Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:15:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008804.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_SRR6008804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:15:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,923,991
Mapped reads	1,706,348 / 88.69%
Unmapped reads	217,643 / 11.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,429 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	74,753 / 3.89%
Duplication rate	3.26%
Clipped reads	776,307 / 40.35%

2.2. ACGT Content

Number/percentage of A's	30,691,906 / 27.15%
Number/percentage of C's	21,879,336 / 19.36%
Number/percentage of T's	34,754,467 / 30.75%
Number/percentage of G's	25,566,460 / 22.62%
Number/percentage of N's	143,818 / 0.13%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.378

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

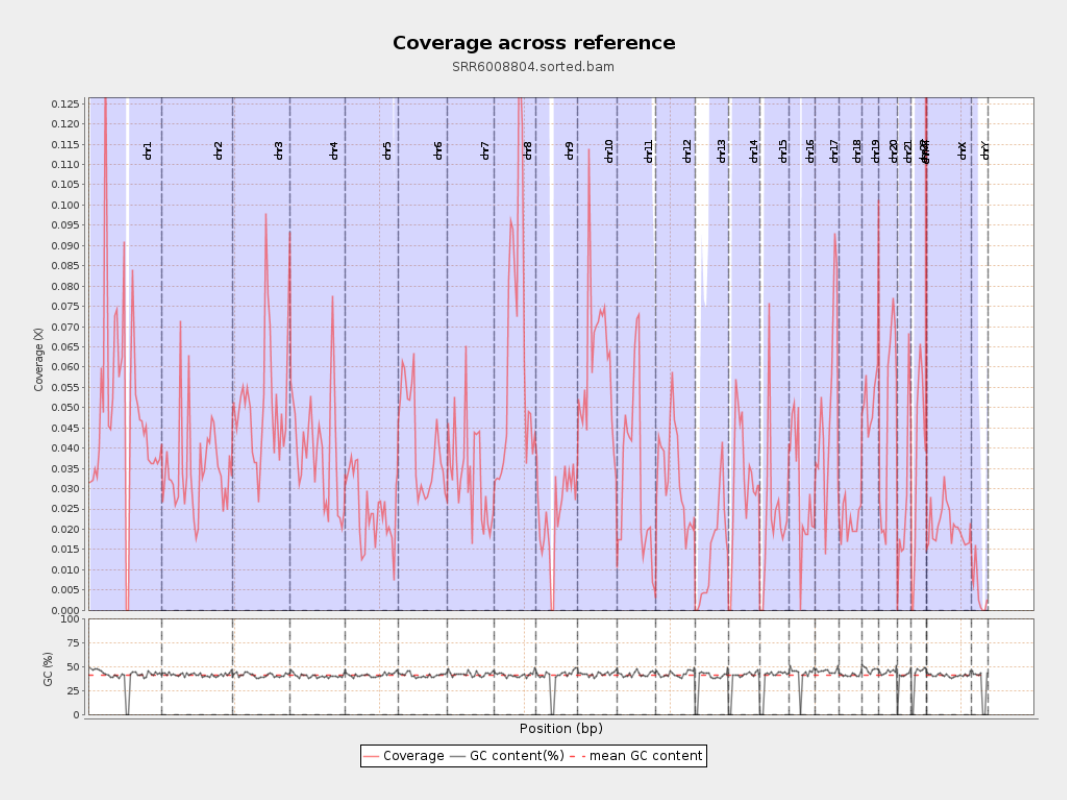
General error rate	0.85%
Mismatches	948,155
Insertions	7,881
Mapped reads with at least one insertion	0.46%
Deletions	33,130
Mapped reads with at least one deletion	1.92%
Homopolymer indels	45.41%

2.6. Chromosome stats

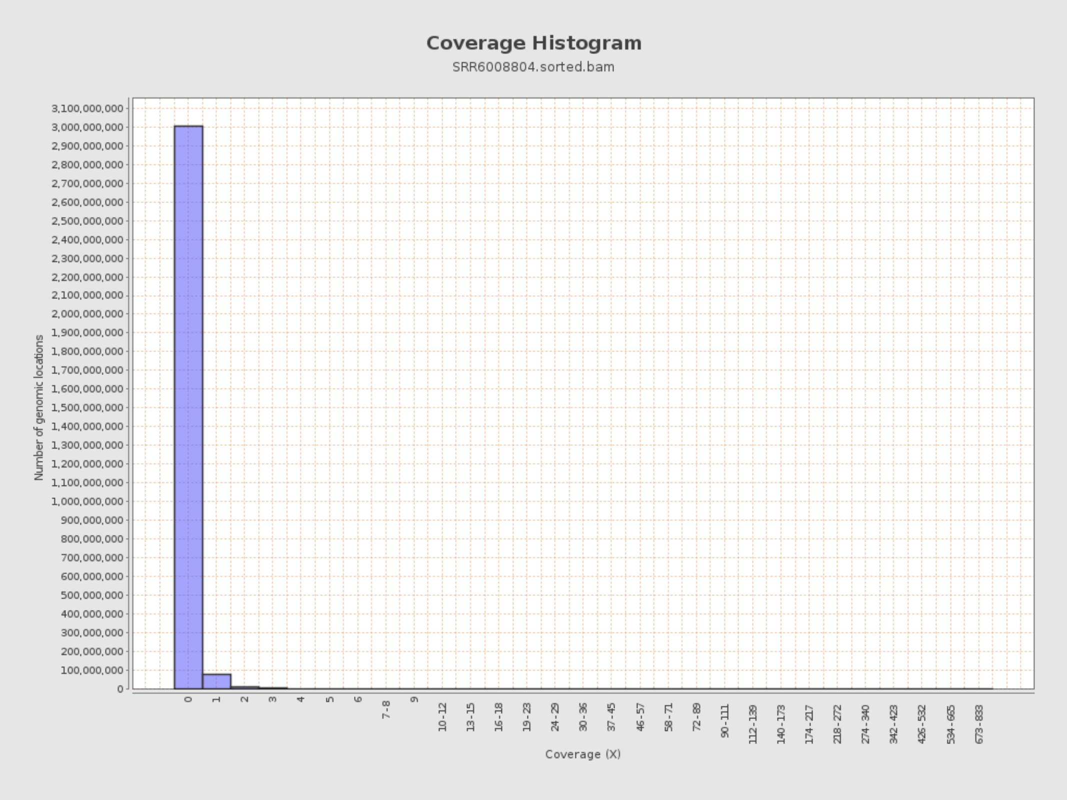
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12193956	0.0489	0.7208
chr2	243199373	8487504	0.0349	0.4005
chr3	198022430	10089912	0.051	0.2936
chr4	191154276	7474240	0.0391	0.2378
chr5	180915260	4519627	0.025	0.1844
chr6	171115067	6977557	0.0408	0.28
chr7	159138663	5349257	0.0336	0.4934

chr8	146364022	9056573	0.0619	0.4466
chr9	141213431	3285513	0.0233	0.2553
chr10	135534747	8323627	0.0614	0.6944
chr11	135006516	4392348	0.0325	0.2627
chr12	133851895	4444313	0.0332	0.2139
chr13	115169878	1669130	0.0145	0.1394
chr14	107349540	3403898	0.0317	0.2134
chr15	102531392	2368507	0.0231	0.1768
chr16	90354753	2636043	0.0292	0.267
chr17	81195210	3938936	0.0485	0.3041
chr18	78077248	1713997	0.022	0.3944
chr19	59128983	3138517	0.0531	0.5171
chr20	63025520	2876060	0.0456	0.2528
chr21	48129895	1340128	0.0278	0.2066
chr22	51304566	1882235	0.0367	0.2242
chrMT	16571	56837	3.4299	3.0197
chrX	155270560	3217863	0.0207	0.1818
chrY	59373566	257843	0.0043	0.1571

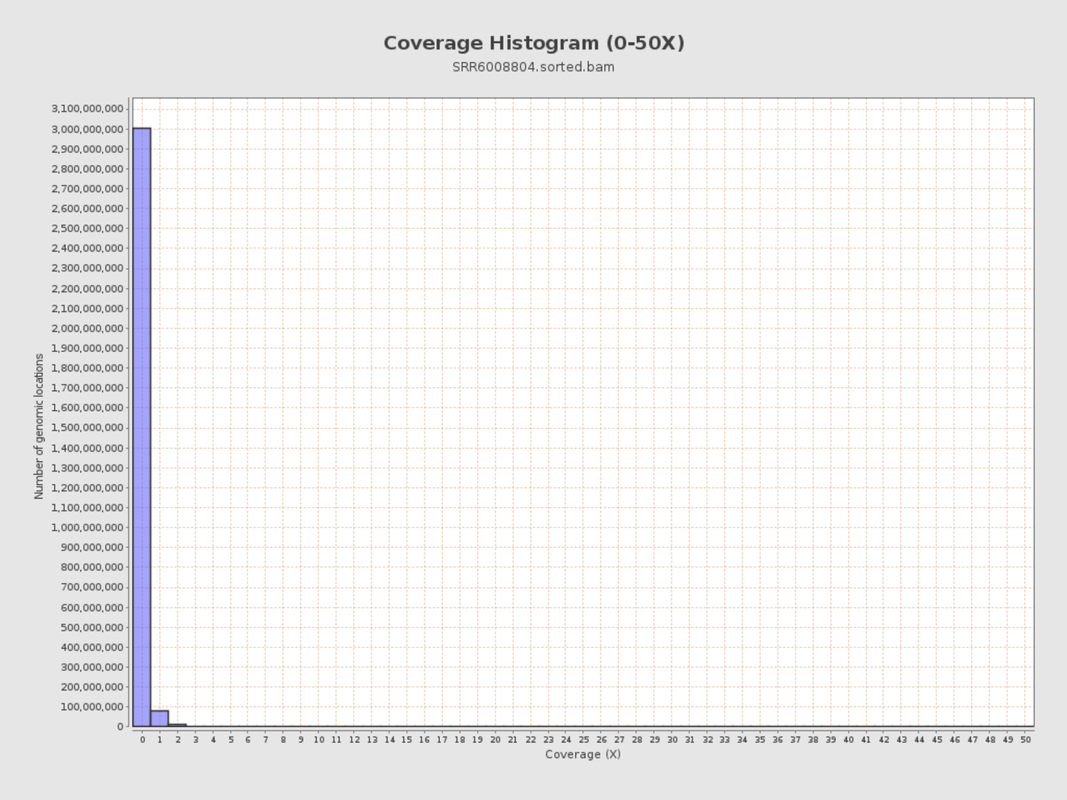
3. Results : Coverage across reference



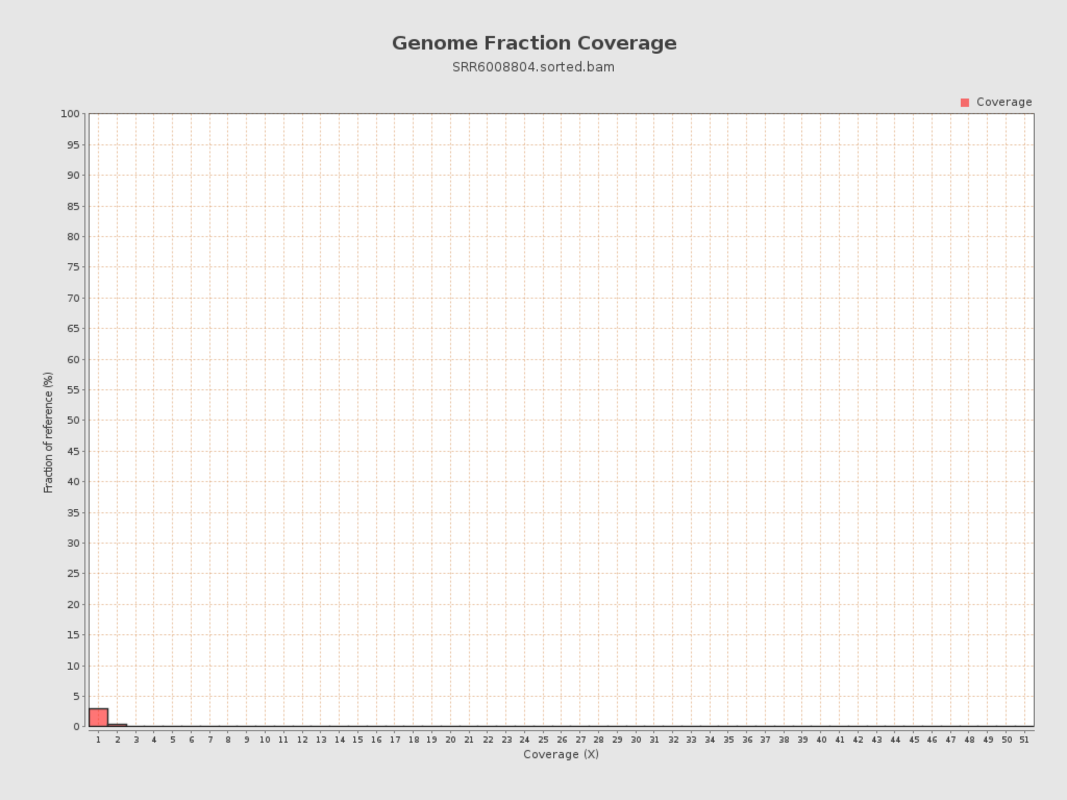
4. Results : Coverage Histogram



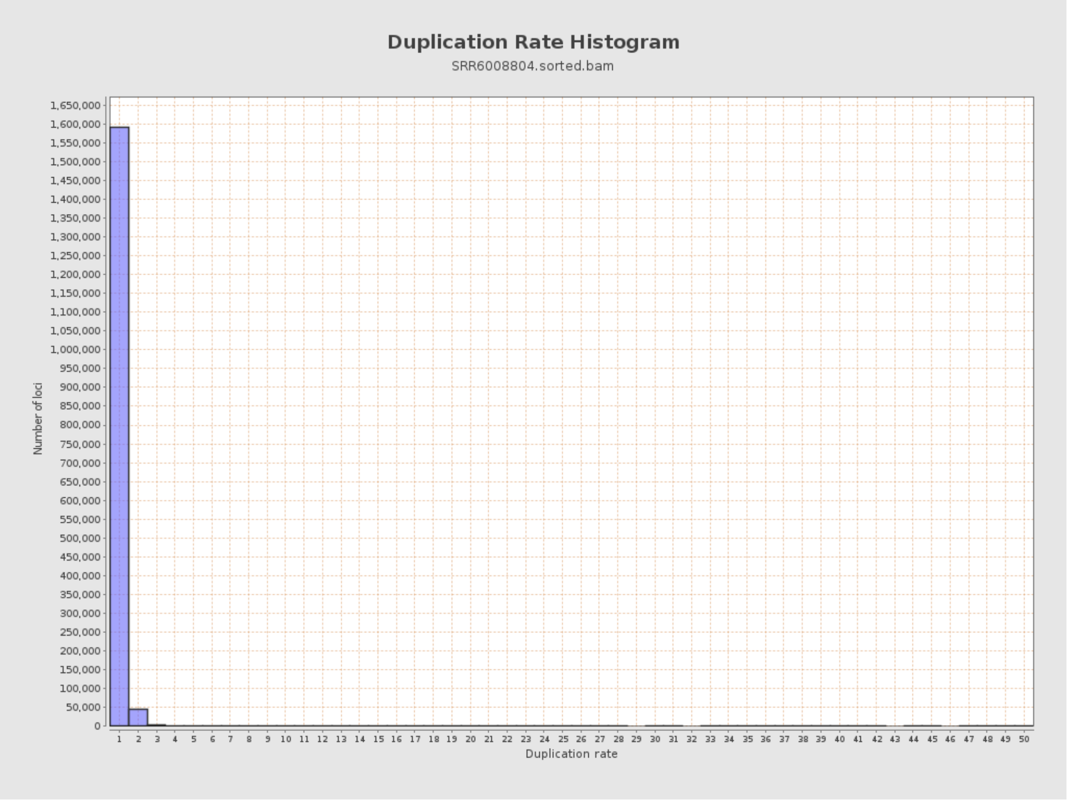
5. Results : Coverage Histogram (0-50X)



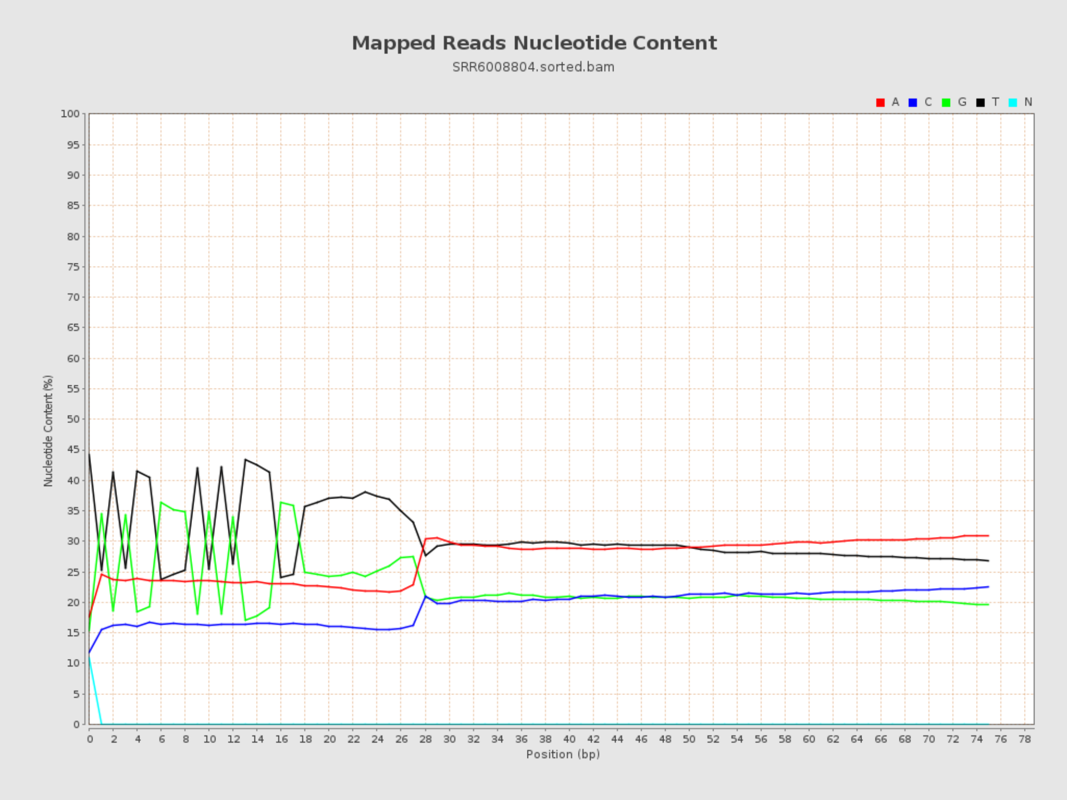
6. Results : Genome Fraction Coverage



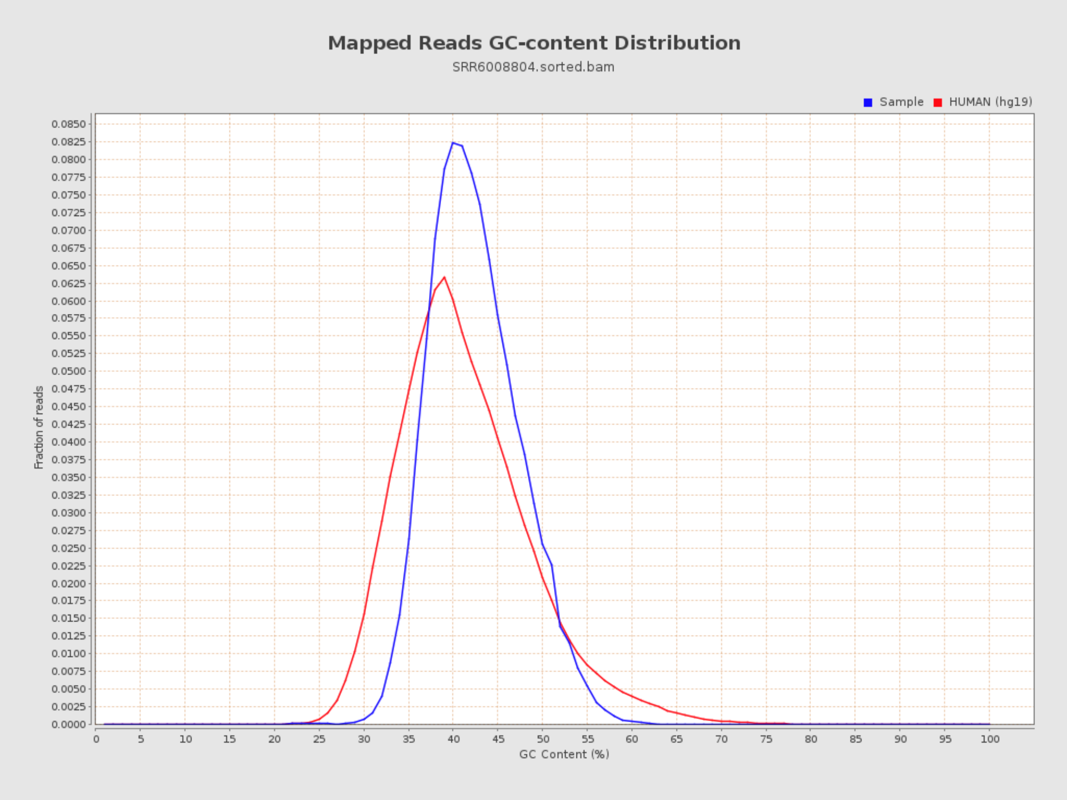
7. Results : Duplication Rate Histogram



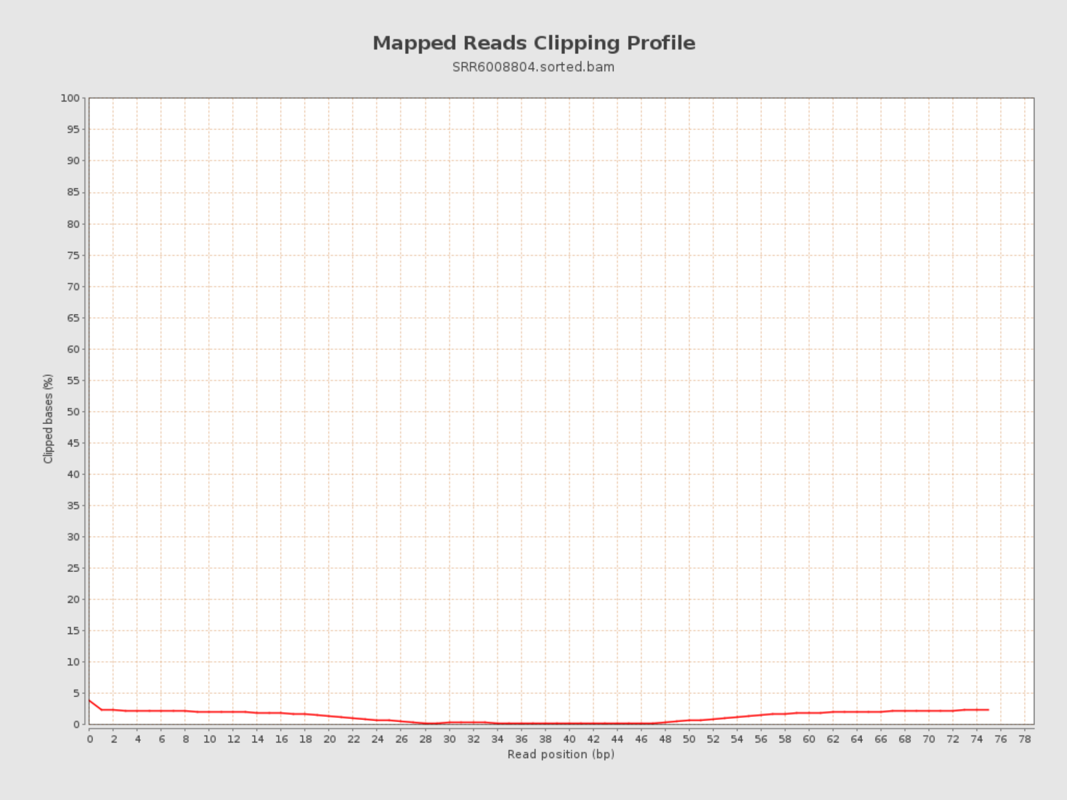
8. Results : Mapped Reads Nucleotide Content



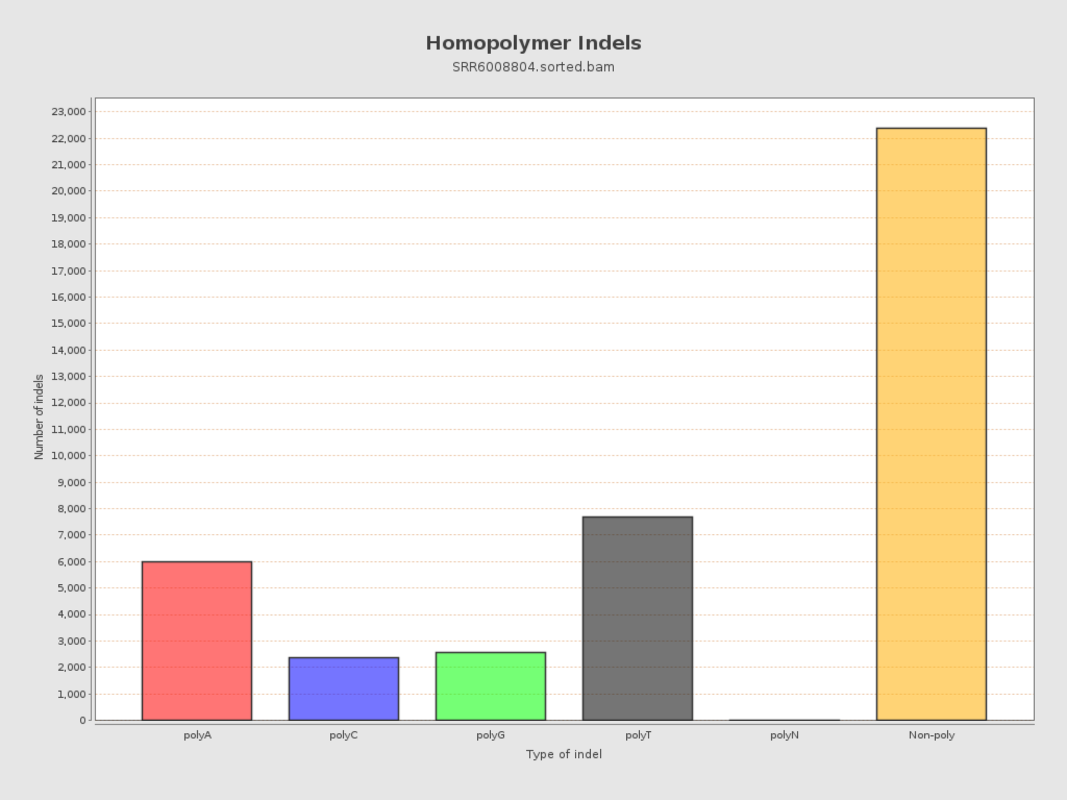
9. Results : Mapped Reads GC-content Distribution



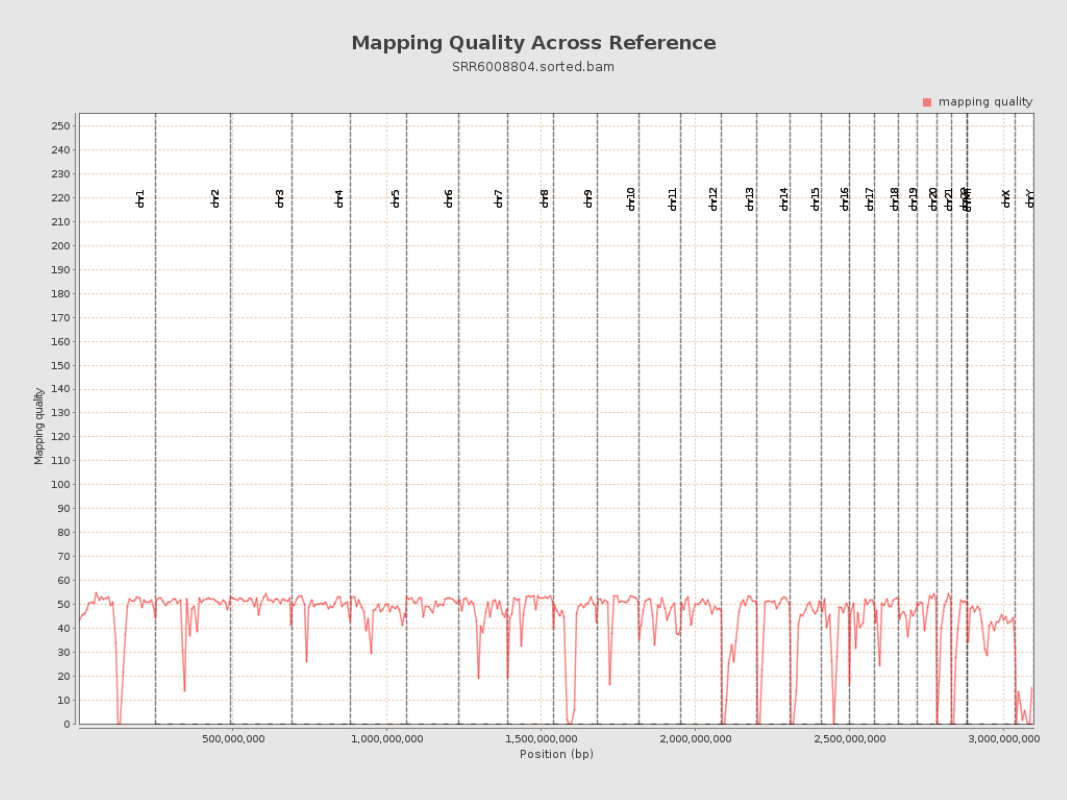
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram