Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:11:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716837.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_SRR9716837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:11:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,085,941
Mapped reads	1,916,691 / 91.89%
Unmapped reads	169,250 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,144 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	133,231 / 6.39%
Duplication rate	5.53%
Clipped reads	1,923,548 / 92.21%

2.2. ACGT Content

Number/percentage of A's	28,532,693 / 25.43%
Number/percentage of C's	22,407,915 / 19.97%
Number/percentage of T's	34,510,291 / 30.76%
Number/percentage of G's	26,731,201 / 23.83%
Number/percentage of N's	888 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3173

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

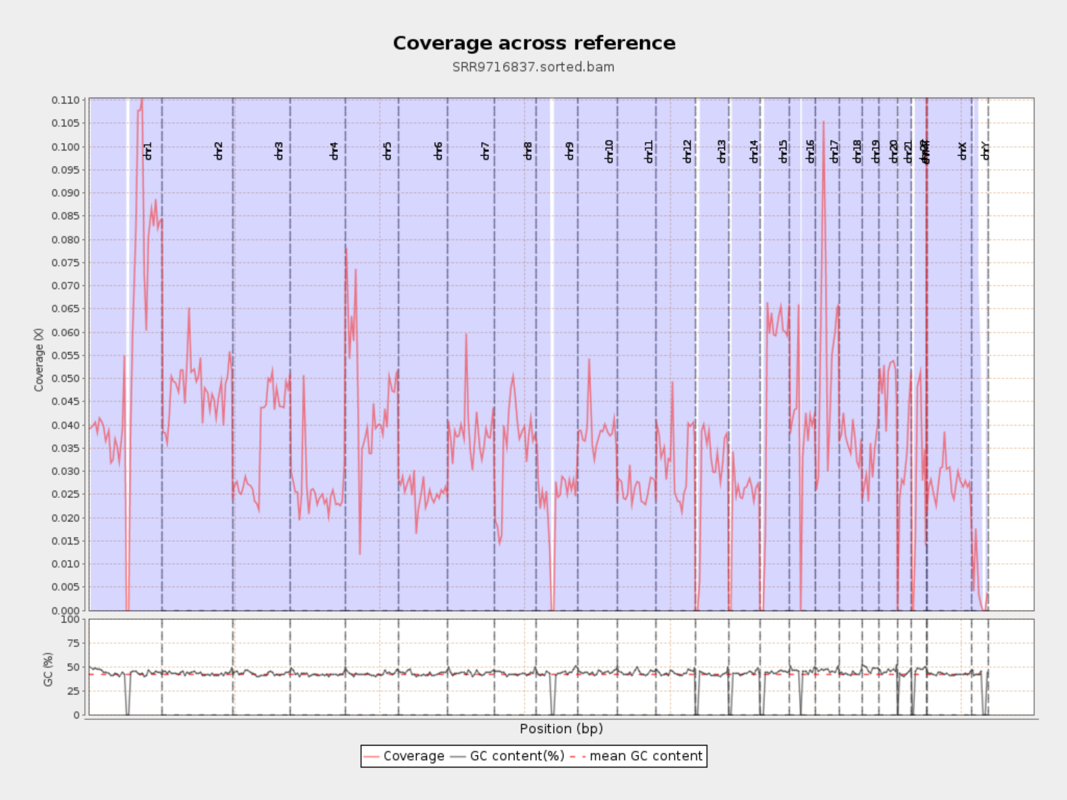
General error rate	0.51%
Mismatches	552,004
Insertions	7,705
Mapped reads with at least one insertion	0.4%
Deletions	19,897
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.71%

2.6. Chromosome stats

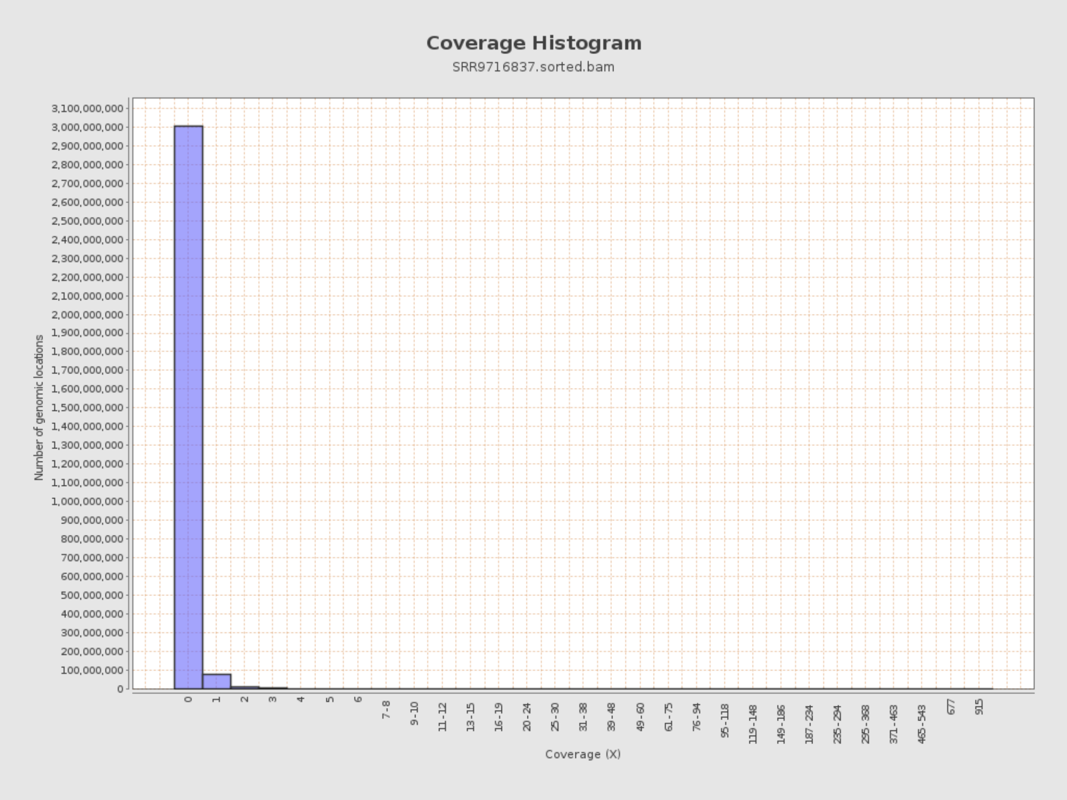
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13796163	0.0554	0.5023
chr2	243199373	11628347	0.0478	0.4759
chr3	198022430	7217582	0.0364	0.2249
chr4	191154276	4901994	0.0256	0.2327
chr5	180915260	8271056	0.0457	0.2531
chr6	171115067	4352566	0.0254	0.2081
chr7	159138663	6100583	0.0383	0.4287

chr8	146364022	5186228	0.0354	0.327
chr9	141213431	3198566	0.0227	0.2347
chr10	135534747	5230645	0.0386	0.3009
chr11	135006516	3532960	0.0262	0.2556
chr12	133851895	4383968	0.0328	0.2156
chr13	115169878	3321324	0.0288	0.2004
chr14	107349540	2501672	0.0233	0.1887
chr15	102531392	5087691	0.0496	0.2634
chr16	90354753	3531268	0.0391	0.2454
chr17	81195210	4595950	0.0566	0.3067
chr18	78077248	2861599	0.0367	0.5062
chr19	59128983	1869930	0.0316	0.3576
chr20	63025520	3142448	0.0499	0.2725
chr21	48129895	1482041	0.0308	0.2271
chr22	51304566	1402236	0.0273	0.1966
chrMT	16571	2186	0.1319	0.4075
chrX	155270560	4323909	0.0278	0.2196
chrY	59373566	291736	0.0049	0.1417

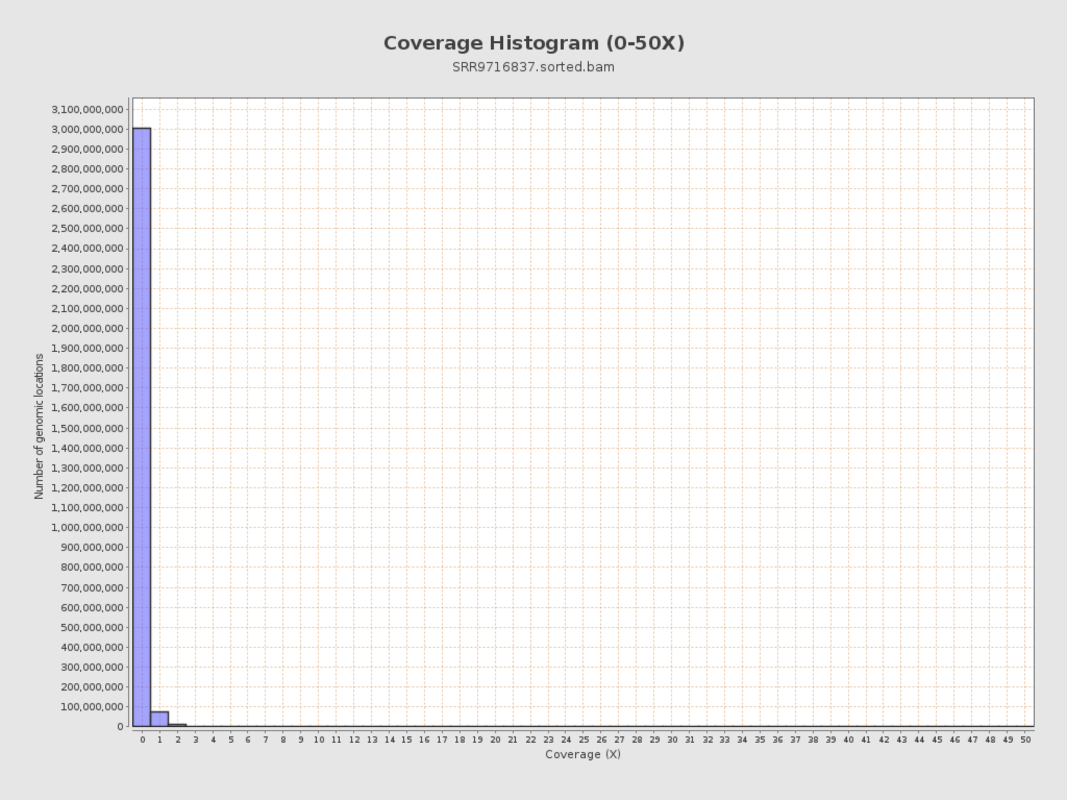
3. Results : Coverage across reference



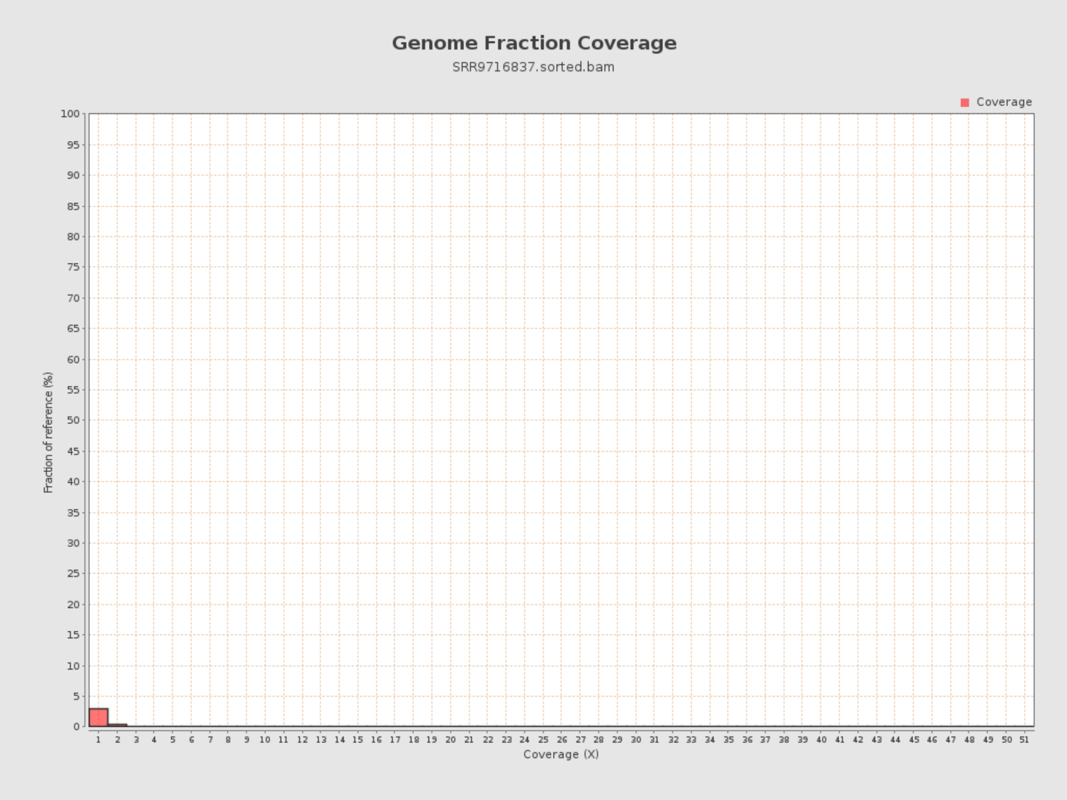
4. Results : Coverage Histogram



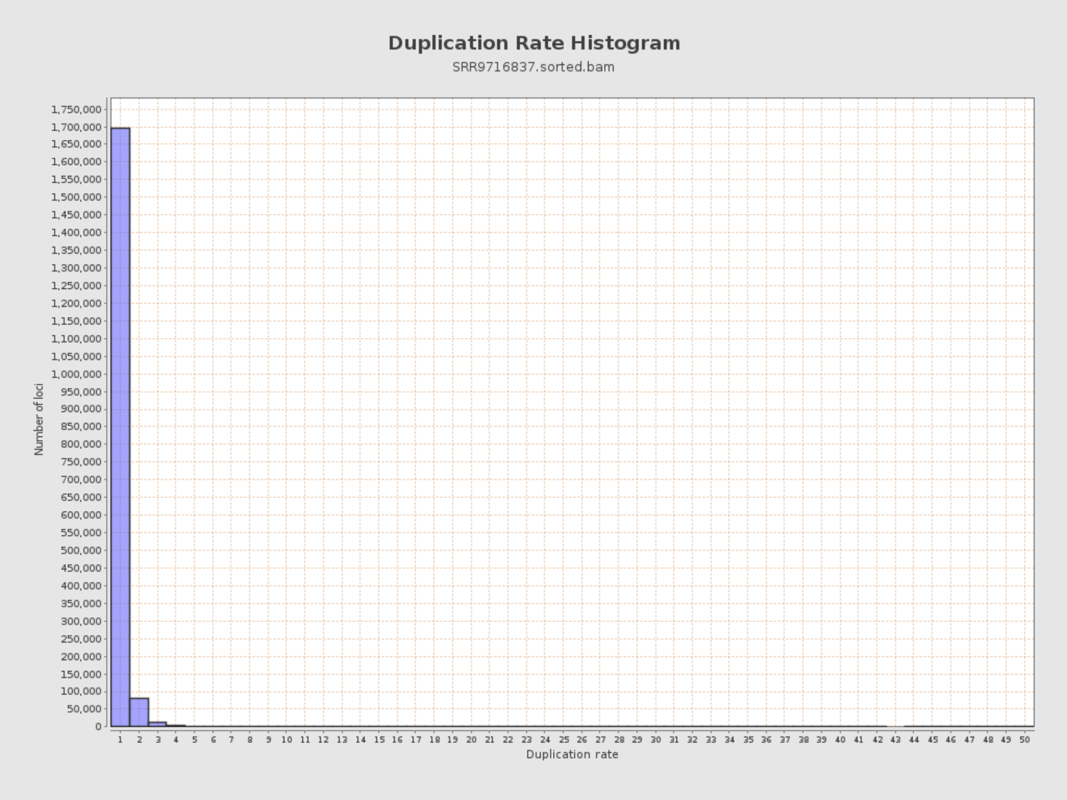
5. Results : Coverage Histogram (0-50X)



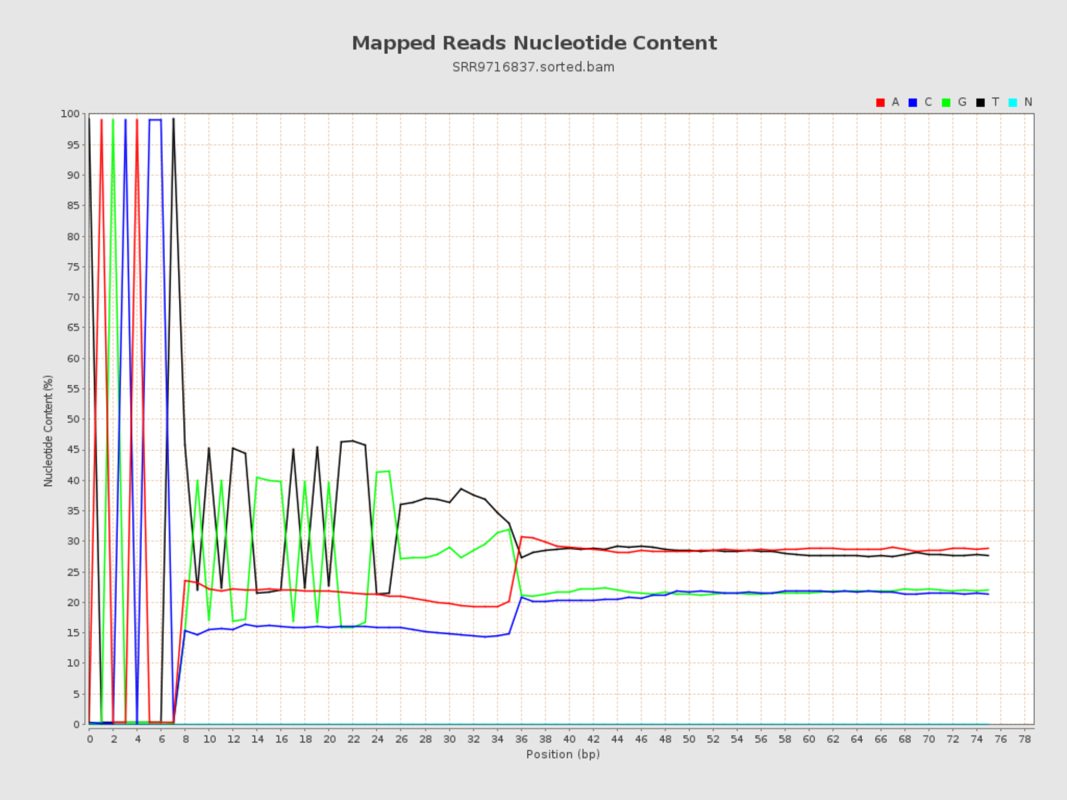
6. Results : Genome Fraction Coverage



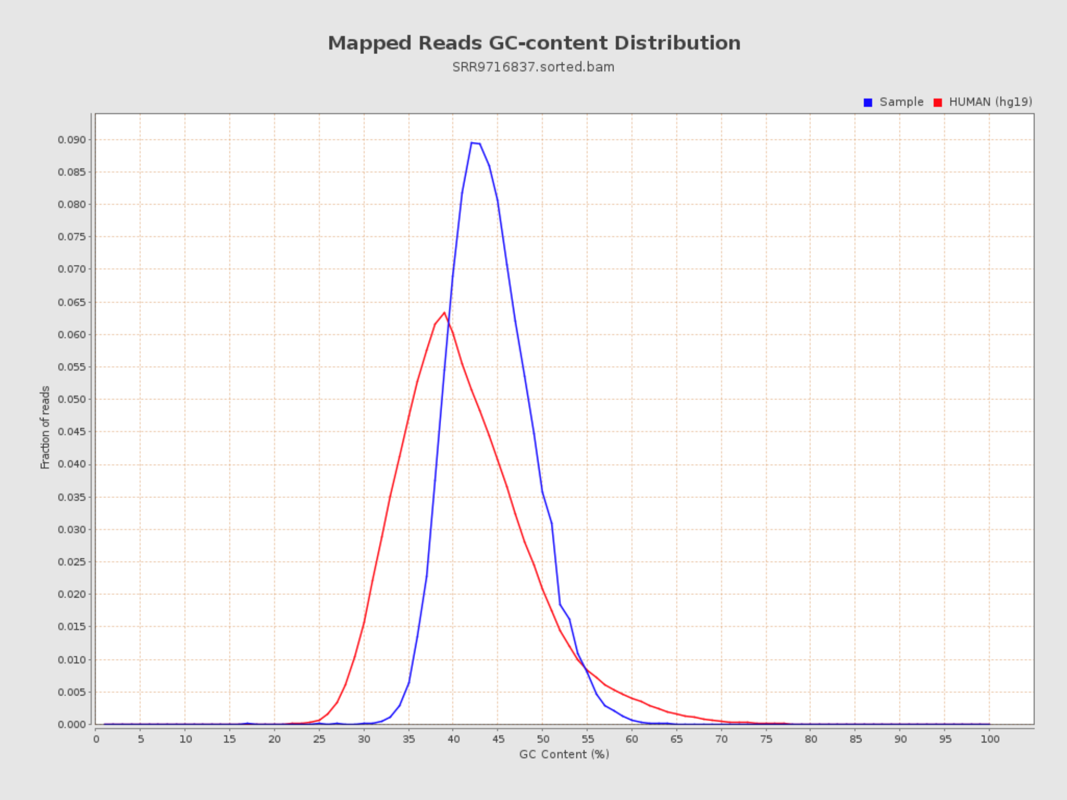
7. Results : Duplication Rate Histogram



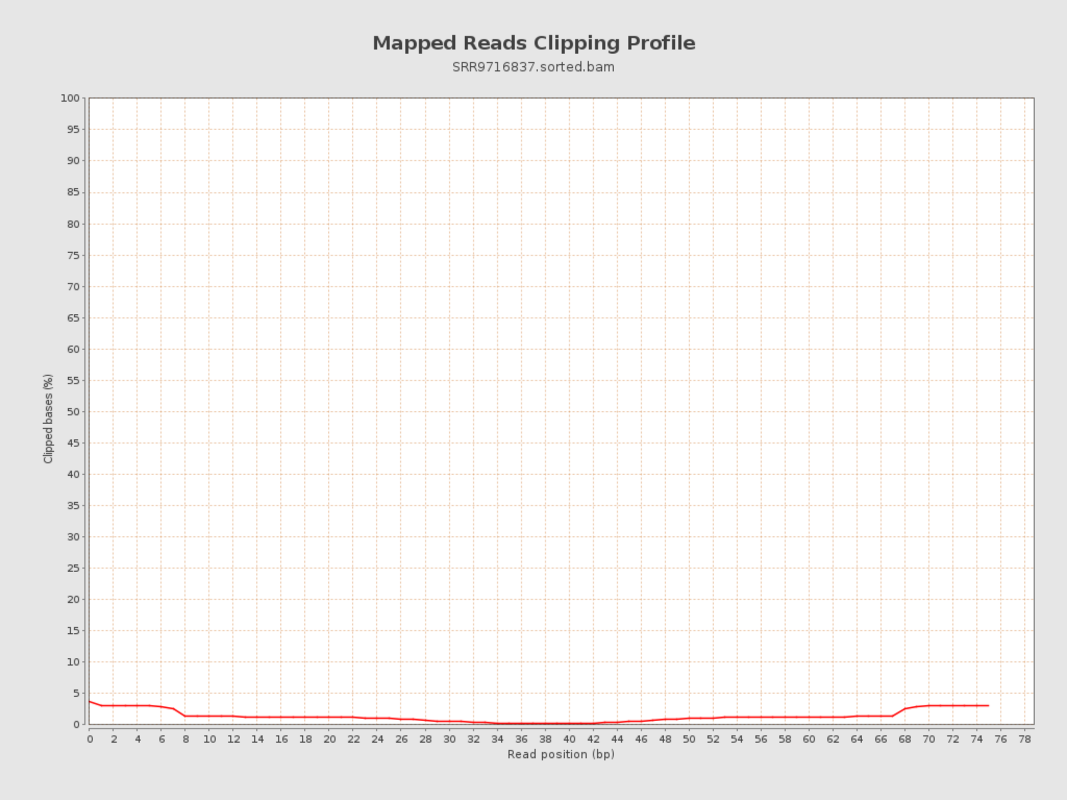
8. Results : Mapped Reads Nucleotide Content



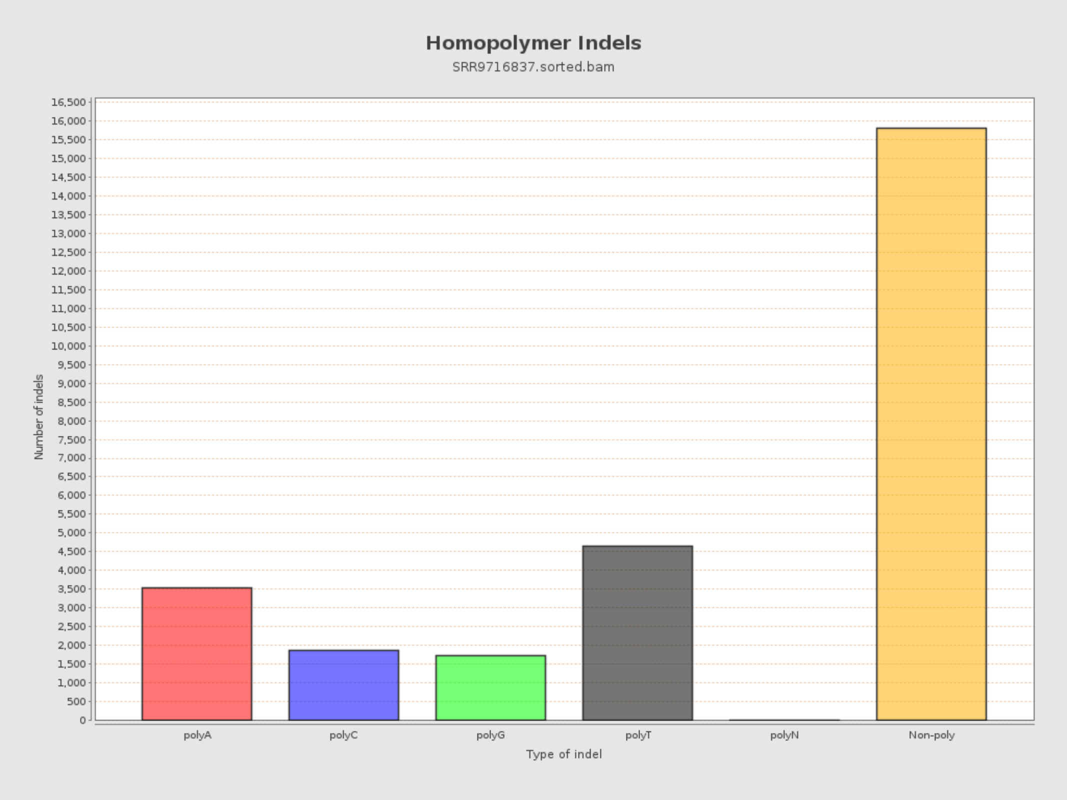
9. Results : Mapped Reads GC-content Distribution



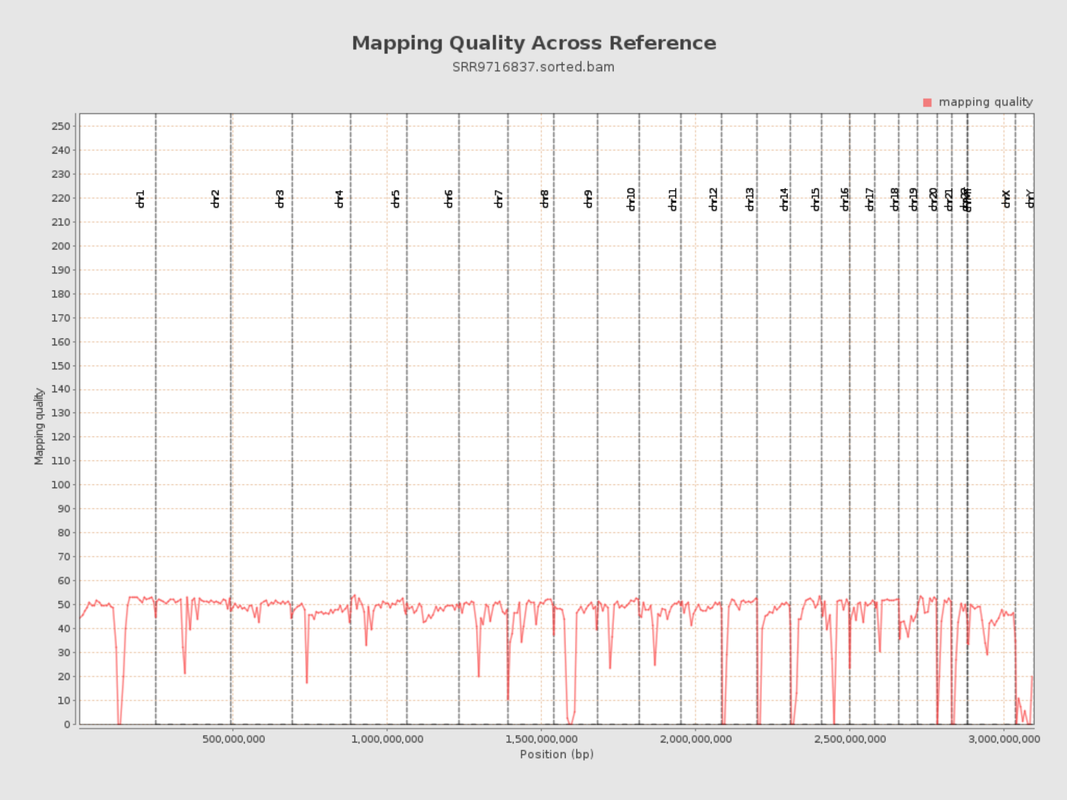
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram