Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 08:20:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524518.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_SRR10524518 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524518.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 08:20:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524518.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,376,651
Mapped reads	2,185,689 / 91.97%
Unmapped reads	190,962 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,881 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	148,850 / 6.26%
Duplication rate	5.21%
Clipped reads	2,189,874 / 92.14%

2.2. ACGT Content

Number/percentage of A's	30,529,903 / 23.9%
Number/percentage of C's	23,080,545 / 18.07%
Number/percentage of T's	41,893,312 / 32.8%
Number/percentage of G's	32,211,001 / 25.22%
Number/percentage of N's	1,802 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0413

Standard Deviation	0.3821

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

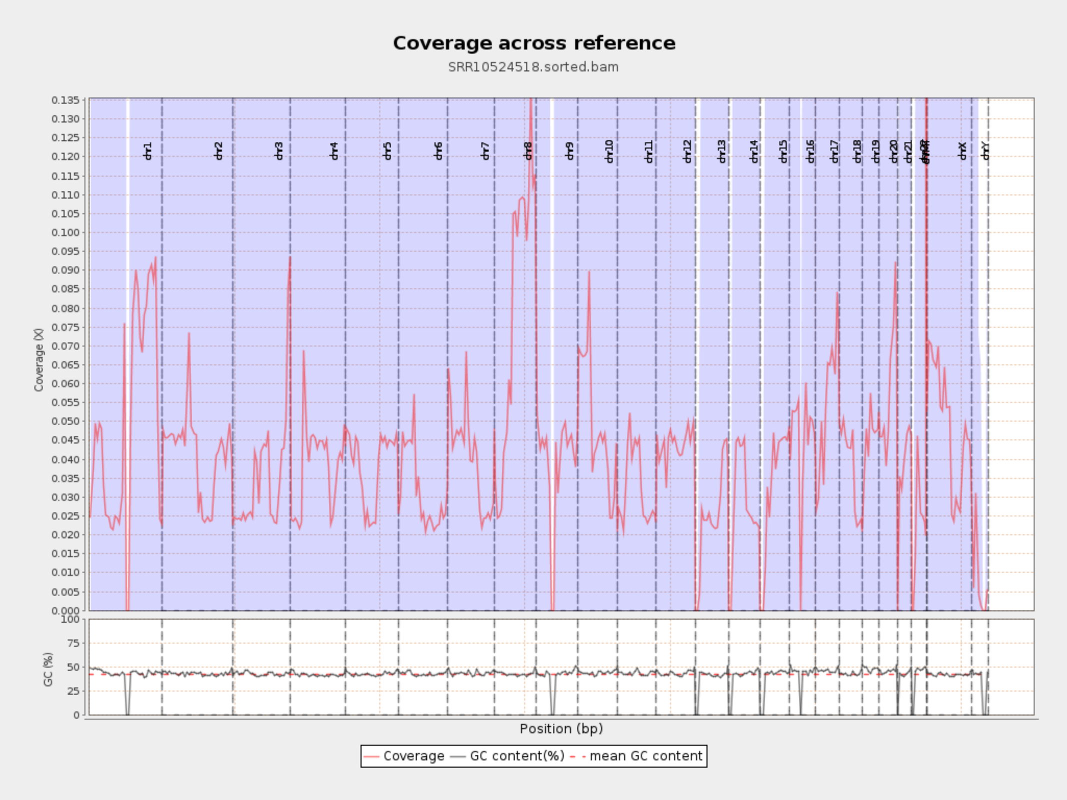
General error rate	0.52%
Mismatches	653,500
Insertions	8,440
Mapped reads with at least one insertion	0.38%
Deletions	23,753
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.16%

2.6. Chromosome stats

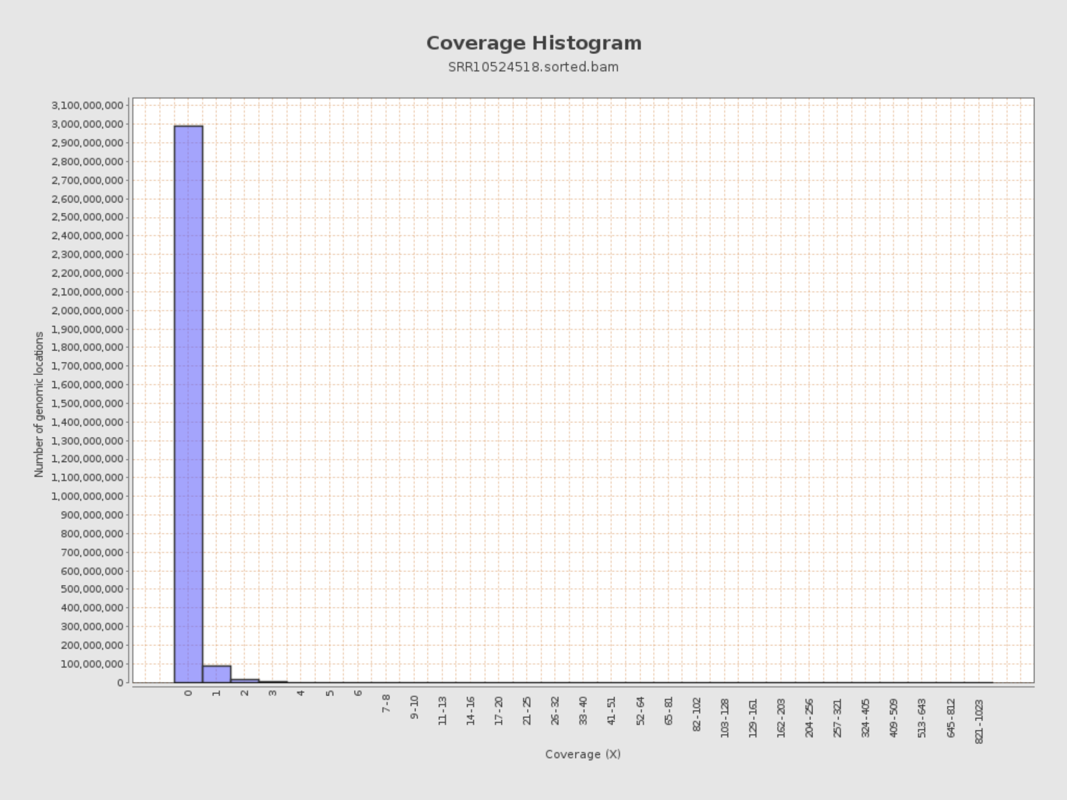
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12406325	0.0498	0.7645
chr2	243199373	10146484	0.0417	0.466
chr3	198022430	6896075	0.0348	0.219
chr4	191154276	7228361	0.0378	0.2802
chr5	180915260	6905571	0.0382	0.2295
chr6	171115067	5390113	0.0315	0.2722
chr7	159138663	6420308	0.0403	0.4326

chr8	146364022	11688782	0.0799	0.3981
chr9	141213431	5404926	0.0383	0.2937
chr10	135534747	6742740	0.0497	0.4269
chr11	135006516	4392839	0.0325	0.313
chr12	133851895	5884686	0.044	0.2464
chr13	115169878	2846834	0.0247	0.1849
chr14	107349540	3015454	0.0281	0.2009
chr15	102531392	3351564	0.0327	0.2142
chr16	90354753	4086769	0.0452	0.27
chr17	81195210	4493132	0.0553	0.2923
chr18	78077248	2989659	0.0383	0.5609
chr19	59128983	2687892	0.0455	0.5156
chr20	63025520	3698873	0.0587	0.2908
chr21	48129895	1792330	0.0372	0.274
chr22	51304566	1083567	0.0211	0.1733
chrMT	16571	78023	4.7084	3.3861
chrX	155270560	7653141	0.0493	0.2895
chrY	59373566	472440	0.008	0.2685

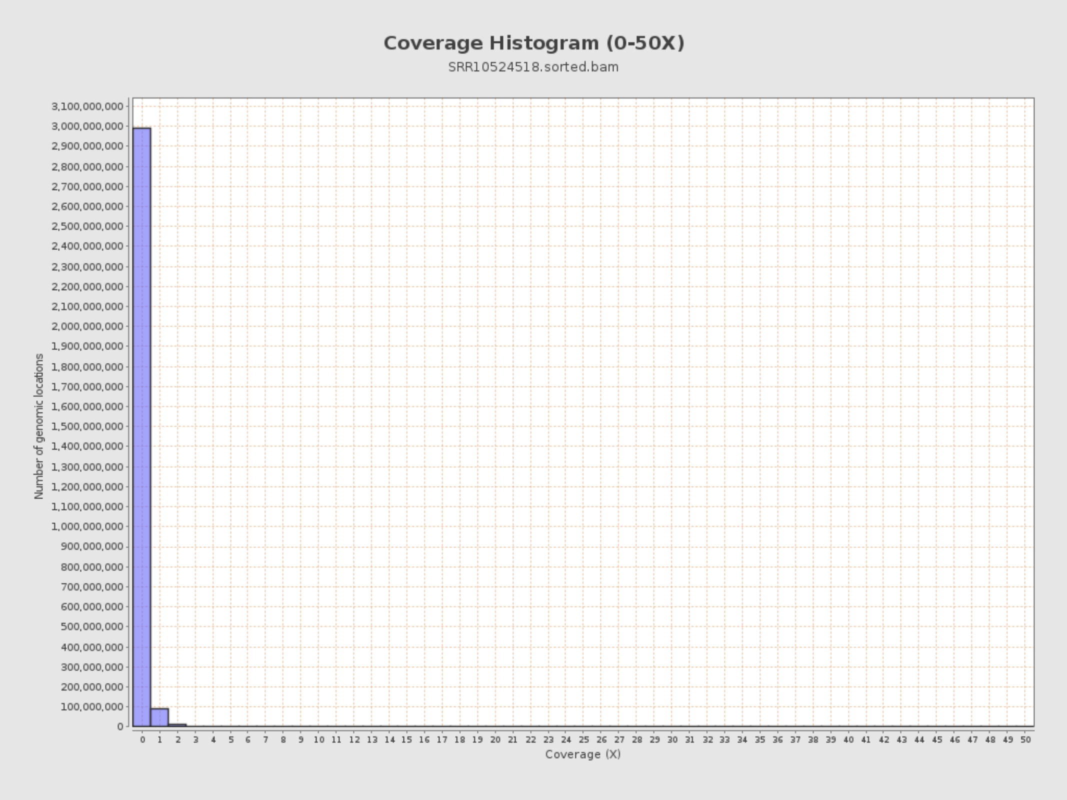
3. Results : Coverage across reference



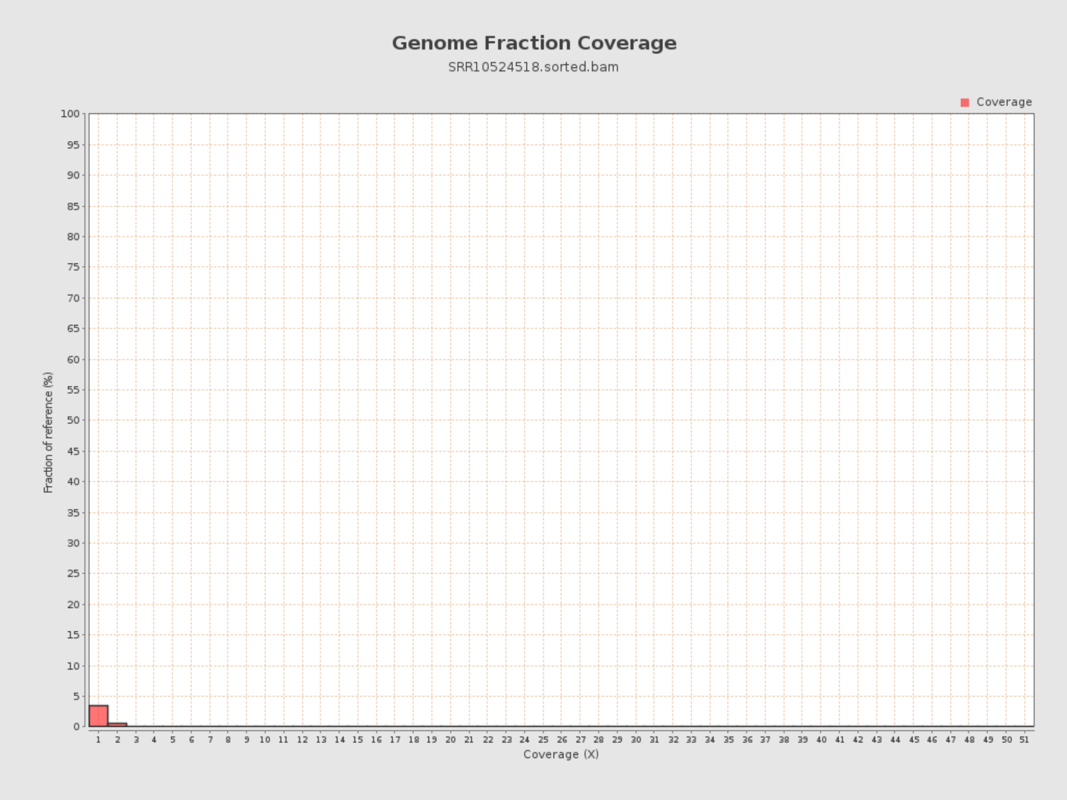
4. Results : Coverage Histogram



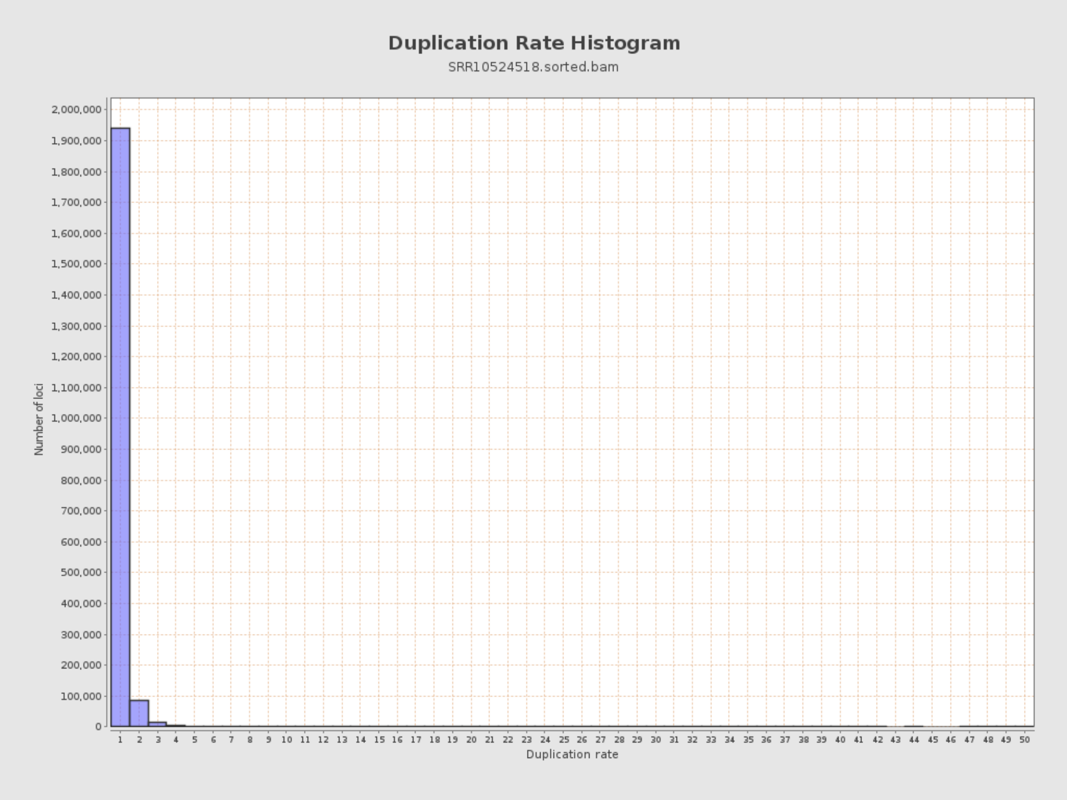
5. Results : Coverage Histogram (0-50X)



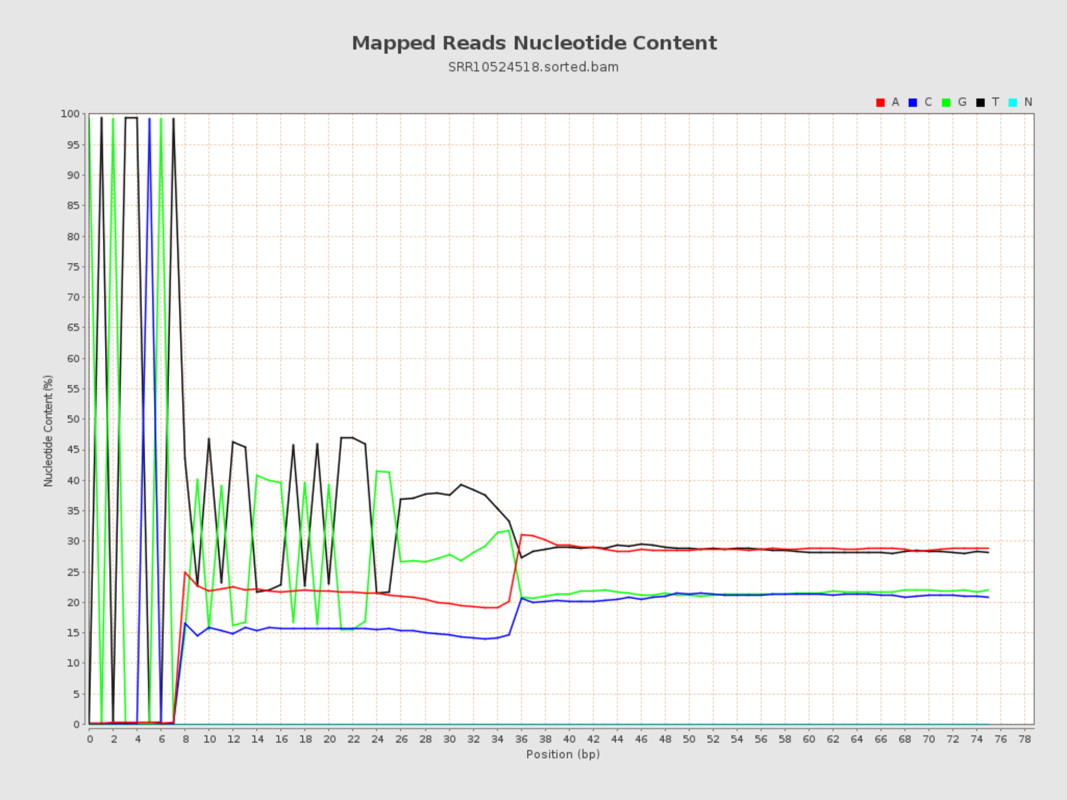
6. Results : Genome Fraction Coverage



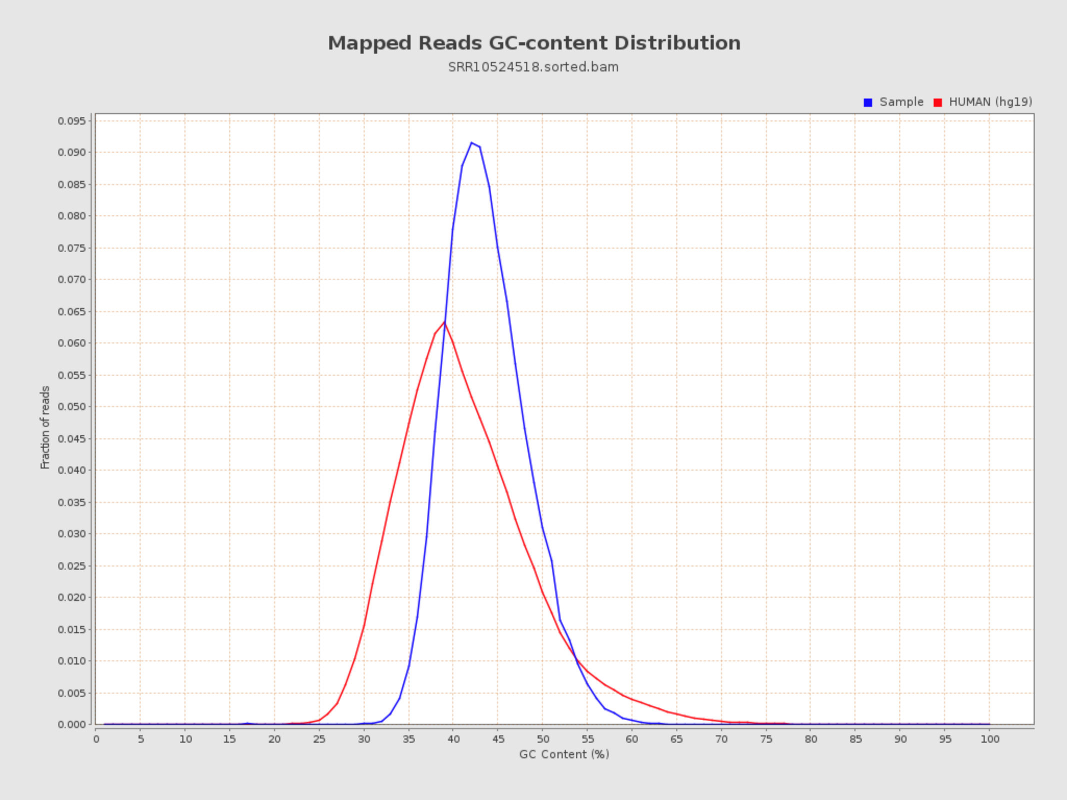
7. Results : Duplication Rate Histogram



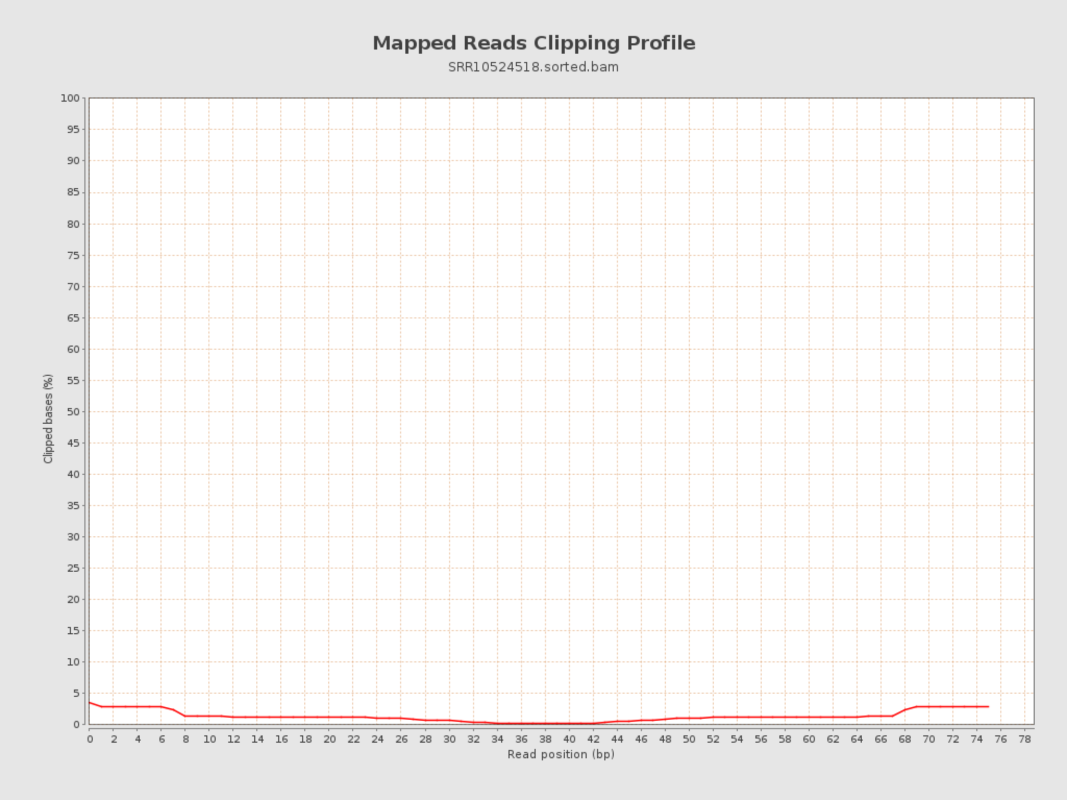
8. Results : Mapped Reads Nucleotide Content



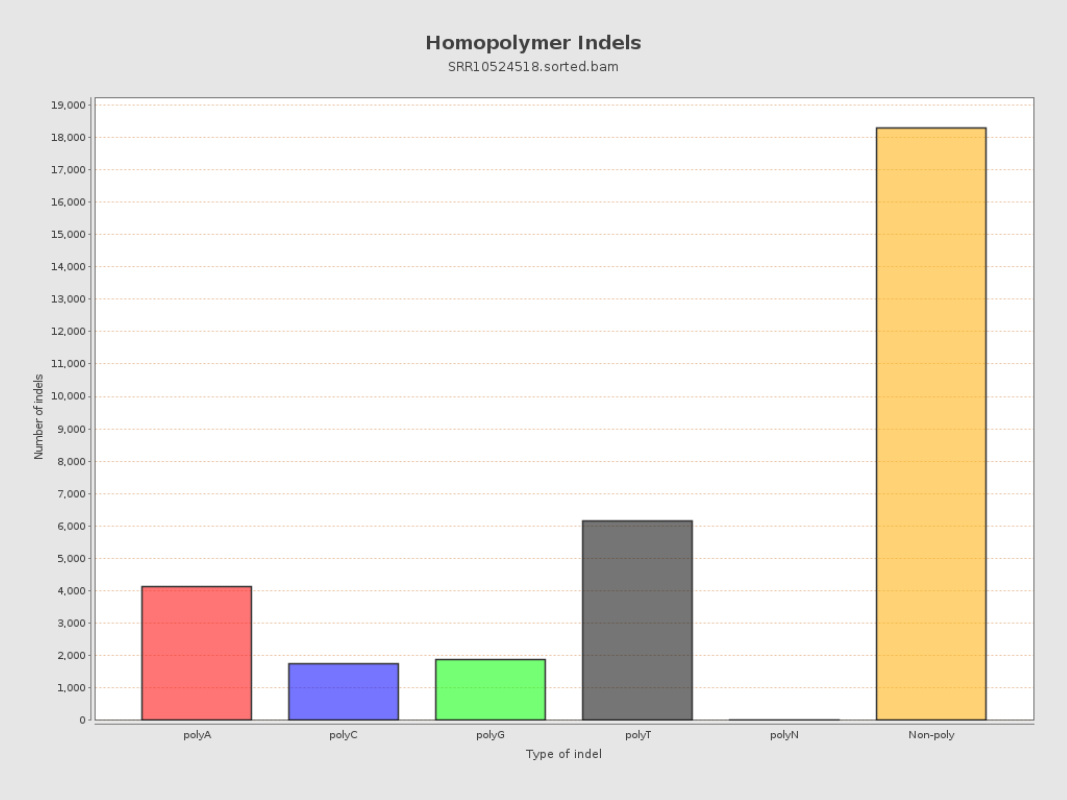
9. Results : Mapped Reads GC-content Distribution



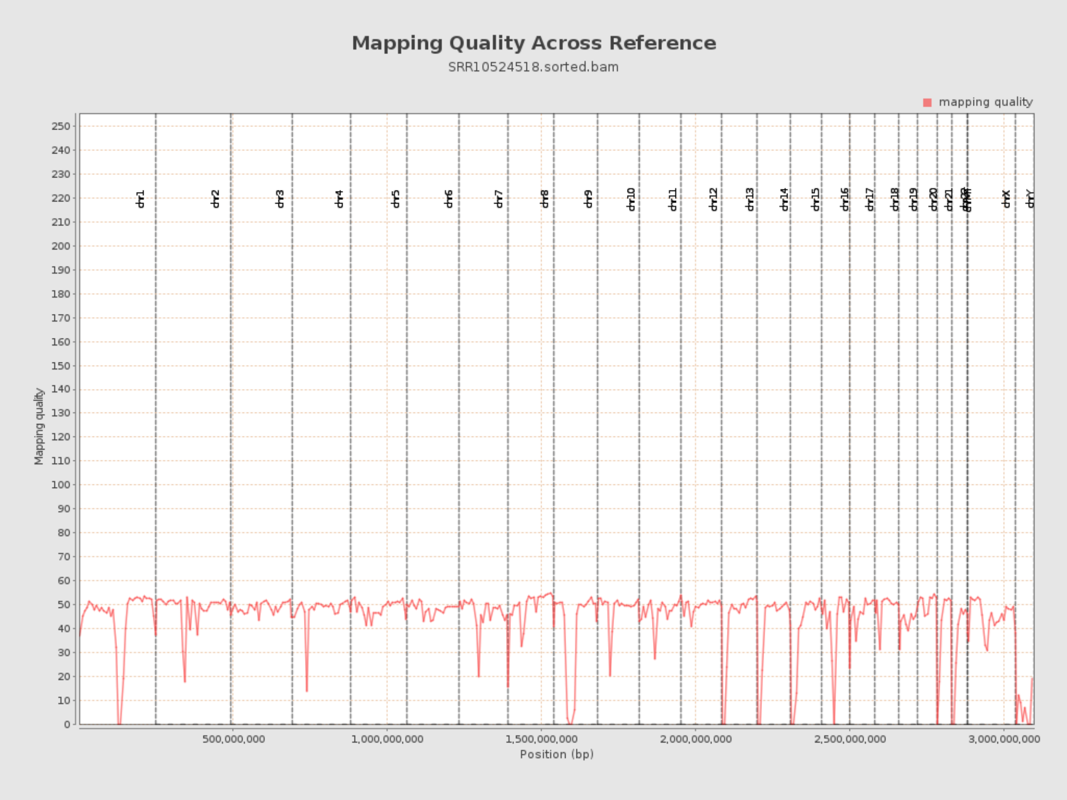
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram