Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:16:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818787.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_SRR1818787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:16:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	177,915
Mapped reads	172,942 / 97.2%
Unmapped reads	4,973 / 2.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,303 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	24,840 / 13.96%
Duplication rate	12.78%
Clipped reads	173,162 / 97.33%

2.2. ACGT Content

Number/percentage of A's	3,134,061 / 26.71%
Number/percentage of C's	2,578,676 / 21.98%
Number/percentage of T's	3,385,429 / 28.85%
Number/percentage of G's	2,635,368 / 22.46%
Number/percentage of N's	732 / 0.01%
GC Percentage	44.43%

2.3. Coverage

Mean	0.0038

Standard Deviation	0.0835

2.4. Mapping Quality

Mean Mapping Quality	47.38

2.5. Mismatches and indels

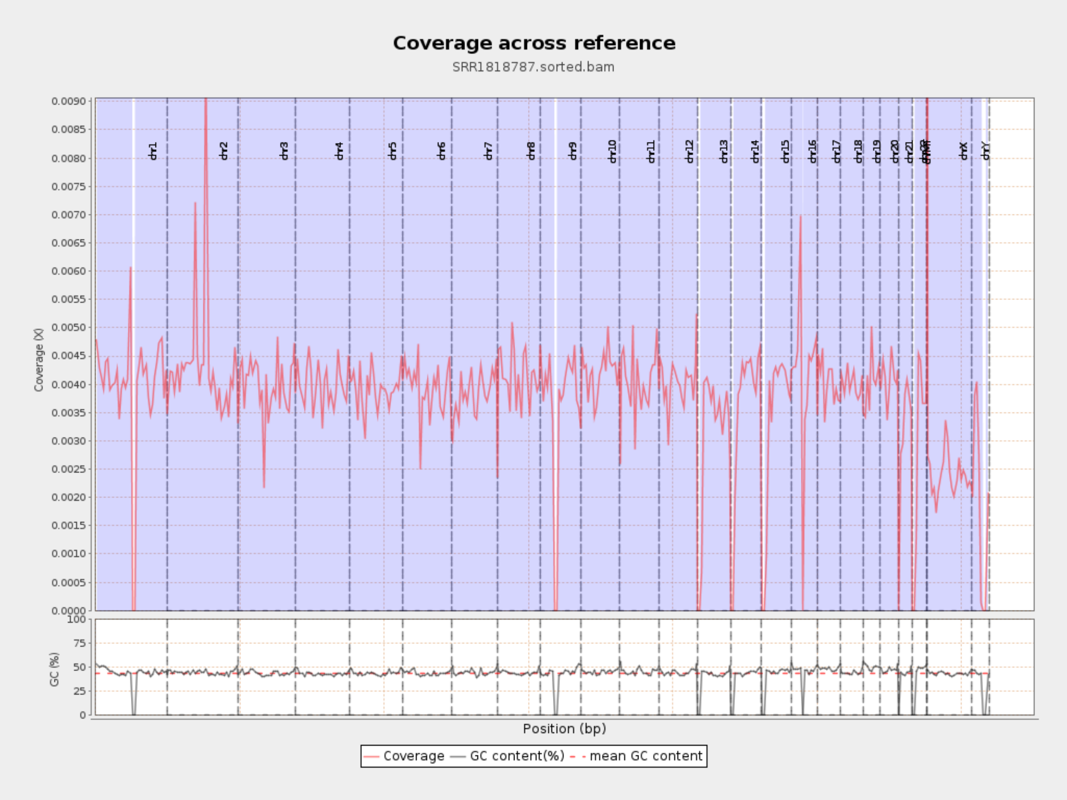
General error rate	0.53%
Mismatches	59,507
Insertions	1,216
Mapped reads with at least one insertion	0.7%
Deletions	3,040
Mapped reads with at least one deletion	1.74%
Homopolymer indels	40.44%

2.6. Chromosome stats

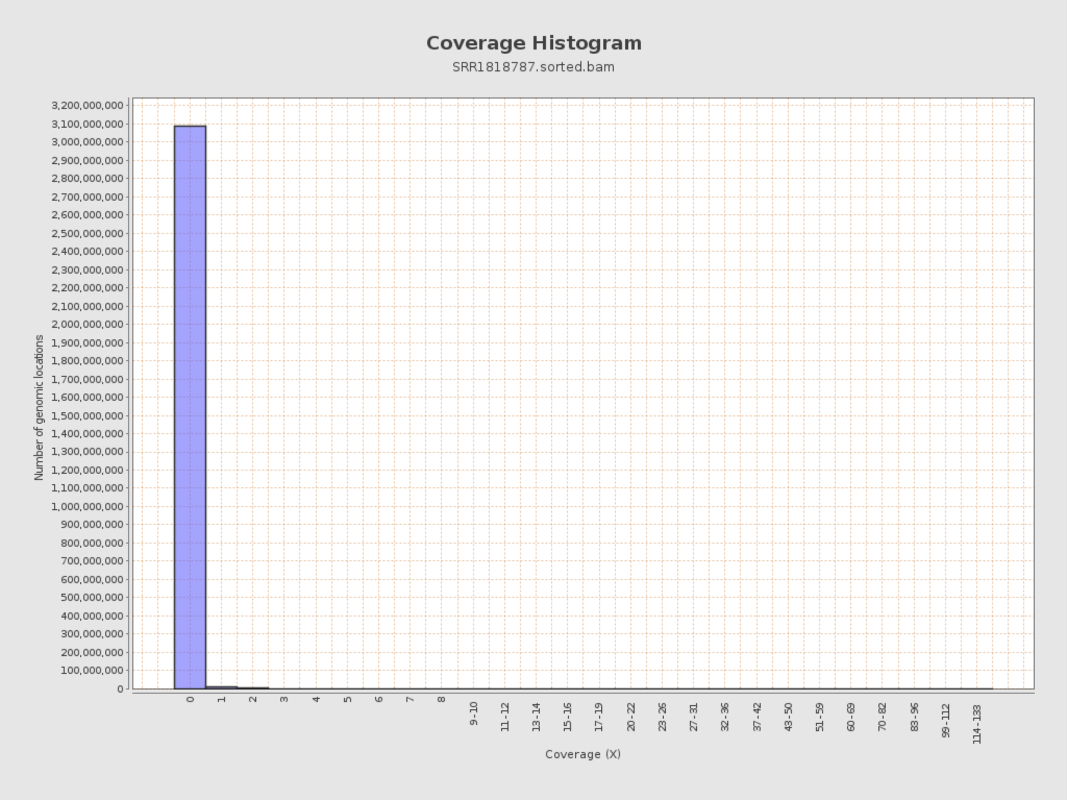
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	981614	0.0039	0.092
chr2	243199373	1063145	0.0044	0.1234
chr3	198022430	784892	0.004	0.0748
chr4	191154276	762147	0.004	0.0764
chr5	180915260	708665	0.0039	0.0748
chr6	171115067	672903	0.0039	0.0774
chr7	159138663	613272	0.0039	0.0764

chr8	146364022	607021	0.0041	0.0789
chr9	141213431	507976	0.0036	0.0777
chr10	135534747	573070	0.0042	0.0886
chr11	135006516	550999	0.0041	0.0779
chr12	133851895	538551	0.004	0.0777
chr13	115169878	353482	0.0031	0.0652
chr14	107349540	378102	0.0035	0.076
chr15	102531392	334098	0.0033	0.0672
chr16	90354753	373982	0.0041	0.0922
chr17	81195210	326754	0.004	0.0771
chr18	78077248	312909	0.004	0.0845
chr19	59128983	239114	0.004	0.0853
chr20	63025520	257495	0.0041	0.0784
chr21	48129895	151346	0.0031	0.0659
chr22	51304566	144729	0.0028	0.0653
chrMT	16571	19984	1.206	1.837
chrX	155270560	373013	0.0024	0.0611
chrY	59373566	109953	0.0019	0.1201

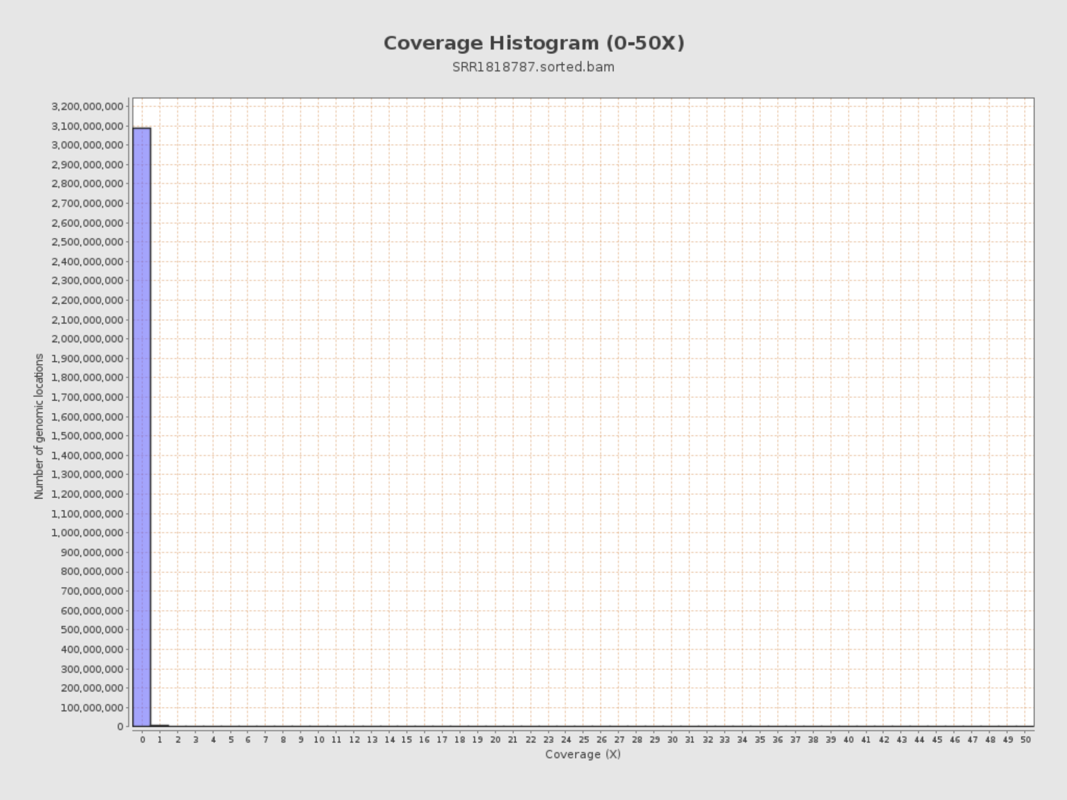
3. Results : Coverage across reference



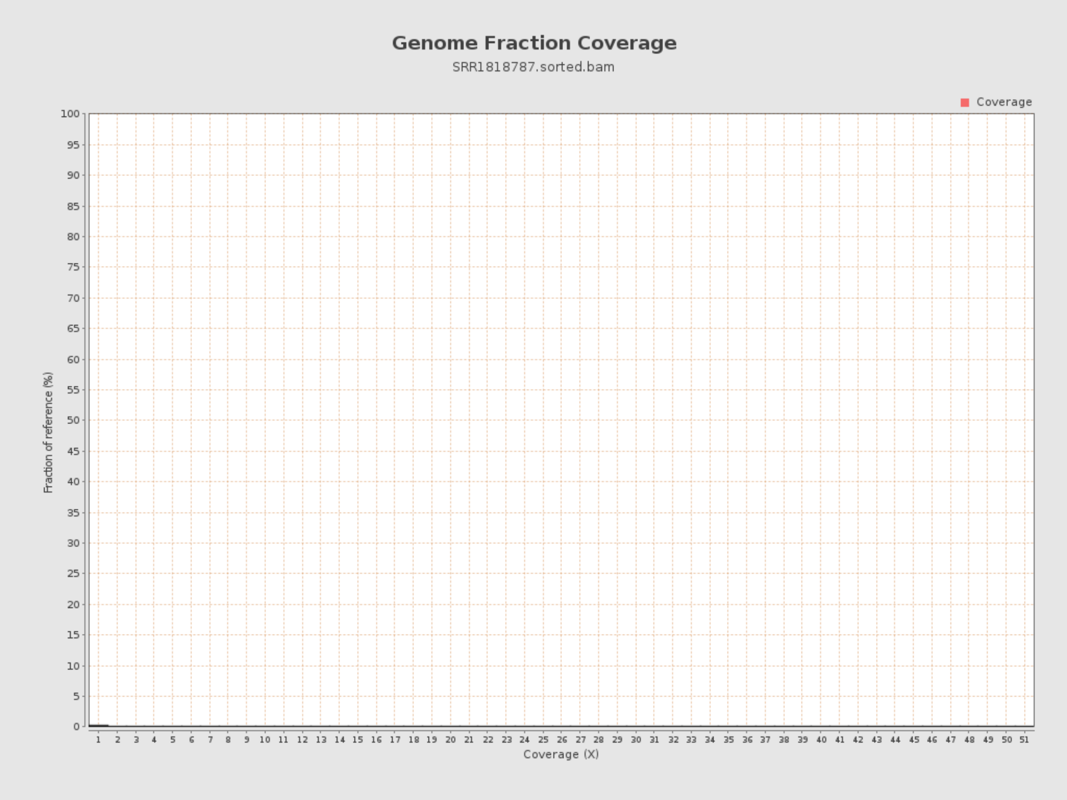
4. Results : Coverage Histogram



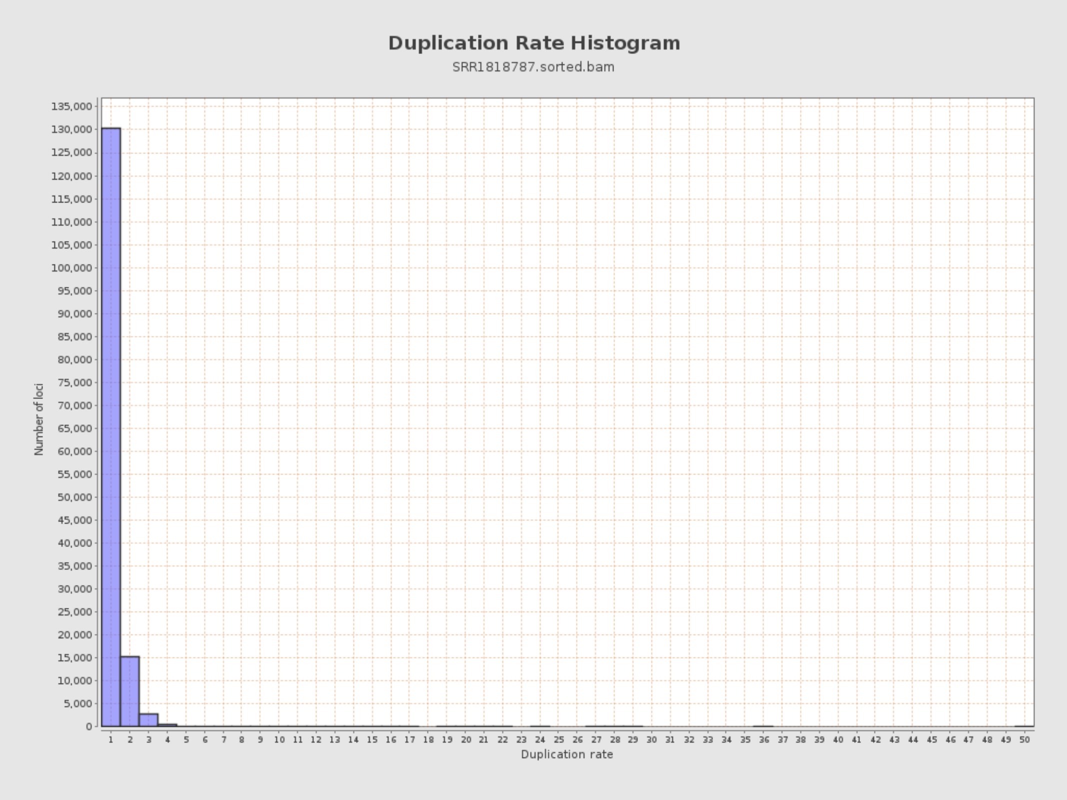
5. Results : Coverage Histogram (0-50X)



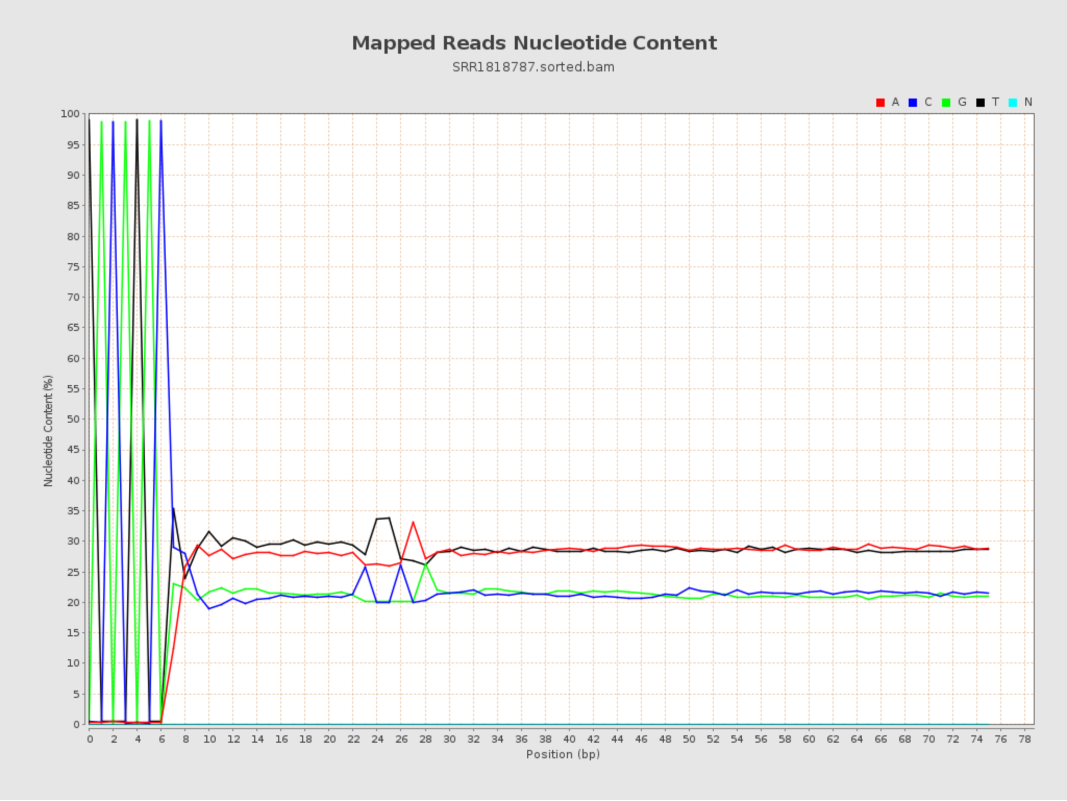
6. Results : Genome Fraction Coverage



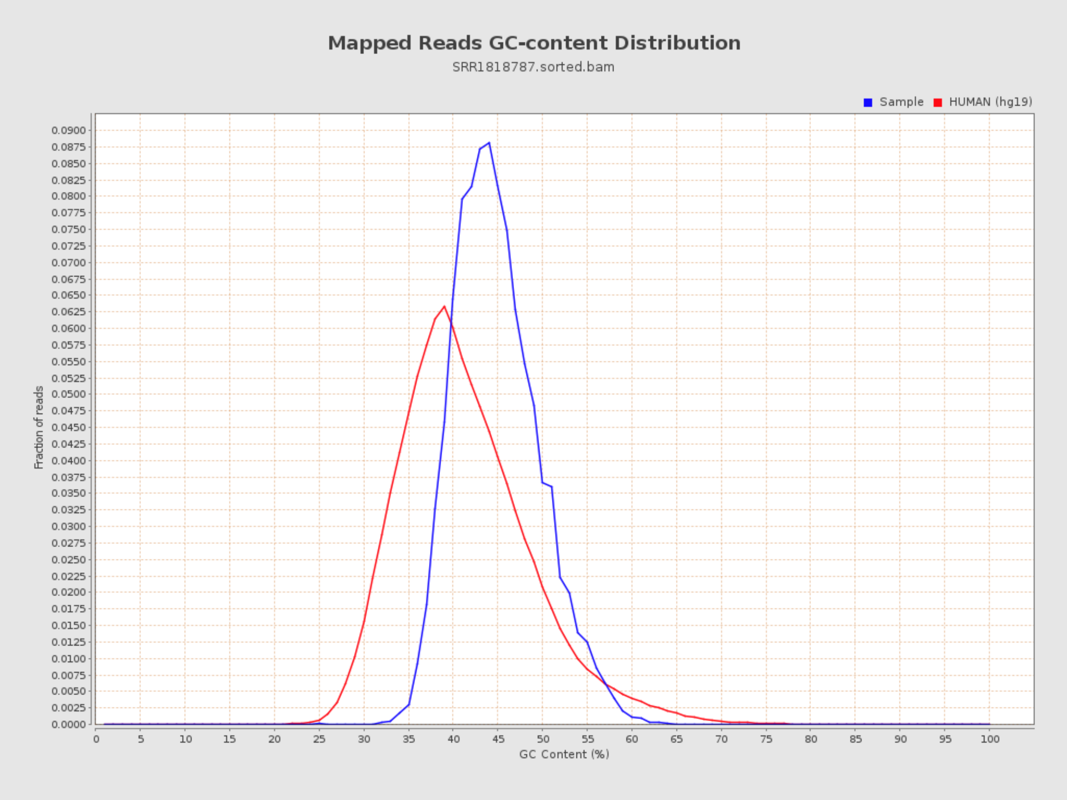
7. Results : Duplication Rate Histogram



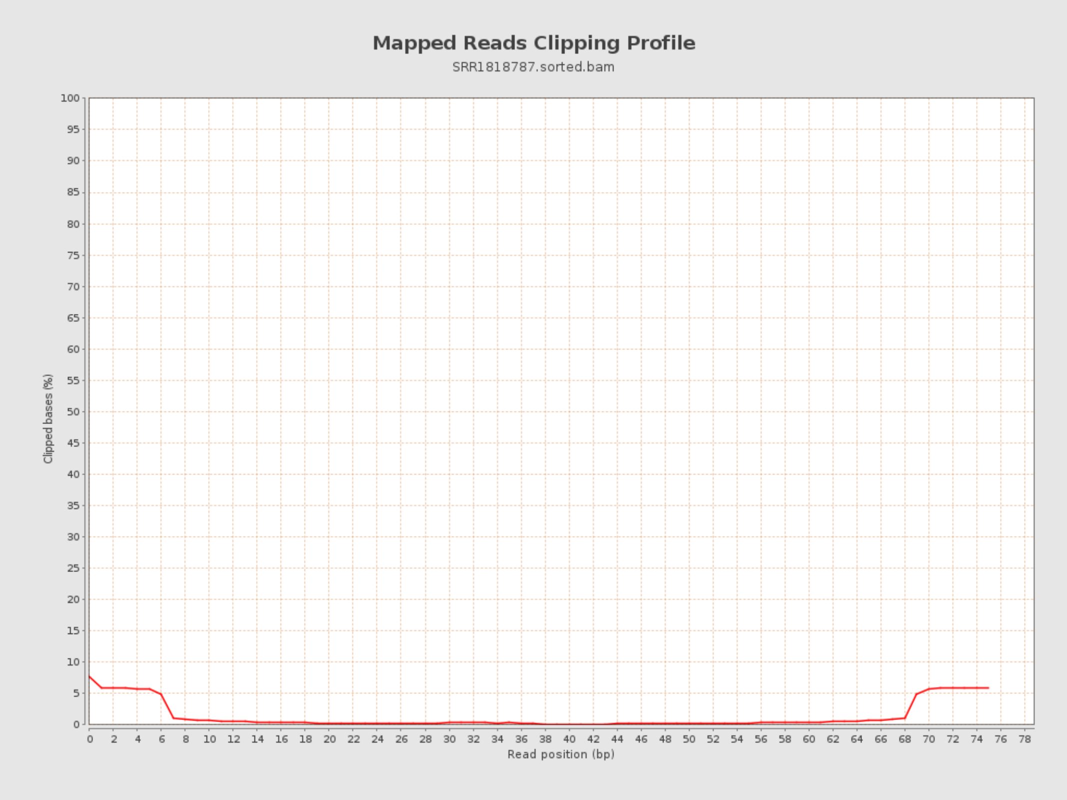
8. Results : Mapped Reads Nucleotide Content



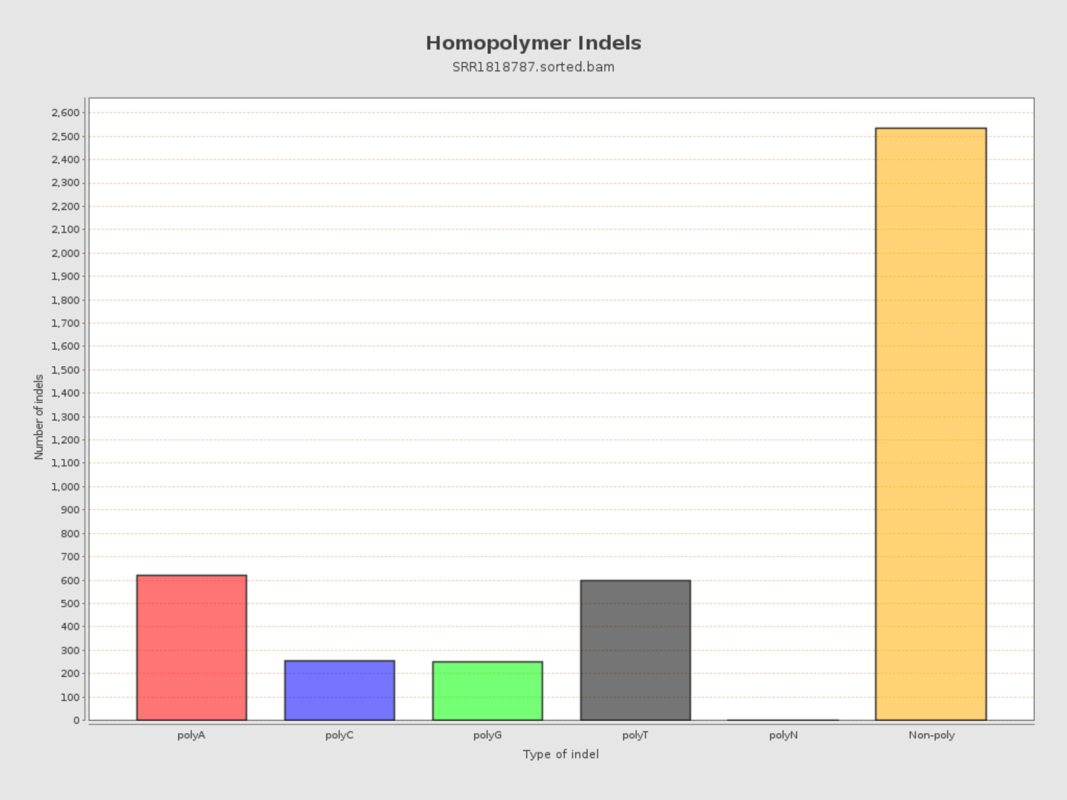
9. Results : Mapped Reads GC-content Distribution



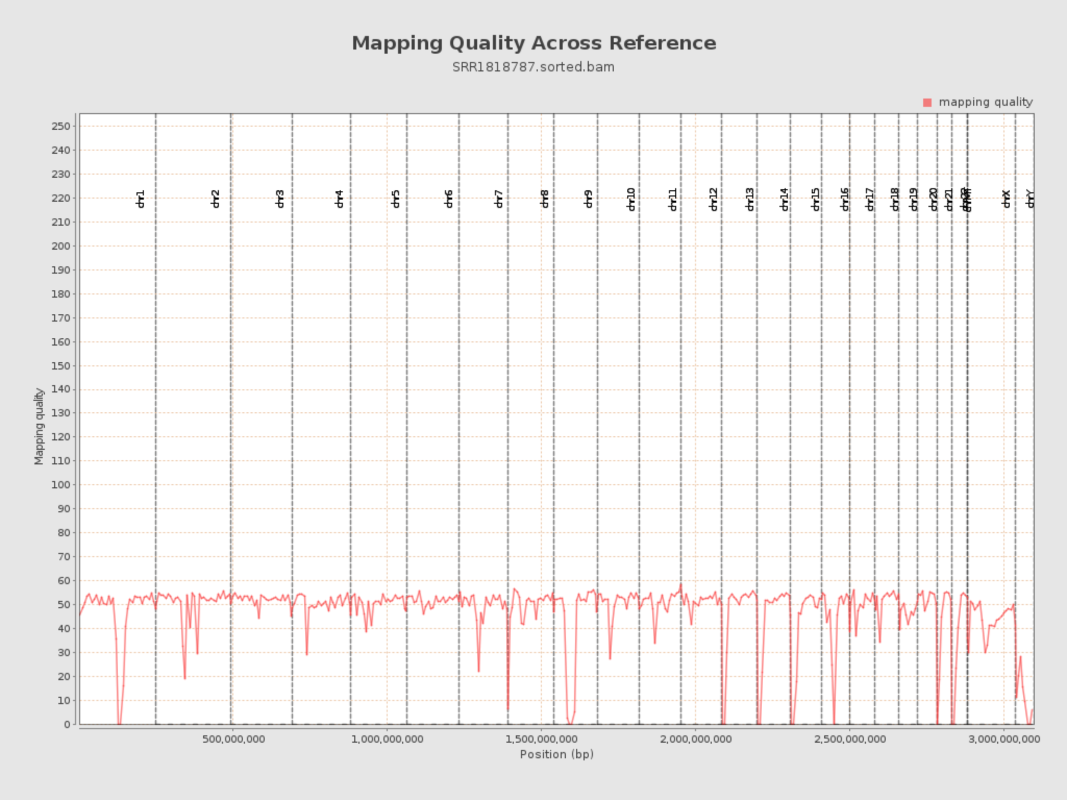
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram