Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:36:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008813.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_SRR6008813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:36:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,127
Mapped reads	1,447,415 / 86.61%
Unmapped reads	223,712 / 13.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,685 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	134,314 / 8.04%
Duplication rate	7.18%
Clipped reads	622,300 / 37.24%

2.2. ACGT Content

Number/percentage of A's	26,304,068 / 27.13%
Number/percentage of C's	18,076,712 / 18.64%
Number/percentage of T's	30,381,525 / 31.34%
Number/percentage of G's	22,151,497 / 22.85%
Number/percentage of N's	39,893 / 0.04%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.3508

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

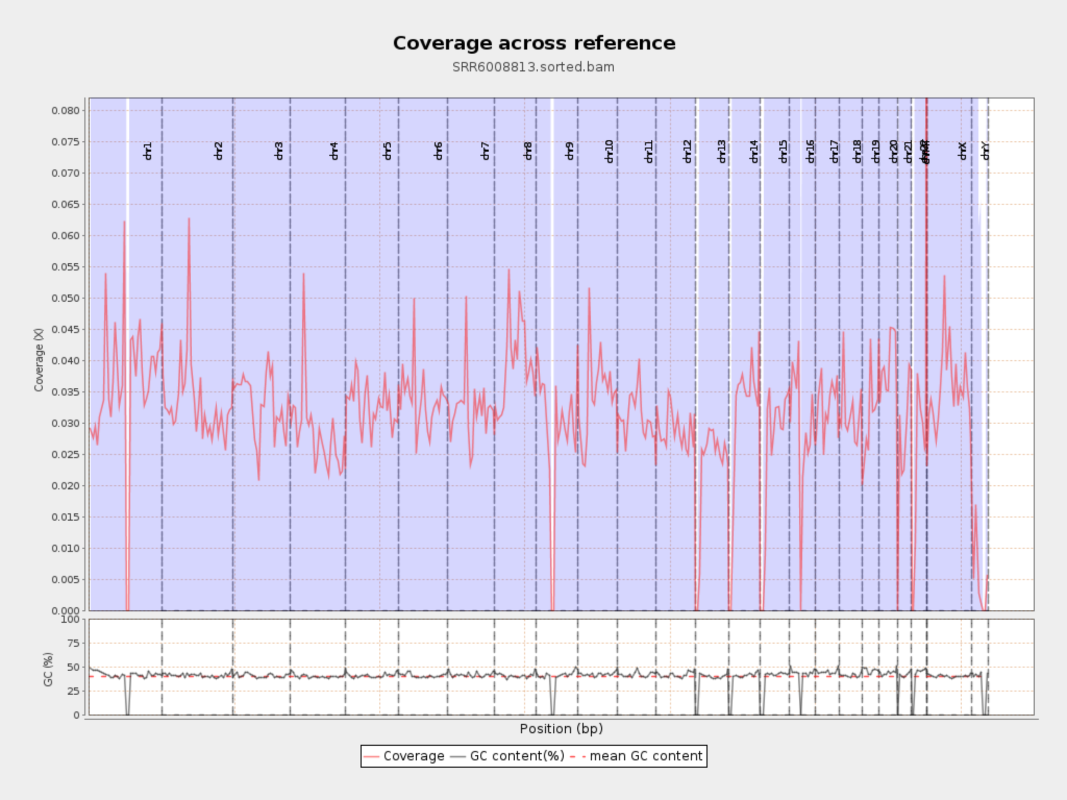
General error rate	0.79%
Mismatches	753,080
Insertions	7,099
Mapped reads with at least one insertion	0.49%
Deletions	19,961
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.76%

2.6. Chromosome stats

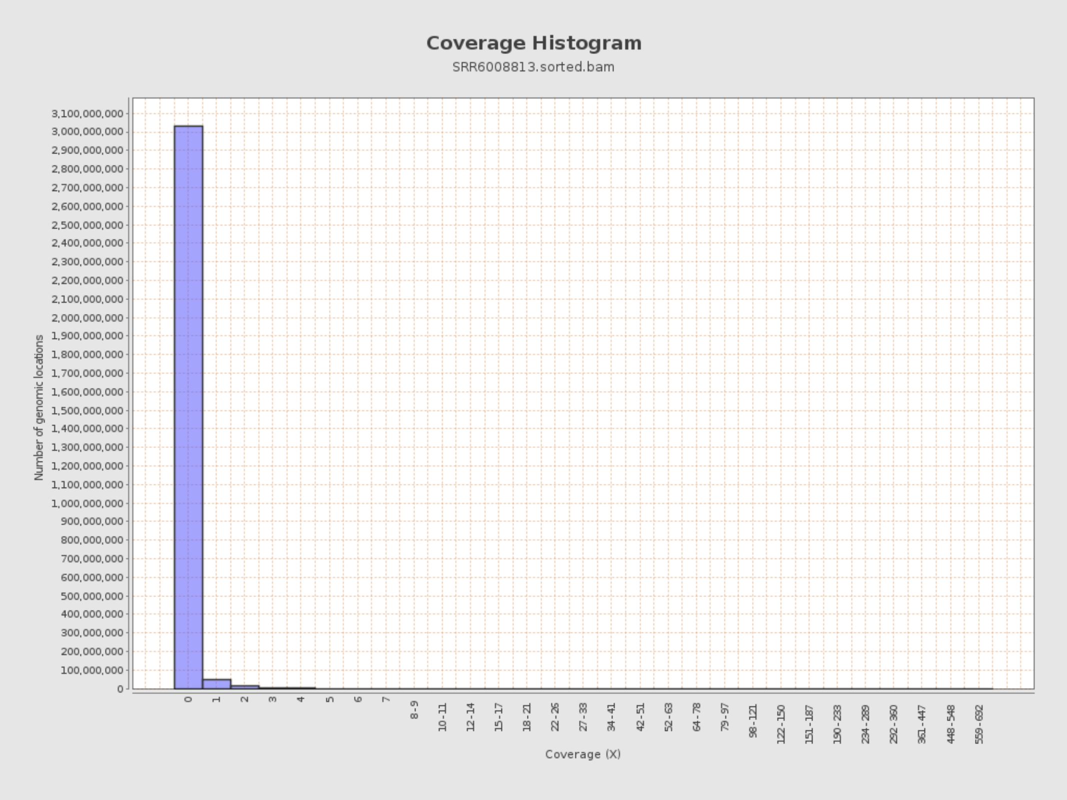
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8886643	0.0357	0.6546
chr2	243199373	8104998	0.0333	0.3684
chr3	198022430	6557982	0.0331	0.2477
chr4	191154276	5393340	0.0282	0.2472
chr5	180915260	5942659	0.0328	0.2473
chr6	171115067	5791171	0.0338	0.2886
chr7	159138663	5117075	0.0322	0.3758

chr8	146364022	5775303	0.0395	0.4797
chr9	141213431	3958111	0.028	0.31
chr10	135534747	4672641	0.0345	0.3342
chr11	135006516	4186346	0.031	0.3229
chr12	133851895	3894961	0.0291	0.2372
chr13	115169878	2544671	0.0221	0.2038
chr14	107349540	3204865	0.0299	0.2466
chr15	102531392	2593766	0.0253	0.2143
chr16	90354753	2634774	0.0292	0.2437
chr17	81195210	2665779	0.0328	0.2724
chr18	78077248	2464493	0.0316	0.5573
chr19	59128983	1833114	0.031	0.3951
chr20	63025520	2483493	0.0394	0.2867
chr21	48129895	1317182	0.0274	0.2415
chr22	51304566	1114103	0.0217	0.198
chrMT	16571	3741	0.2258	0.5786
chrX	155270560	5543637	0.0357	0.2944
chrY	59373566	303629	0.0051	0.1332

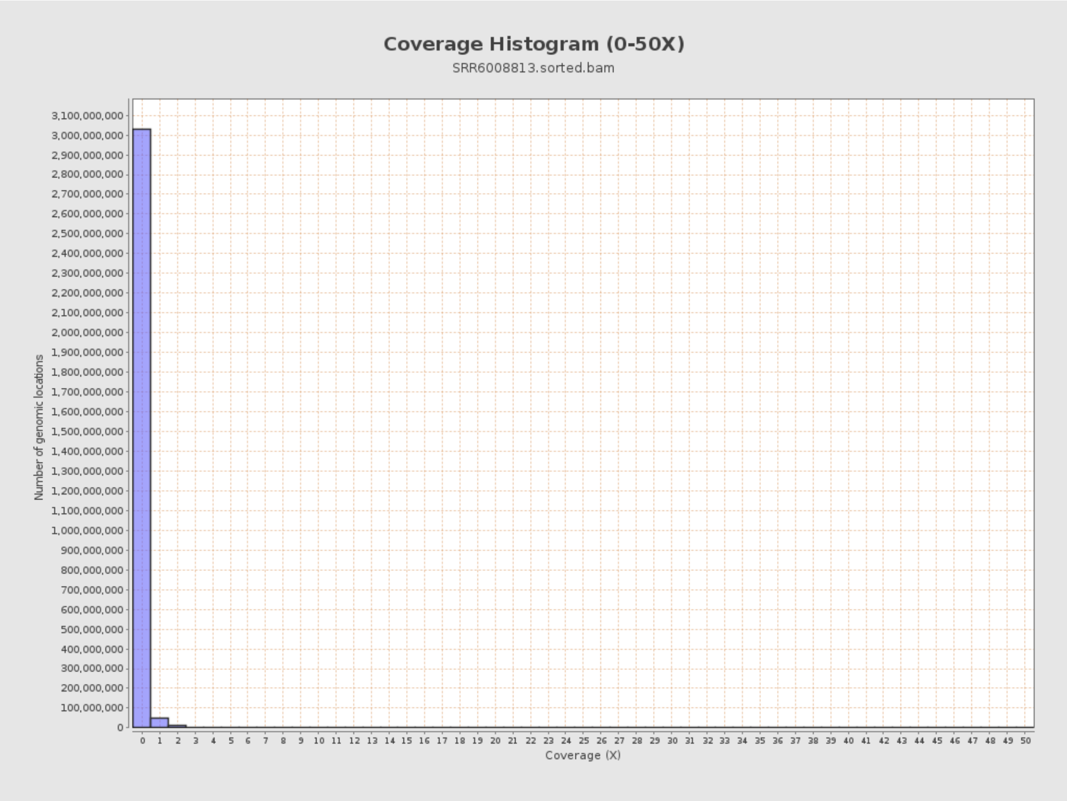
3. Results : Coverage across reference



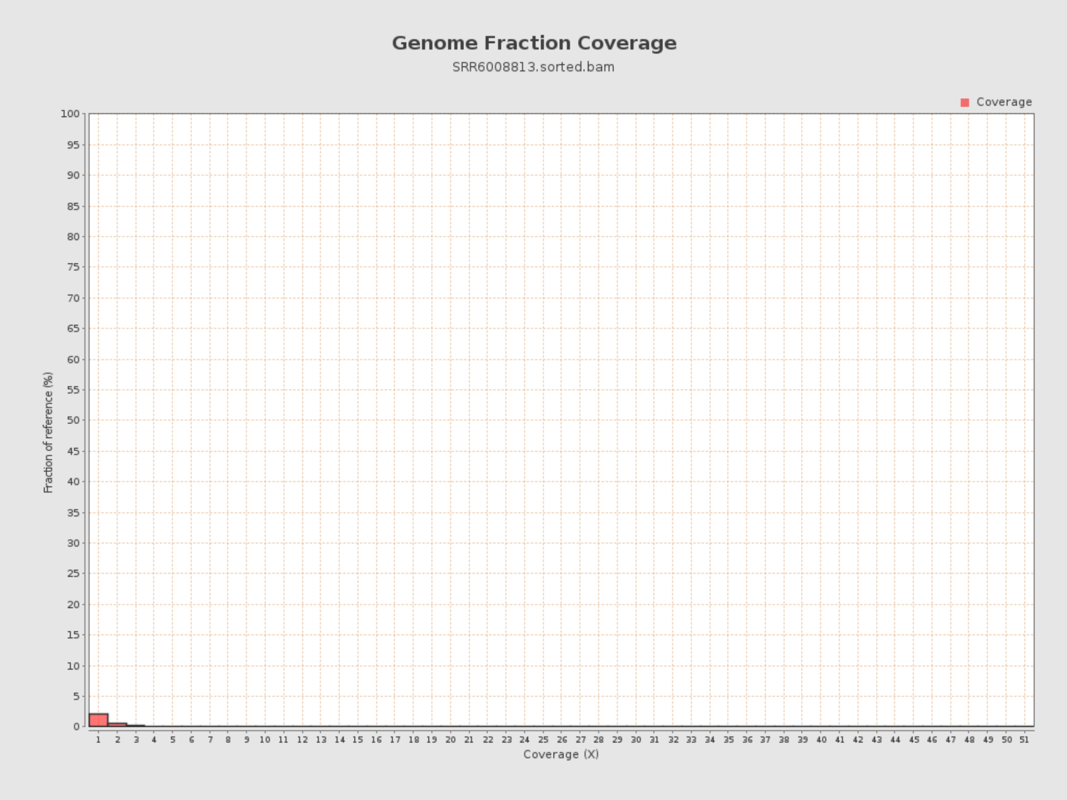
4. Results : Coverage Histogram



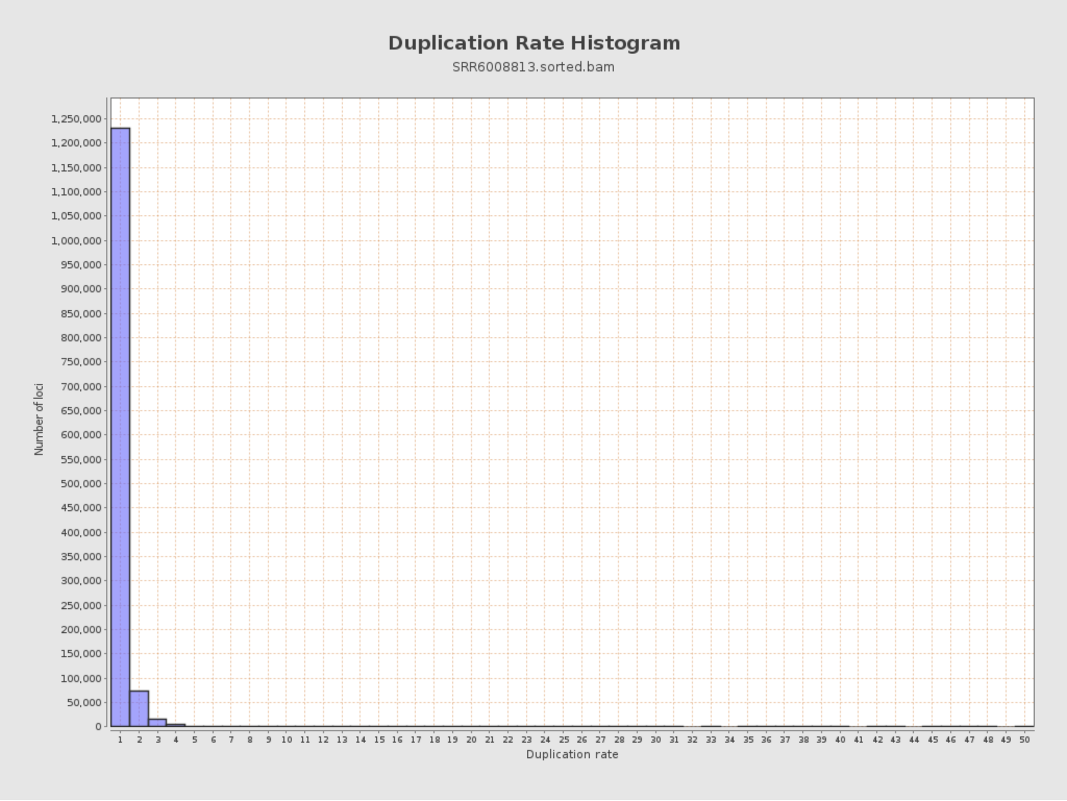
5. Results : Coverage Histogram (0-50X)



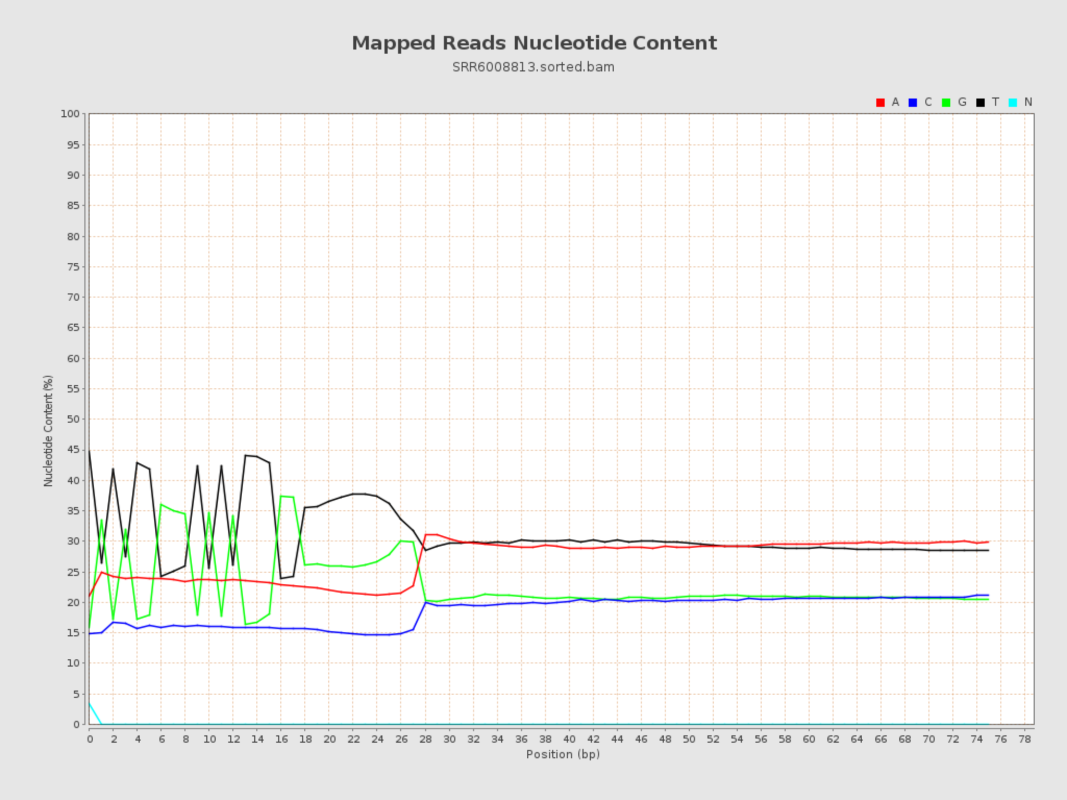
6. Results : Genome Fraction Coverage



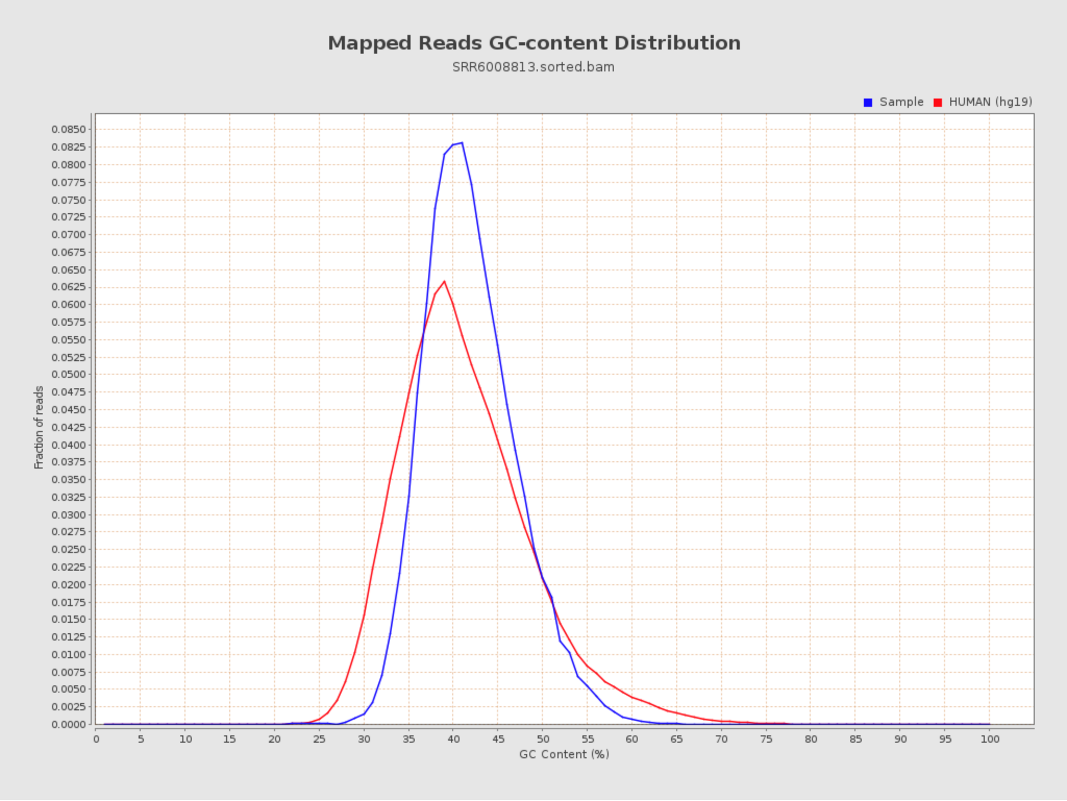
7. Results : Duplication Rate Histogram



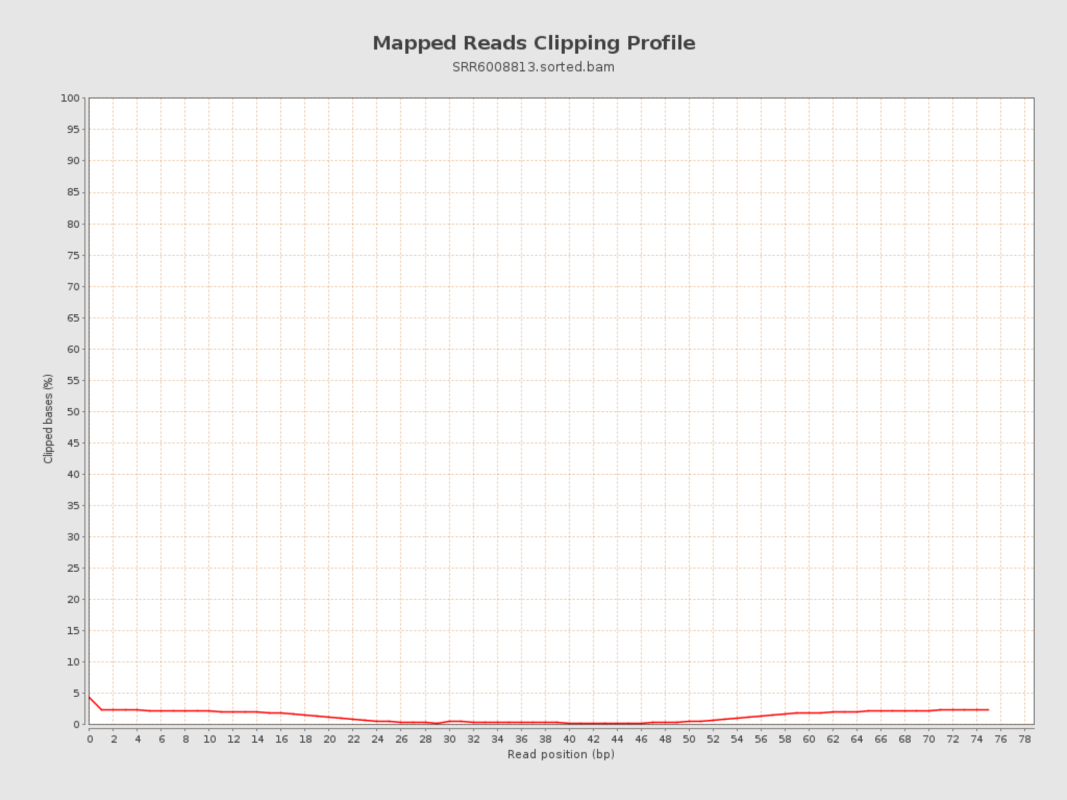
8. Results : Mapped Reads Nucleotide Content



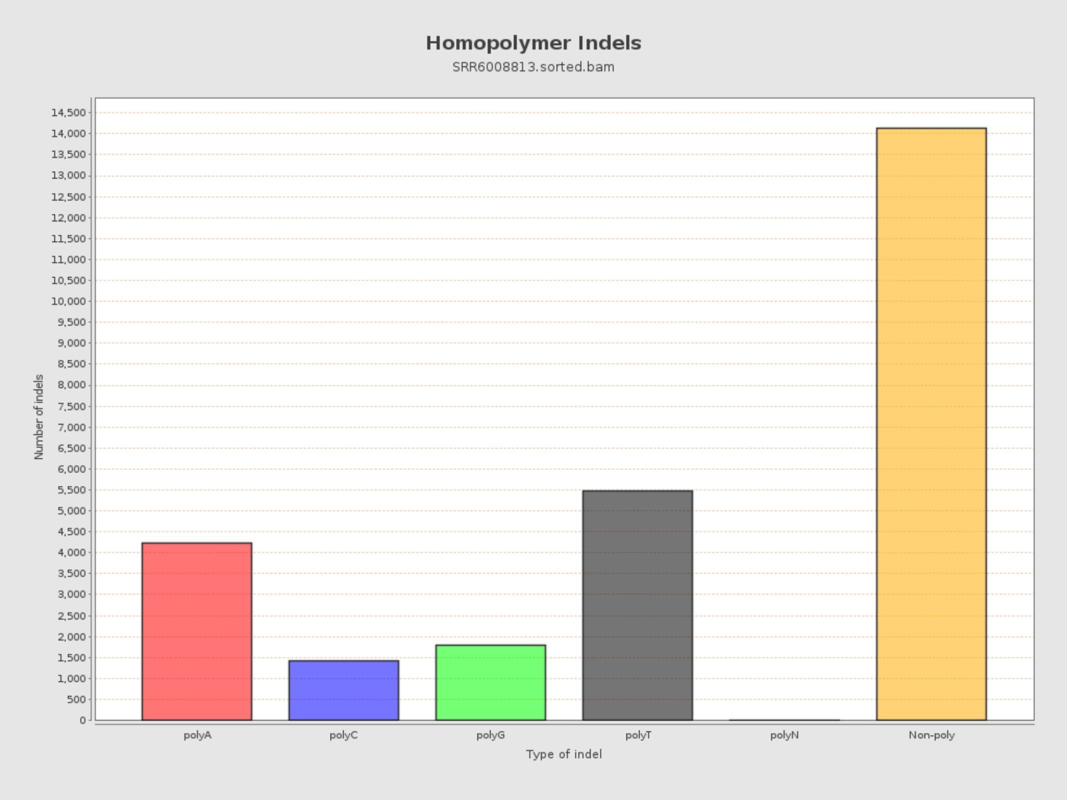
9. Results : Mapped Reads GC-content Distribution



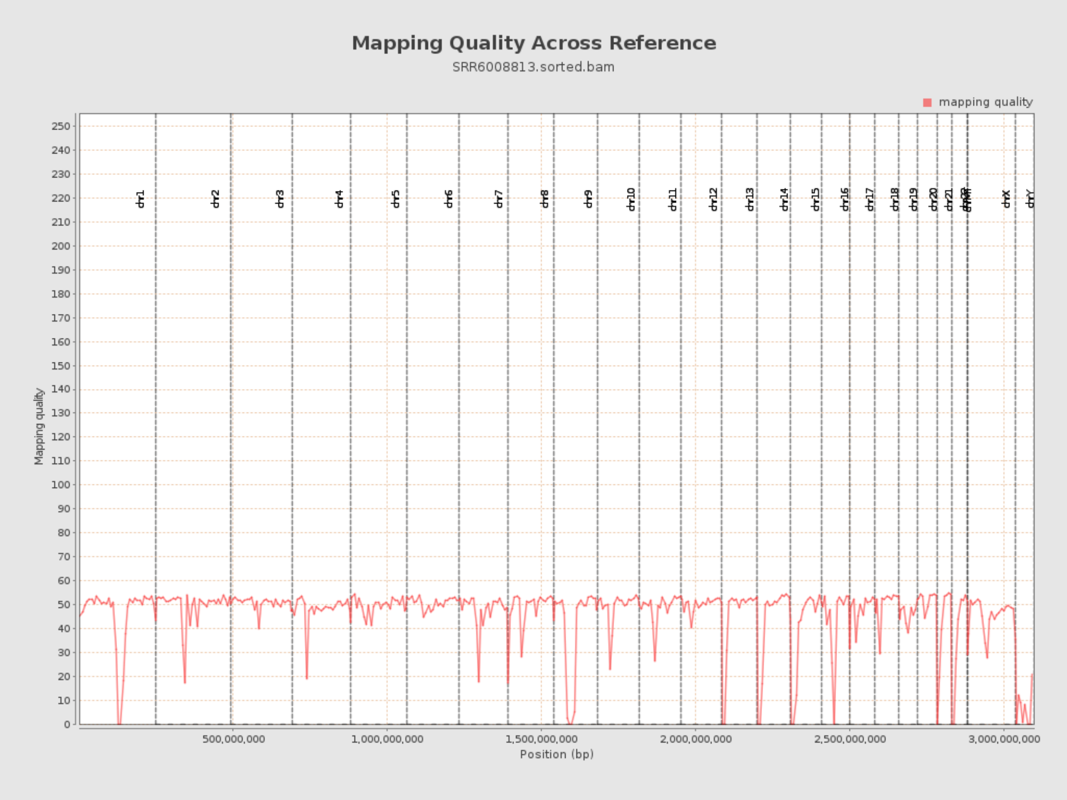
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram