Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:13:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818757.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_SRR1818757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:13:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,940,798
Mapped reads	1,891,484 / 97.46%
Unmapped reads	49,314 / 2.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,390 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	1,100,399 / 56.7%
Duplication rate	47.87%
Clipped reads	1,900,896 / 97.94%

2.2. ACGT Content

Number/percentage of A's	37,284,957 / 29.05%
Number/percentage of C's	28,220,533 / 21.99%
Number/percentage of T's	36,335,775 / 28.32%
Number/percentage of G's	26,477,189 / 20.63%
Number/percentage of N's	7,870 / 0.01%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.5678

2.4. Mapping Quality

Mean Mapping Quality	47.82

2.5. Mismatches and indels

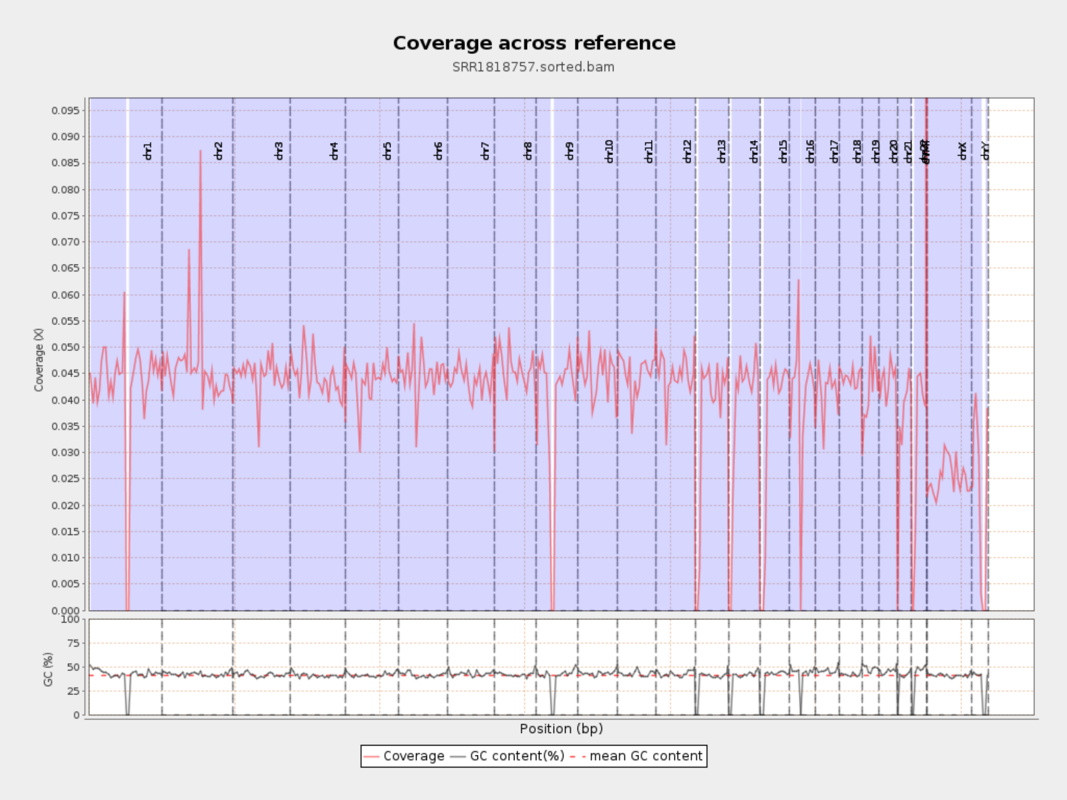
General error rate	0.53%
Mismatches	651,061
Insertions	12,932
Mapped reads with at least one insertion	0.67%
Deletions	32,465
Mapped reads with at least one deletion	1.7%
Homopolymer indels	42.34%

2.6. Chromosome stats

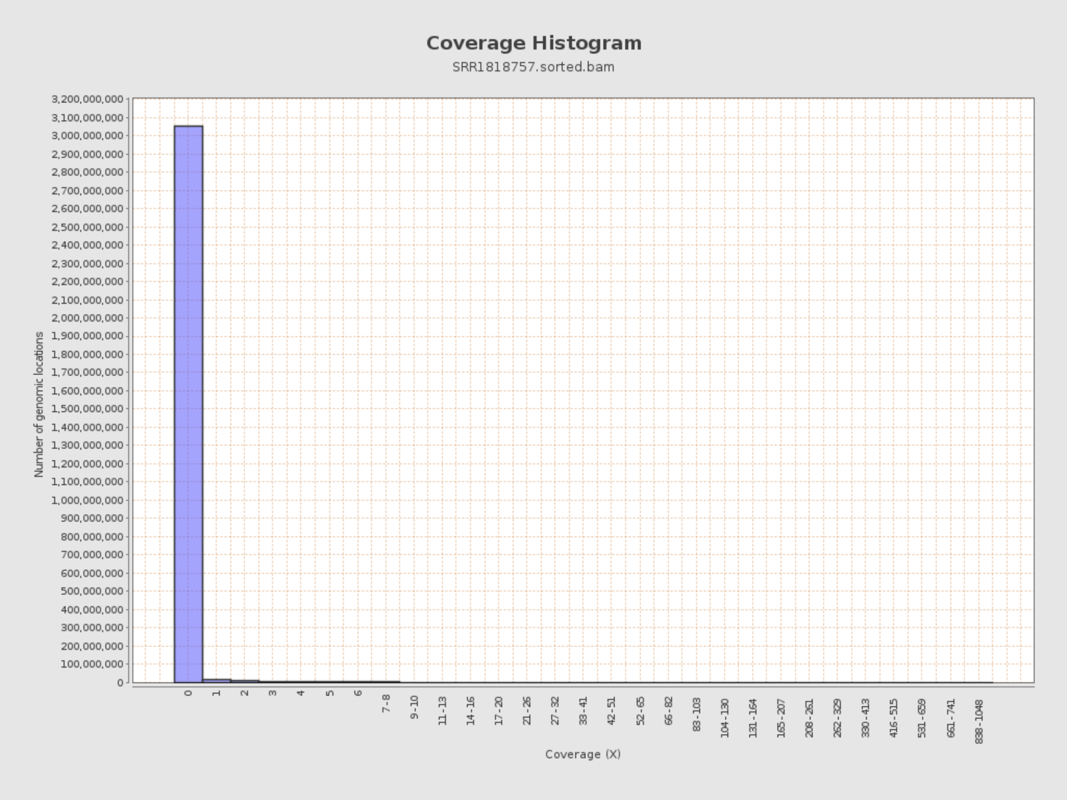
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10571725	0.0424	0.6958
chr2	243199373	11347594	0.0467	0.8648
chr3	198022430	8846651	0.0447	0.4773
chr4	191154276	8521697	0.0446	0.5129
chr5	180915260	7923529	0.0438	0.4756
chr6	171115067	7699748	0.045	0.5076
chr7	159138663	6991333	0.0439	0.5276

chr8	146364022	6774733	0.0463	0.5262
chr9	141213431	5529939	0.0392	0.4841
chr10	135534747	6098617	0.045	0.5681
chr11	135006516	6076633	0.045	0.5115
chr12	133851895	5980597	0.0447	0.5357
chr13	115169878	4177181	0.0363	0.4351
chr14	107349540	4028766	0.0375	0.4643
chr15	102531392	3631945	0.0354	0.4248
chr16	90354753	3677502	0.0407	0.6364
chr17	81195210	3366902	0.0415	0.4835
chr18	78077248	3460728	0.0443	0.597
chr19	59128983	2489146	0.0421	0.613
chr20	63025520	2736159	0.0434	0.4964
chr21	48129895	1705648	0.0354	0.4377
chr22	51304566	1502109	0.0293	0.4131
chrMT	16571	52500	3.1682	5.4114
chrX	155270560	3917743	0.0252	0.3716
chrY	59373566	1268768	0.0214	0.9627

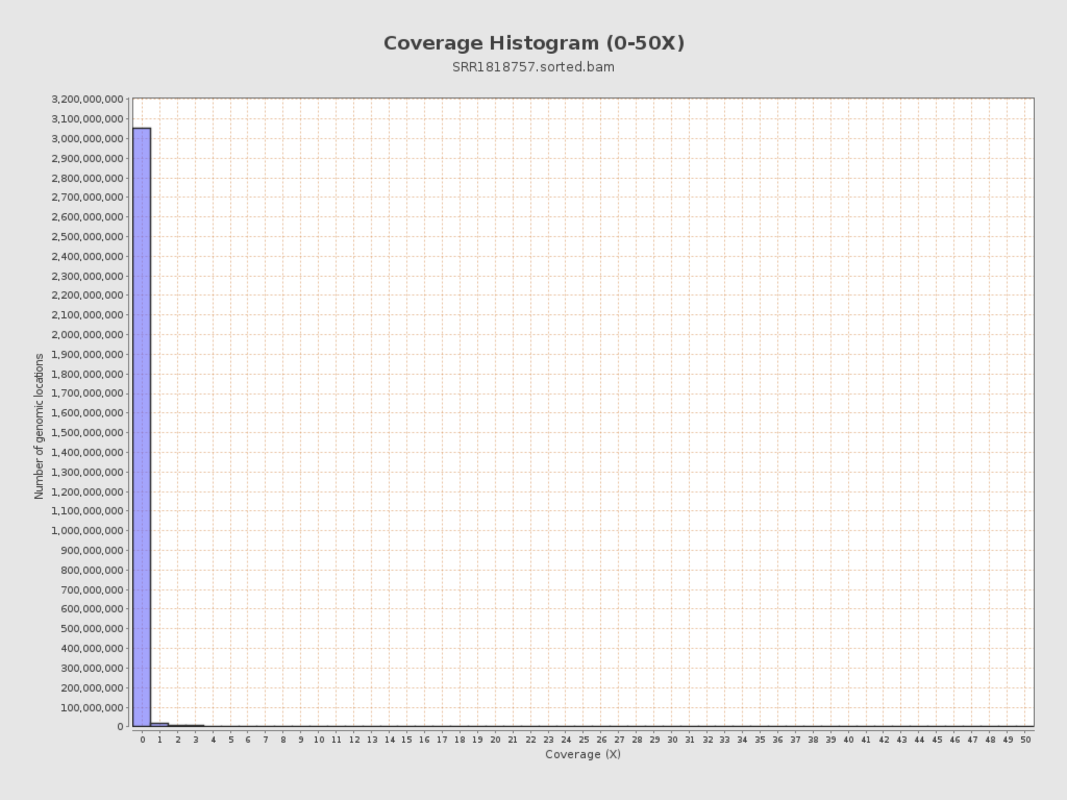
3. Results : Coverage across reference



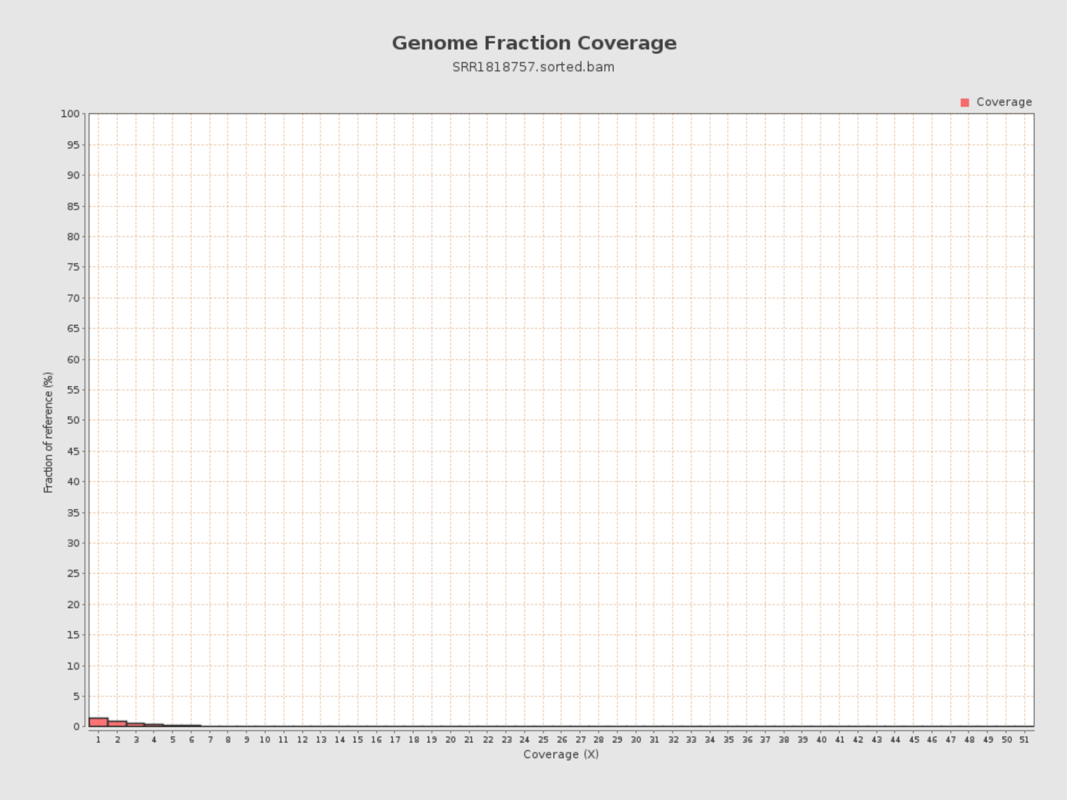
4. Results : Coverage Histogram



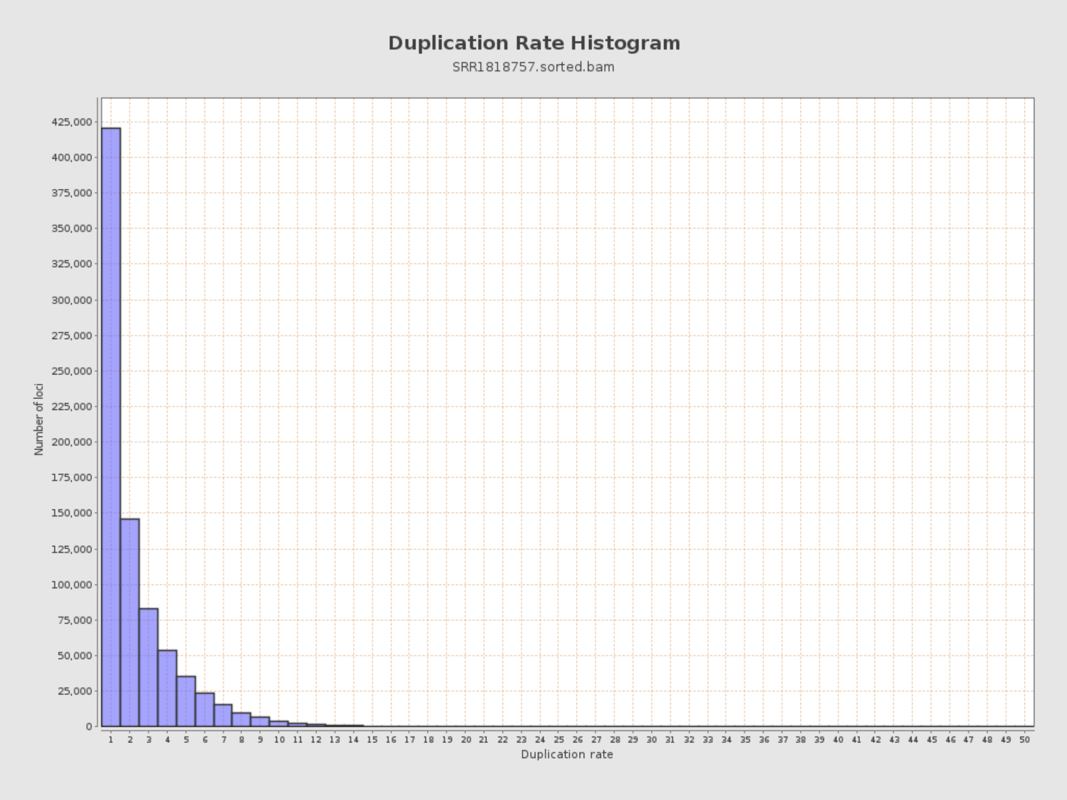
5. Results : Coverage Histogram (0-50X)



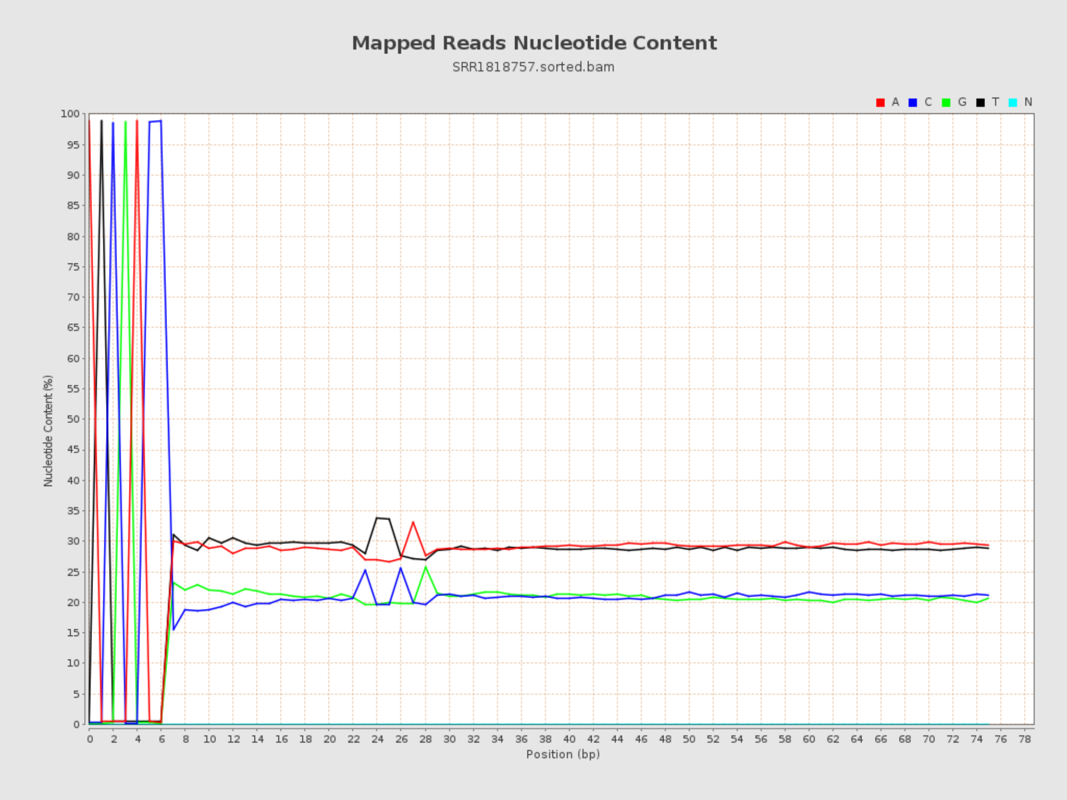
6. Results : Genome Fraction Coverage



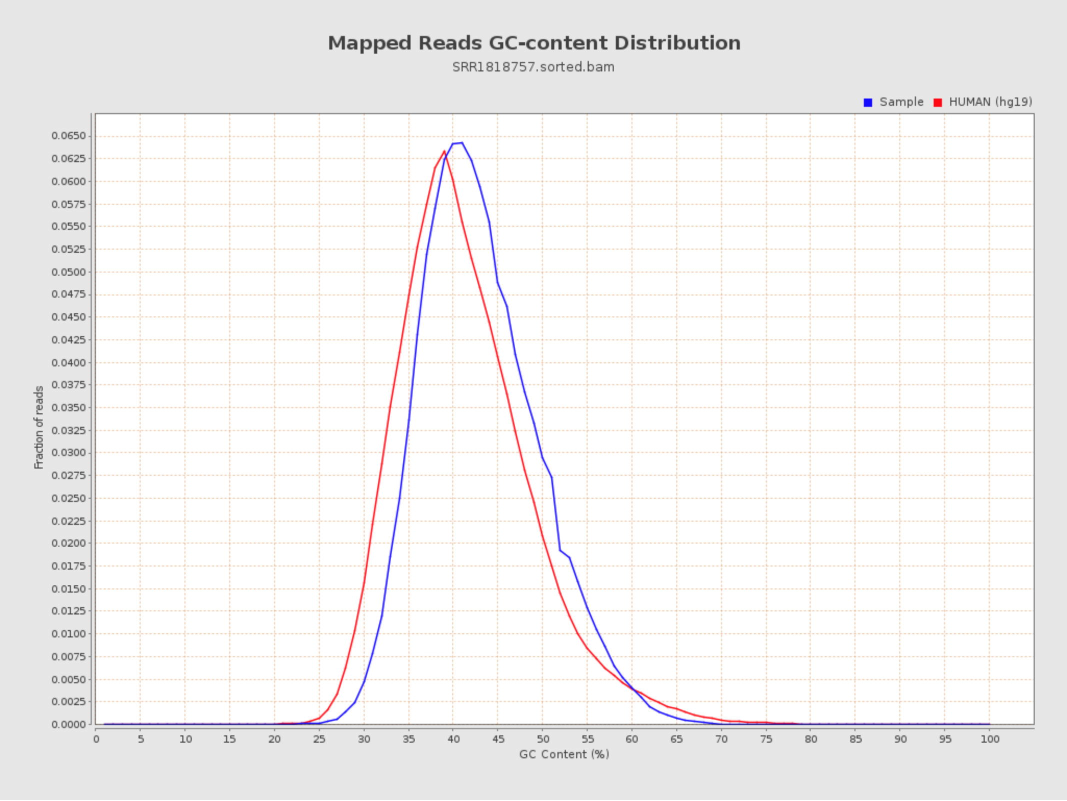
7. Results : Duplication Rate Histogram



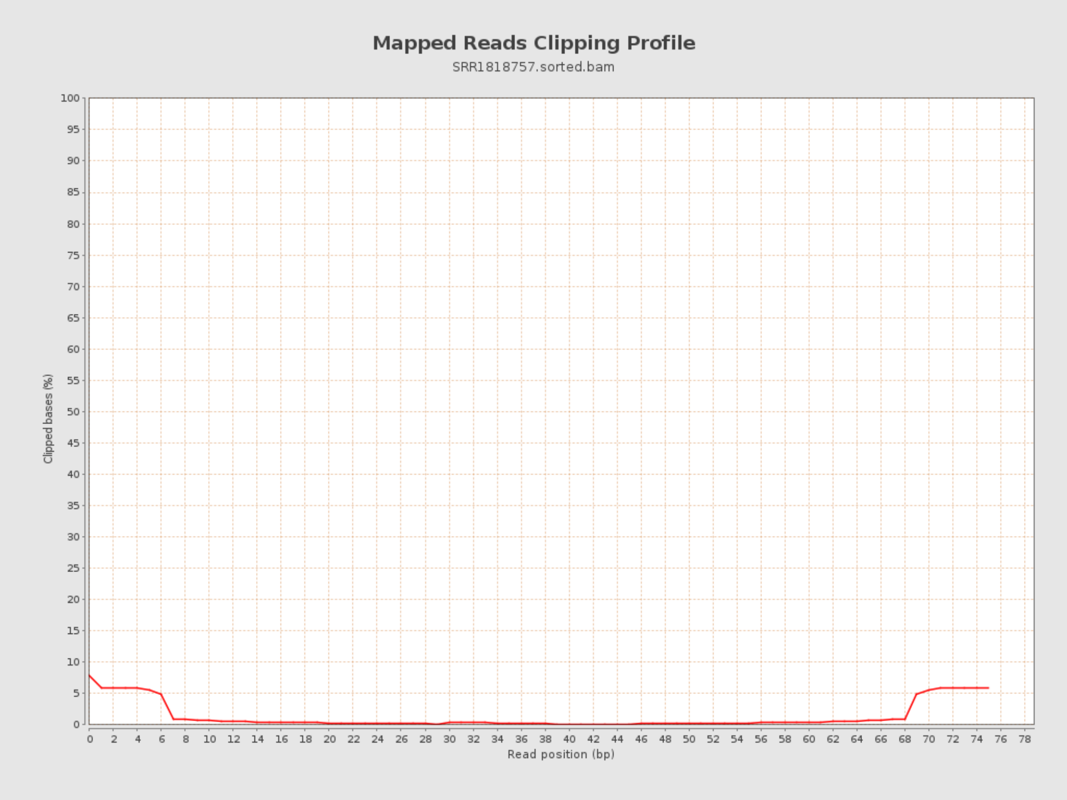
8. Results : Mapped Reads Nucleotide Content



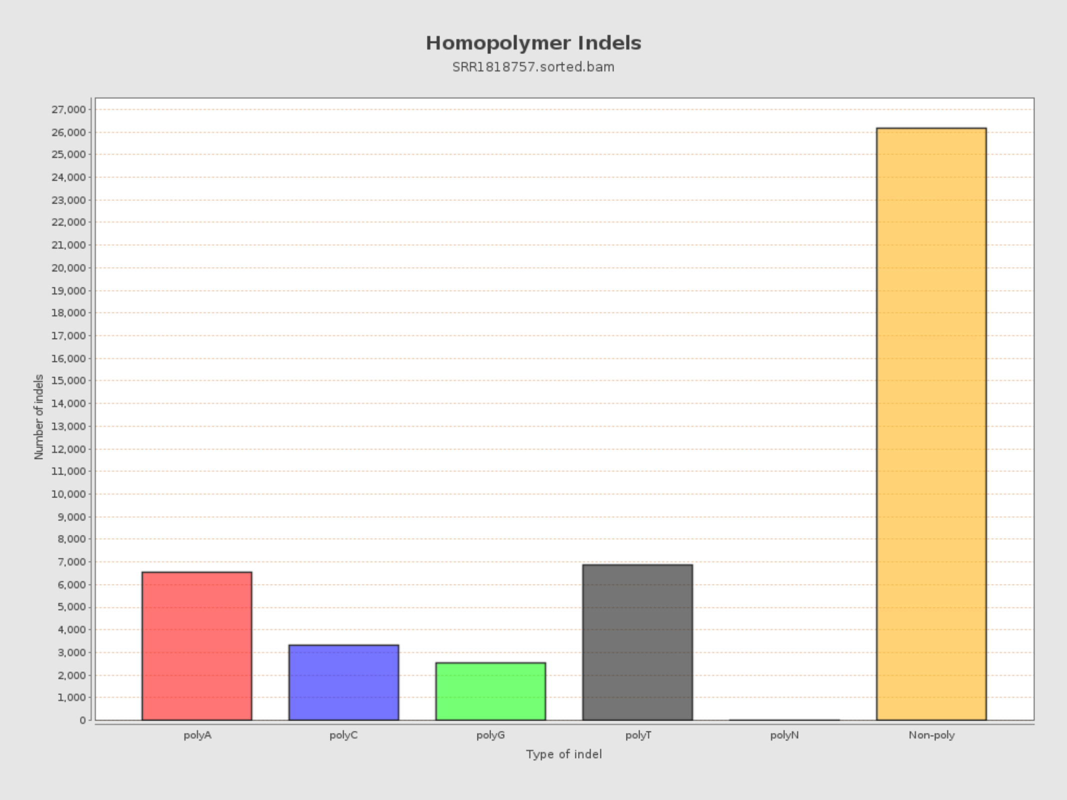
9. Results : Mapped Reads GC-content Distribution



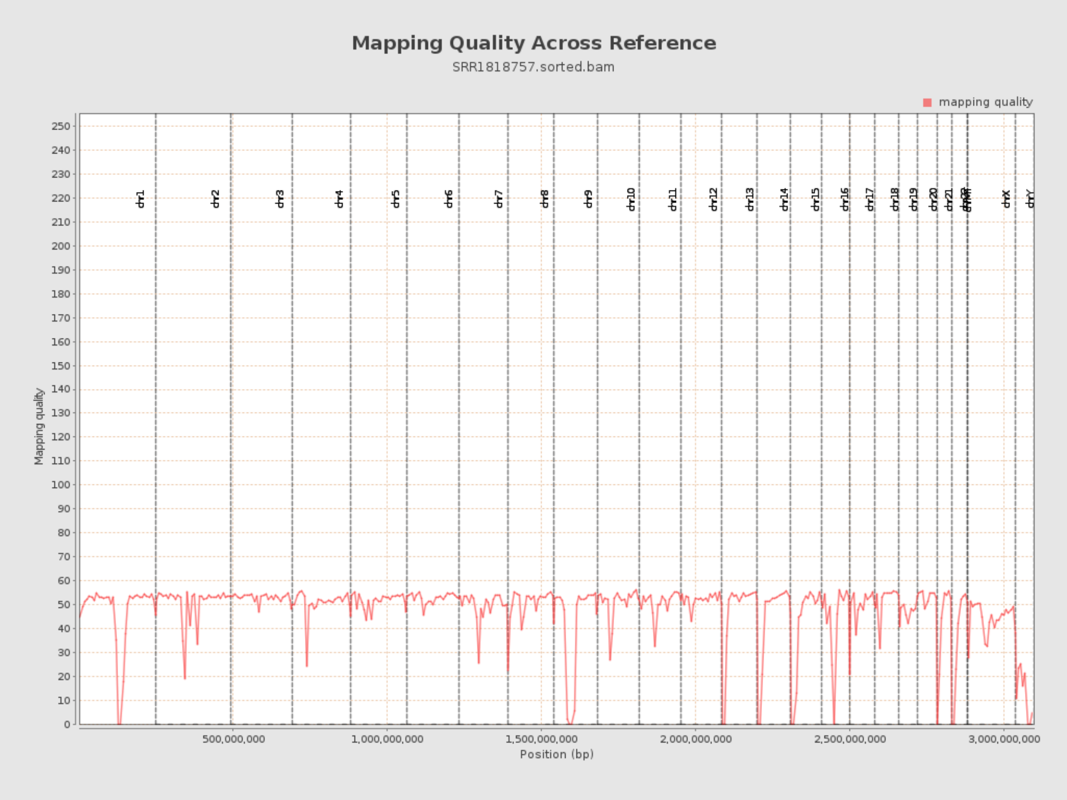
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram