Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:01:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548994.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_SRR1548994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:01:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,870,292
Mapped reads	5,048,271 / 86%
Unmapped reads	822,021 / 14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	327,571 / 5.58%
Duplication rate	5.74%
Clipped reads	234,150 / 3.99%

2.2. ACGT Content

Number/percentage of A's	61,036,935 / 30.44%
Number/percentage of C's	39,349,799 / 19.62%
Number/percentage of T's	59,727,769 / 29.78%
Number/percentage of G's	40,416,425 / 20.15%
Number/percentage of N's	1,553 / 0%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0648
Standard Deviation	0.6398

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

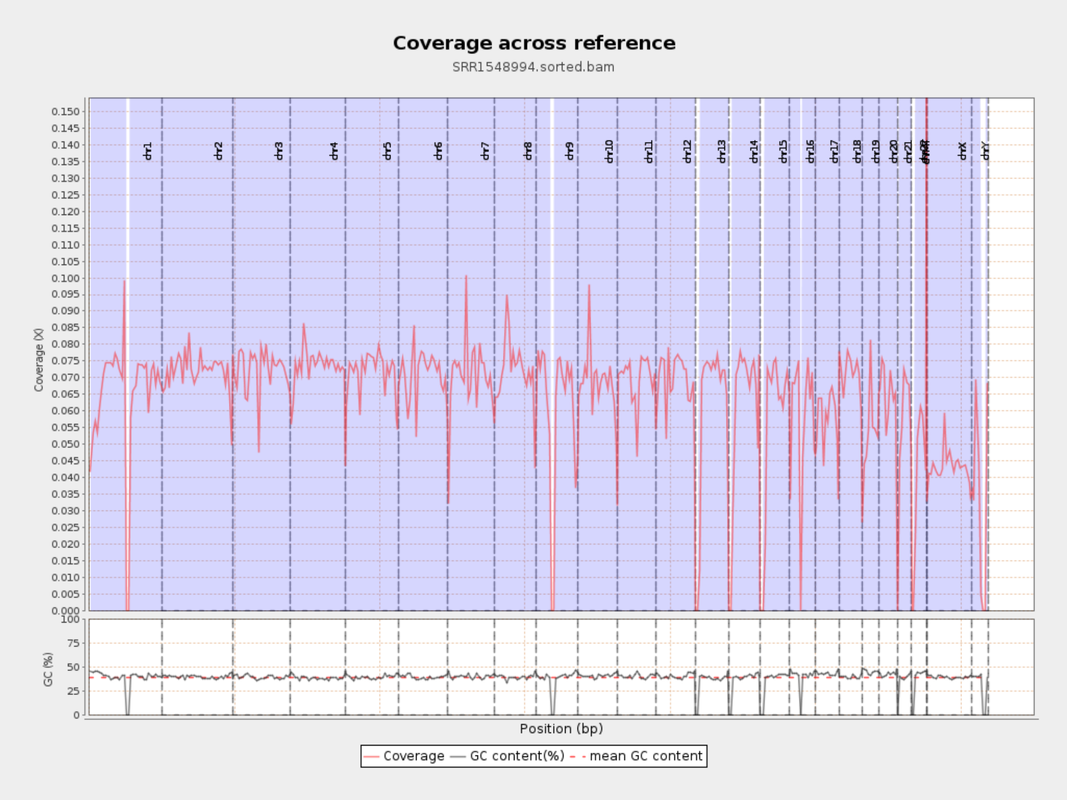
General error rate	0.31%
Mismatches	608,167
Insertions	5,603
Mapped reads with at least one insertion	0.11%
Deletions	16,440
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.56%

2.6. Chromosome stats

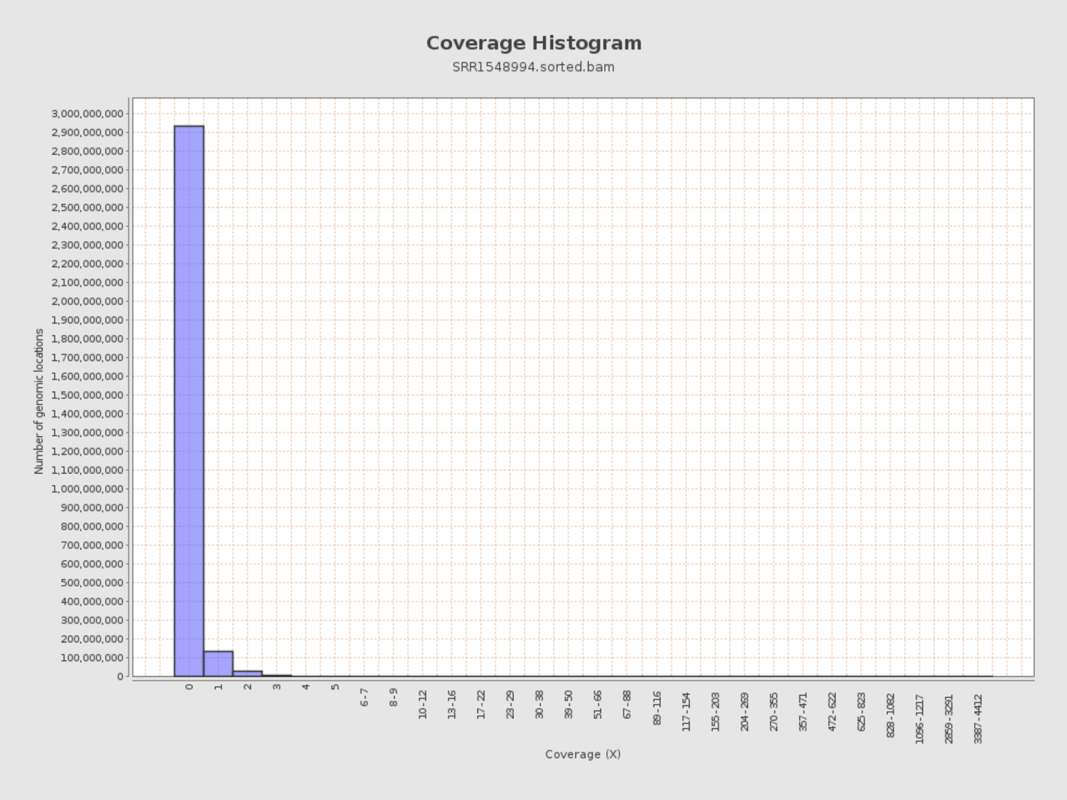
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16140191	0.0648	0.8433
chr2	243199373	17554479	0.0722	0.4014
chr3	198022430	14354214	0.0725	0.3234
chr4	191154276	14058278	0.0735	0.3454
chr5	180915260	13003654	0.0719	0.3236
chr6	171115067	12184714	0.0712	0.3555
chr7	159138663	11322416	0.0711	0.5808
chr8	146364022	10532818	0.072	2.1749

chr9	141213431	8536953	0.0605	0.3625
chr10	135534747	9397479	0.0693	0.4285
chr11	135006516	9320872	0.069	0.3791
chr12	133851895	9311859	0.0696	0.3252
chr13	115169878	6879660	0.0597	0.2911
chr14	107349540	6330564	0.059	0.3333
chr15	102531392	5692266	0.0555	0.2793
chr16	90354753	5255664	0.0582	0.3084
chr17	81195210	4626287	0.057	0.306
chr18	78077248	5595587	0.0717	0.6966
chr19	59128983	3211200	0.0543	0.6371
chr20	63025520	4056198	0.0644	0.3173
chr21	48129895	2632293	0.0547	0.3202
chr22	51304566	1957045	0.0381	0.2461
chrMT	16571	4547	0.2744	0.609
chrX	155270560	6703576	0.0432	0.2882
chrY	59373566	1890856	0.0318	0.3763

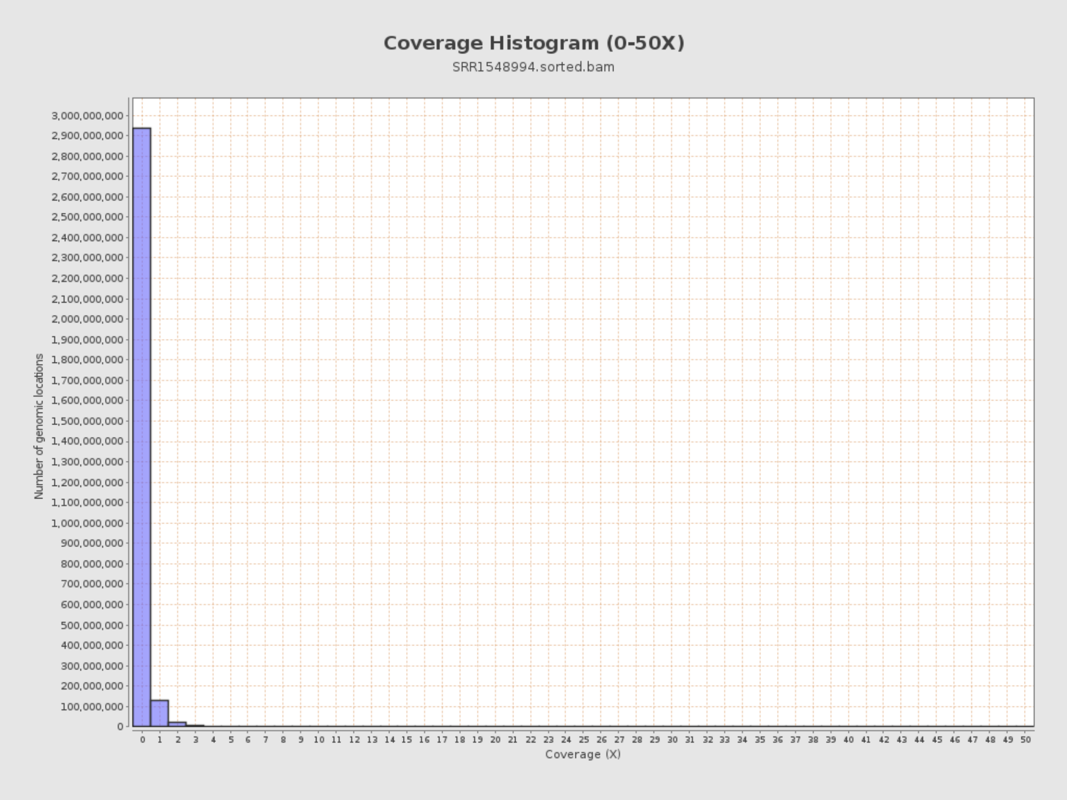
3. Results : Coverage across reference



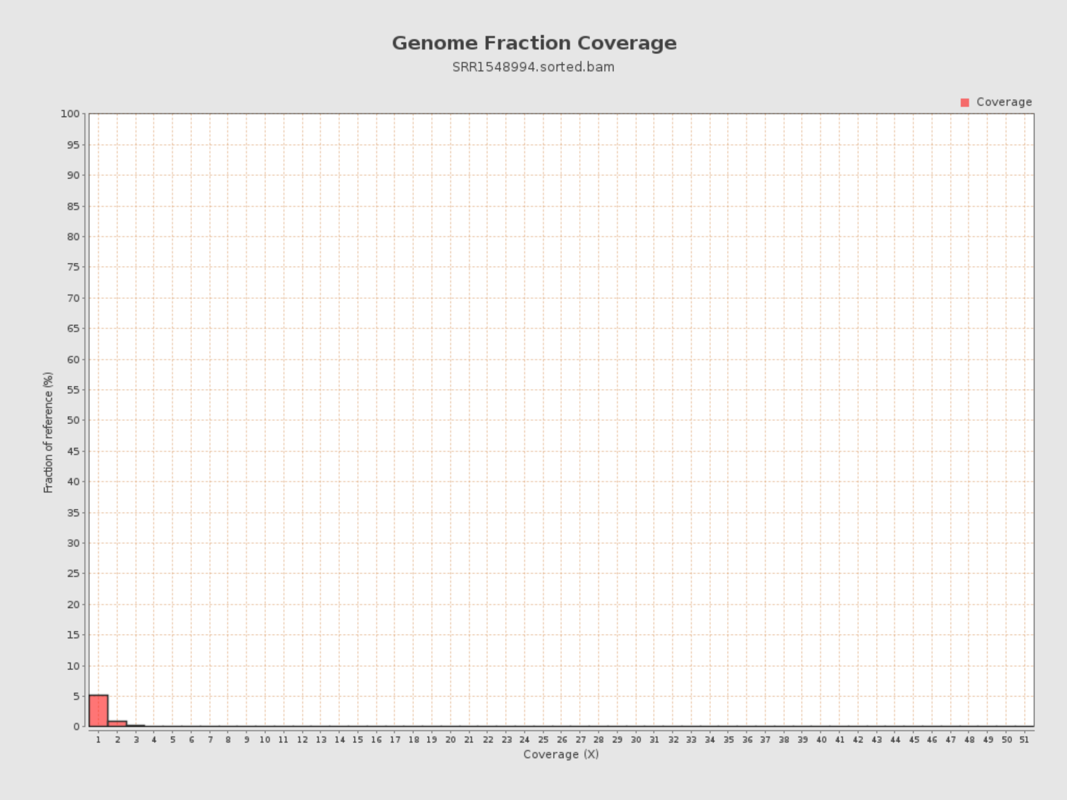
4. Results : Coverage Histogram



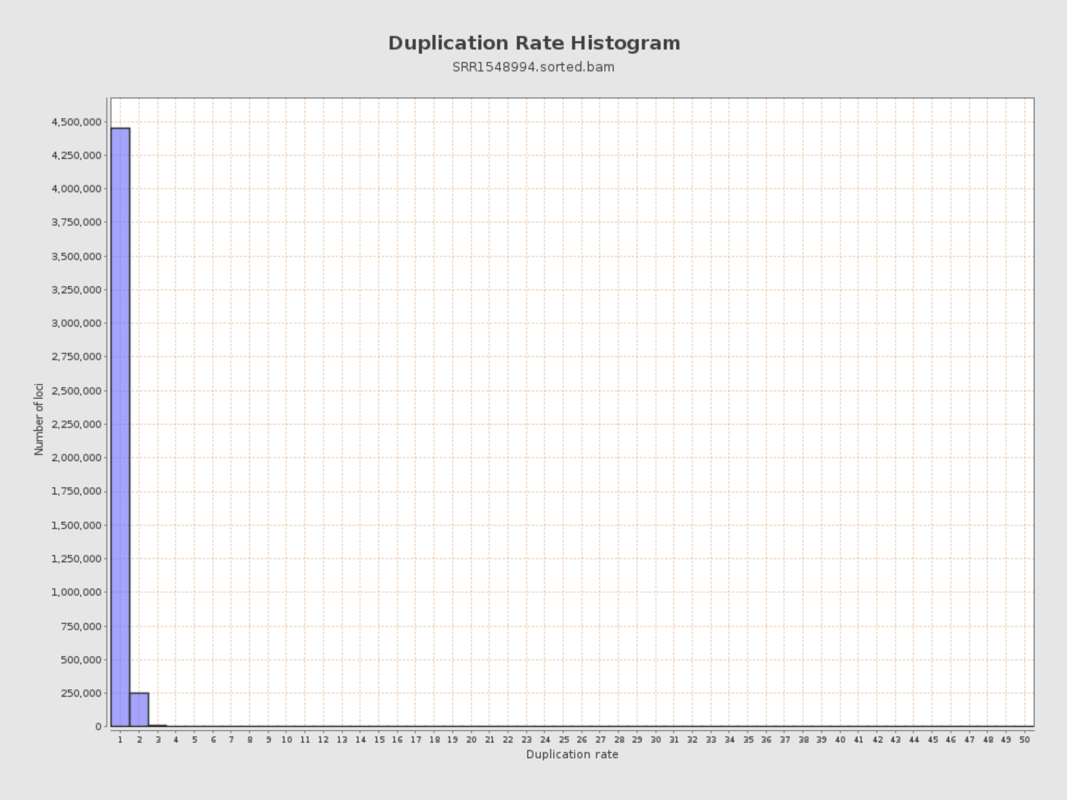
5. Results : Coverage Histogram (0-50X)



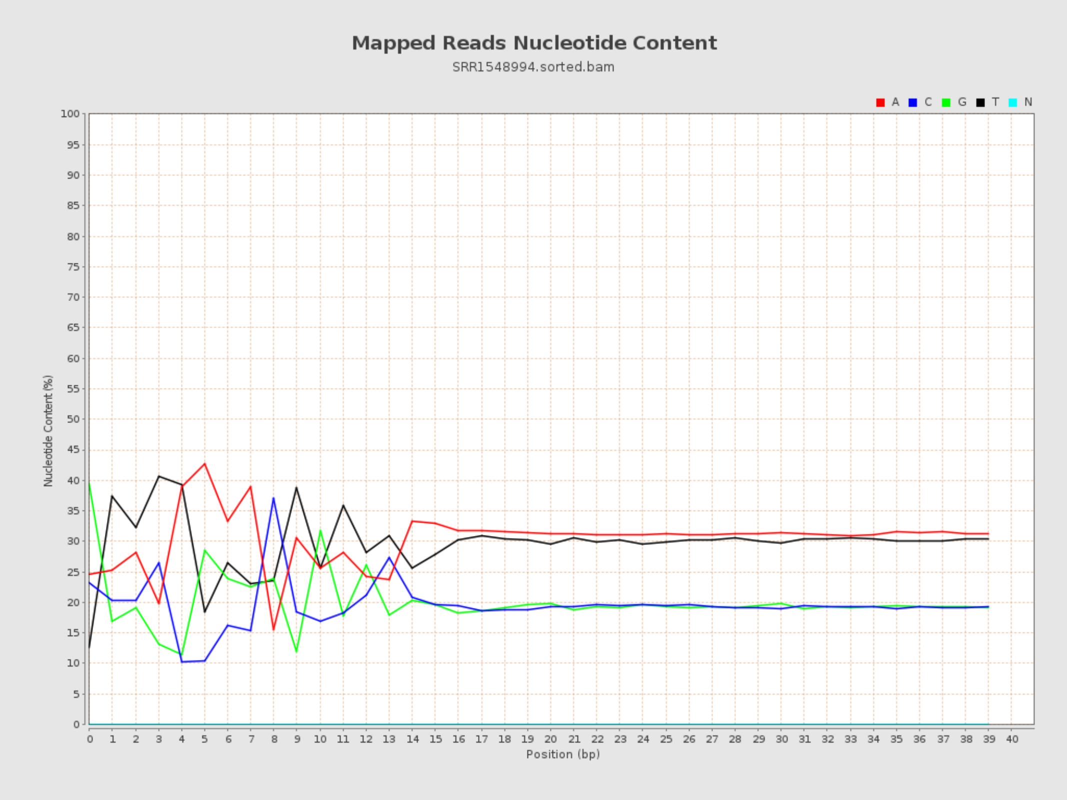
6. Results : Genome Fraction Coverage



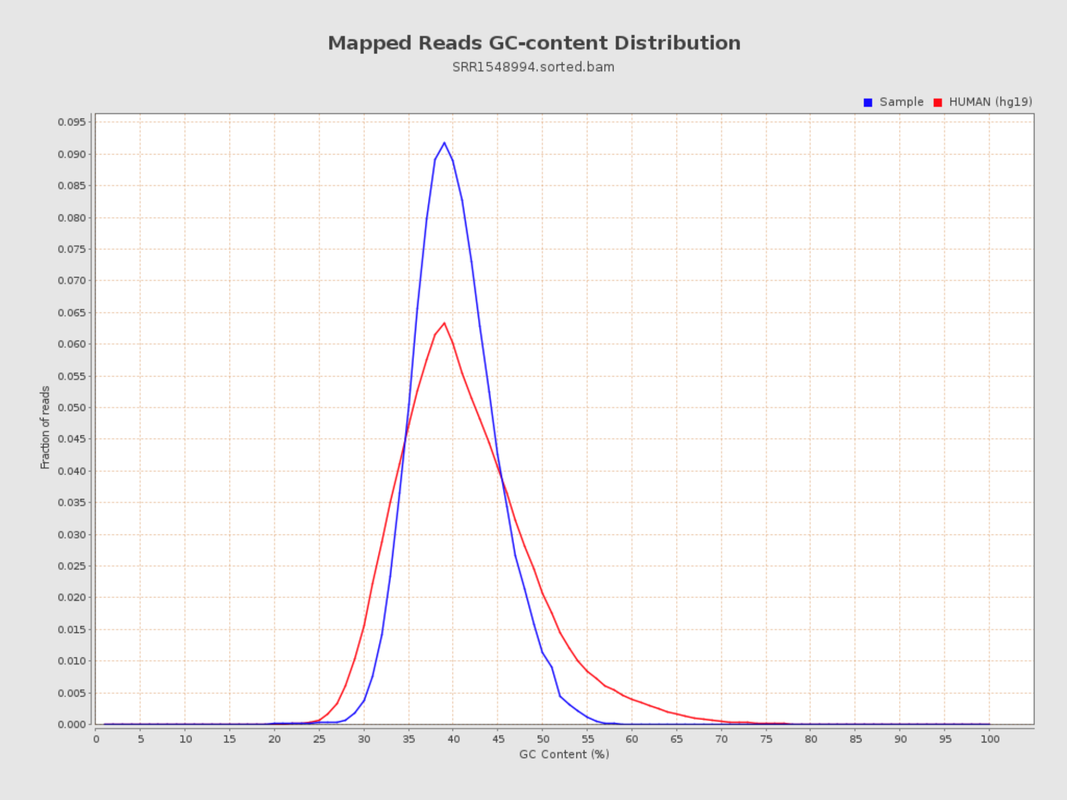
7. Results : Duplication Rate Histogram



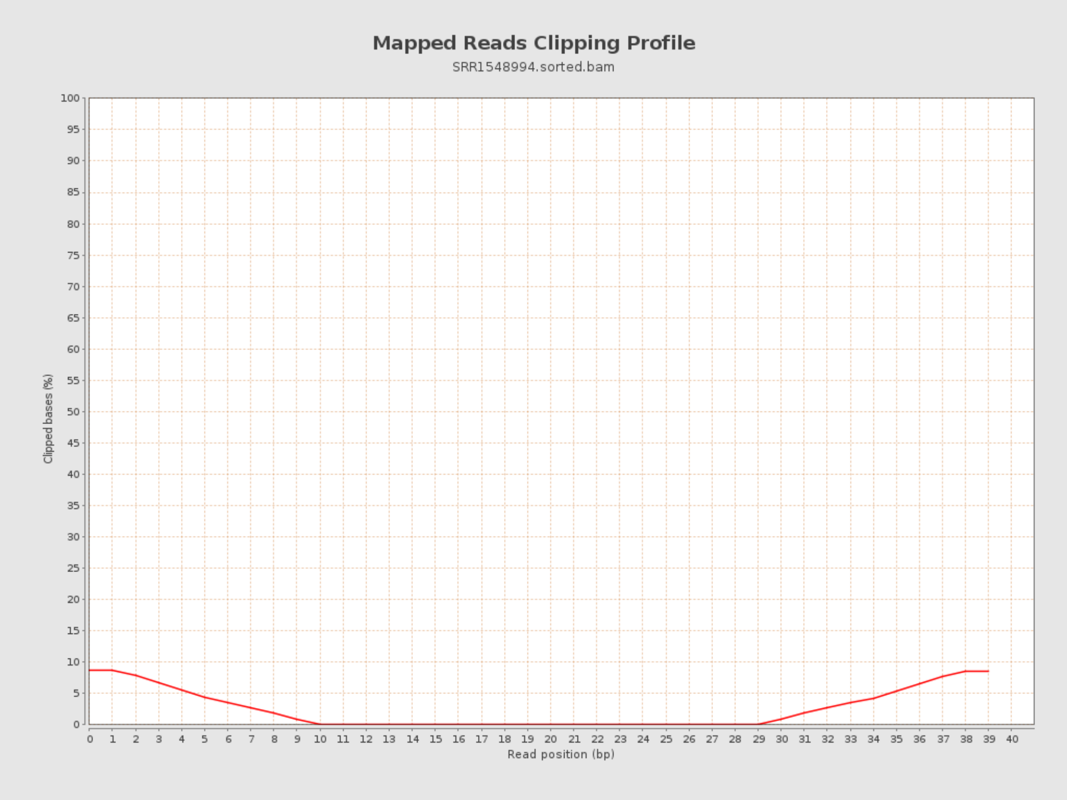
8. Results : Mapped Reads Nucleotide Content



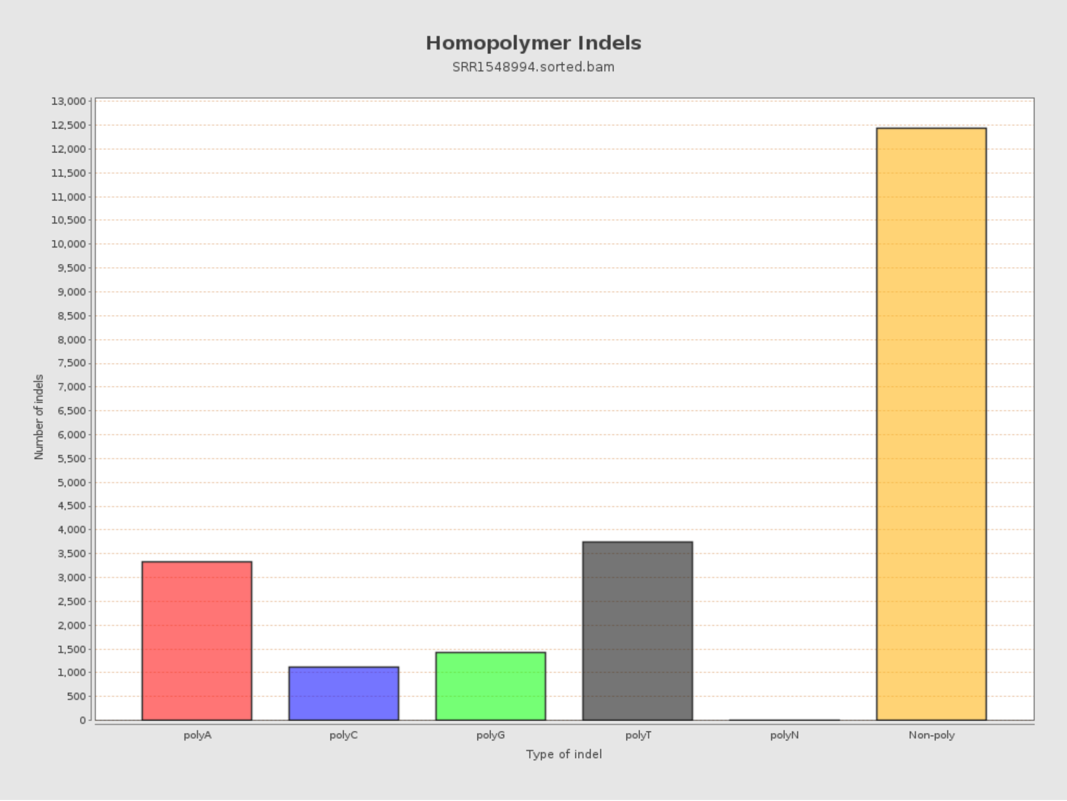
9. Results : Mapped Reads GC-content Distribution



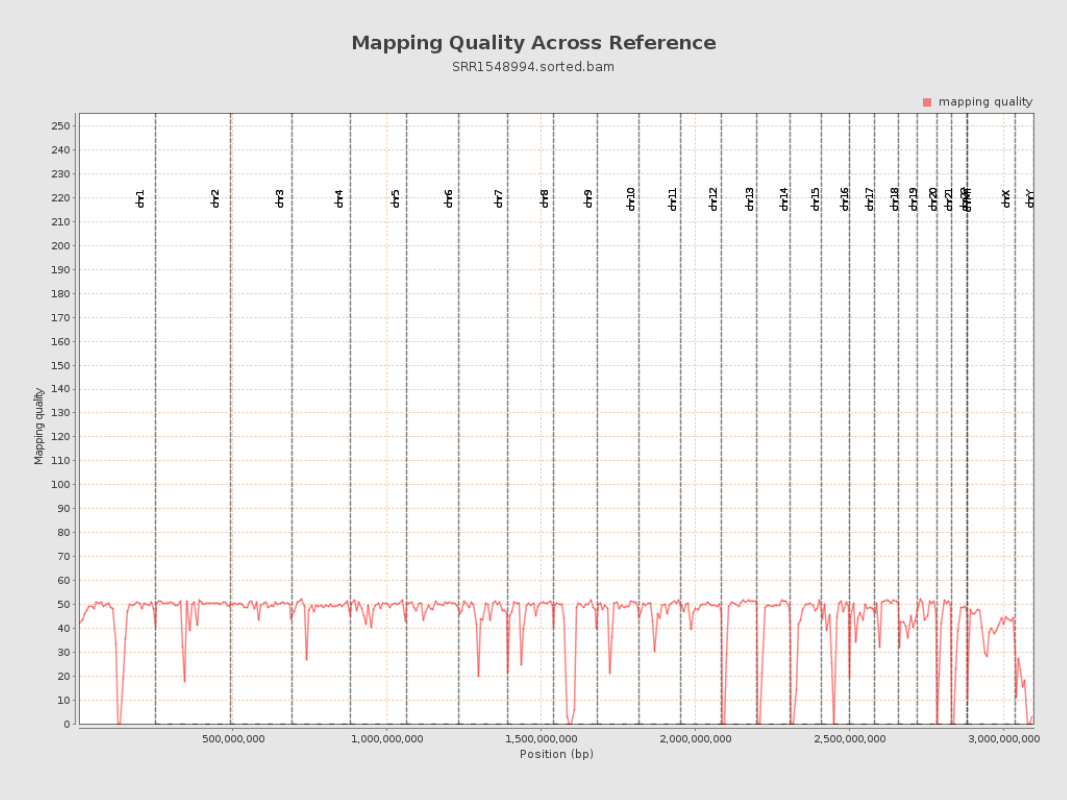
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram