

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:37:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240040.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_SRR6240040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:37:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,253,891
Mapped reads	1,795,259 / 79.65%
Unmapped reads	458,632 / 20.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,928 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	317,765 / 14.1%
Duplication rate	12.48%
Clipped reads	1,015,939 / 45.07%

2.2. ACGT Content

Number/percentage of A's	31,601,002 / 27.75%
Number/percentage of C's	20,309,261 / 17.83%
Number/percentage of T's	36,708,640 / 32.24%
Number/percentage of G's	25,173,988 / 22.11%
Number/percentage of N's	80,689 / 0.07%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.4426
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2.4. Mapping Quality

Mean Mapping Quality	45.85
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2.5. Mismatches and indels

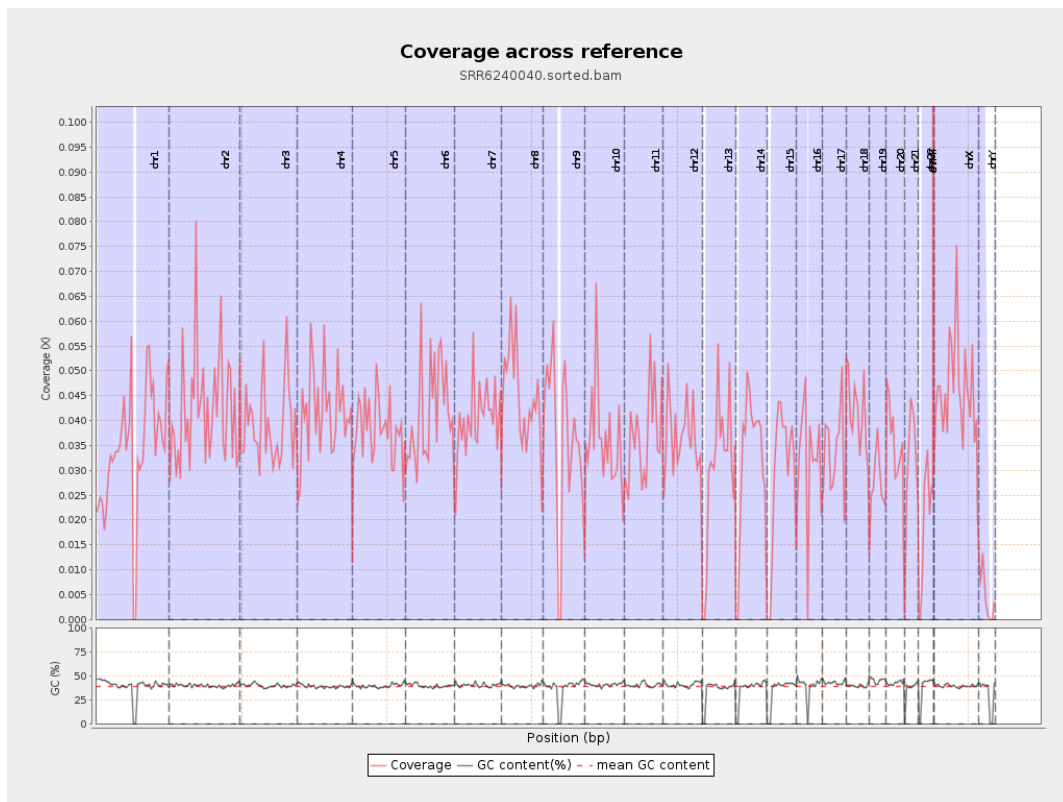
General error rate	0.87%
Mismatches	971,072
Insertions	7,879
Mapped reads with at least one insertion	0.44%
Deletions	25,567
Mapped reads with at least one deletion	1.41%
Homopolymer indels	47.49%

2.6. Chromosome stats

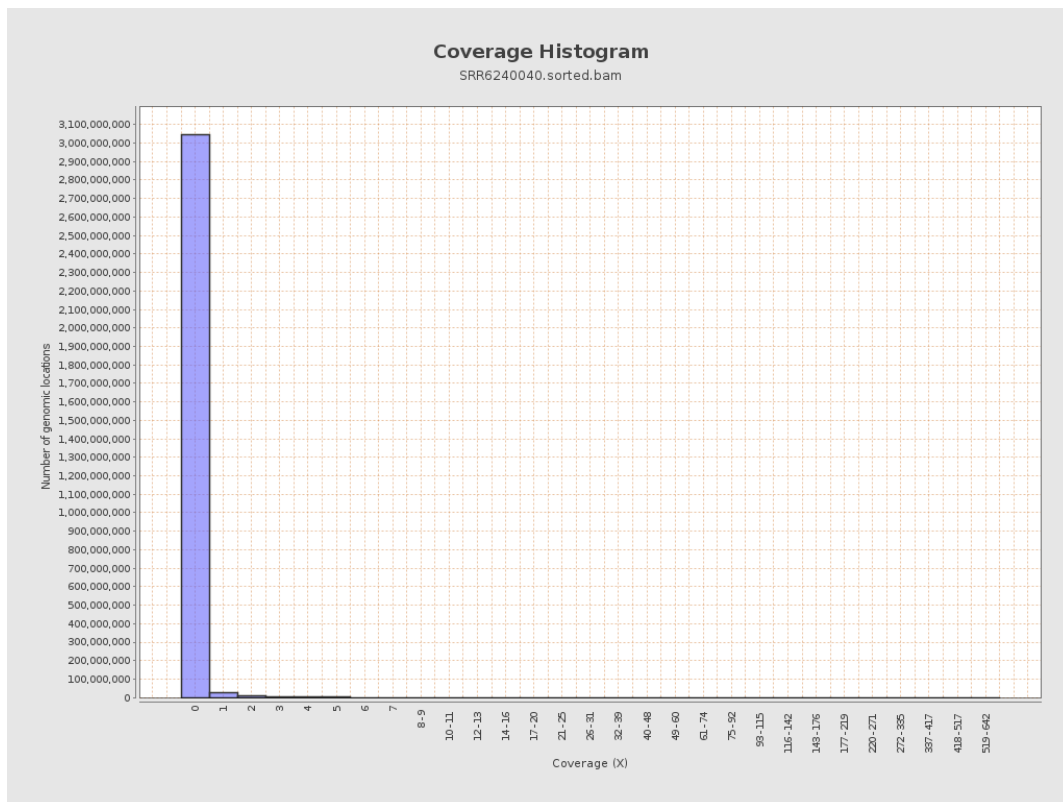
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8546121	0.0343	0.6201
chr2	243199373	10216089	0.042	0.5282
chr3	198022430	7780515	0.0393	0.3788
chr4	191154276	7946539	0.0416	0.4328
chr5	180915260	6900301	0.0381	0.3729
chr6	171115067	7088963	0.0414	0.4286
chr7	159138663	6480943	0.0407	0.5051

chr8	146364022	6543601	0.0447	0.4929
chr9	141213431	5130376	0.0363	0.4272
chr10	135534747	4903110	0.0362	0.4502
chr11	135006516	5012236	0.0371	0.3787
chr12	133851895	4865278	0.0363	0.3661
chr13	115169878	3493598	0.0303	0.3375
chr14	107349540	3451138	0.0321	0.3805
chr15	102531392	2994582	0.0292	0.4039
chr16	90354753	2913848	0.0322	0.3412
chr17	81195210	2647507	0.0326	0.3497
chr18	78077248	3242073	0.0415	0.6354
chr19	59128983	1645621	0.0278	0.4547
chr20	63025520	2250367	0.0357	0.354
chr21	48129895	1489482	0.0309	0.328
chr22	51304566	965394	0.0188	0.2406
chrMT	16571	31638	1.9092	3.2944
chrX	155270560	7104078	0.0458	0.4259
chrY	59373566	273355	0.0046	0.1309

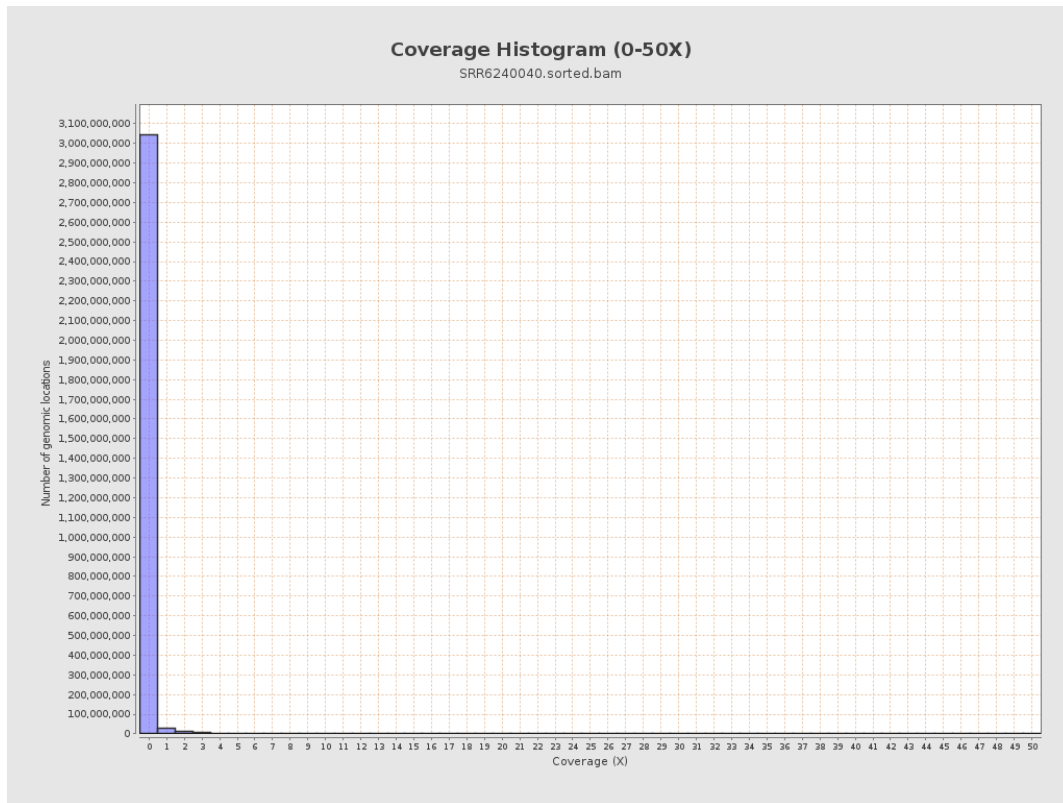
3. Results : Coverage across reference



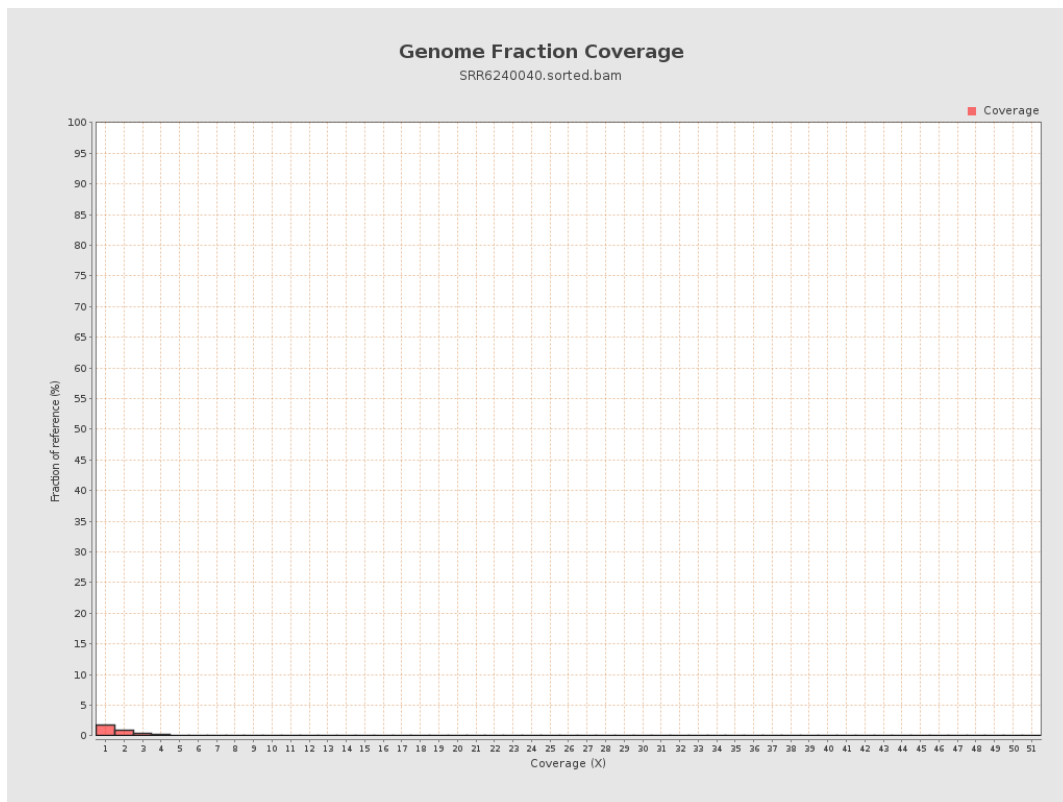
4. Results : Coverage Histogram



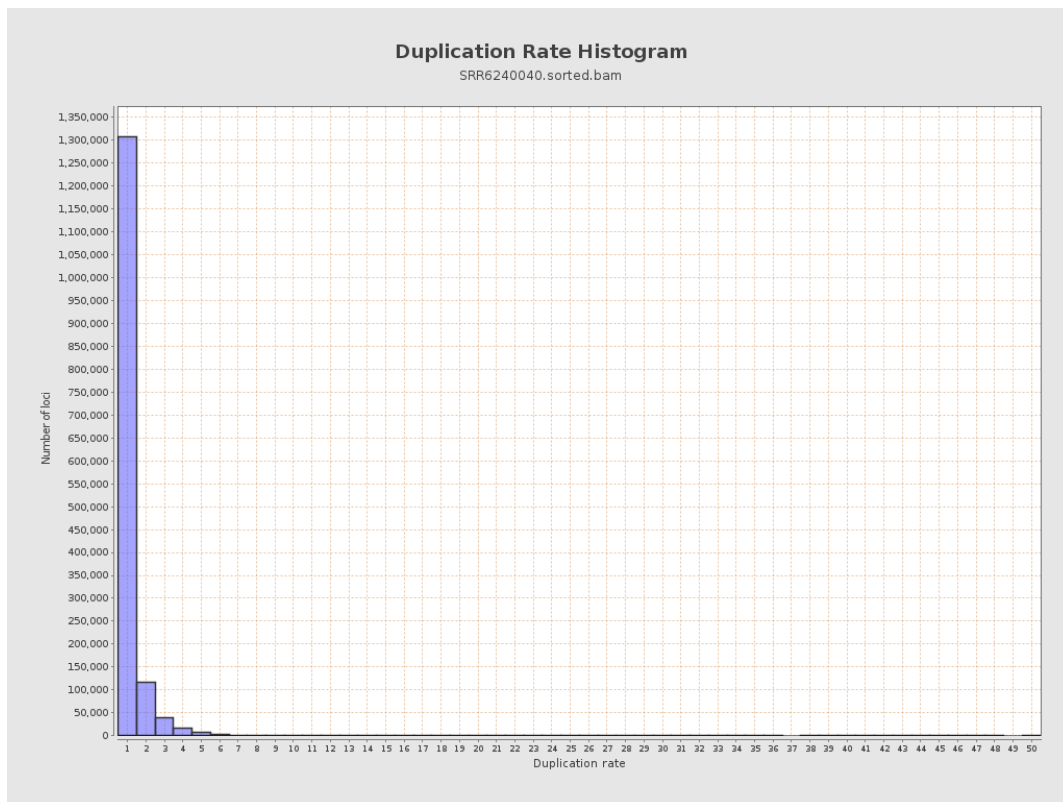
5. Results : Coverage Histogram (0-50X)



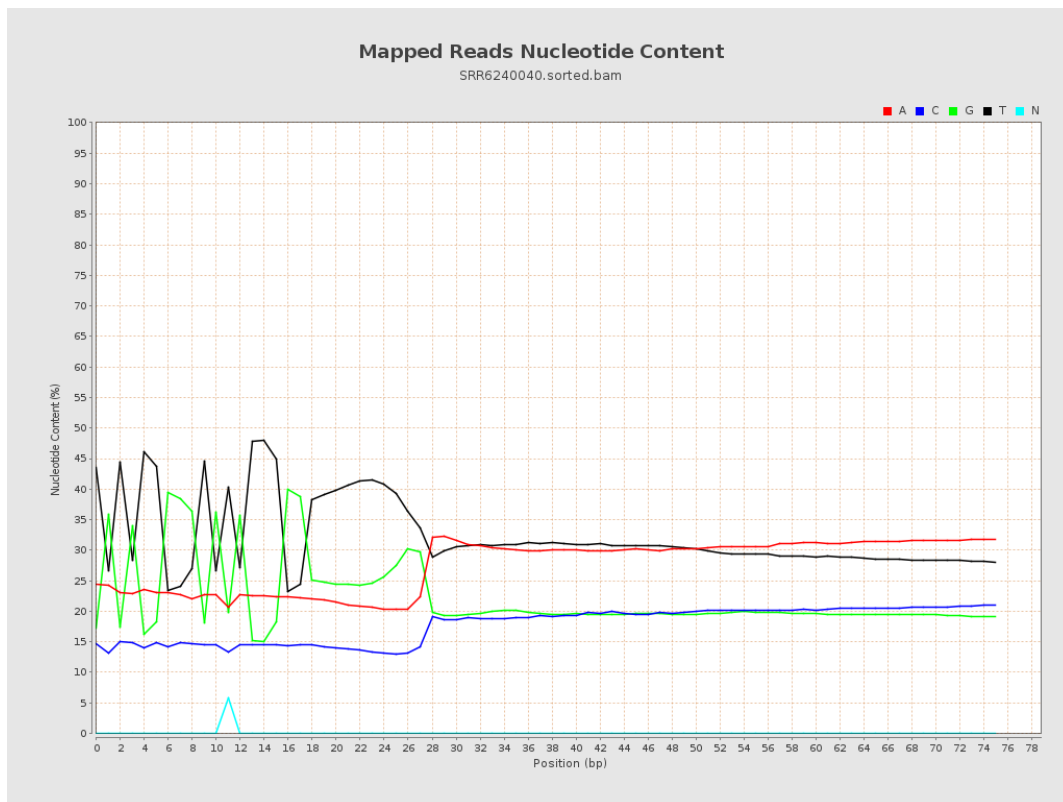
6. Results : Genome Fraction Coverage



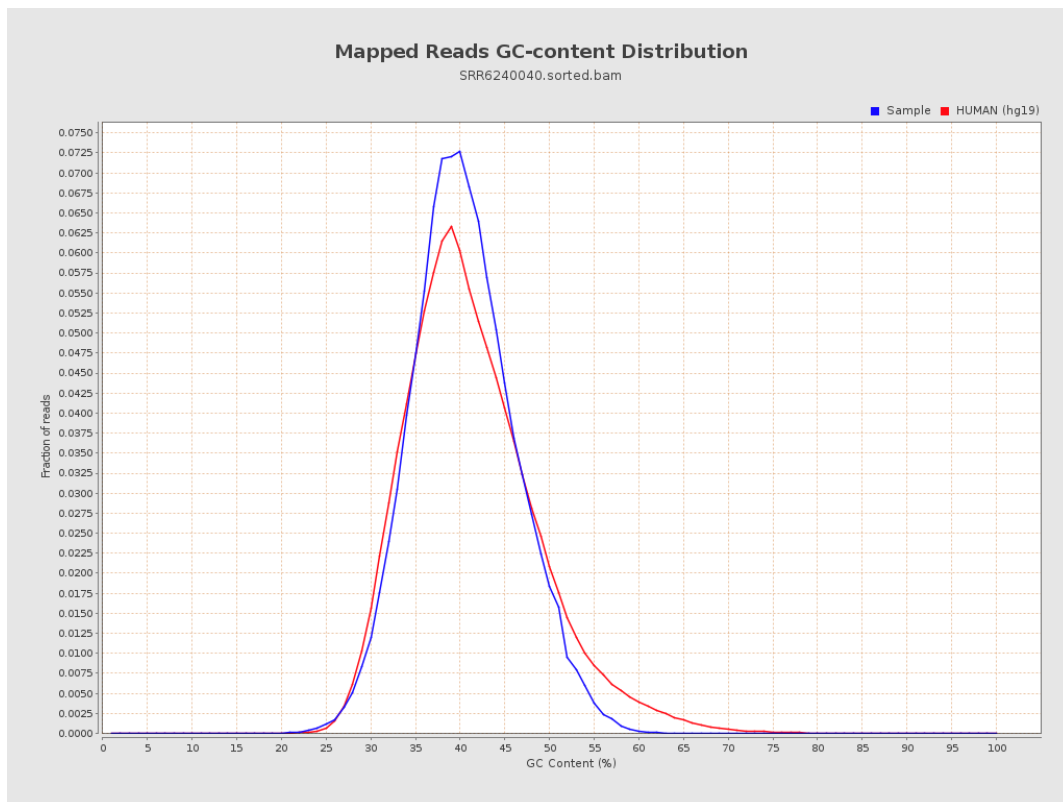
7. Results : Duplication Rate Histogram



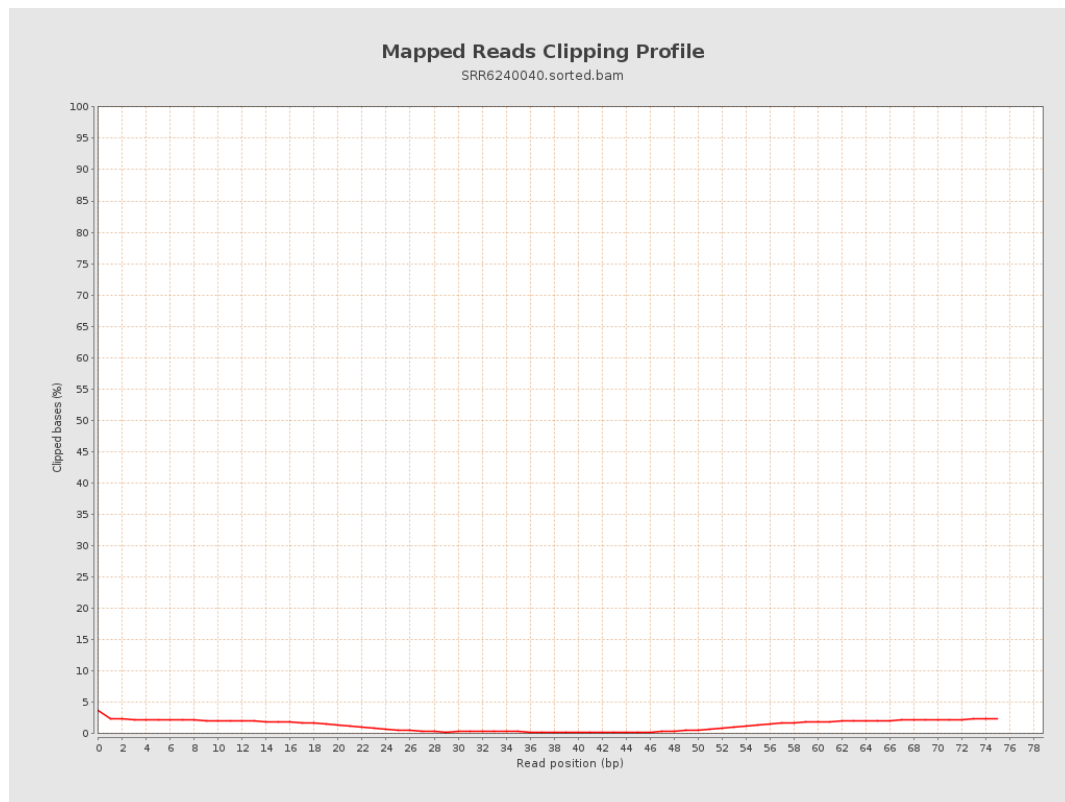
8. Results : Mapped Reads Nucleotide Content



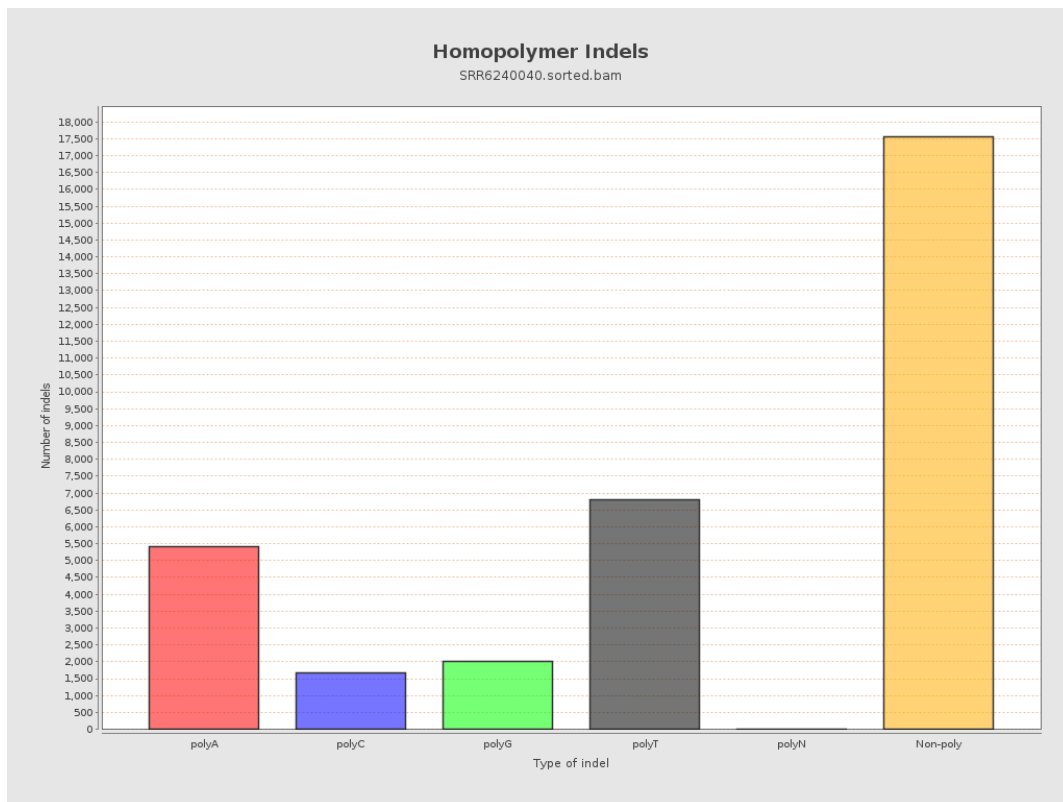
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

