Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:33:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716888.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_SRR9716888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716888.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:33:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,386,932
Mapped reads	3,143,488 / 92.81%
Unmapped reads	243,444 / 7.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,895 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	183,228 / 5.41%
Duplication rate	4.29%
Clipped reads	3,157,319 / 93.22%

2.2. ACGT Content

Number/percentage of A's	47,482,751 / 25.84%
Number/percentage of C's	37,712,657 / 20.52%
Number/percentage of T's	55,730,634 / 30.32%
Number/percentage of G's	42,855,605 / 23.32%
Number/percentage of N's	5,207 / 0%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0594

Standard Deviation	0.5603

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

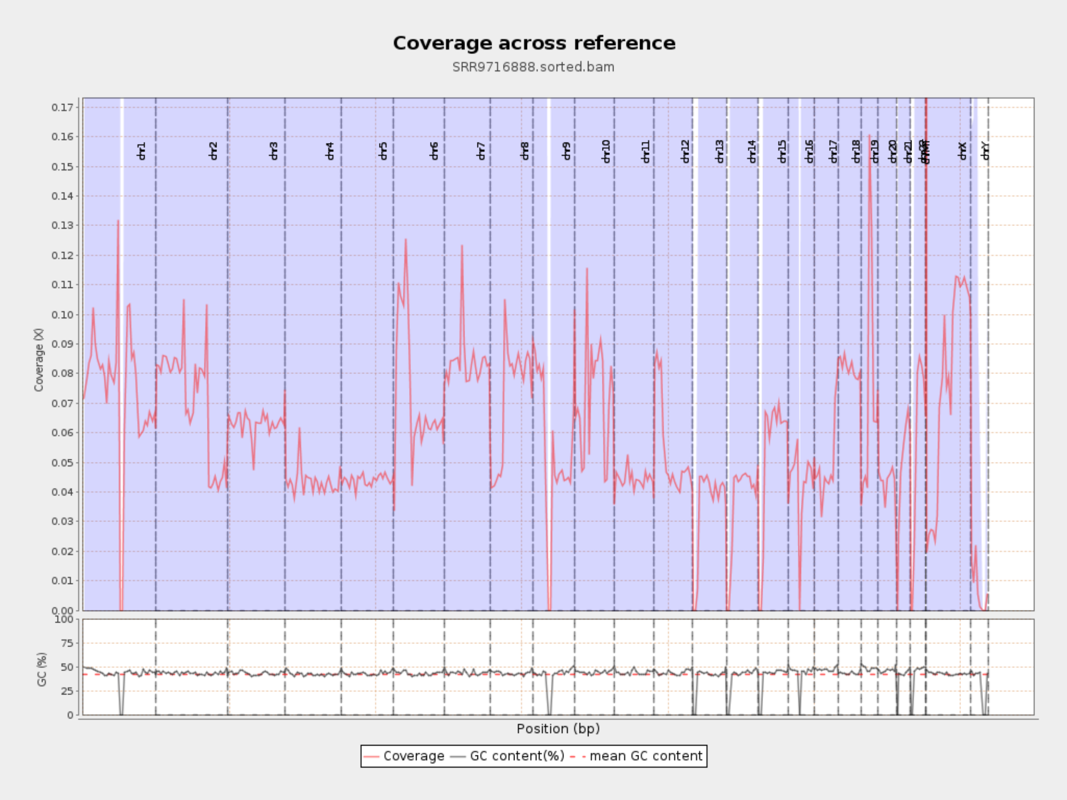
General error rate	0.49%
Mismatches	890,352
Insertions	10,369
Mapped reads with at least one insertion	0.33%
Deletions	32,603
Mapped reads with at least one deletion	1.03%
Homopolymer indels	45.71%

2.6. Chromosome stats

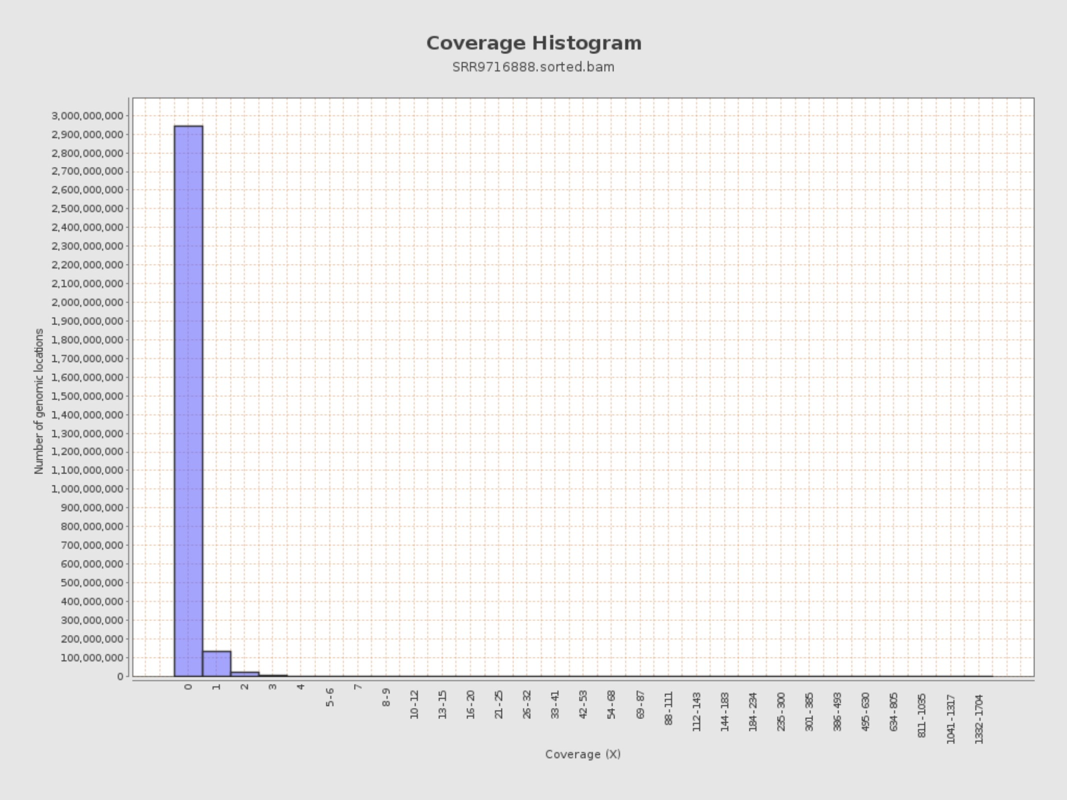
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18606061	0.0746	1.2828
chr2	243199373	17240824	0.0709	0.6543
chr3	198022430	12485367	0.0631	0.2958
chr4	191154276	8342088	0.0436	0.2717
chr5	180915260	7965995	0.044	0.2558
chr6	171115067	12524880	0.0732	0.3854
chr7	159138663	13436301	0.0844	0.8154

chr8	146364022	10494255	0.0717	0.4121
chr9	141213431	7497623	0.0531	0.4267
chr10	135534747	9706066	0.0716	0.4908
chr11	135006516	5993147	0.0444	0.3844
chr12	133851895	7320585	0.0547	0.2876
chr13	115169878	4054661	0.0352	0.2204
chr14	107349540	3943754	0.0367	0.2677
chr15	102531392	5360437	0.0523	0.2715
chr16	90354753	3762918	0.0416	0.2784
chr17	81195210	3895790	0.048	0.2774
chr18	78077248	6401844	0.082	0.8388
chr19	59128983	4503834	0.0762	0.802
chr20	63025520	2741870	0.0435	0.2518
chr21	48129895	2312109	0.048	0.2903
chr22	51304566	2834509	0.0552	0.2769
chrMT	16571	183960	11.1013	6.3533
chrX	155270560	11800172	0.076	0.4004
chrY	59373566	429147	0.0072	0.158

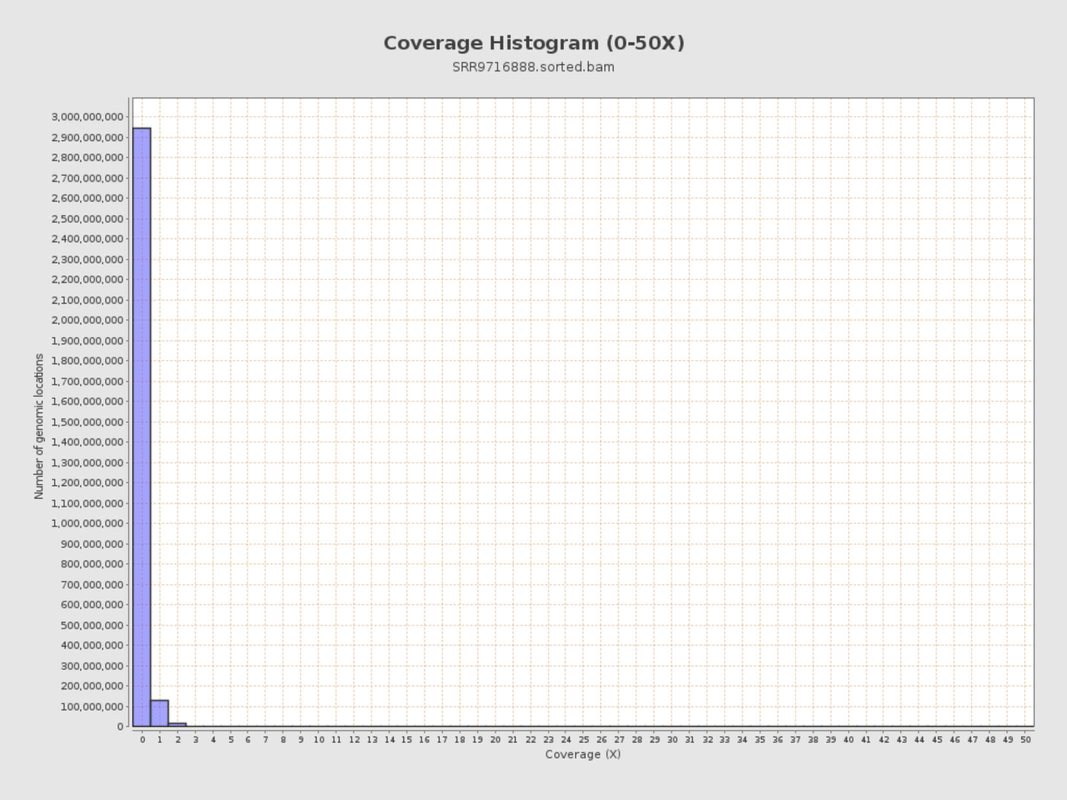
3. Results : Coverage across reference



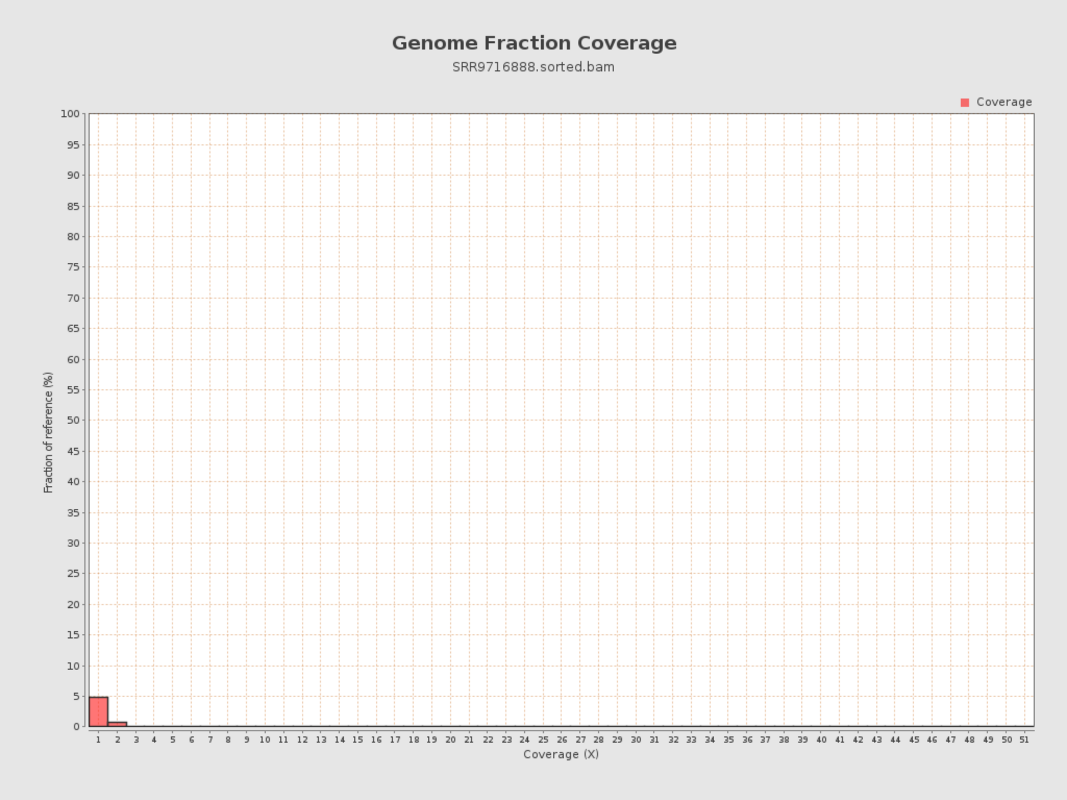
4. Results : Coverage Histogram



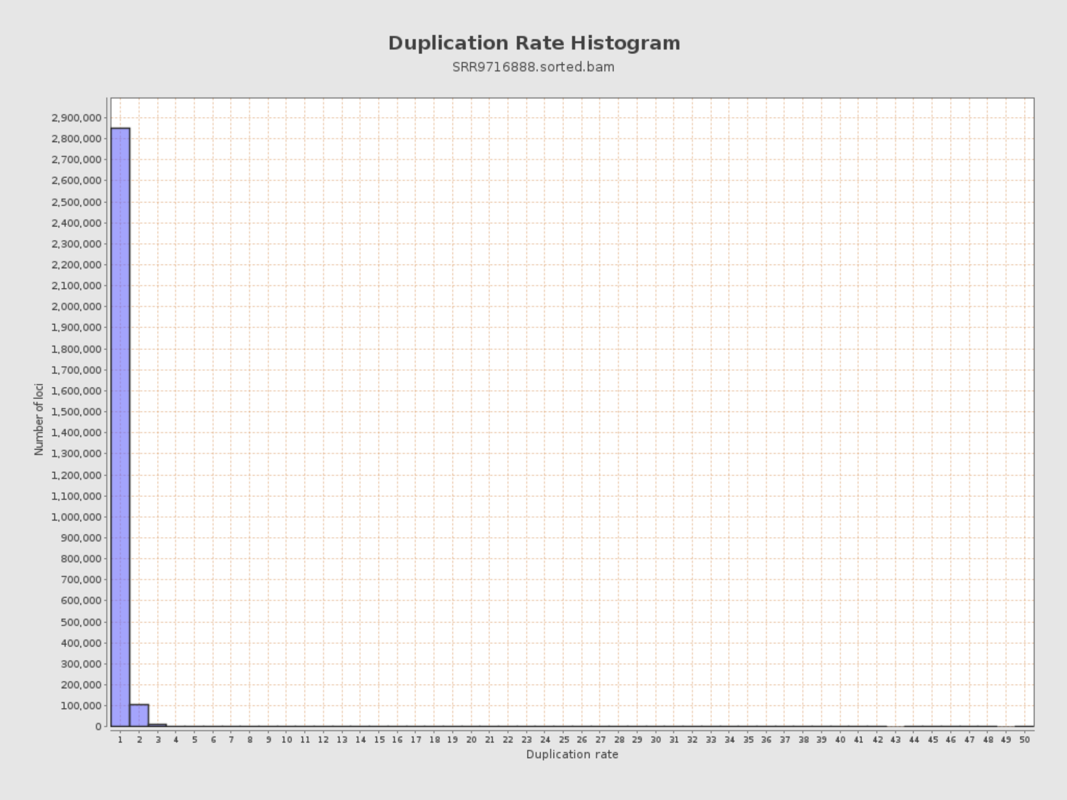
5. Results : Coverage Histogram (0-50X)



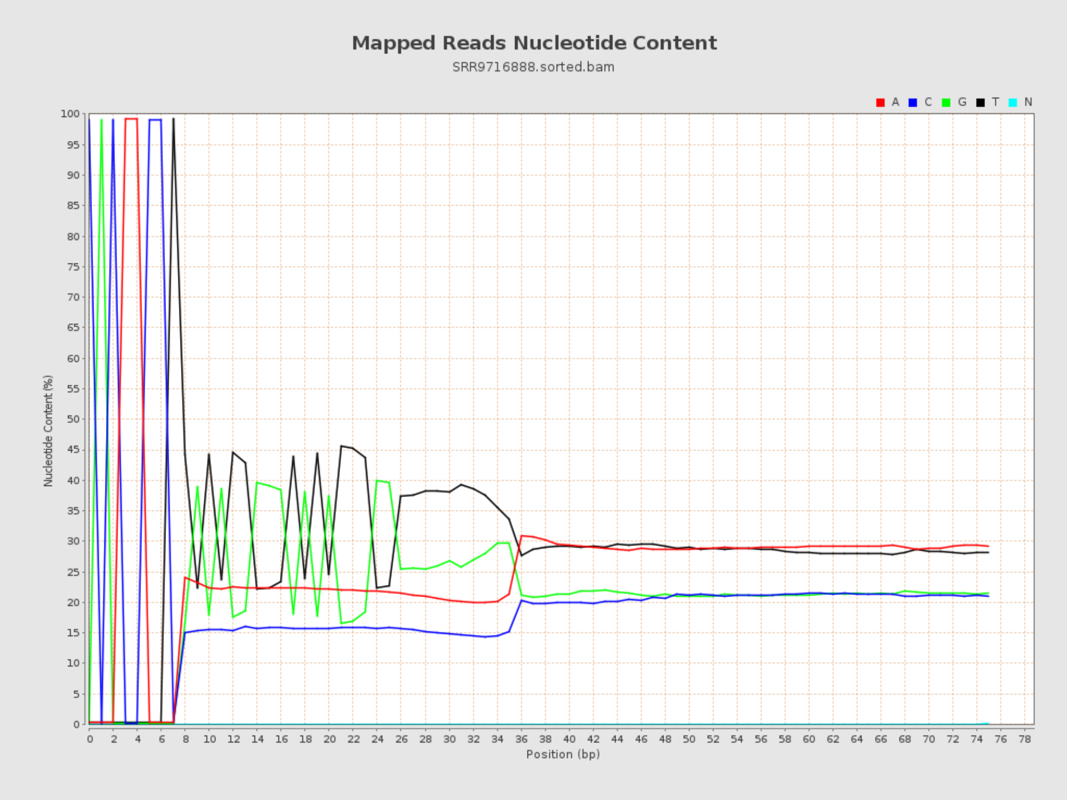
6. Results : Genome Fraction Coverage



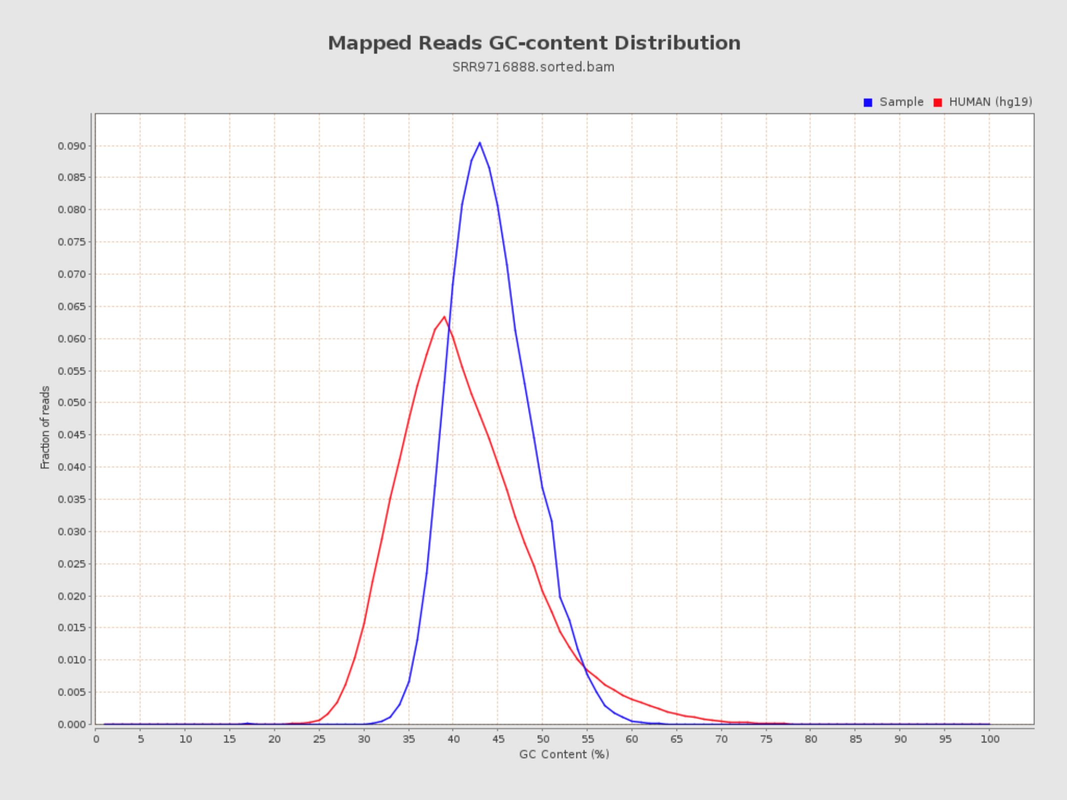
7. Results : Duplication Rate Histogram



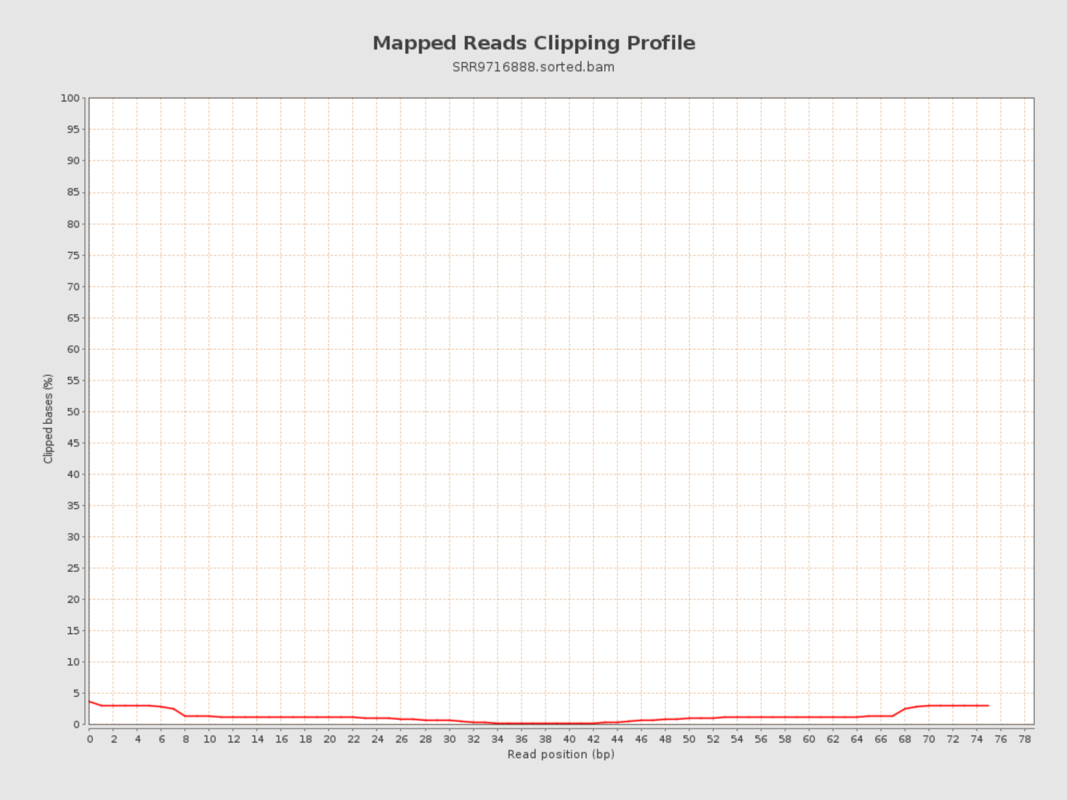
8. Results : Mapped Reads Nucleotide Content



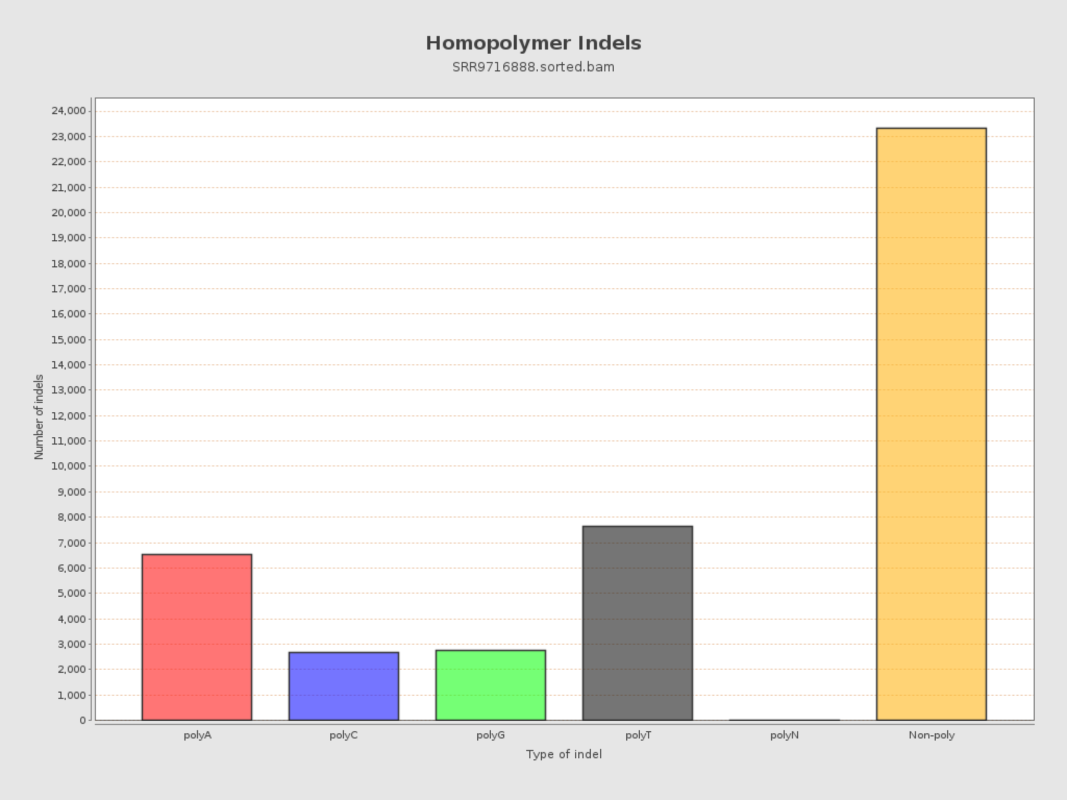
9. Results : Mapped Reads GC-content Distribution



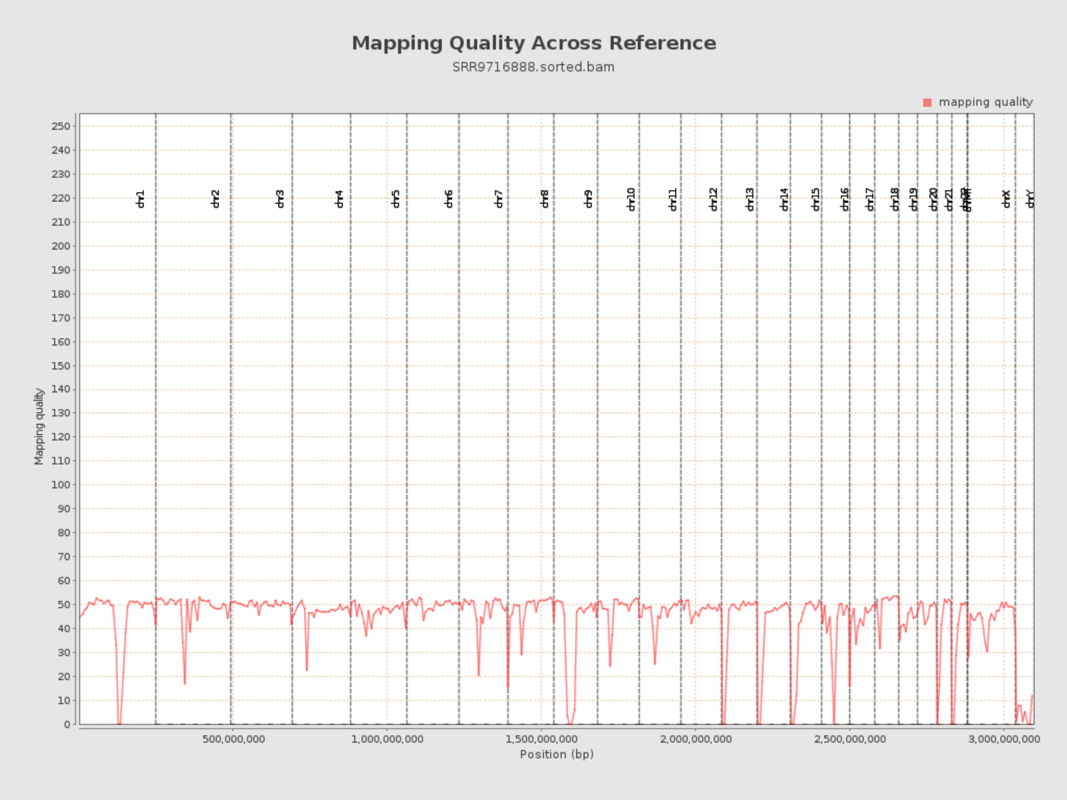
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram