

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:07:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548944.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_SRR1548944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:07:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,059,628
Mapped reads	4,329,262 / 85.56%
Unmapped reads	730,366 / 14.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	265,404 / 5.25%
Duplication rate	2.72%
Clipped reads	491,429 / 9.71%

2.2. ACGT Content

Number/percentage of A's	47,597,207 / 27.93%
Number/percentage of C's	37,727,915 / 22.14%
Number/percentage of T's	47,900,219 / 28.11%
Number/percentage of G's	37,202,874 / 21.83%
Number/percentage of N's	1,438 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0551
Standard Deviation	1.0151

2.4. Mapping Quality

Mean Mapping Quality	28.82
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2.5. Mismatches and indels

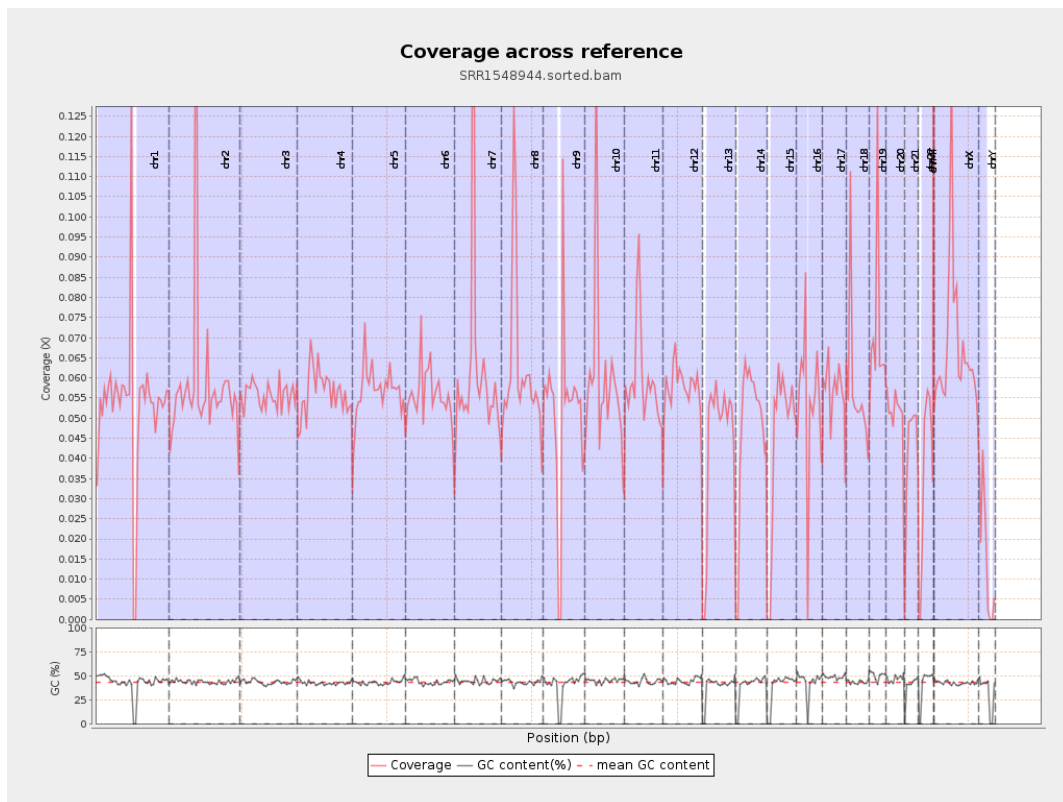
General error rate	0.45%
Mismatches	763,495
Insertions	7,737
Mapped reads with at least one insertion	0.18%
Deletions	13,181
Mapped reads with at least one deletion	0.3%
Homopolymer indels	34.2%

2.6. Chromosome stats

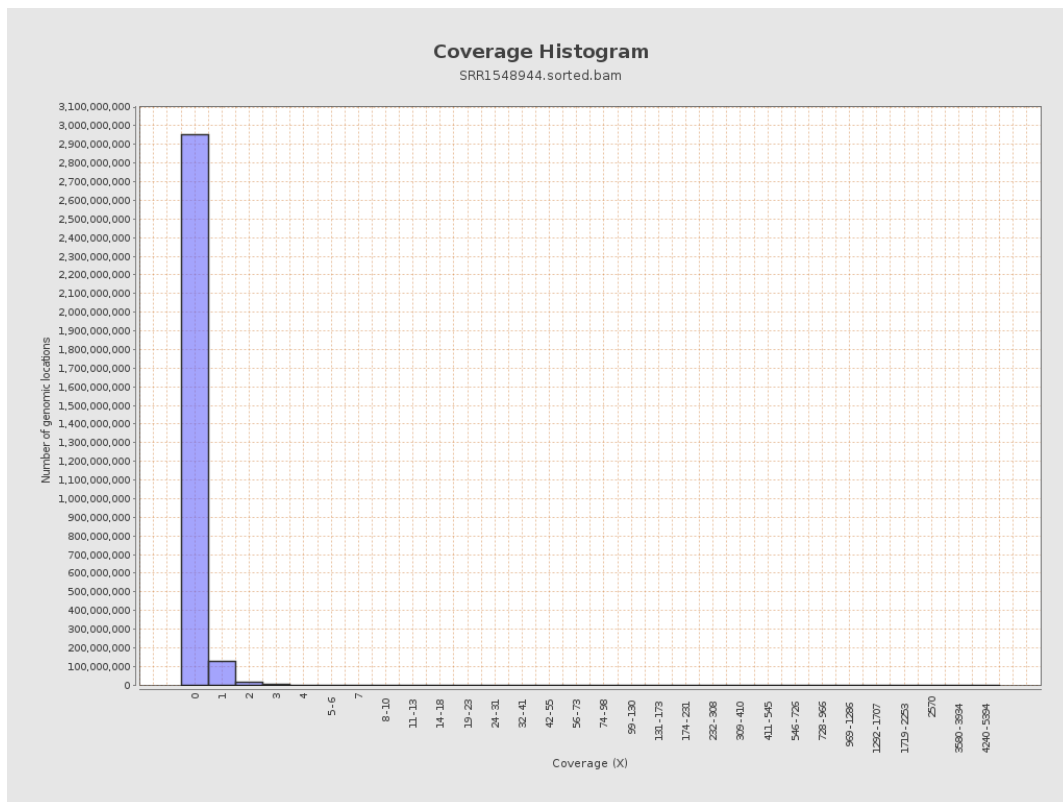
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13302635	0.0534	1.5105
chr2	243199373	14286054	0.0587	0.9843
chr3	198022430	11018236	0.0556	0.2895
chr4	191154276	10762513	0.0563	0.296
chr5	180915260	10336618	0.0571	0.3317
chr6	171115067	9505155	0.0555	0.3547
chr7	159138663	9974172	0.0627	1.3292
chr8	146364022	8973957	0.0613	2.6613

chr9	141213431	7226592	0.0512	1.0205
chr10	135534747	8039719	0.0593	0.7528
chr11	135006516	7919162	0.0587	0.8355
chr12	133851895	7754138	0.0579	0.3678
chr13	115169878	5014090	0.0435	0.231
chr14	107349540	5086082	0.0474	0.5099
chr15	102531392	4613921	0.045	0.2592
chr16	90354753	4832289	0.0535	0.479
chr17	81195210	4571538	0.0563	0.3535
chr18	78077248	4513384	0.0578	2.0902
chr19	59128983	4260247	0.0721	1.7004
chr20	63025520	3226745	0.0512	0.3337
chr21	48129895	1982166	0.0412	0.3879
chr22	51304566	1826992	0.0356	0.254
chrMT	16571	4140	0.2498	0.5877
chrX	155270560	10529185	0.0678	0.5833
chrY	59373566	886100	0.0149	0.1902

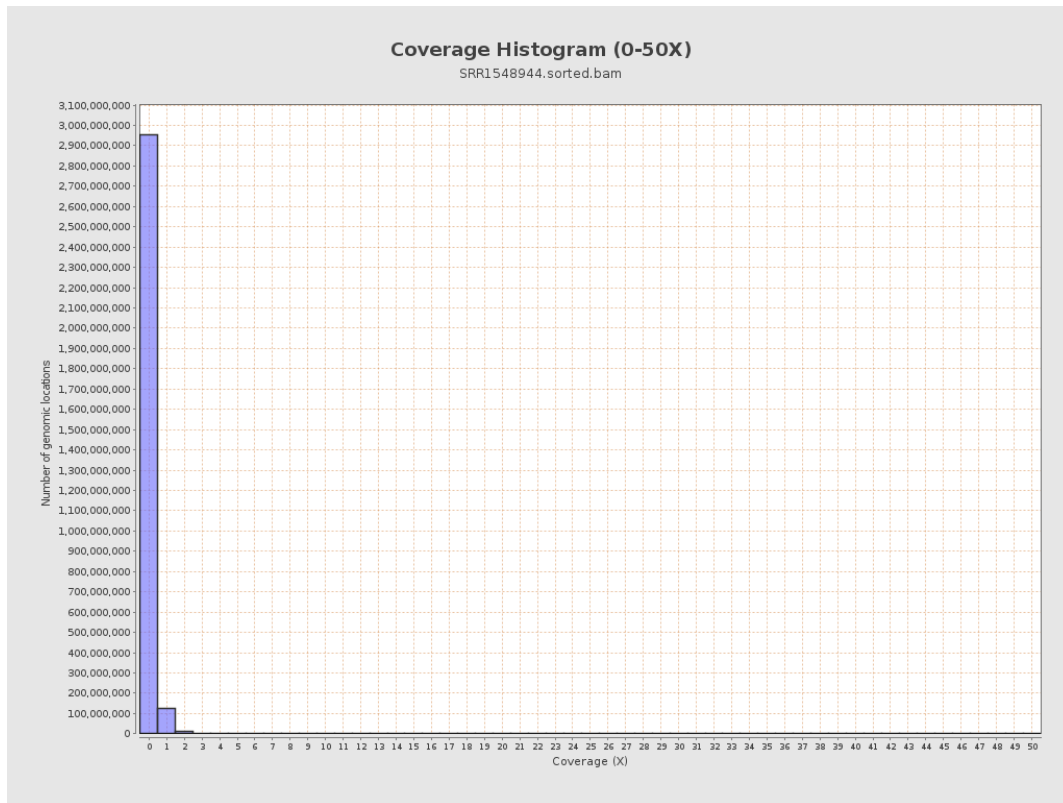
3. Results : Coverage across reference



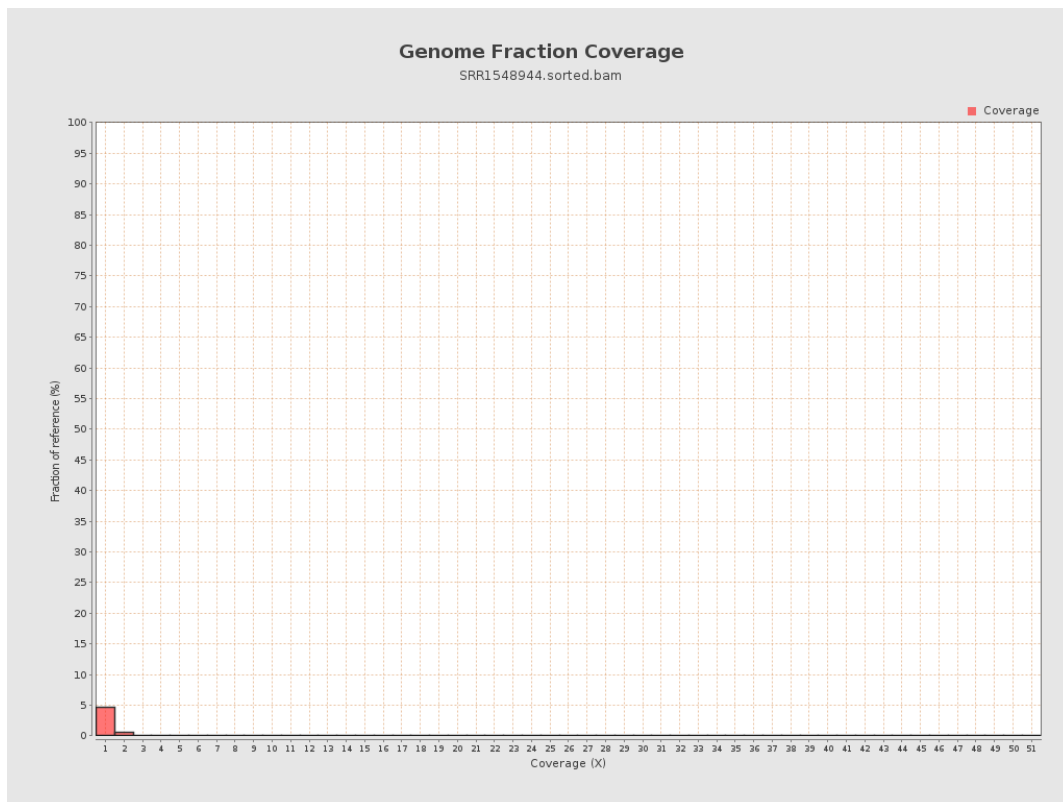
4. Results : Coverage Histogram



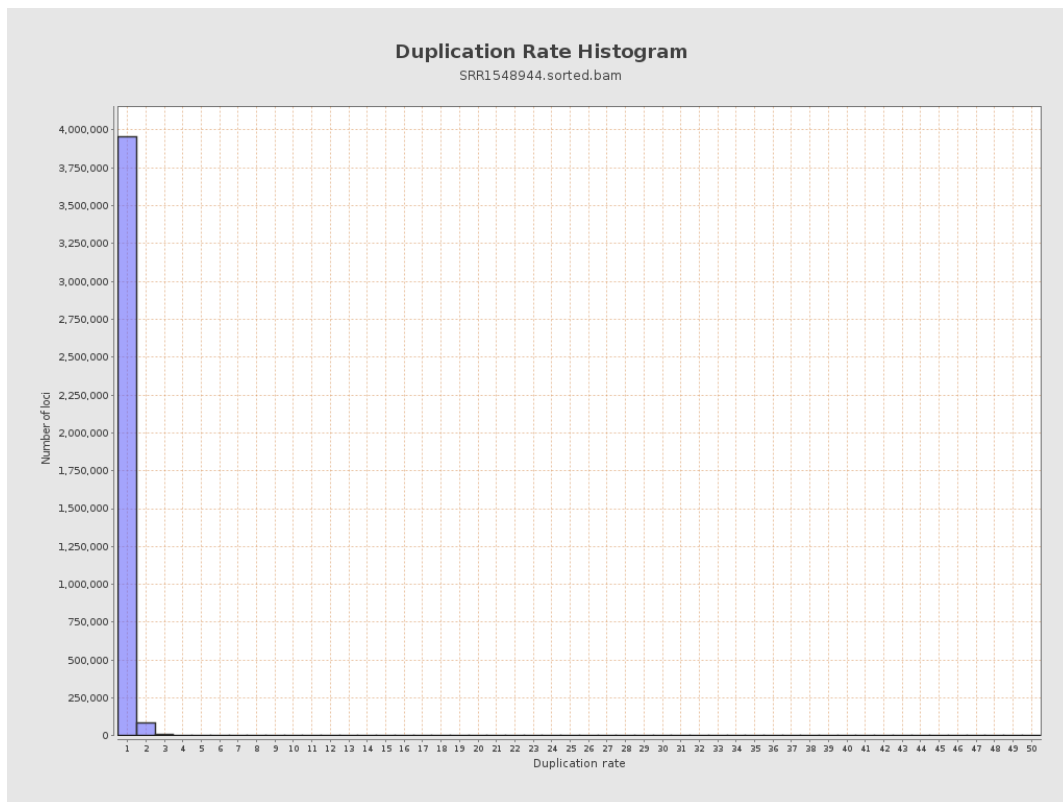
5. Results : Coverage Histogram (0-50X)



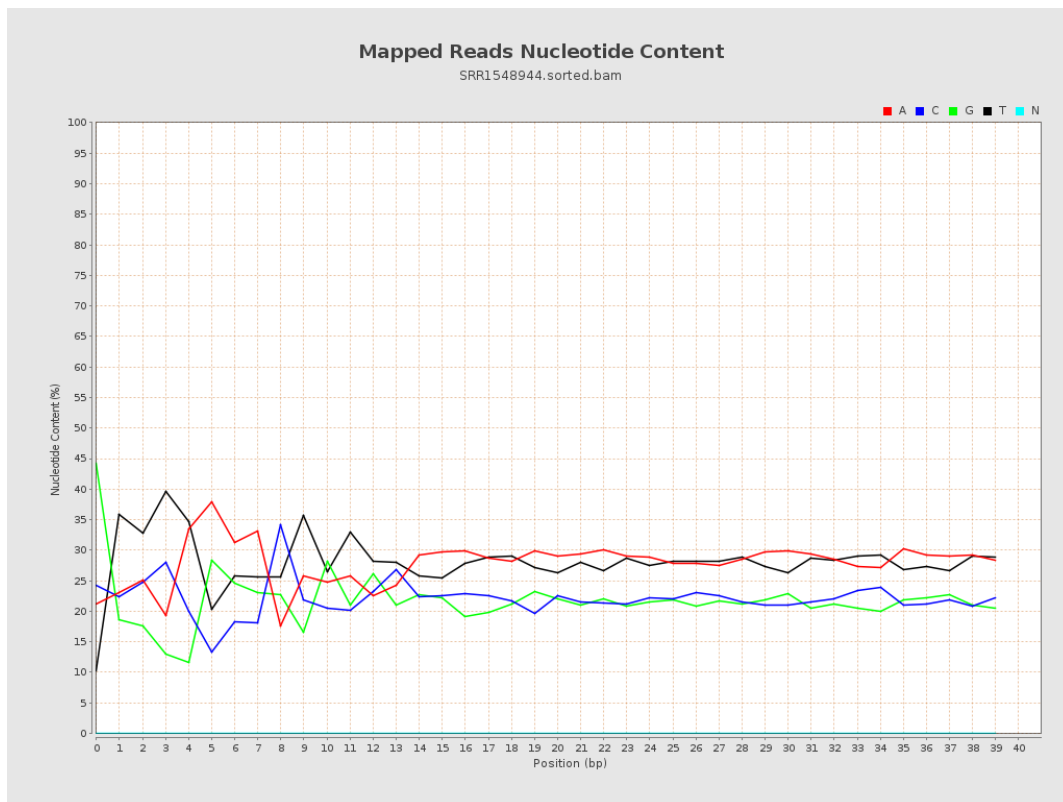
6. Results : Genome Fraction Coverage



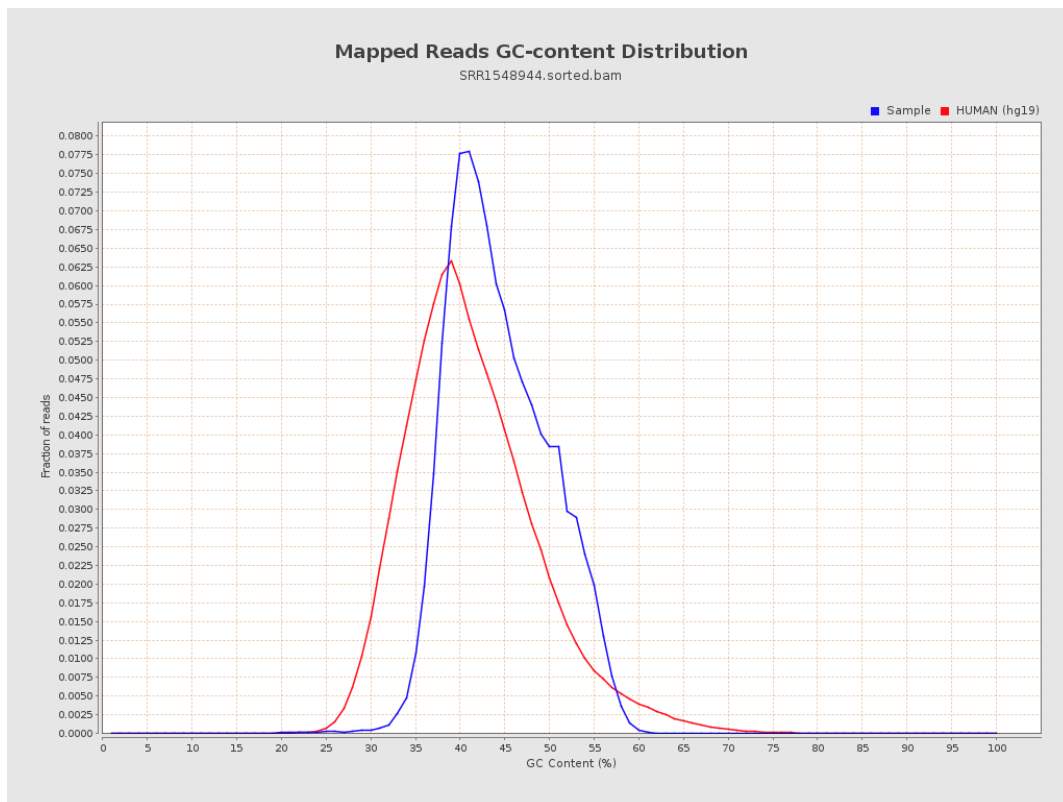
7. Results : Duplication Rate Histogram



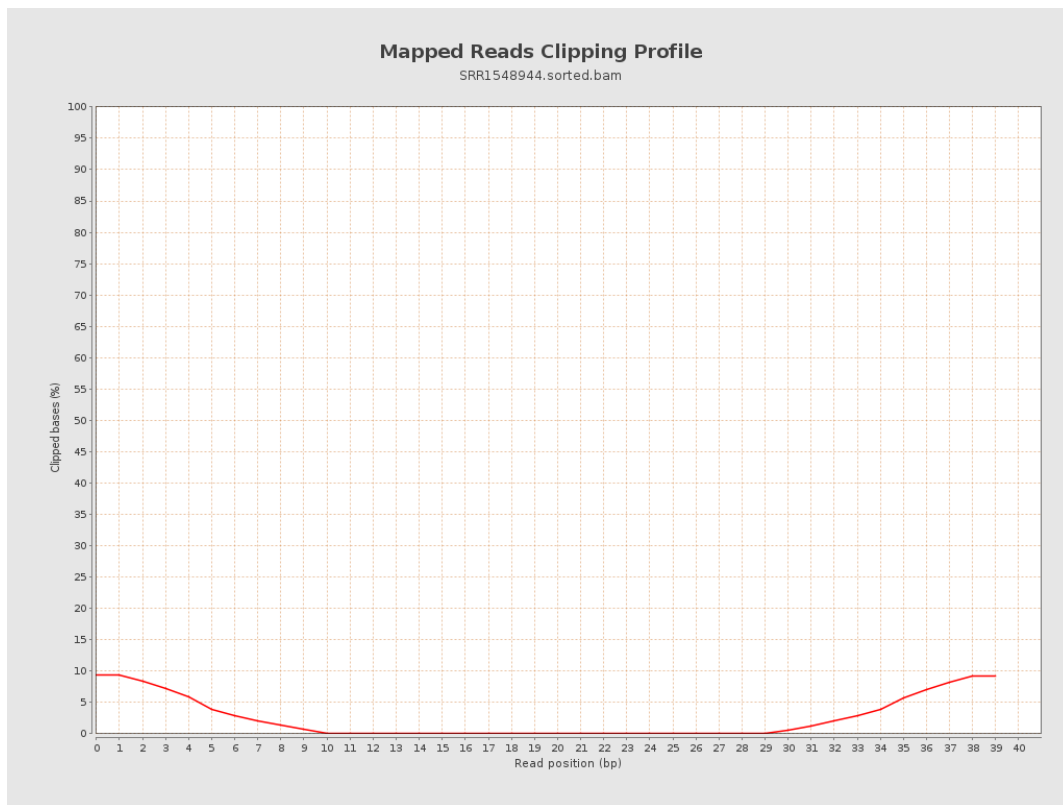
8. Results : Mapped Reads Nucleotide Content



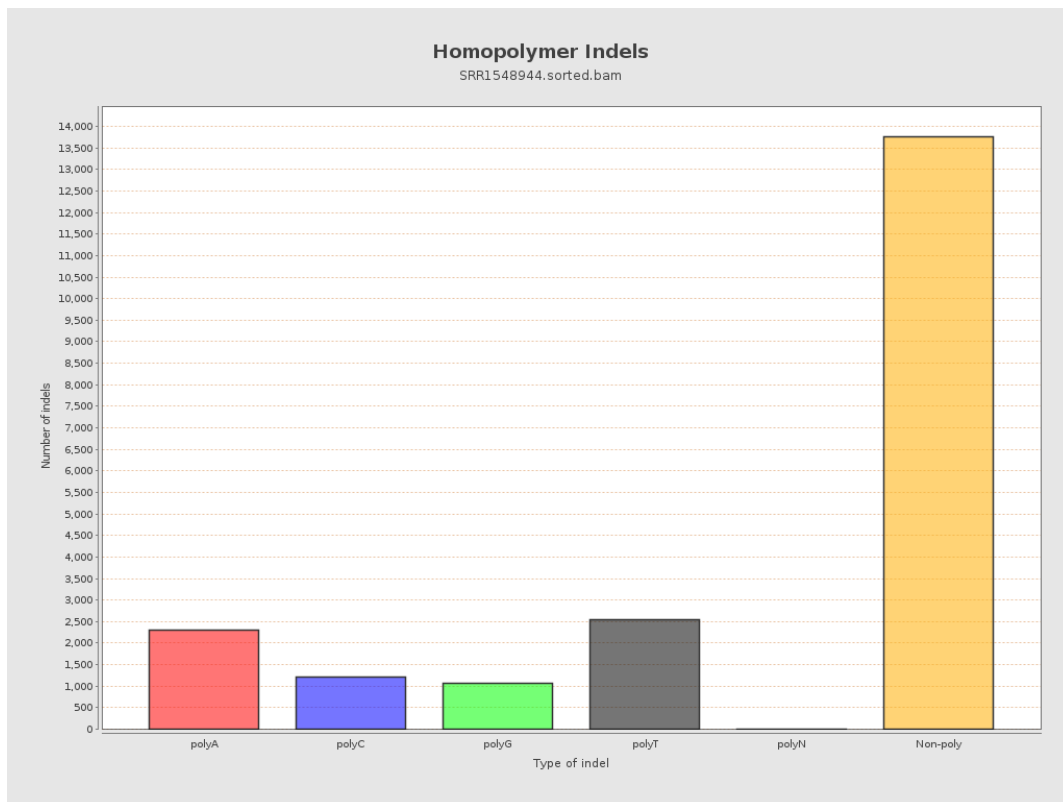
9. Results : Mapped Reads GC-content Distribution



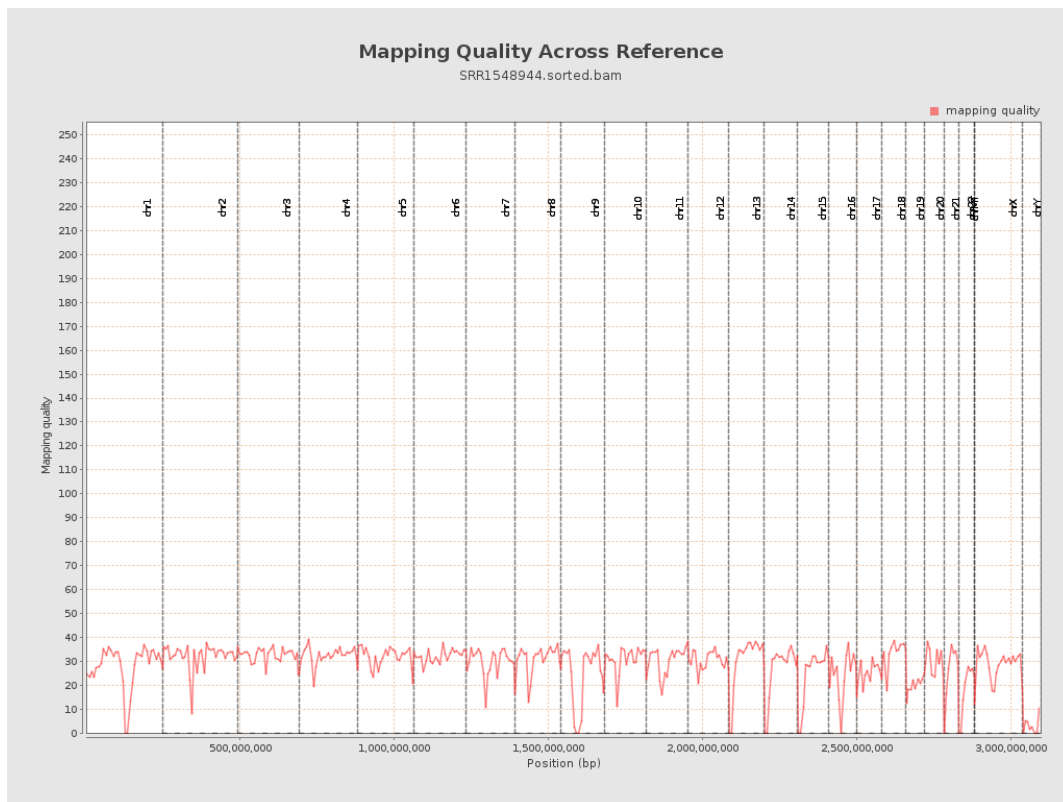
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

