Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:58:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008773.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_SRR6008773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:58:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,677,234
Mapped reads	1,467,843 / 87.52%
Unmapped reads	209,391 / 12.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,200 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	54,825 / 3.27%
Duplication rate	2.7%
Clipped reads	715,777 / 42.68%

2.2. ACGT Content

Number/percentage of A's	26,596,538 / 27.66%
Number/percentage of C's	17,416,759 / 18.12%
Number/percentage of T's	30,341,711 / 31.56%
Number/percentage of G's	21,771,181 / 22.64%
Number/percentage of N's	17,984 / 0.02%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.3113

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

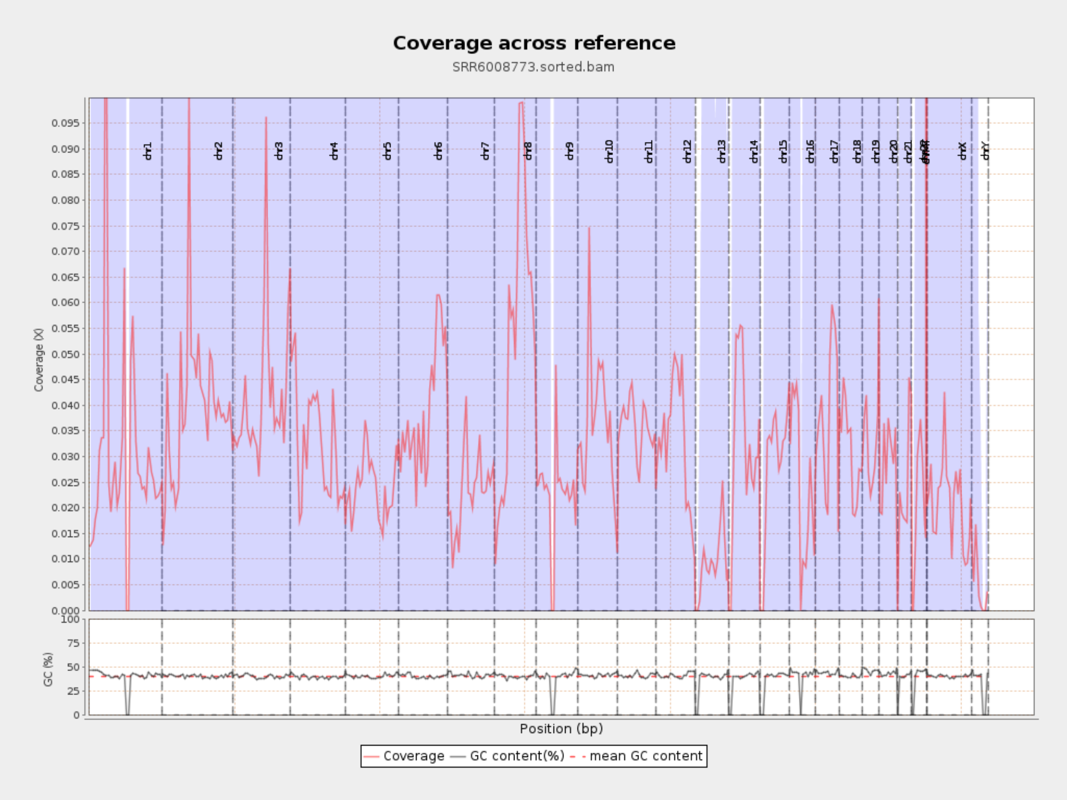
General error rate	0.81%
Mismatches	758,917
Insertions	8,326
Mapped reads with at least one insertion	0.56%
Deletions	29,325
Mapped reads with at least one deletion	1.97%
Homopolymer indels	47.07%

2.6. Chromosome stats

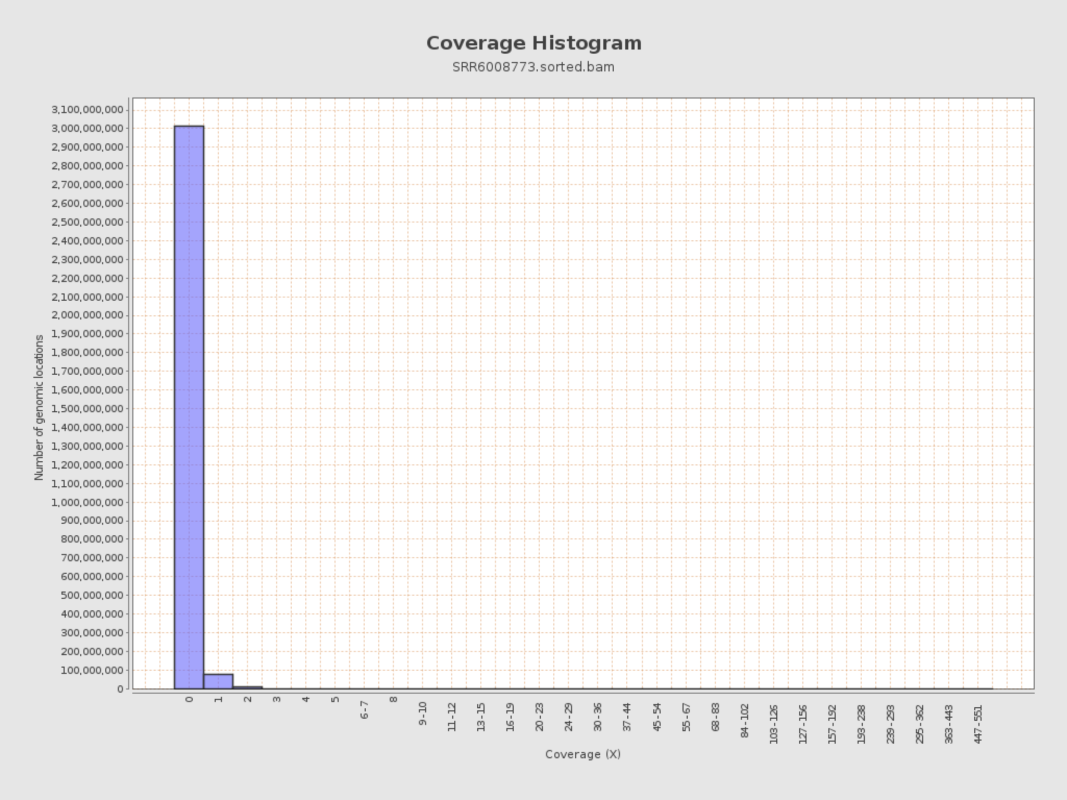
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7445743	0.0299	0.4453
chr2	243199373	9745468	0.0401	0.4494
chr3	198022430	8188385	0.0414	0.2281
chr4	191154276	6227177	0.0326	0.2106
chr5	180915260	4333590	0.024	0.1716
chr6	171115067	6704669	0.0392	0.2426
chr7	159138663	3674680	0.0231	0.2964

chr8	146364022	7789424	0.0532	0.4397
chr9	141213431	3182569	0.0225	0.3371
chr10	135534747	4999984	0.0369	0.3555
chr11	135006516	4767237	0.0353	0.3731
chr12	133851895	4482288	0.0335	0.2065
chr13	115169878	1063443	0.0092	0.1058
chr14	107349540	3469241	0.0323	0.2056
chr15	102531392	2856587	0.0279	0.1834
chr16	90354753	2213394	0.0245	0.2071
chr17	81195210	3113452	0.0383	0.2622
chr18	78077248	2418783	0.031	0.6128
chr19	59128983	1907642	0.0323	0.3295
chr20	63025520	1833515	0.0291	0.1934
chr21	48129895	1158400	0.0241	0.1911
chr22	51304566	1000440	0.0195	0.1514
chrMT	16571	43392	2.6186	2.1142
chrX	155270560	3295480	0.0212	0.1967
chrY	59373566	277495	0.0047	0.1403

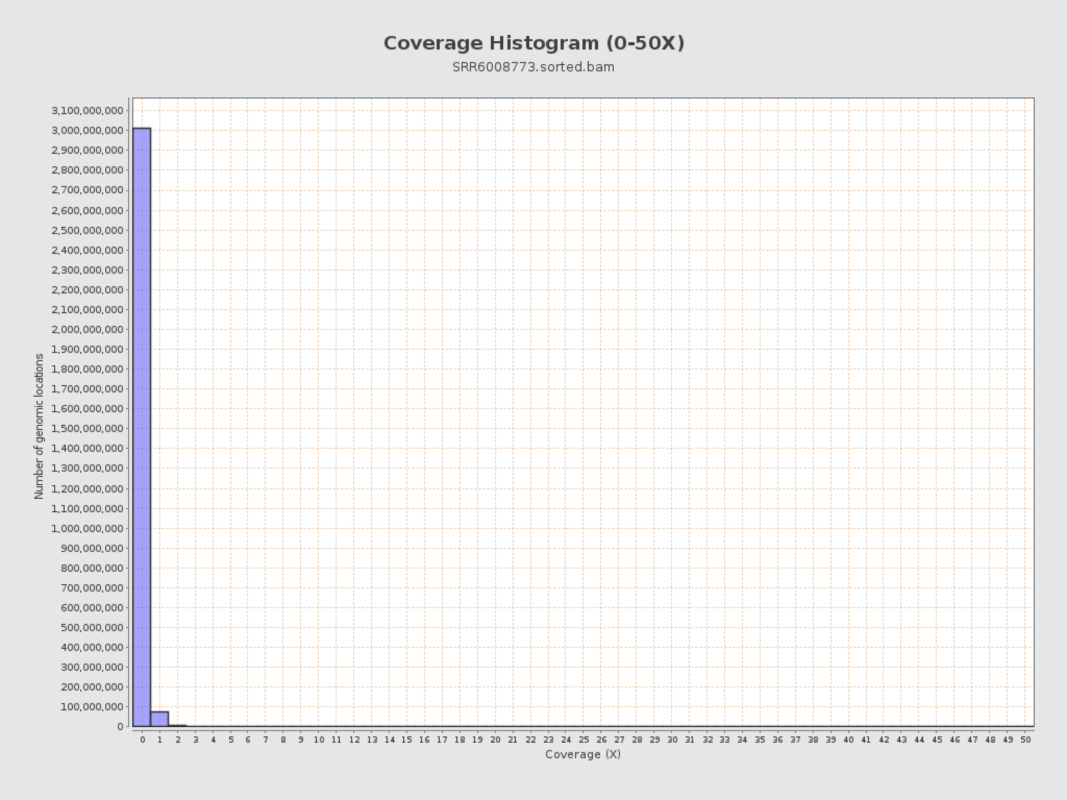
3. Results : Coverage across reference



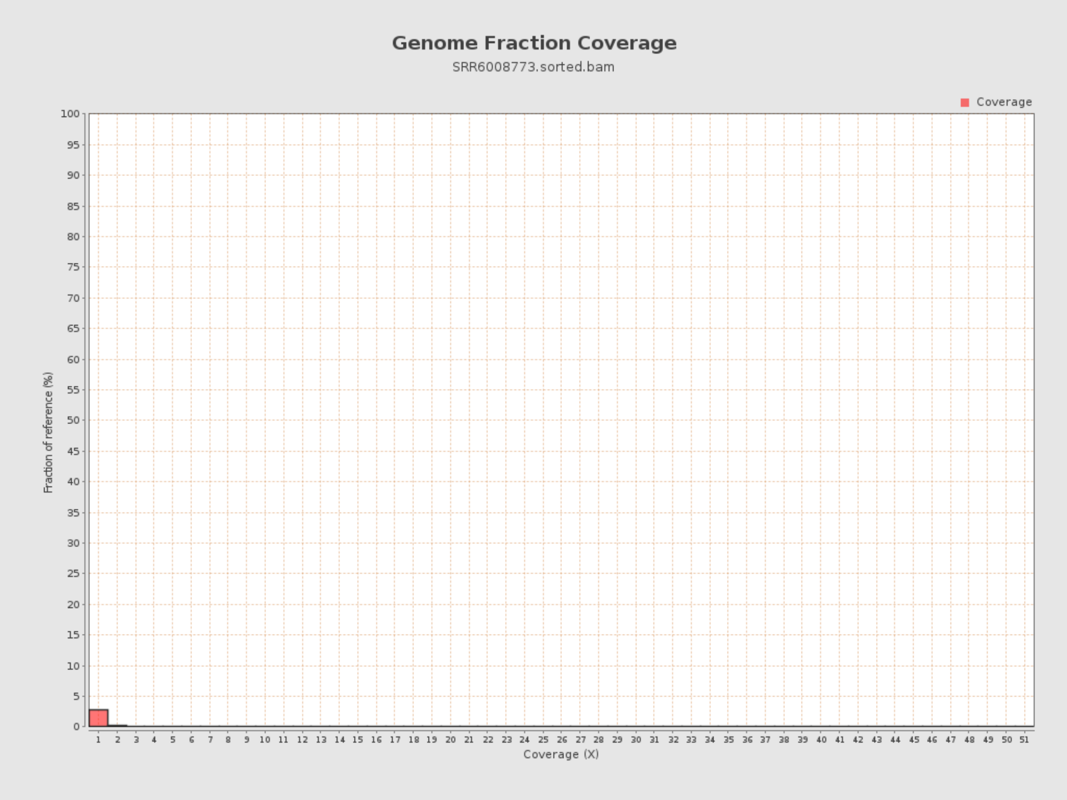
4. Results : Coverage Histogram



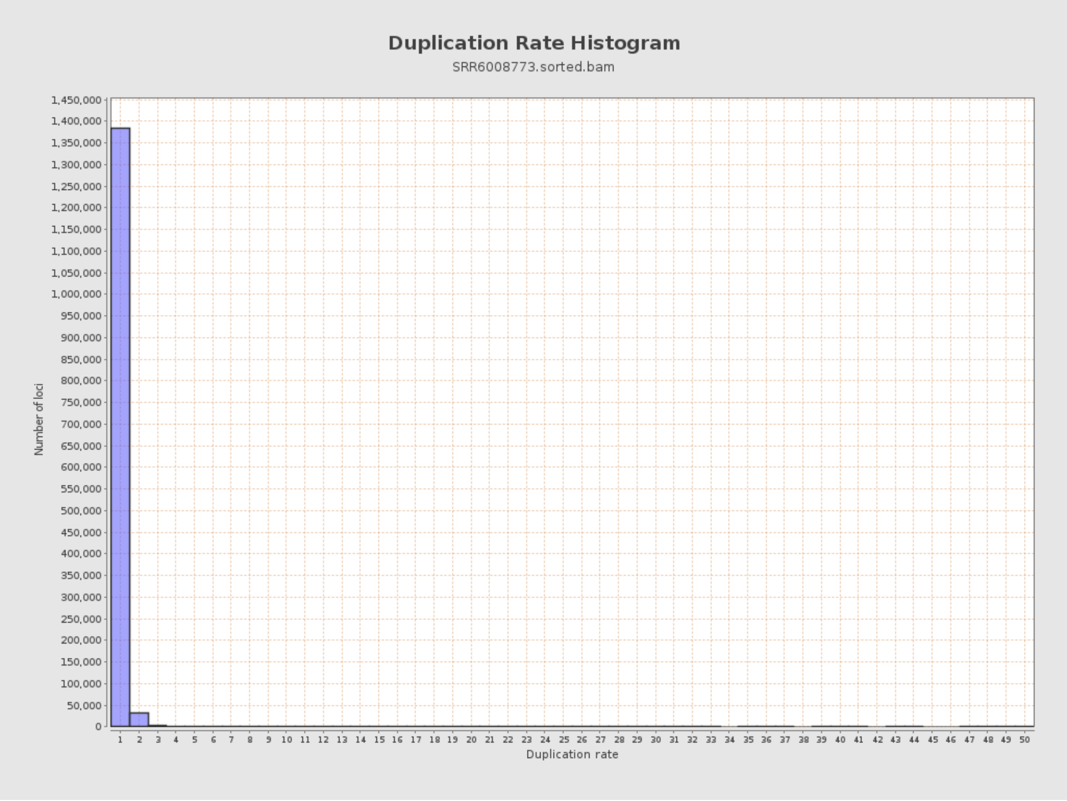
5. Results : Coverage Histogram (0-50X)



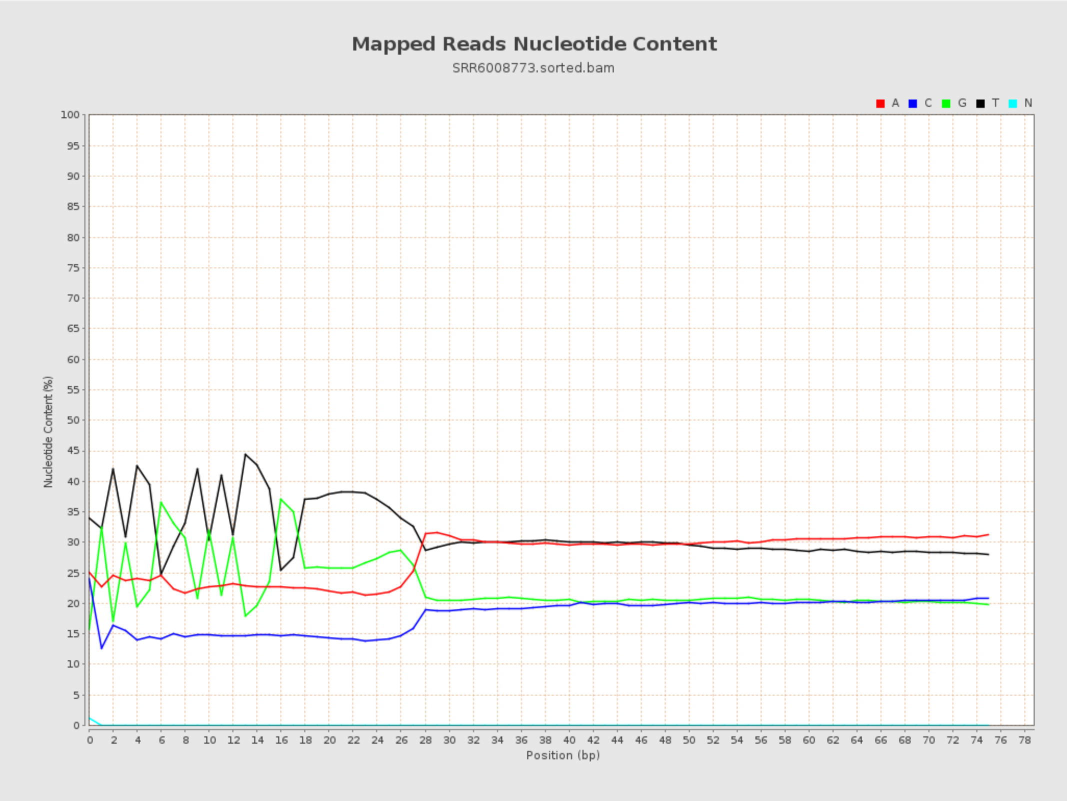
6. Results : Genome Fraction Coverage



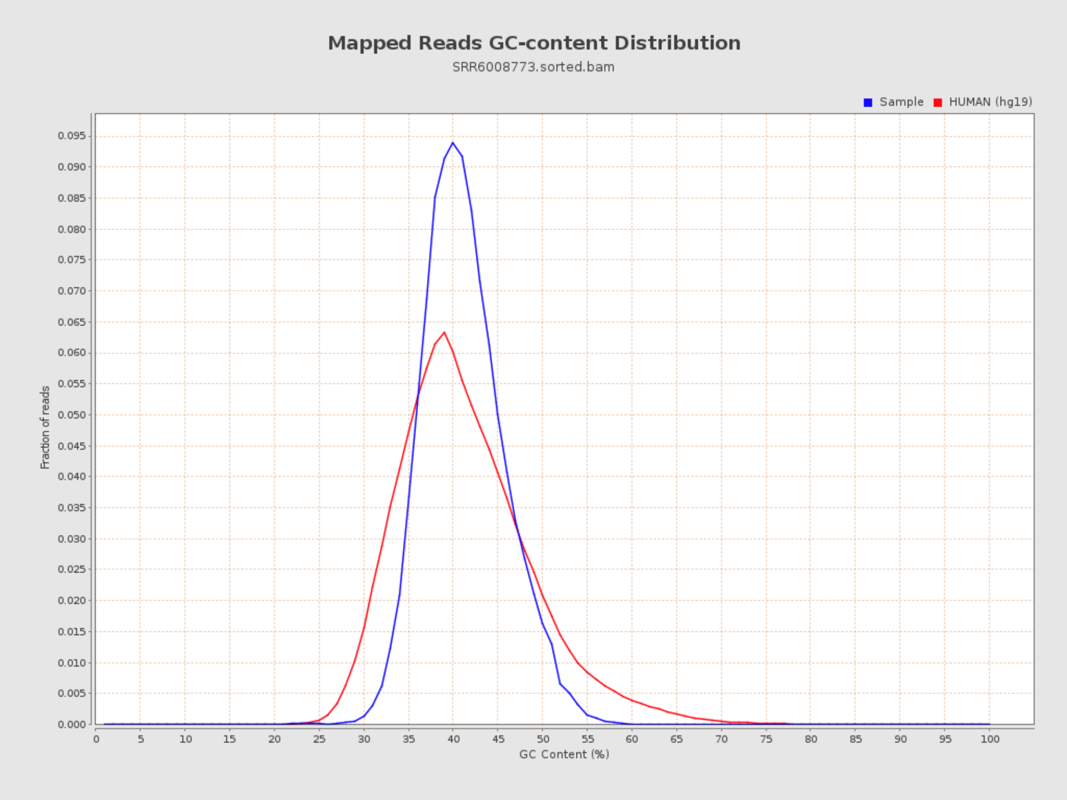
7. Results : Duplication Rate Histogram



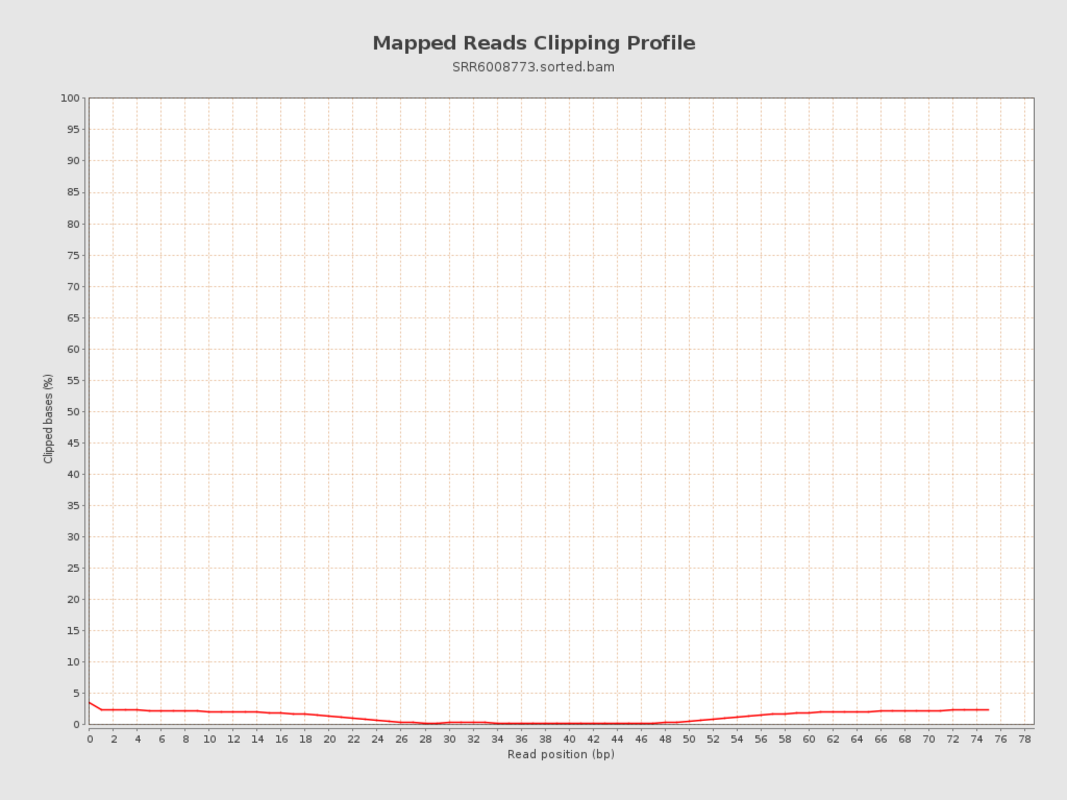
8. Results : Mapped Reads Nucleotide Content



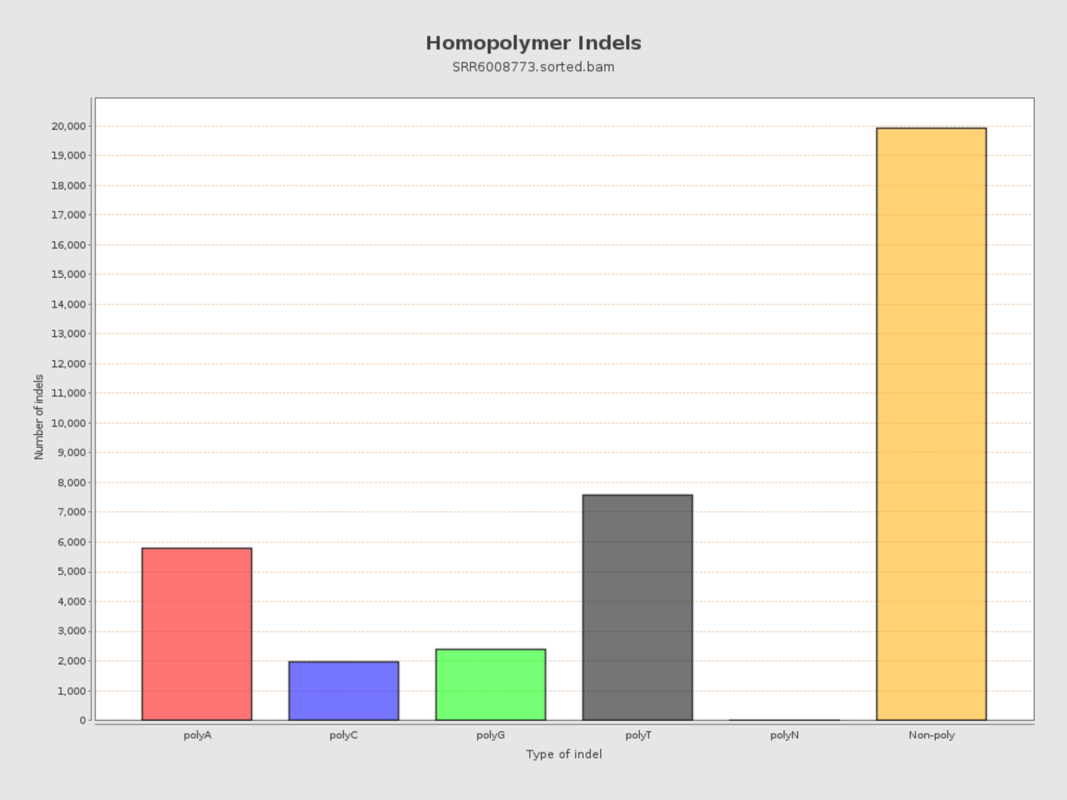
9. Results : Mapped Reads GC-content Distribution



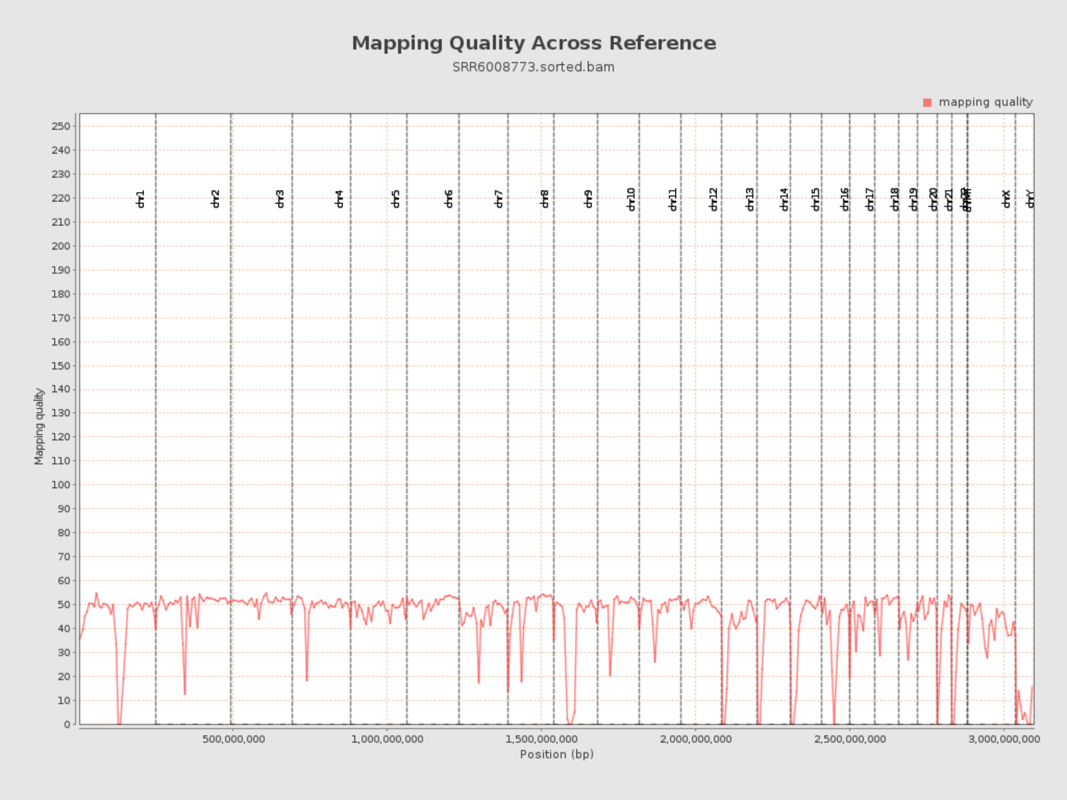
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram