Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:41:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548987.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_SRR1548987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:41:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,944,288
Mapped reads	3,421,877 / 43.07%
Unmapped reads	4,522,411 / 56.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	101,038 / 1.27%
Duplication rate	2.22%
Clipped reads	407,702 / 5.13%

2.2. ACGT Content

Number/percentage of A's	40,174,164 / 29.82%
Number/percentage of C's	26,964,699 / 20.01%
Number/percentage of T's	40,605,159 / 30.14%
Number/percentage of G's	26,992,934 / 20.03%
Number/percentage of N's	7,213 / 0.01%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0435
Standard Deviation	0.3589

2.4. Mapping Quality

Mean Mapping Quality	42.52

2.5. Mismatches and indels

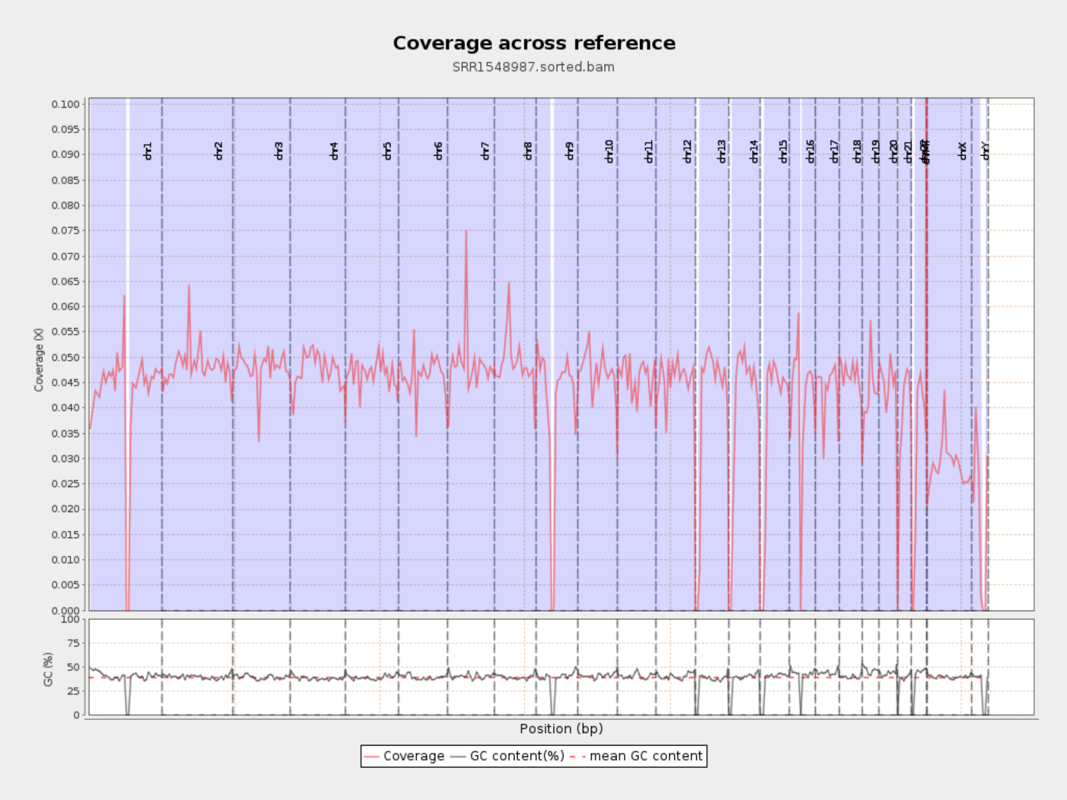
General error rate	0.33%
Mismatches	442,006
Insertions	6,598
Mapped reads with at least one insertion	0.19%
Deletions	14,485
Mapped reads with at least one deletion	0.42%
Homopolymer indels	43.4%

2.6. Chromosome stats

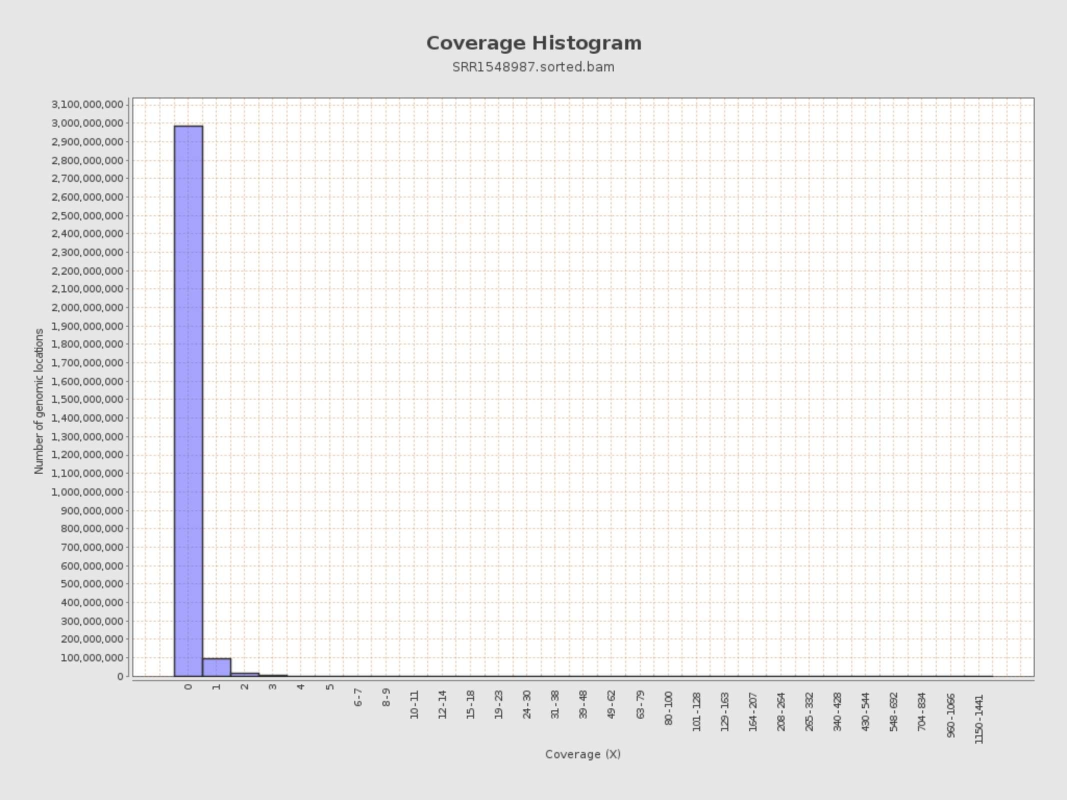
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10687491	0.0429	0.5691
chr2	243199373	11815356	0.0486	0.3263
chr3	198022430	9519300	0.0481	0.2591
chr4	191154276	9077916	0.0475	0.2652
chr5	180915260	8496085	0.047	0.2577
chr6	171115067	7964643	0.0465	0.2858
chr7	159138663	7776167	0.0489	0.4708
chr8	146364022	7145081	0.0488	0.7537

chr9	141213431	5710682	0.0404	0.2789
chr10	135534747	6449572	0.0476	0.2928
chr11	135006516	6215530	0.046	0.3054
chr12	133851895	6120260	0.0457	0.2589
chr13	115169878	4584781	0.0398	0.2371
chr14	107349540	4235730	0.0395	0.2537
chr15	102531392	3802699	0.0371	0.2271
chr16	90354753	3758175	0.0416	0.2482
chr17	81195210	3533840	0.0435	0.2565
chr18	78077248	3652838	0.0468	0.4234
chr19	59128983	2565318	0.0434	0.4728
chr20	63025520	2823931	0.0448	0.2541
chr21	48129895	1762490	0.0366	0.2398
chr22	51304566	1521162	0.0296	0.2363
chrMT	16571	6428	0.3879	0.6765
chrX	155270560	4462144	0.0287	0.2247
chrY	59373566	1074549	0.0181	0.2035

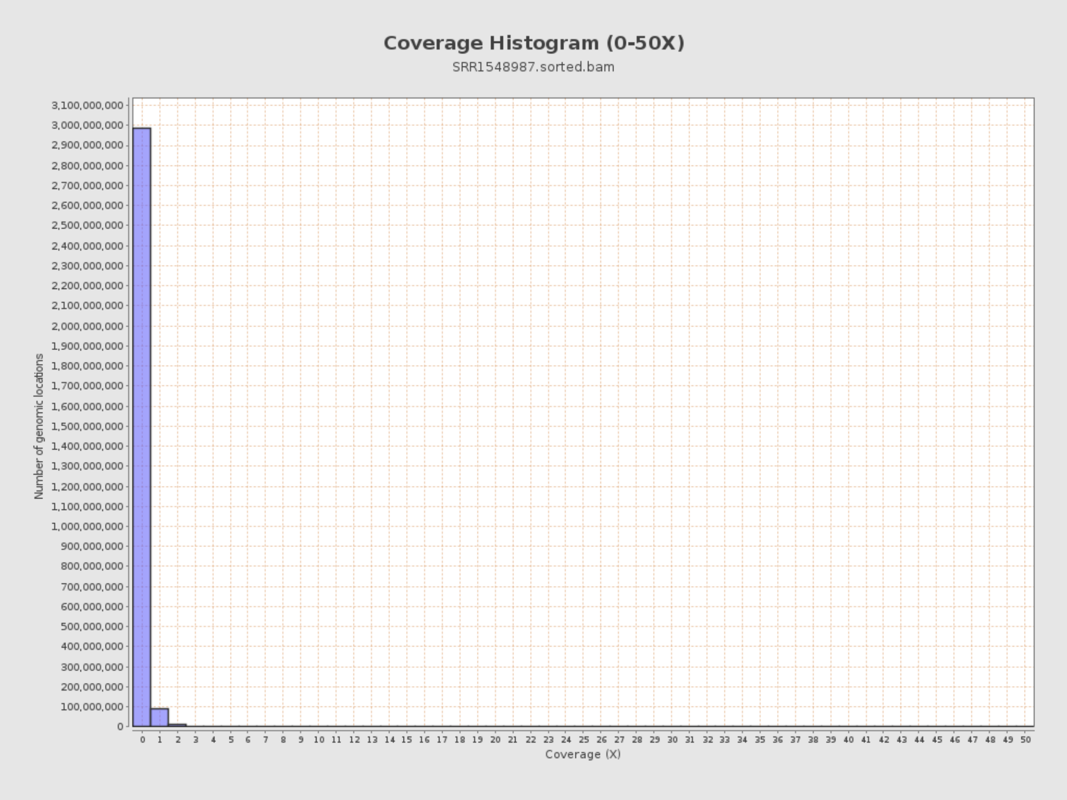
3. Results : Coverage across reference



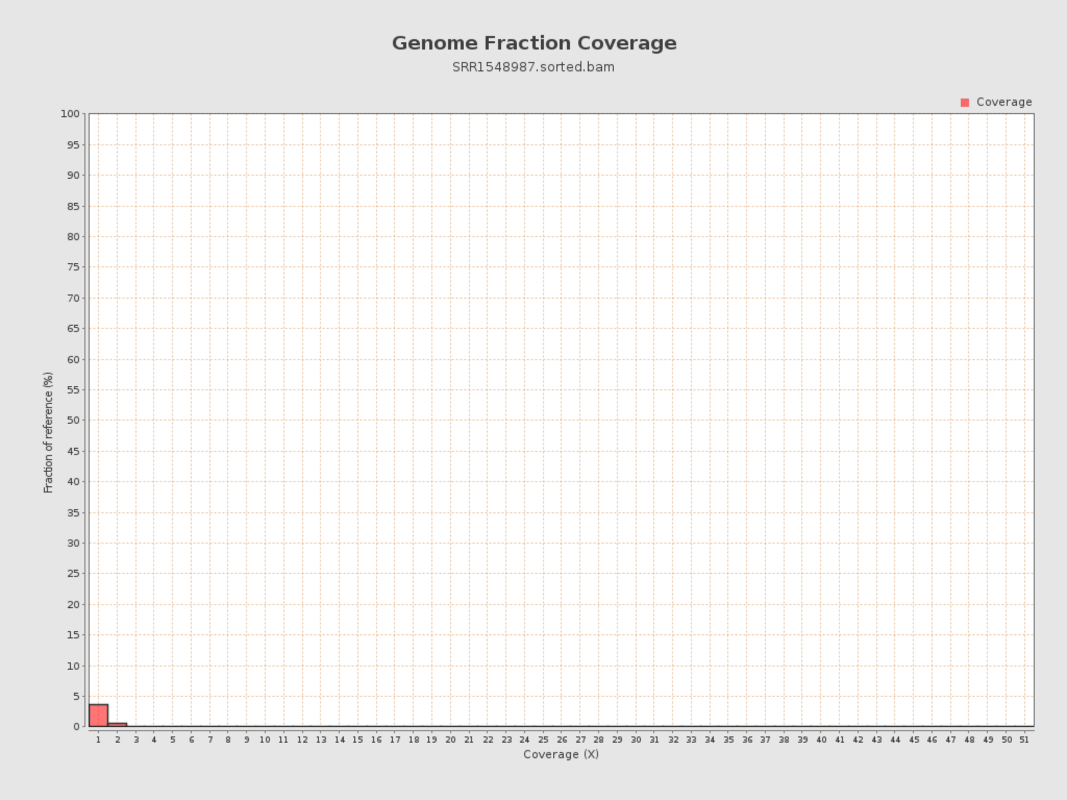
4. Results : Coverage Histogram



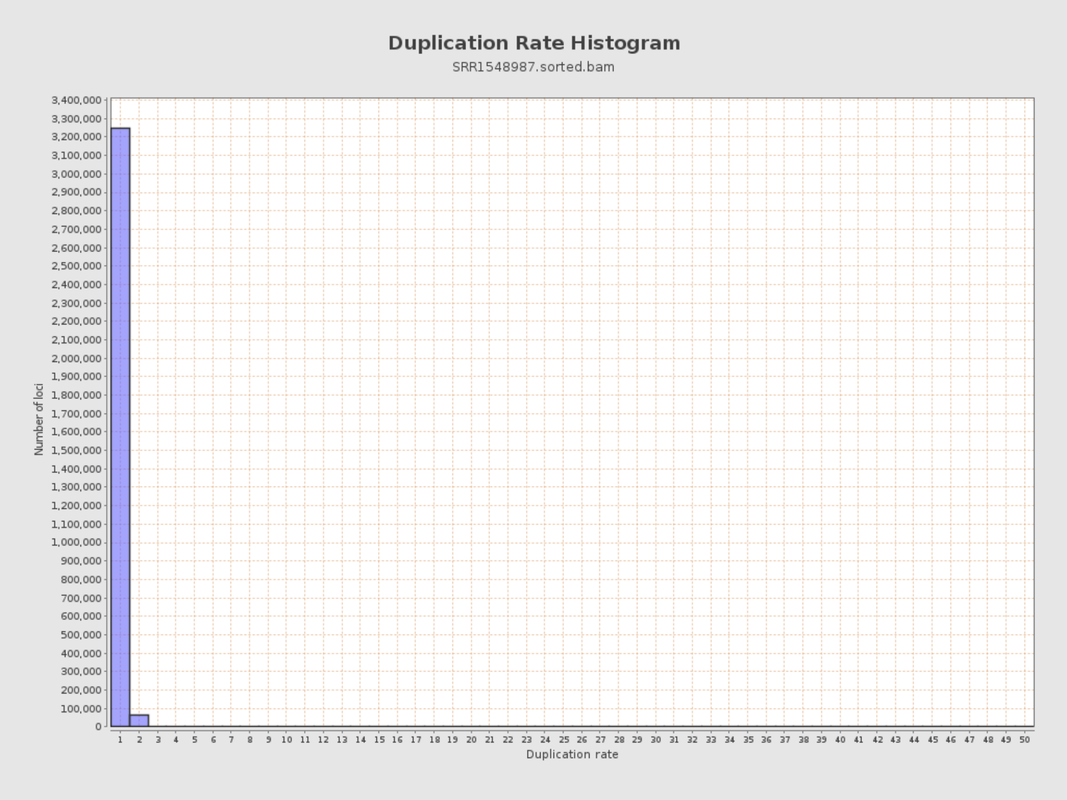
5. Results : Coverage Histogram (0-50X)



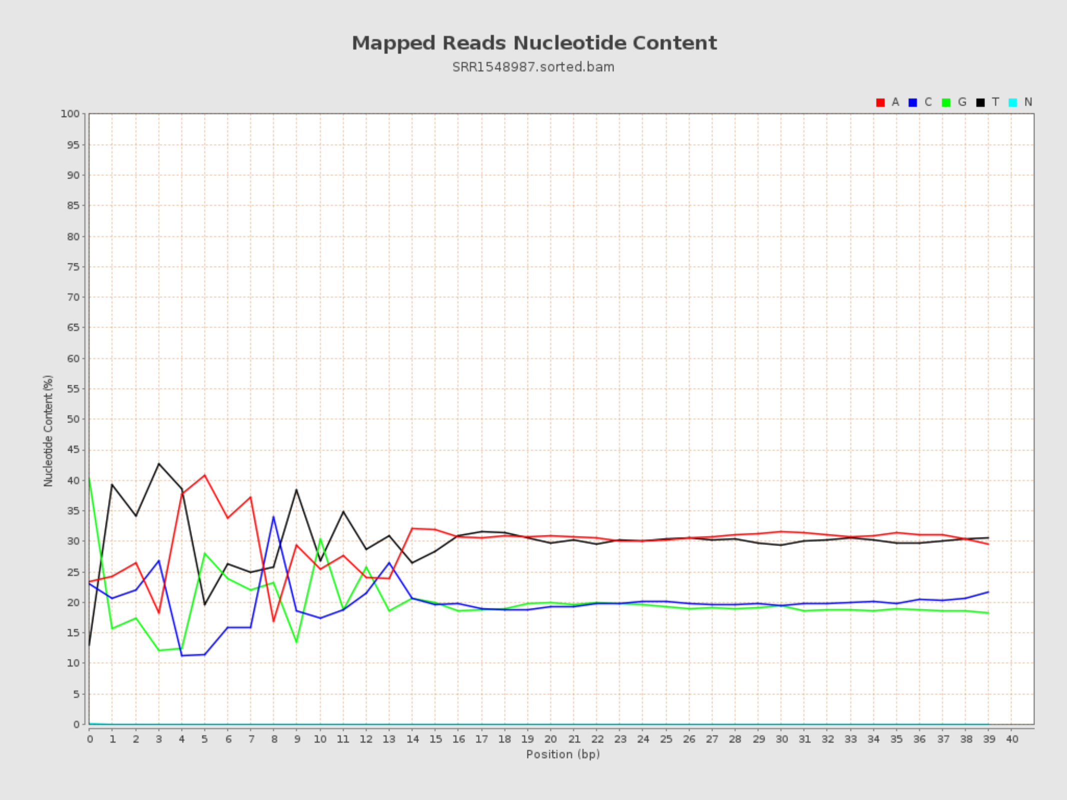
6. Results : Genome Fraction Coverage



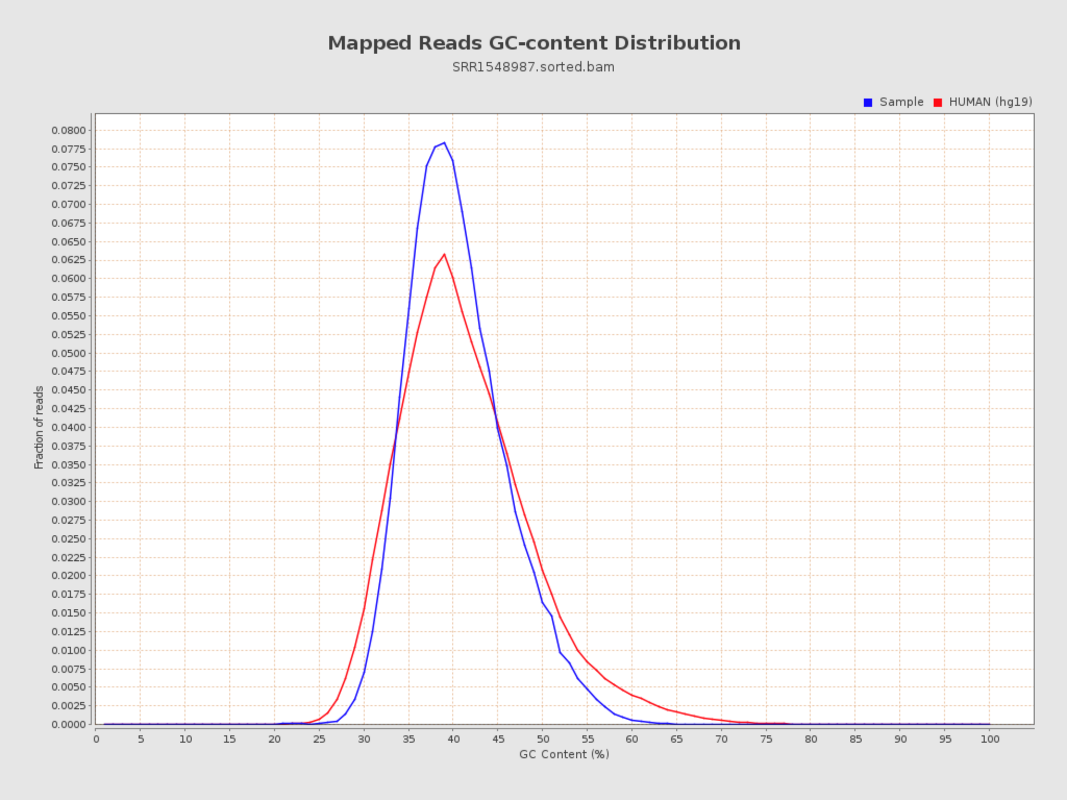
7. Results : Duplication Rate Histogram



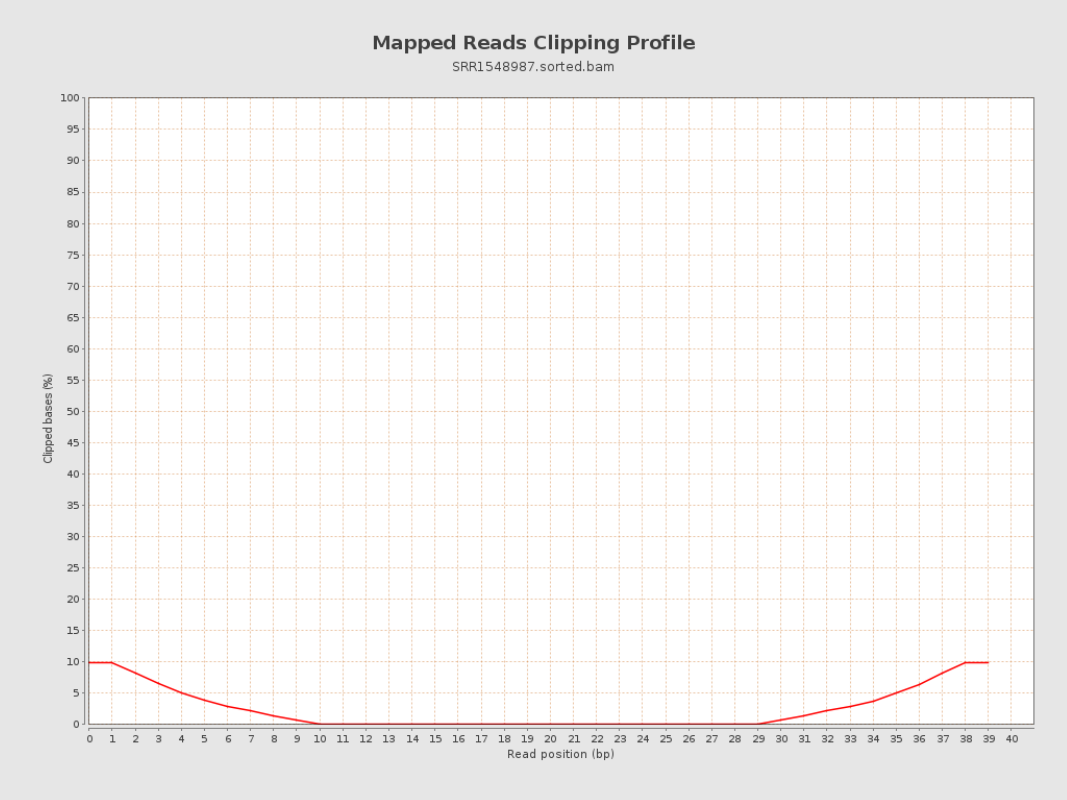
8. Results : Mapped Reads Nucleotide Content



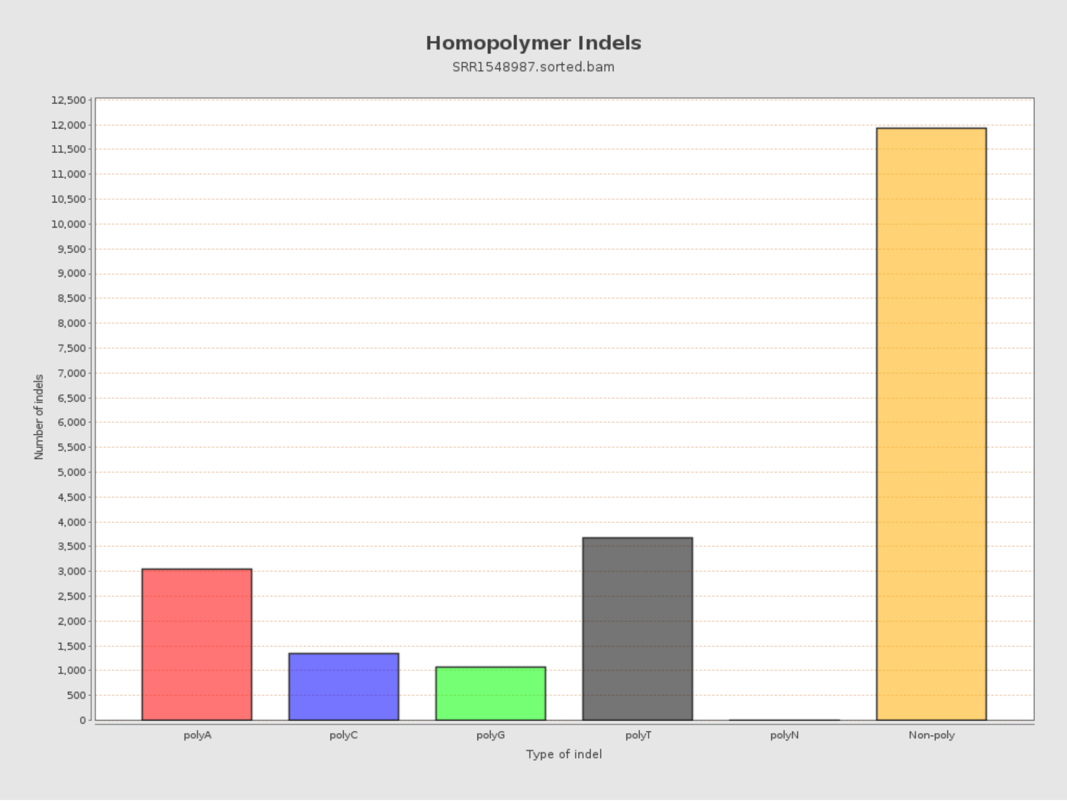
9. Results : Mapped Reads GC-content Distribution



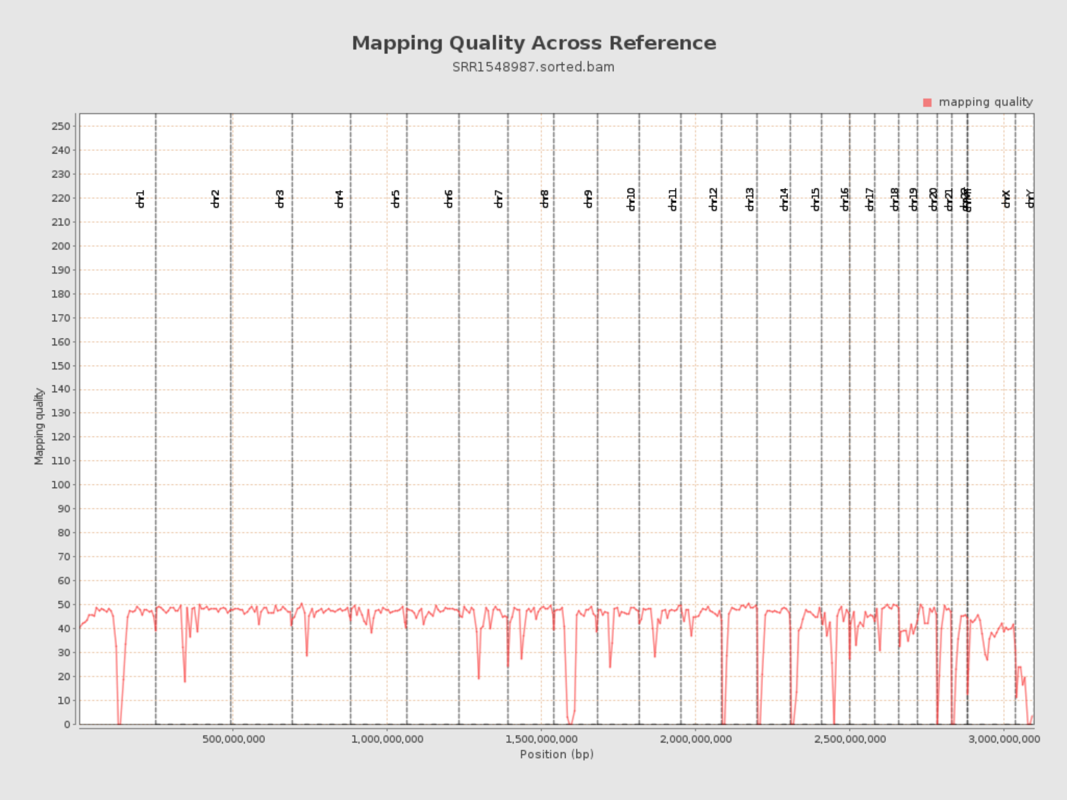
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram