Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:19:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549153.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_SRR1549153 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:19:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,914,571
Mapped reads	13,945,588 / 87.63%
Unmapped reads	1,968,983 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	928,491 / 5.83%
Duplication rate	5.58%
Clipped reads	706,952 / 4.44%

2.2. ACGT Content

Number/percentage of A's	158,974,047 / 28.72%
Number/percentage of C's	116,019,262 / 20.96%
Number/percentage of T's	161,588,996 / 29.19%
Number/percentage of G's	116,883,122 / 21.11%
Number/percentage of N's	112,412 / 0.02%
GC Percentage	42.07%

2.3. Coverage

Mean	0.1788
Standard Deviation	0.9162

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

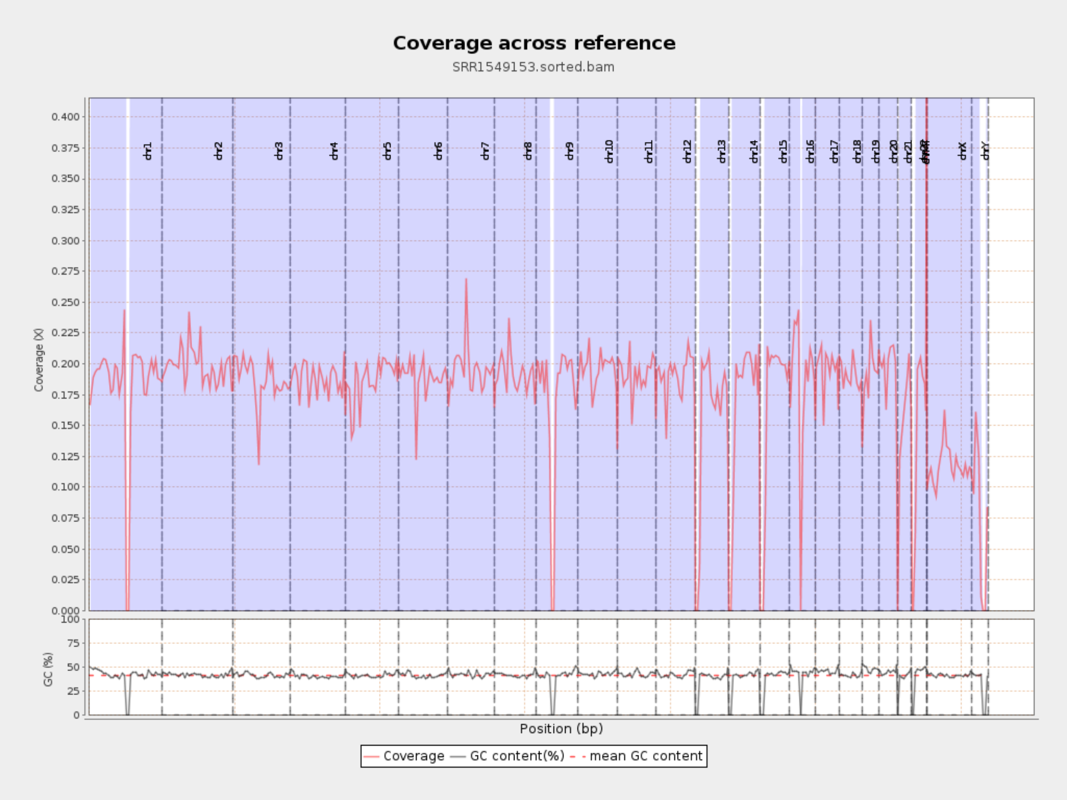
General error rate	0.31%
Mismatches	1,693,492
Insertions	13,791
Mapped reads with at least one insertion	0.1%
Deletions	41,689
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.7%

2.6. Chromosome stats

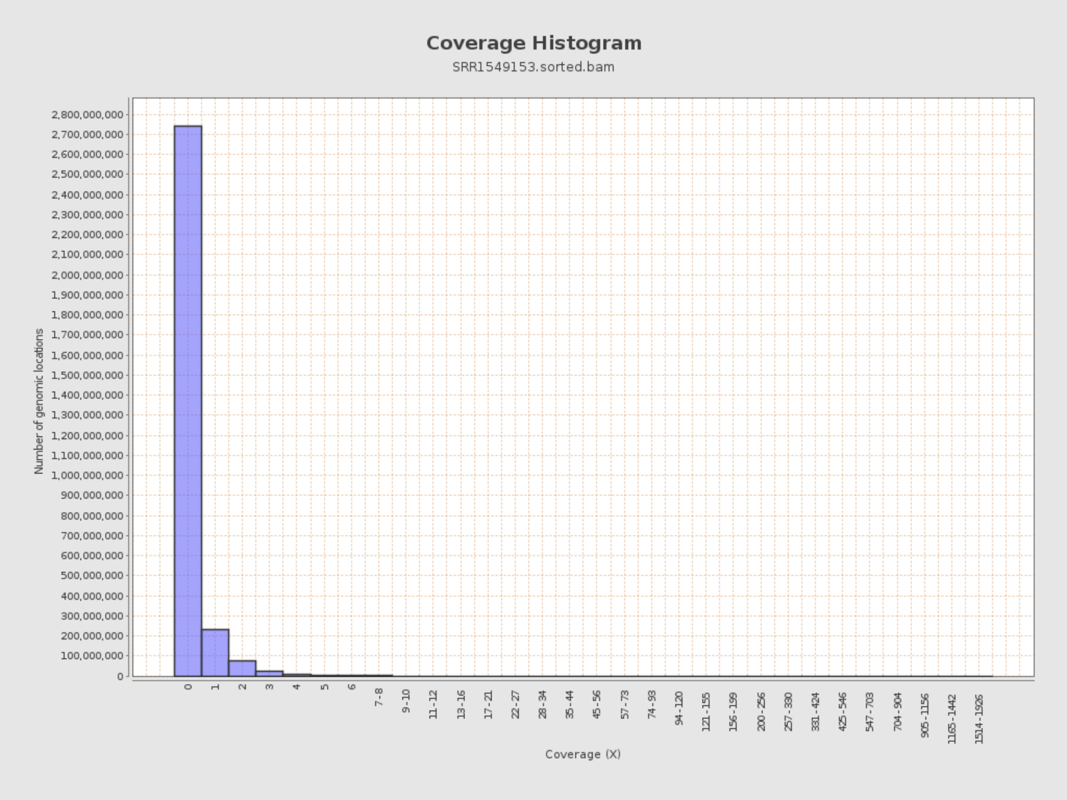
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	45261275	0.1816	1.6018
chr2	243199373	48353601	0.1988	0.9005
chr3	198022430	36975559	0.1867	0.6193
chr4	191154276	35845881	0.1875	0.6528
chr5	180915260	33739133	0.1865	0.6298
chr6	171115067	32341231	0.189	0.7019
chr7	159138663	31291825	0.1966	1.2952
chr8	146364022	28162373	0.1924	1.0218

chr9	141213431	23809422	0.1686	0.854
chr10	135534747	26652259	0.1966	0.8602
chr11	135006516	25752042	0.1907	0.8144
chr12	133851895	25578015	0.1911	0.6525
chr13	115169878	17649912	0.1533	0.5578
chr14	107349540	17493643	0.163	0.7326
chr15	102531392	16856060	0.1644	0.5817
chr16	90354753	16752025	0.1854	0.6836
chr17	81195210	15882860	0.1956	0.6945
chr18	78077248	14937283	0.1913	1.6546
chr19	59128983	11443712	0.1935	1.4106
chr20	63025520	12410141	0.1969	0.6828
chr21	48129895	7155234	0.1487	0.6525
chr22	51304566	6806087	0.1327	0.5665
chrMT	16571	10050	0.6065	1.054
chrX	155270560	18252424	0.1176	0.59
chrY	59373566	4218123	0.071	0.5147

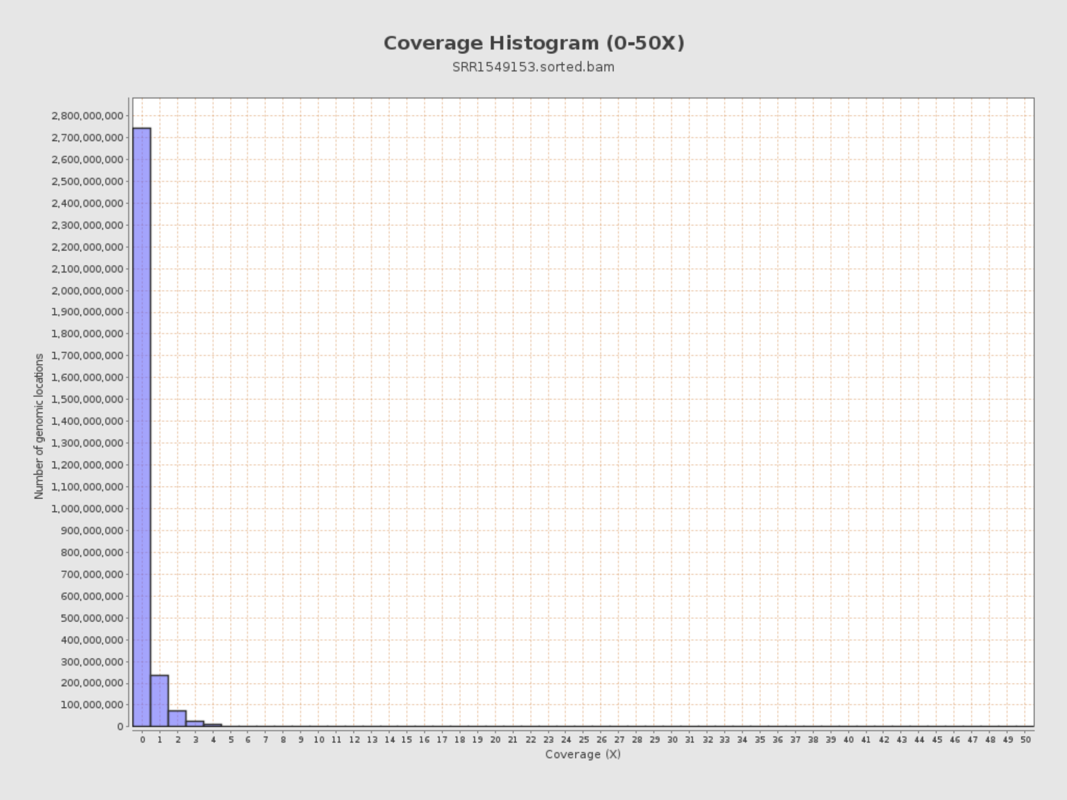
3. Results : Coverage across reference



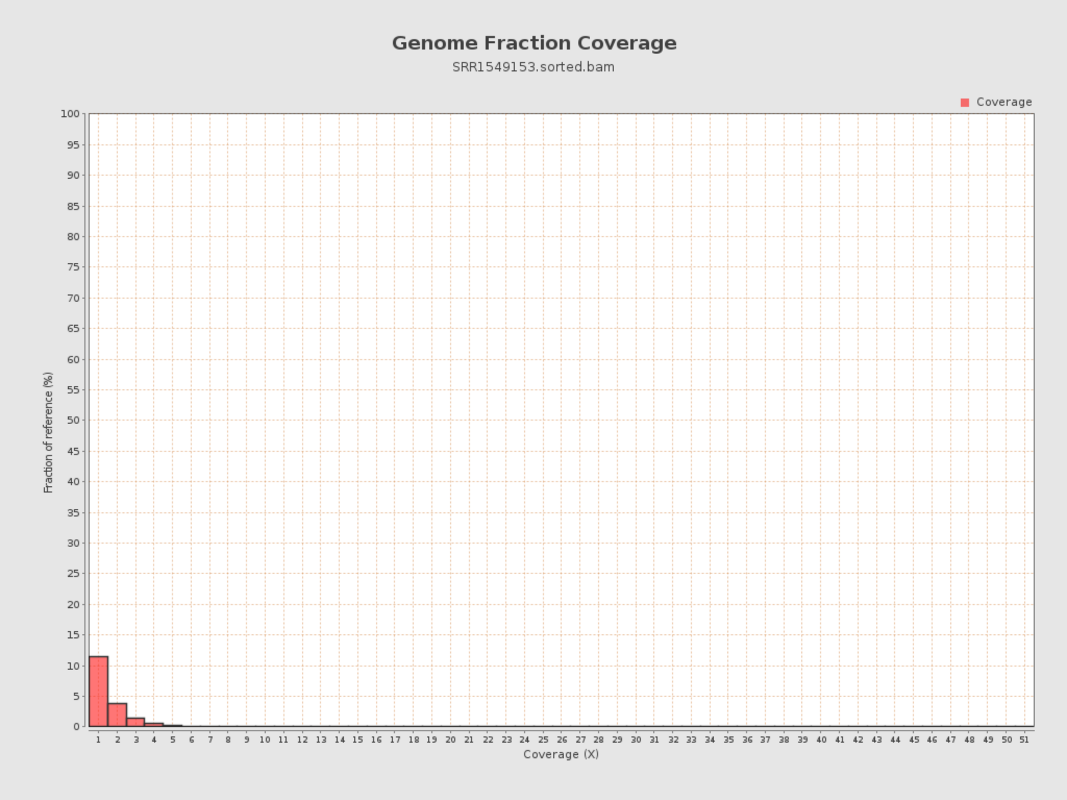
4. Results : Coverage Histogram



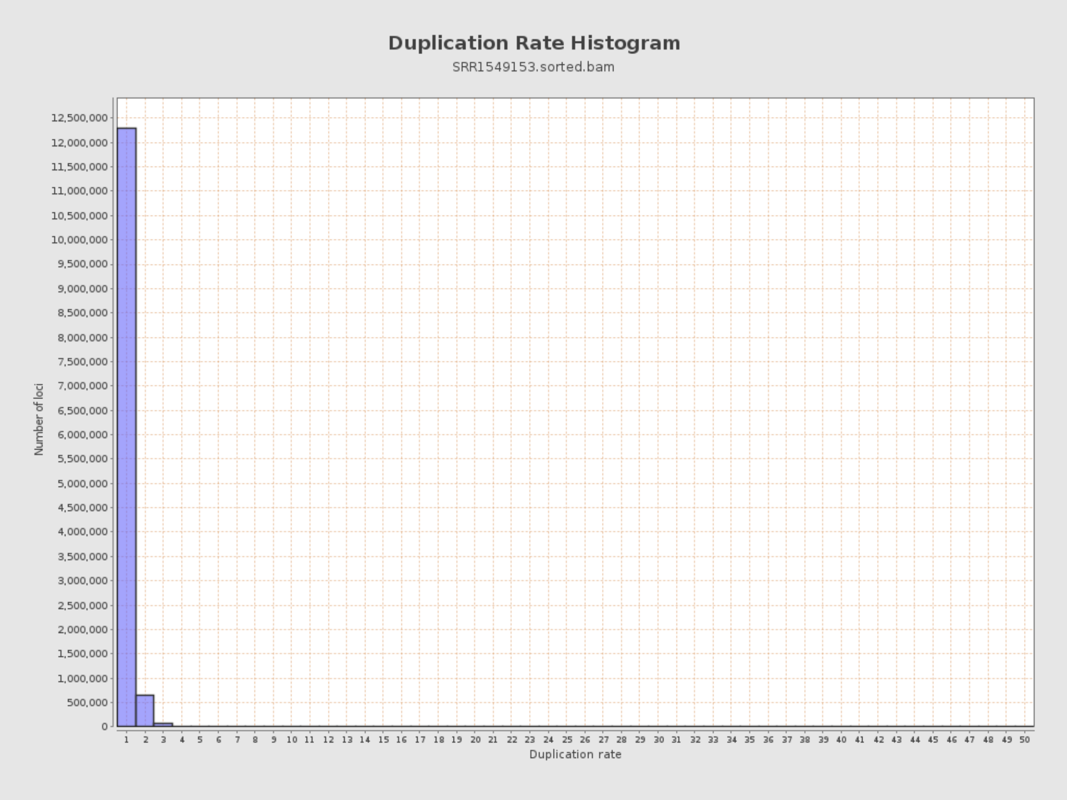
5. Results : Coverage Histogram (0-50X)



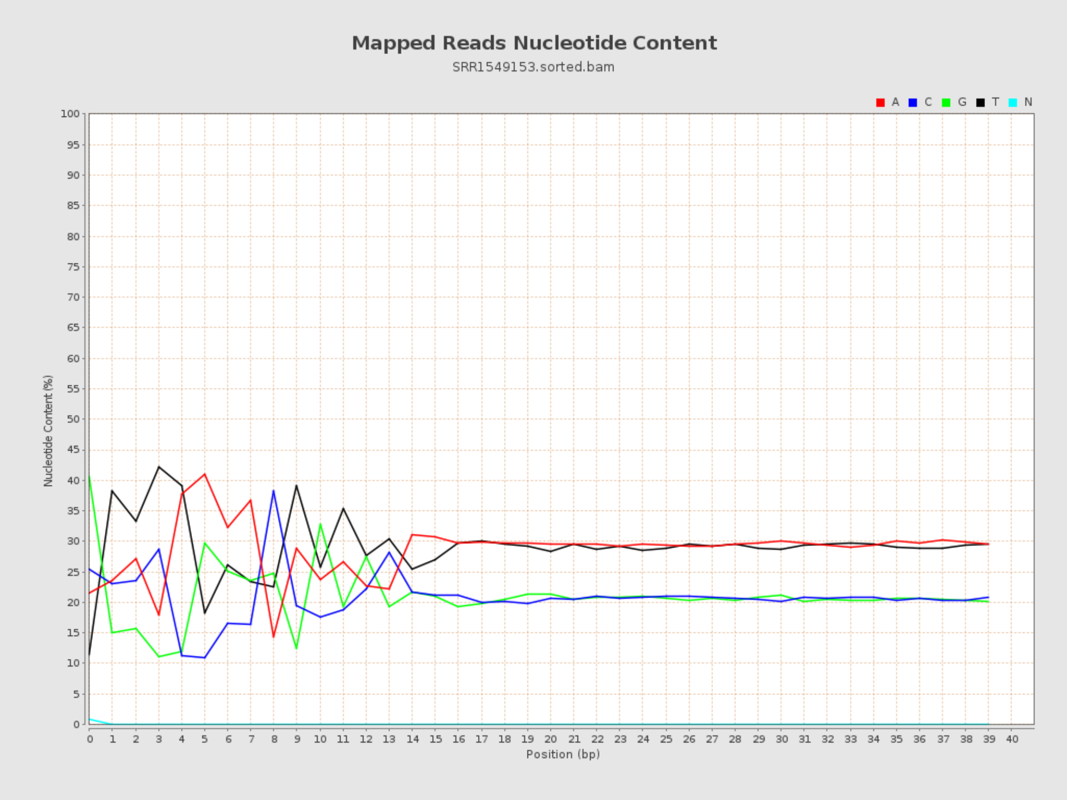
6. Results : Genome Fraction Coverage



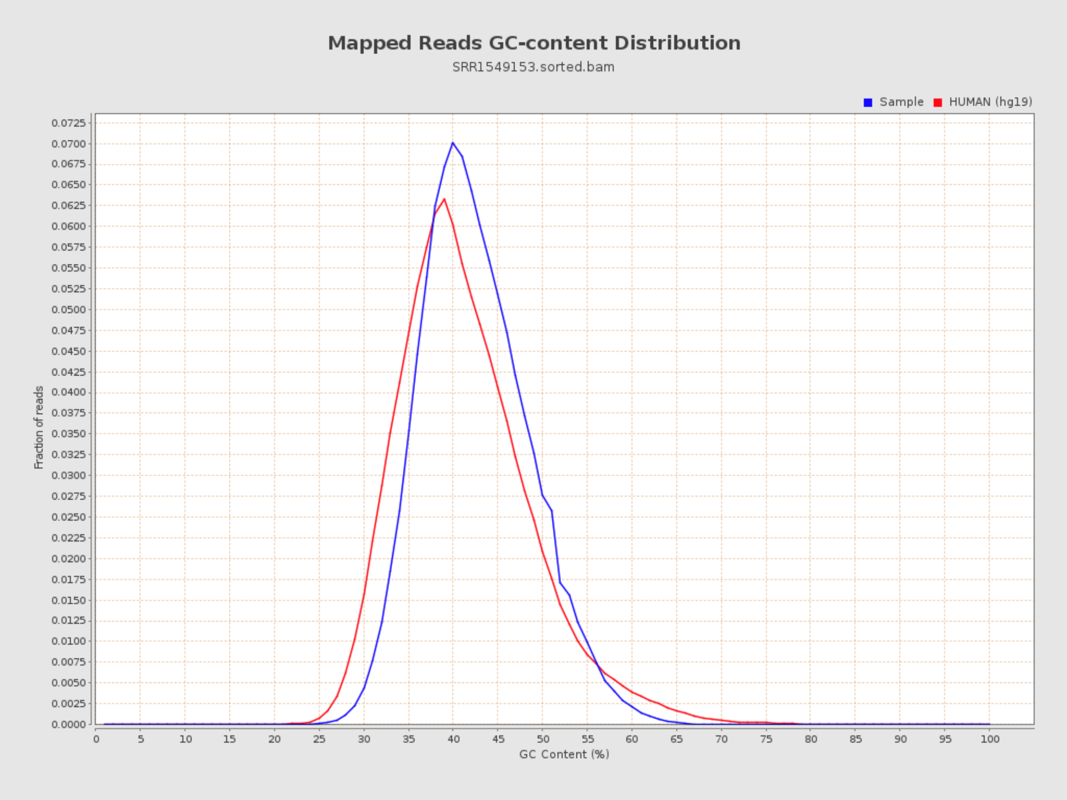
7. Results : Duplication Rate Histogram



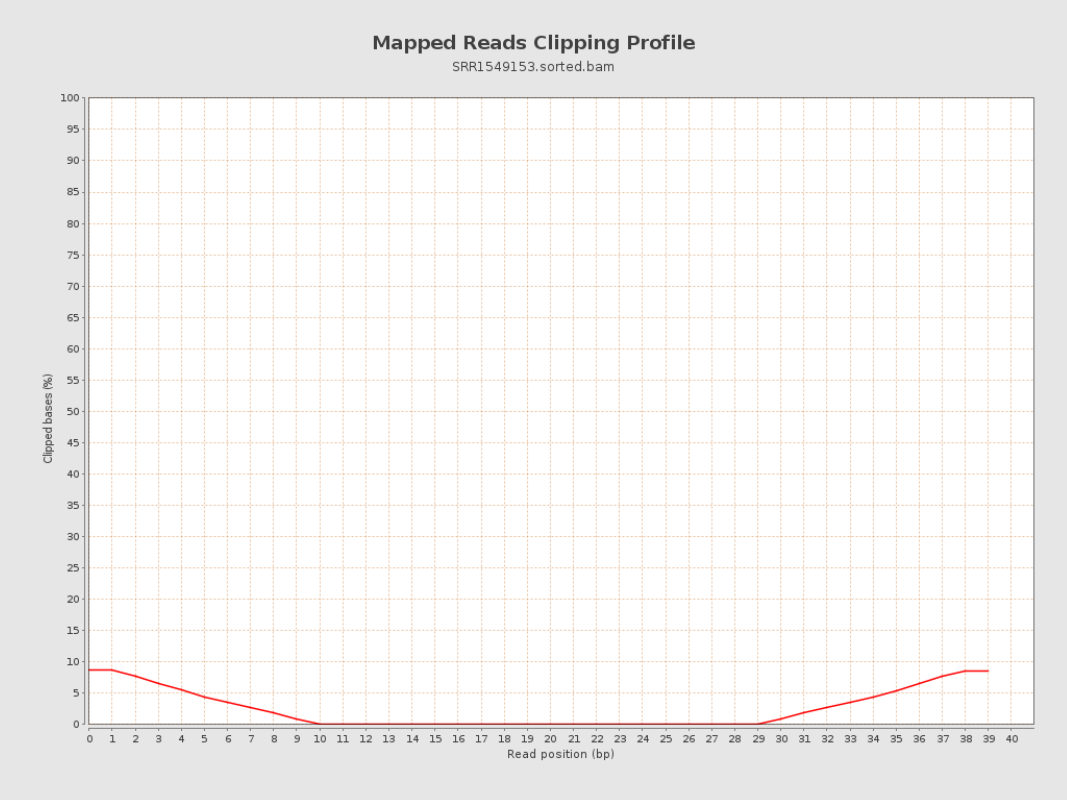
8. Results : Mapped Reads Nucleotide Content



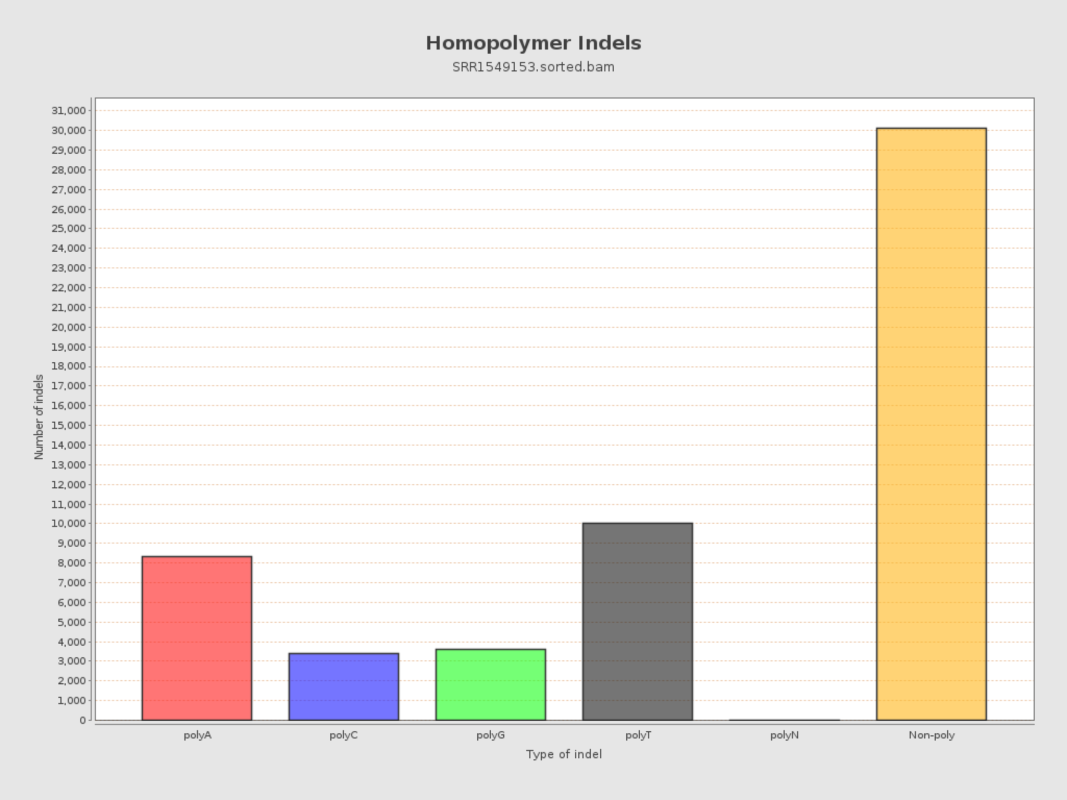
9. Results : Mapped Reads GC-content Distribution



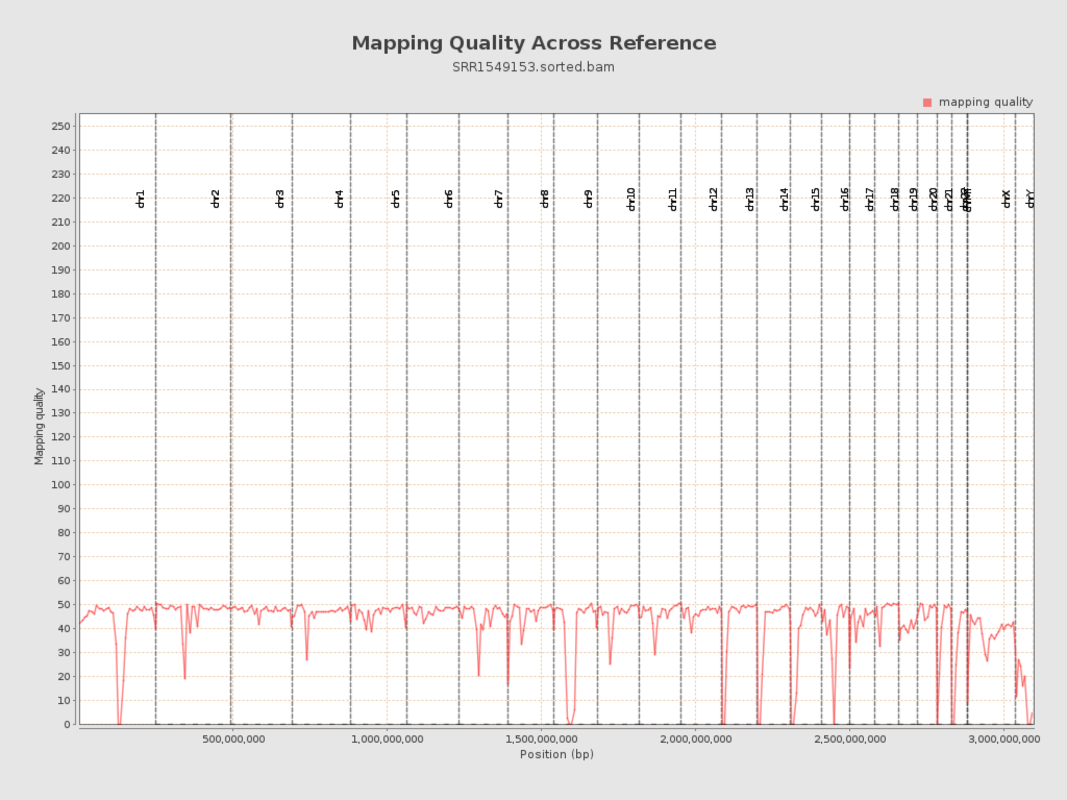
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram