Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:19:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818739.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_SRR1818739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:19:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,180,489
Mapped reads	2,126,632 / 97.53%
Unmapped reads	53,857 / 2.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,237 / 0.88%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	1,189,306 / 54.54%
Duplication rate	46.6%
Clipped reads	2,134,627 / 97.9%

2.2. ACGT Content

Number/percentage of A's	40,544,083 / 28.11%
Number/percentage of C's	31,415,888 / 21.78%
Number/percentage of T's	41,329,721 / 28.65%
Number/percentage of G's	30,937,644 / 21.45%
Number/percentage of N's	8,948 / 0.01%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.5975

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

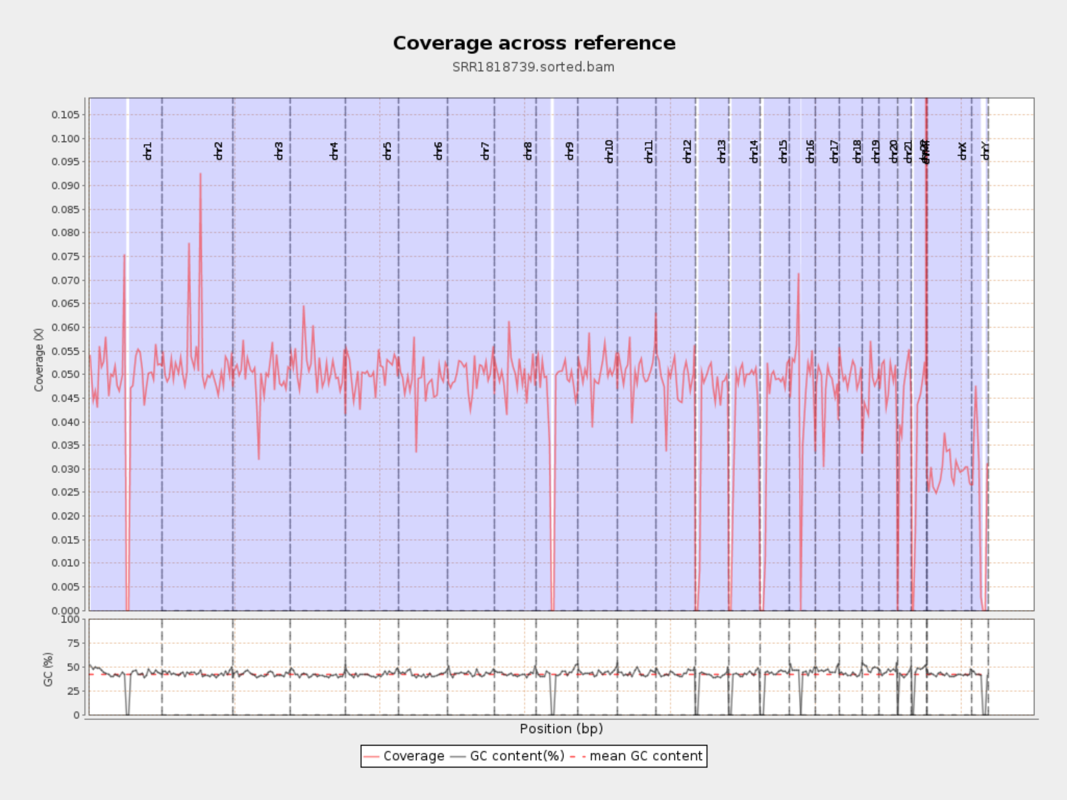
General error rate	0.52%
Mismatches	719,948
Insertions	17,321
Mapped reads with at least one insertion	0.81%
Deletions	36,604
Mapped reads with at least one deletion	1.71%
Homopolymer indels	39.24%

2.6. Chromosome stats

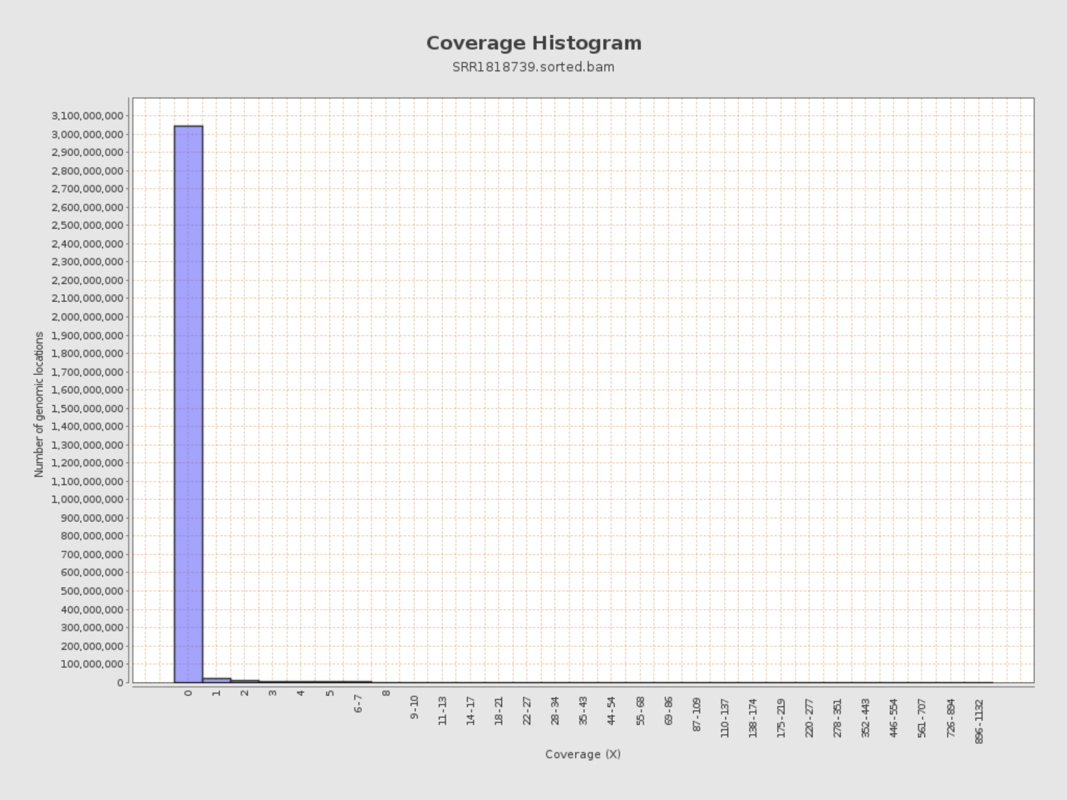
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11952738	0.048	0.7962
chr2	243199373	12842011	0.0528	0.9203
chr3	198022430	9826754	0.0496	0.4843
chr4	191154276	9854606	0.0516	0.5279
chr5	180915260	9122198	0.0504	0.4944
chr6	171115067	8332187	0.0487	0.5076
chr7	159138663	7952603	0.05	0.5443

chr8	146364022	7345881	0.0502	0.5521
chr9	141213431	6162854	0.0436	0.5101
chr10	135534747	6861570	0.0506	0.593
chr11	135006516	6864480	0.0508	0.5272
chr12	133851895	6535575	0.0488	0.5016
chr13	115169878	4680885	0.0406	0.44
chr14	107349540	4432354	0.0413	0.4841
chr15	102531392	4068771	0.0397	0.4346
chr16	90354753	4220642	0.0467	0.6557
chr17	81195210	3797107	0.0468	0.4888
chr18	78077248	3913452	0.0501	0.6581
chr19	59128983	2769177	0.0468	0.682
chr20	63025520	3080681	0.0489	0.518
chr21	48129895	2019475	0.042	0.4889
chr22	51304566	1704455	0.0332	0.4363
chrMT	16571	91118	5.4986	7.0115
chrX	155270560	4572781	0.0295	0.3903
chrY	59373566	1289518	0.0217	0.9716

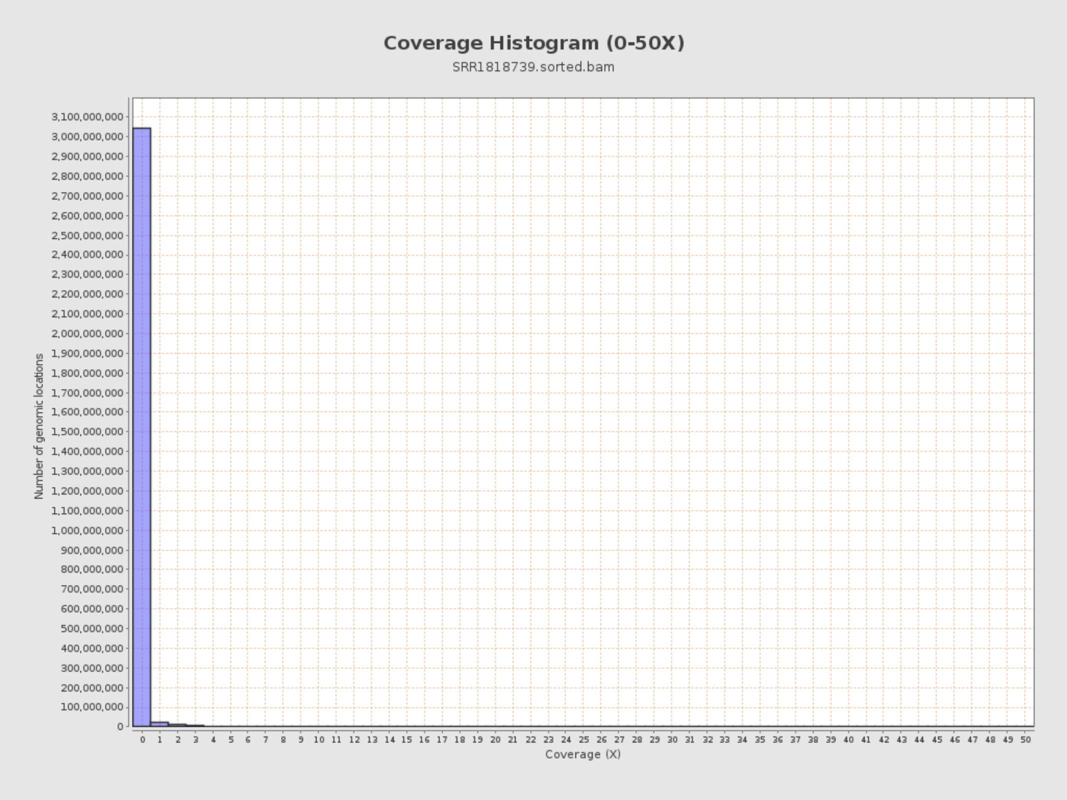
3. Results : Coverage across reference



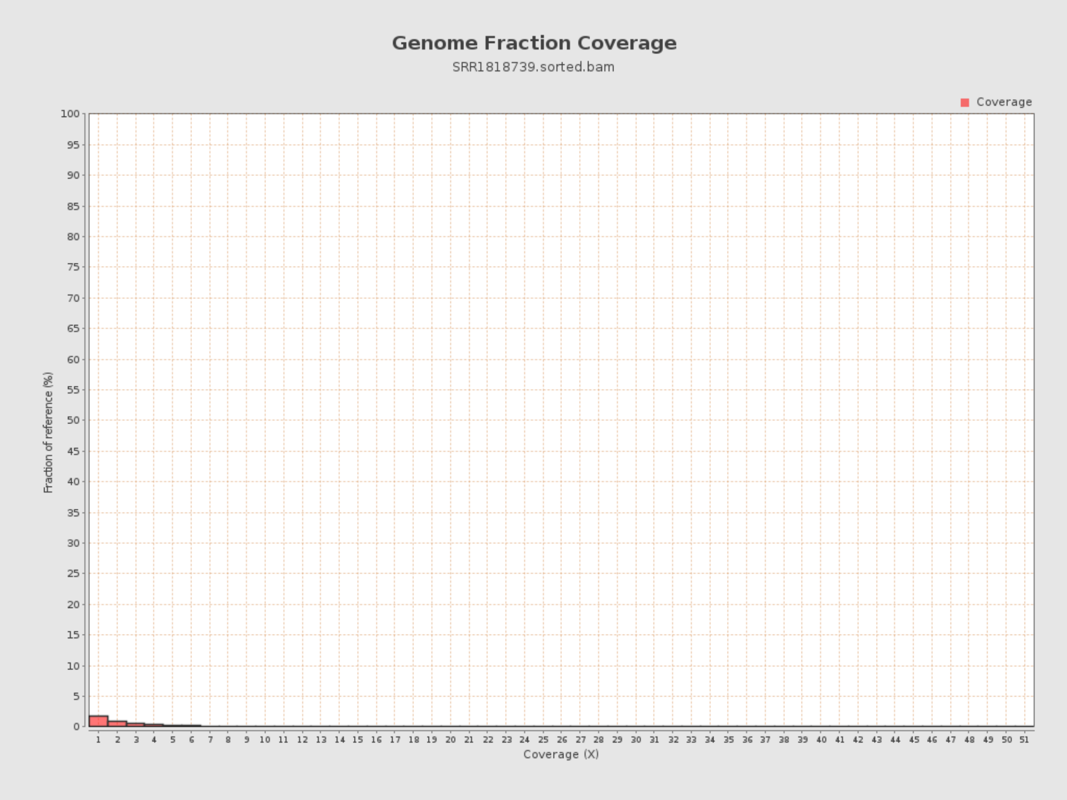
4. Results : Coverage Histogram



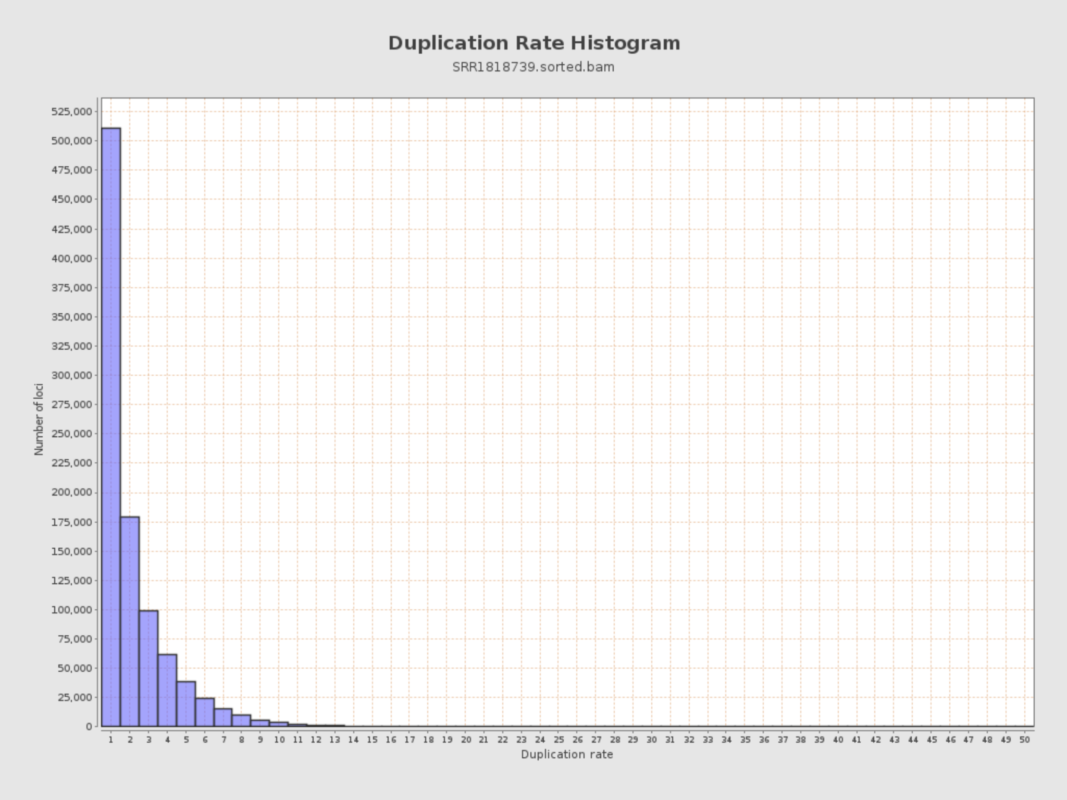
5. Results : Coverage Histogram (0-50X)



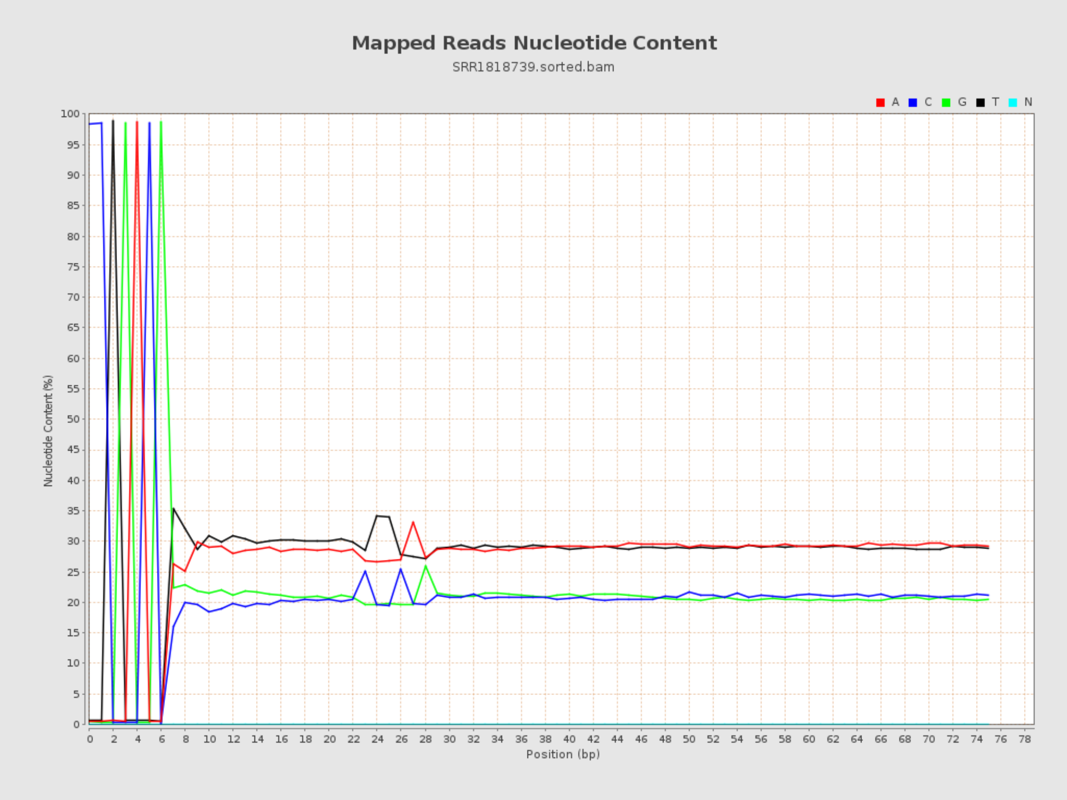
6. Results : Genome Fraction Coverage



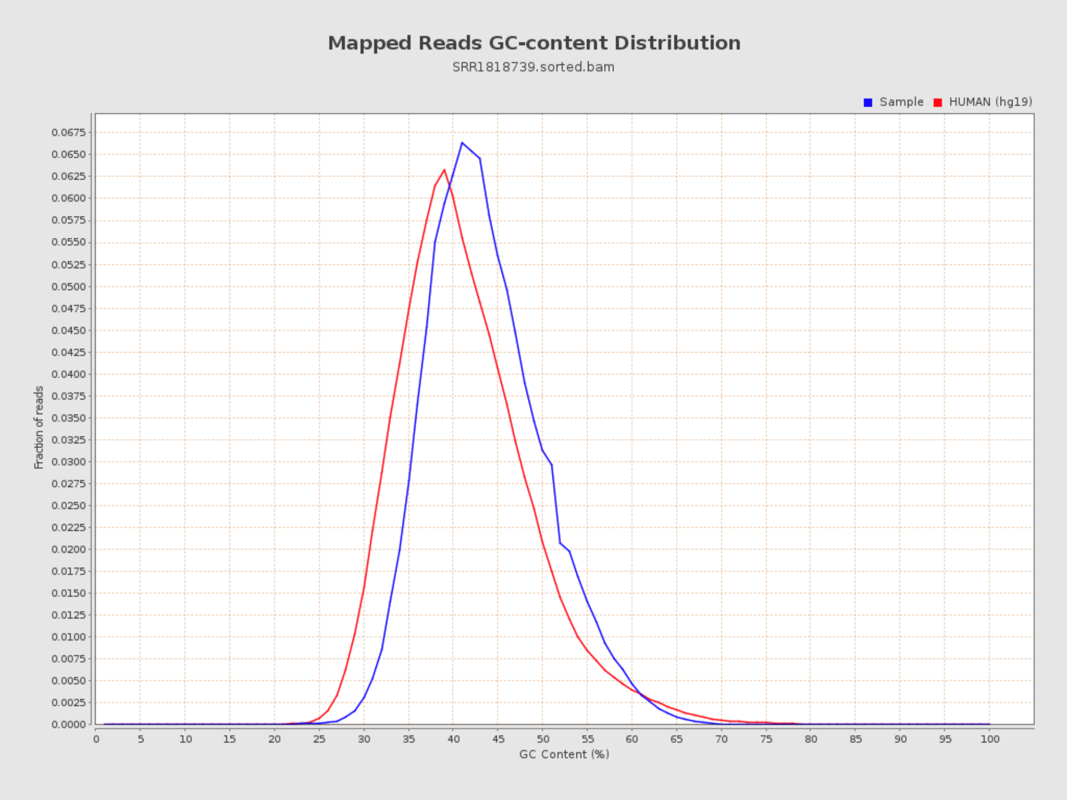
7. Results : Duplication Rate Histogram



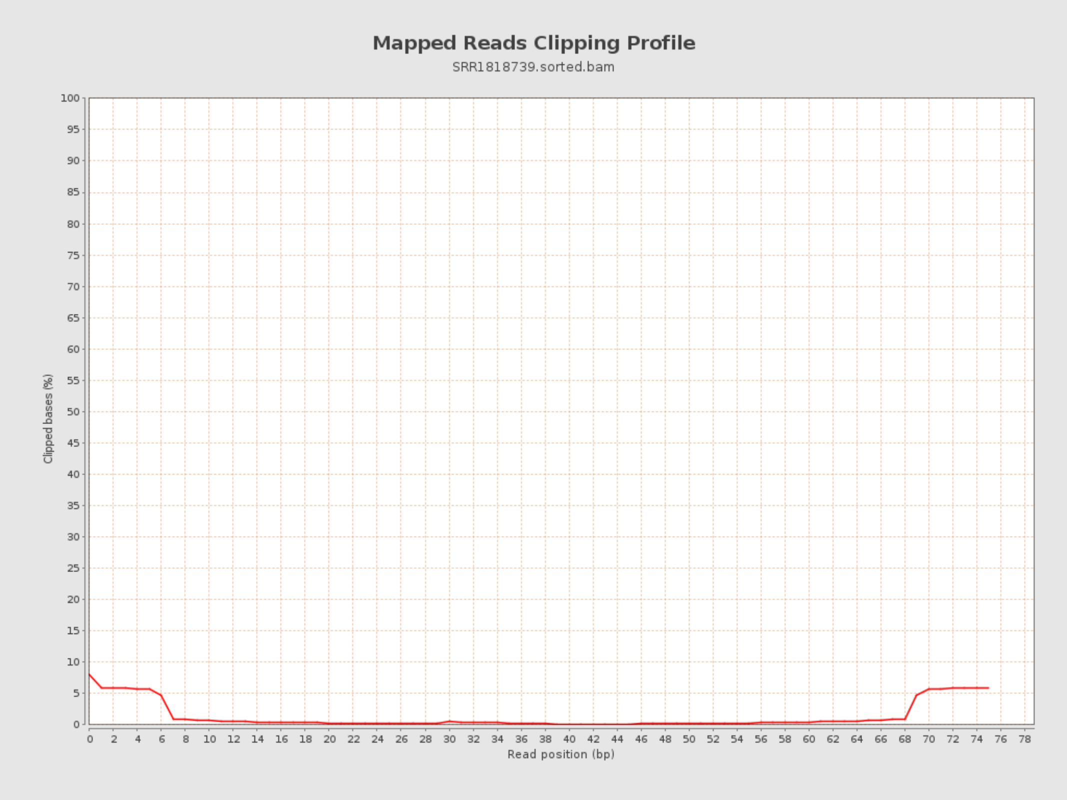
8. Results : Mapped Reads Nucleotide Content



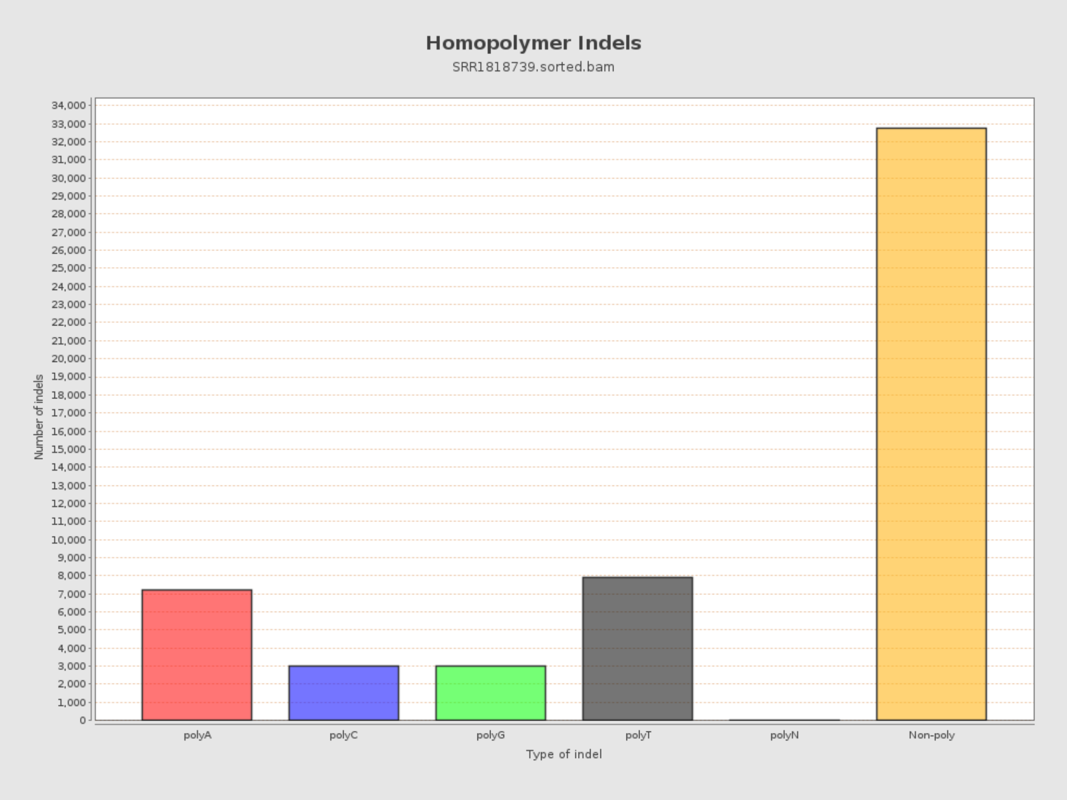
9. Results : Mapped Reads GC-content Distribution



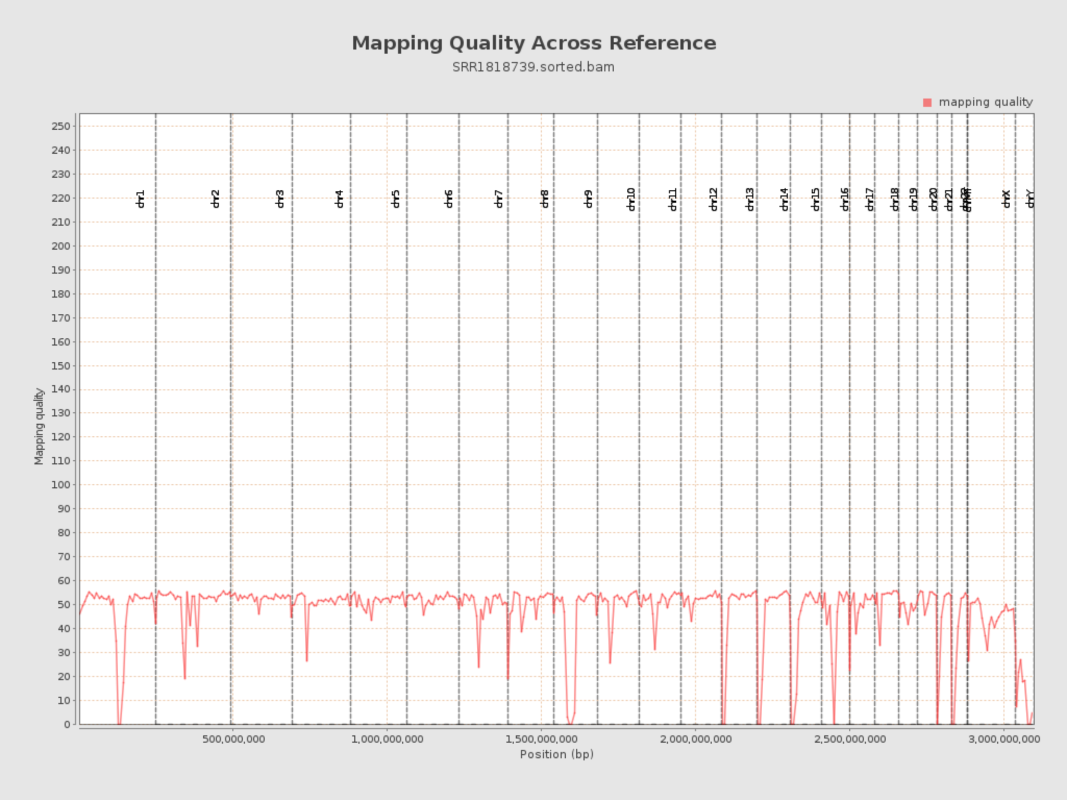
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram