Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:57:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549141.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_SRR1549141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:57:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,930,174
Mapped reads	11,429,842 / 88.4%
Unmapped reads	1,500,332 / 11.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	593,078 / 4.59%
Duplication rate	4.09%
Clipped reads	605,151 / 4.68%

2.2. ACGT Content

Number/percentage of A's	127,136,350 / 28.03%
Number/percentage of C's	98,957,568 / 21.82%
Number/percentage of T's	128,548,434 / 28.34%
Number/percentage of G's	98,861,619 / 21.79%
Number/percentage of N's	100,179 / 0.02%
GC Percentage	43.61%

2.3. Coverage

Mean	0.1465
Standard Deviation	0.8021

2.4. Mapping Quality

Mean Mapping Quality	42.43

2.5. Mismatches and indels

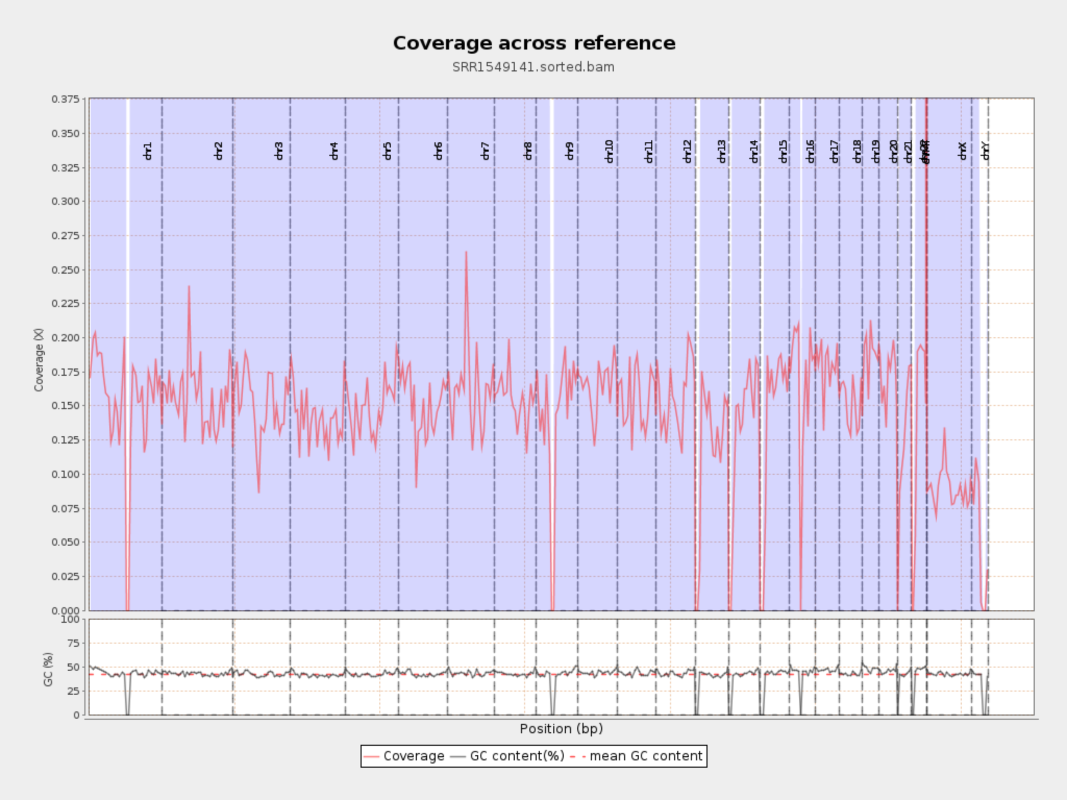
General error rate	0.33%
Mismatches	1,469,018
Insertions	12,343
Mapped reads with at least one insertion	0.11%
Deletions	36,819
Mapped reads with at least one deletion	0.32%
Homopolymer indels	46.73%

2.6. Chromosome stats

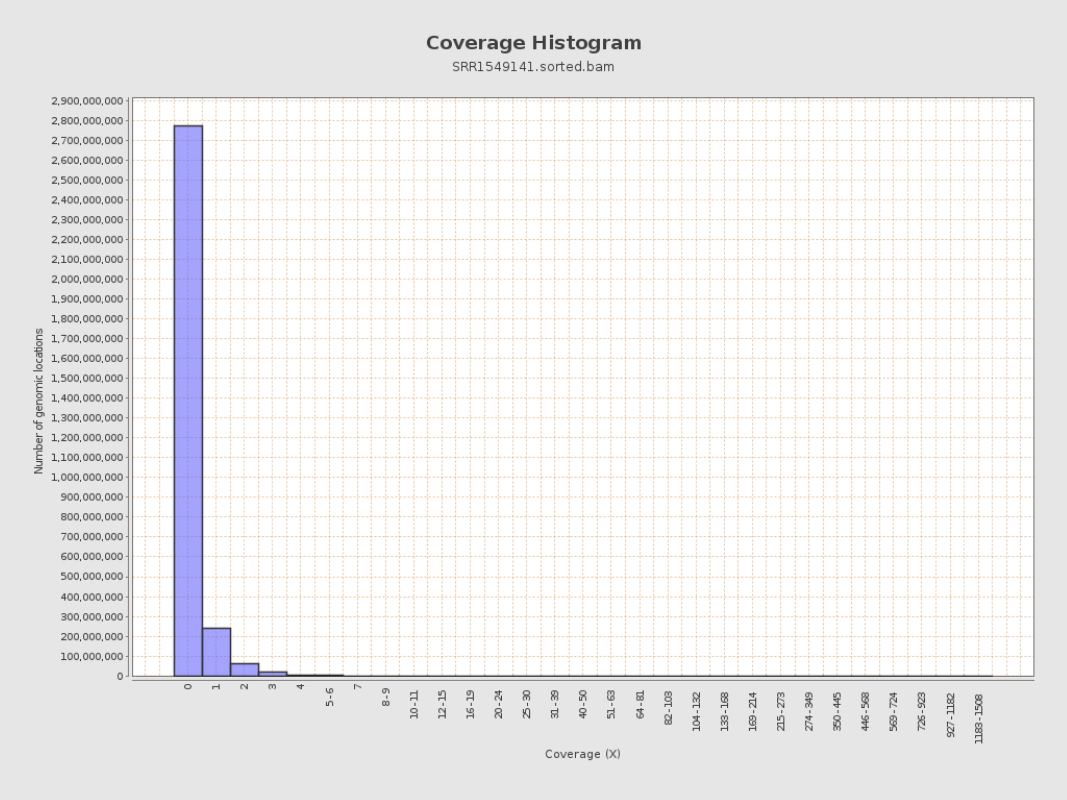
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37953970	0.1523	1.2357
chr2	243199373	38273839	0.1574	0.8503
chr3	198022430	29944140	0.1512	0.519
chr4	191154276	26914208	0.1408	0.5168
chr5	180915260	27026624	0.1494	0.5364
chr6	171115067	25926878	0.1515	0.6167
chr7	159138663	25790793	0.1621	1.3715
chr8	146364022	22719977	0.1552	0.7847

chr9	141213431	19565012	0.1385	0.8095
chr10	135534747	22336623	0.1648	0.7097
chr11	135006516	20993744	0.1555	0.7099
chr12	133851895	21080602	0.1575	0.5585
chr13	115169878	13569750	0.1178	0.4527
chr14	107349540	14123687	0.1316	0.6255
chr15	102531392	14375646	0.1402	0.4967
chr16	90354753	15106301	0.1672	0.6088
chr17	81195210	14589323	0.1797	0.6084
chr18	78077248	11877650	0.1521	1.6096
chr19	59128983	11119800	0.1881	1.2284
chr20	63025520	10780035	0.171	0.589
chr21	48129895	5920323	0.123	0.5863
chr22	51304566	6657966	0.1298	0.5568
chrMT	16571	97358	5.8752	10.1136
chrX	155270560	13971334	0.09	0.5319
chrY	59373566	2935285	0.0494	0.3091

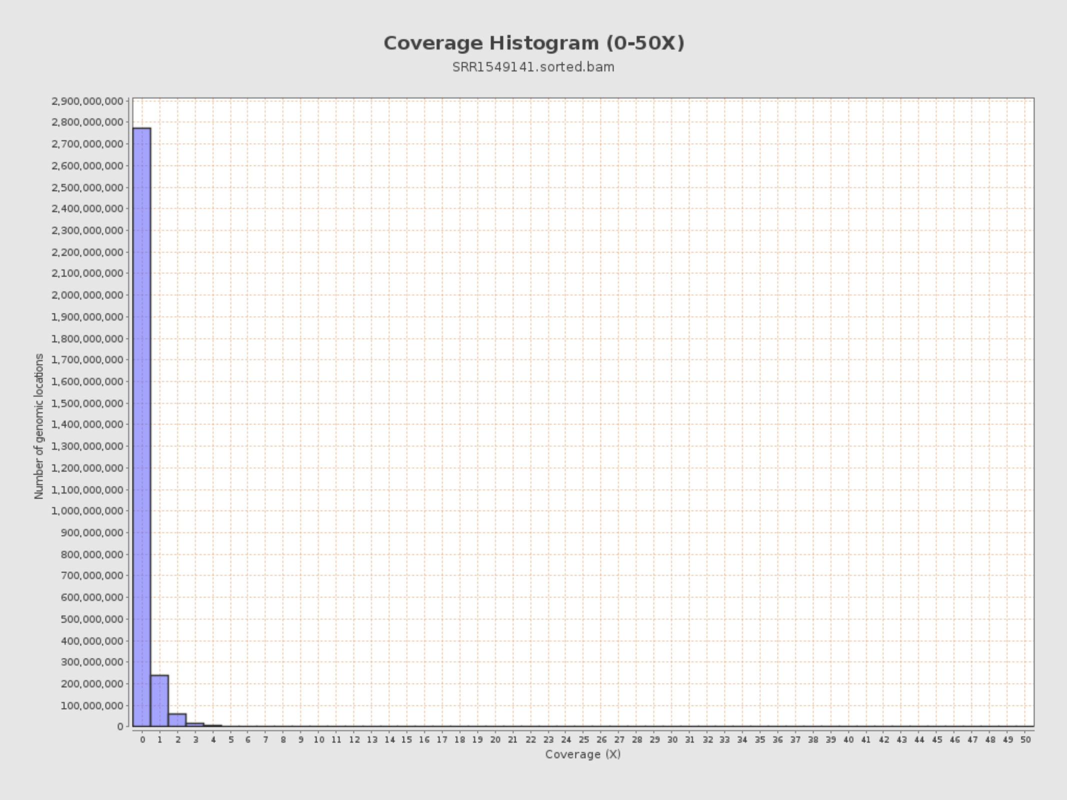
3. Results : Coverage across reference



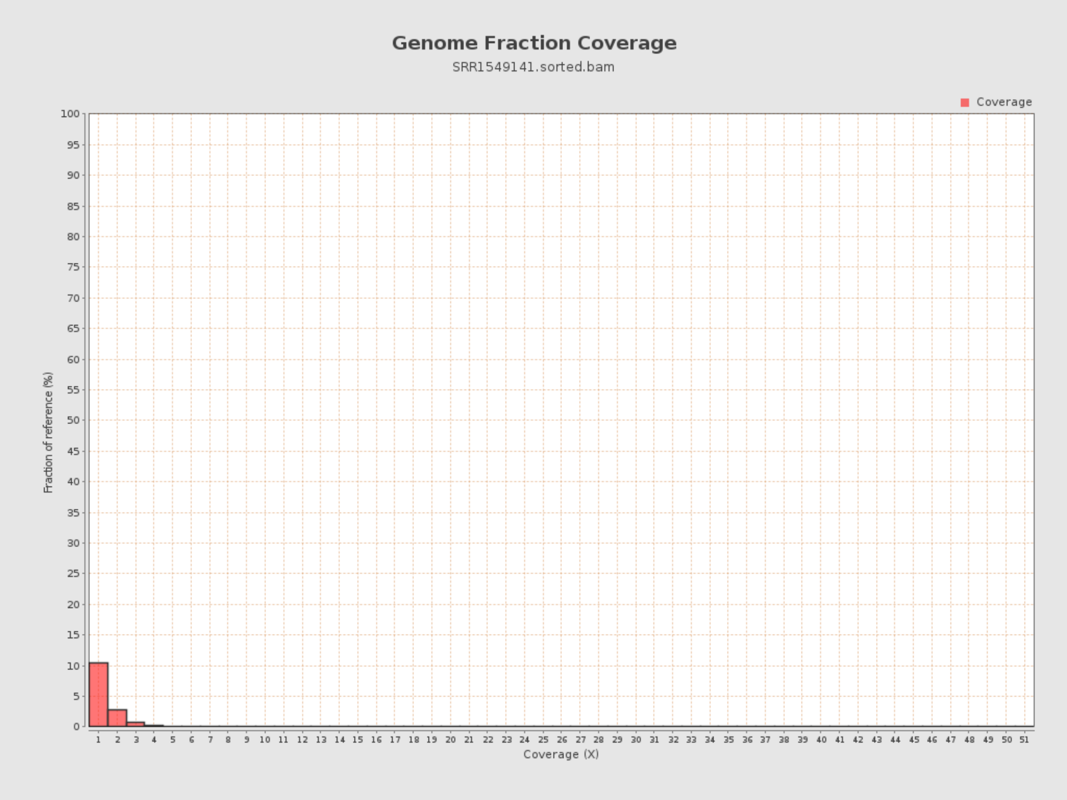
4. Results : Coverage Histogram



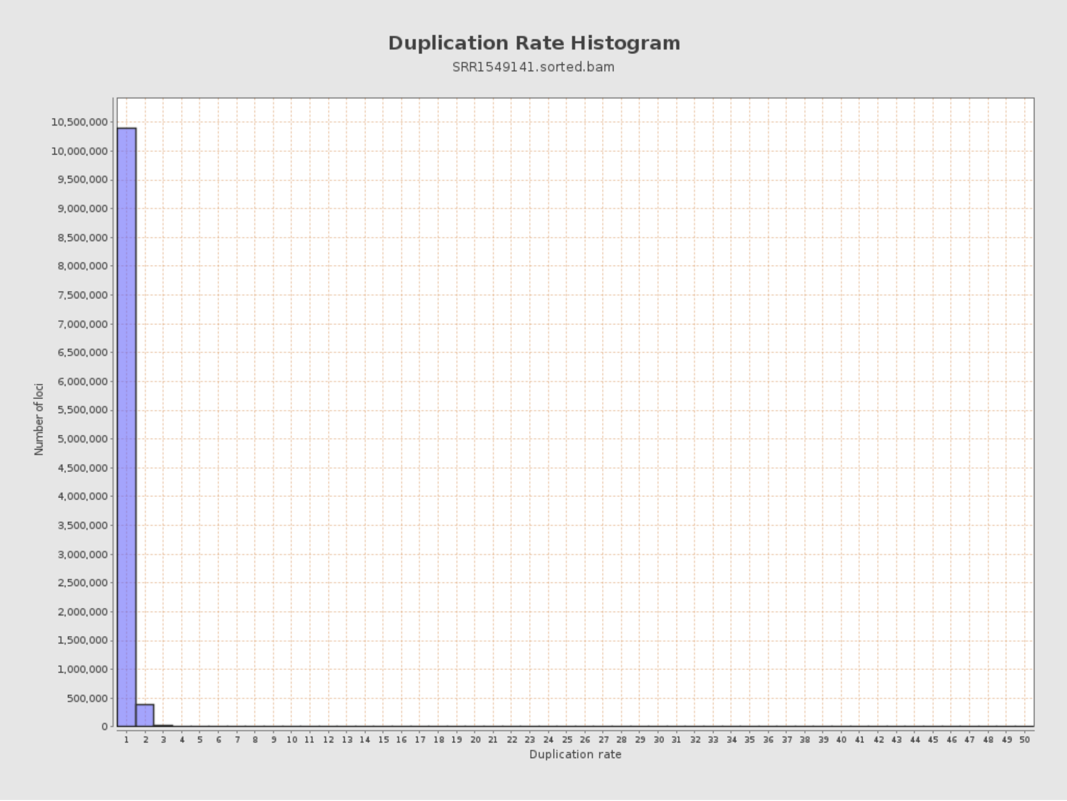
5. Results : Coverage Histogram (0-50X)



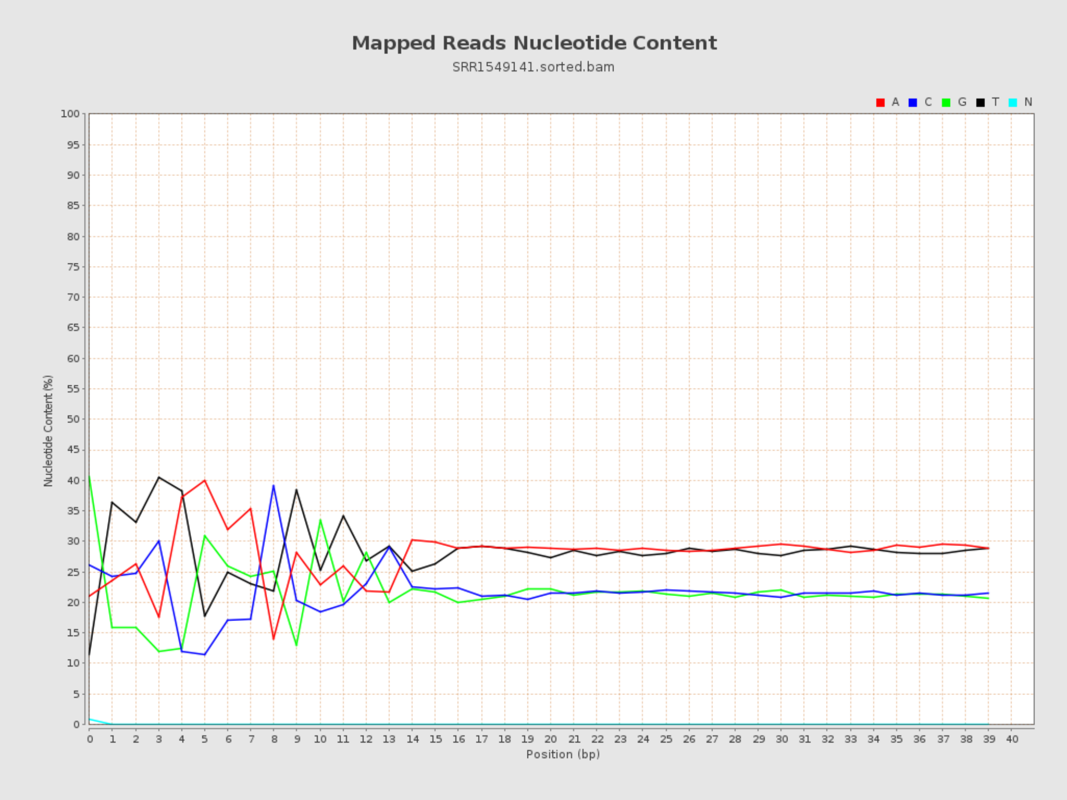
6. Results : Genome Fraction Coverage



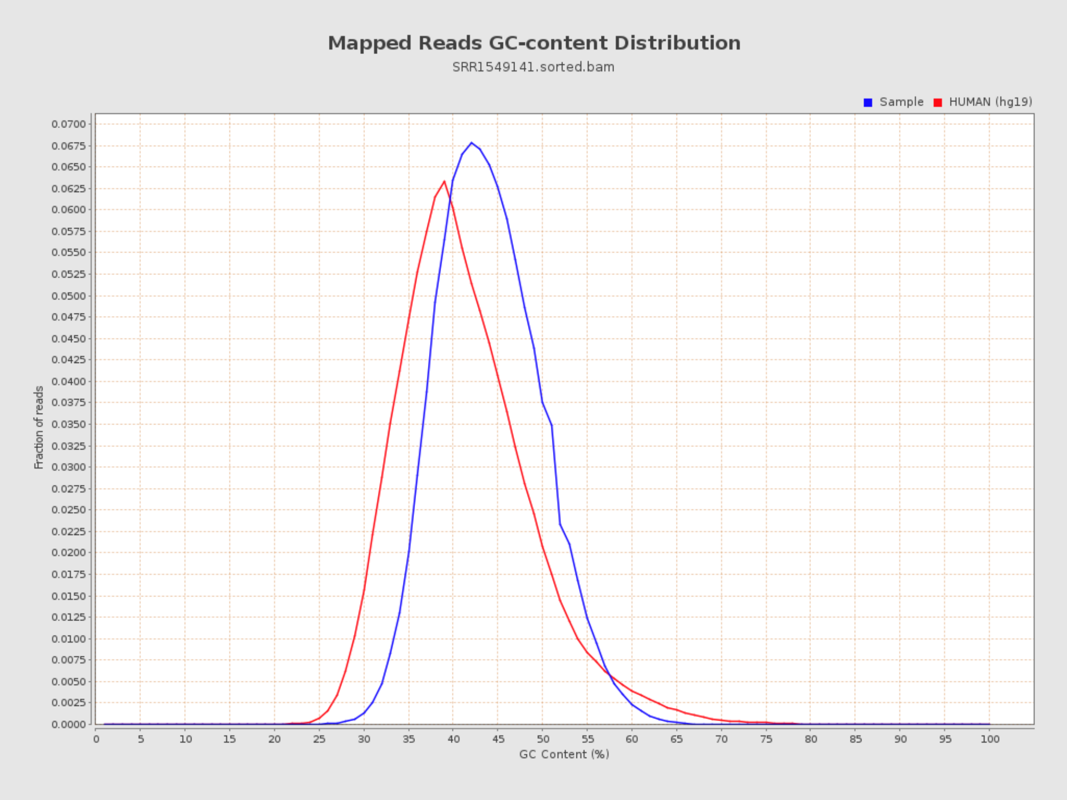
7. Results : Duplication Rate Histogram



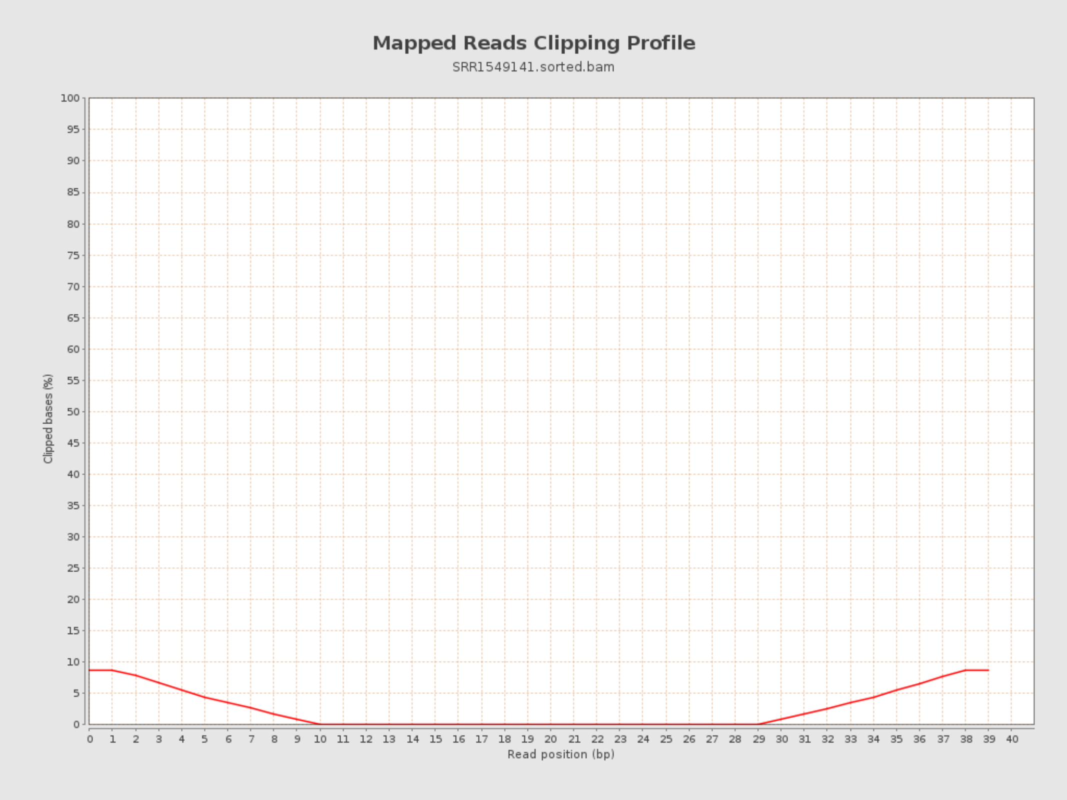
8. Results : Mapped Reads Nucleotide Content



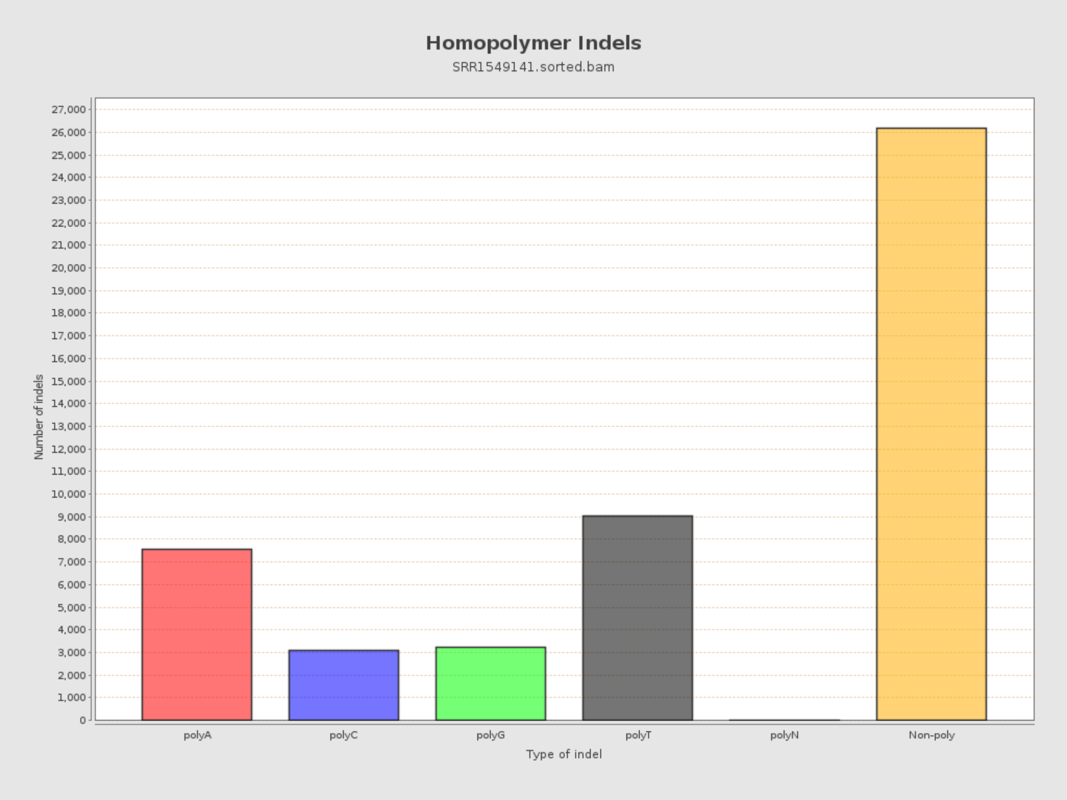
9. Results : Mapped Reads GC-content Distribution



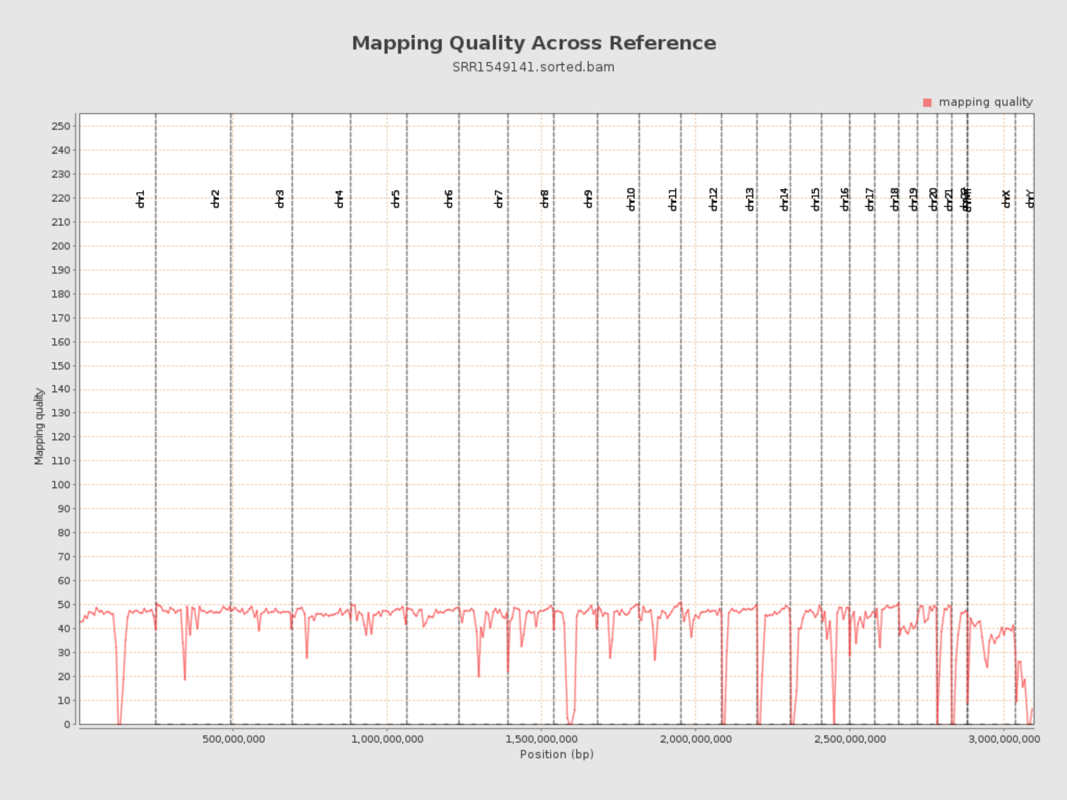
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram