Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:23:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818763.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_SRR1818763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,552,012
Mapped reads	1,482,421 / 95.52%
Unmapped reads	69,591 / 4.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,593 / 0.88%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	726,065 / 46.78%
Duplication rate	41.41%
Clipped reads	1,482,526 / 95.52%

2.2. ACGT Content

Number/percentage of A's	28,466,102 / 28.34%
Number/percentage of C's	22,924,664 / 22.82%
Number/percentage of T's	29,255,542 / 29.12%
Number/percentage of G's	19,802,322 / 19.71%
Number/percentage of N's	6,255 / 0.01%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.4427

2.4. Mapping Quality

Mean Mapping Quality	47.79

2.5. Mismatches and indels

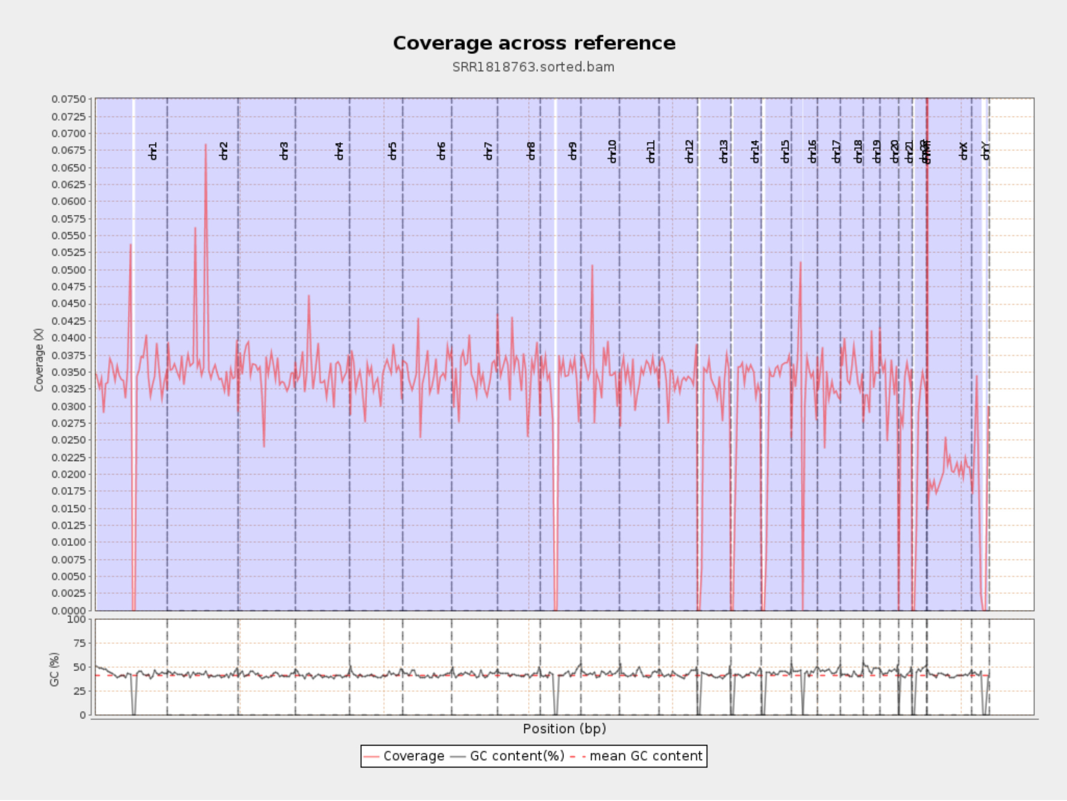
General error rate	0.56%
Mismatches	541,491
Insertions	12,488
Mapped reads with at least one insertion	0.83%
Deletions	26,521
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.01%

2.6. Chromosome stats

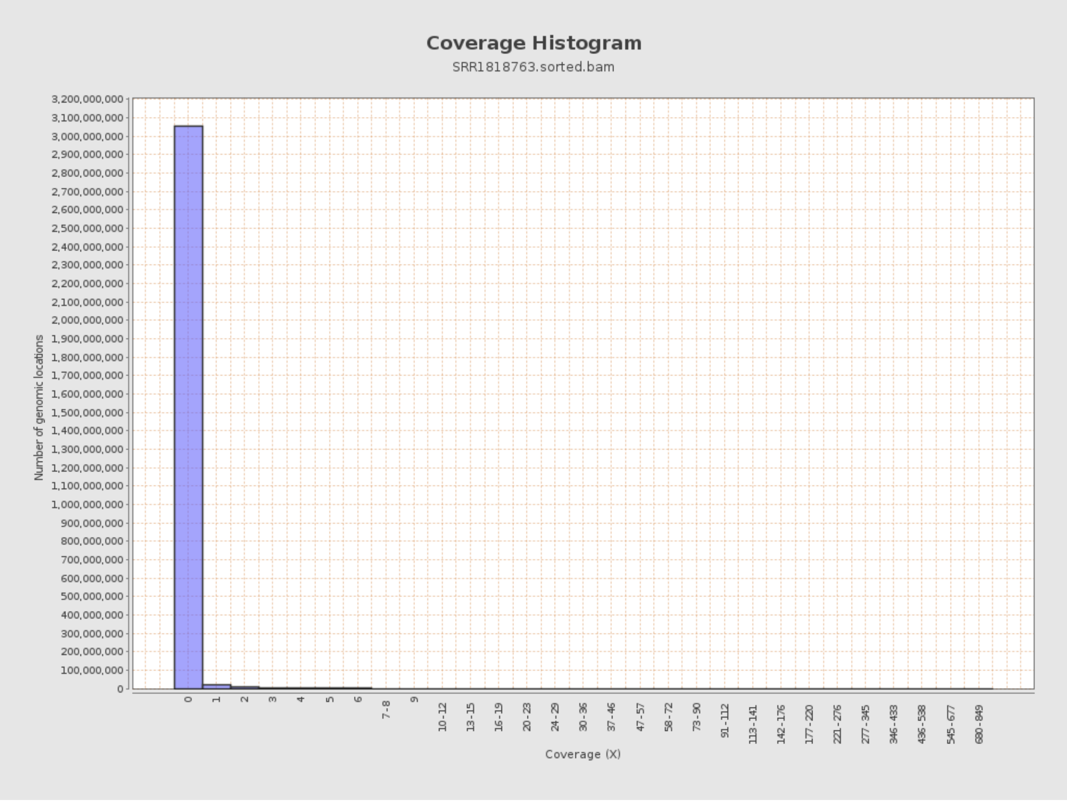
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8215839	0.033	0.599
chr2	243199373	8990636	0.037	0.6802
chr3	198022430	6896976	0.0348	0.3594
chr4	191154276	6734923	0.0352	0.3986
chr5	180915260	6255551	0.0346	0.3649
chr6	171115067	5956879	0.0348	0.3838
chr7	159138663	5493110	0.0345	0.416

chr8	146364022	5174215	0.0354	0.4034
chr9	141213431	4350799	0.0308	0.3796
chr10	135534747	4820479	0.0356	0.4496
chr11	135006516	4672980	0.0346	0.3891
chr12	133851895	4584535	0.0343	0.3849
chr13	115169878	3259518	0.0283	0.3224
chr14	107349540	3068103	0.0286	0.3533
chr15	102531392	2926051	0.0285	0.33
chr16	90354753	2900662	0.0321	0.4876
chr17	81195210	2636397	0.0325	0.3659
chr18	78077248	2777308	0.0356	0.4931
chr19	59128983	1992950	0.0337	0.5146
chr20	63025520	2084087	0.0331	0.3624
chr21	48129895	1413725	0.0294	0.3465
chr22	51304566	1146860	0.0224	0.2999
chrMT	16571	71582	4.3197	4.5346
chrX	155270560	3134341	0.0202	0.294
chrY	59373566	938670	0.0158	0.6351

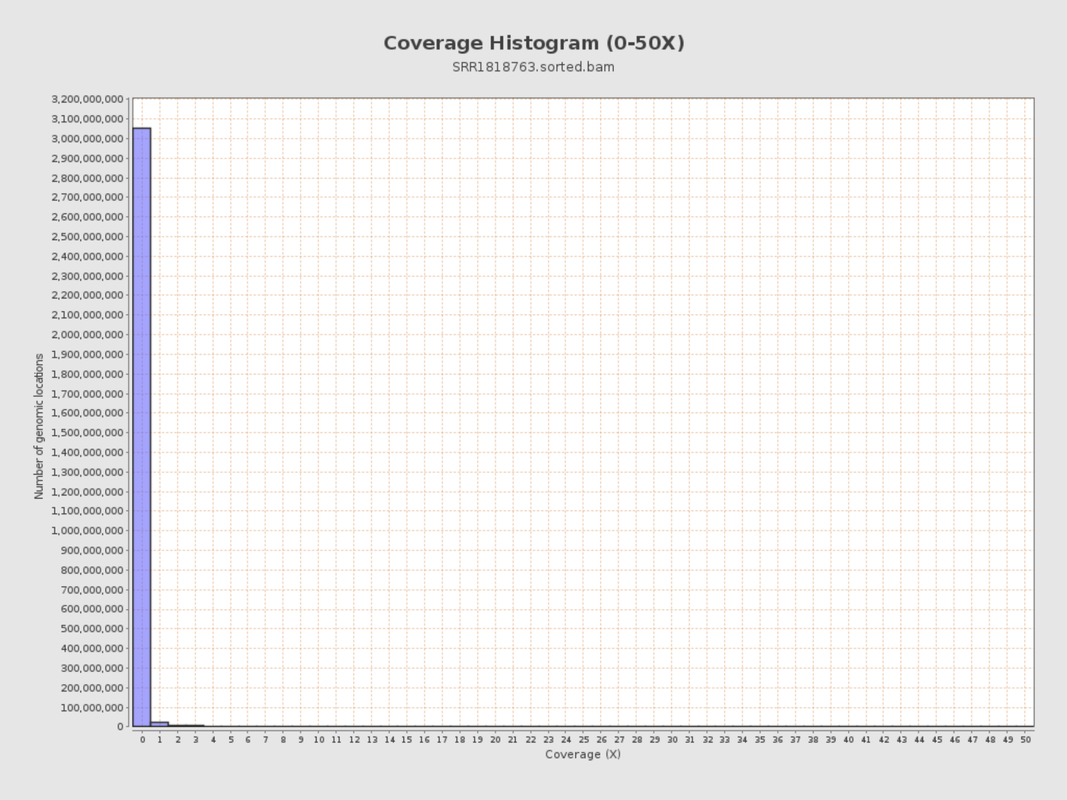
3. Results : Coverage across reference



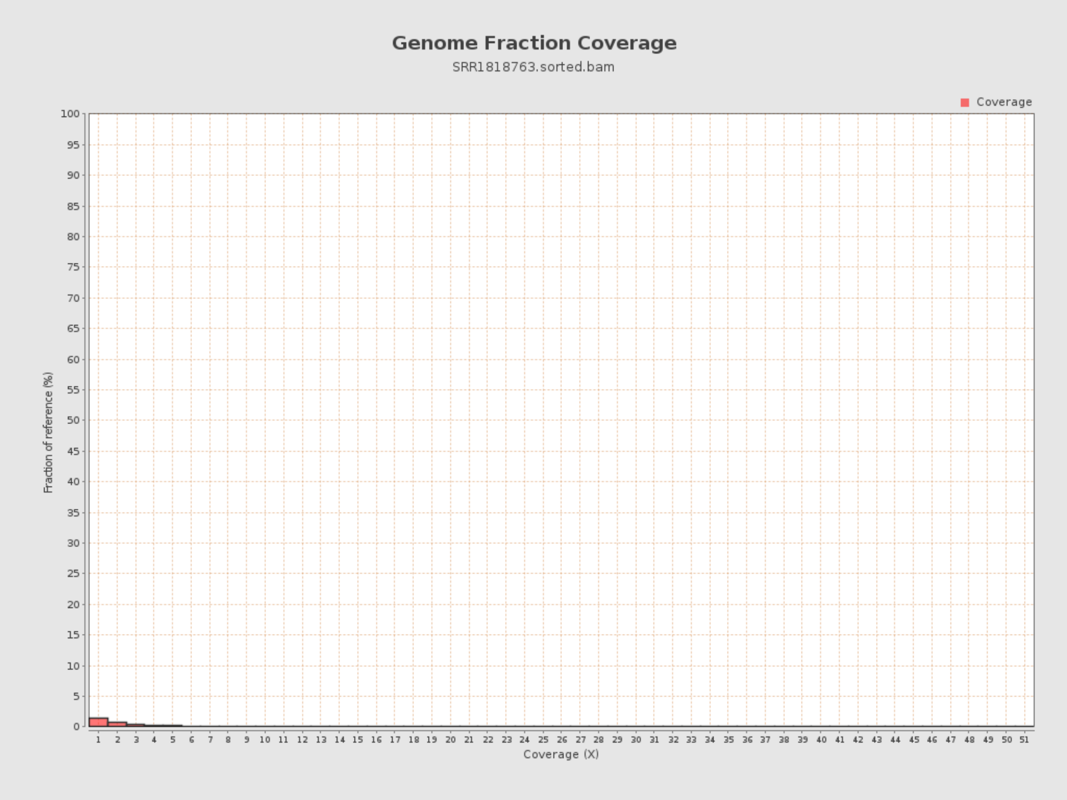
4. Results : Coverage Histogram



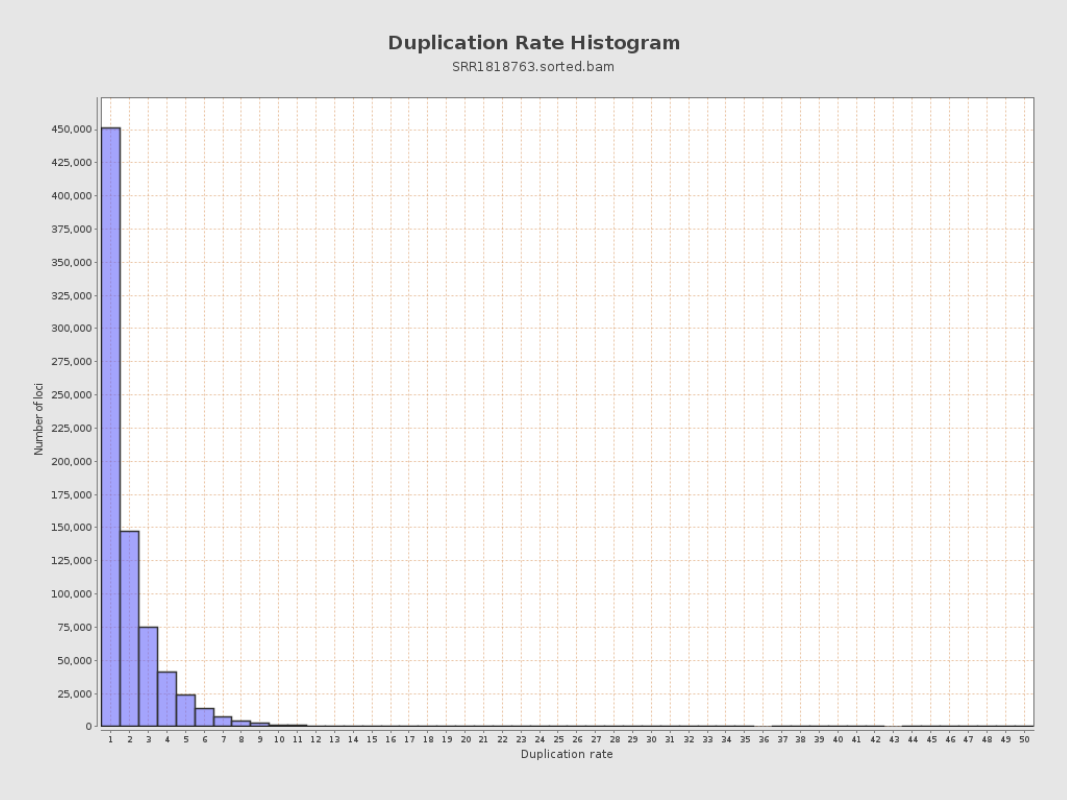
5. Results : Coverage Histogram (0-50X)



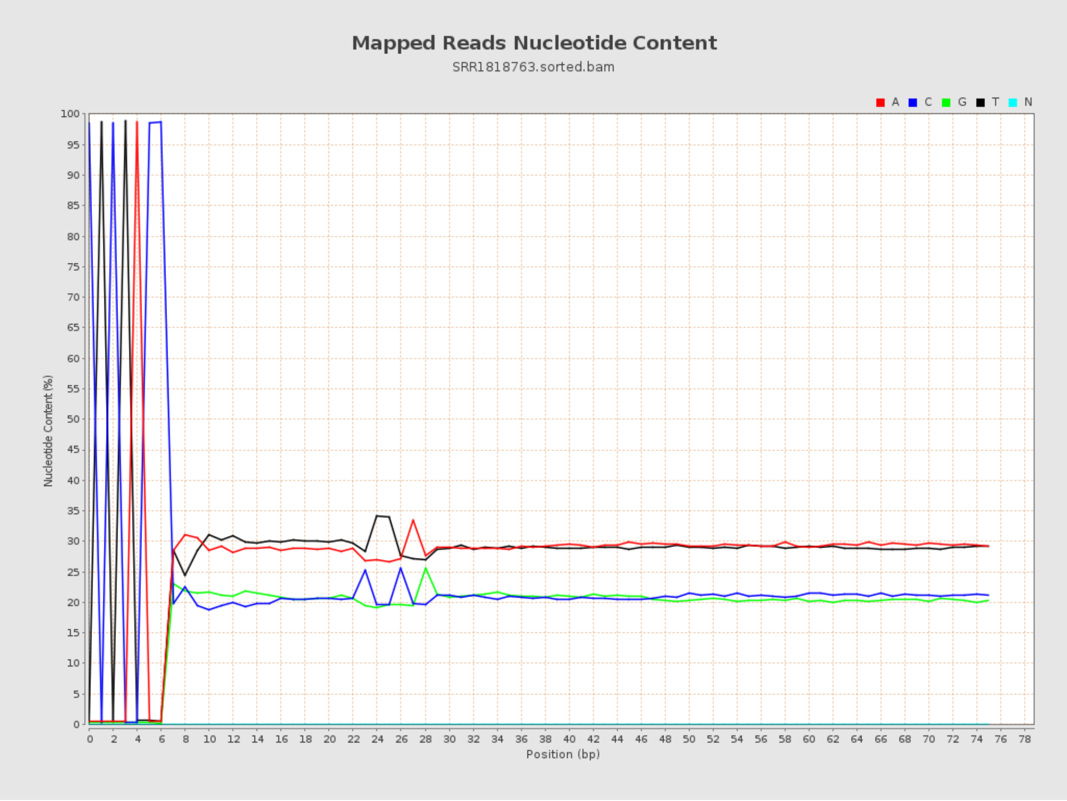
6. Results : Genome Fraction Coverage



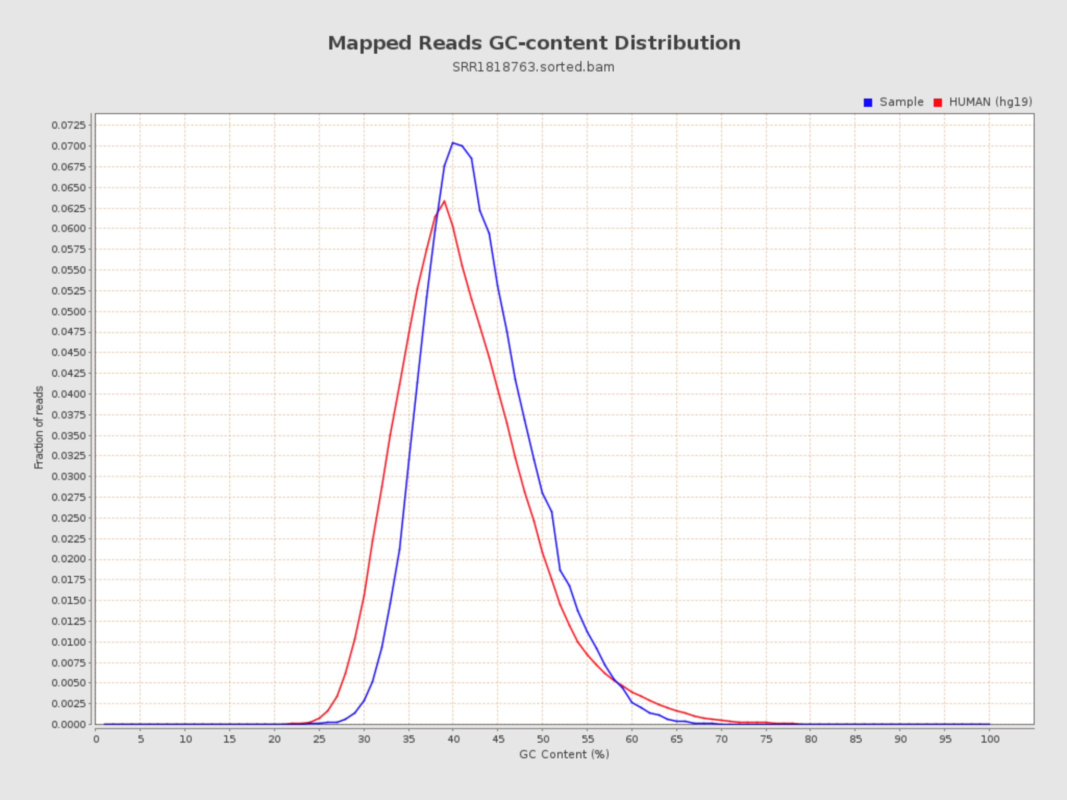
7. Results : Duplication Rate Histogram



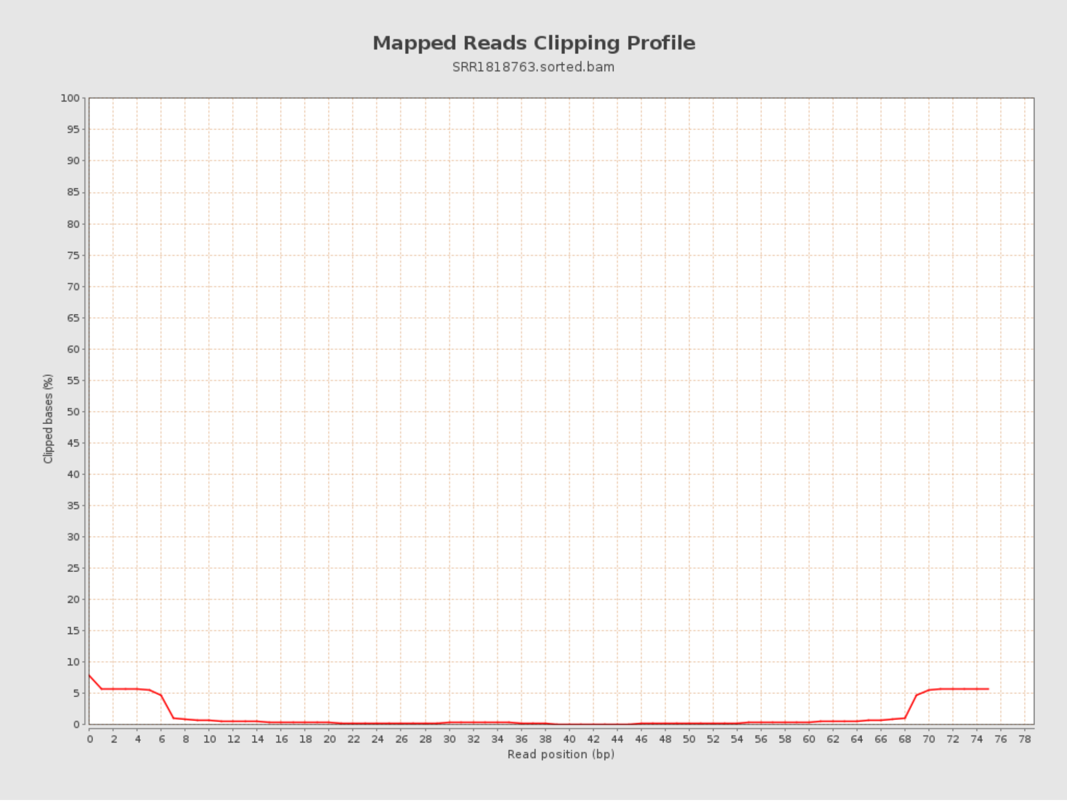
8. Results : Mapped Reads Nucleotide Content



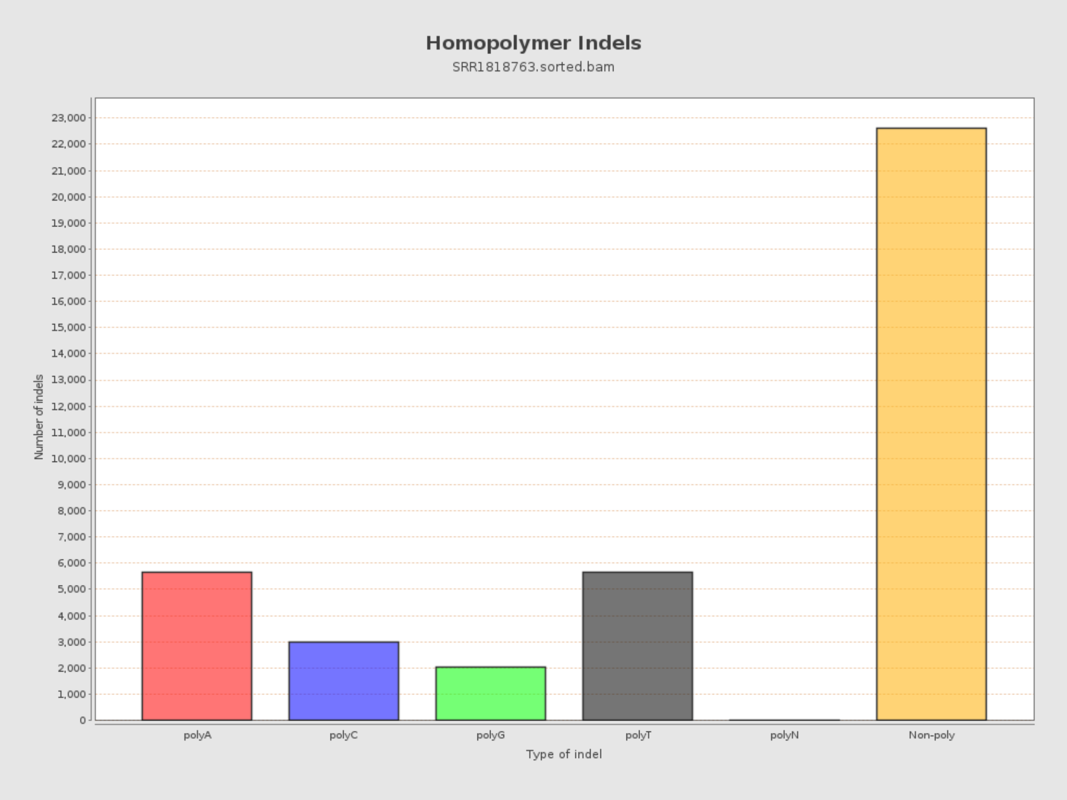
9. Results : Mapped Reads GC-content Distribution



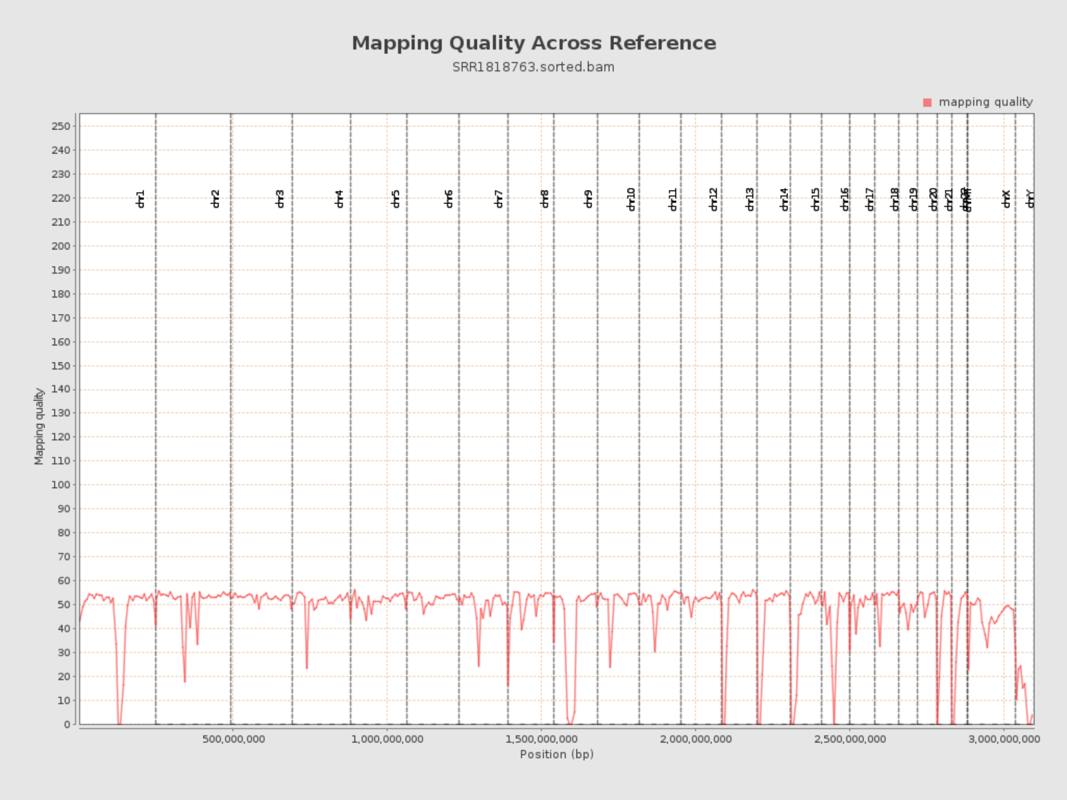
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram