Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:00:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818742.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_SRR1818742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:00:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,341,421
Mapped reads	2,272,055 / 97.04%
Unmapped reads	69,366 / 2.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,838 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,109,548 / 47.39%
Duplication rate	40.97%
Clipped reads	2,270,040 / 96.95%

2.2. ACGT Content

Number/percentage of A's	45,698,531 / 29.62%
Number/percentage of C's	31,529,675 / 20.43%
Number/percentage of T's	44,284,068 / 28.7%
Number/percentage of G's	32,780,451 / 21.24%
Number/percentage of N's	9,612 / 0.01%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.5838

2.4. Mapping Quality

Mean Mapping Quality	47.69

2.5. Mismatches and indels

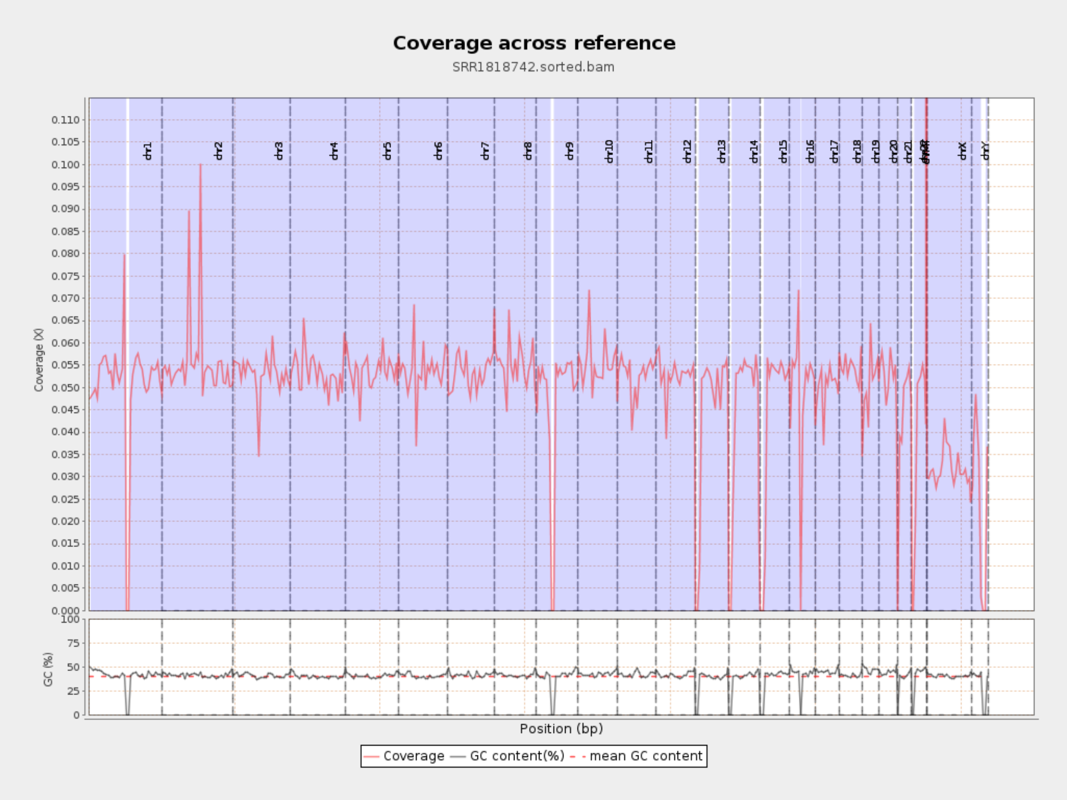
General error rate	0.53%
Mismatches	769,109
Insertions	23,479
Mapped reads with at least one insertion	1.02%
Deletions	39,619
Mapped reads with at least one deletion	1.73%
Homopolymer indels	37.89%

2.6. Chromosome stats

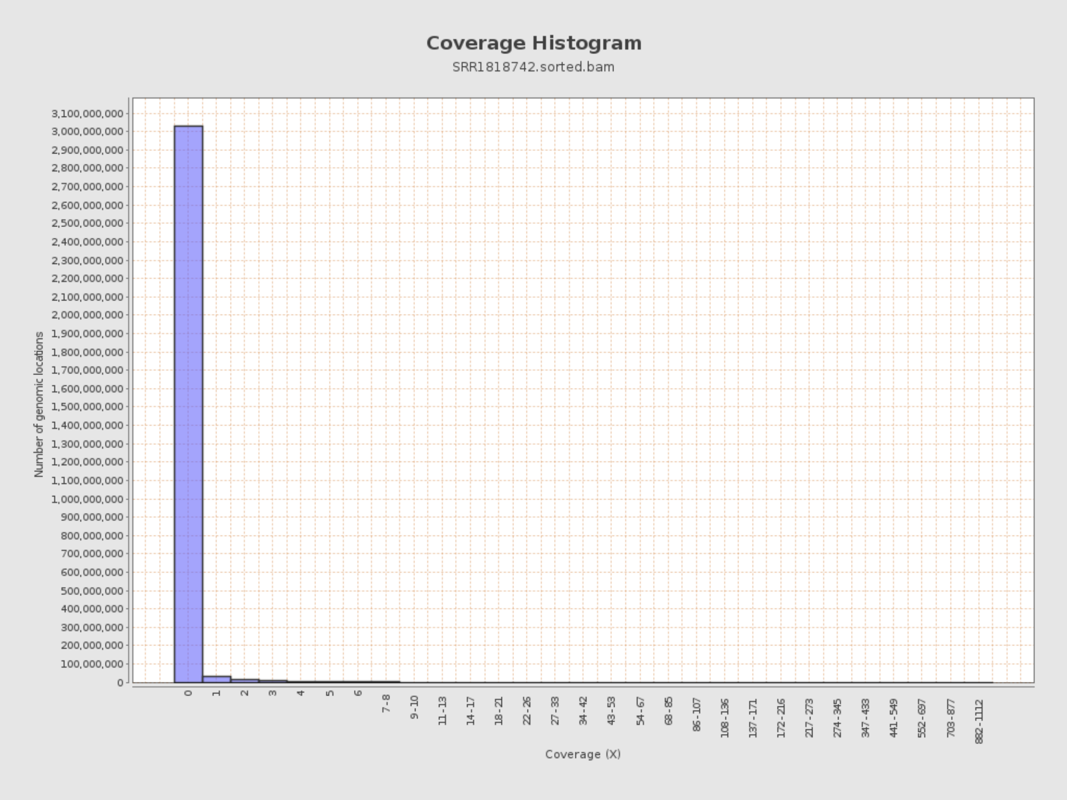
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12568459	0.0504	0.8554
chr2	243199373	13615551	0.056	0.8652
chr3	198022430	10493821	0.053	0.4583
chr4	191154276	10214265	0.0534	0.4994
chr5	180915260	9705795	0.0536	0.4666
chr6	171115067	9222826	0.0539	0.5024
chr7	159138663	8468277	0.0532	0.5238

chr8	146364022	8084609	0.0552	0.5353
chr9	141213431	6586857	0.0466	0.5092
chr10	135534747	7509444	0.0554	0.601
chr11	135006516	7116048	0.0527	0.5013
chr12	133851895	7049195	0.0527	0.4809
chr13	115169878	4994376	0.0434	0.4146
chr14	107349540	4799818	0.0447	0.4622
chr15	102531392	4443698	0.0433	0.4125
chr16	90354753	4472922	0.0495	0.6052
chr17	81195210	4051334	0.0499	0.4628
chr18	78077248	4242143	0.0543	0.7182
chr19	59128983	3011666	0.0509	0.7328
chr20	63025520	3335964	0.0529	0.4794
chr21	48129895	2046089	0.0425	0.4508
chr22	51304566	1857642	0.0362	0.4075
chrMT	16571	148863	8.9833	9.5103
chrX	155270560	4938970	0.0318	0.3859
chrY	59373566	1387339	0.0234	0.8341

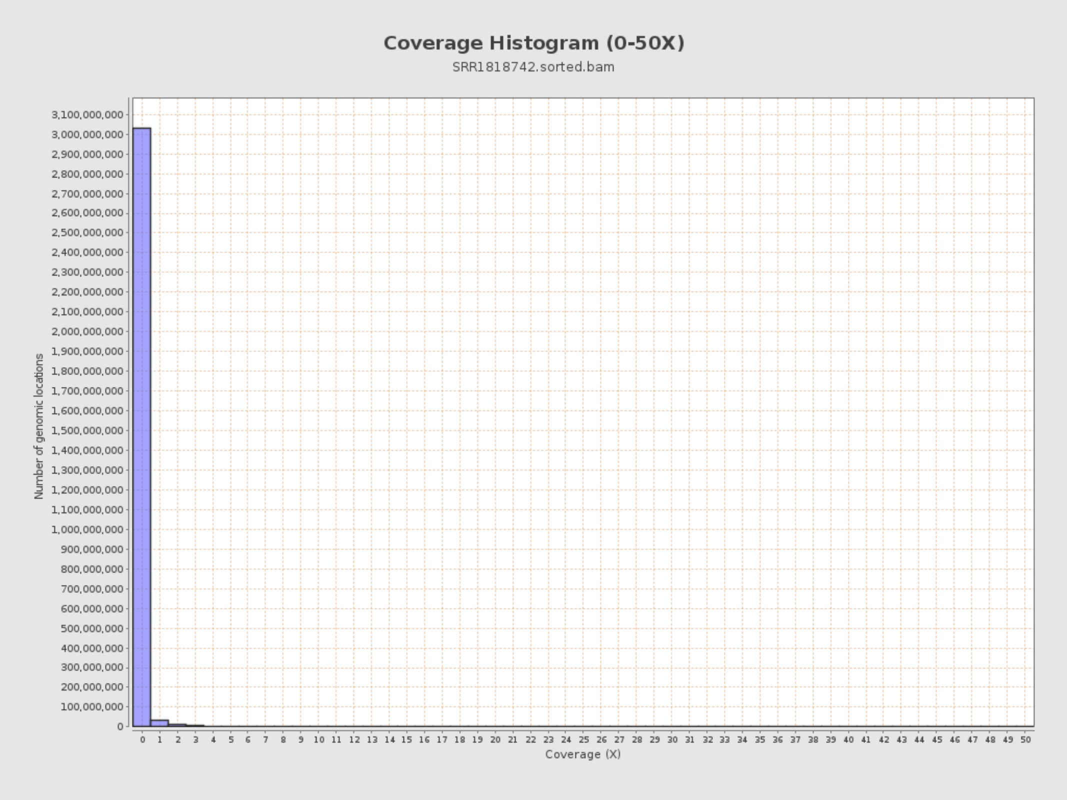
3. Results : Coverage across reference



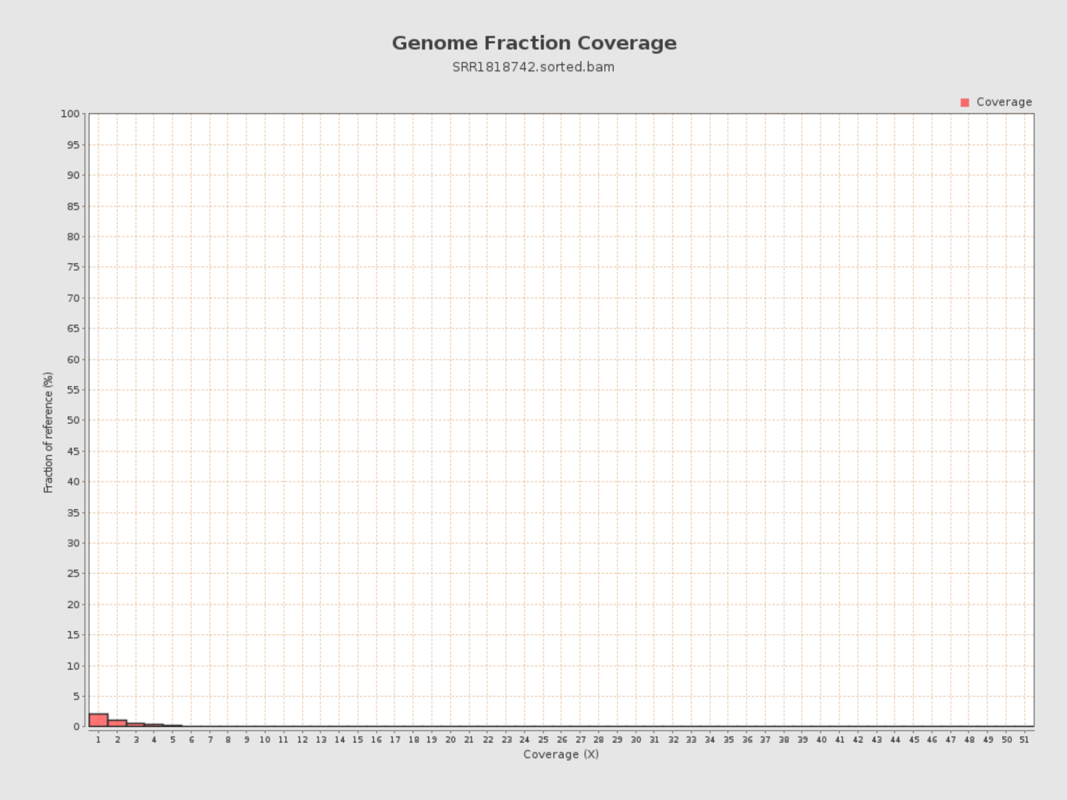
4. Results : Coverage Histogram



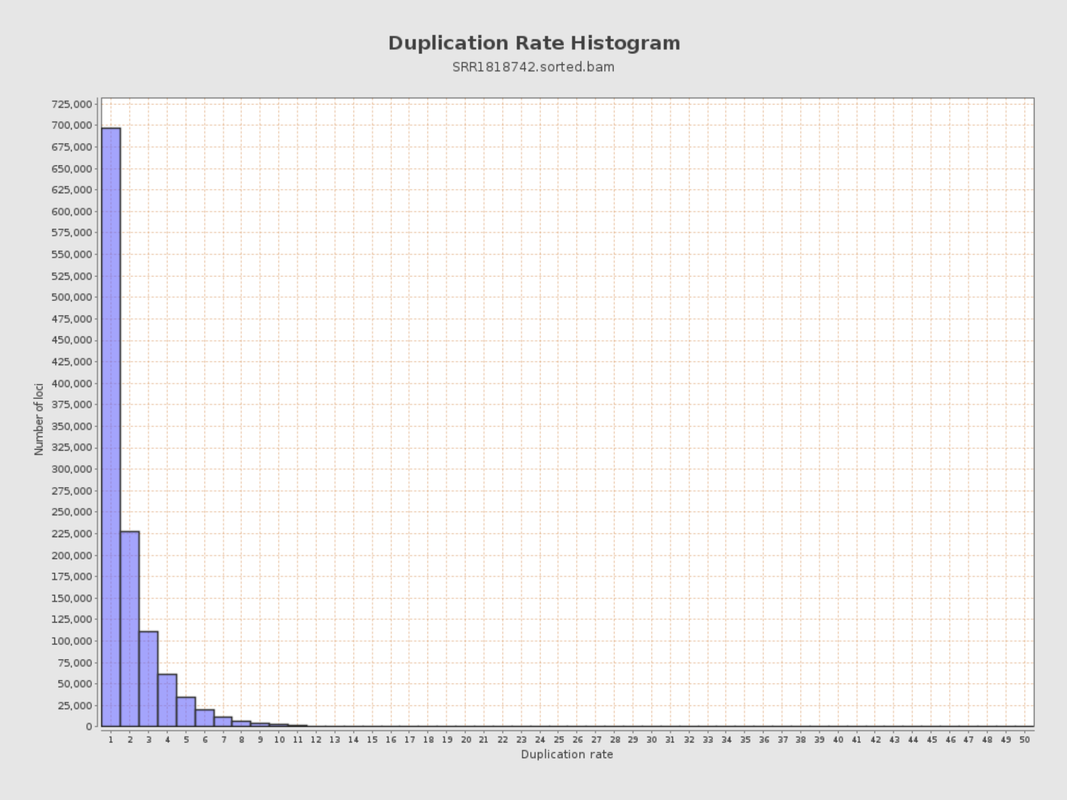
5. Results : Coverage Histogram (0-50X)



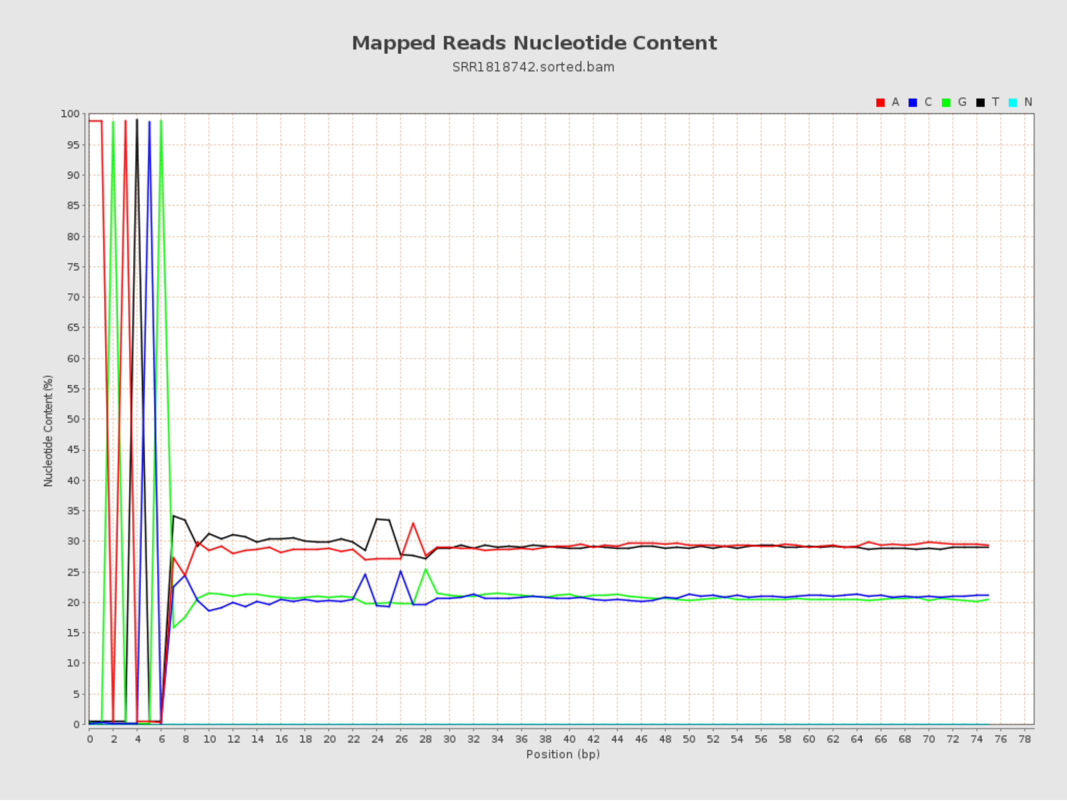
6. Results : Genome Fraction Coverage



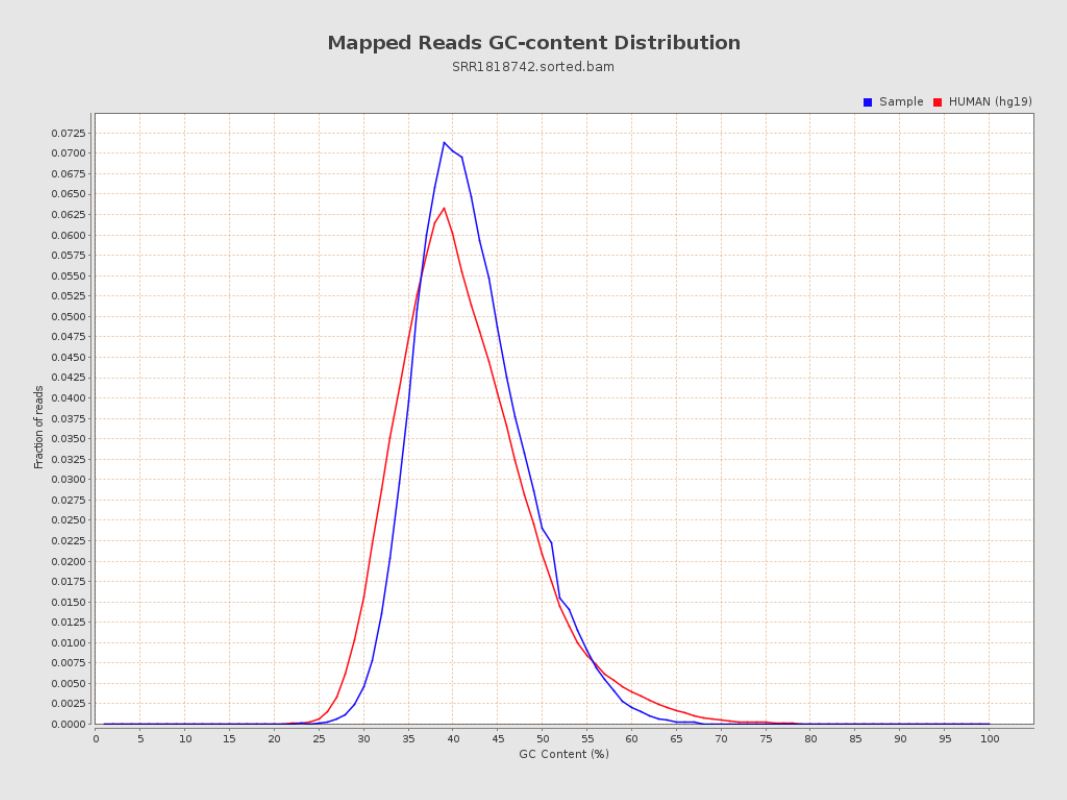
7. Results : Duplication Rate Histogram



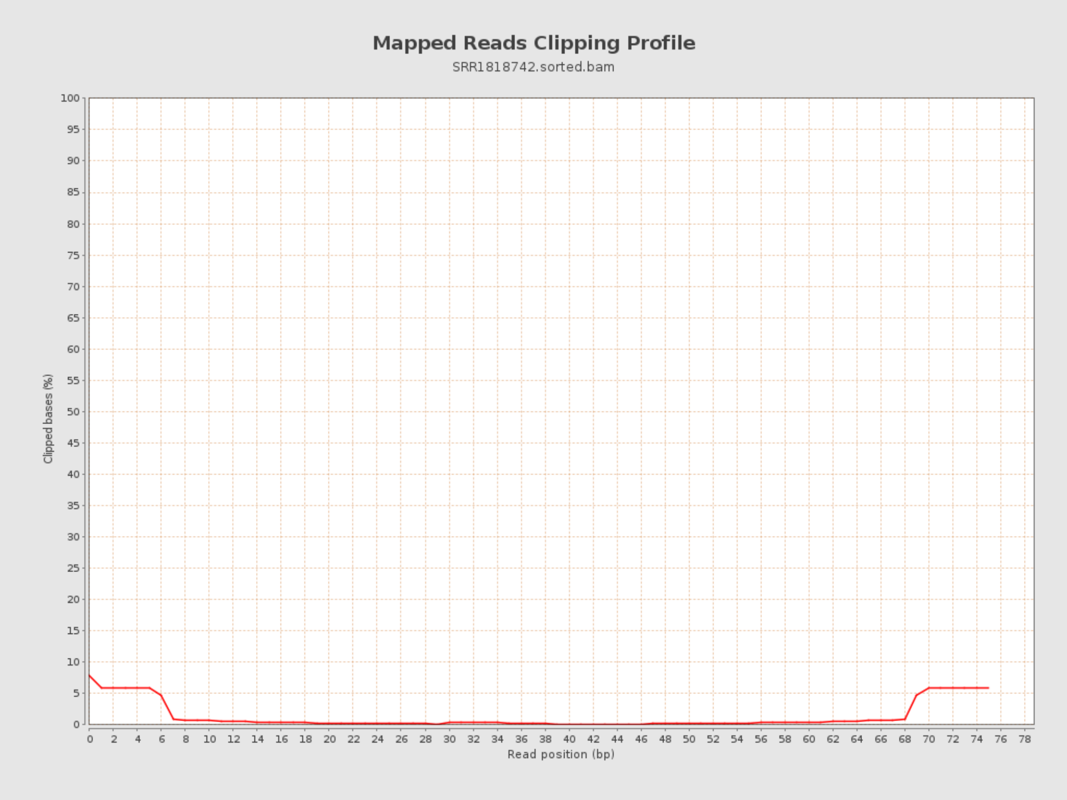
8. Results : Mapped Reads Nucleotide Content



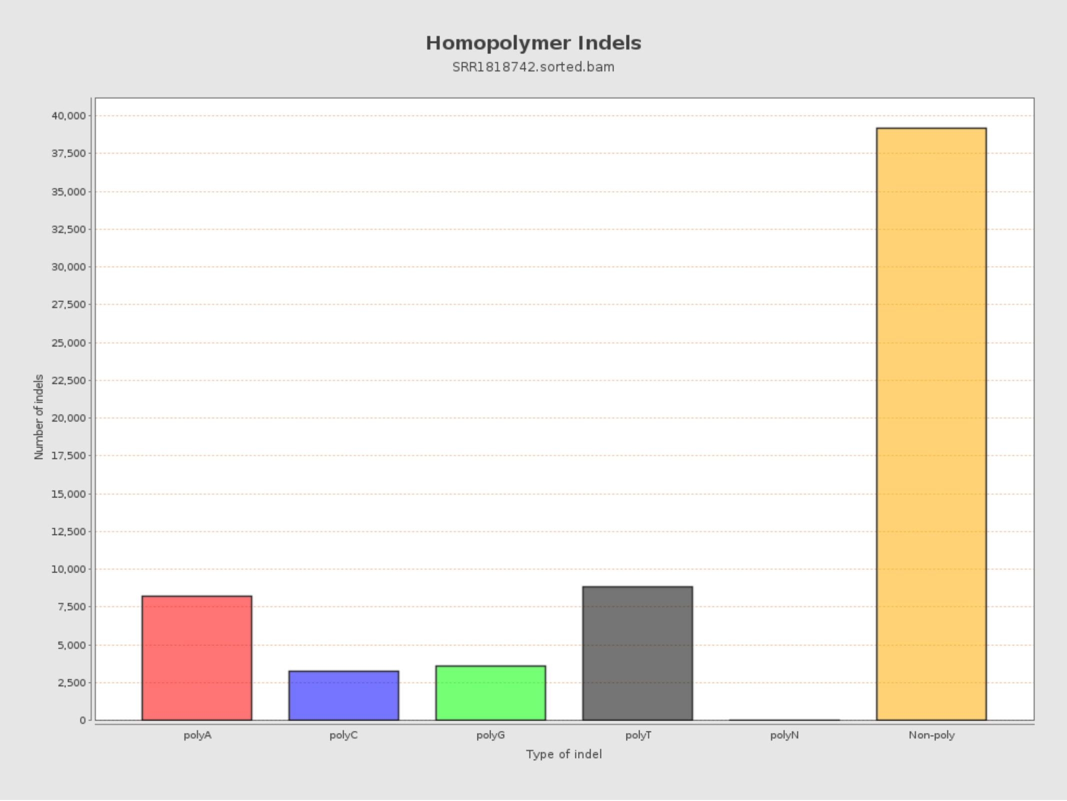
9. Results : Mapped Reads GC-content Distribution



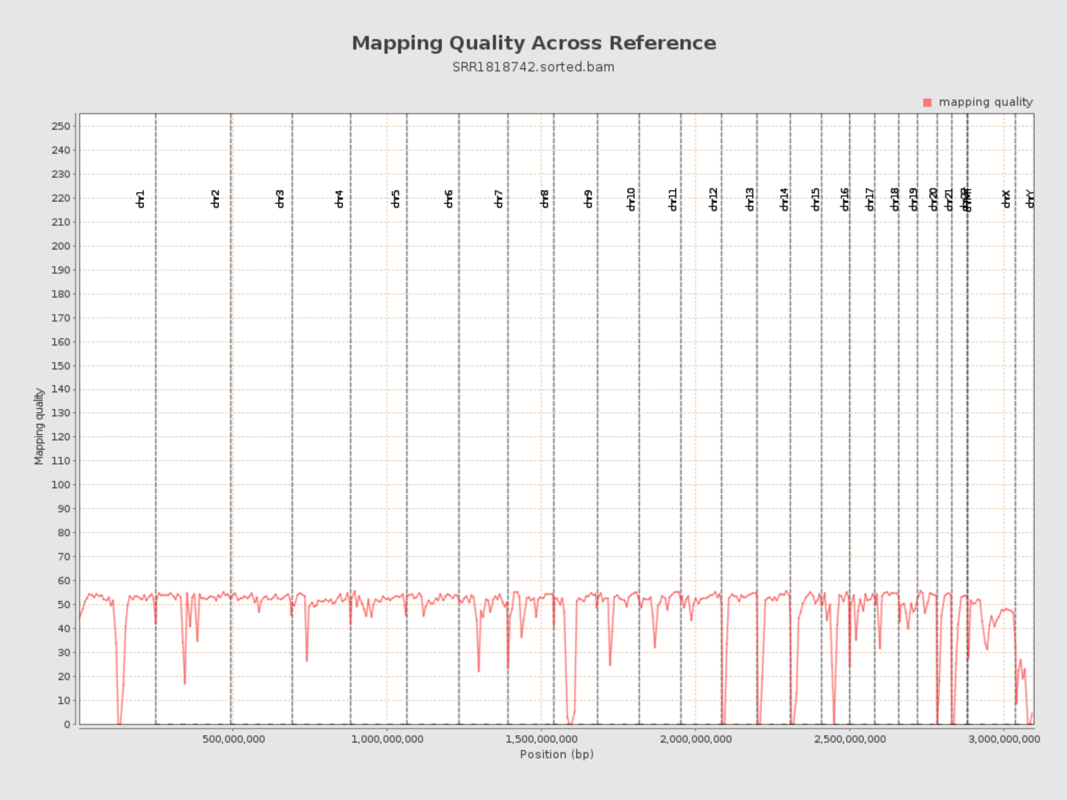
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram