

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548985.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_SRR1548985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:23:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,802,047
Mapped reads	3,430,435 / 43.97%
Unmapped reads	4,371,612 / 56.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	73,683 / 0.94%
Duplication rate	1.43%
Clipped reads	285,187 / 3.66%

2.2. ACGT Content

Number/percentage of A's	39,598,531 / 29.19%
Number/percentage of C's	27,960,682 / 20.61%
Number/percentage of T's	39,946,717 / 29.45%
Number/percentage of G's	28,130,755 / 20.74%
Number/percentage of N's	7,296 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0438
Standard Deviation	0.3283

2.4. Mapping Quality

Mean Mapping Quality	42.86
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2.5. Mismatches and indels

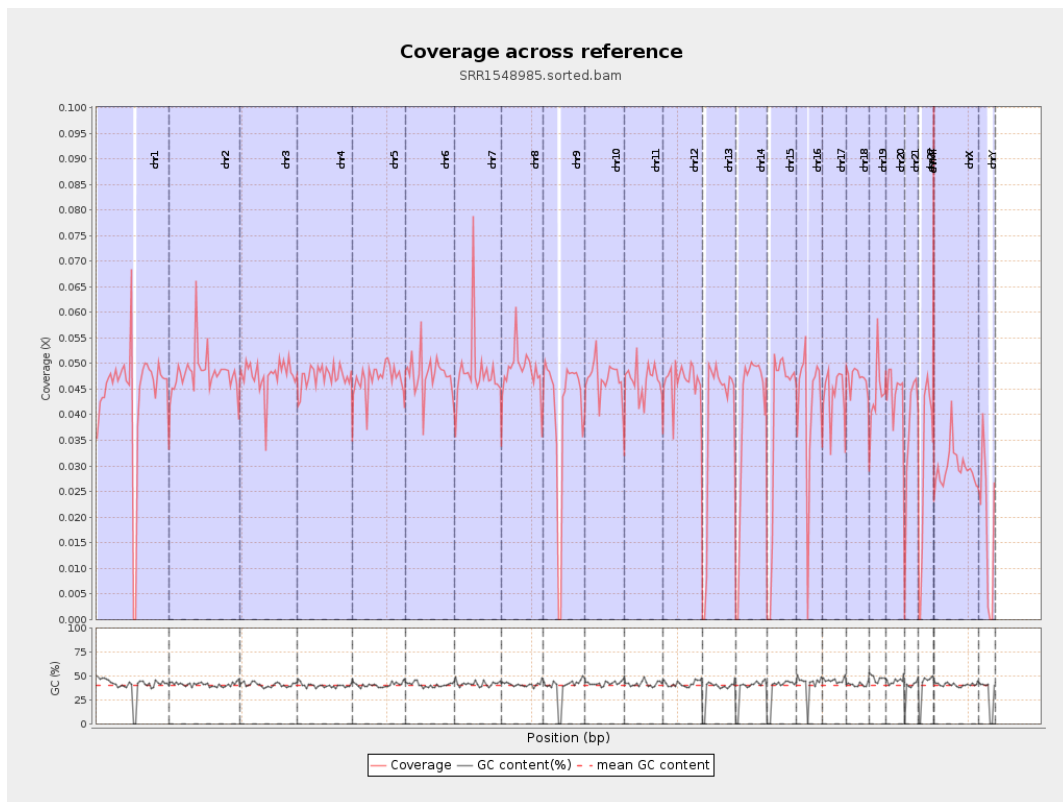
General error rate	0.3%
Mismatches	400,195
Insertions	4,812
Mapped reads with at least one insertion	0.14%
Deletions	13,257
Mapped reads with at least one deletion	0.39%
Homopolymer indels	43.02%

2.6. Chromosome stats

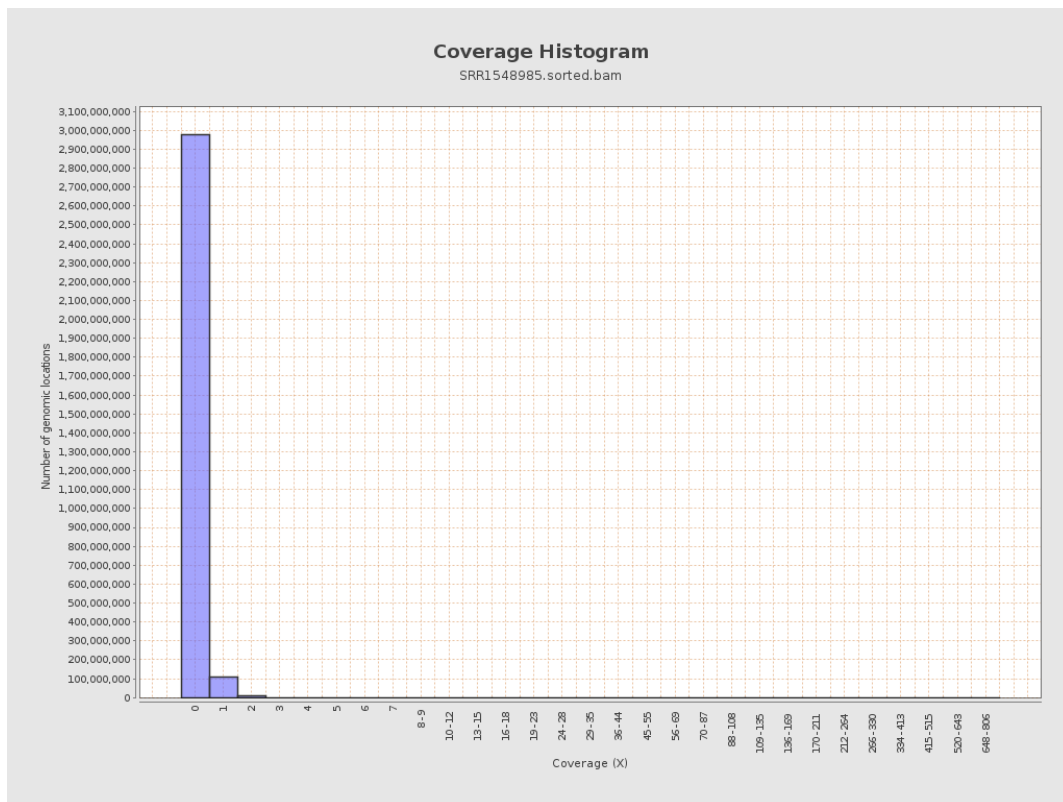
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11000551	0.0441	0.5959
chr2	243199373	11727552	0.0482	0.3037
chr3	198022430	9442356	0.0477	0.2388
chr4	191154276	9070320	0.0475	0.2411
chr5	180915260	8514665	0.0471	0.2392
chr6	171115067	8184821	0.0478	0.2772
chr7	159138663	7736317	0.0486	0.505
chr8	146364022	7120237	0.0486	0.4066

chr9	141213431	5753338	0.0407	0.2788
chr10	135534747	6406025	0.0473	0.2776
chr11	135006516	6270227	0.0464	0.2855
chr12	133851895	6233771	0.0466	0.2409
chr13	115169878	4498124	0.0391	0.2142
chr14	107349540	4269388	0.0398	0.241
chr15	102531392	4028616	0.0393	0.2158
chr16	90354753	3797926	0.042	0.2346
chr17	81195210	3545973	0.0437	0.2425
chr18	78077248	3679750	0.0471	0.4274
chr19	59128983	2635100	0.0446	0.4796
chr20	63025520	2784495	0.0442	0.2352
chr21	48129895	1768287	0.0367	0.2259
chr22	51304566	1543448	0.0301	0.2153
chrMT	16571	1753	0.1058	0.3281
chrX	155270560	4595694	0.0296	0.2185
chrY	59373566	1052188	0.0177	0.1854

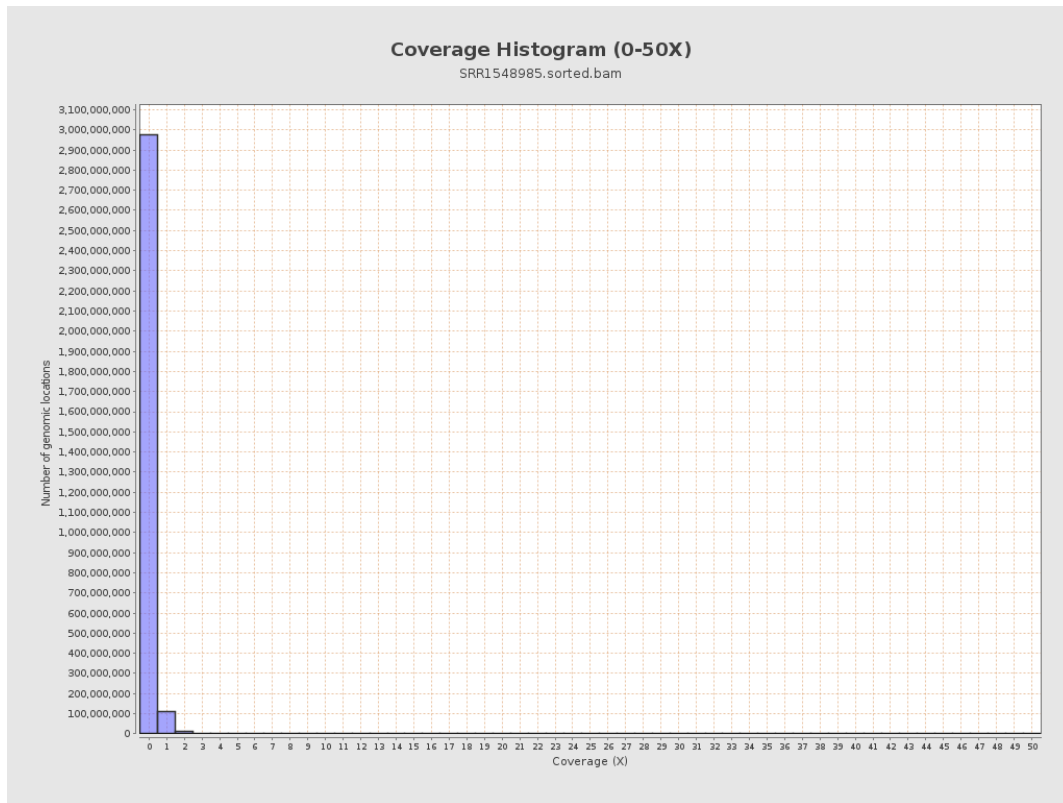
3. Results : Coverage across reference



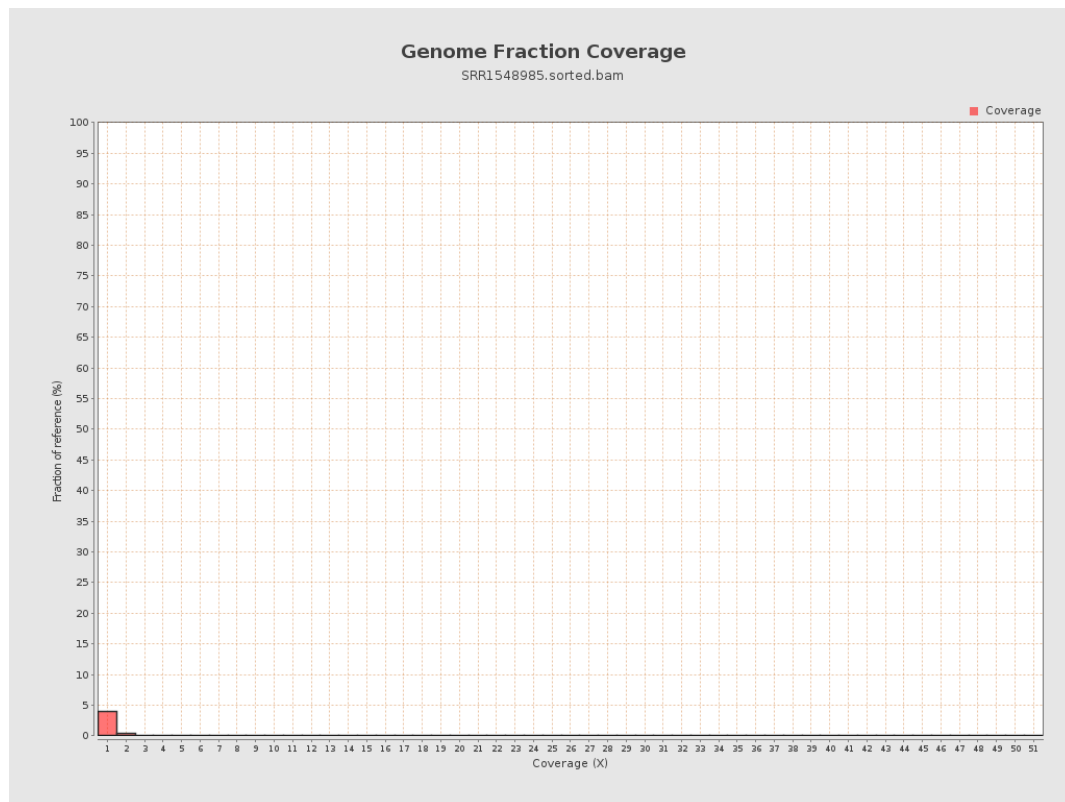
4. Results : Coverage Histogram



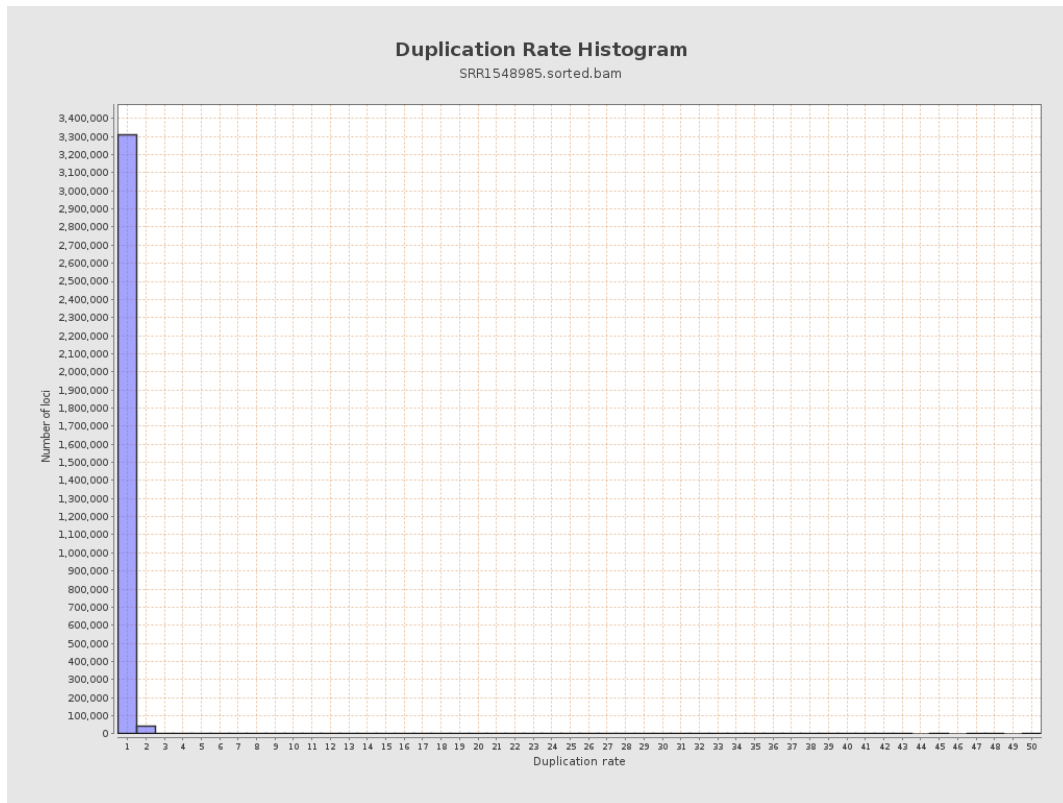
5. Results : Coverage Histogram (0-50X)



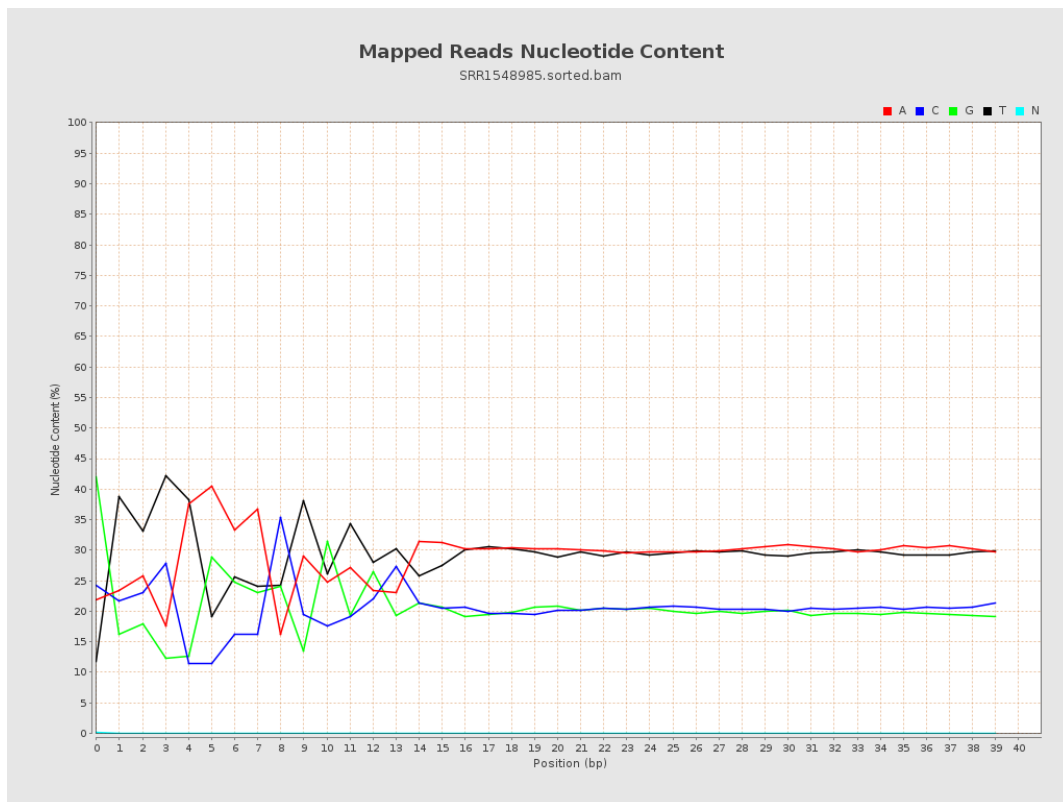
6. Results : Genome Fraction Coverage



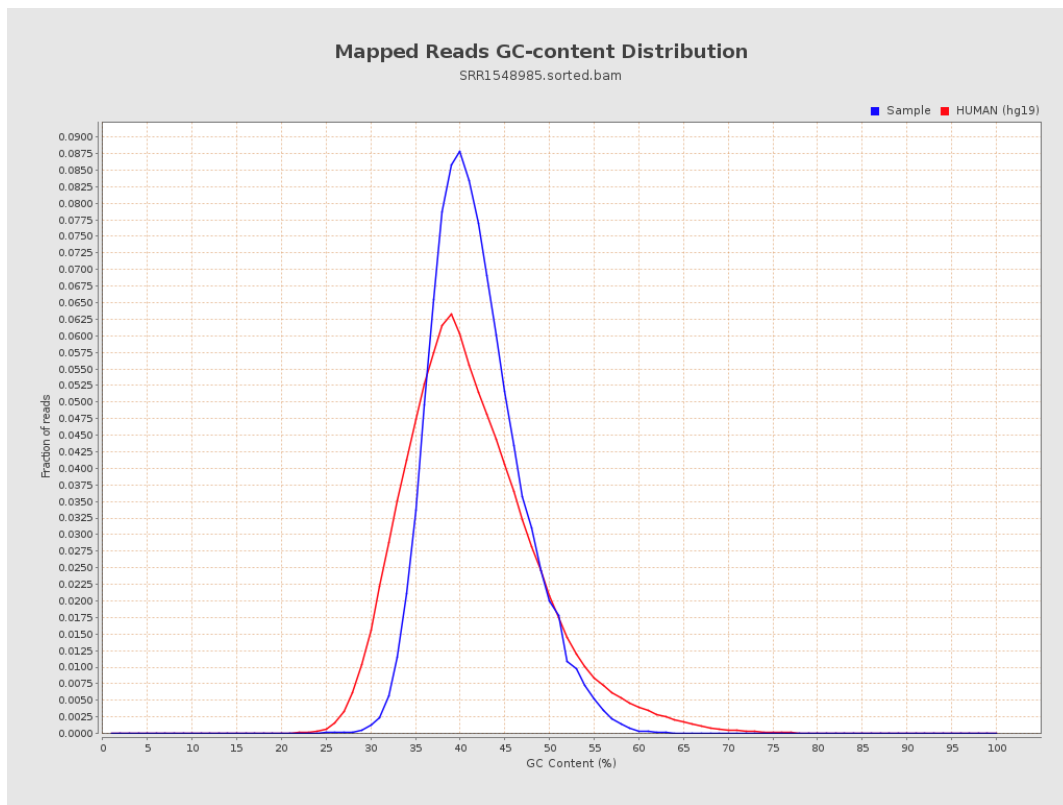
7. Results : Duplication Rate Histogram



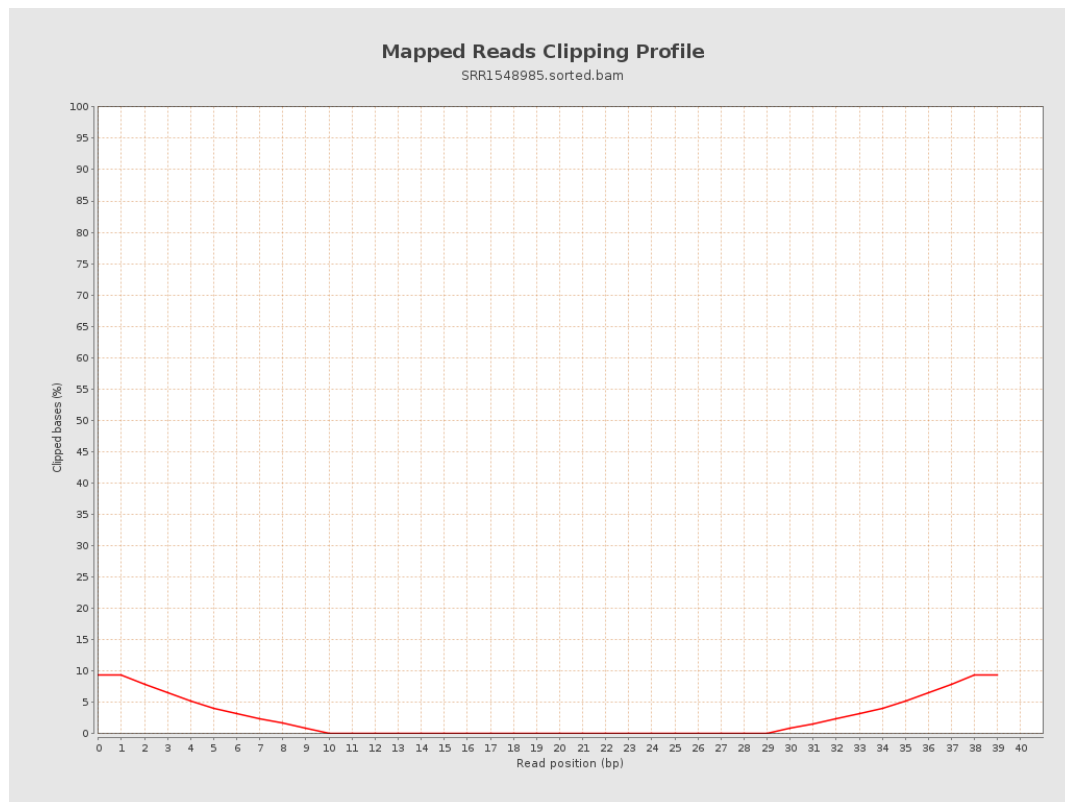
8. Results : Mapped Reads Nucleotide Content



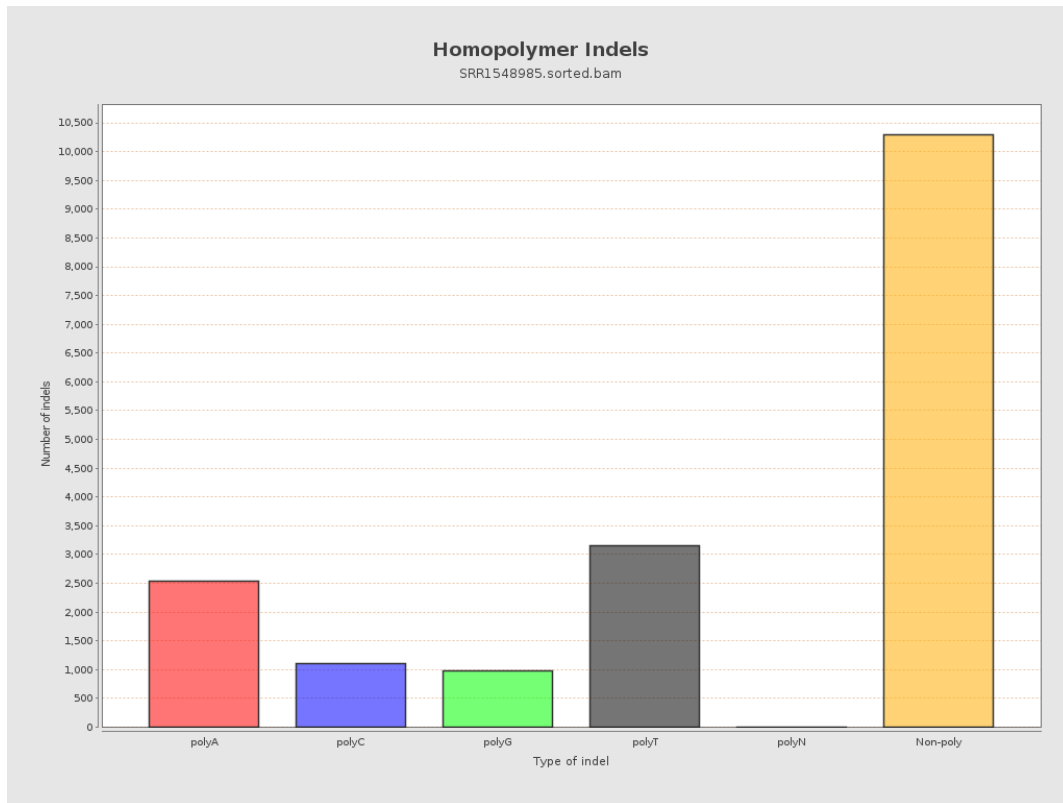
9. Results : Mapped Reads GC-content Distribution



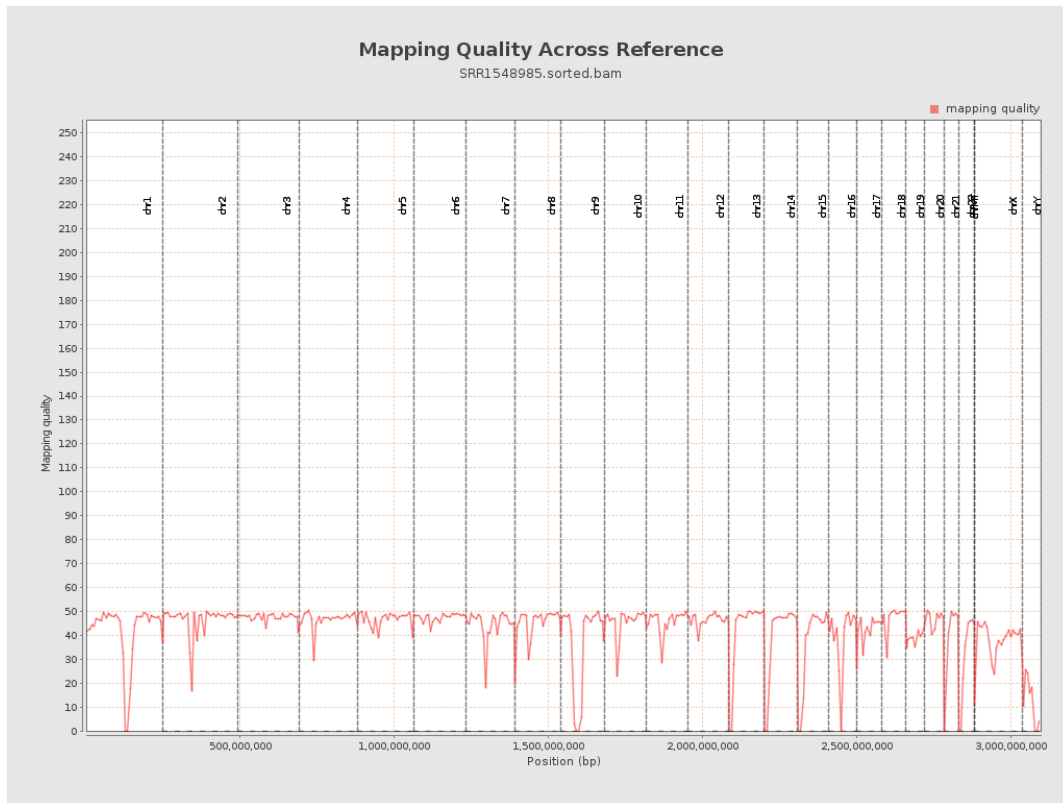
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

