Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:24:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818921.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_SRR1818921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,390,210
Mapped reads	2,356,910 / 98.61%
Unmapped reads	33,300 / 1.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,395 / 1.44%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	694,582 / 29.06%
Duplication rate	25.04%
Clipped reads	2,366,680 / 99.02%

2.2. ACGT Content

Number/percentage of A's	63,425,063 / 29.06%
Number/percentage of C's	44,820,746 / 20.53%
Number/percentage of T's	61,248,093 / 28.06%
Number/percentage of G's	48,773,376 / 22.35%
Number/percentage of N's	3,058 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0706

Standard Deviation	0.8641

2.4. Mapping Quality

Mean Mapping Quality	49.3

2.5. Mismatches and indels

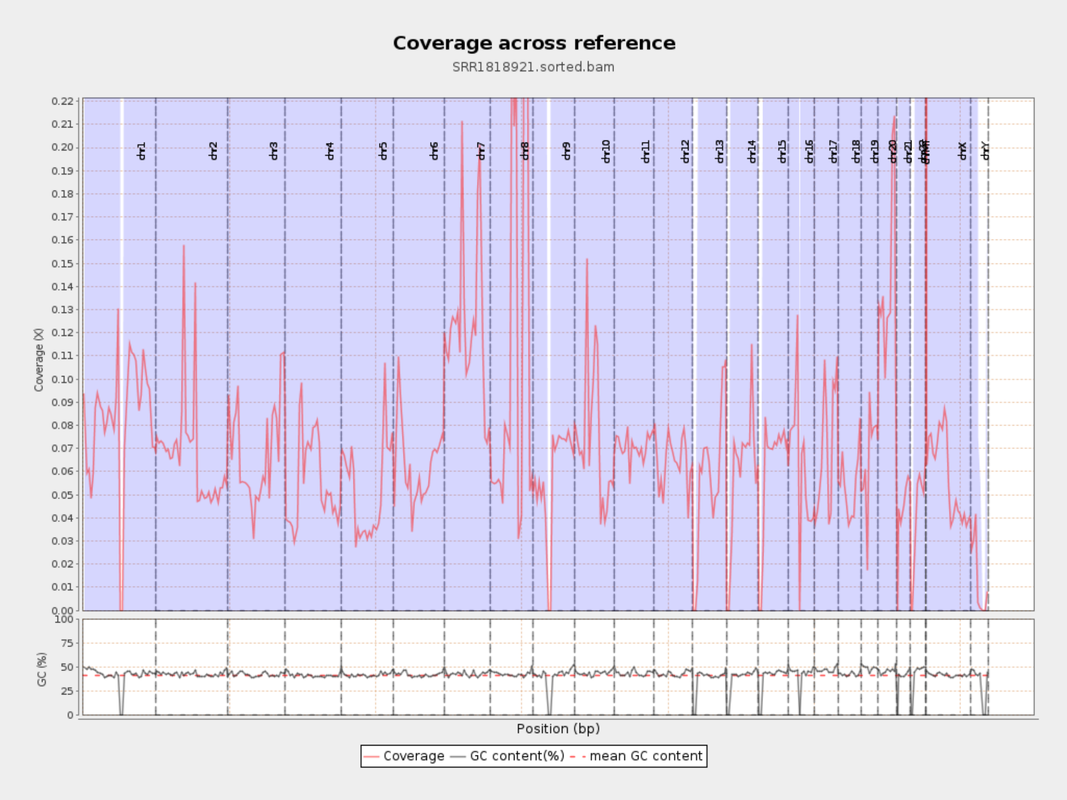
General error rate	0.64%
Mismatches	1,313,068
Insertions	32,002
Mapped reads with at least one insertion	1.31%
Deletions	75,092
Mapped reads with at least one deletion	3.09%
Homopolymer indels	39.66%

2.6. Chromosome stats

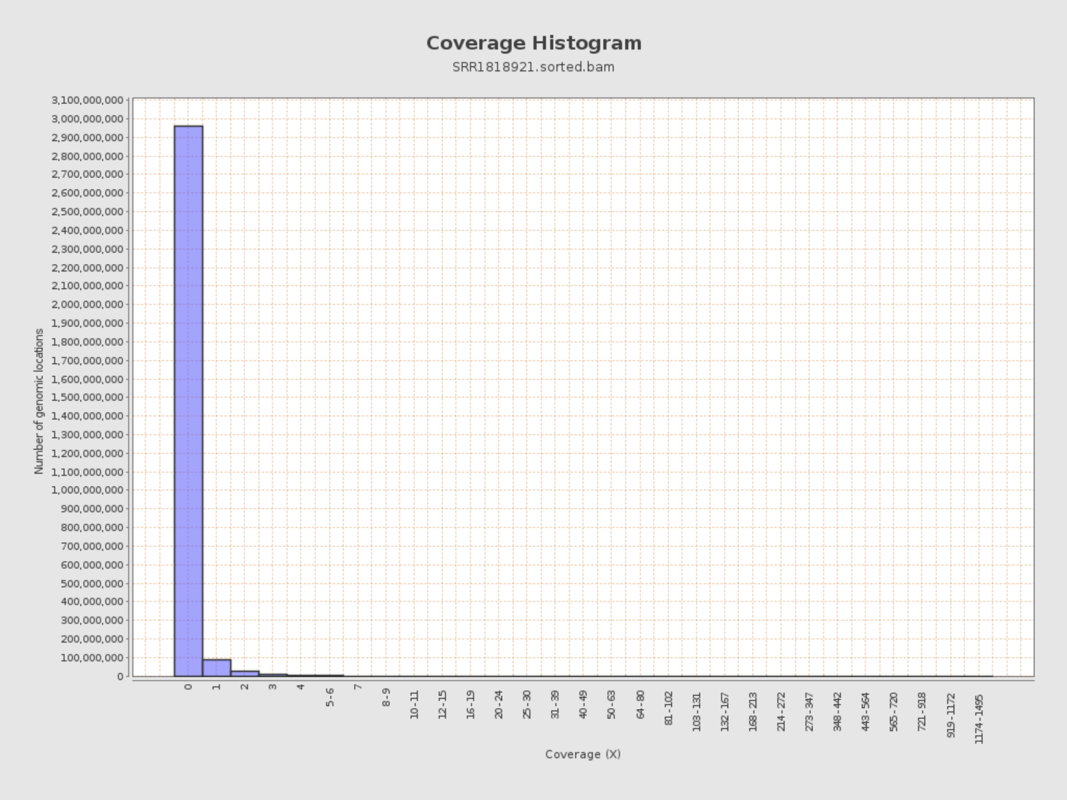
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20648160	0.0828	1.2063
chr2	243199373	16473259	0.0677	1.3746
chr3	198022430	13593048	0.0686	0.3879
chr4	191154276	10726837	0.0561	0.496
chr5	180915260	9492158	0.0525	0.3874
chr6	171115067	10779821	0.063	0.4235
chr7	159138663	19661748	0.1236	1.9425

chr8	146364022	19088070	0.1304	0.6865
chr9	141213431	8156473	0.0578	0.6667
chr10	135534747	9978656	0.0736	1.0002
chr11	135006516	9548933	0.0707	0.504
chr12	133851895	8639237	0.0645	0.3832
chr13	115169878	6596681	0.0573	0.3525
chr14	107349540	6469578	0.0603	0.4125
chr15	102531392	6124637	0.0597	0.3611
chr16	90354753	5517702	0.0611	1.0305
chr17	81195210	5544546	0.0683	0.5241
chr18	78077248	4205112	0.0539	0.7694
chr19	59128983	3867044	0.0654	1.0914
chr20	63025520	9127399	0.1448	0.6324
chr21	48129895	2116481	0.044	0.3643
chr22	51304566	1991632	0.0388	0.346
chrMT	16571	285956	17.2564	11.4299
chrX	155270560	8993353	0.0579	0.4344
chrY	59373566	790885	0.0133	1.1306

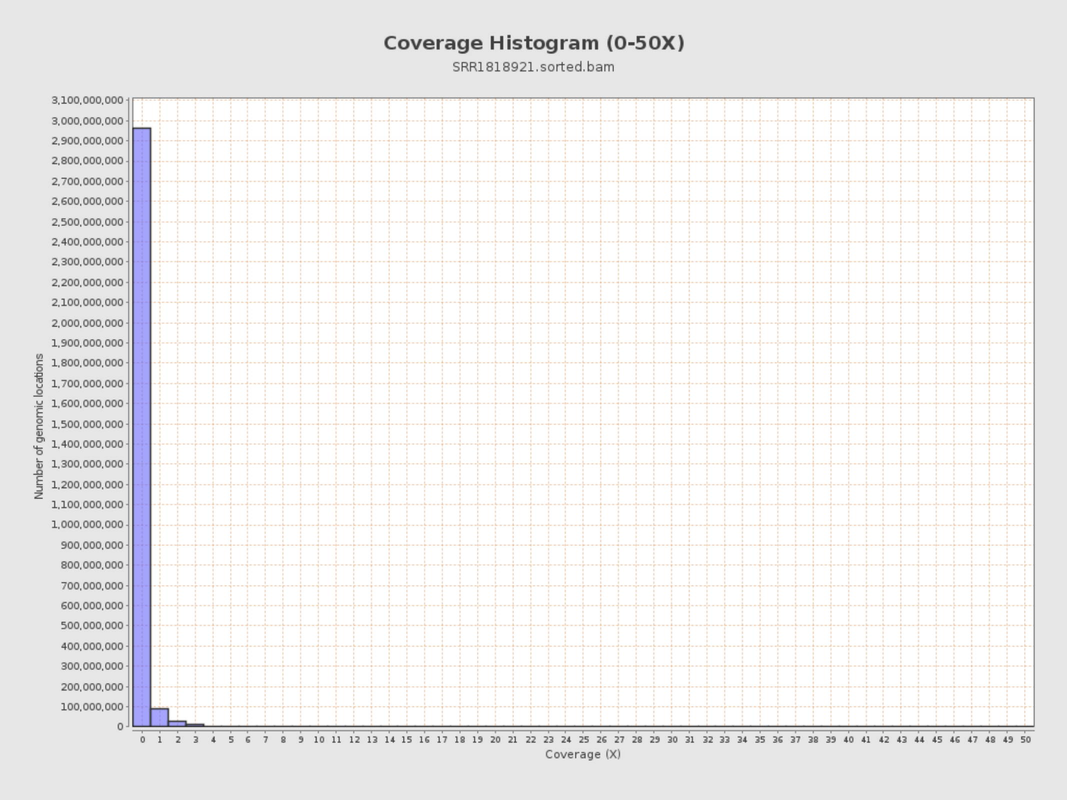
3. Results : Coverage across reference



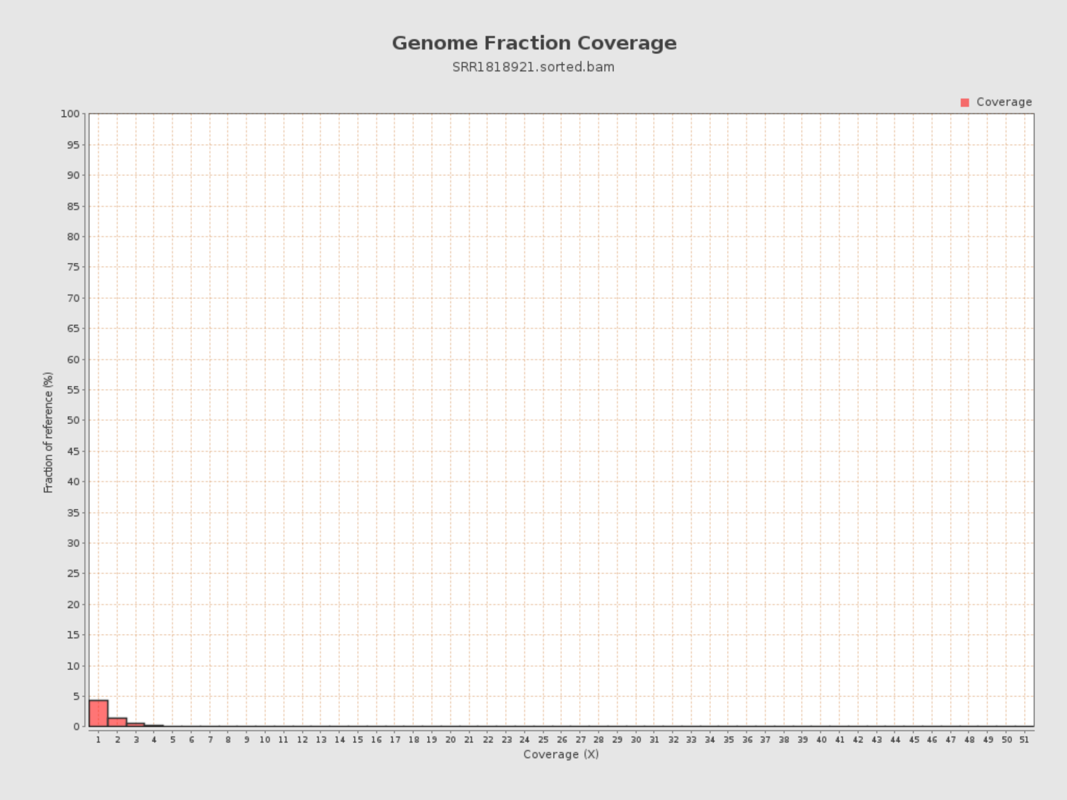
4. Results : Coverage Histogram



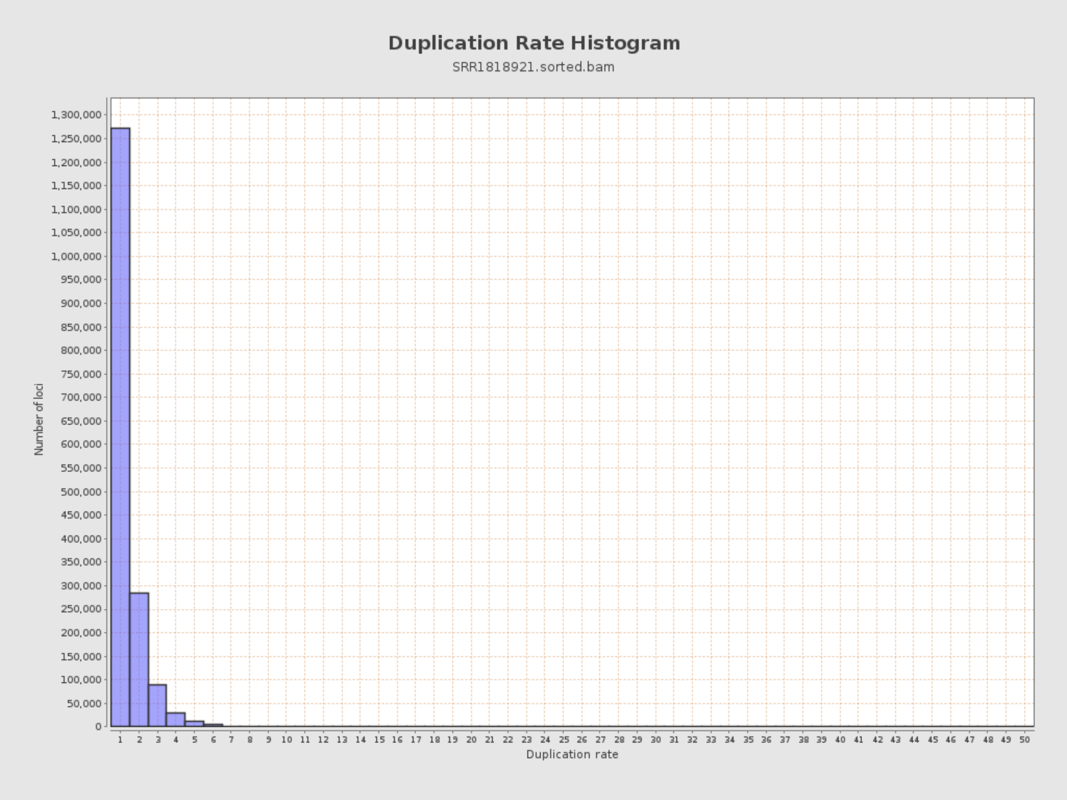
5. Results : Coverage Histogram (0-50X)



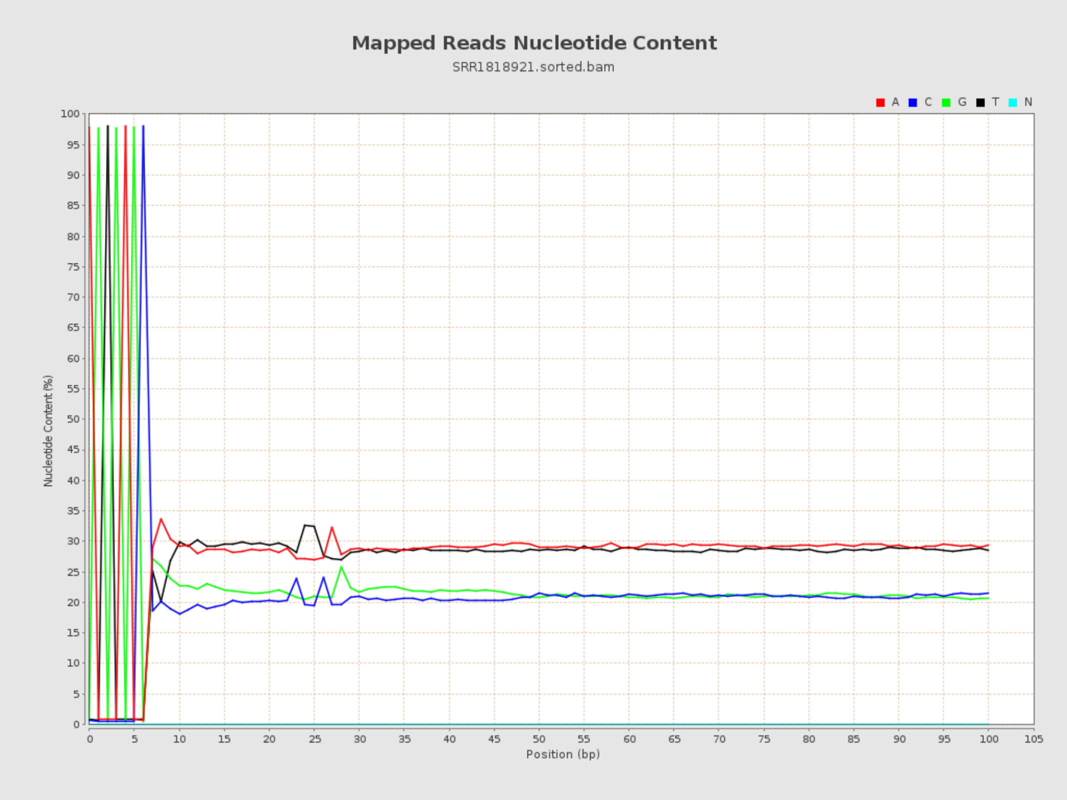
6. Results : Genome Fraction Coverage



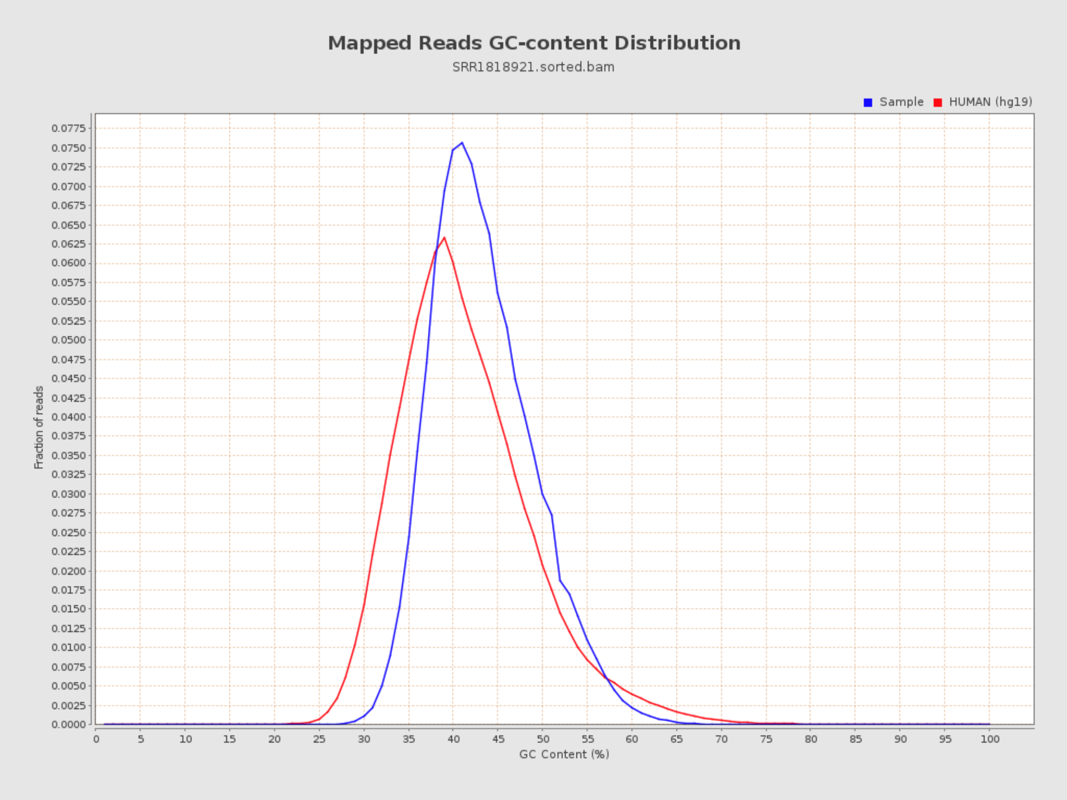
7. Results : Duplication Rate Histogram



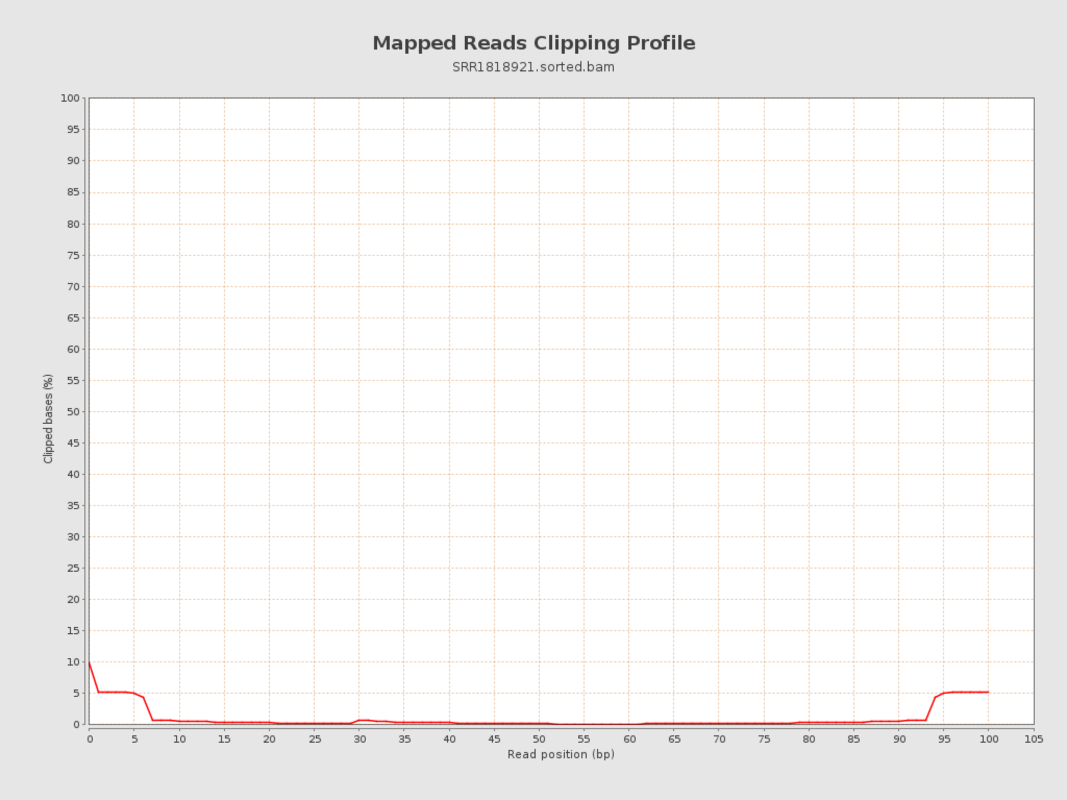
8. Results : Mapped Reads Nucleotide Content



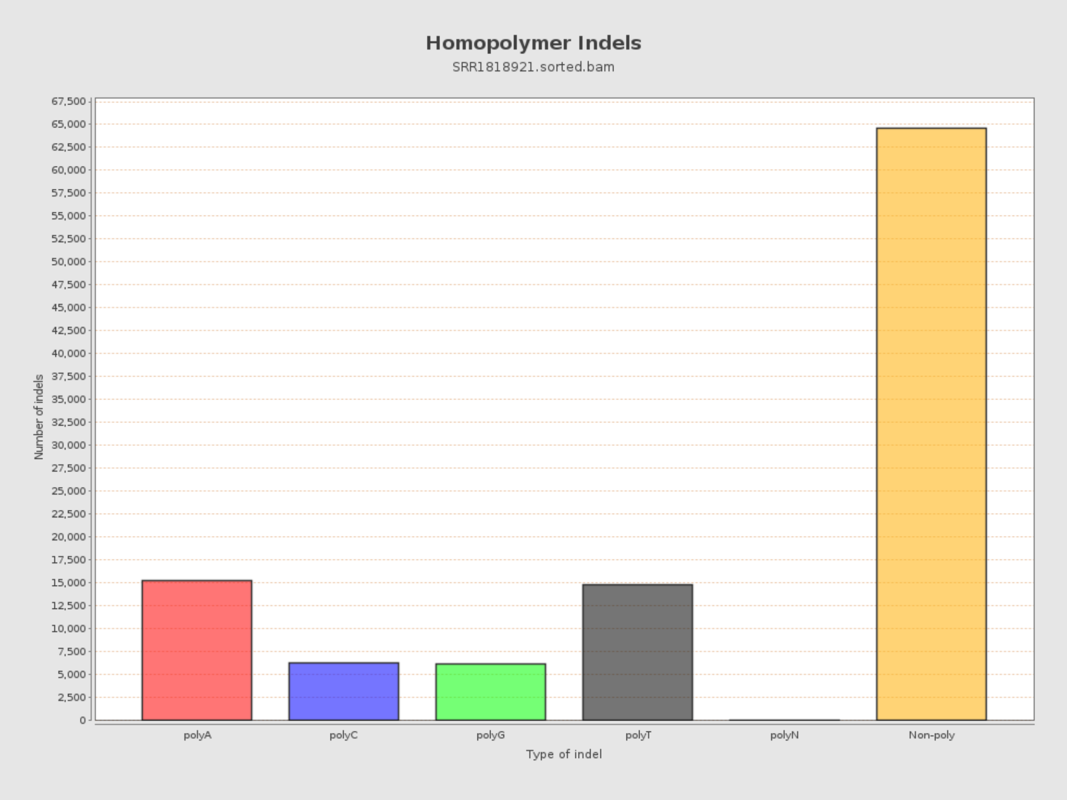
9. Results : Mapped Reads GC-content Distribution



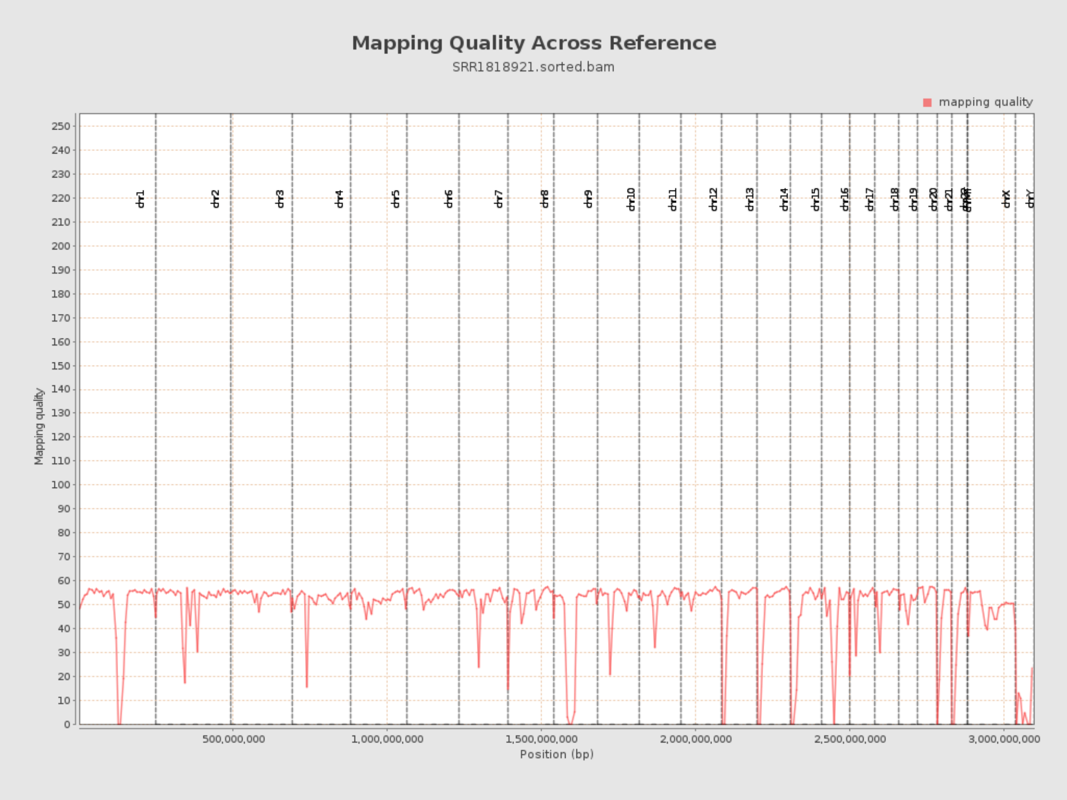
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram