Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:14:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505918.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_SRR1505918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:14:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,714,736
Mapped reads	4,603,718 / 68.56%
Unmapped reads	2,111,018 / 31.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	219 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	212,824 / 3.17%
Duplication rate	3.45%
Clipped reads	894,107 / 13.32%

2.2. ACGT Content

Number/percentage of A's	62,913,077 / 29.68%
Number/percentage of C's	42,985,632 / 20.28%
Number/percentage of T's	62,462,041 / 29.46%
Number/percentage of G's	43,642,850 / 20.59%
Number/percentage of N's	722 / 0%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0685

Standard Deviation	0.5821

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Mismatches and indels

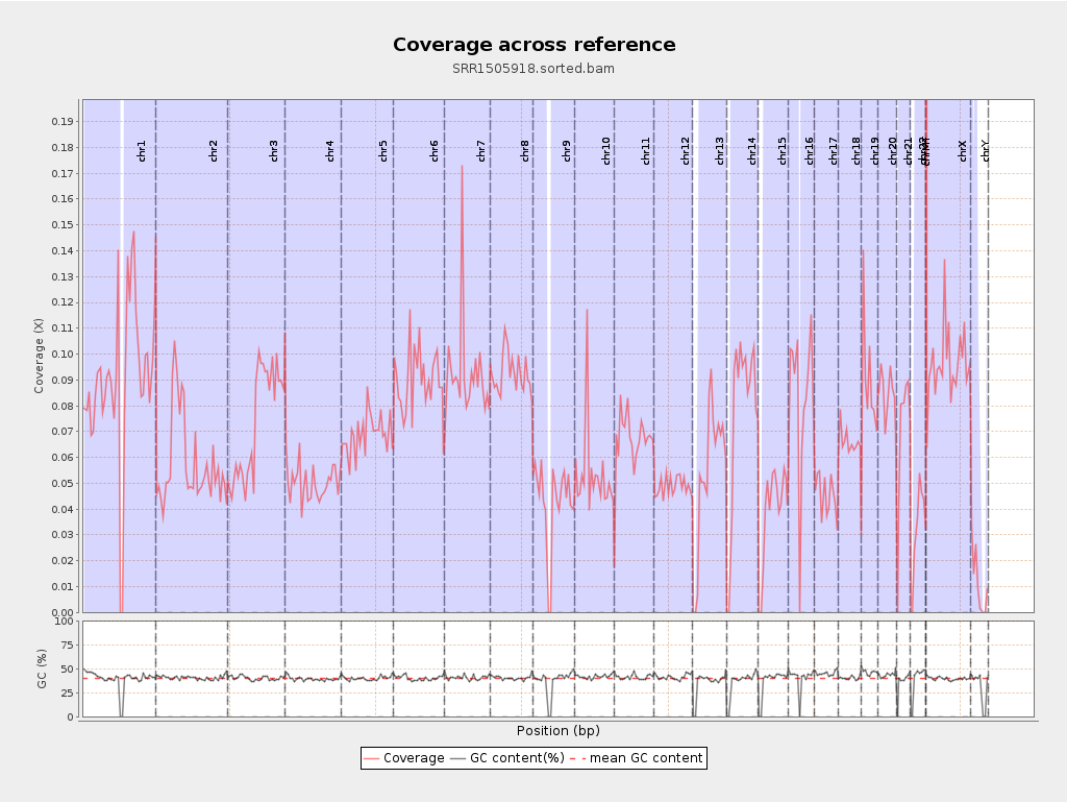
General error rate	0.51%
Mismatches	1,075,526
Insertions	9,755
Mapped reads with at least one insertion	0.21%
Deletions	32,168
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.71%

2.6. Chromosome stats

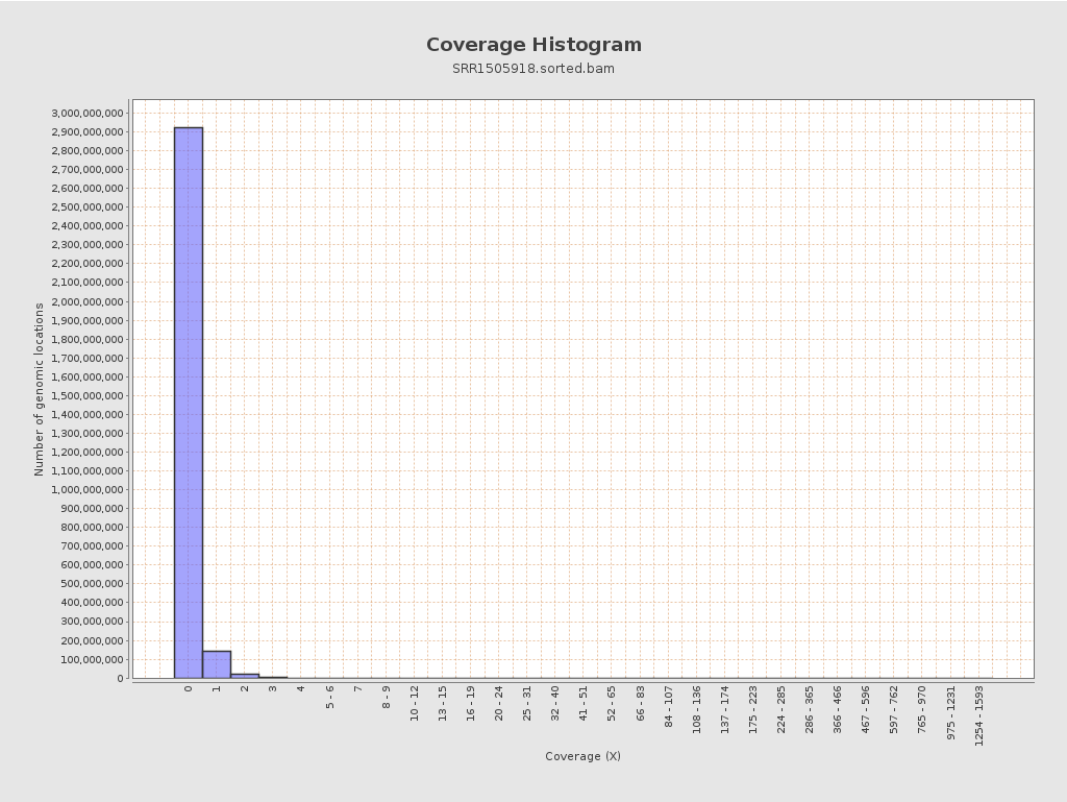
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22660718	0.0909	1.1526
chr2	243199373	14100311	0.058	0.398
chr3	198022430	14490214	0.0732	0.3223
chr4	191154276	9610302	0.0503	0.2691
chr5	180915260	12490477	0.069	0.3131
chr6	171115067	15462675	0.0904	0.4476
chr7	159138663	14646708	0.092	1.1361

chr8	146364022	13495028	0.0922	0.7764
chr9	141213431	6062636	0.0429	0.3414
chr10	135534747	7179144	0.053	0.6245
chr11	135006516	9122401	0.0676	0.4462
chr12	133851895	6518423	0.0487	0.2801
chr13	115169878	6335640	0.055	0.2743
chr14	107349540	8394650	0.0782	0.5598
chr15	102531392	3956744	0.0386	0.2274
chr16	90354753	7335463	0.0812	0.396
chr17	81195210	3709059	0.0457	0.2887
chr18	78077248	5172369	0.0662	0.64
chr19	59128983	5225464	0.0884	0.8749
chr20	63025520	5347694	0.0848	0.3523
chr21	48129895	3306882	0.0687	0.3256
chr22	51304566	1655171	0.0323	0.2101
chrMT	16571	168142	10.1468	7.0351
chrX	155270560	14955213	0.0963	0.412
chrY	59373566	647776	0.0109	0.1454

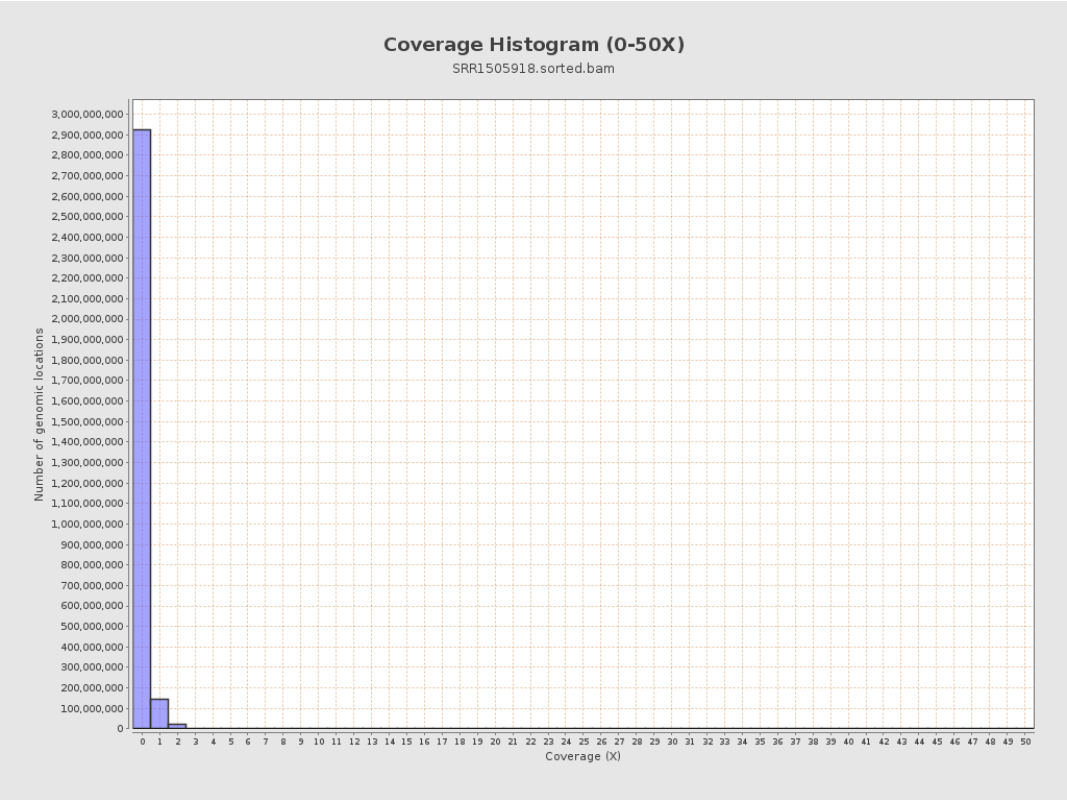
3. Results : Coverage across reference



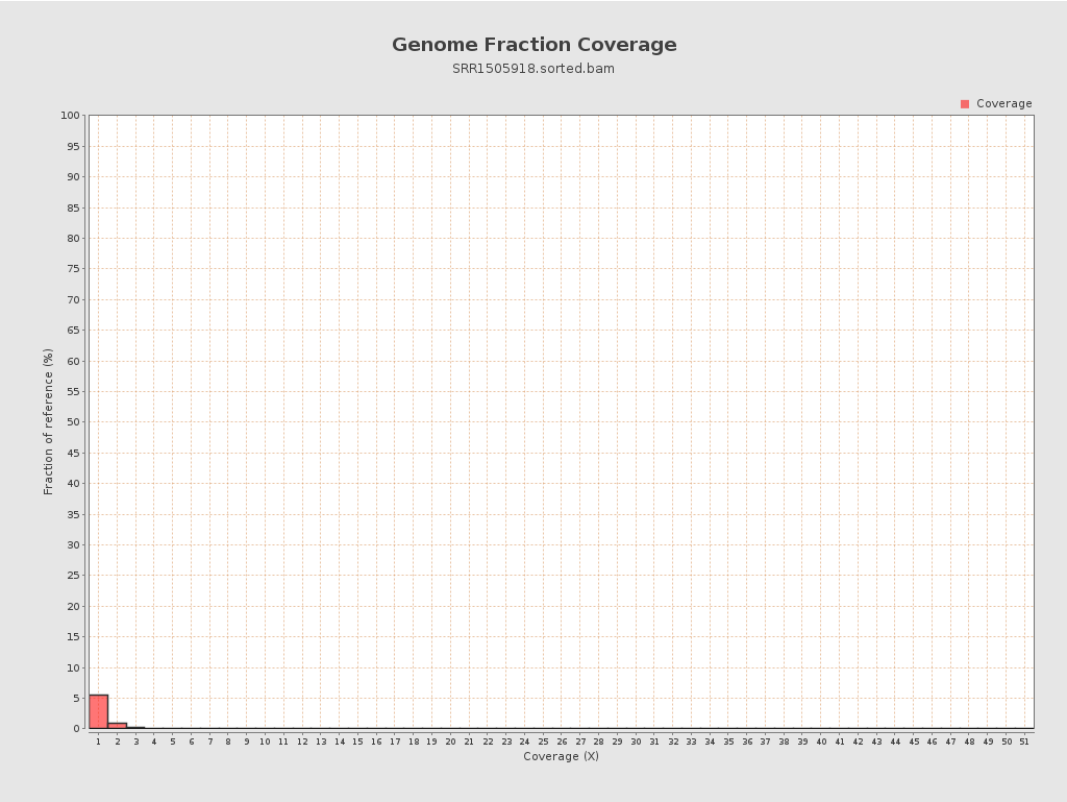
4. Results : Coverage Histogram



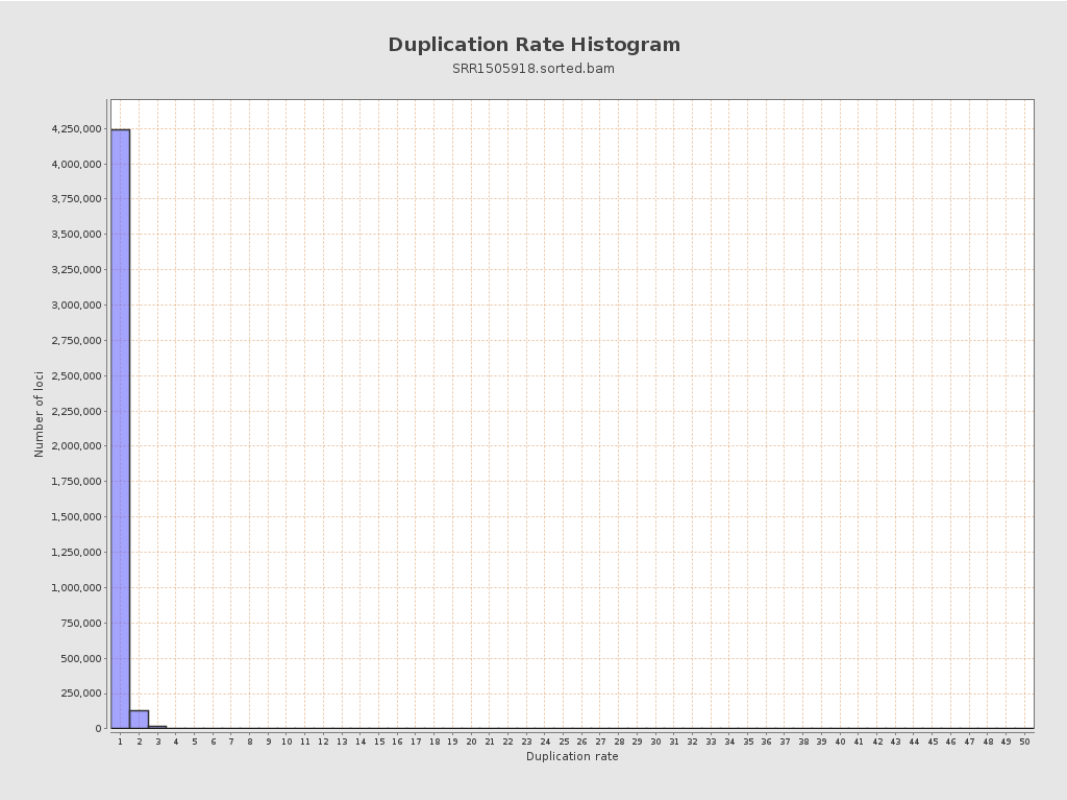
5. Results : Coverage Histogram (0-50X)



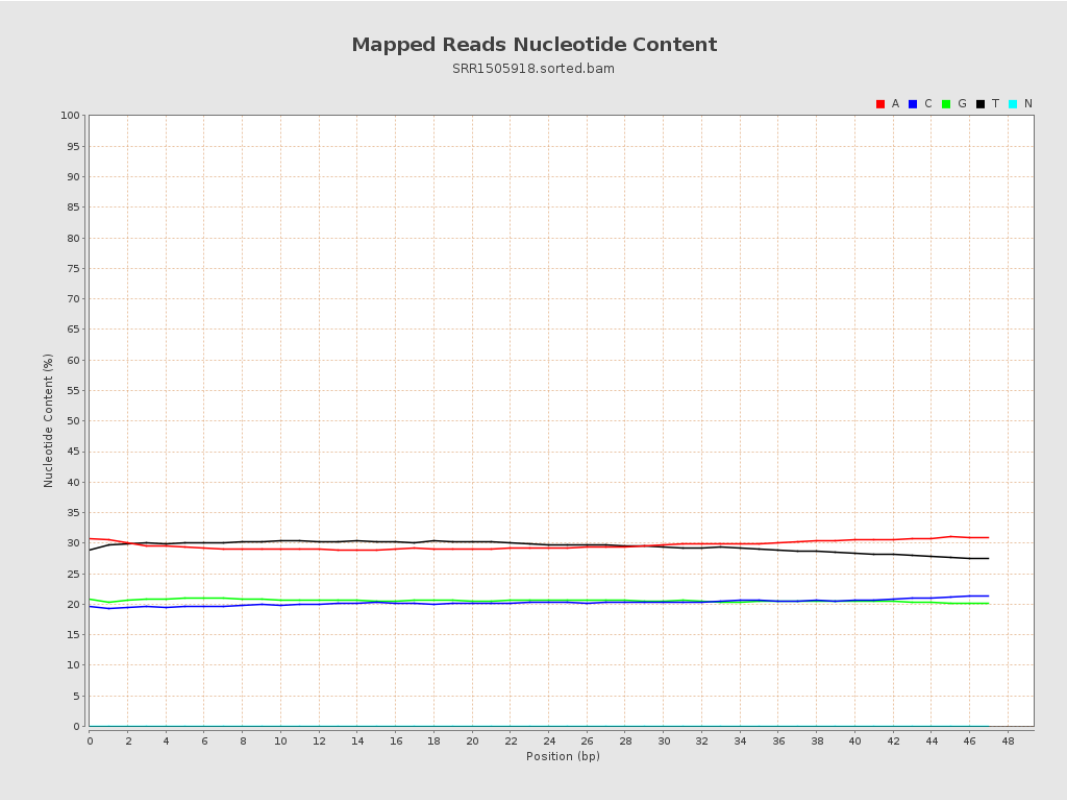
6. Results : Genome Fraction Coverage



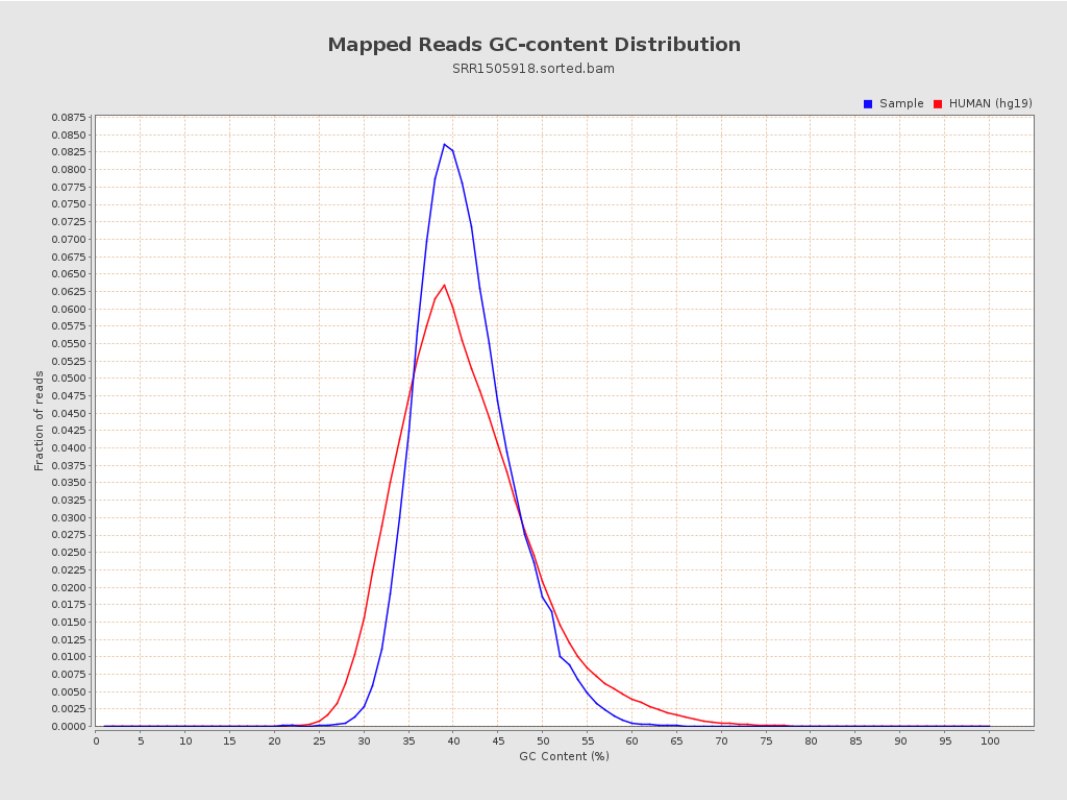
7. Results : Duplication Rate Histogram



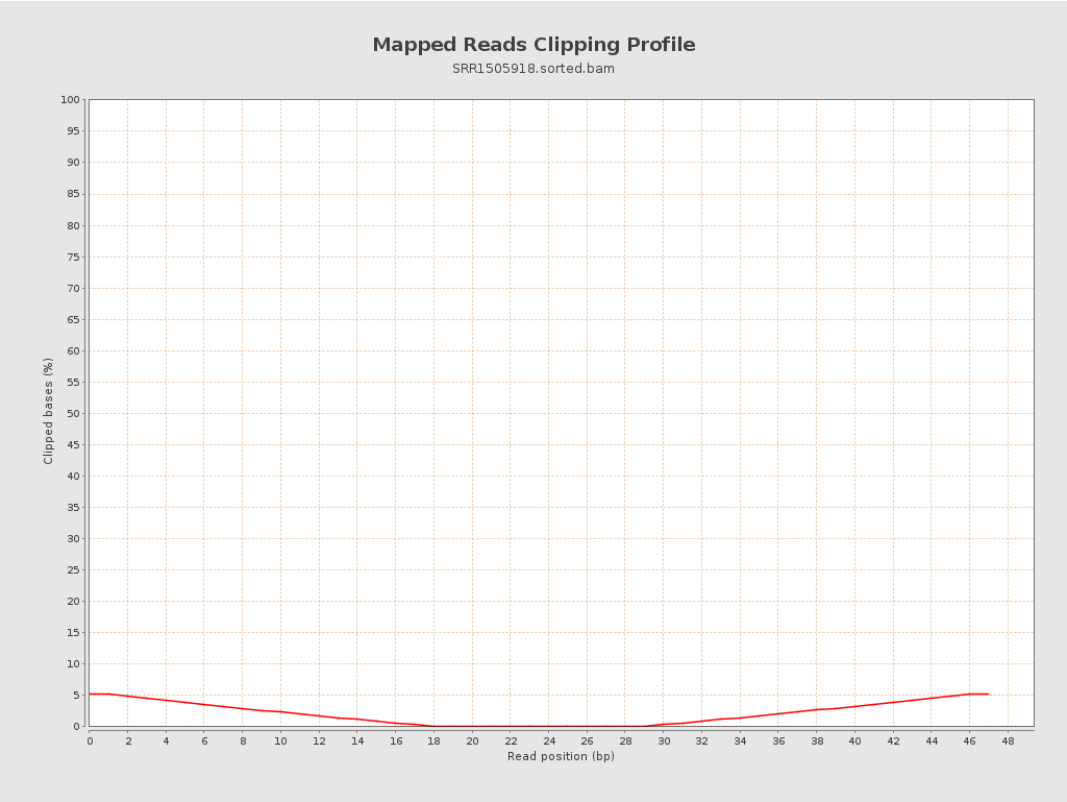
8. Results : Mapped Reads Nucleotide Content



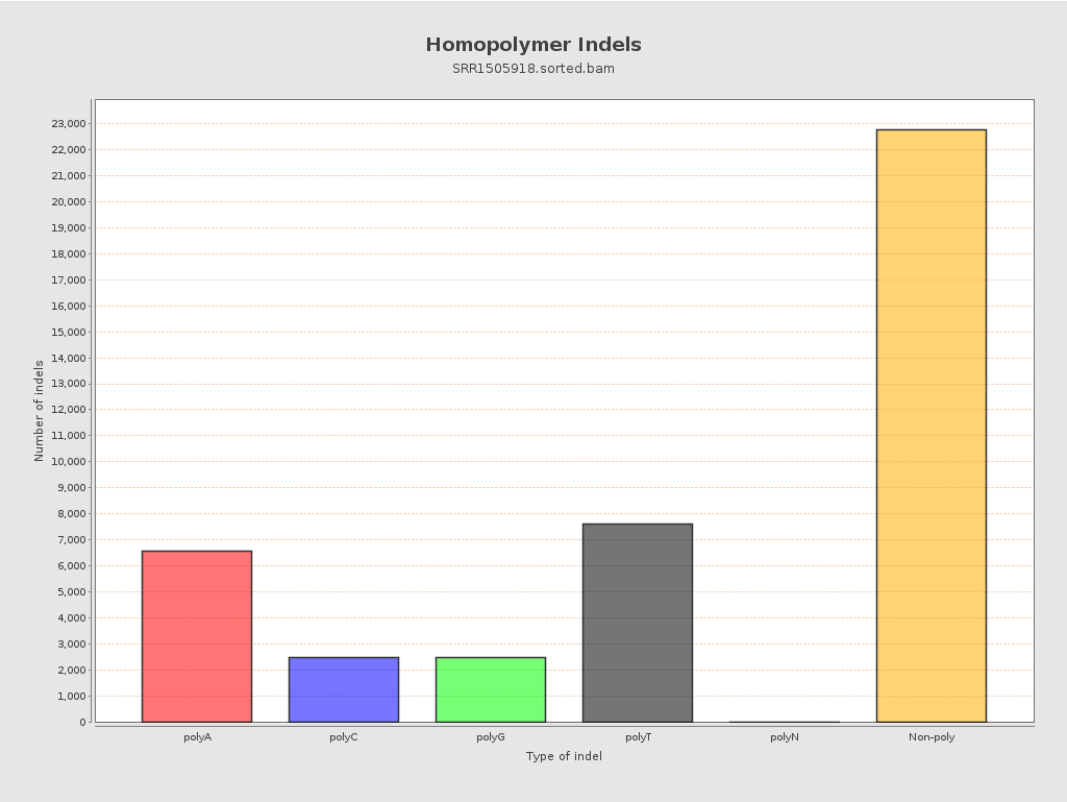
9. Results : Mapped Reads GC-content Distribution



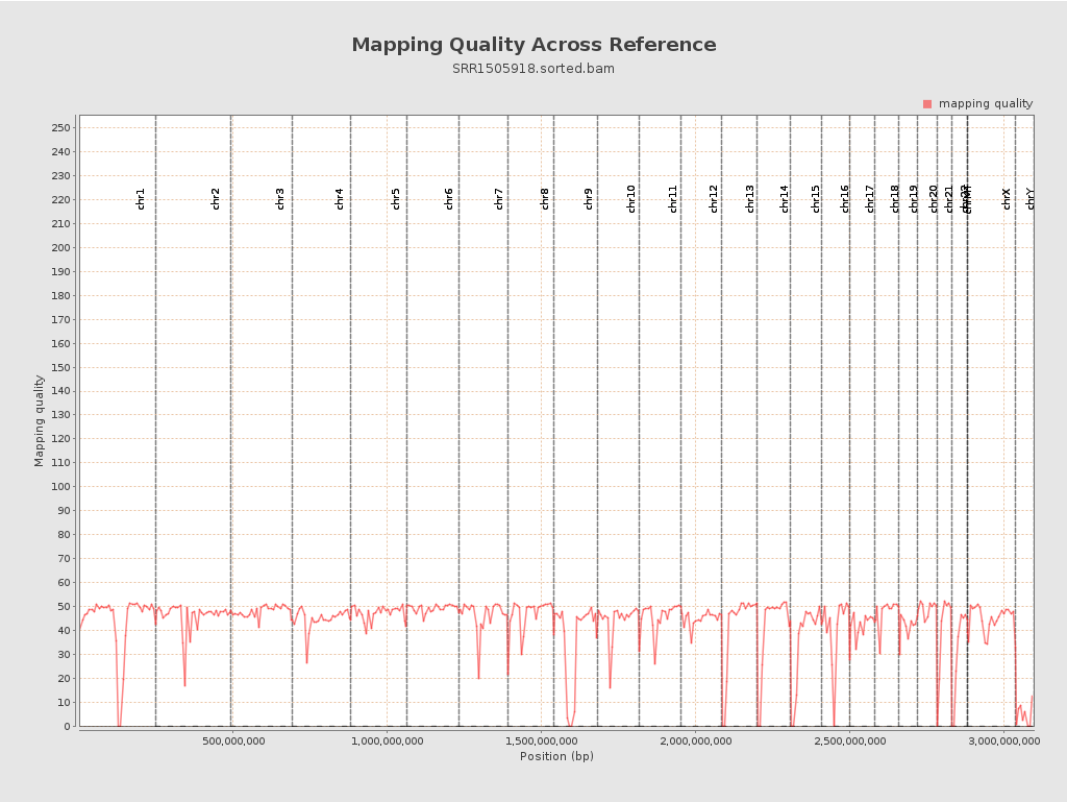
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram