

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:36:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548975.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_SRR1548975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548975.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:36:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,697,809
Mapped reads	3,391,889 / 44.06%
Unmapped reads	4,305,920 / 55.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	89,052 / 1.16%
Duplication rate	1.92%
Clipped reads	359,800 / 4.67%

2.2. ACGT Content

Number/percentage of A's	41,700,124 / 31.17%
Number/percentage of C's	25,021,632 / 18.7%
Number/percentage of T's	41,783,607 / 31.23%
Number/percentage of G's	25,280,132 / 18.9%
Number/percentage of N's	6,526 / 0%
GC Percentage	37.6%

2.3. Coverage

Mean	0.0432
Standard Deviation	0.3323

2.4. Mapping Quality

Mean Mapping Quality	43.63
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2.5. Mismatches and indels

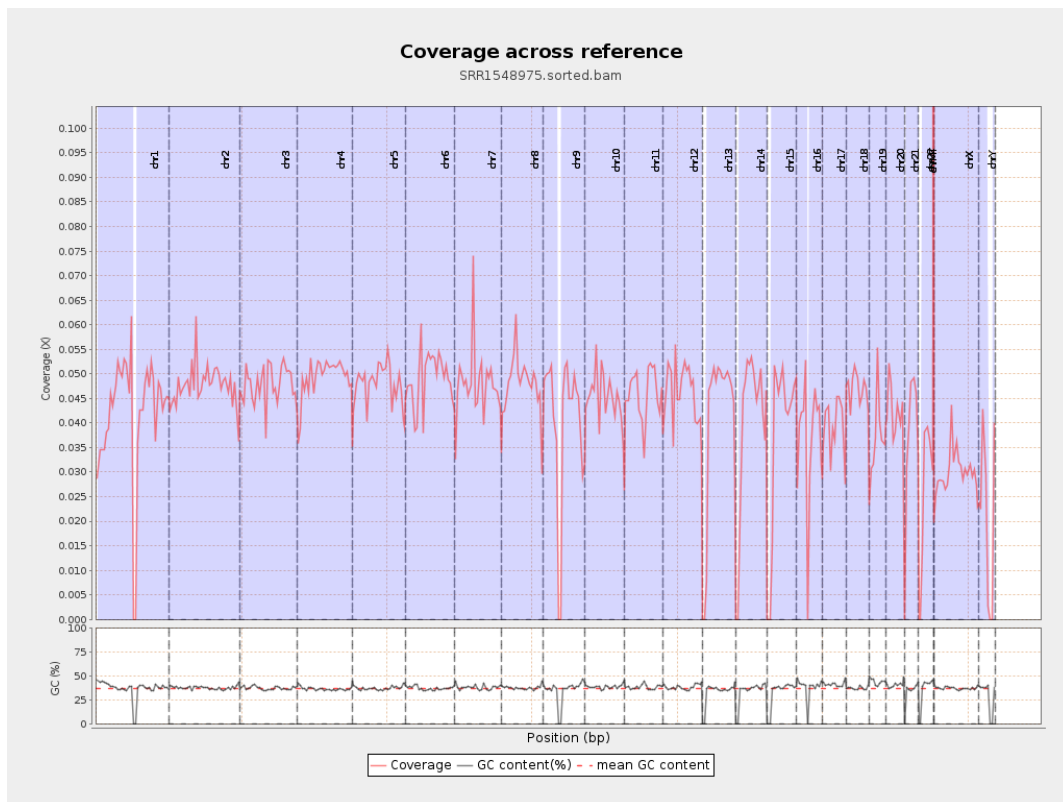
General error rate	0.34%
Mismatches	443,808
Insertions	6,261
Mapped reads with at least one insertion	0.18%
Deletions	15,274
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.05%

2.6. Chromosome stats

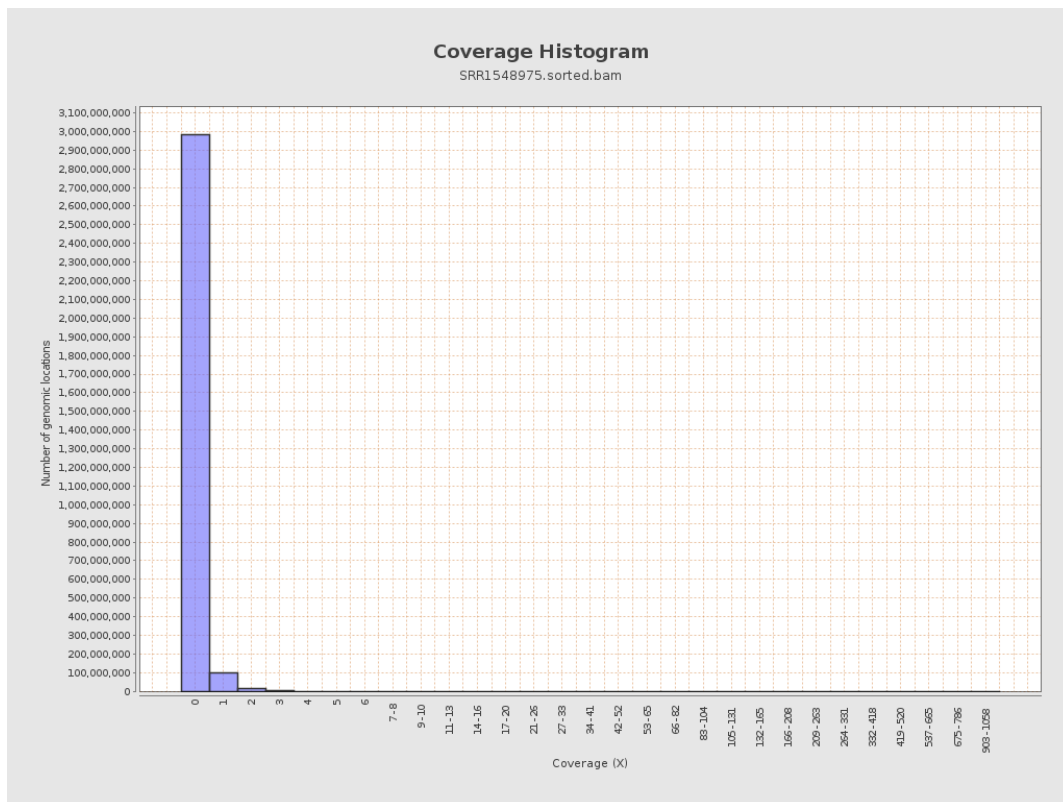
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10485960	0.0421	0.5073
chr2	243199373	11617040	0.0478	0.3097
chr3	198022430	9482928	0.0479	0.2511
chr4	191154276	9425329	0.0493	0.2608
chr5	180915260	8686140	0.048	0.2546
chr6	171115067	8385992	0.049	0.2818
chr7	159138663	7692189	0.0483	0.4559
chr8	146364022	7009782	0.0479	0.5778

chr9	141213431	5705698	0.0404	0.28
chr10	135534747	6171018	0.0455	0.2846
chr11	135006516	6172864	0.0457	0.3041
chr12	133851895	6203105	0.0463	0.2527
chr13	115169878	4657435	0.0404	0.2304
chr14	107349540	4256472	0.0397	0.2549
chr15	102531392	3874827	0.0378	0.2214
chr16	90354753	3337893	0.0369	0.2272
chr17	81195210	3157479	0.0389	0.2335
chr18	78077248	3667462	0.047	0.4588
chr19	59128983	2215312	0.0375	0.5022
chr20	63025520	2648324	0.042	0.2394
chr21	48129895	1818473	0.0378	0.2401
chr22	51304566	1303774	0.0254	0.2013
chrMT	16571	5668	0.342	0.6442
chrX	155270560	4643513	0.0299	0.2269
chrY	59373566	1186443	0.02	0.2379

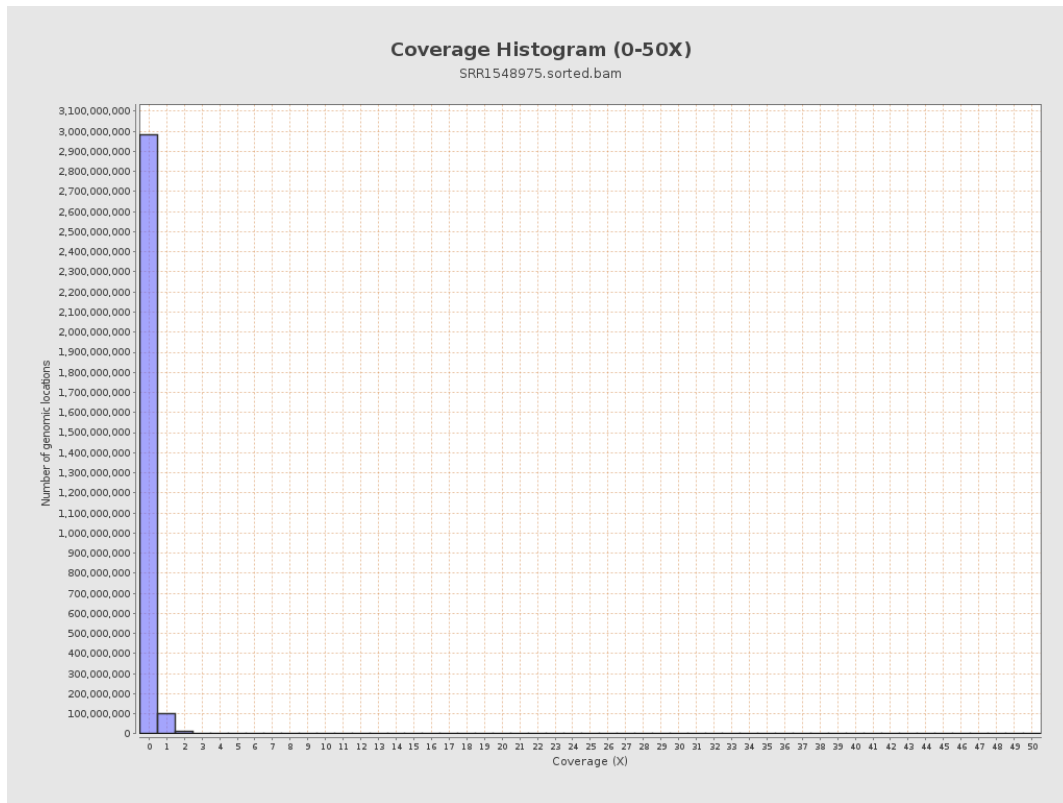
3. Results : Coverage across reference



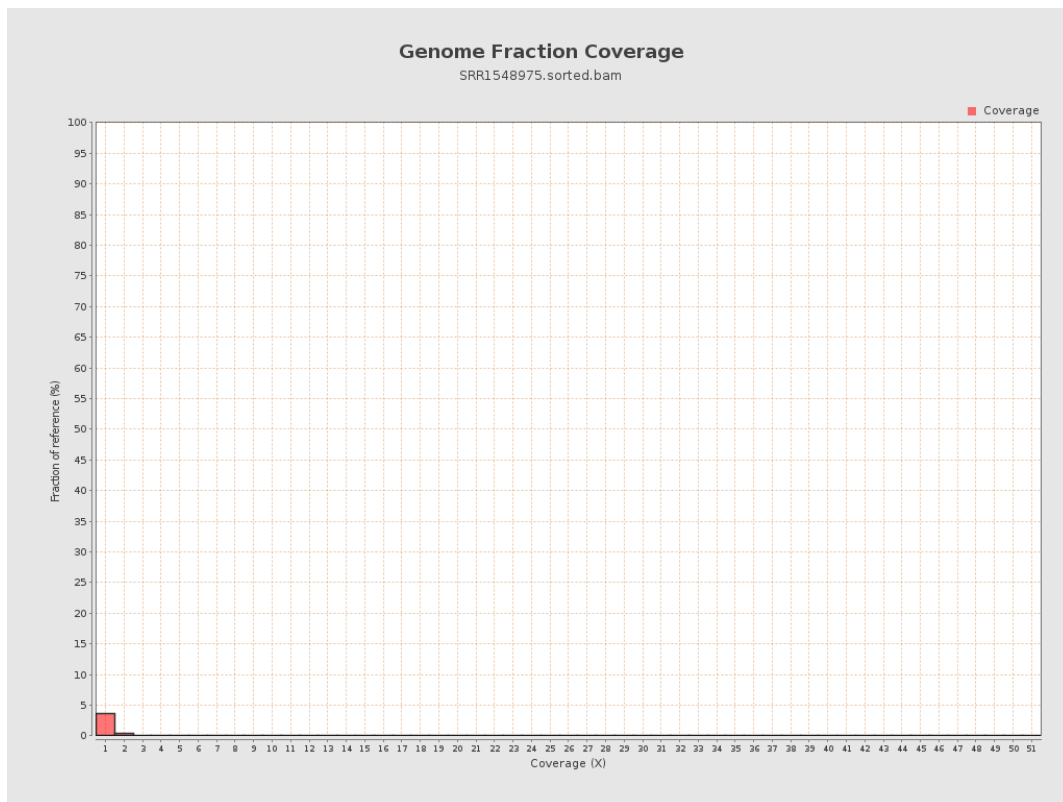
4. Results : Coverage Histogram



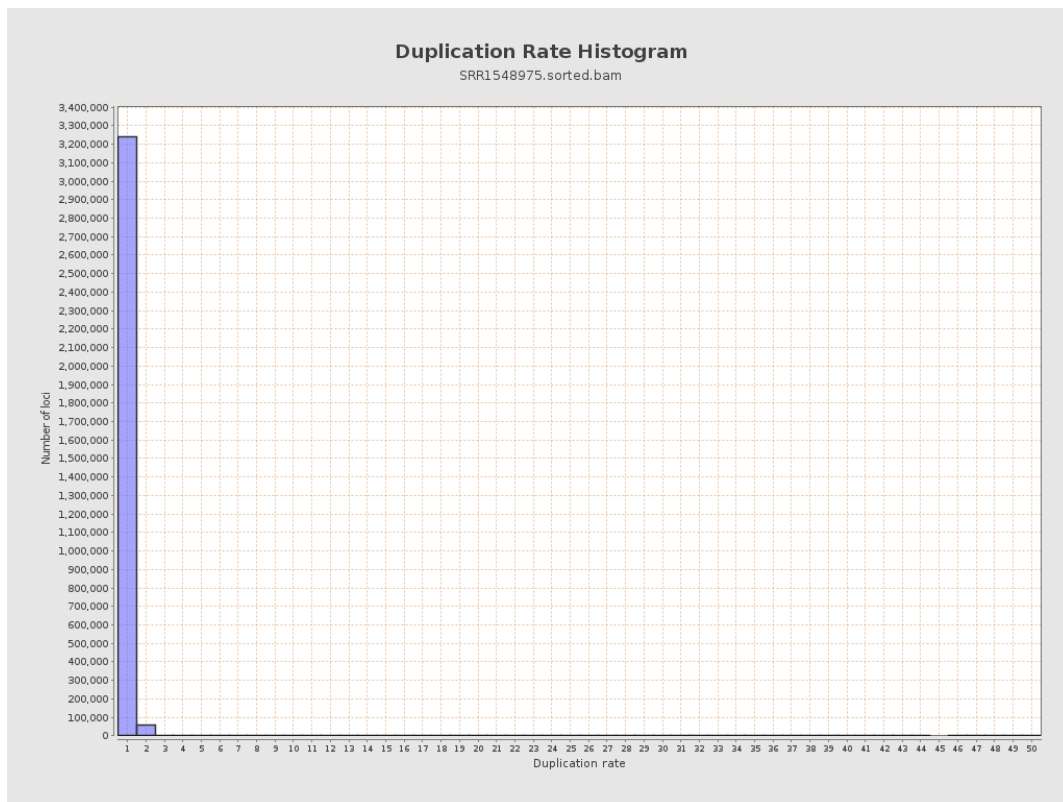
5. Results : Coverage Histogram (0-50X)



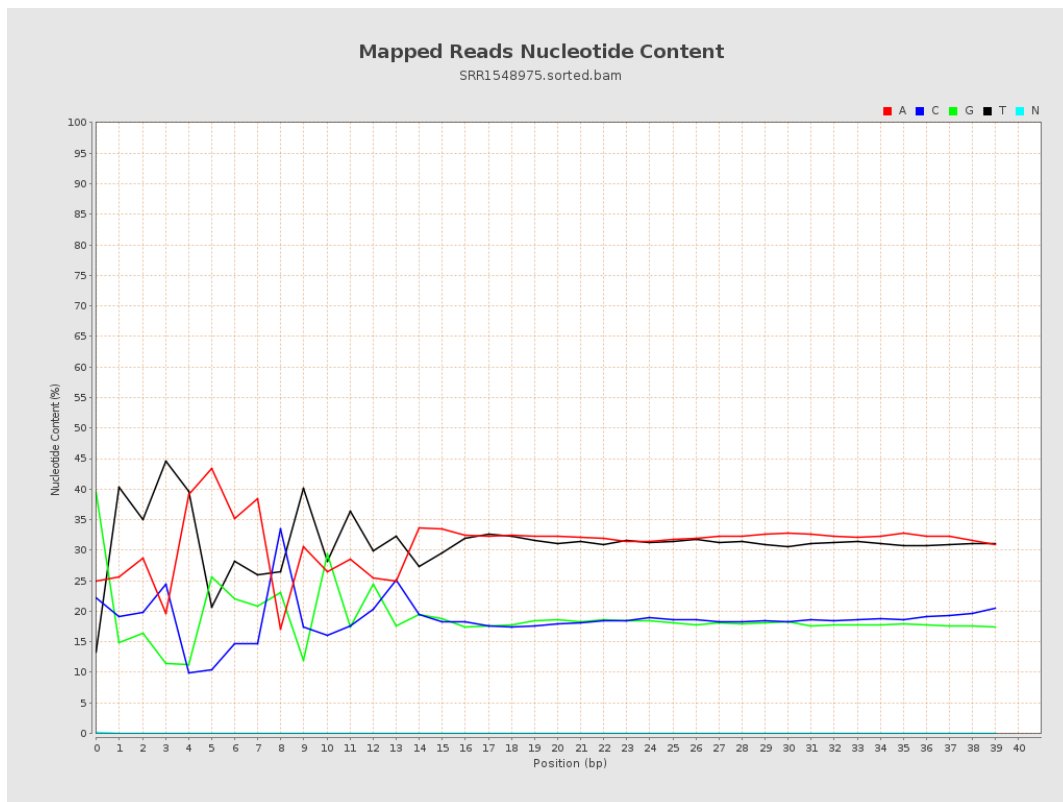
6. Results : Genome Fraction Coverage



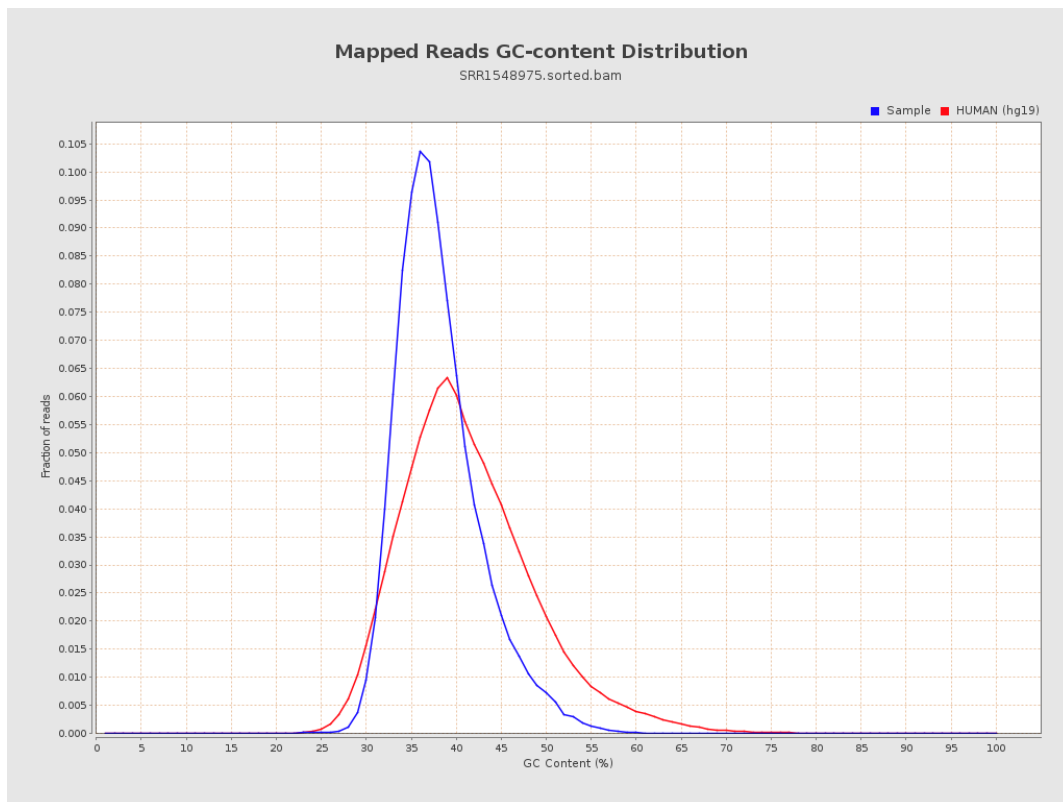
7. Results : Duplication Rate Histogram



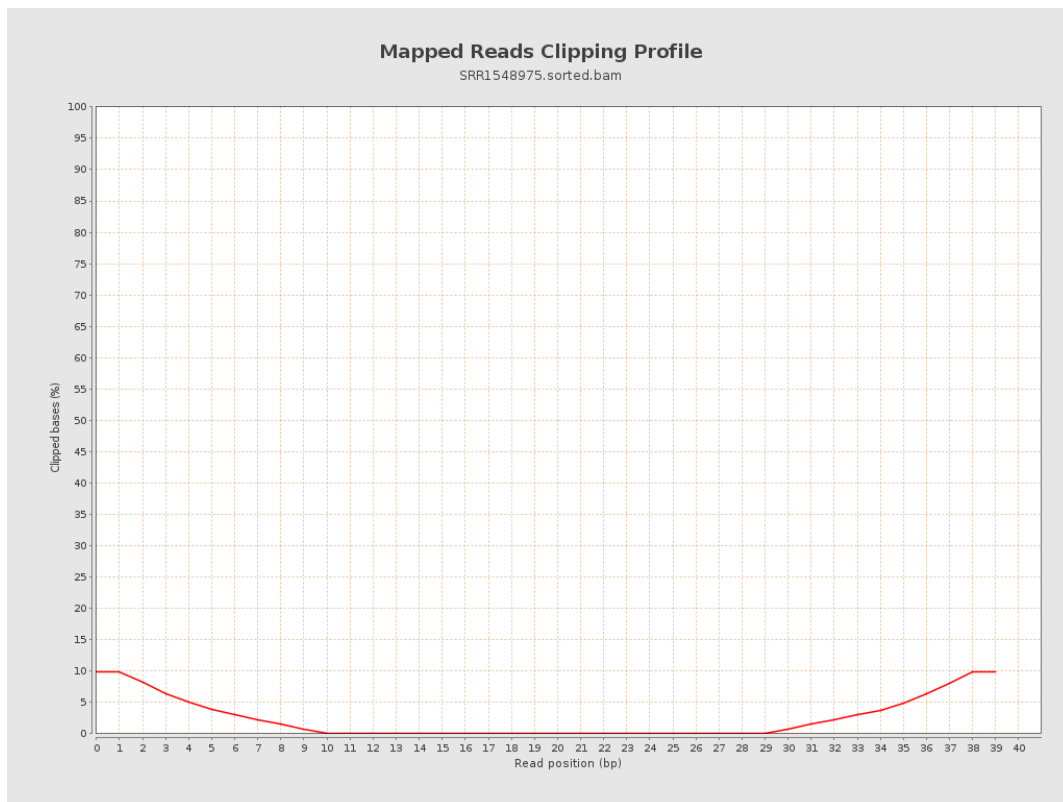
8. Results : Mapped Reads Nucleotide Content



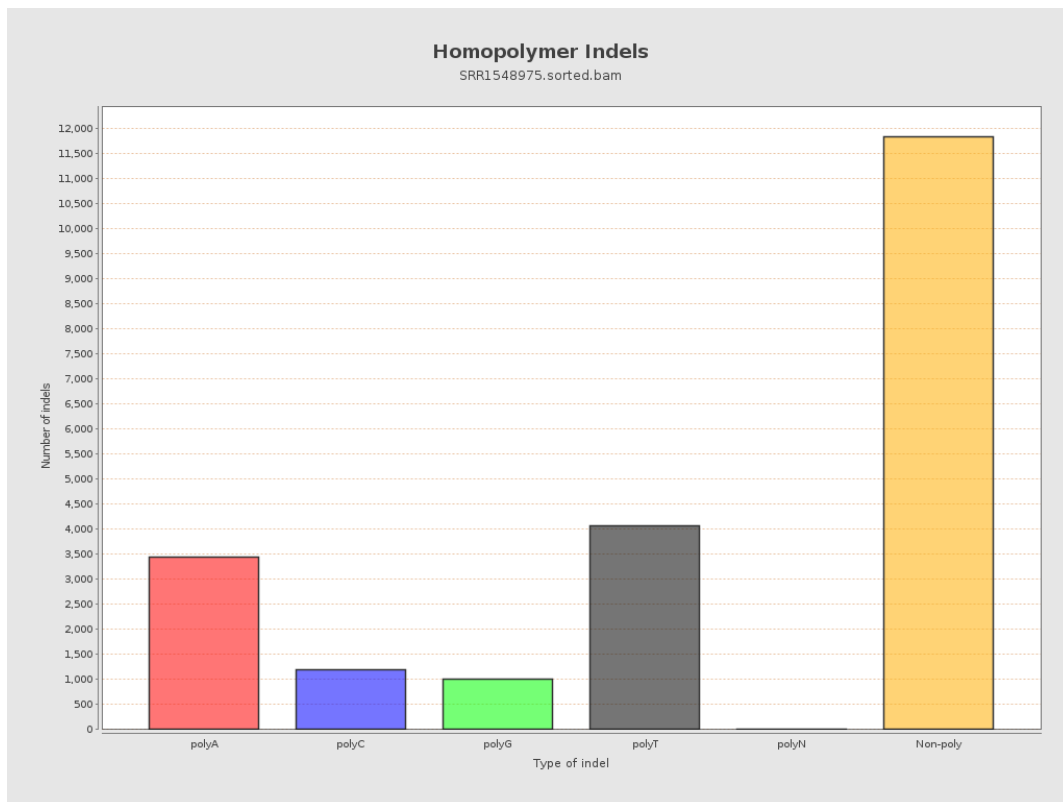
9. Results : Mapped Reads GC-content Distribution



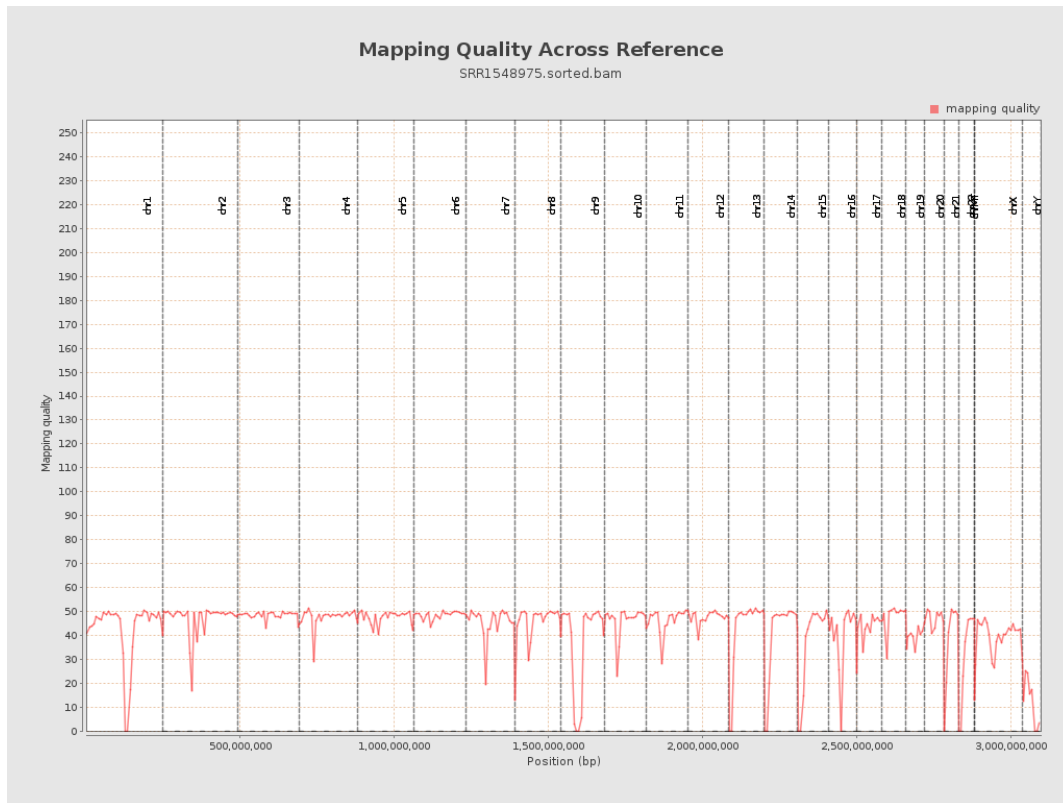
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

