Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:09:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008668.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_SRR6008668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,305,941
Mapped reads	2,117,133 / 91.81%
Unmapped reads	188,808 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,391 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	74,244 / 3.22%
Duplication rate	2.28%
Clipped reads	992,013 / 43.02%

2.2. ACGT Content

Number/percentage of A's	38,981,618 / 27.66%
Number/percentage of C's	26,144,149 / 18.55%
Number/percentage of T's	43,693,498 / 31%
Number/percentage of G's	32,067,525 / 22.75%
Number/percentage of N's	44,886 / 0.03%
GC Percentage	41.3%

2.3. Coverage

Mean	0.0455

Standard Deviation	0.4634

2.4. Mapping Quality

Mean Mapping Quality	43.54

2.5. Mismatches and indels

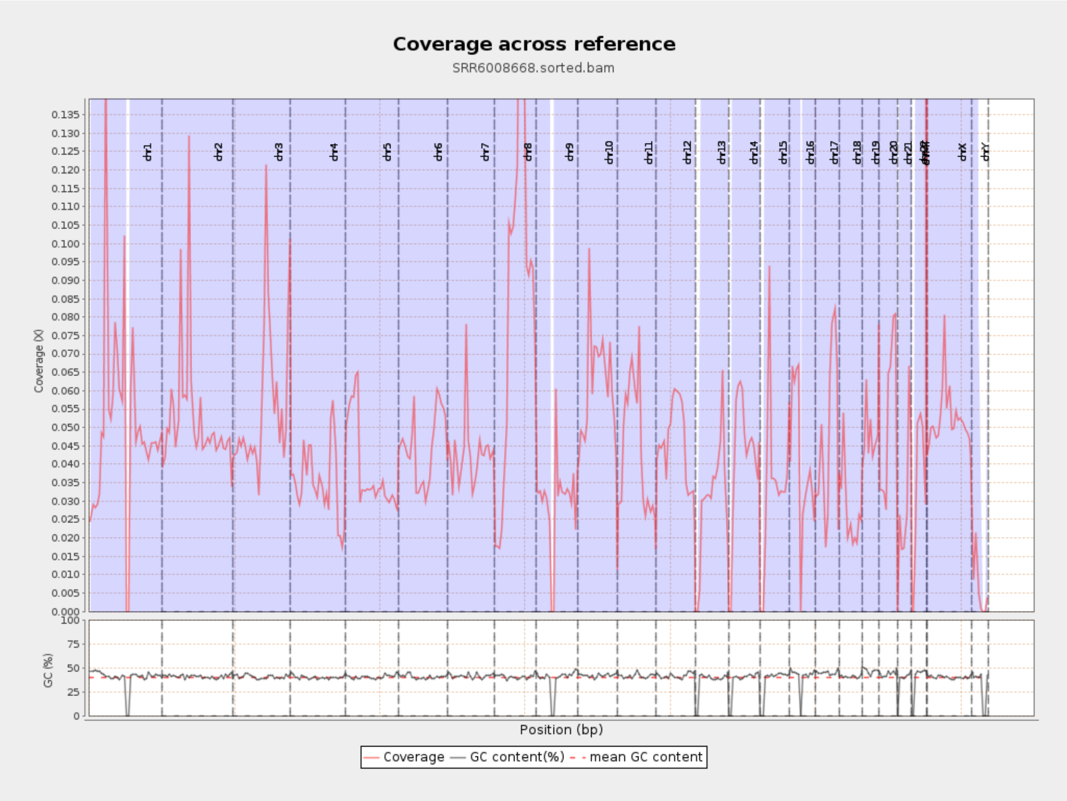
General error rate	0.89%
Mismatches	1,236,872
Insertions	11,804
Mapped reads with at least one insertion	0.55%
Deletions	46,083
Mapped reads with at least one deletion	2.15%
Homopolymer indels	44.81%

2.6. Chromosome stats

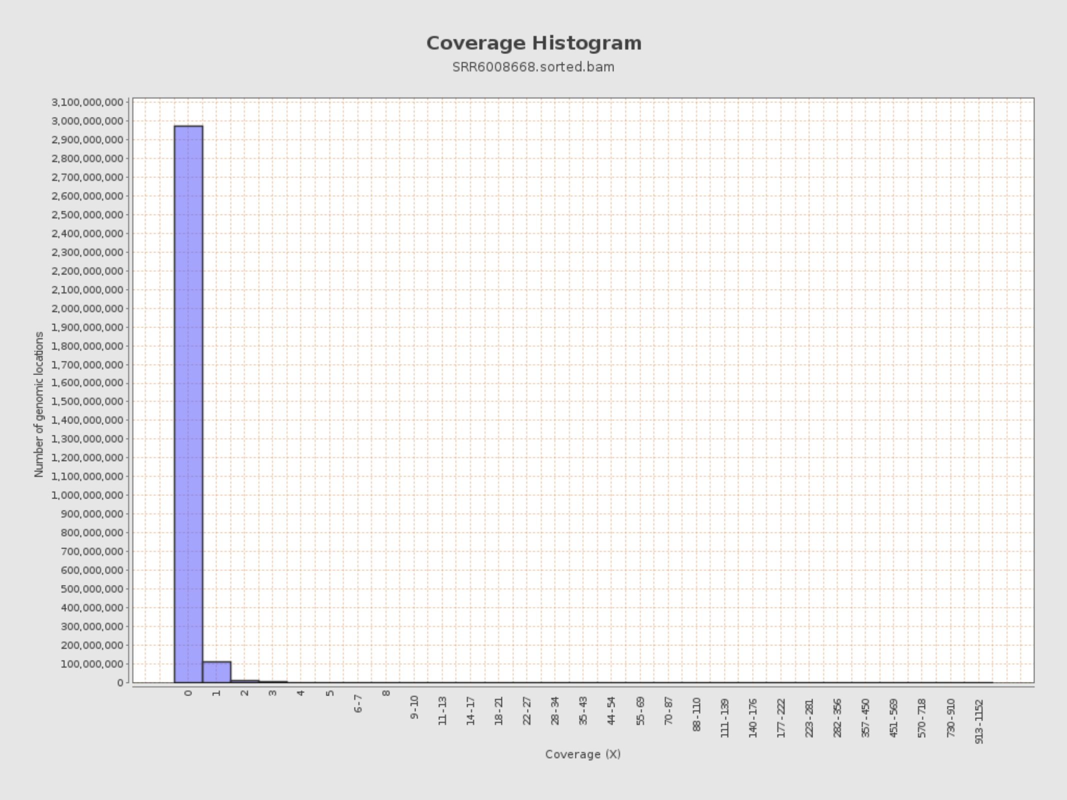
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12556086	0.0504	0.9324
chr2	243199373	12905486	0.0531	0.5839
chr3	198022430	10952871	0.0553	0.2622
chr4	191154276	6641878	0.0347	0.2275
chr5	180915260	7042149	0.0389	0.2209
chr6	171115067	7638915	0.0446	0.2847
chr7	159138663	6820445	0.0429	0.4885

chr8	146364022	12671595	0.0866	0.6029
chr9	141213431	4169801	0.0295	0.4314
chr10	135534747	8377557	0.0618	0.4421
chr11	135006516	5943180	0.044	0.5396
chr12	133851895	6173099	0.0461	0.2423
chr13	115169878	3510857	0.0305	0.1898
chr14	107349540	4489661	0.0418	0.2434
chr15	102531392	3533515	0.0345	0.2204
chr16	90354753	3704207	0.041	0.275
chr17	81195210	3834895	0.0472	0.3513
chr18	78077248	2185285	0.028	0.7745
chr19	59128983	2886027	0.0488	0.6229
chr20	63025520	3313774	0.0526	0.265
chr21	48129895	1410783	0.0293	0.2074
chr22	51304566	1679048	0.0327	0.1971
chrMT	16571	35221	2.1255	2.2029
chrX	155270560	8128912	0.0524	0.3087
chrY	59373566	402090	0.0068	0.176

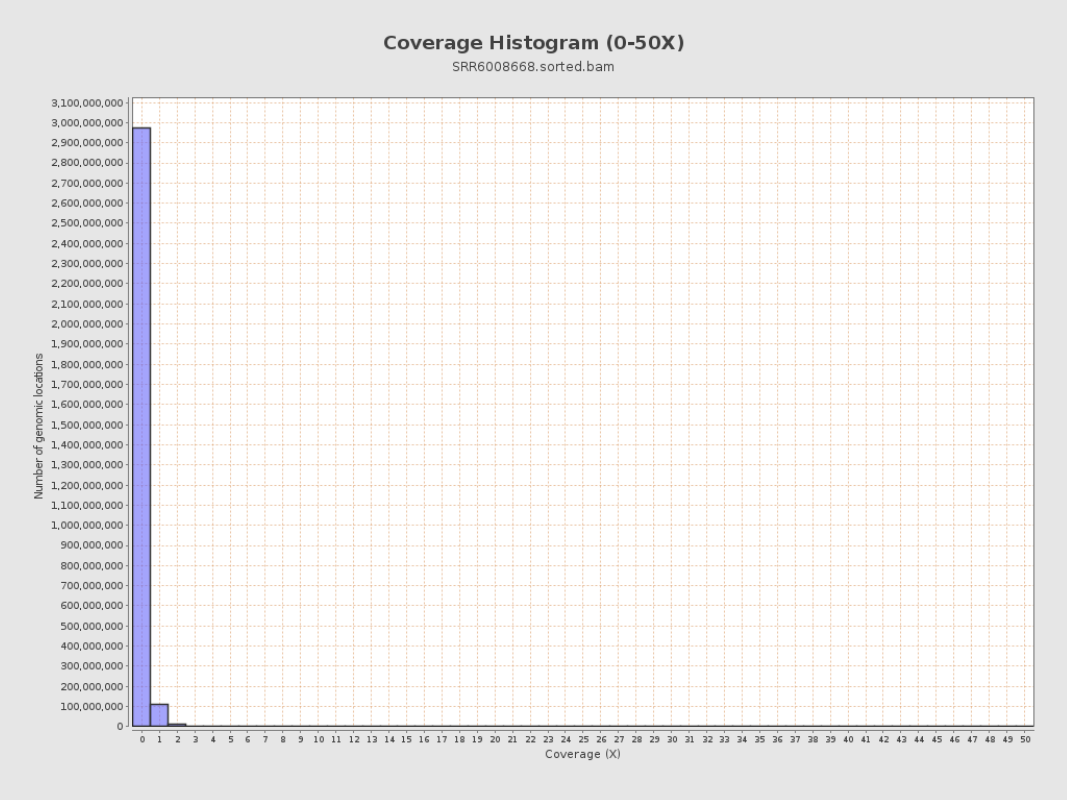
3. Results : Coverage across reference



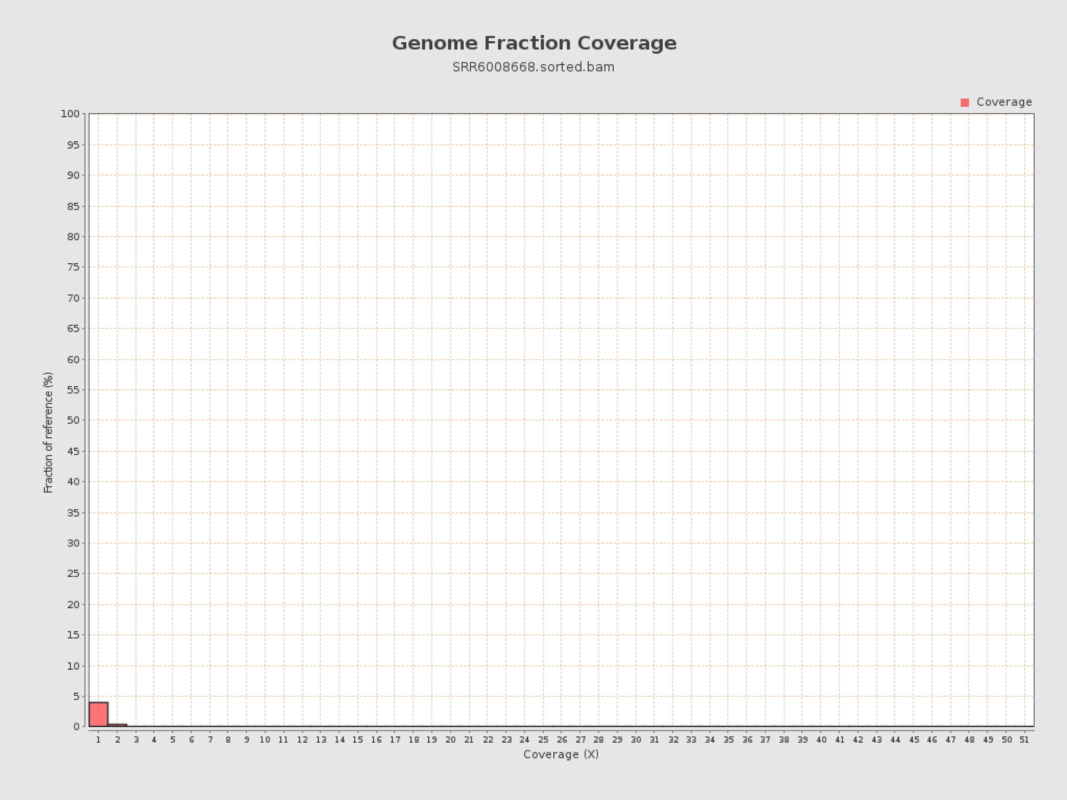
4. Results : Coverage Histogram



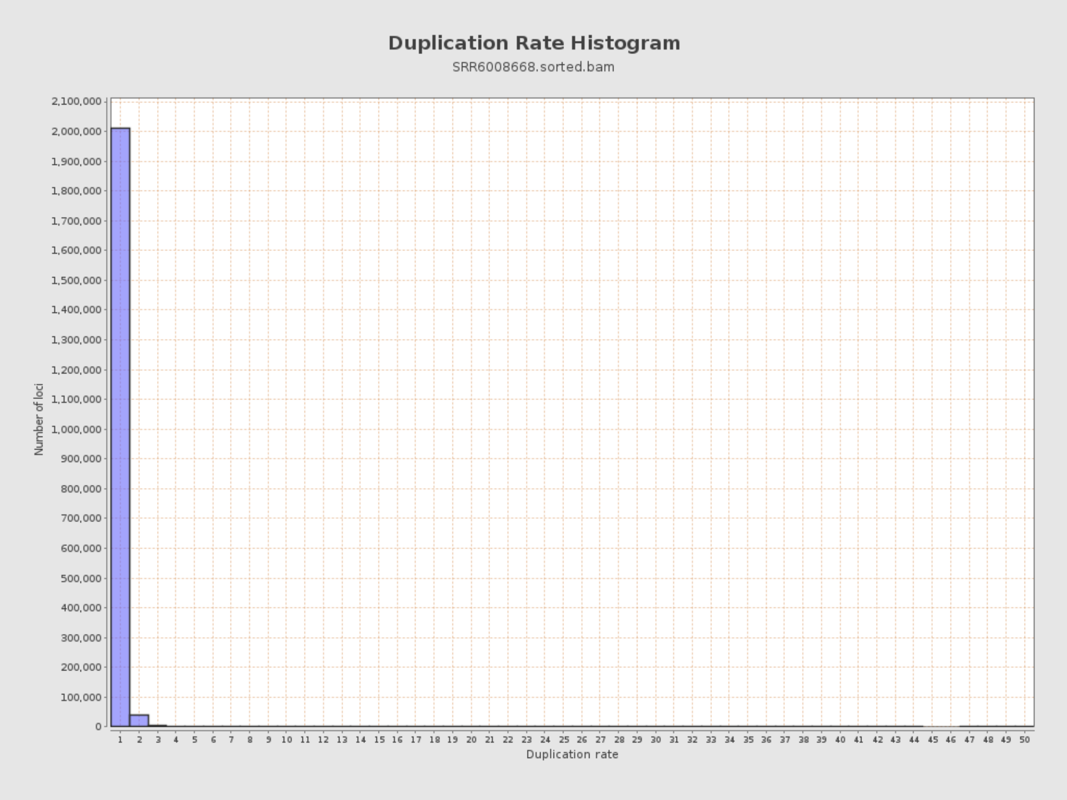
5. Results : Coverage Histogram (0-50X)



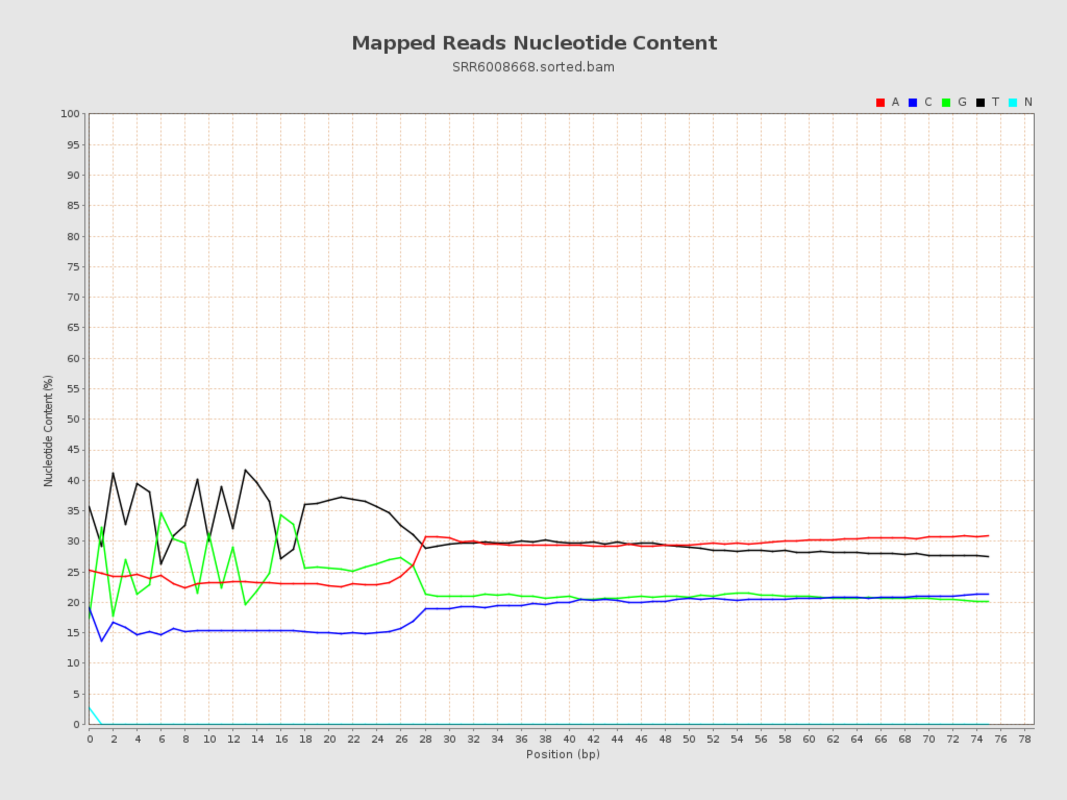
6. Results : Genome Fraction Coverage



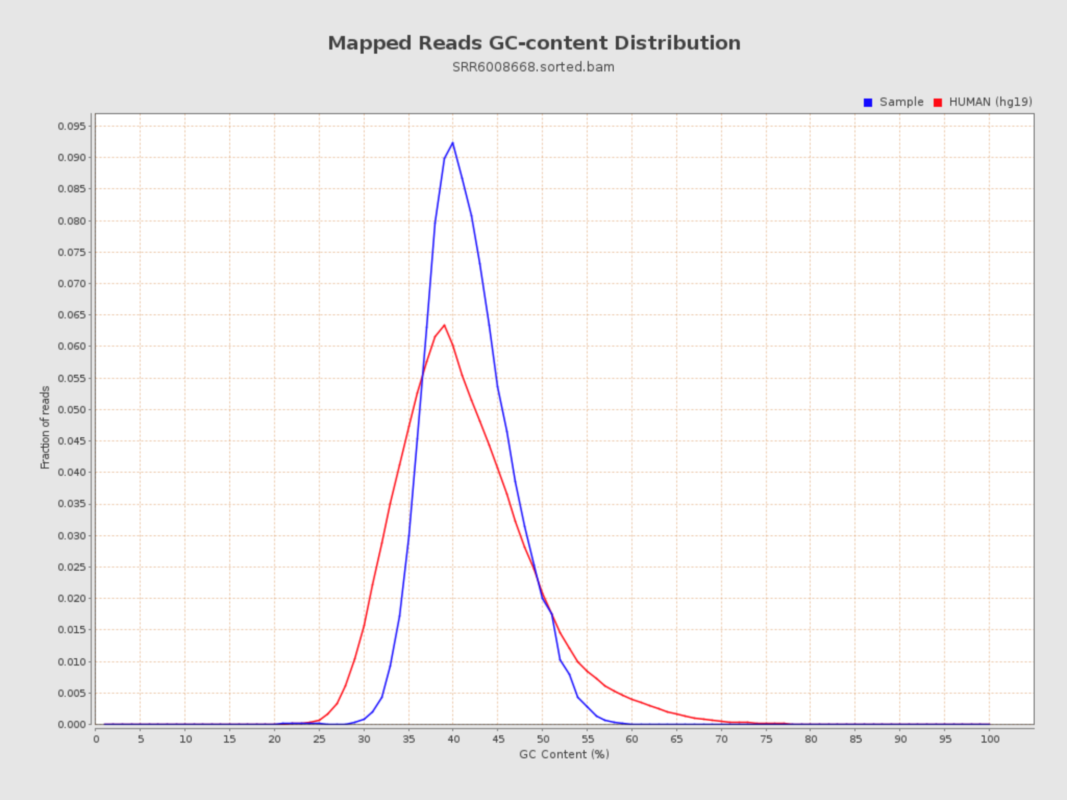
7. Results : Duplication Rate Histogram



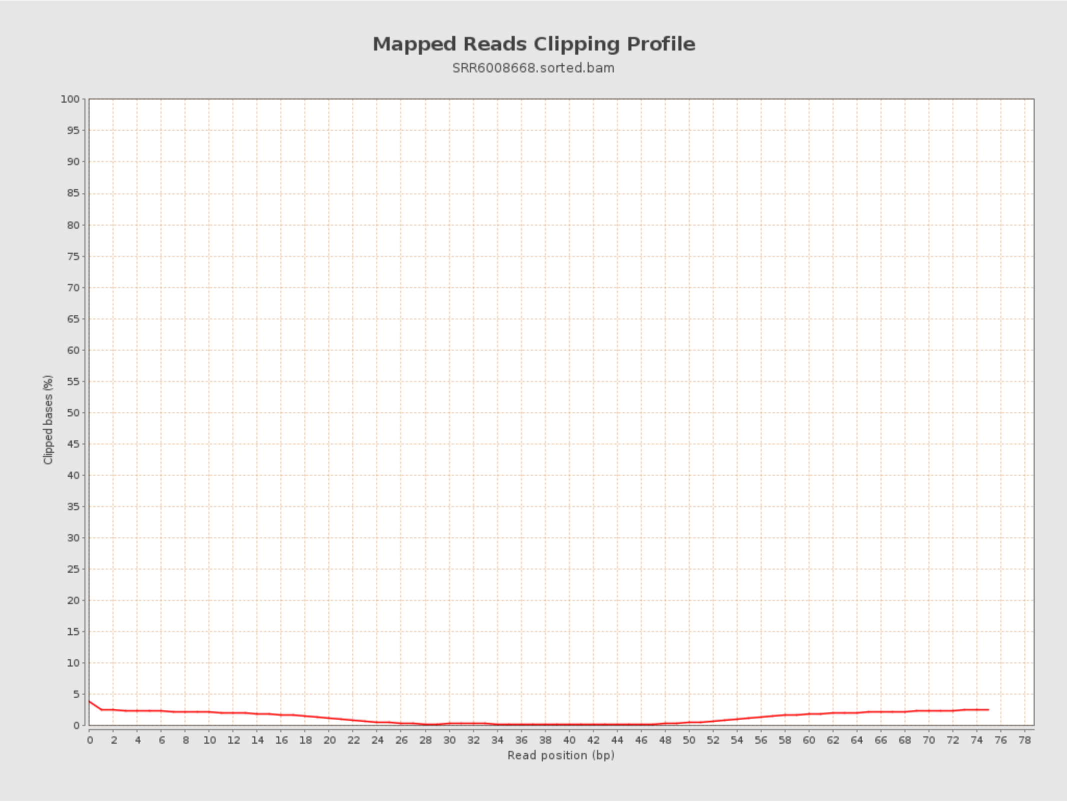
8. Results : Mapped Reads Nucleotide Content



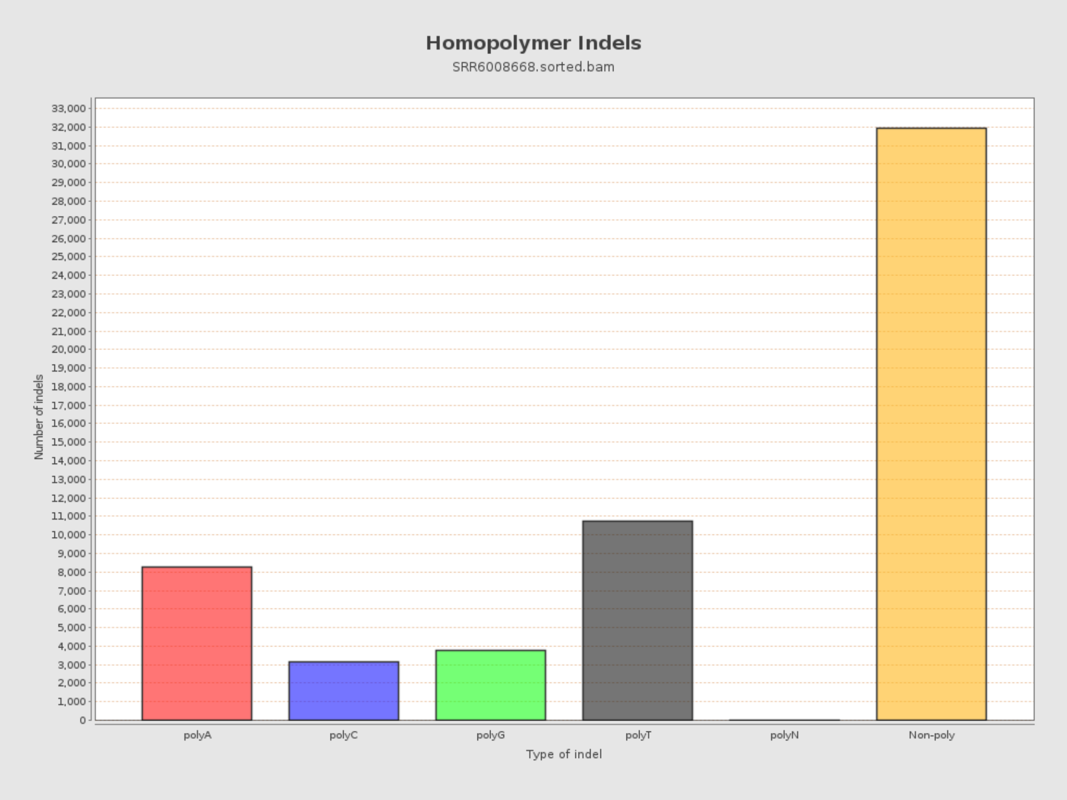
9. Results : Mapped Reads GC-content Distribution



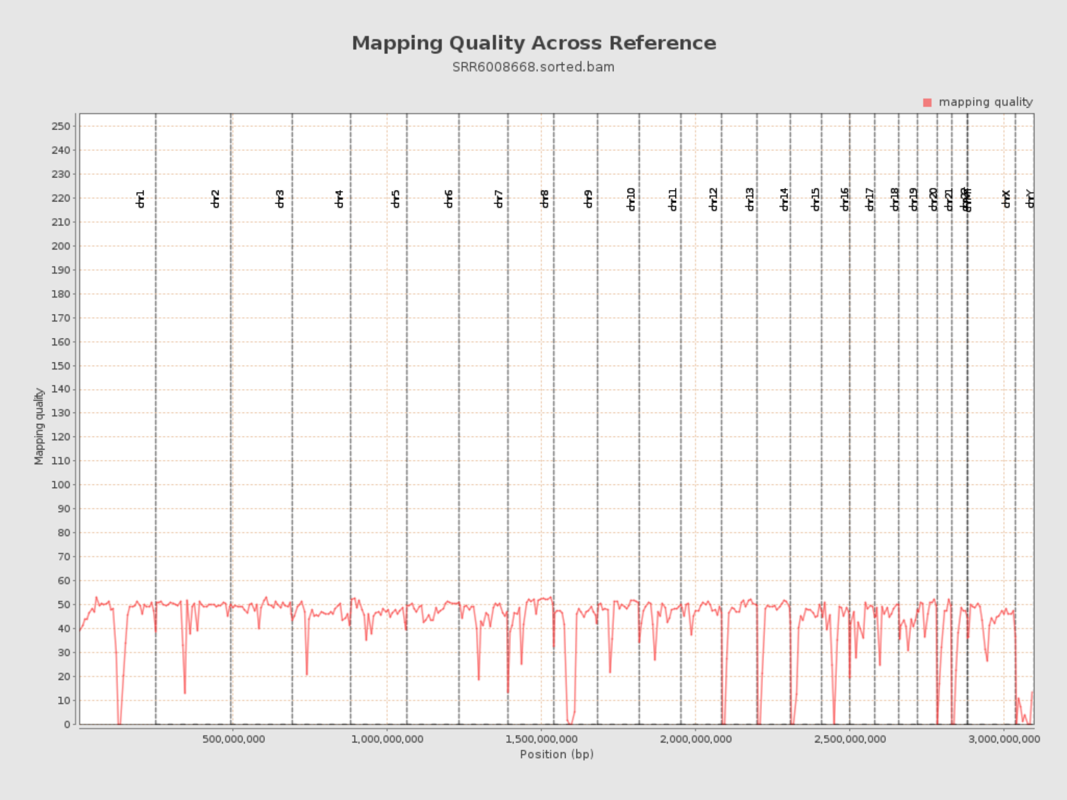
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram