Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:20:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524618.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_SRR10524618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:20:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,279,774
Mapped reads	2,126,257 / 93.27%
Unmapped reads	153,517 / 6.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,956 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	115,901 / 5.08%
Duplication rate	4.22%
Clipped reads	2,124,228 / 93.18%

2.2. ACGT Content

Number/percentage of A's	29,781,424 / 23.97%
Number/percentage of C's	24,032,366 / 19.34%
Number/percentage of T's	41,050,690 / 33.04%
Number/percentage of G's	29,384,741 / 23.65%
Number/percentage of N's	760 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3361

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

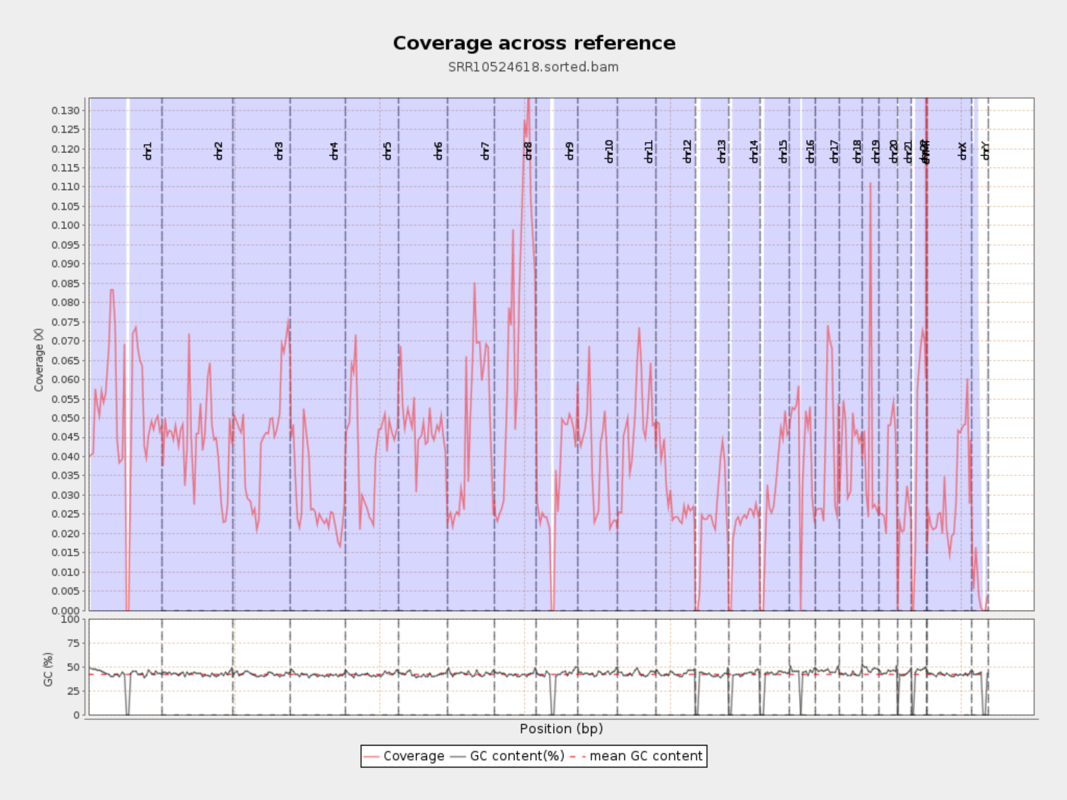
General error rate	0.48%
Mismatches	577,785
Insertions	7,981
Mapped reads with at least one insertion	0.37%
Deletions	23,146
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.27%

2.6. Chromosome stats

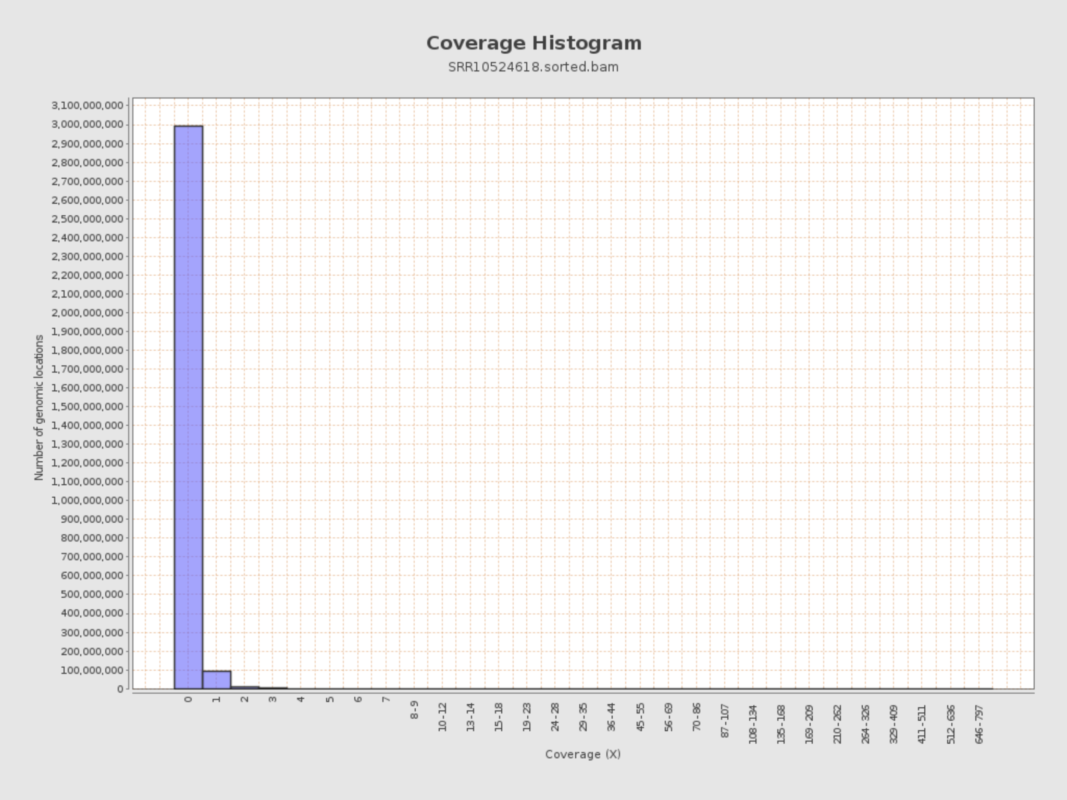
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12927480	0.0519	0.607
chr2	243199373	10692284	0.044	0.3922
chr3	198022430	9023435	0.0456	0.2453
chr4	191154276	5395883	0.0282	0.2216
chr5	180915260	7700036	0.0426	0.236
chr6	171115067	8178784	0.0478	0.2726
chr7	159138663	7482229	0.047	0.4488

chr8	146364022	10822065	0.0739	0.4395
chr9	141213431	4571120	0.0324	0.3055
chr10	135534747	5122882	0.0378	0.3178
chr11	135006516	6468942	0.0479	0.33
chr12	133851895	4077299	0.0305	0.2089
chr13	115169878	2710254	0.0235	0.177
chr14	107349540	2279782	0.0212	0.1768
chr15	102531392	3175109	0.031	0.2131
chr16	90354753	3780184	0.0418	0.2507
chr17	81195210	3412692	0.042	0.2413
chr18	78077248	3371766	0.0432	0.4926
chr19	59128983	2432946	0.0411	0.4149
chr20	63025520	2313741	0.0367	0.225
chr21	48129895	1075077	0.0223	0.1861
chr22	51304566	2318565	0.0452	0.2432
chrMT	16571	12021	0.7254	1.0555
chrX	155270560	4655826	0.03	0.2278
chrY	59373566	289176	0.0049	0.1312

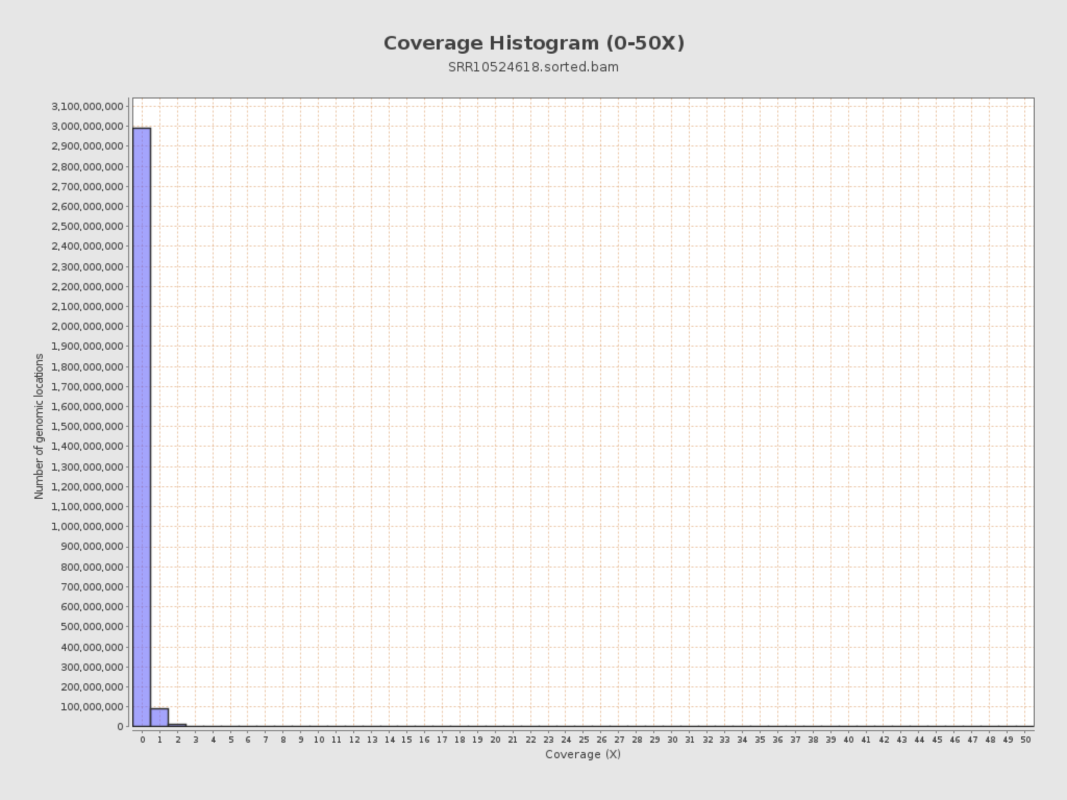
3. Results : Coverage across reference



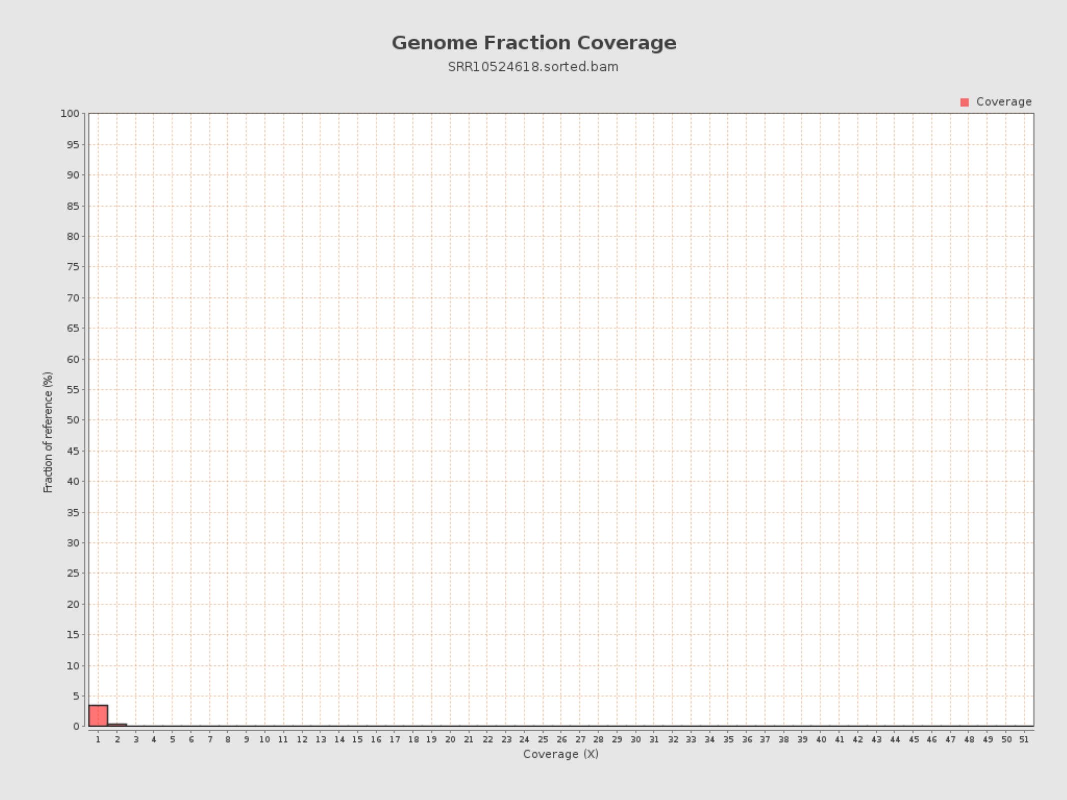
4. Results : Coverage Histogram



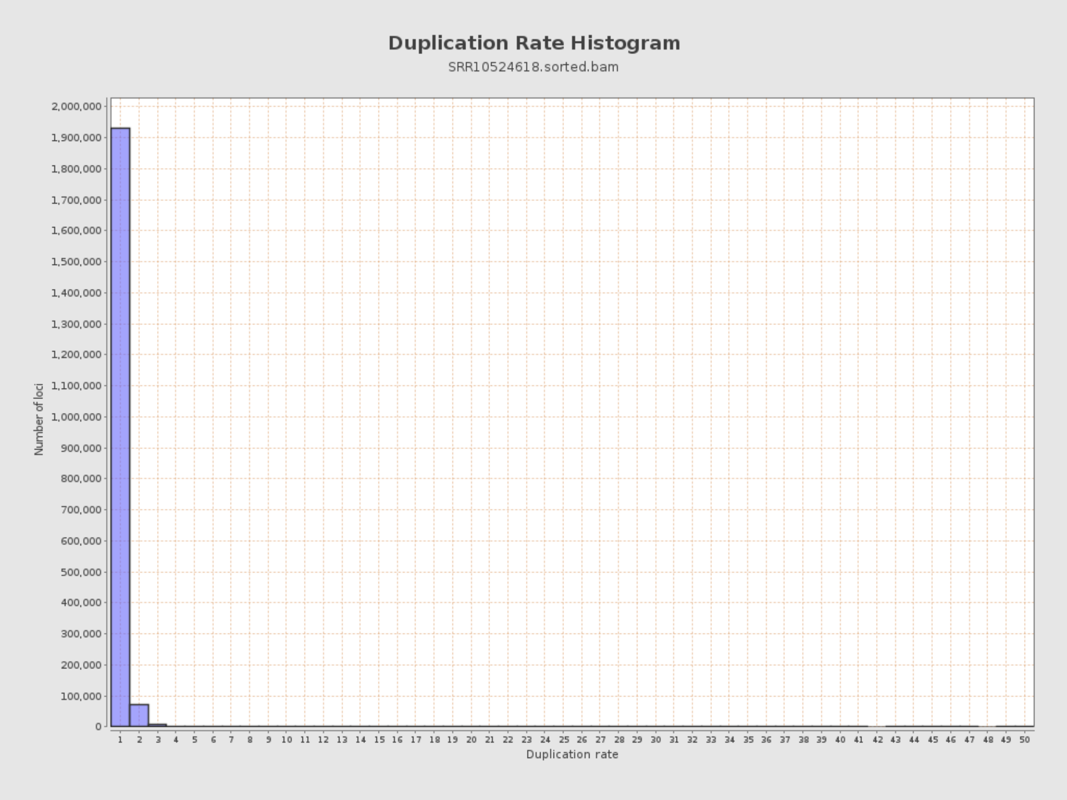
5. Results : Coverage Histogram (0-50X)



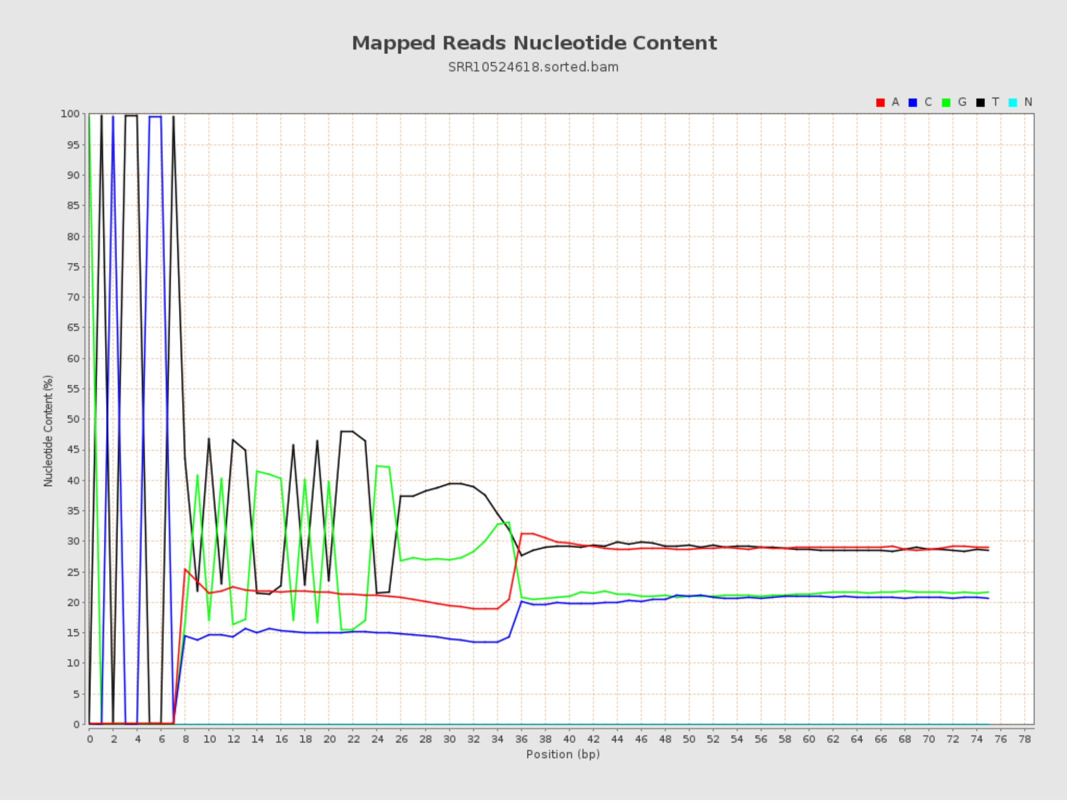
6. Results : Genome Fraction Coverage



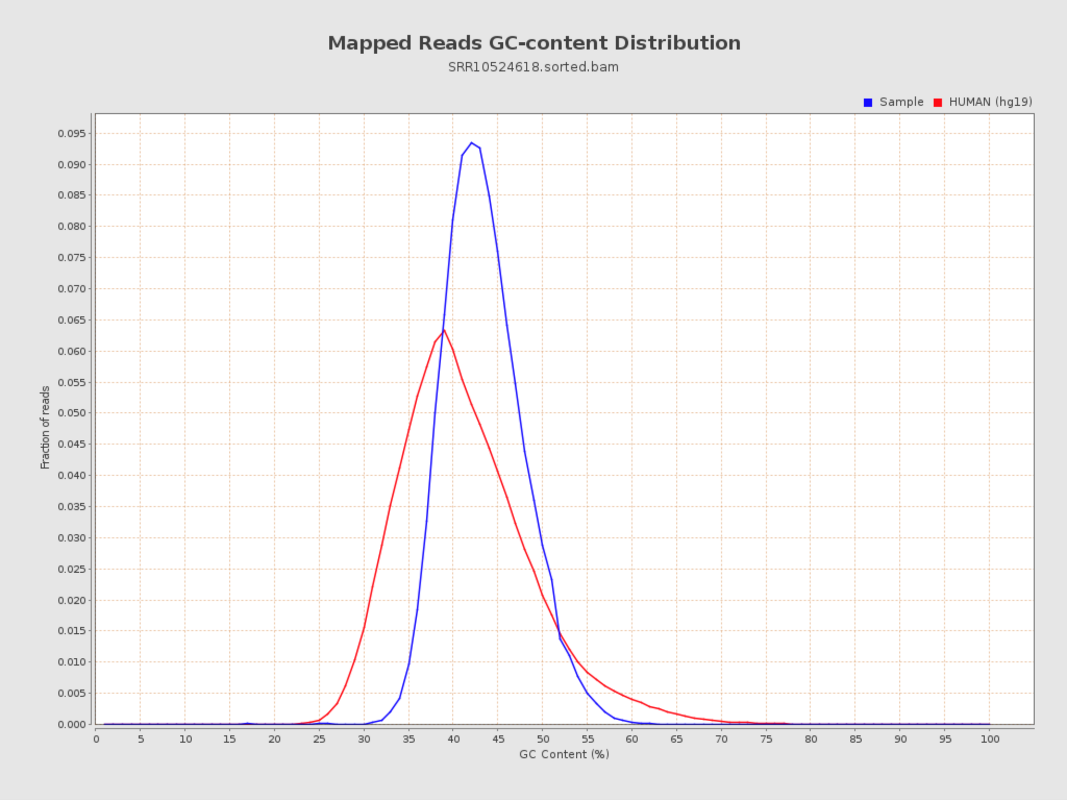
7. Results : Duplication Rate Histogram



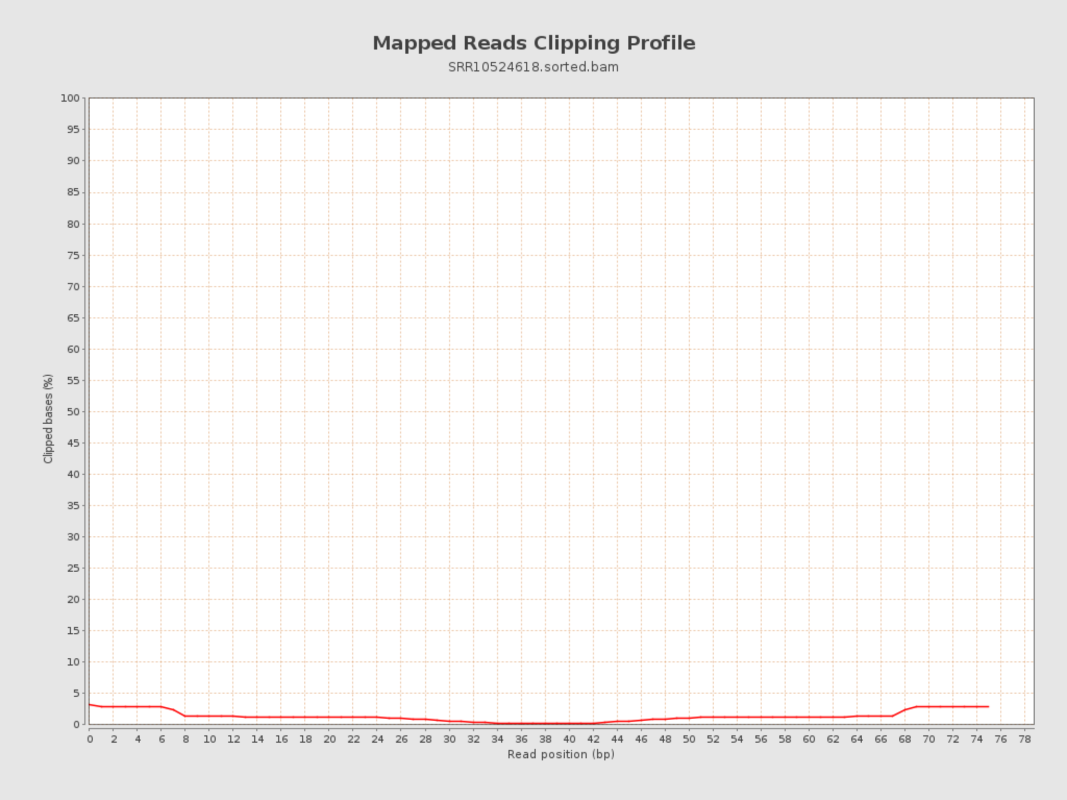
8. Results : Mapped Reads Nucleotide Content



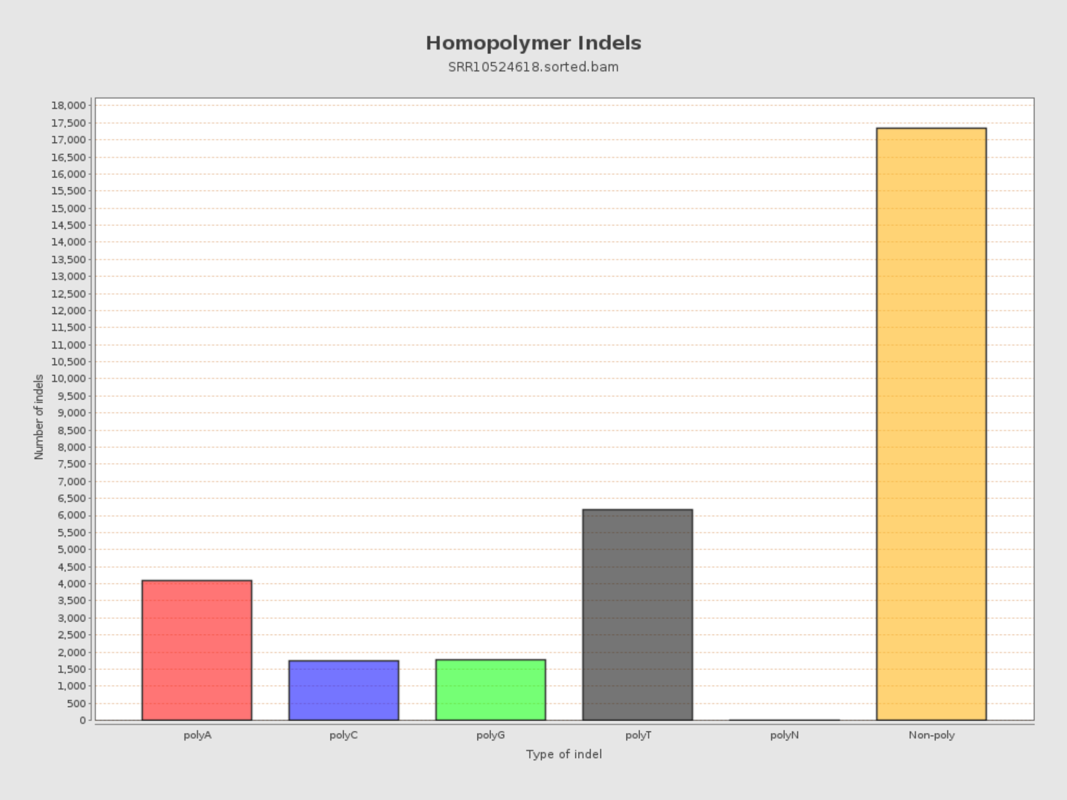
9. Results : Mapped Reads GC-content Distribution



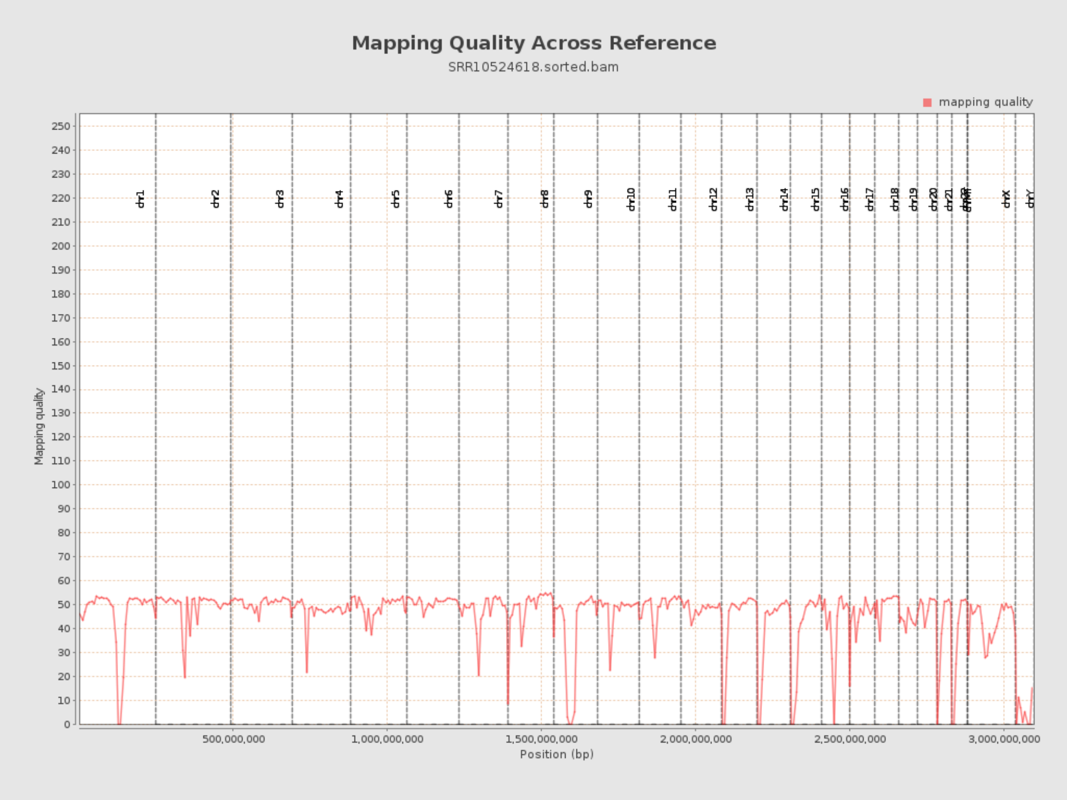
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram