Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:59:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818756.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_SRR1818756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:59:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	938,630
Mapped reads	757,962 / 80.75%
Unmapped reads	180,668 / 19.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,824 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	259,087 / 27.6%
Duplication rate	30.76%
Clipped reads	758,115 / 80.77%

2.2. ACGT Content

Number/percentage of A's	15,276,790 / 29.71%
Number/percentage of C's	10,455,025 / 20.33%
Number/percentage of T's	14,716,348 / 28.62%
Number/percentage of G's	10,972,352 / 21.34%
Number/percentage of N's	3,321 / 0.01%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.2382

2.4. Mapping Quality

Mean Mapping Quality	47.66

2.5. Mismatches and indels

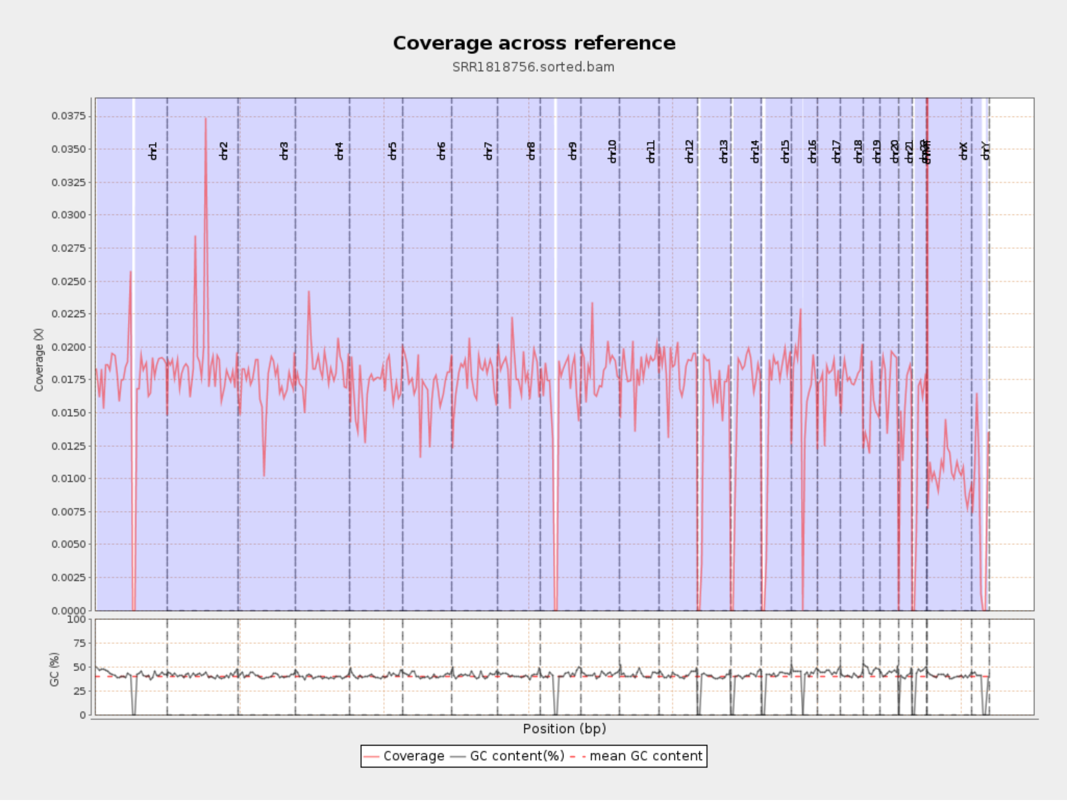
General error rate	0.53%
Mismatches	261,892
Insertions	5,626
Mapped reads with at least one insertion	0.74%
Deletions	13,379
Mapped reads with at least one deletion	1.75%
Homopolymer indels	42.6%

2.6. Chromosome stats

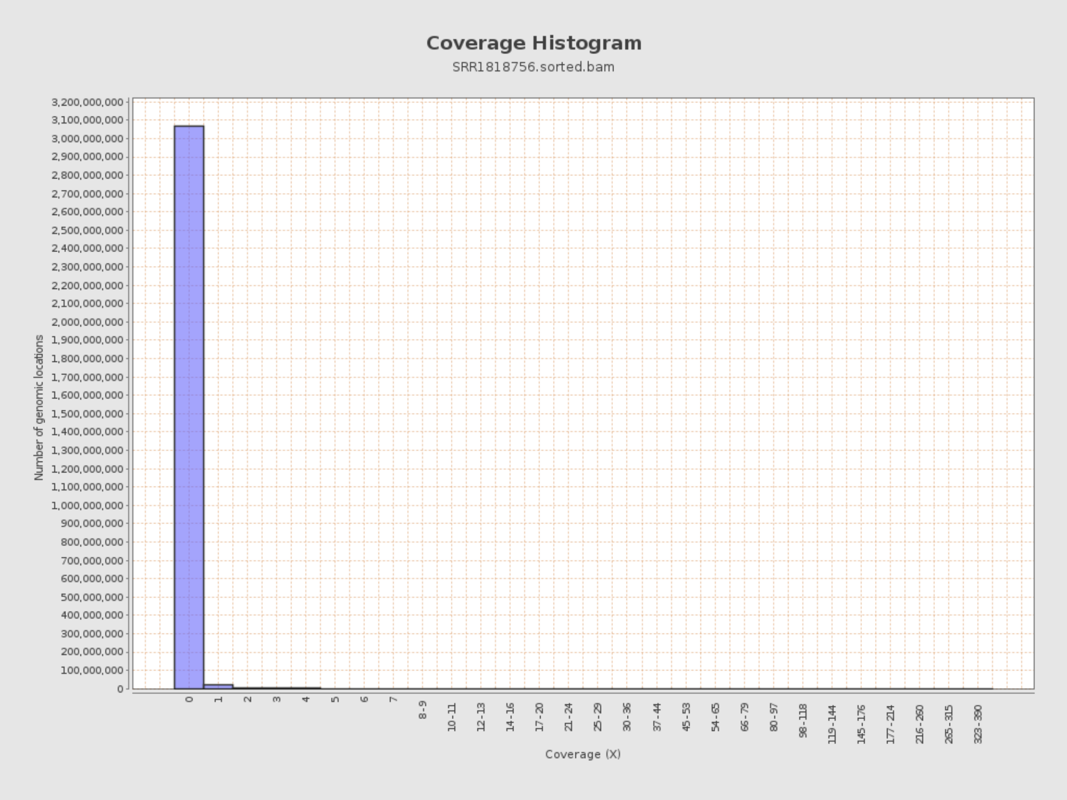
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4271485	0.0171	0.2811
chr2	243199373	4642517	0.0191	0.3481
chr3	198022430	3390648	0.0171	0.2019
chr4	191154276	3525254	0.0184	0.2227
chr5	180915260	3070992	0.017	0.2041
chr6	171115067	2916688	0.017	0.2093
chr7	159138663	2802973	0.0176	0.2283

chr8	146364022	2675692	0.0183	0.2274
chr9	141213431	2199997	0.0156	0.2163
chr10	135534747	2494285	0.0184	0.2644
chr11	135006516	2470925	0.0183	0.2258
chr12	133851895	2462575	0.0184	0.2183
chr13	115169878	1670189	0.0145	0.1866
chr14	107349540	1655340	0.0154	0.2039
chr15	102531392	1532391	0.0149	0.1888
chr16	90354753	1455154	0.0161	0.2569
chr17	81195210	1401447	0.0173	0.2125
chr18	78077248	1389937	0.0178	0.2911
chr19	59128983	866512	0.0147	0.2421
chr20	63025520	1115334	0.0177	0.2125
chr21	48129895	694992	0.0144	0.1991
chr22	51304566	604707	0.0118	0.1771
chrMT	16571	63842	3.8526	3.8406
chrX	155270560	1618303	0.0104	0.1645
chrY	59373566	453321	0.0076	0.3141

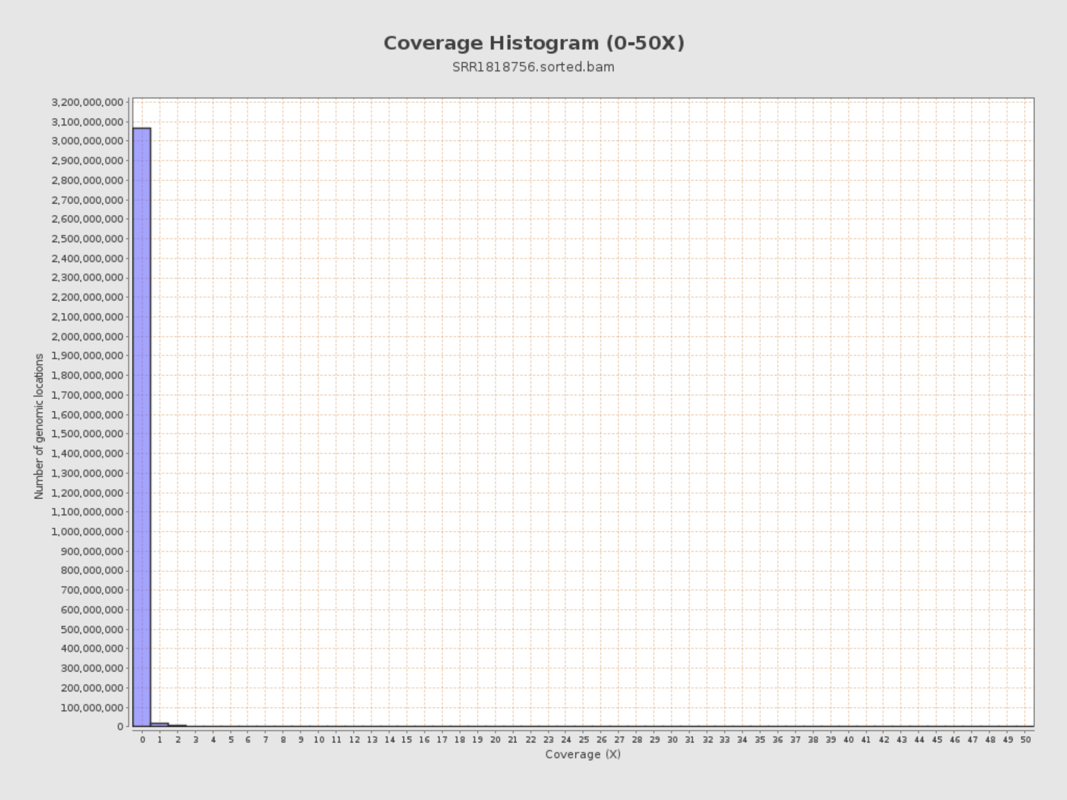
3. Results : Coverage across reference



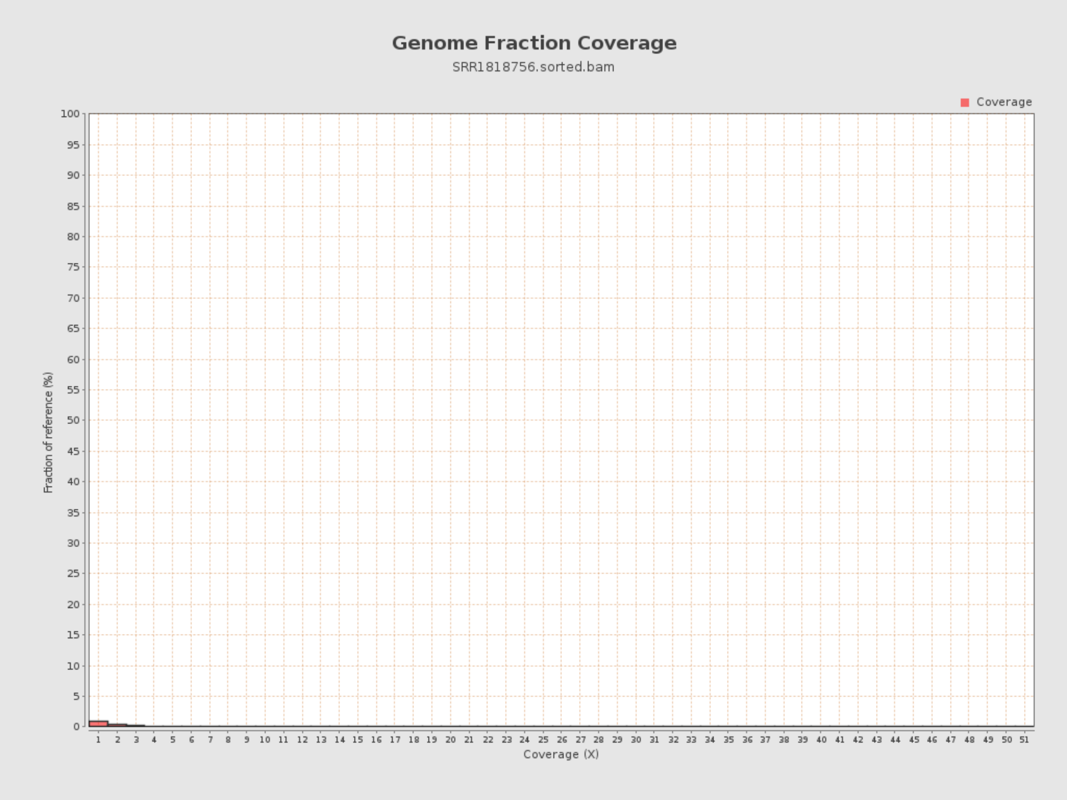
4. Results : Coverage Histogram



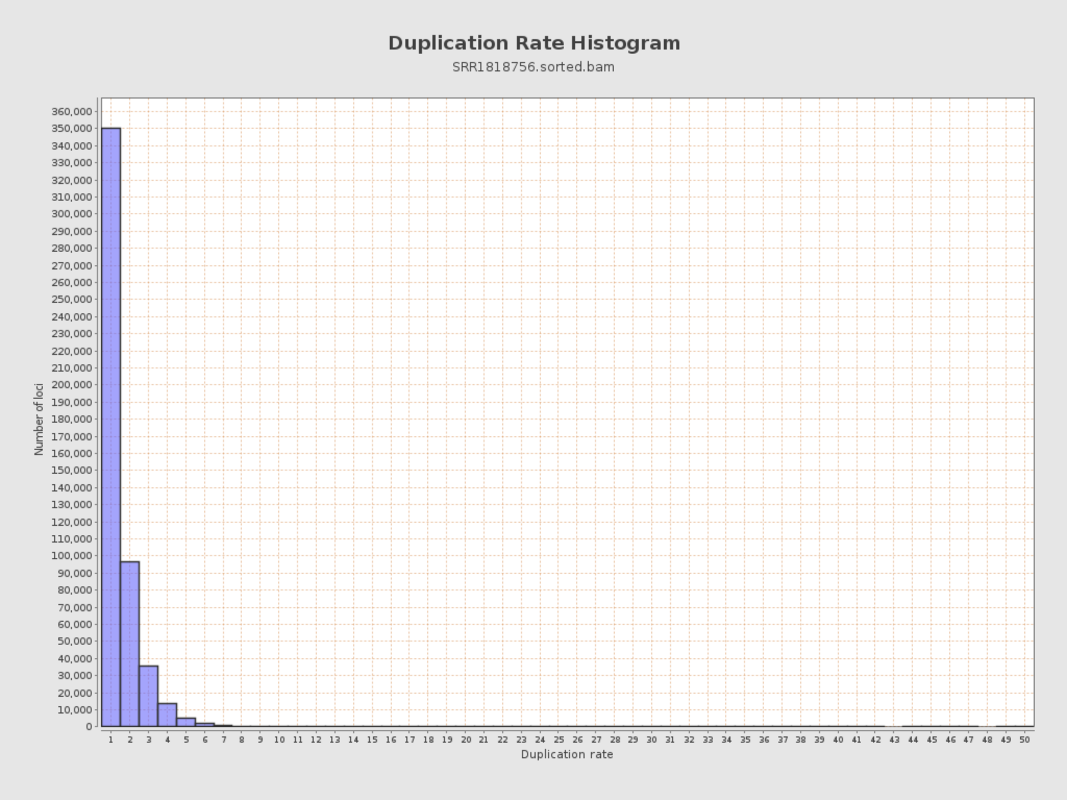
5. Results : Coverage Histogram (0-50X)



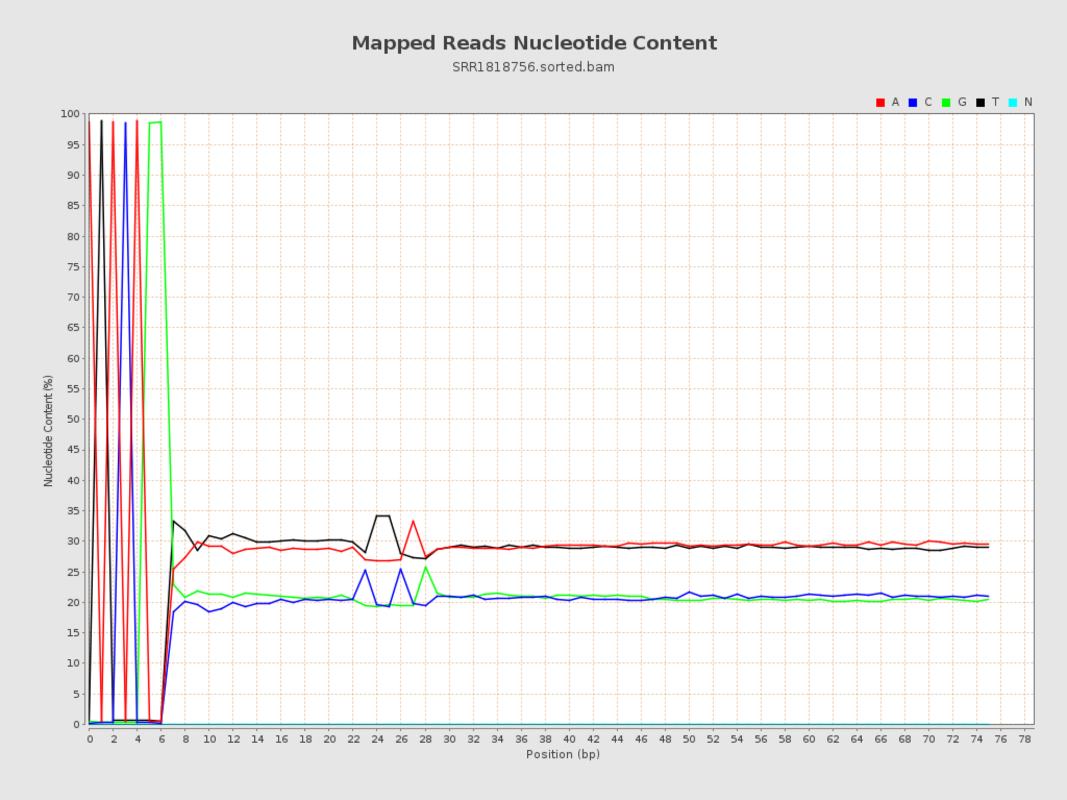
6. Results : Genome Fraction Coverage



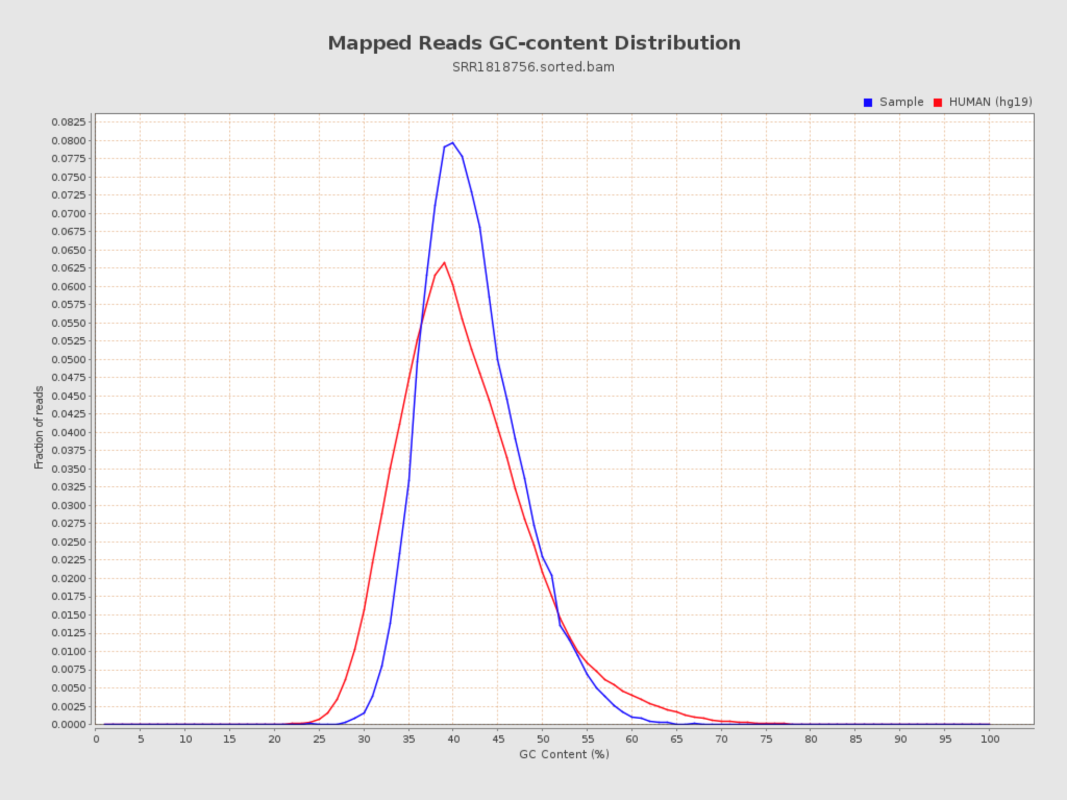
7. Results : Duplication Rate Histogram



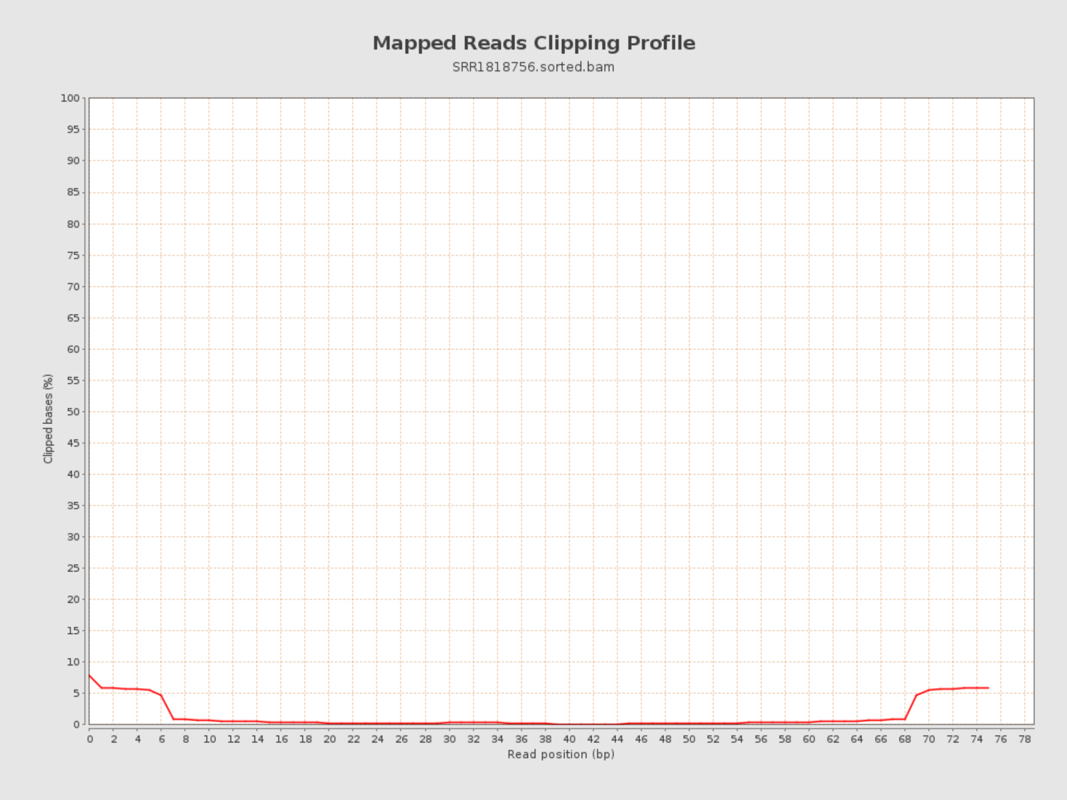
8. Results : Mapped Reads Nucleotide Content



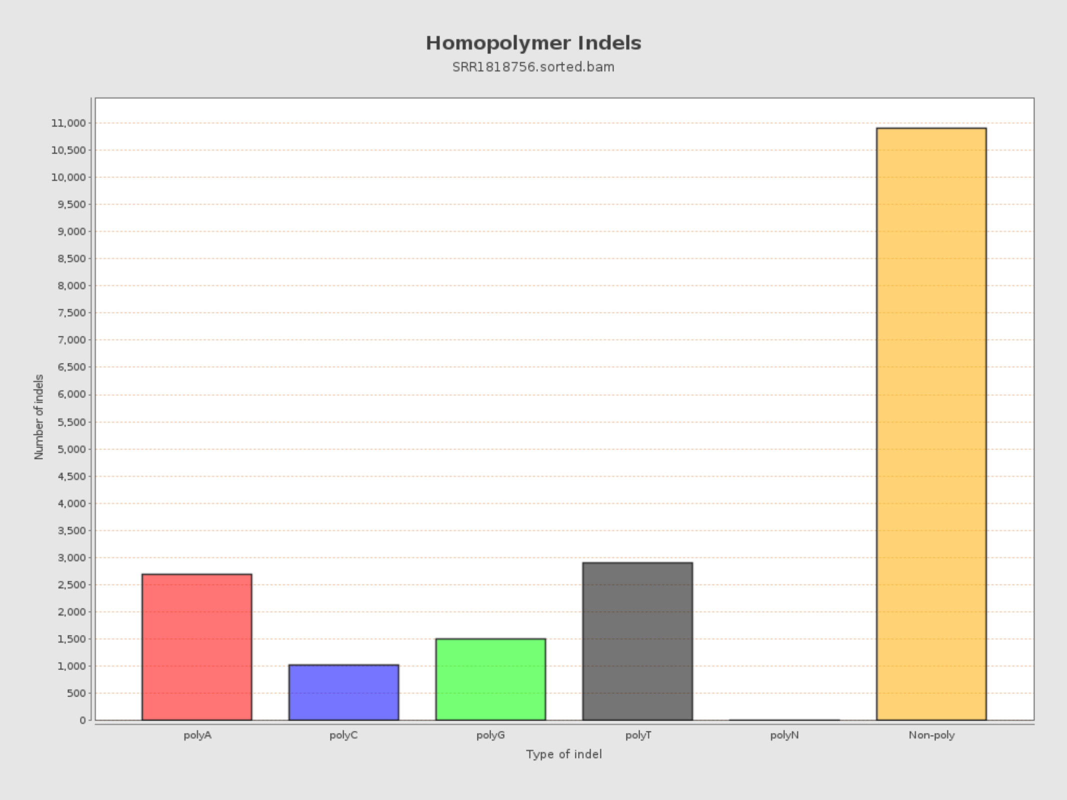
9. Results : Mapped Reads GC-content Distribution



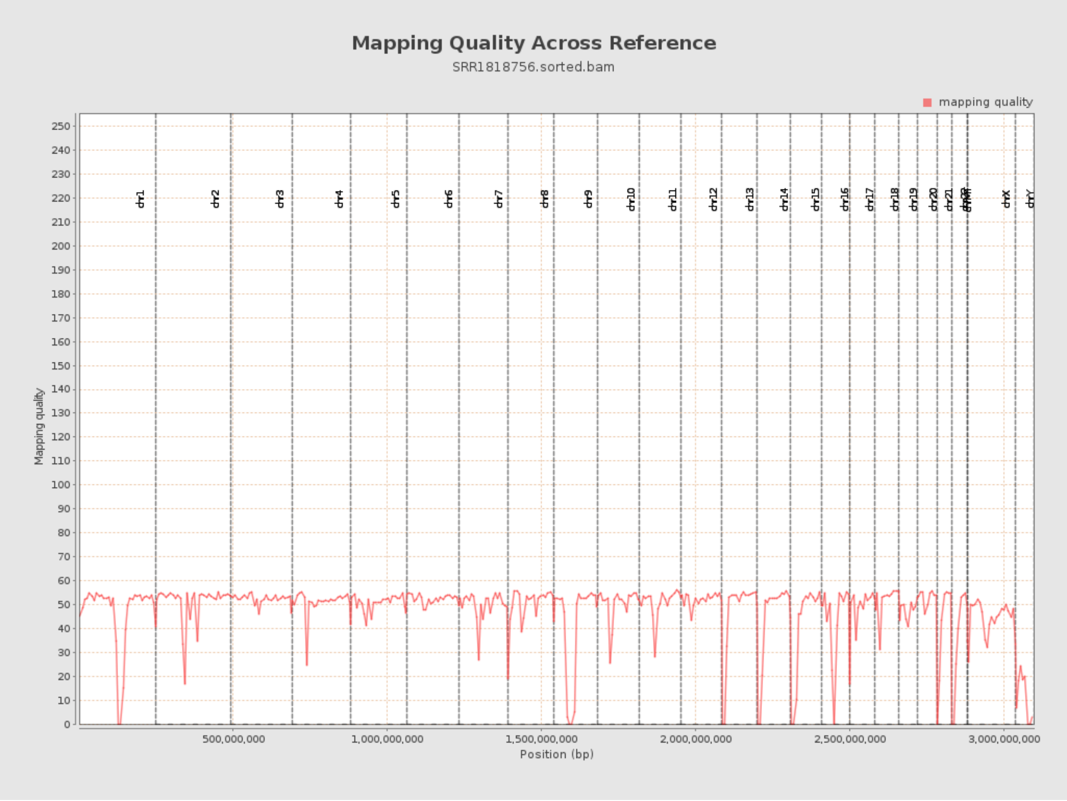
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram