Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:51:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013186.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_SRR6013186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:51:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,812,440
Mapped reads	2,511,037 / 89.28%
Unmapped reads	301,403 / 10.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,949 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	216,567 / 7.7%
Duplication rate	6.62%
Clipped reads	1,227,135 / 43.63%

2.2. ACGT Content

Number/percentage of A's	44,913,153 / 27.24%
Number/percentage of C's	31,085,325 / 18.85%
Number/percentage of T's	51,302,874 / 31.11%
Number/percentage of G's	37,571,472 / 22.79%
Number/percentage of N's	19,080 / 0.01%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0533

Standard Deviation	0.5233

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

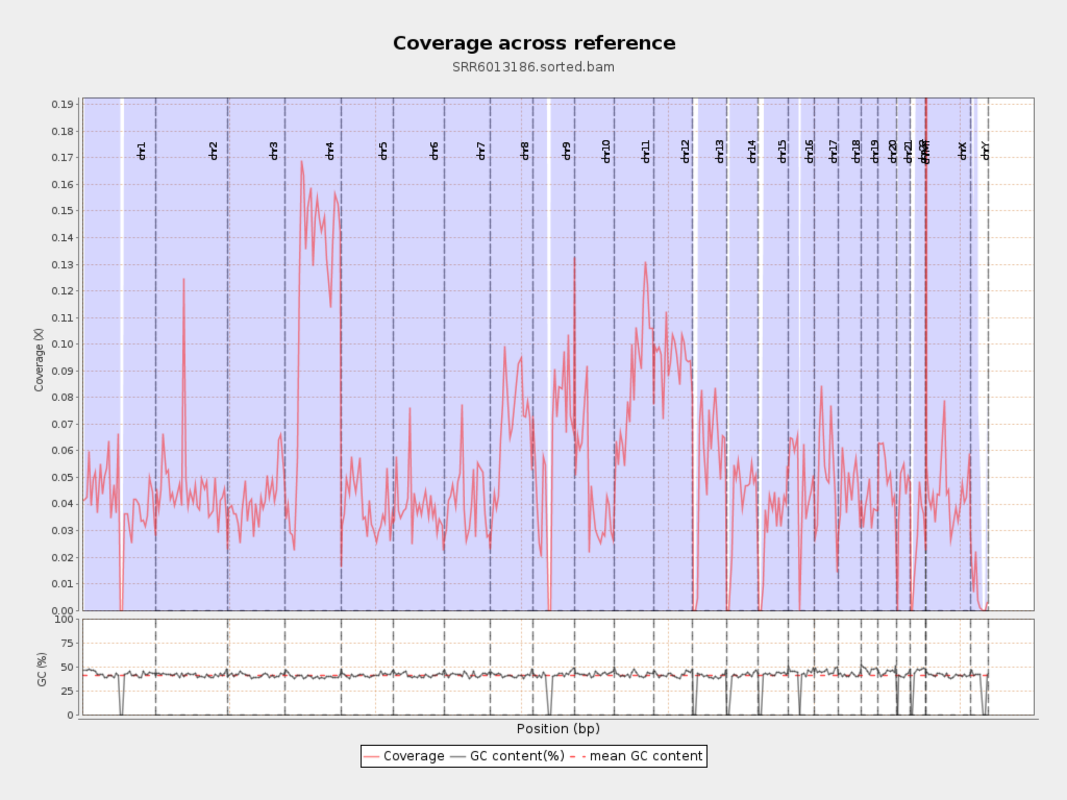
General error rate	0.78%
Mismatches	1,255,767
Insertions	11,689
Mapped reads with at least one insertion	0.46%
Deletions	42,445
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.68%

2.6. Chromosome stats

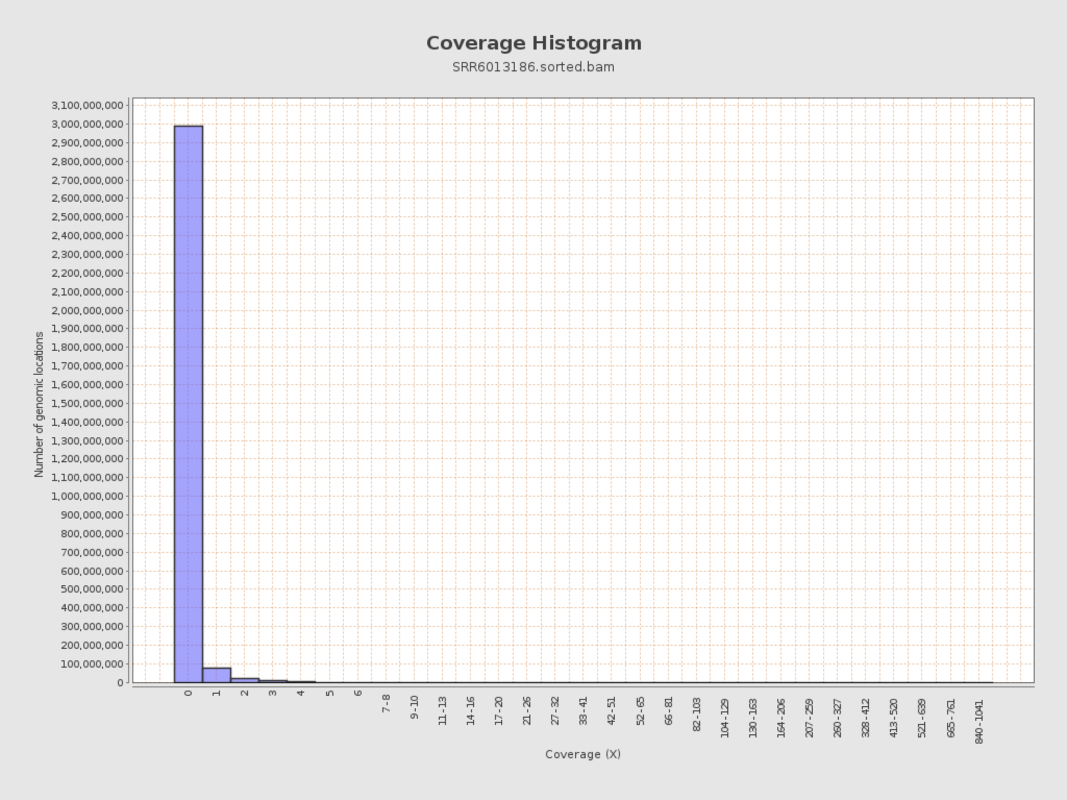
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9992690	0.0401	0.5957
chr2	243199373	11228258	0.0462	0.5992
chr3	198022430	8203793	0.0414	0.2924
chr4	191154276	22644502	0.1185	0.5199
chr5	180915260	7012652	0.0388	0.2899
chr6	171115067	6744557	0.0394	0.3403
chr7	159138663	6668629	0.0419	0.7175

chr8	146364022	10059132	0.0687	0.7152
chr9	141213431	8446993	0.0598	0.5057
chr10	135534747	6022523	0.0444	0.5381
chr11	135006516	11810711	0.0875	0.5267
chr12	133851895	12776321	0.0955	0.4517
chr13	115169878	6281462	0.0545	0.3453
chr14	107349540	4382010	0.0408	0.3739
chr15	102531392	3181509	0.031	0.2616
chr16	90354753	4269911	0.0473	0.3361
chr17	81195210	4255298	0.0524	0.377
chr18	78077248	3621206	0.0464	0.7846
chr19	59128983	2284544	0.0386	0.484
chr20	63025520	3282106	0.0521	0.3488
chr21	48129895	2048026	0.0426	0.3348
chr22	51304566	1318636	0.0257	0.2265
chrMT	16571	1197419	72.2599	39.9281
chrX	155270560	6854993	0.0441	0.3505
chrY	59373566	378085	0.0064	0.2134

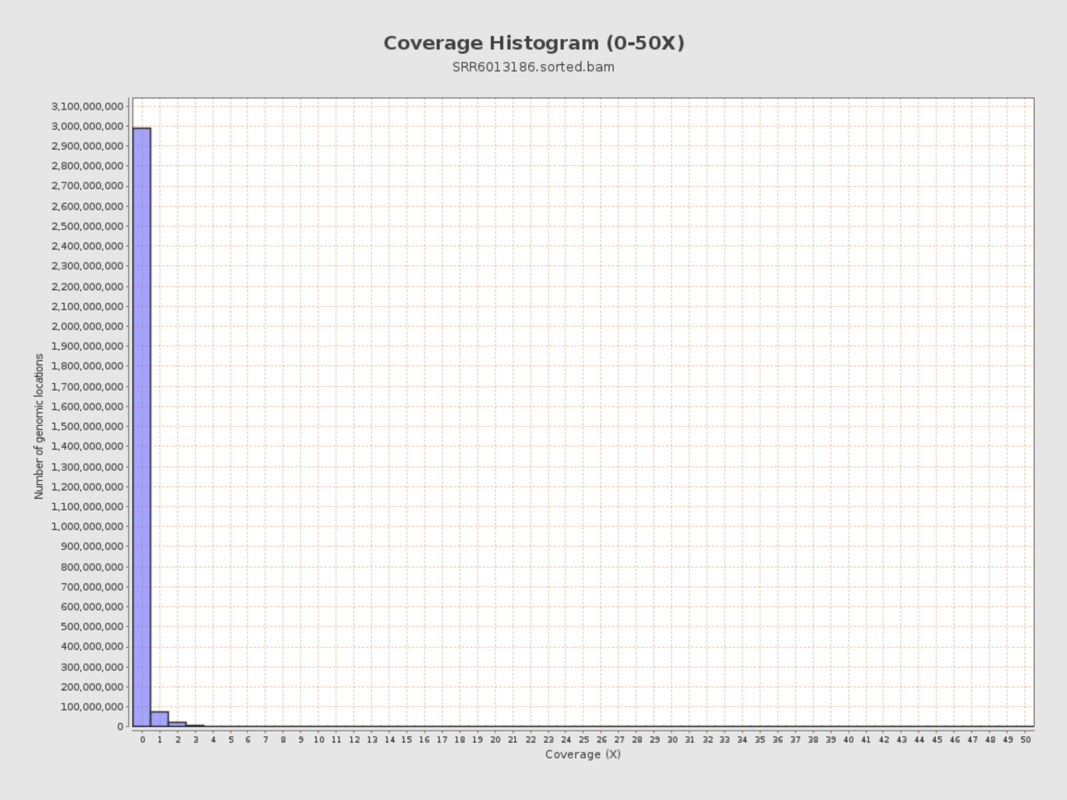
3. Results : Coverage across reference



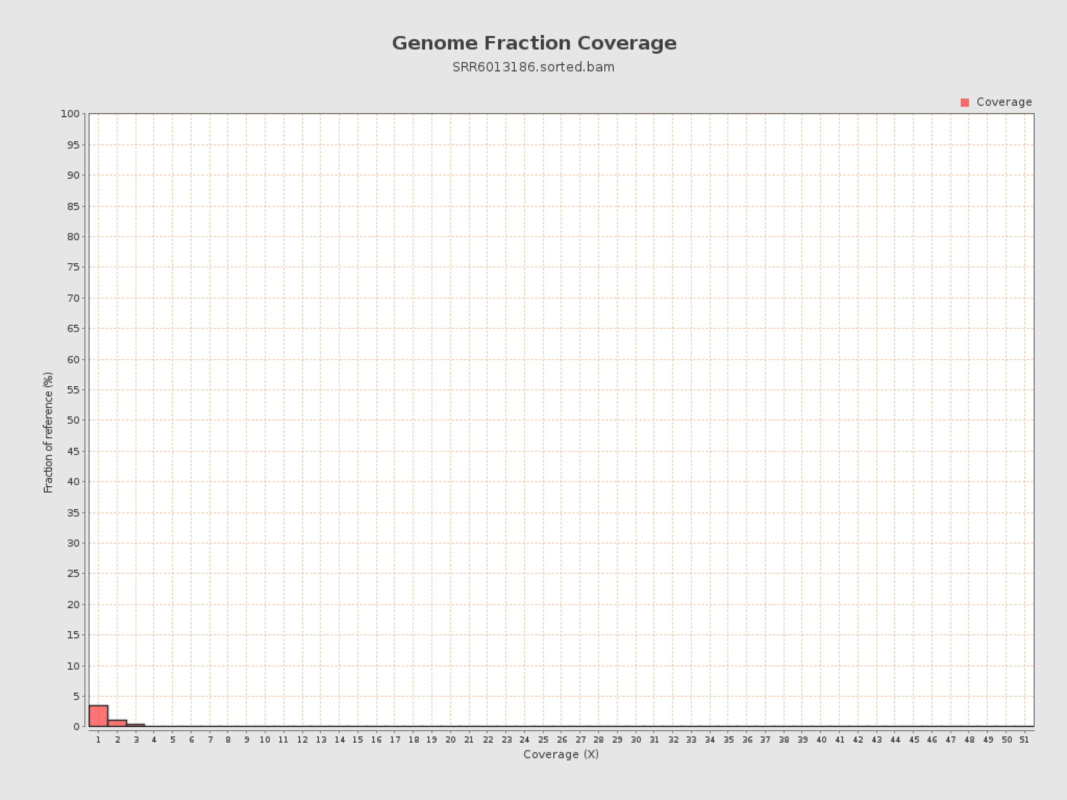
4. Results : Coverage Histogram



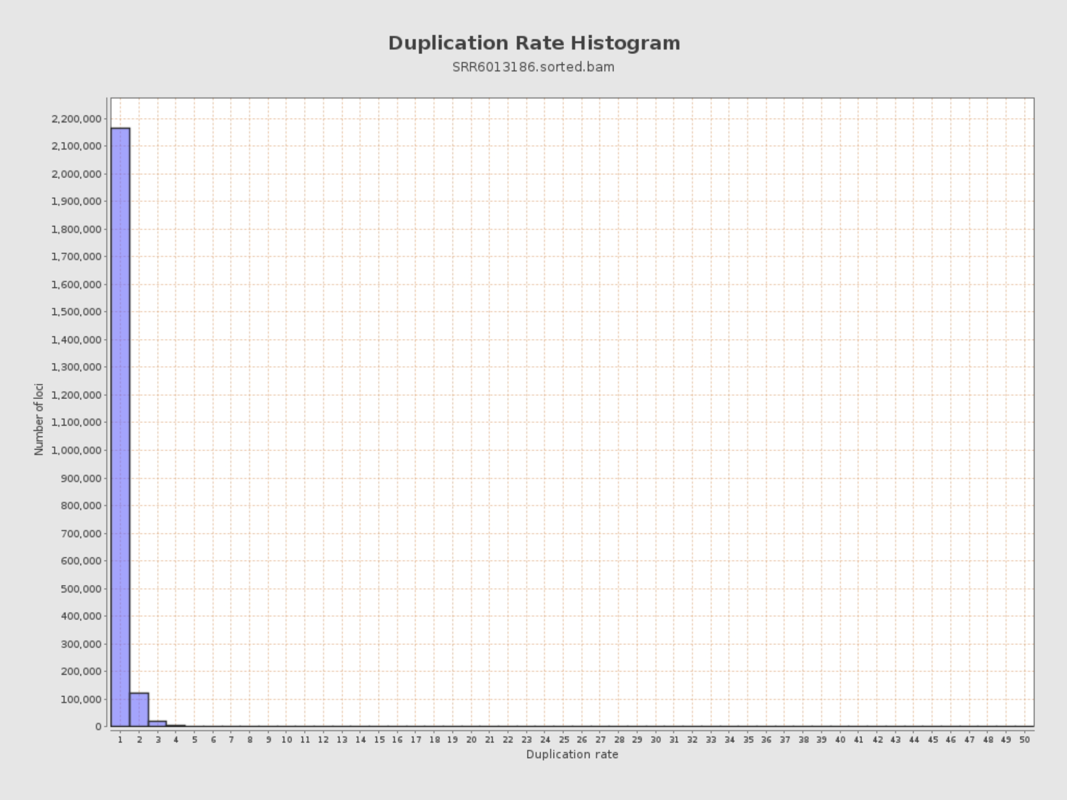
5. Results : Coverage Histogram (0-50X)



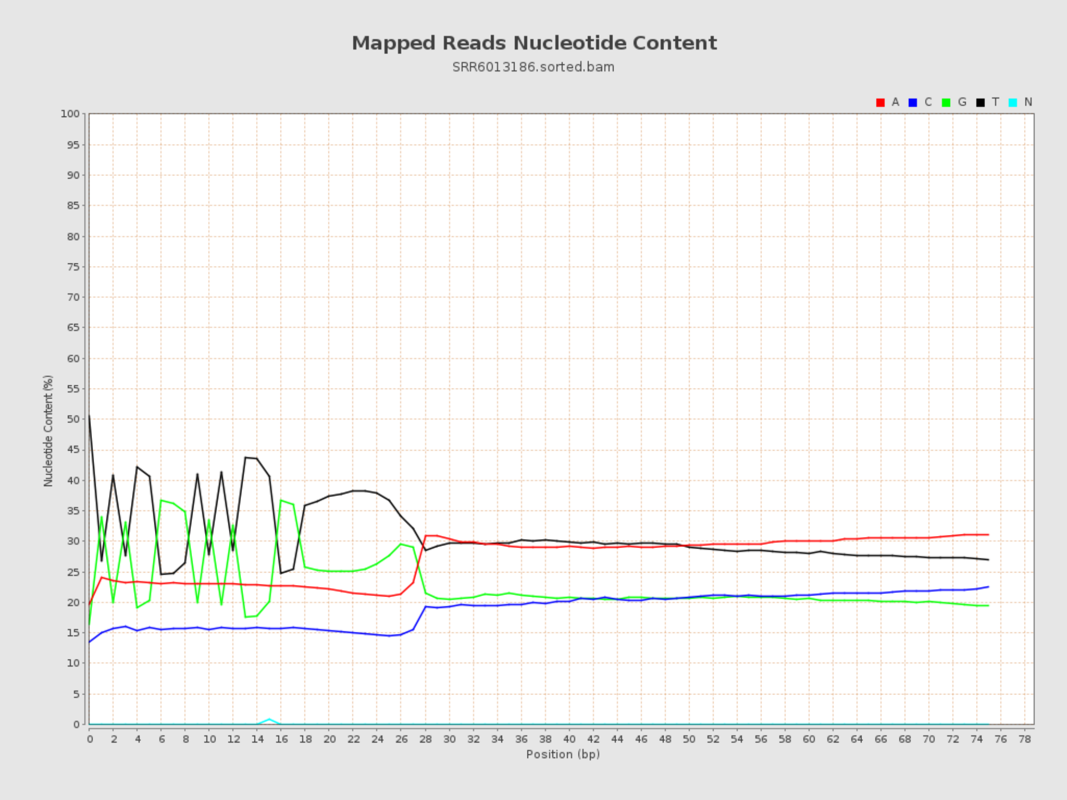
6. Results : Genome Fraction Coverage



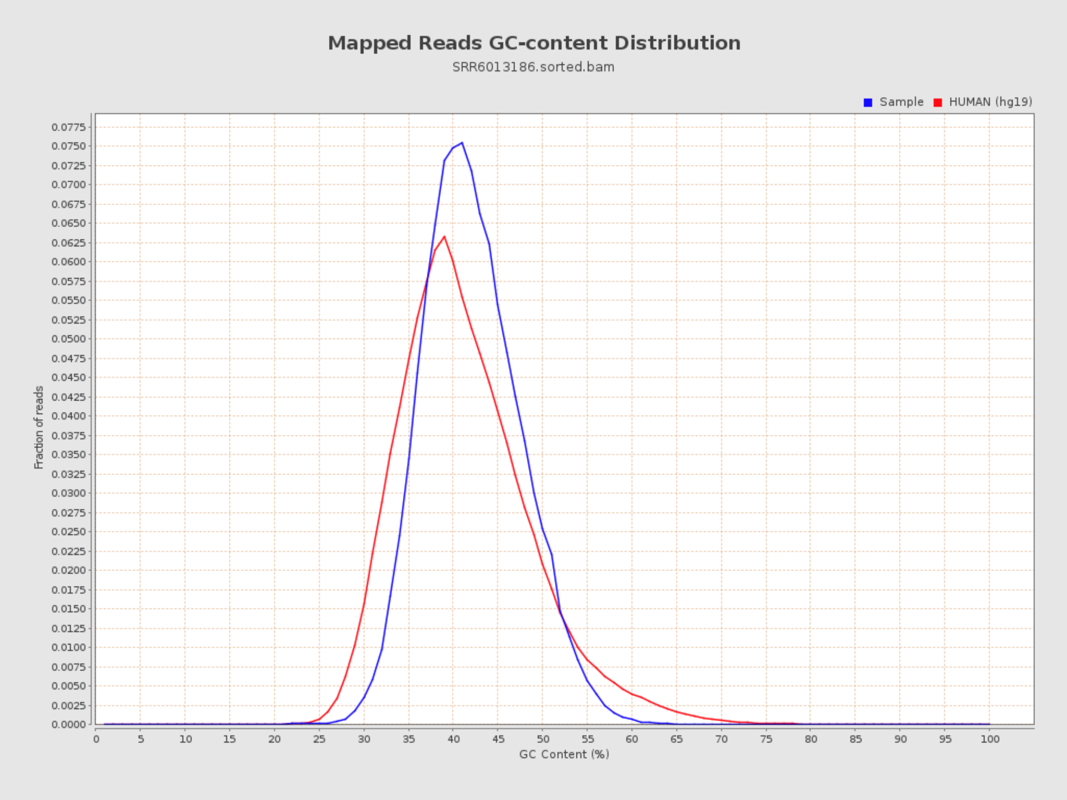
7. Results : Duplication Rate Histogram



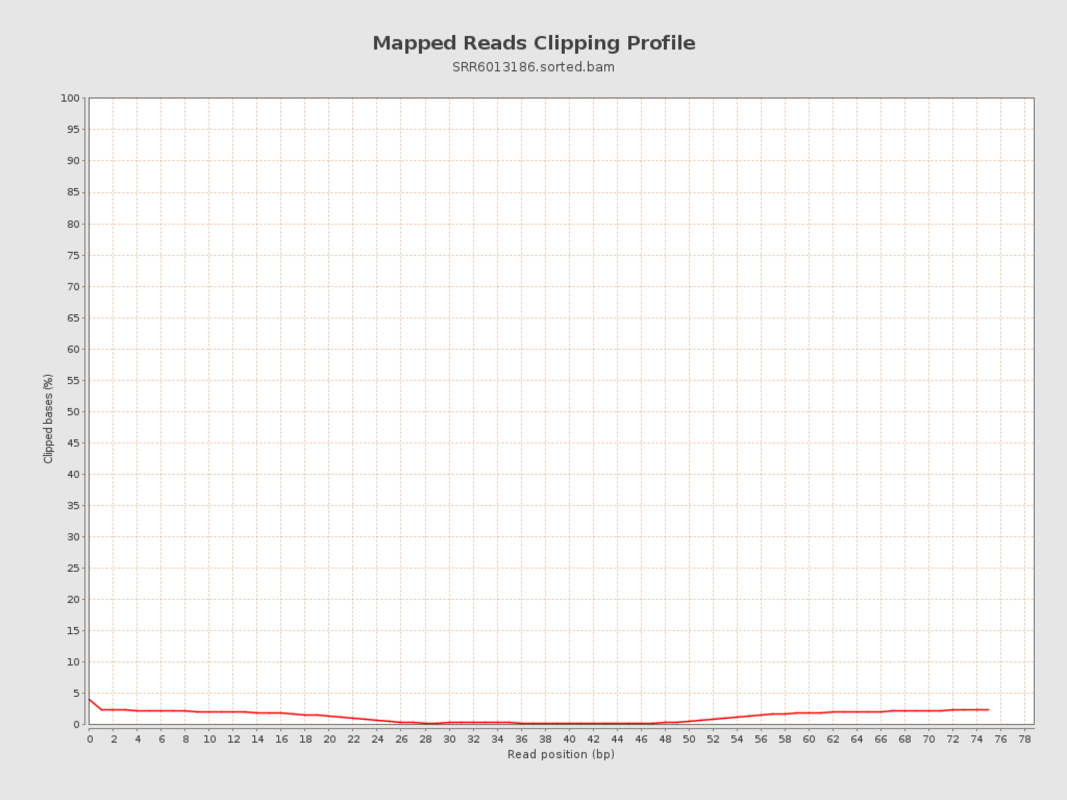
8. Results : Mapped Reads Nucleotide Content



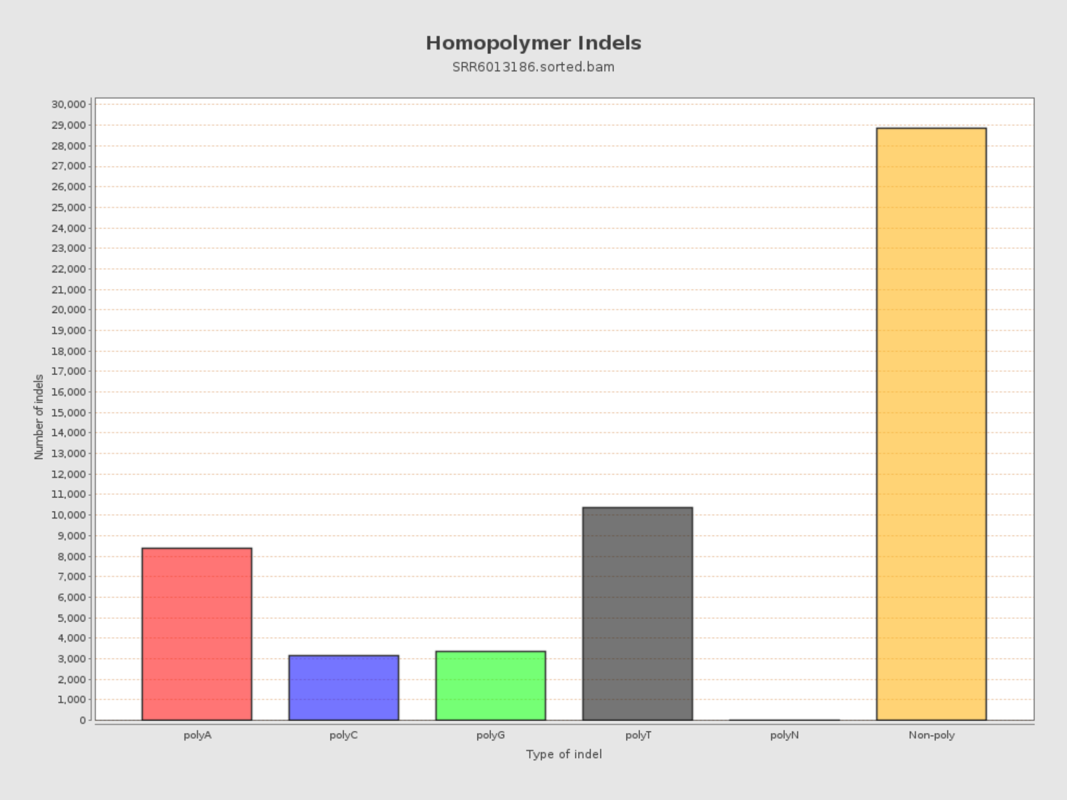
9. Results : Mapped Reads GC-content Distribution



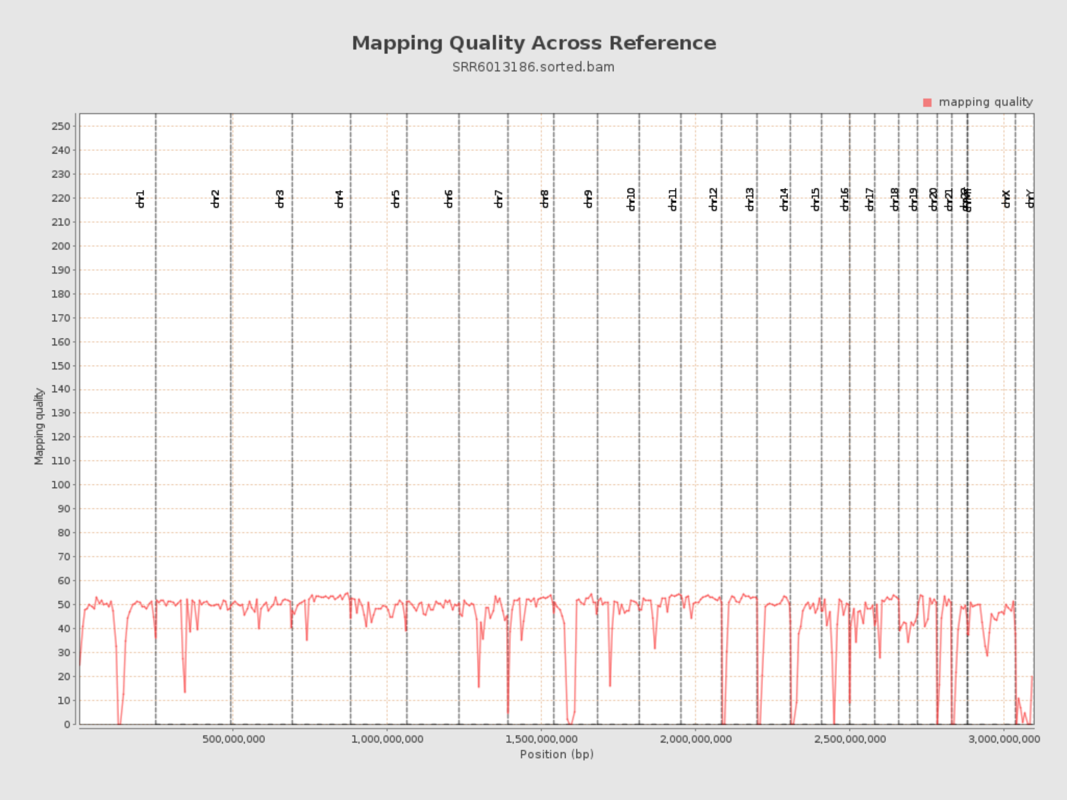
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram