Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:39:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008679.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_SRR6008679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:39:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,020,323
Mapped reads	1,833,114 / 90.73%
Unmapped reads	187,209 / 9.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,690 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	65,049 / 3.22%
Duplication rate	2.77%
Clipped reads	909,586 / 45.02%

2.2. ACGT Content

Number/percentage of A's	32,890,016 / 27.51%
Number/percentage of C's	22,039,123 / 18.43%
Number/percentage of T's	37,292,037 / 31.19%
Number/percentage of G's	27,333,098 / 22.86%
Number/percentage of N's	22,707 / 0.02%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3277

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

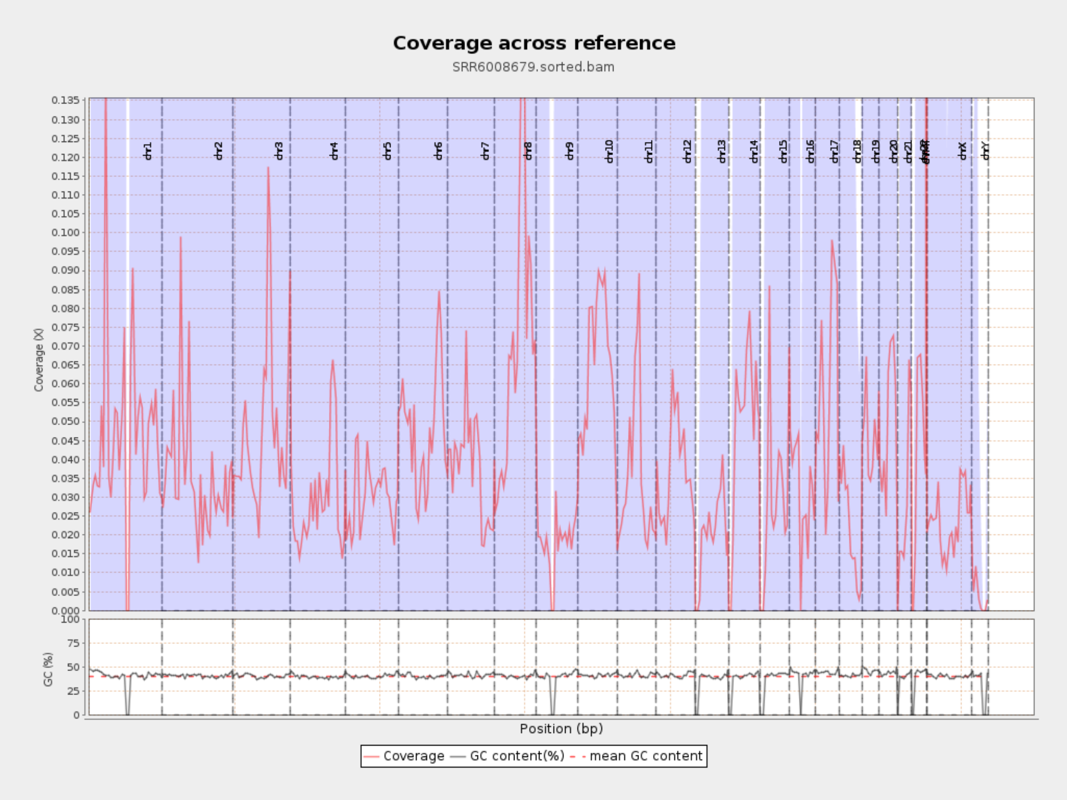
General error rate	0.71%
Mismatches	830,187
Insertions	9,895
Mapped reads with at least one insertion	0.54%
Deletions	29,859
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.04%

2.6. Chromosome stats

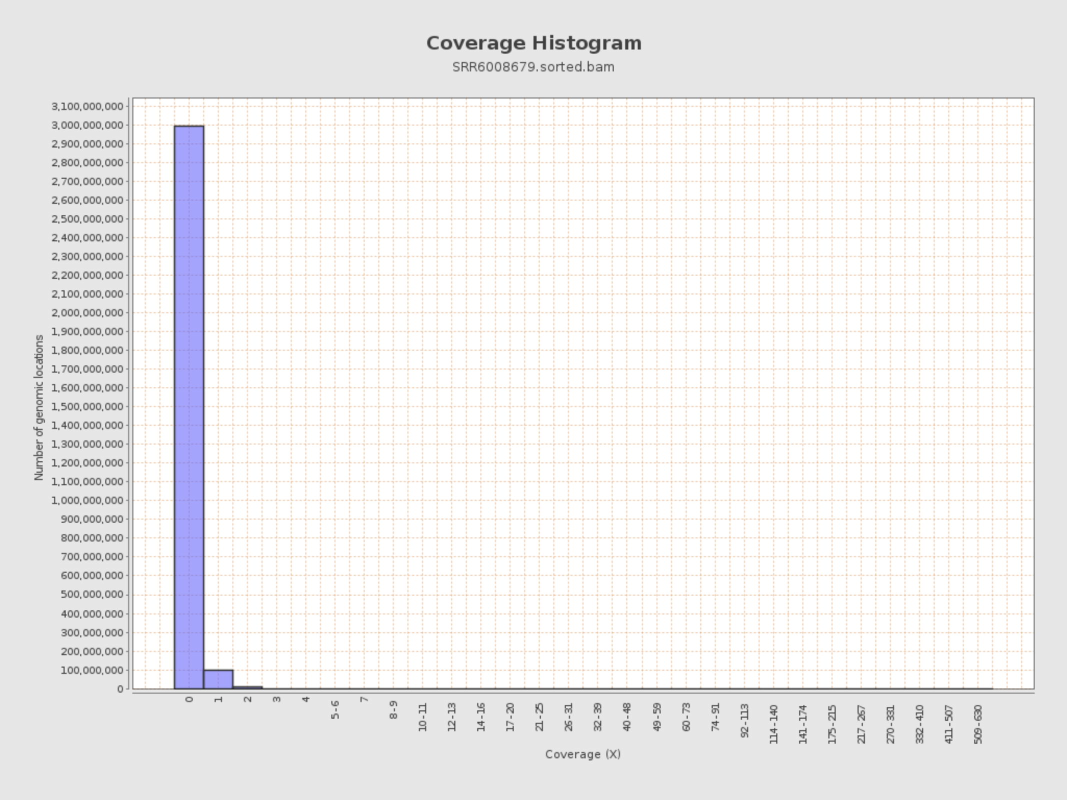
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11523743	0.0462	0.5717
chr2	243199373	8755300	0.036	0.3707
chr3	198022430	9291265	0.0469	0.2375
chr4	191154276	5471861	0.0286	0.1896
chr5	180915260	5471012	0.0302	0.1907
chr6	171115067	8232589	0.0481	0.286
chr7	159138663	6019015	0.0378	0.4745

chr8	146364022	10429115	0.0713	0.3969
chr9	141213431	2482585	0.0176	0.2753
chr10	135534747	8972138	0.0662	0.3632
chr11	135006516	4819313	0.0357	0.2943
chr12	133851895	5007058	0.0374	0.2136
chr13	115169878	2344375	0.0204	0.1551
chr14	107349540	5274026	0.0491	0.2446
chr15	102531392	2965682	0.0289	0.188
chr16	90354753	2812309	0.0311	0.218
chr17	81195210	4846684	0.0597	0.326
chr18	78077248	1672661	0.0214	0.524
chr19	59128983	2702697	0.0457	0.4047
chr20	63025520	3144075	0.0499	0.2468
chr21	48129895	1359409	0.0282	0.1909
chr22	51304566	1999039	0.039	0.2149
chrMT	16571	169545	10.2314	6.1682
chrX	155270560	3632497	0.0234	0.1827
chrY	59373566	228624	0.0039	0.1035

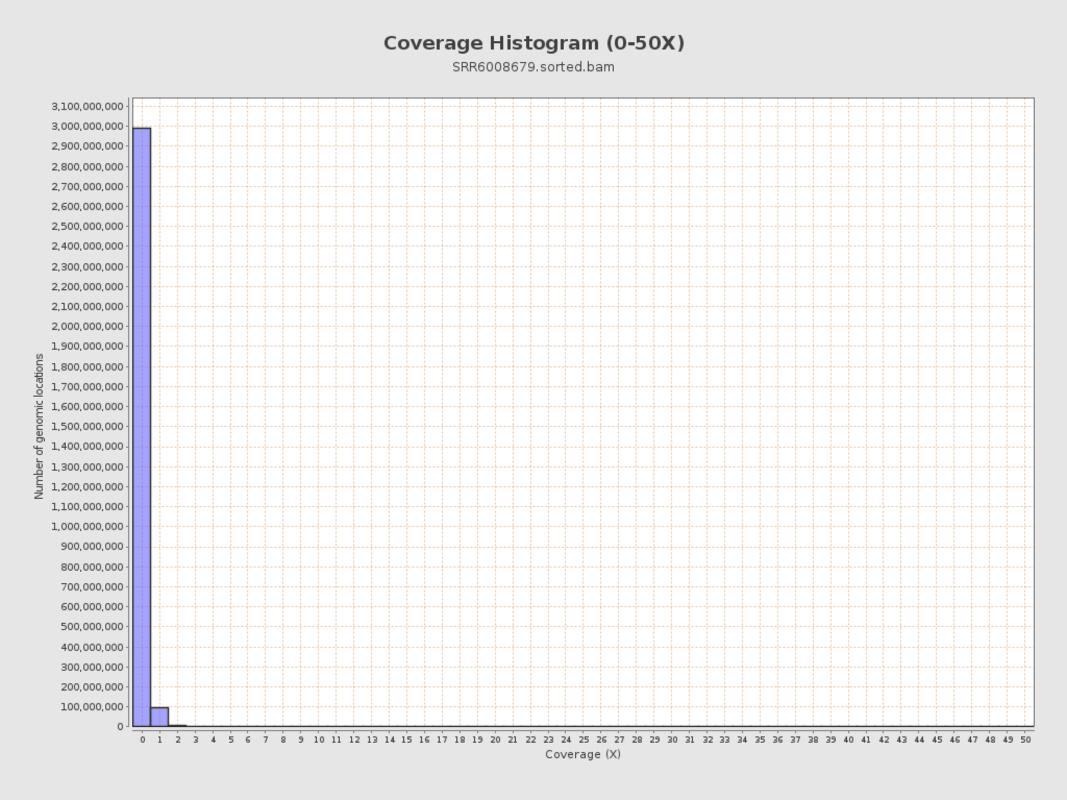
3. Results : Coverage across reference



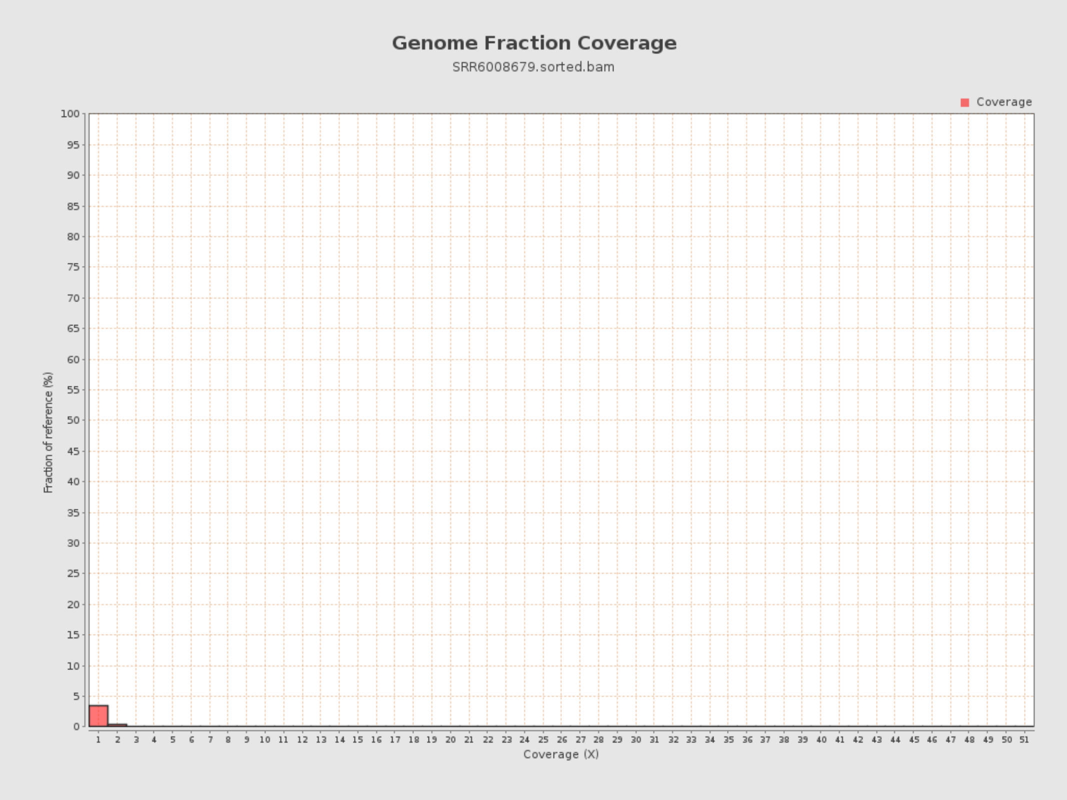
4. Results : Coverage Histogram



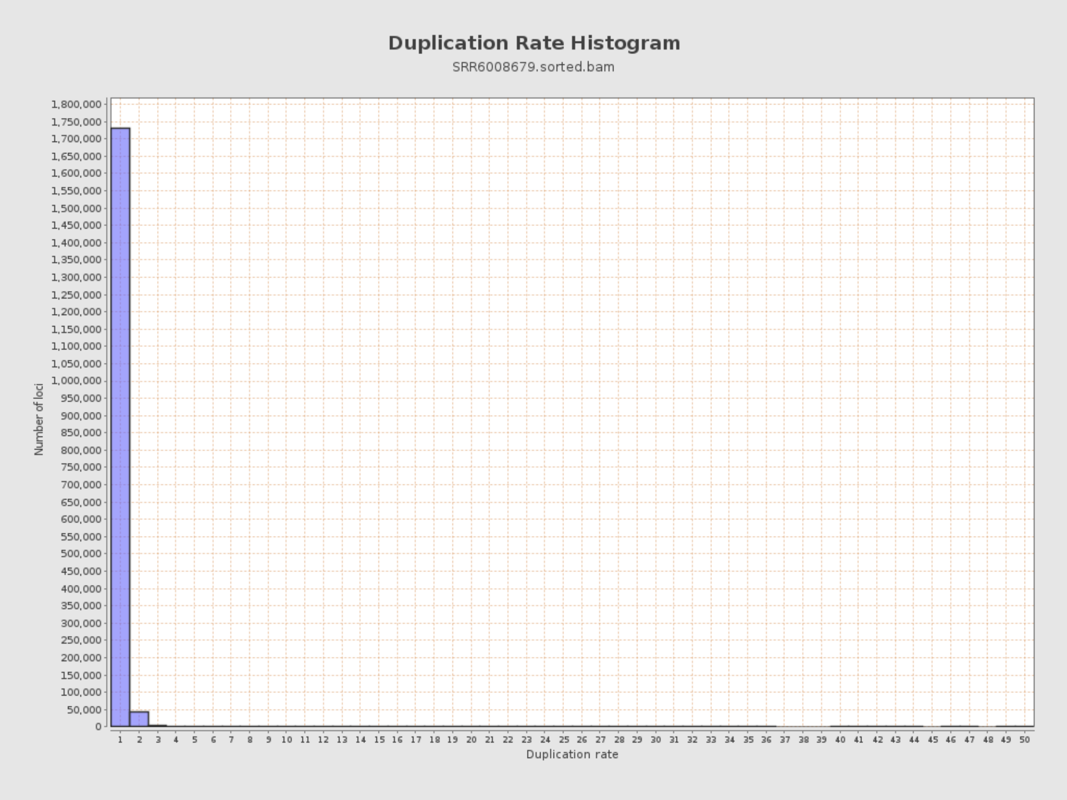
5. Results : Coverage Histogram (0-50X)



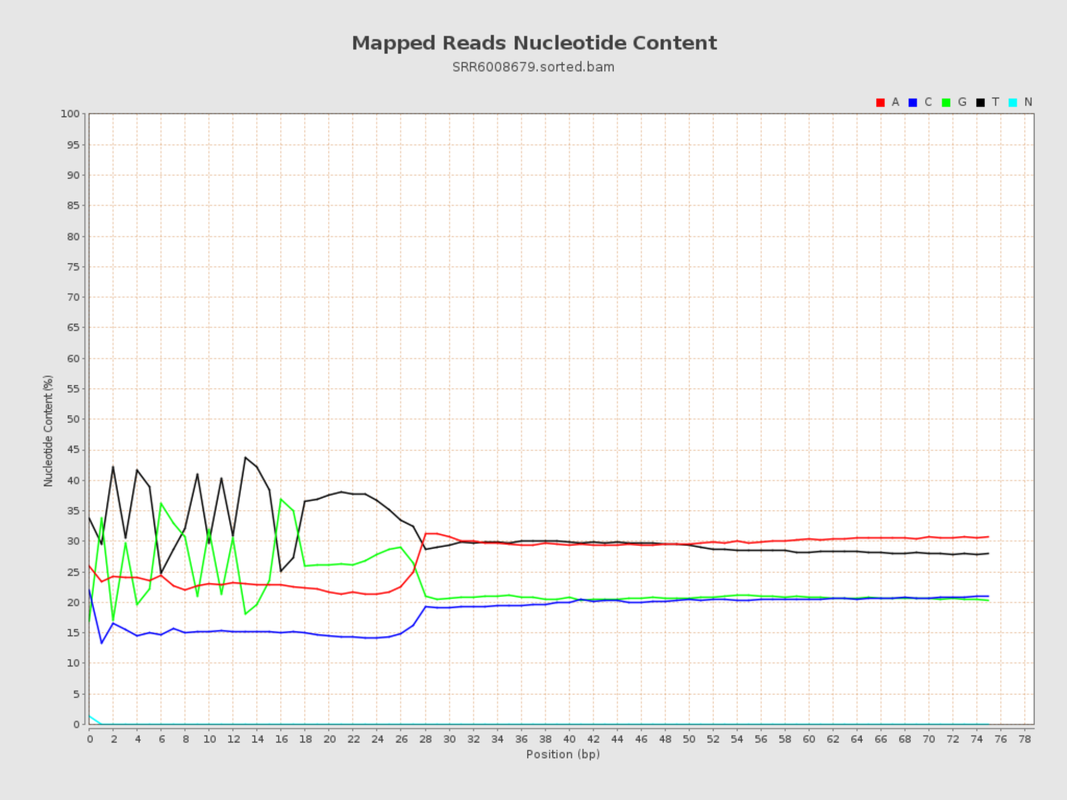
6. Results : Genome Fraction Coverage



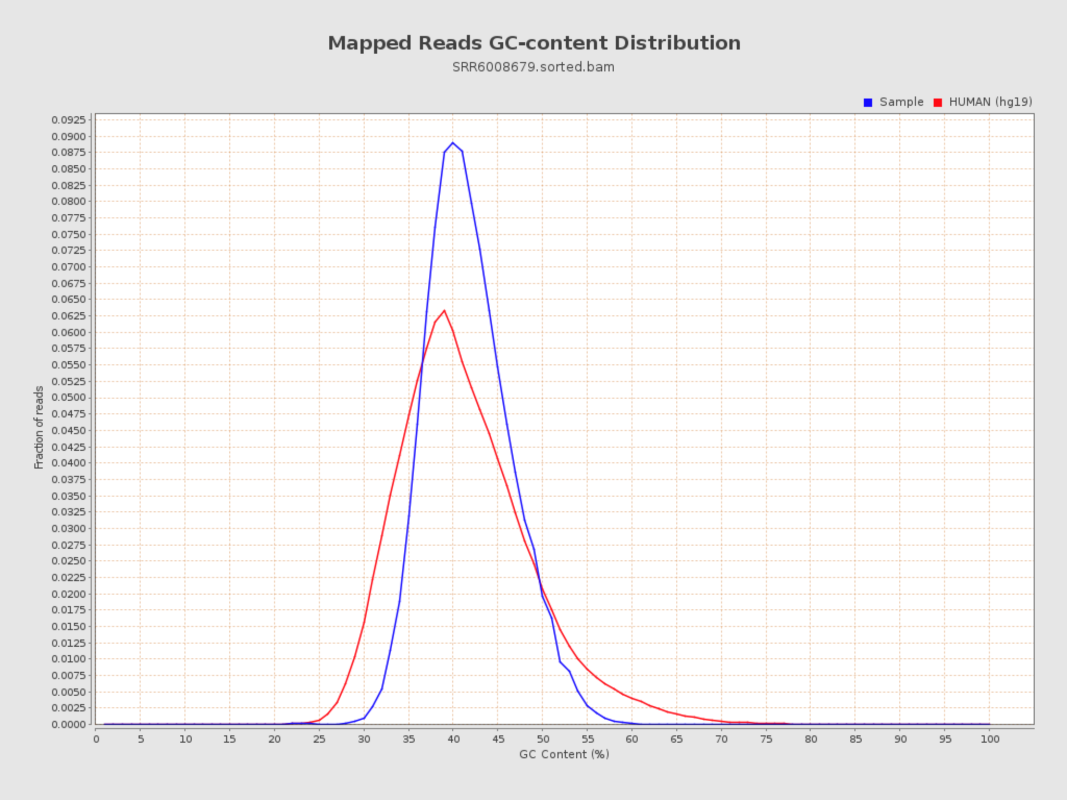
7. Results : Duplication Rate Histogram



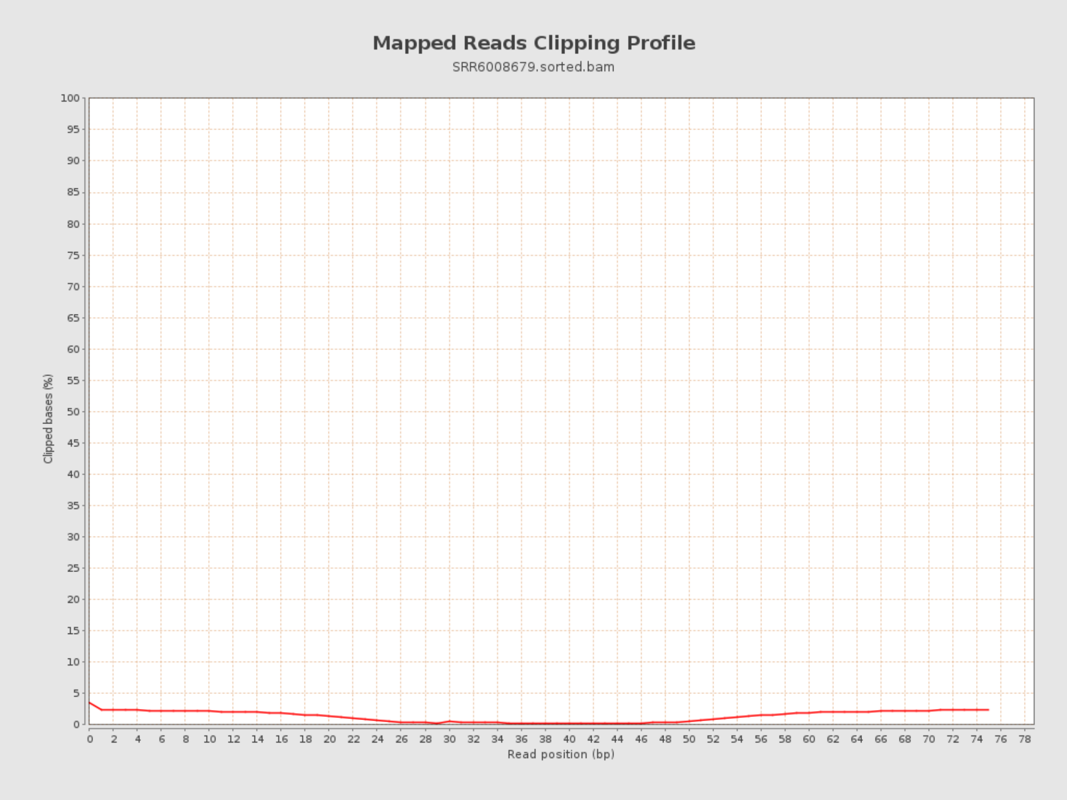
8. Results : Mapped Reads Nucleotide Content



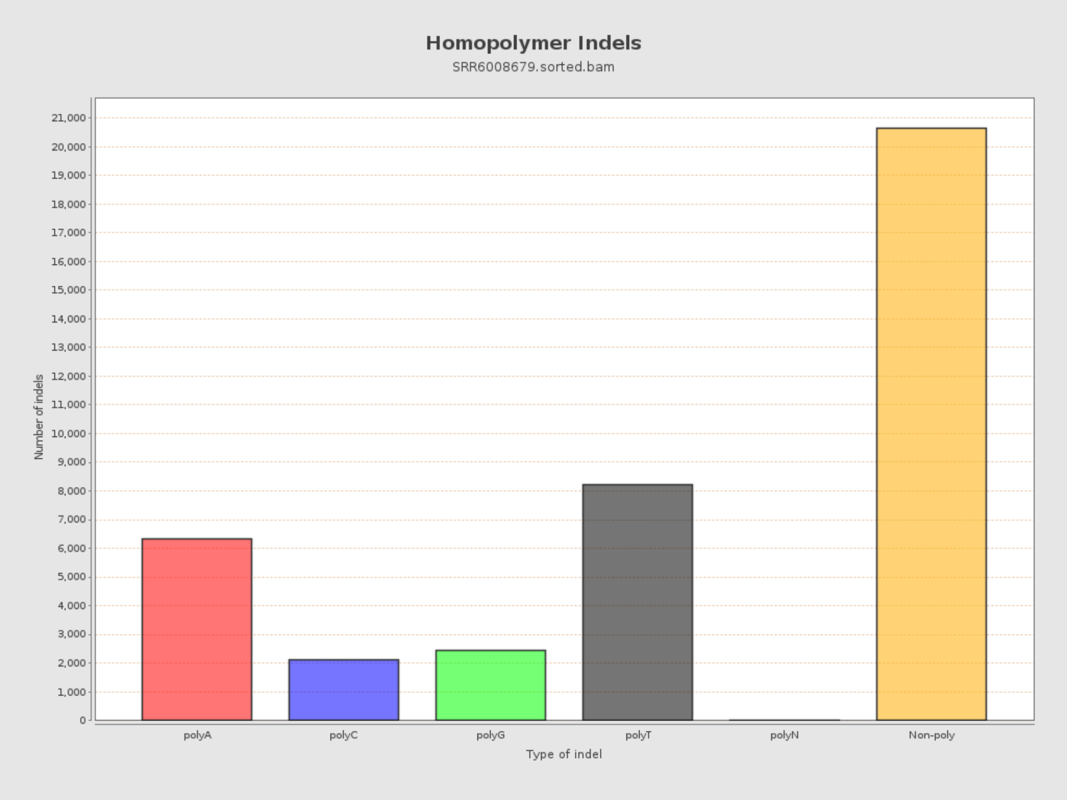
9. Results : Mapped Reads GC-content Distribution



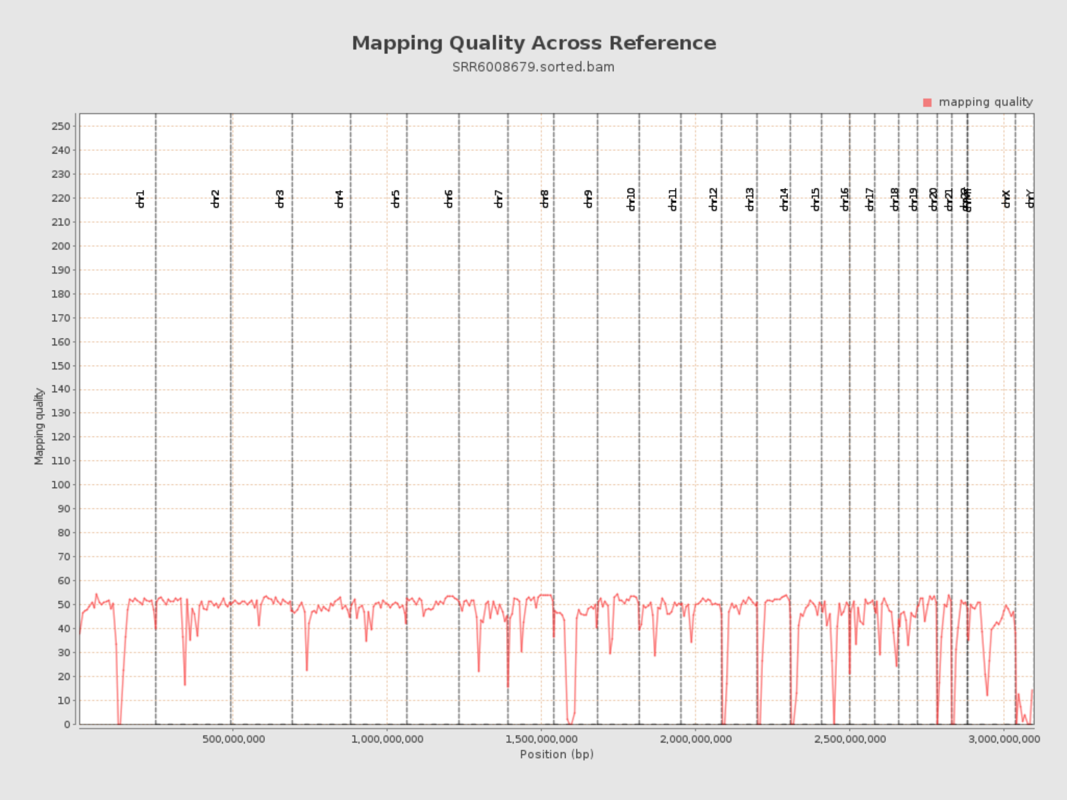
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram