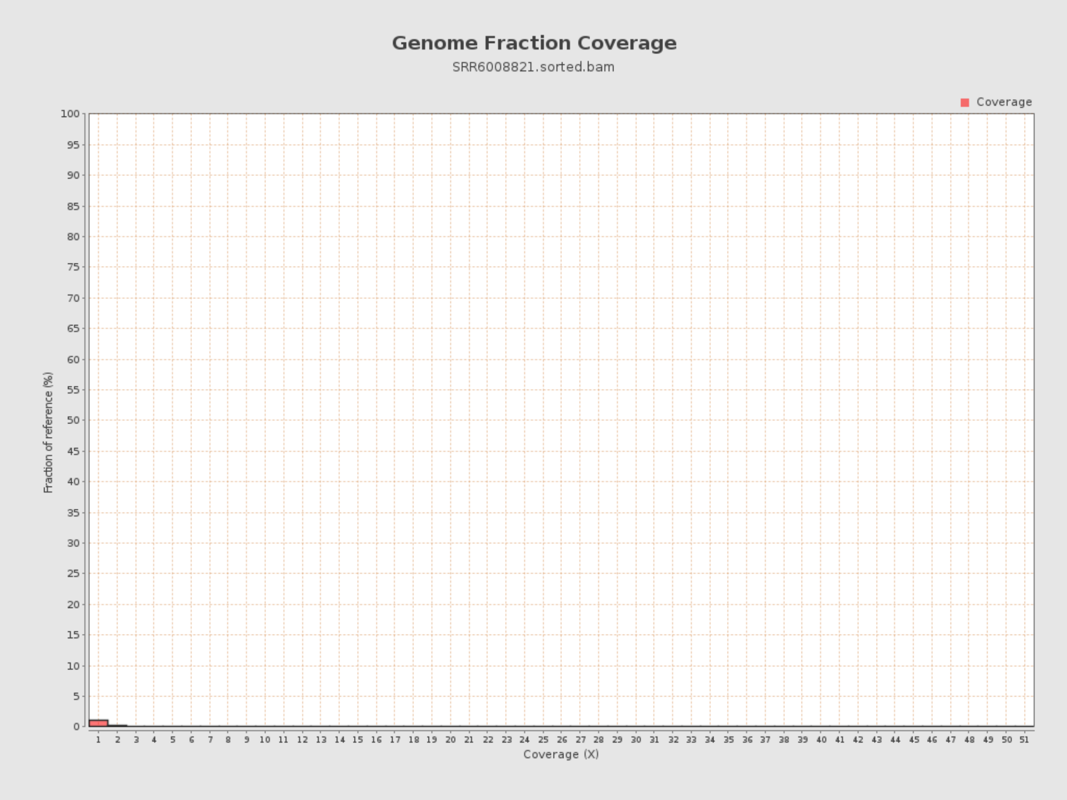
4. Results : Coverage Histogram



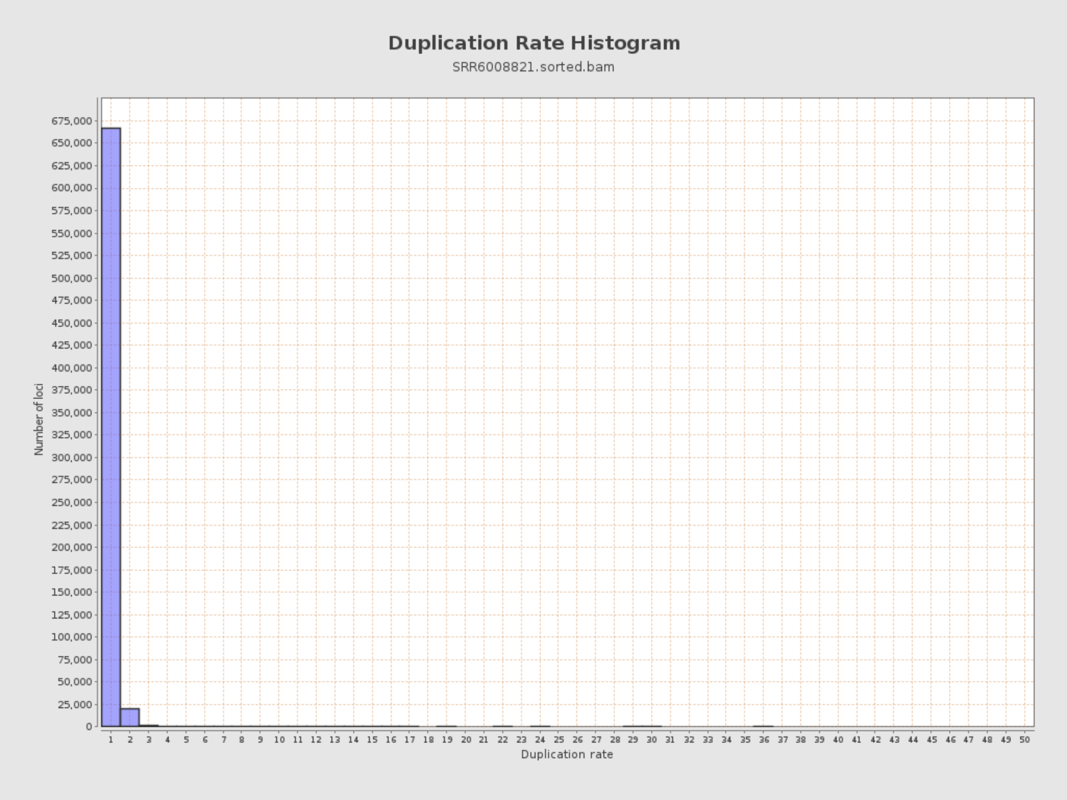
5. Results : Coverage Histogram (0-50X)



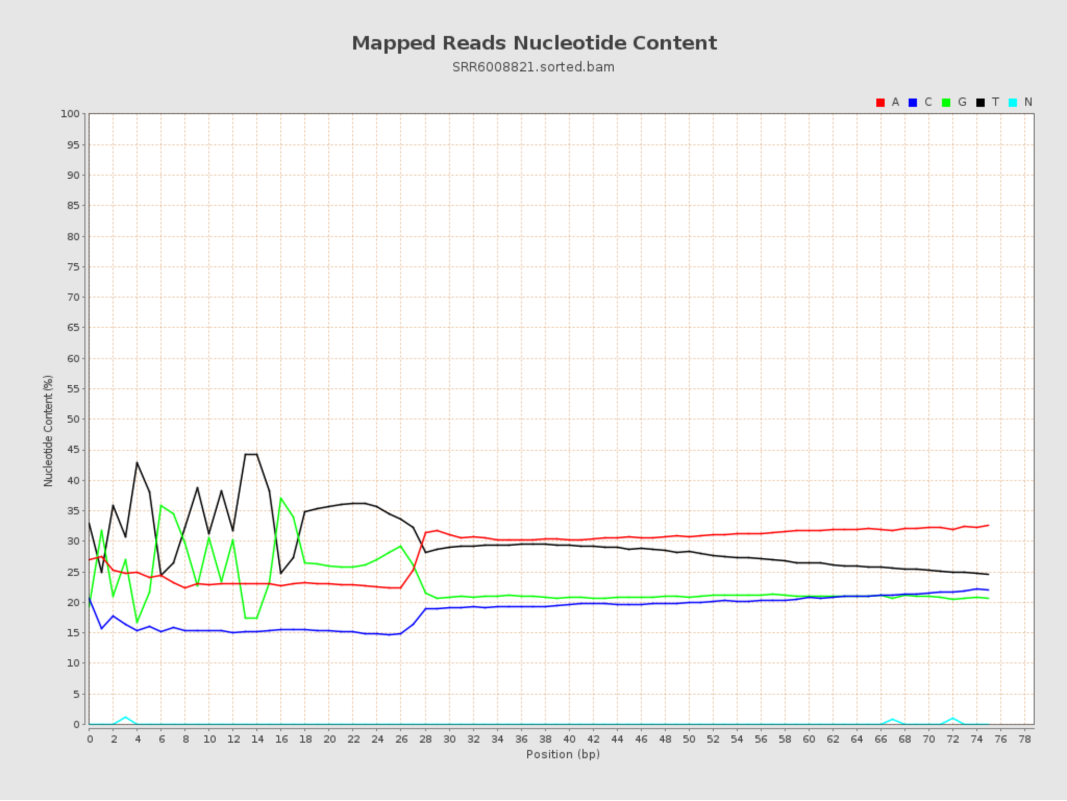
6. Results : Genome Fraction Coverage



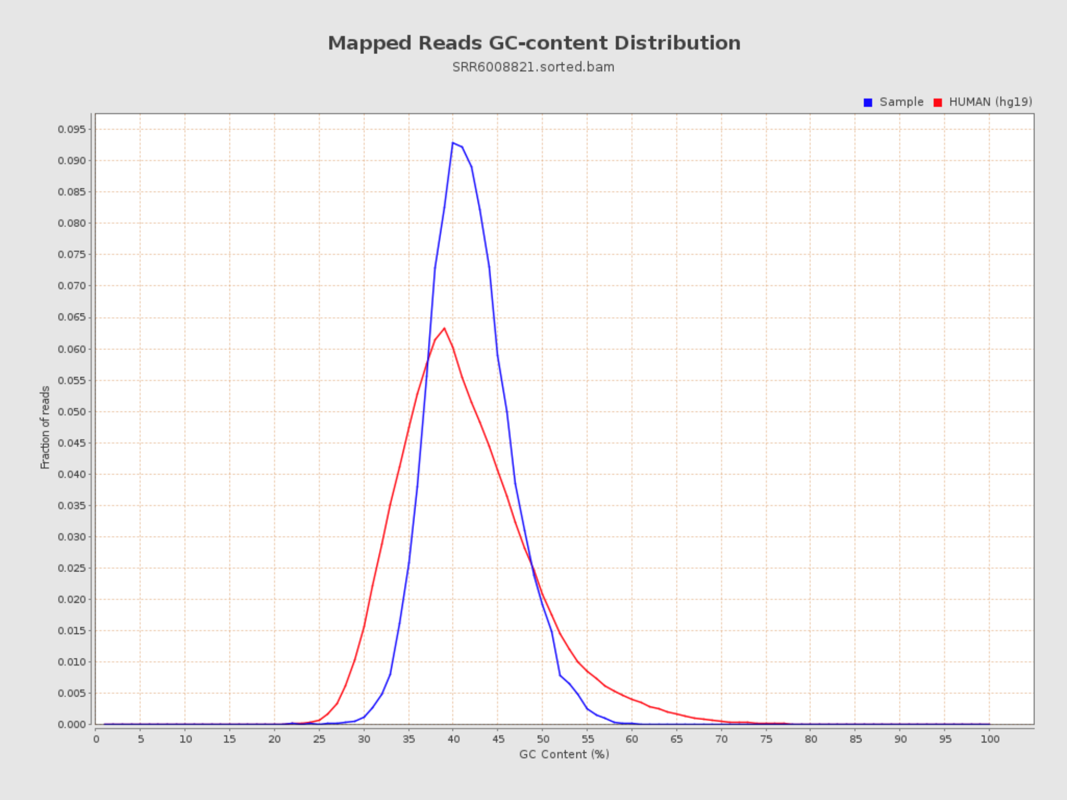
7. Results : Duplication Rate Histogram



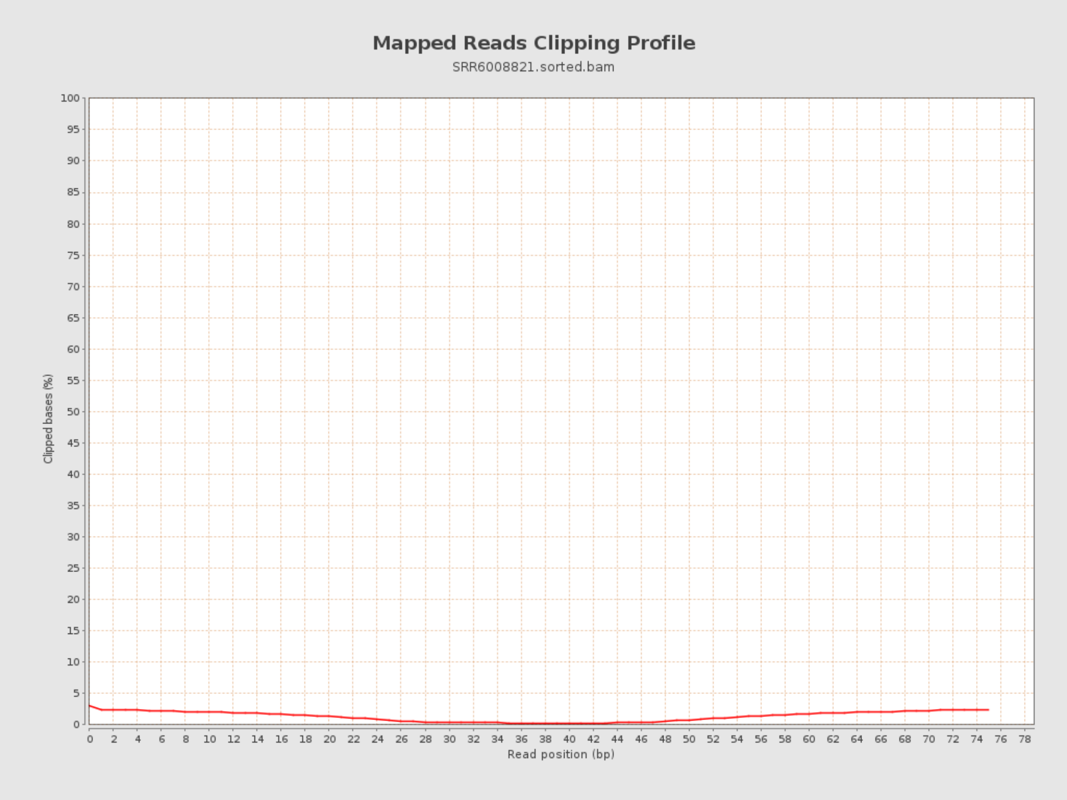
8. Results : Mapped Reads Nucleotide Content



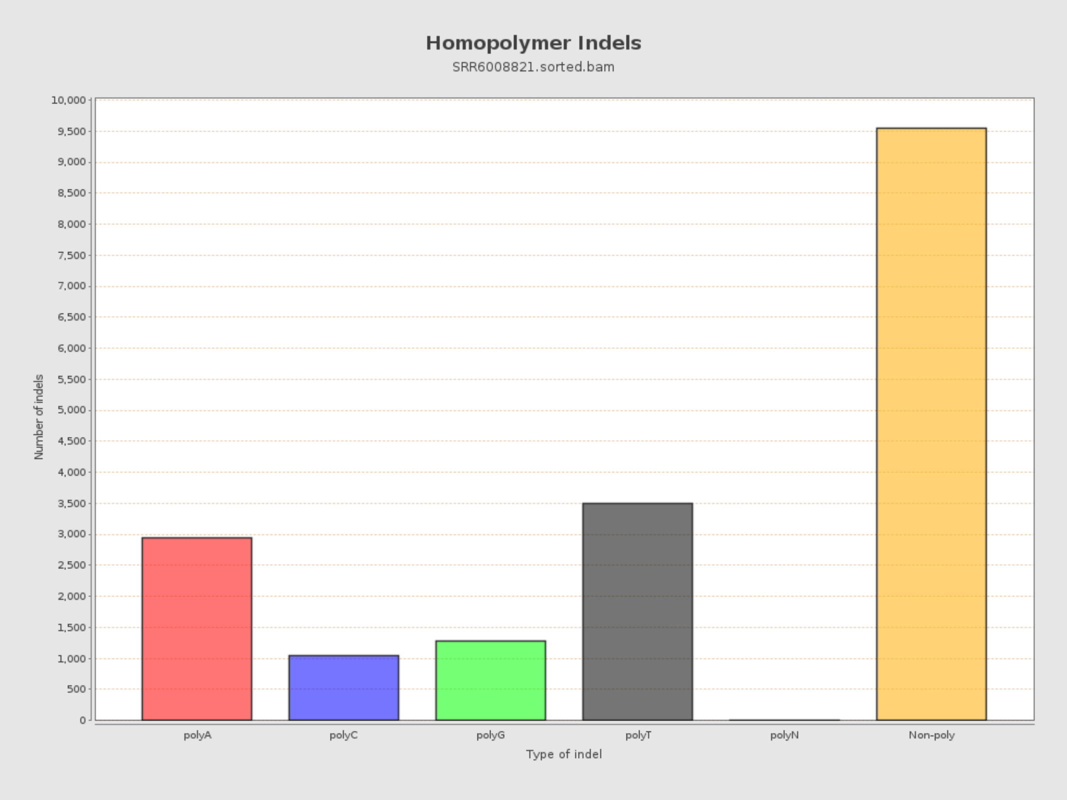
9. Results : Mapped Reads GC-content Distribution



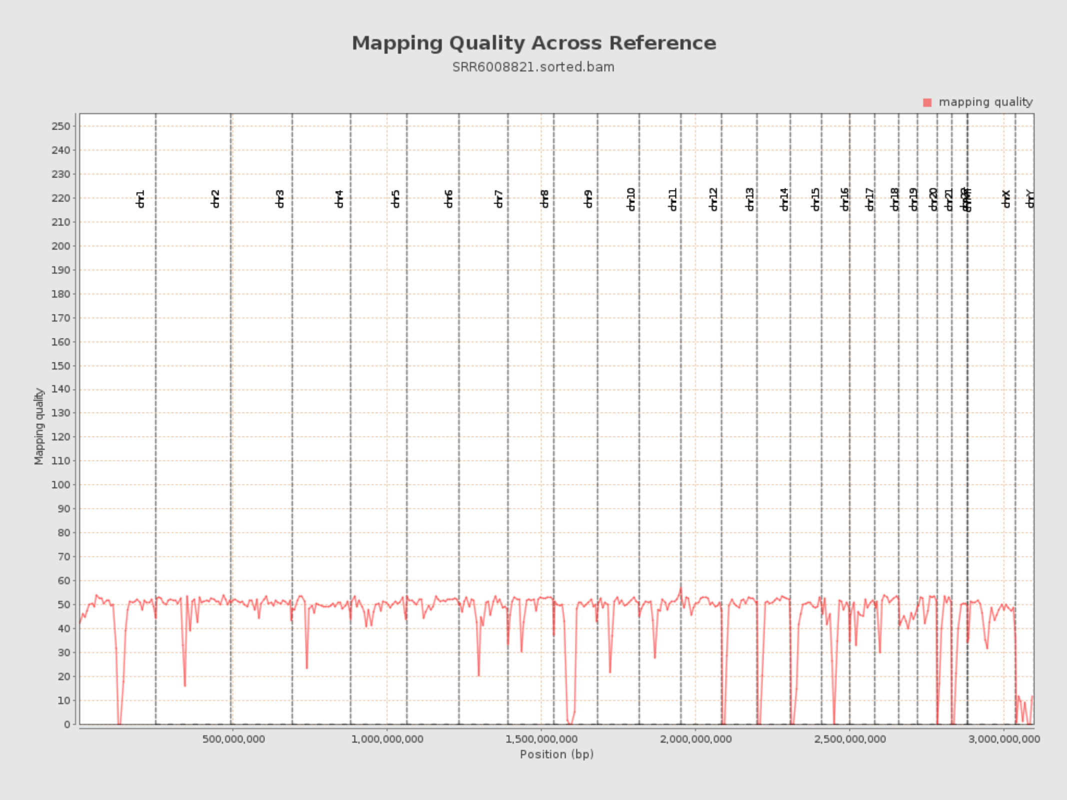
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram