Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:43:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549026.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_SRR1549026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:43:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,792,261
Mapped reads	7,705,844 / 87.64%
Unmapped reads	1,086,417 / 12.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	326,146 / 3.71%
Duplication rate	3.25%
Clipped reads	601,388 / 6.84%

2.2. ACGT Content

Number/percentage of A's	88,346,225 / 28.98%
Number/percentage of C's	63,607,129 / 20.86%
Number/percentage of T's	88,891,011 / 29.16%
Number/percentage of G's	64,022,610 / 21%
Number/percentage of N's	2,936 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0985
Standard Deviation	1.0263

2.4. Mapping Quality

Mean Mapping Quality	40.69

2.5. Mismatches and indels

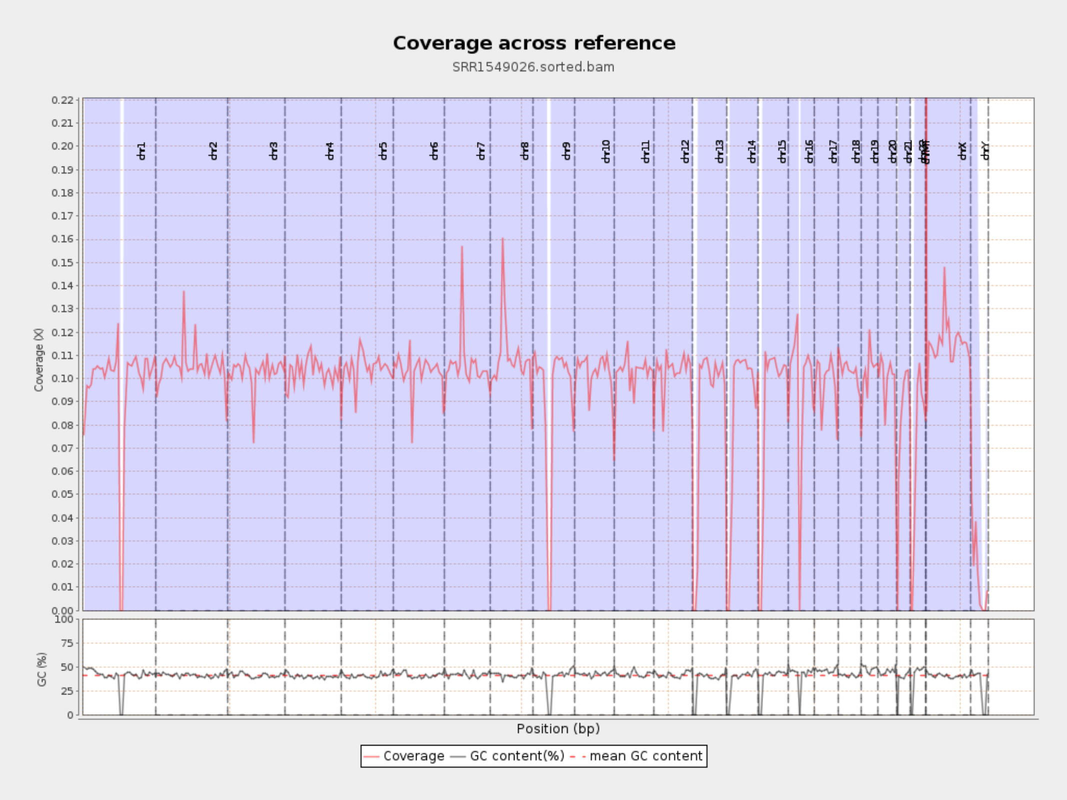
General error rate	0.29%
Mismatches	861,682
Insertions	10,239
Mapped reads with at least one insertion	0.13%
Deletions	24,091
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.98%

2.6. Chromosome stats

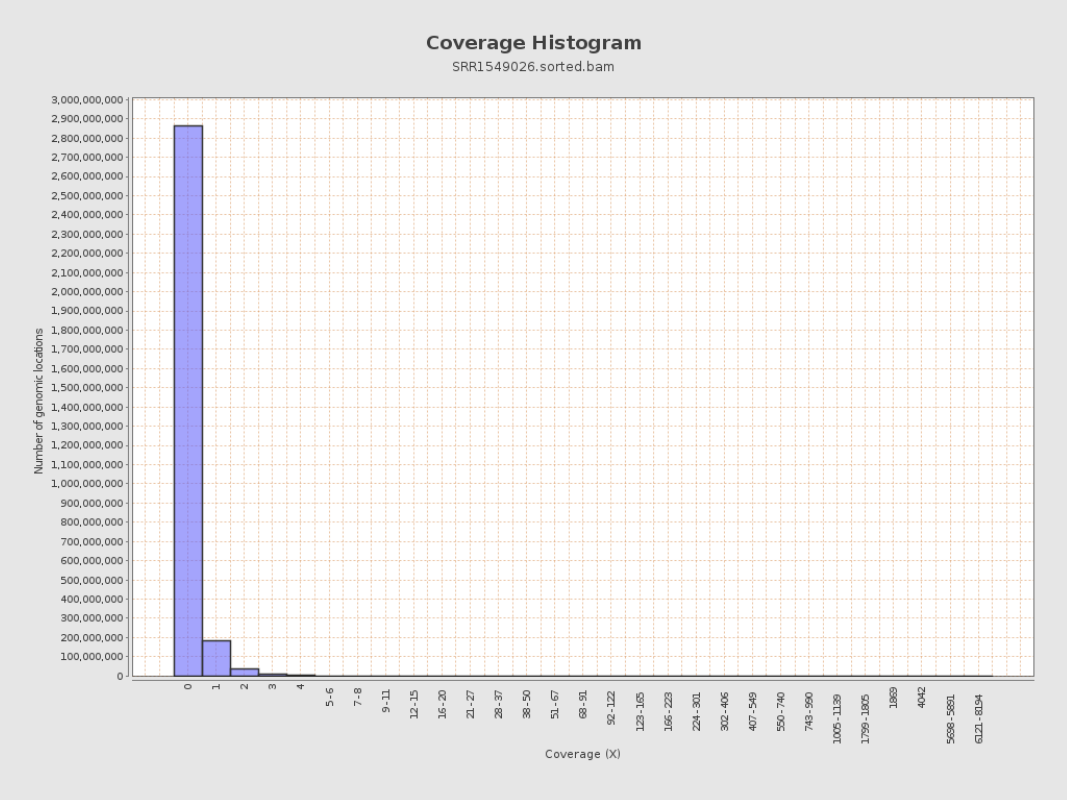
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24041580	0.0965	0.8318
chr2	243199373	25735111	0.1058	0.5957
chr3	198022430	20379534	0.1029	0.4022
chr4	191154276	19741693	0.1033	0.4119
chr5	180915260	18867558	0.1043	0.4111
chr6	171115067	17686274	0.1034	0.4485
chr7	159138663	16897501	0.1062	0.8352
chr8	146364022	15957214	0.109	3.9729

chr9	141213431	12852808	0.091	0.5918
chr10	135534747	13968653	0.1031	0.483
chr11	135006516	13846081	0.1026	0.7147
chr12	133851895	13804715	0.1031	0.4151
chr13	115169878	9879059	0.0858	0.3651
chr14	107349540	9304867	0.0867	0.4477
chr15	102531392	8832346	0.0861	0.3677
chr16	90354753	8497444	0.094	0.421
chr17	81195210	8070187	0.0994	0.4369
chr18	78077248	8070656	0.1034	1.0481
chr19	59128983	6114199	0.1034	0.8226
chr20	63025520	6255488	0.0993	0.4075
chr21	48129895	3853368	0.0801	0.4049
chr22	51304566	3422558	0.0667	0.3881
chrMT	16571	27898	1.6835	2.1608
chrX	155270560	17882434	0.1152	0.5132
chrY	59373566	911903	0.0154	0.185

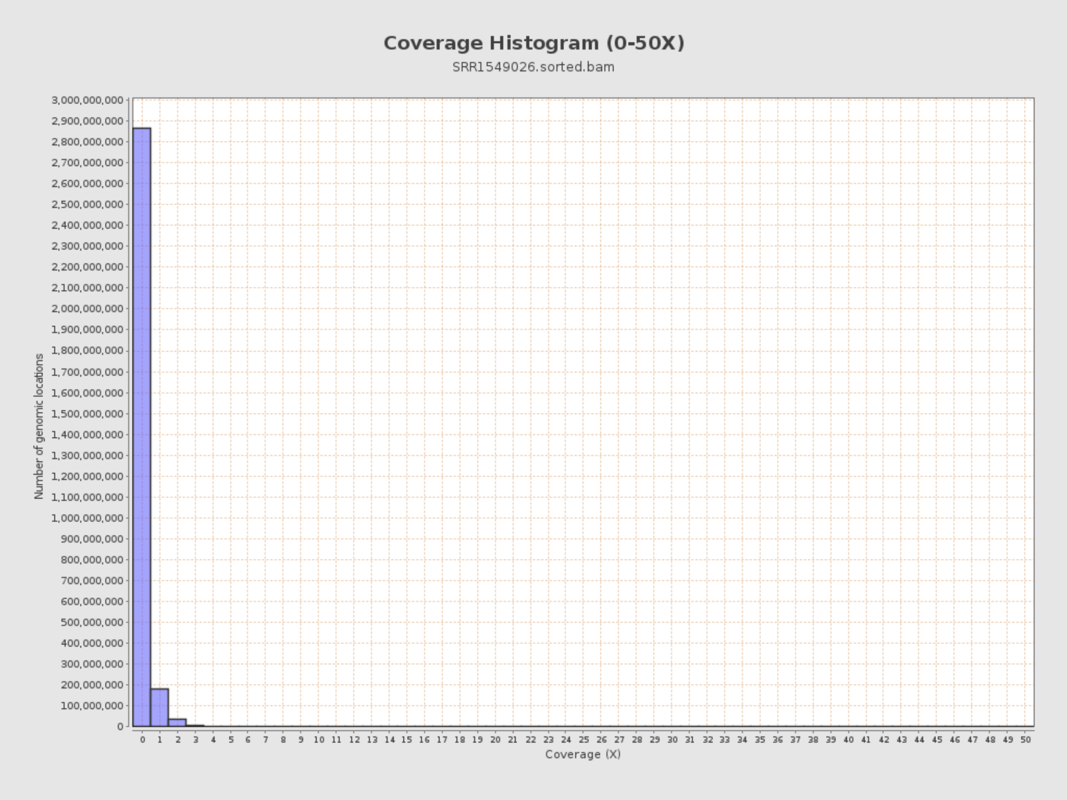
3. Results : Coverage across reference



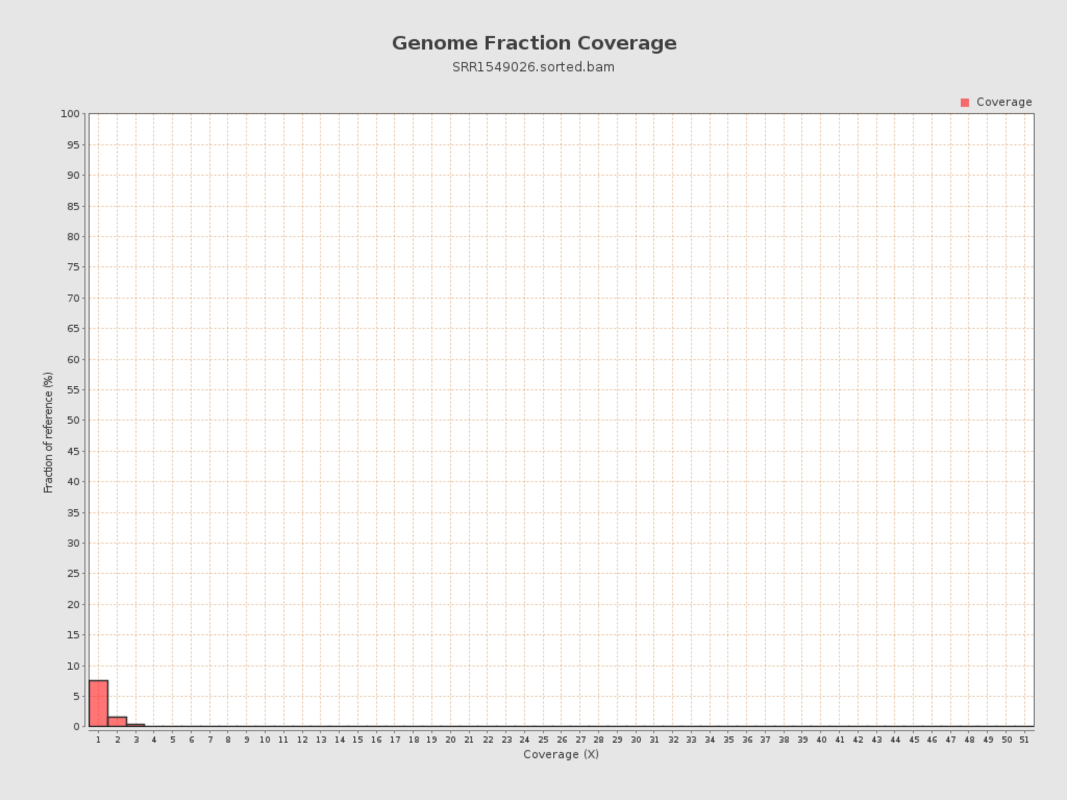
4. Results : Coverage Histogram



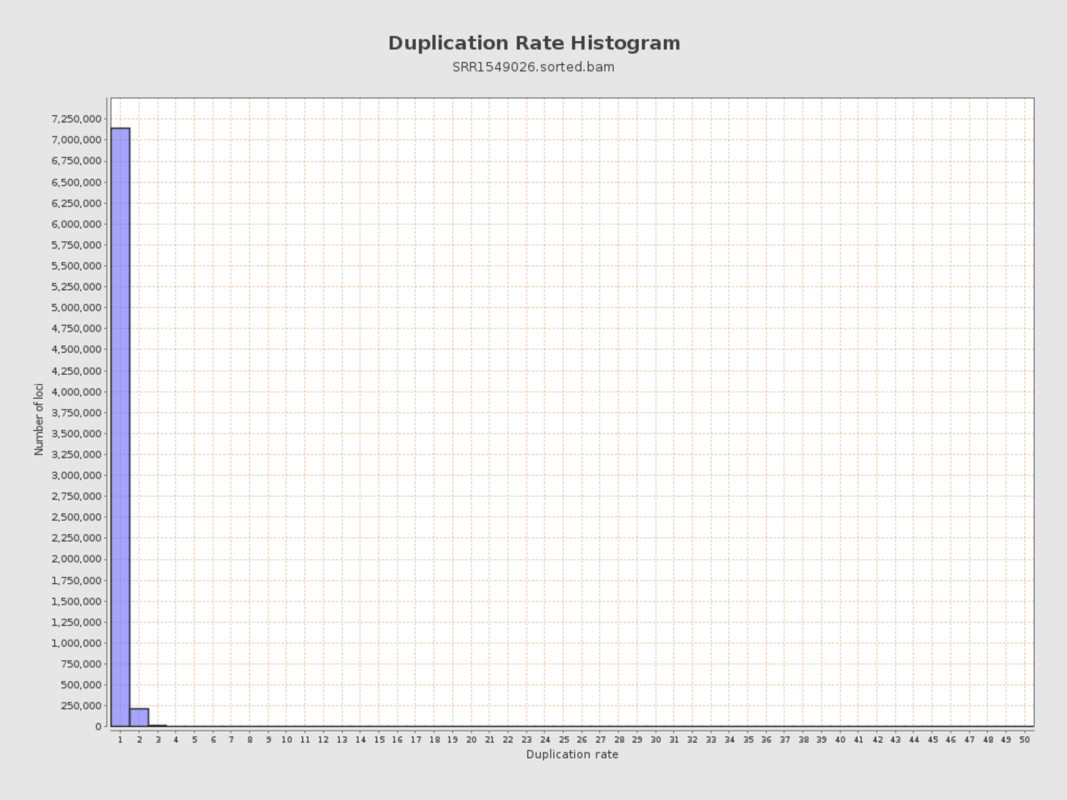
5. Results : Coverage Histogram (0-50X)



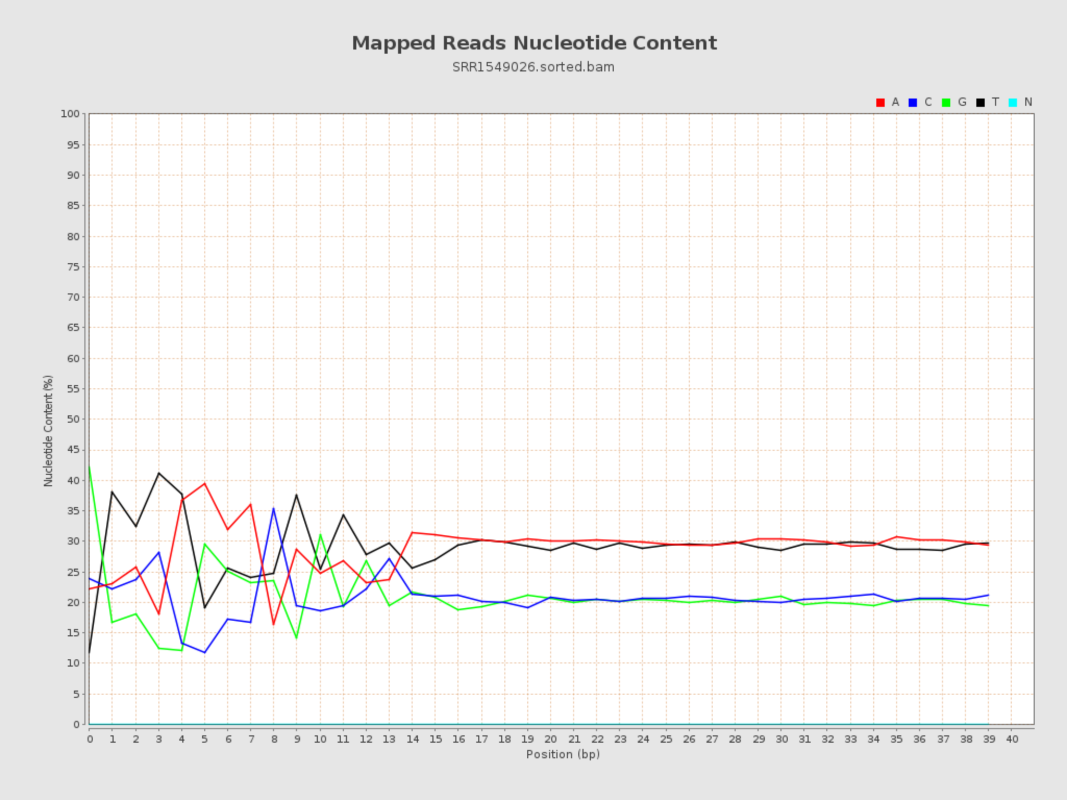
6. Results : Genome Fraction Coverage



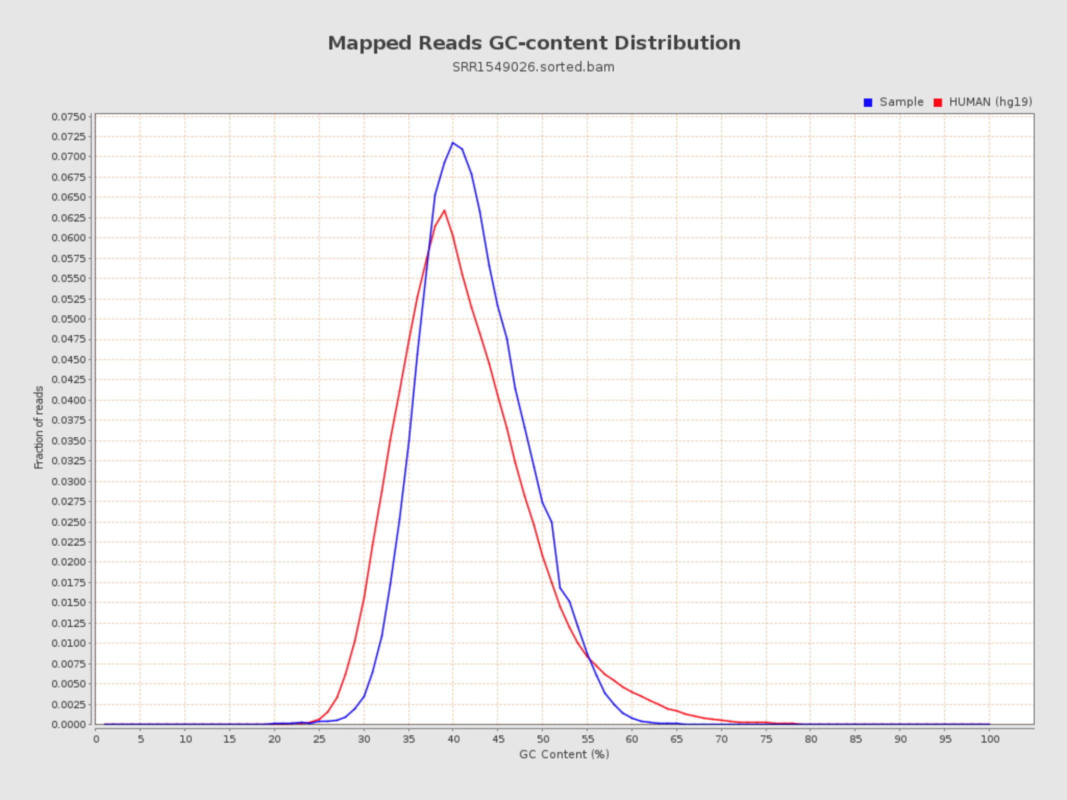
7. Results : Duplication Rate Histogram



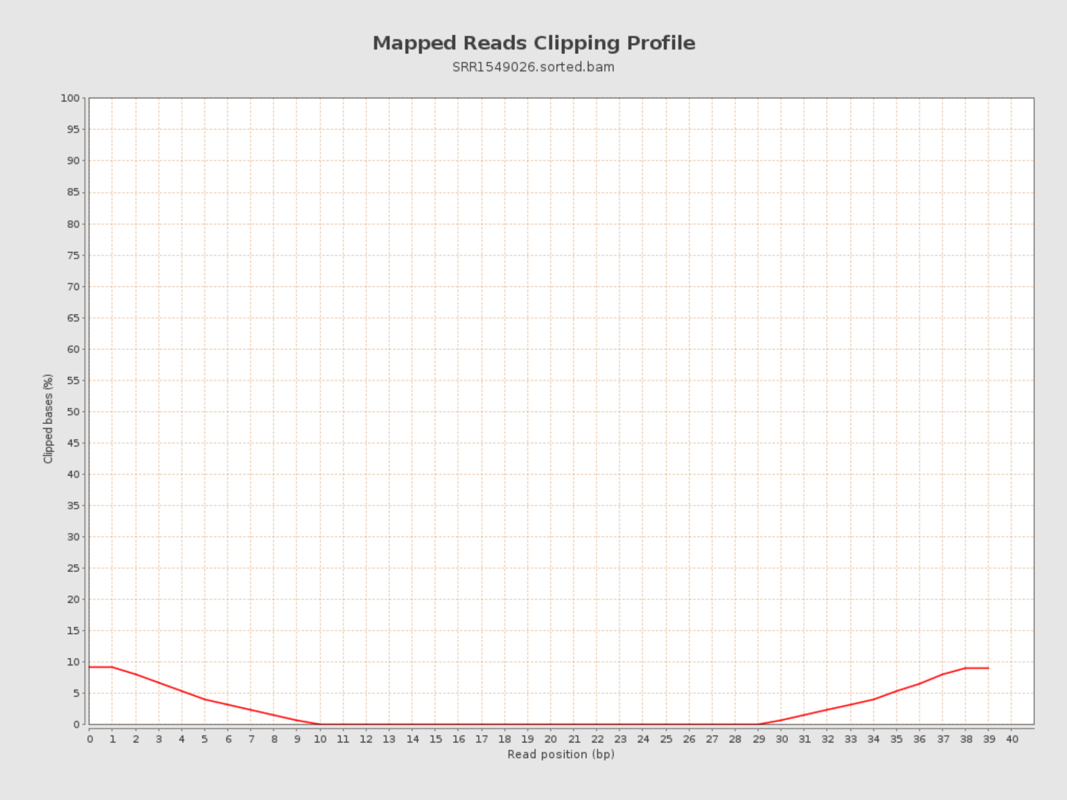
8. Results : Mapped Reads Nucleotide Content



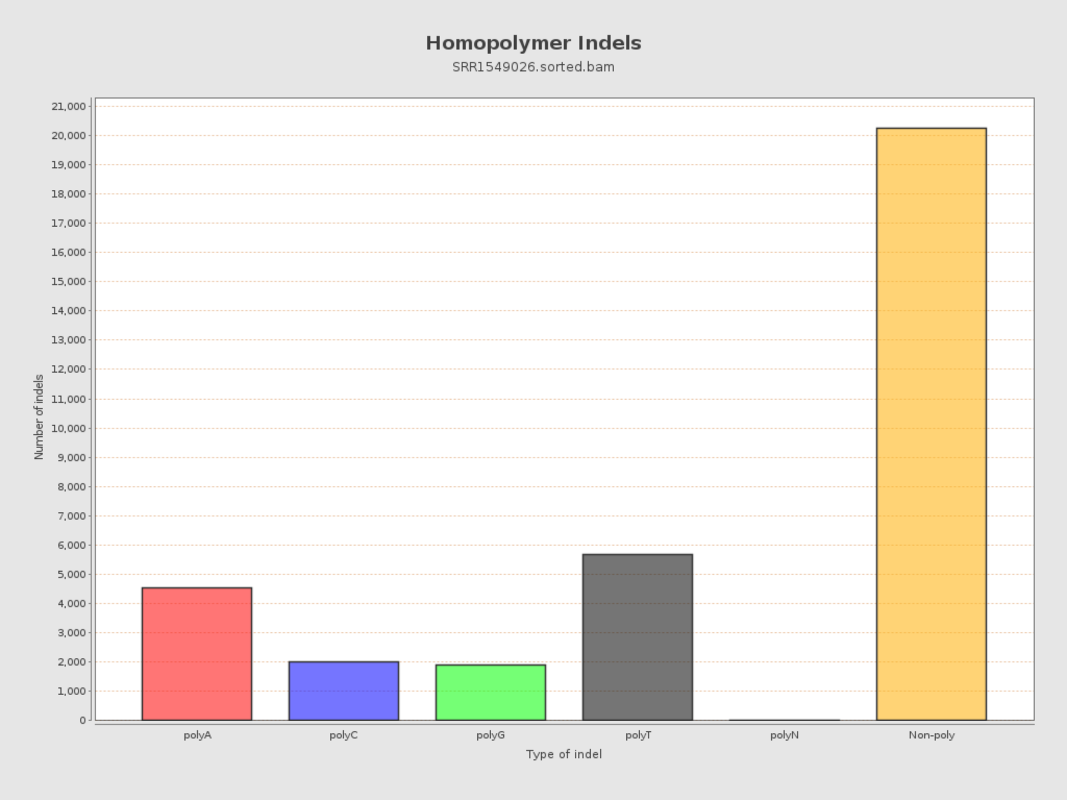
9. Results : Mapped Reads GC-content Distribution



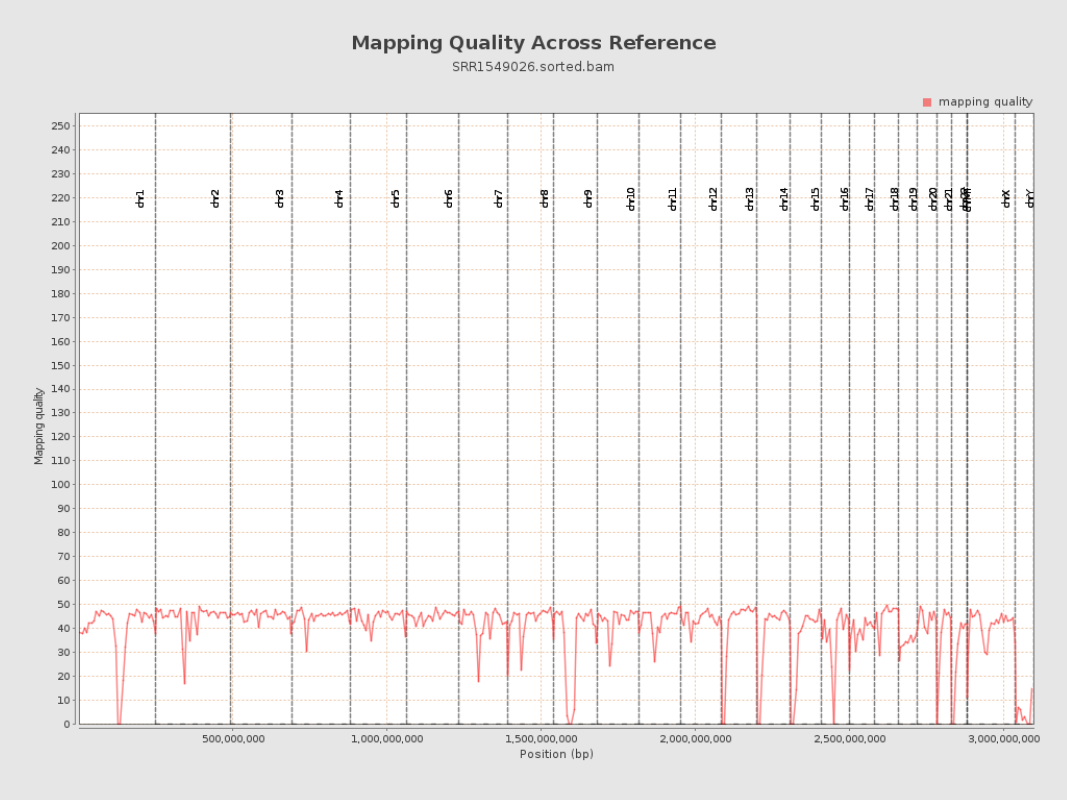
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram