

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:26:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240247.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_SRR6240247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:26:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,718,998
Mapped reads	1,223,834 / 71.19%
Unmapped reads	495,164 / 28.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,921 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	269,102 / 15.65%
Duplication rate	14.49%
Clipped reads	729,597 / 42.44%

2.2. ACGT Content

Number/percentage of A's	20,974,385 / 27.21%
Number/percentage of C's	13,378,258 / 17.36%
Number/percentage of T's	25,589,808 / 33.2%
Number/percentage of G's	17,124,307 / 22.22%
Number/percentage of N's	6,745 / 0.01%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.3694
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2.4. Mapping Quality

Mean Mapping Quality	45.93
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2.5. Mismatches and indels

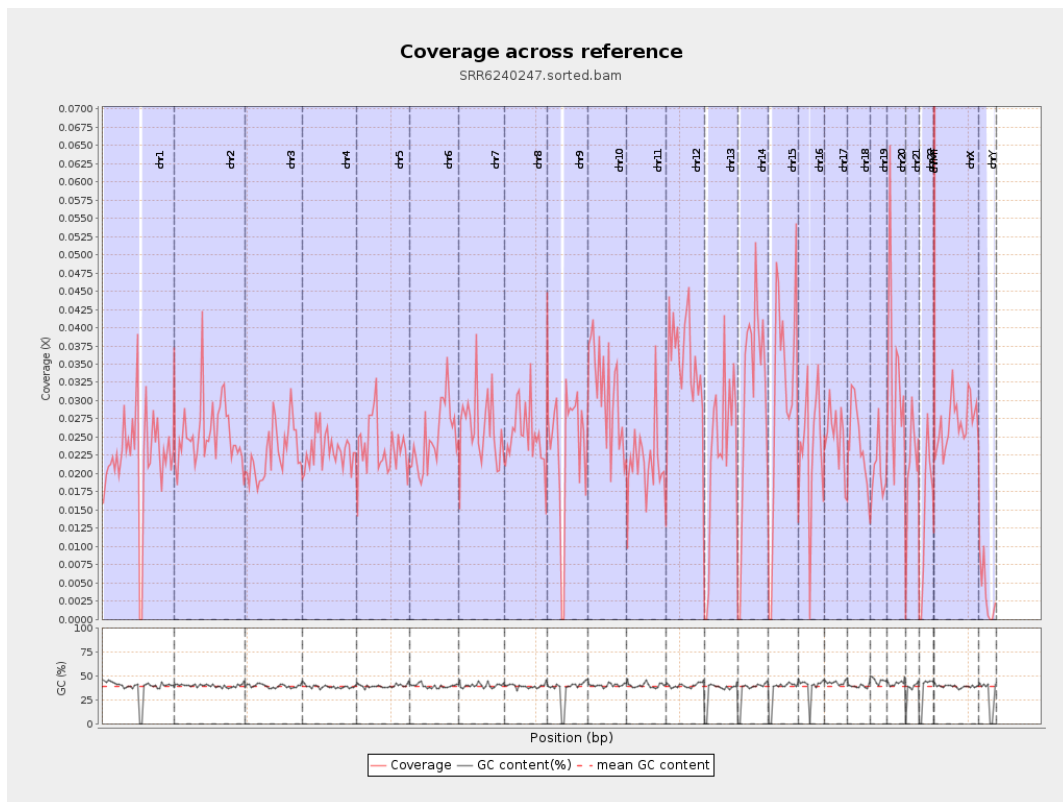
General error rate	0.91%
Mismatches	689,883
Insertions	5,477
Mapped reads with at least one insertion	0.44%
Deletions	23,442
Mapped reads with at least one deletion	1.89%
Homopolymer indels	49.05%

2.6. Chromosome stats

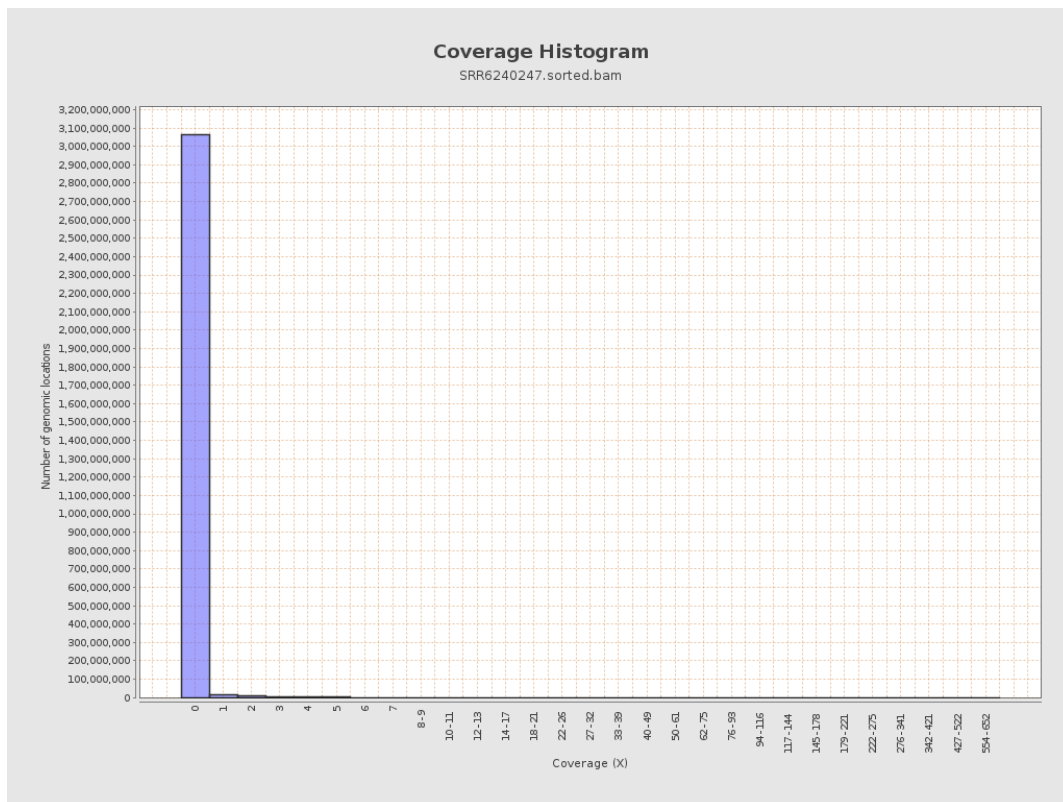
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5533406	0.0222	0.467
chr2	243199373	6201209	0.0255	0.3742
chr3	198022430	4520977	0.0228	0.2989
chr4	191154276	4434986	0.0232	0.3118
chr5	180915260	4301417	0.0238	0.3163
chr6	171115067	4255443	0.0249	0.3331
chr7	159138663	4203855	0.0264	0.4246

chr8	146364022	3683764	0.0252	0.4979
chr9	141213431	3341880	0.0237	0.3573
chr10	135534747	4210584	0.0311	0.3852
chr11	135006516	2929920	0.0217	0.331
chr12	133851895	4729090	0.0353	0.4005
chr13	115169878	2652065	0.023	0.3275
chr14	107349540	3315658	0.0309	0.3852
chr15	102531392	3186423	0.0311	0.3737
chr16	90354753	2103020	0.0233	0.3117
chr17	81195210	2025807	0.0249	0.3316
chr18	78077248	1914018	0.0245	0.4922
chr19	59128983	1210680	0.0205	0.3264
chr20	63025520	2111784	0.0335	0.3845
chr21	48129895	1032836	0.0215	0.3012
chr22	51304566	758932	0.0148	0.2376
chrMT	16571	39109	2.3601	3.3639
chrX	155270560	4208877	0.0271	0.3397
chrY	59373566	207841	0.0035	0.1165

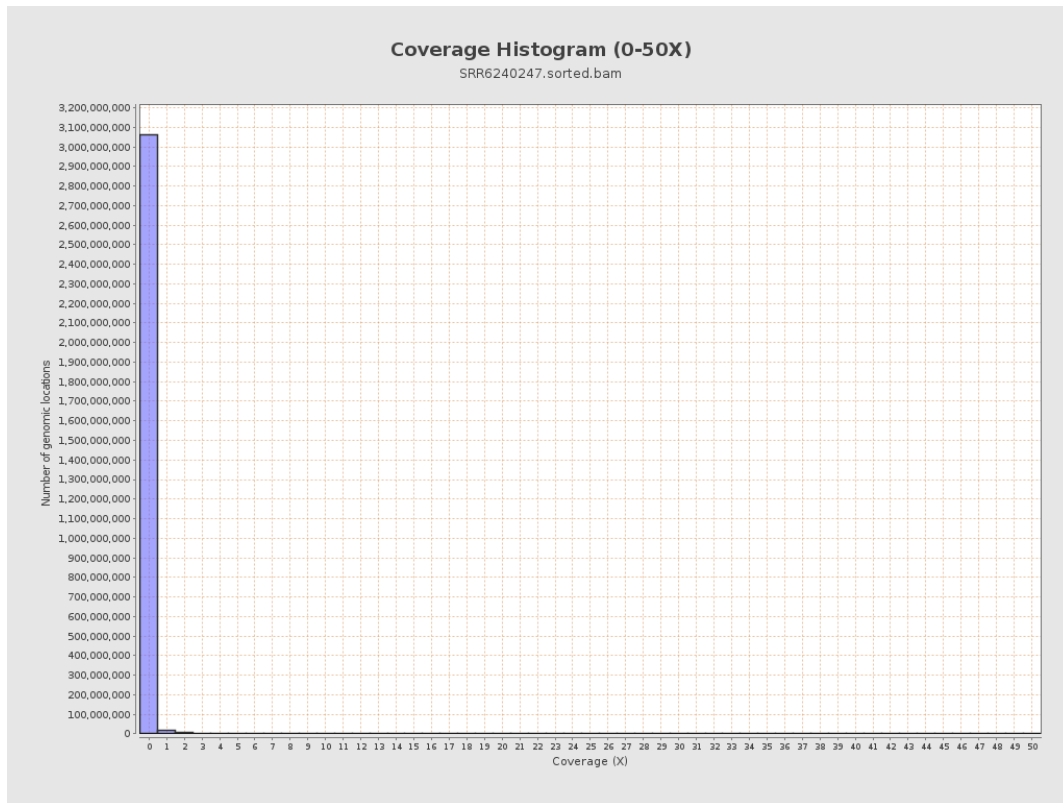
3. Results : Coverage across reference



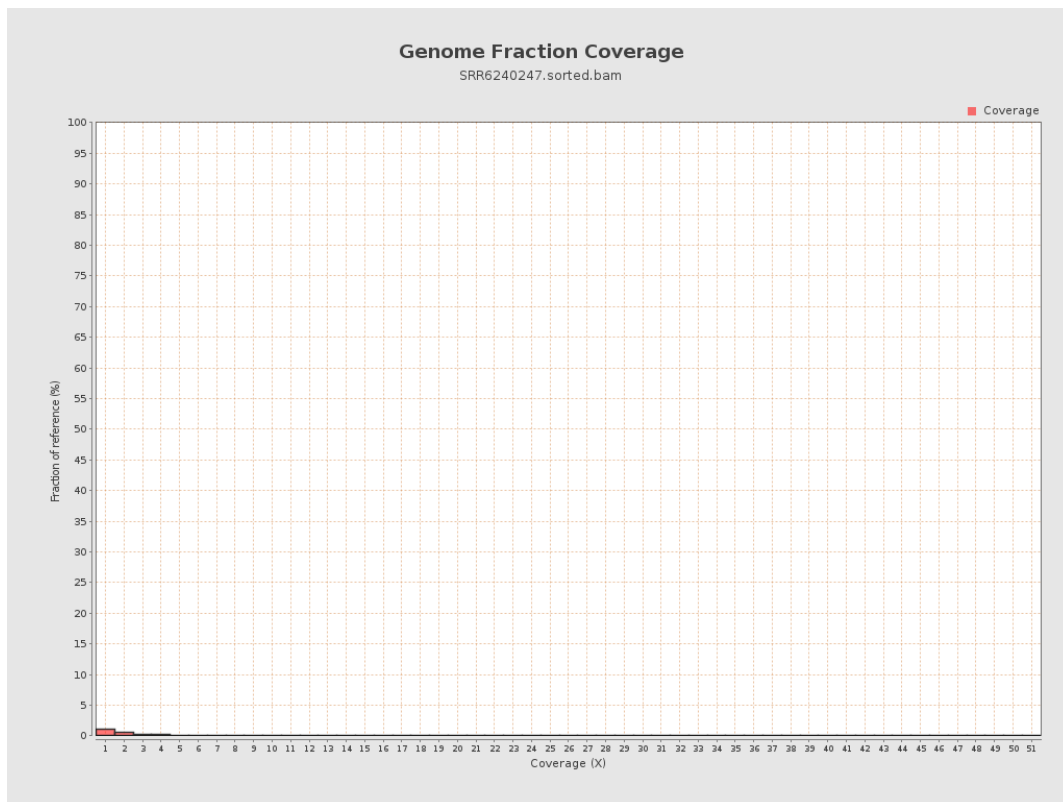
4. Results : Coverage Histogram



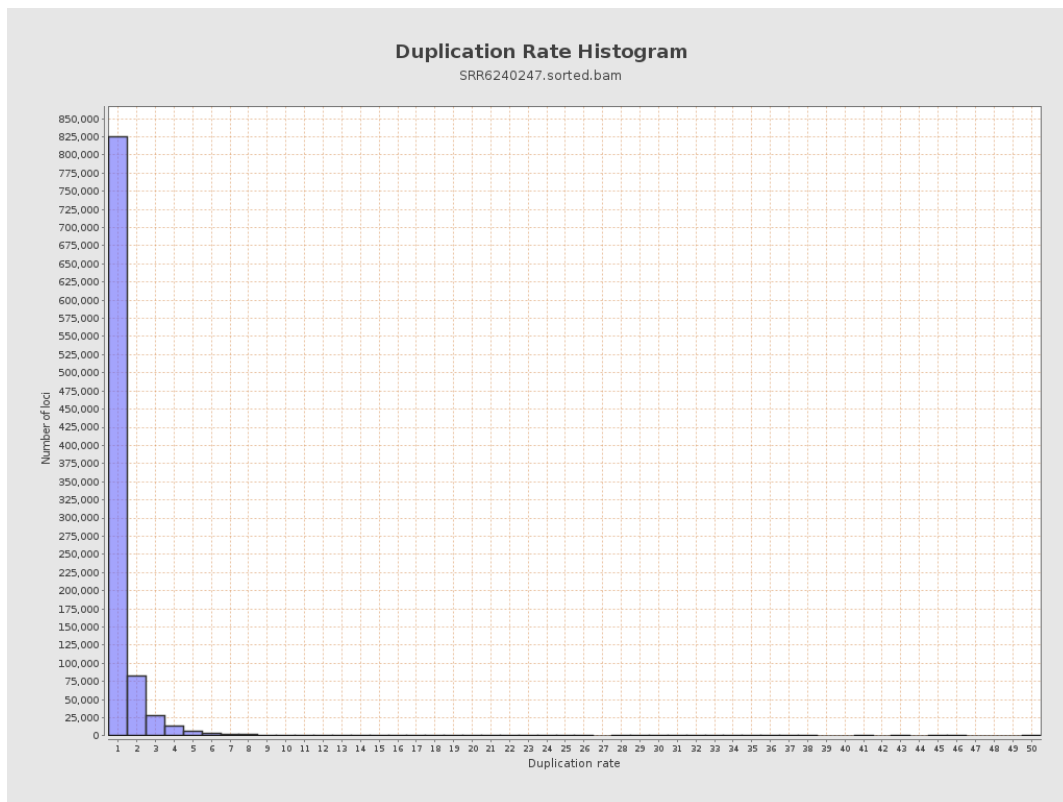
5. Results : Coverage Histogram (0-50X)



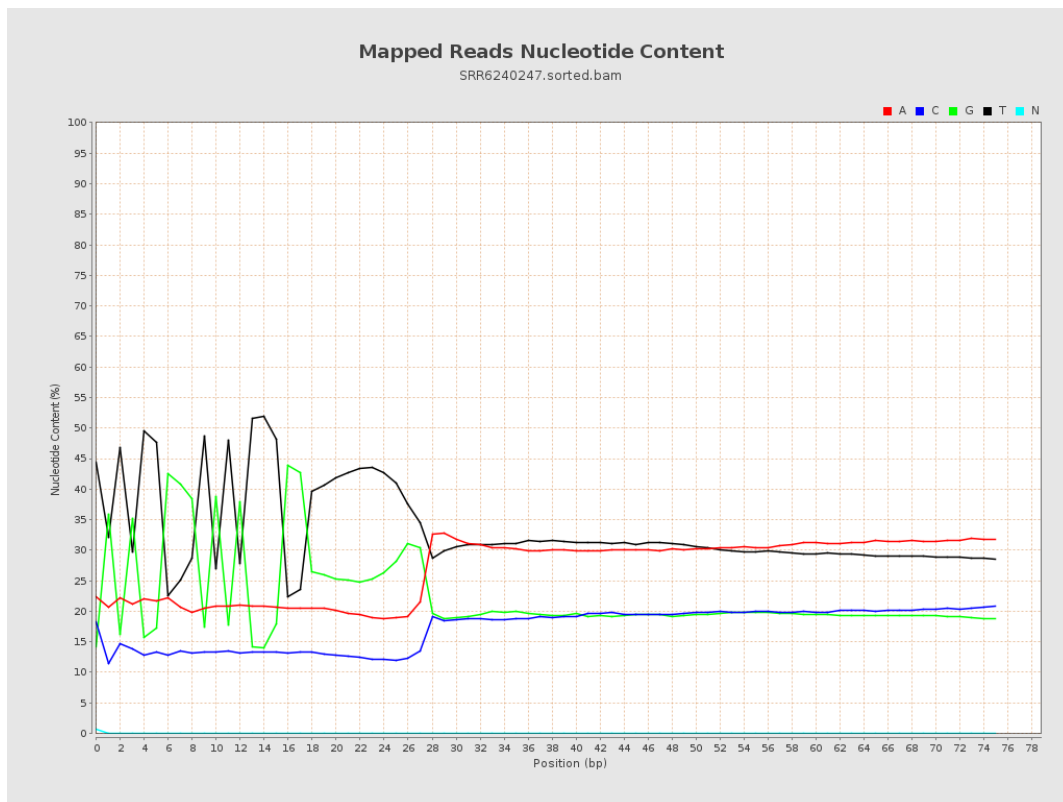
6. Results : Genome Fraction Coverage



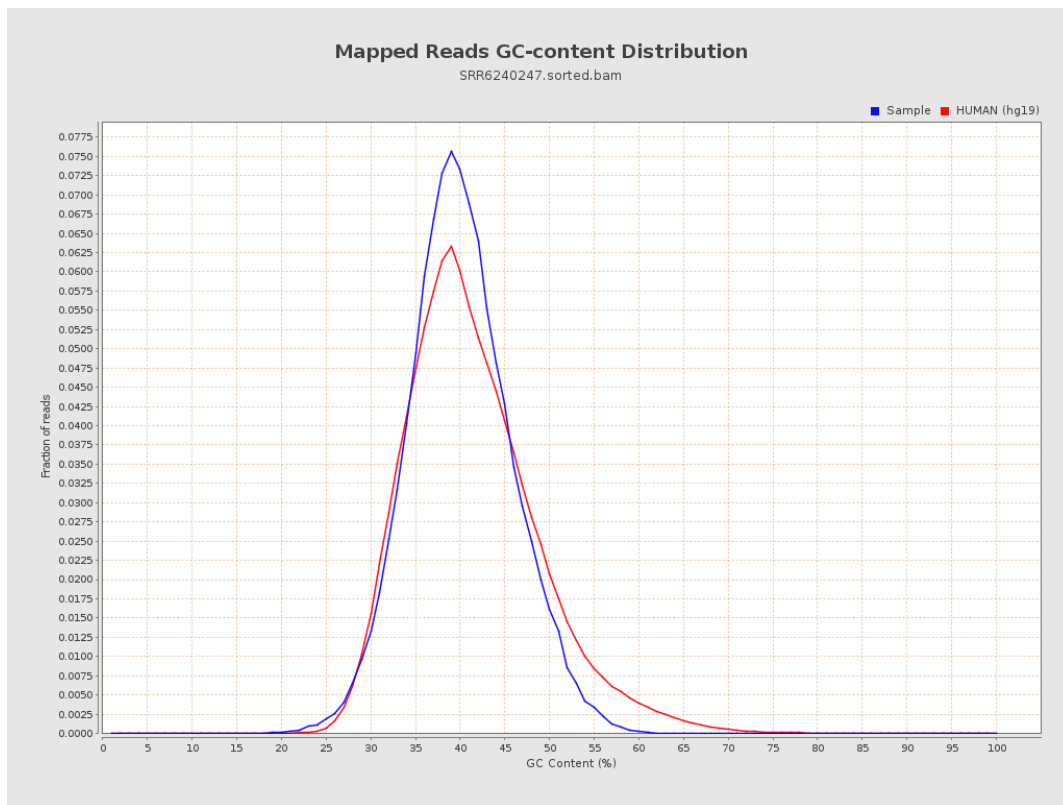
7. Results : Duplication Rate Histogram



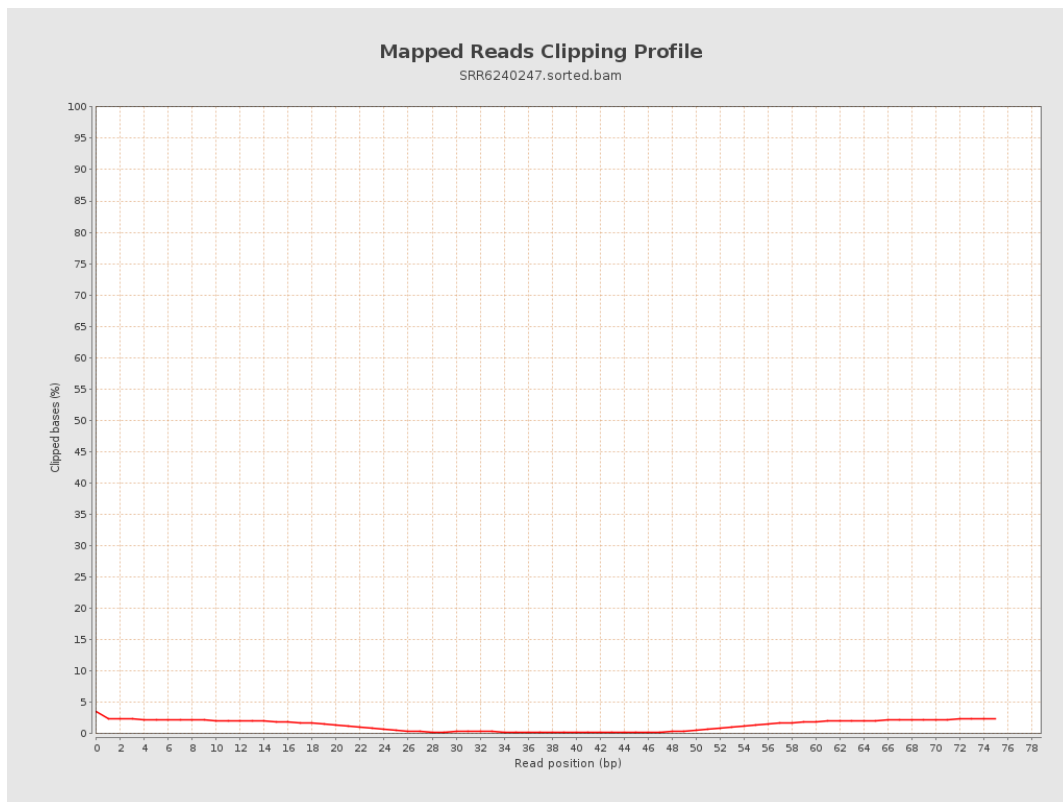
8. Results : Mapped Reads Nucleotide Content



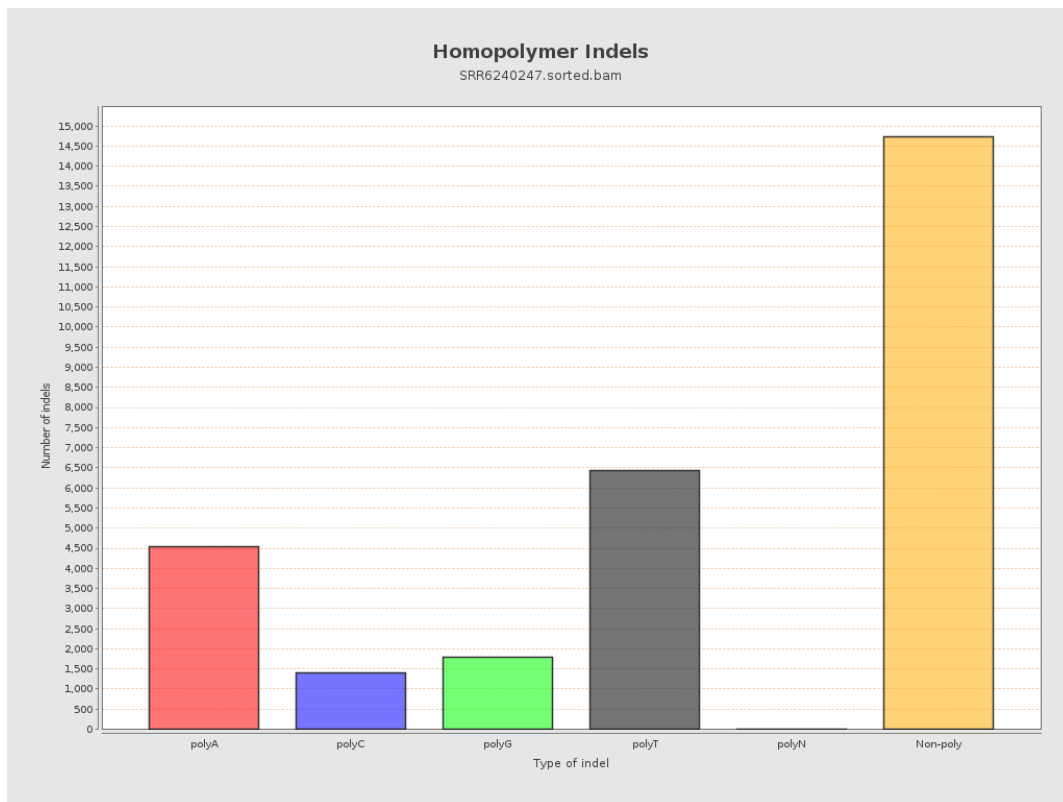
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

