Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:51:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716148.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_SRR9716148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:51:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,074,552
Mapped reads	1,910,639 / 92.1%
Unmapped reads	163,913 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,993 / 0.58%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	77,901 / 3.76%
Duplication rate	2.98%
Clipped reads	1,920,940 / 92.6%

2.2. ACGT Content

Number/percentage of A's	28,648,106 / 25.67%
Number/percentage of C's	22,718,328 / 20.36%
Number/percentage of T's	34,002,119 / 30.47%
Number/percentage of G's	26,238,636 / 23.51%
Number/percentage of N's	1,420 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0361

Standard Deviation	0.334

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

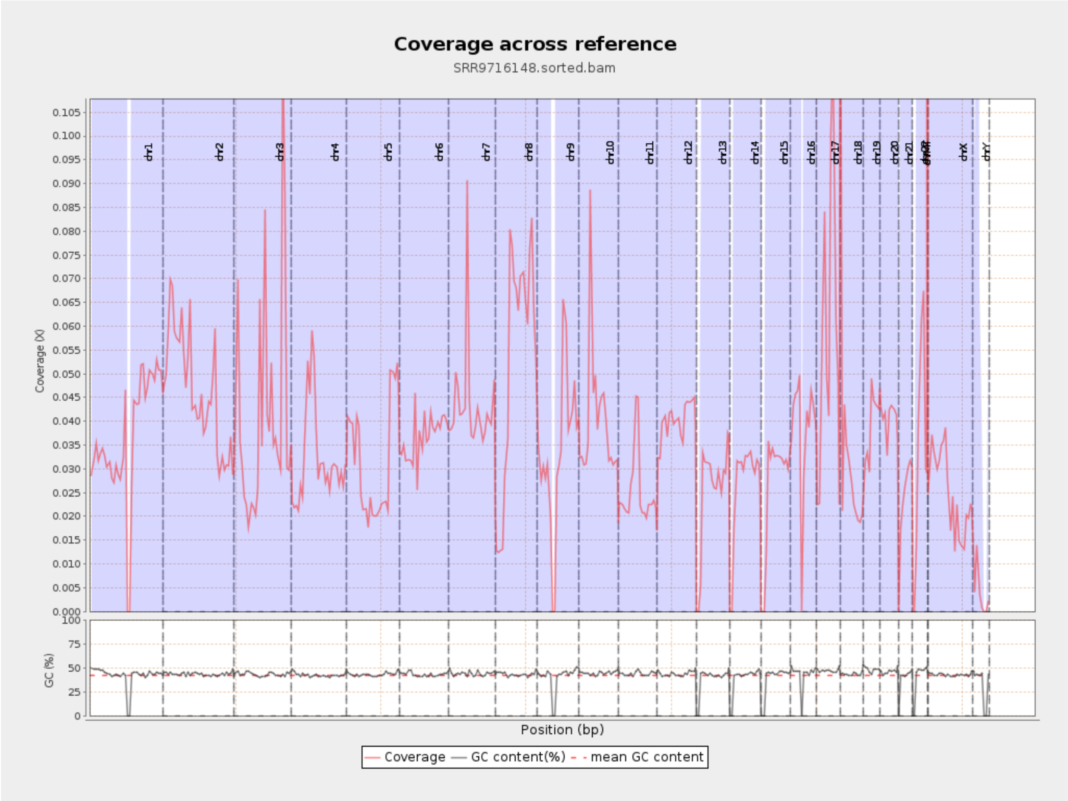
General error rate	0.5%
Mismatches	550,541
Insertions	6,081
Mapped reads with at least one insertion	0.32%
Deletions	19,275
Mapped reads with at least one deletion	1%
Homopolymer indels	42.27%

2.6. Chromosome stats

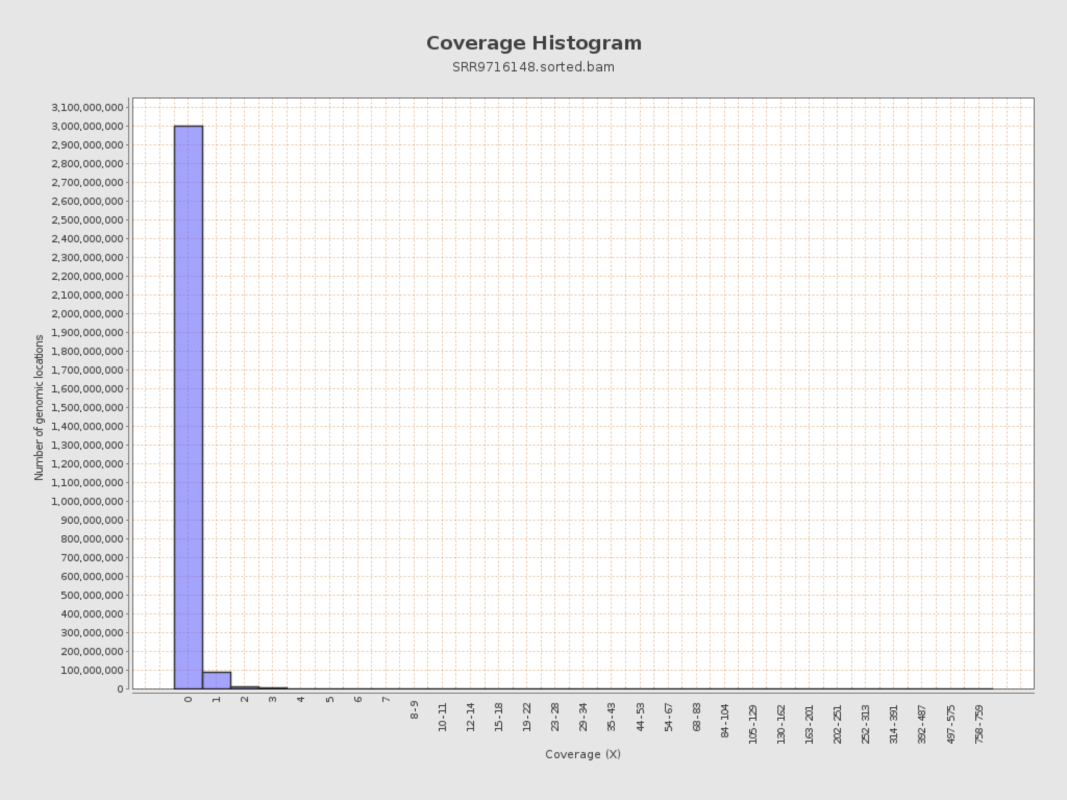
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9126317	0.0366	0.4535
chr2	243199373	11362633	0.0467	0.4103
chr3	198022430	8240369	0.0416	0.2473
chr4	191154276	6143518	0.0321	0.2245
chr5	180915260	5663091	0.0313	0.1983
chr6	171115067	6275803	0.0367	0.2309
chr7	159138663	6931979	0.0436	0.7449

chr8	146364022	7829923	0.0535	0.3525
chr9	141213431	4692692	0.0332	0.2335
chr10	135534747	5441152	0.0401	0.4494
chr11	135006516	3384871	0.0251	0.2268
chr12	133851895	5354247	0.04	0.2525
chr13	115169878	2882786	0.025	0.1756
chr14	107349540	2842614	0.0265	0.1879
chr15	102531392	2714481	0.0265	0.1844
chr16	90354753	3480801	0.0385	0.2301
chr17	81195210	4800460	0.0591	0.2861
chr18	78077248	2514641	0.0322	0.3622
chr19	59128983	2286832	0.0387	0.4127
chr20	63025520	2561645	0.0406	0.2379
chr21	48129895	1141018	0.0237	0.1838
chr22	51304566	1710050	0.0333	0.2041
chrMT	16571	90389	5.4546	3.7715
chrX	155270560	3914793	0.0252	0.2038
chrY	59373566	251989	0.0042	0.1165

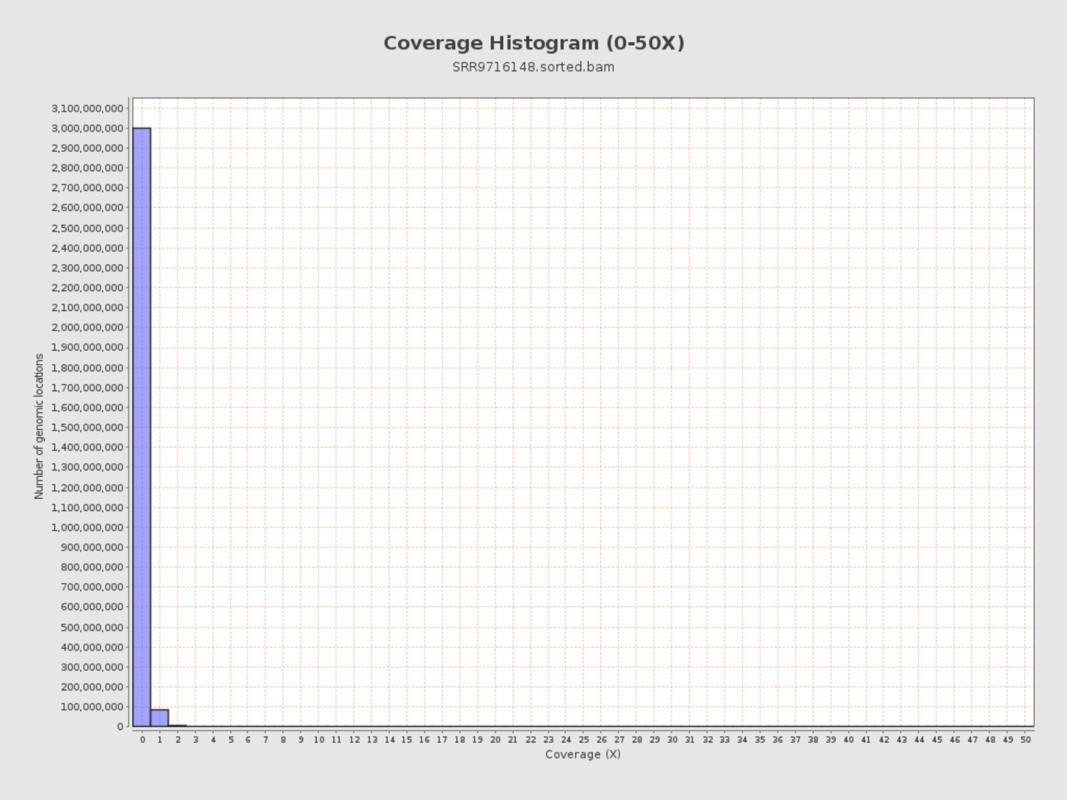
3. Results : Coverage across reference



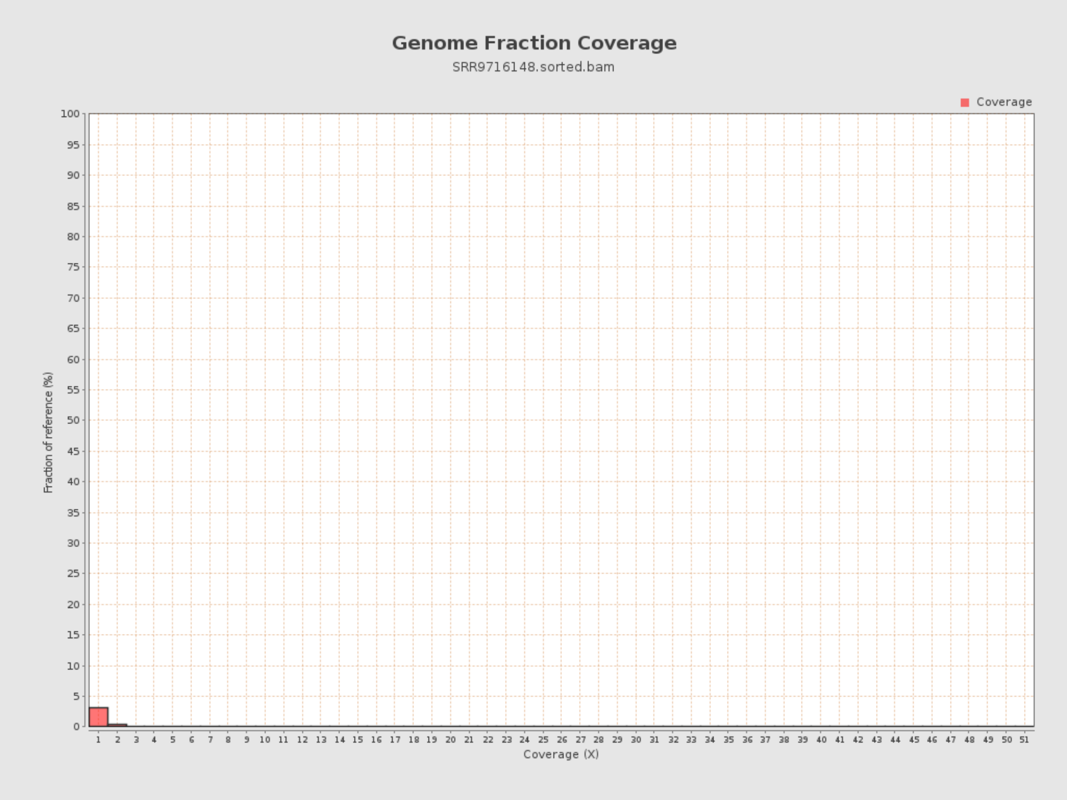
4. Results : Coverage Histogram



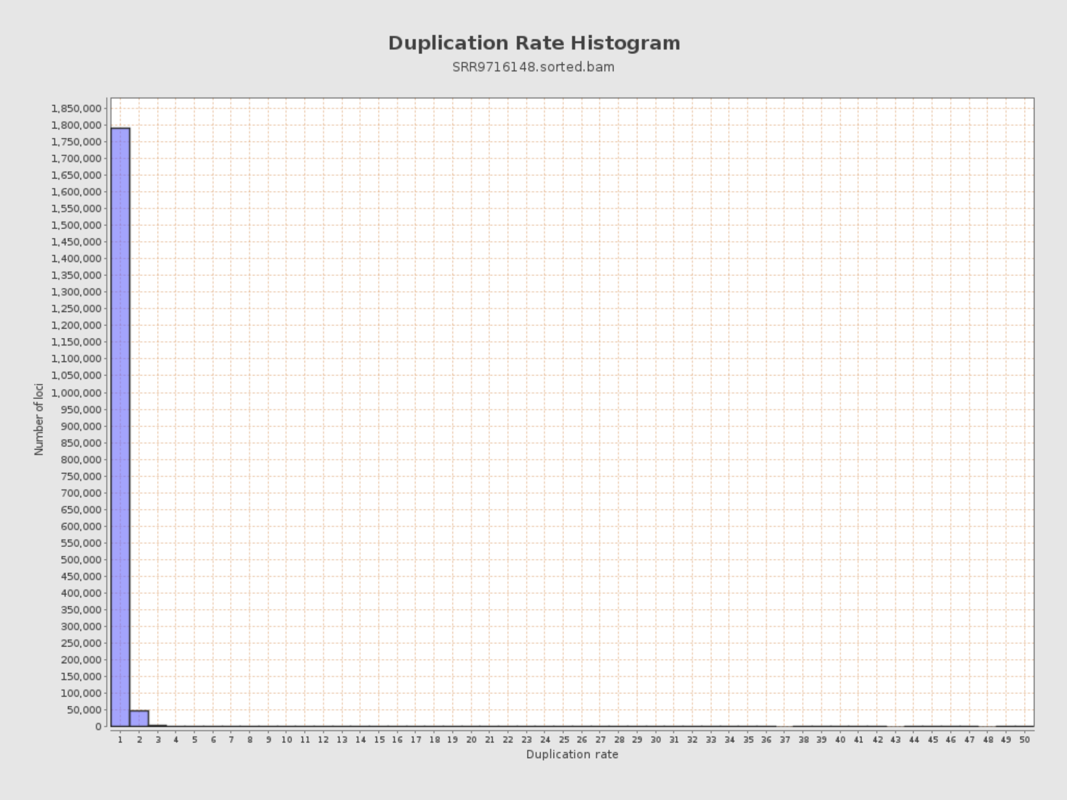
5. Results : Coverage Histogram (0-50X)



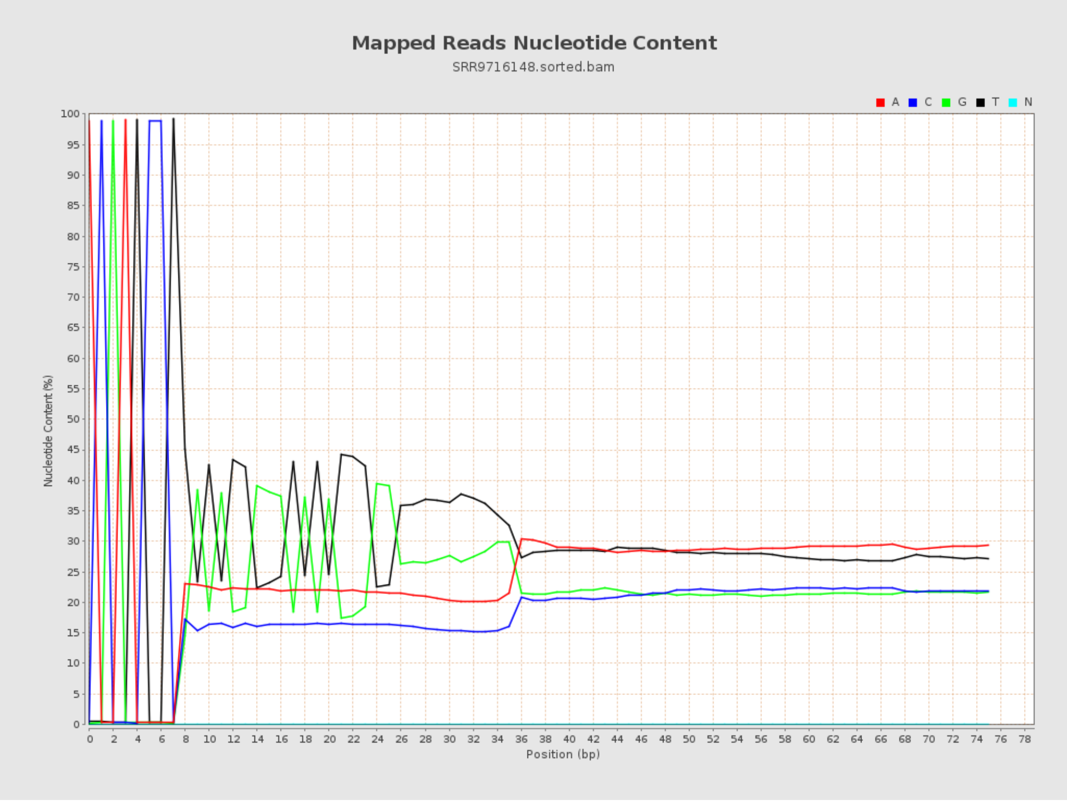
6. Results : Genome Fraction Coverage



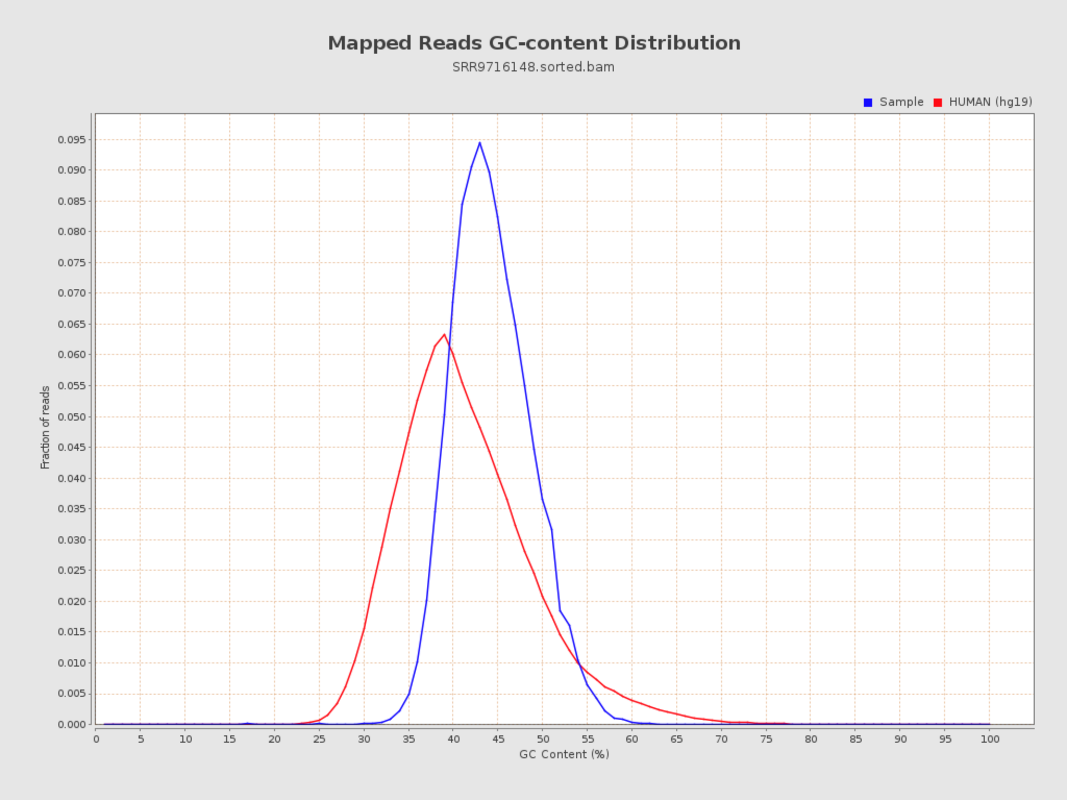
7. Results : Duplication Rate Histogram



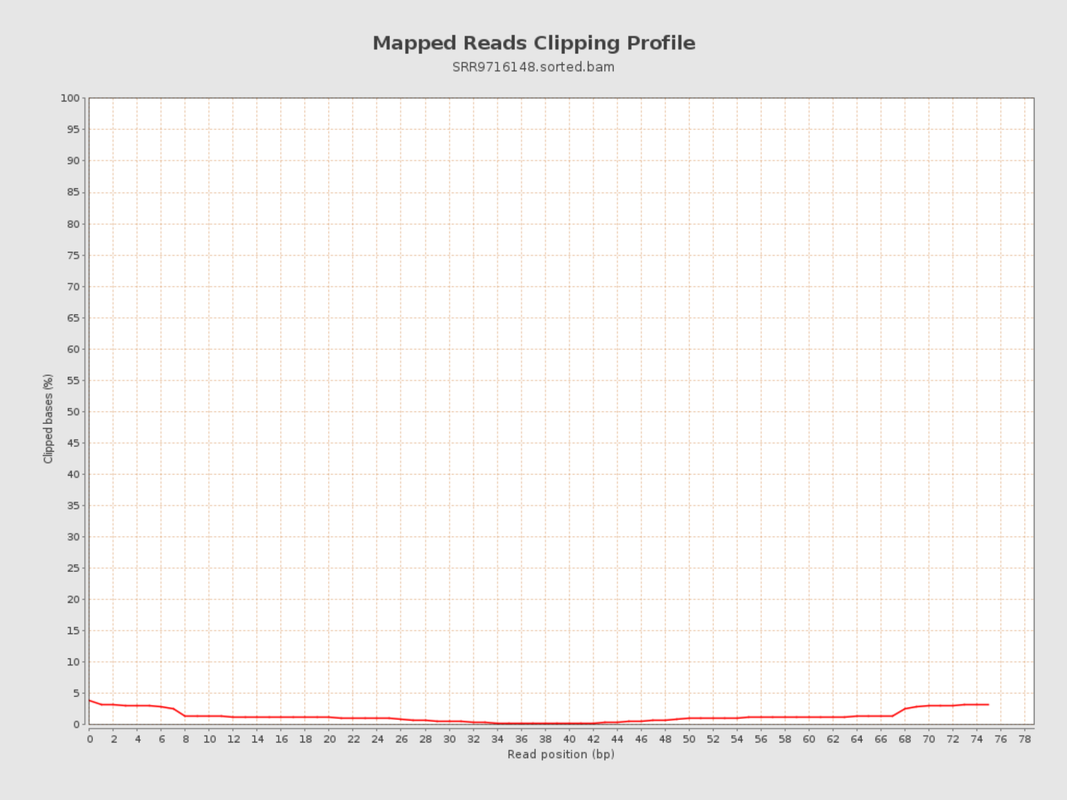
8. Results : Mapped Reads Nucleotide Content



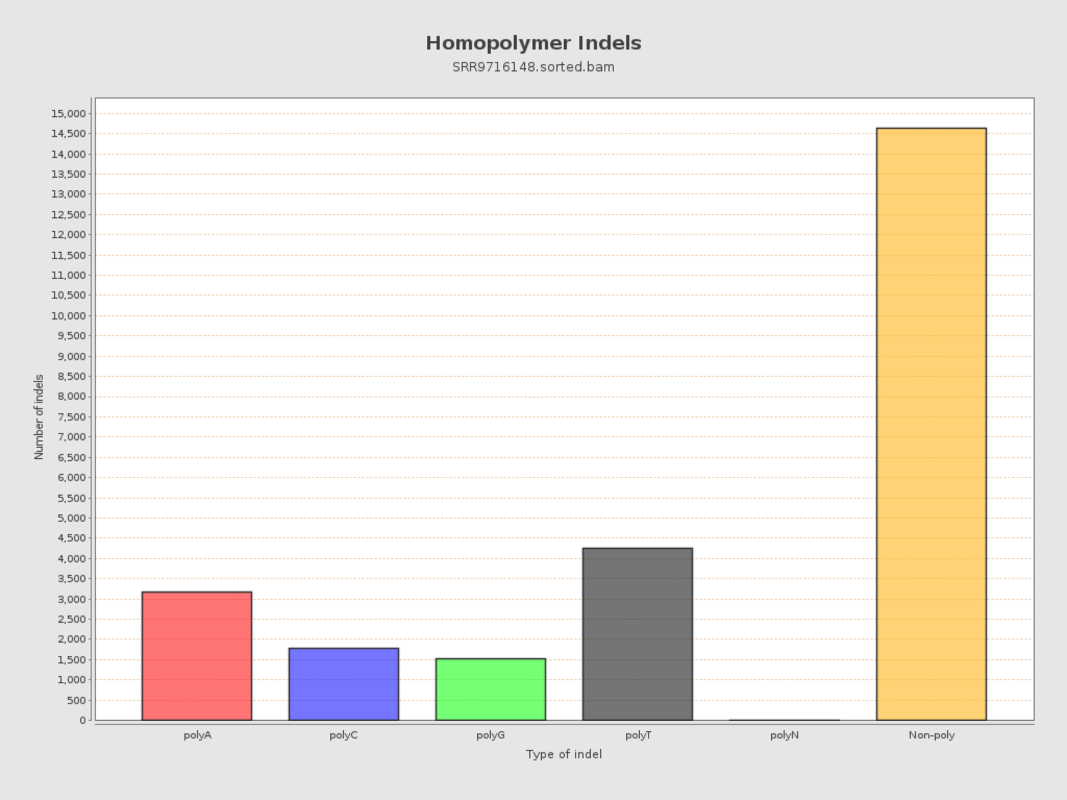
9. Results : Mapped Reads GC-content Distribution



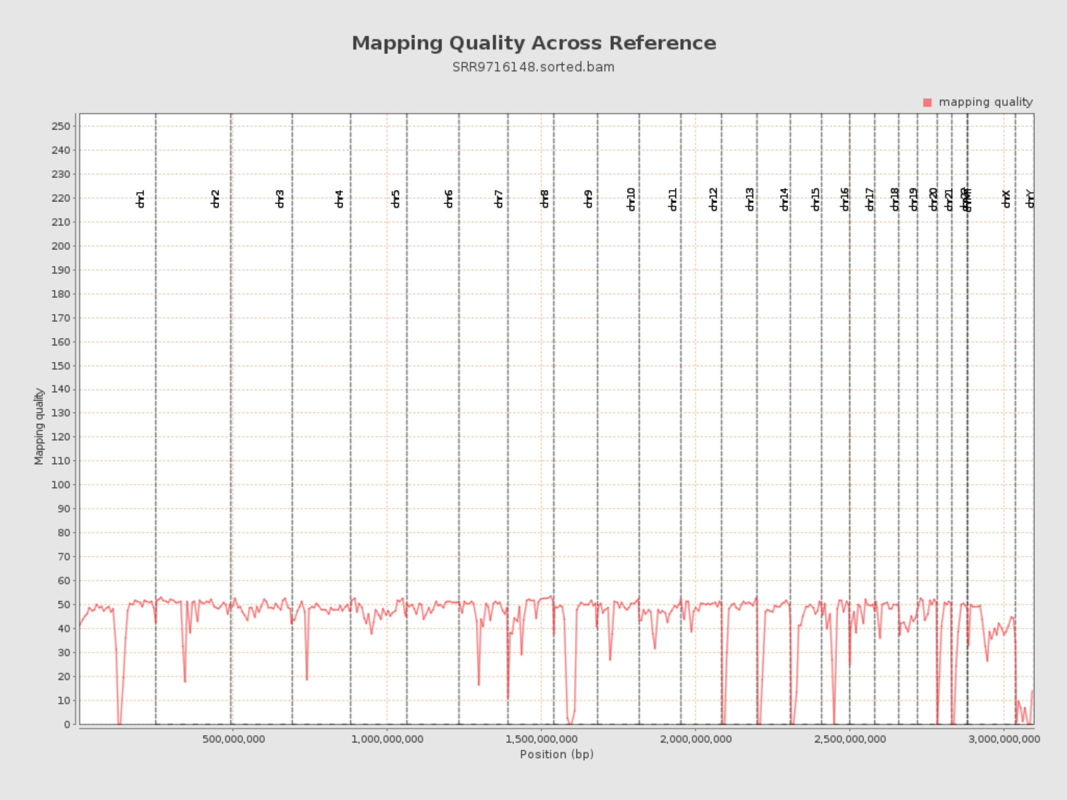
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram