

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:12:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240265.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_SRR6240265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240265.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:12:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,602,591
Mapped reads	1,214,699 / 75.8%
Unmapped reads	387,892 / 24.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,257 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	160,665 / 10.03%
Duplication rate	9.95%
Clipped reads	975,975 / 60.9%

2.2. ACGT Content

Number/percentage of A's	18,601,451 / 26.5%
Number/percentage of C's	11,059,249 / 15.76%
Number/percentage of T's	23,325,728 / 33.23%
Number/percentage of G's	17,190,744 / 24.49%
Number/percentage of N's	14,566 / 0.02%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.2764
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2.4. Mapping Quality

Mean Mapping Quality	43.51
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2.5. Mismatches and indels

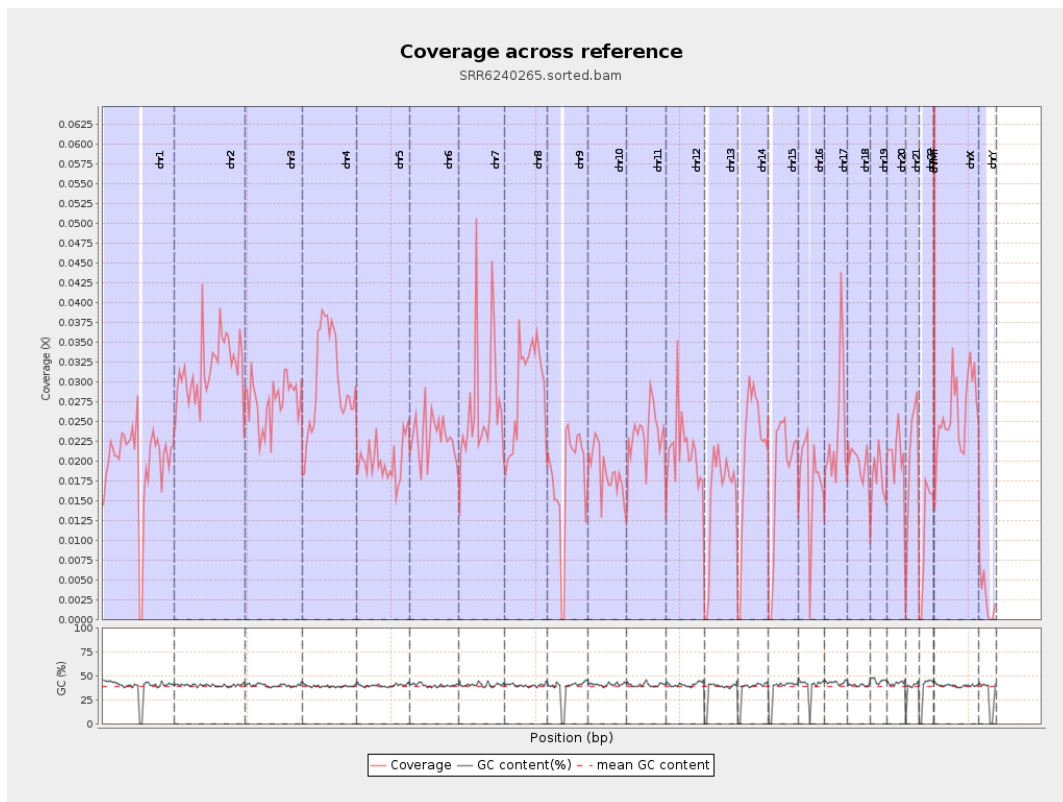
General error rate	1.06%
Mismatches	735,155
Insertions	4,929
Mapped reads with at least one insertion	0.4%
Deletions	26,166
Mapped reads with at least one deletion	2.13%
Homopolymer indels	50.75%

2.6. Chromosome stats

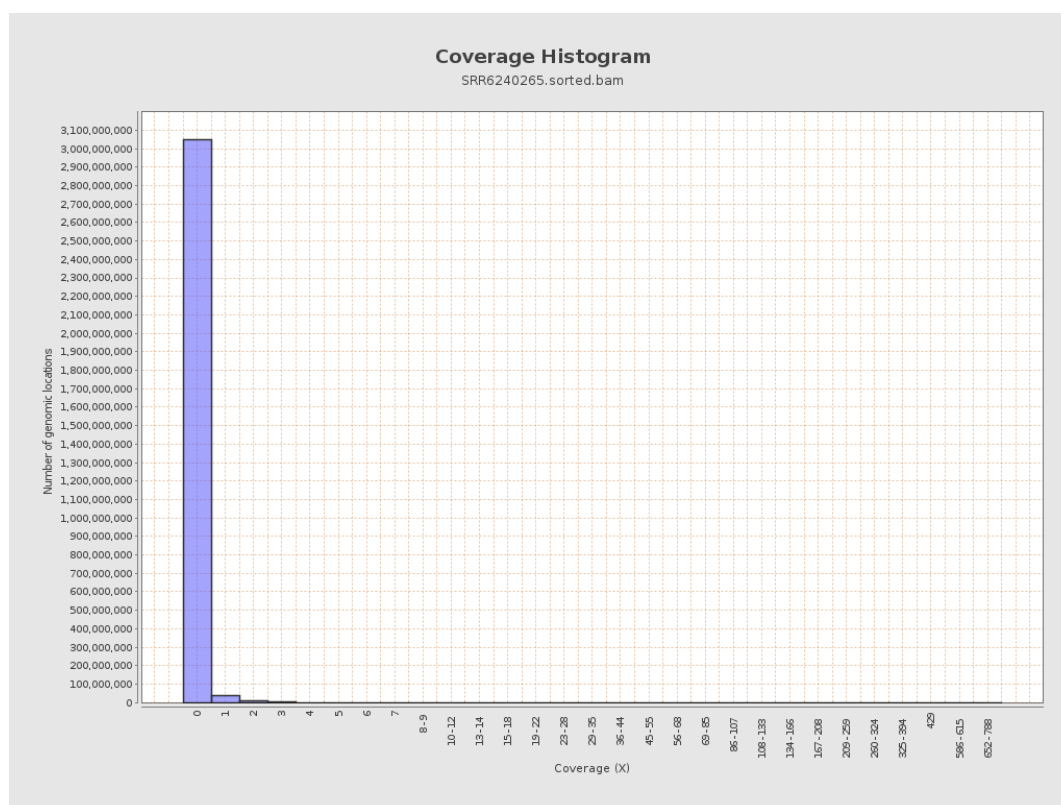
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4929224	0.0198	0.2685
chr2	243199373	7729920	0.0318	0.3324
chr3	198022430	5459205	0.0276	0.2488
chr4	191154276	5709133	0.0299	0.2587
chr5	180915260	3635172	0.0201	0.2051
chr6	171115067	3924257	0.0229	0.2372
chr7	159138663	4254511	0.0267	0.6298

chr8	146364022	4277099	0.0292	0.2885
chr9	141213431	2496679	0.0177	0.2284
chr10	135534747	2512123	0.0185	0.203
chr11	135006516	3171673	0.0235	0.2469
chr12	133851895	2834943	0.0212	0.2071
chr13	115169878	1781325	0.0155	0.1789
chr14	107349540	2316457	0.0216	0.2186
chr15	102531392	1879685	0.0183	0.2133
chr16	90354753	1563859	0.0173	0.1831
chr17	81195210	1948067	0.024	0.2268
chr18	78077248	1548965	0.0198	0.2847
chr19	59128983	1071543	0.0181	0.2248
chr20	63025520	1304870	0.0207	0.2114
chr21	48129895	978617	0.0203	0.2071
chr22	51304566	588613	0.0115	0.147
chrMT	16571	75427	4.5517	6.3983
chrX	155270560	4087027	0.0263	0.2508
chrY	59373566	156780	0.0026	0.0686

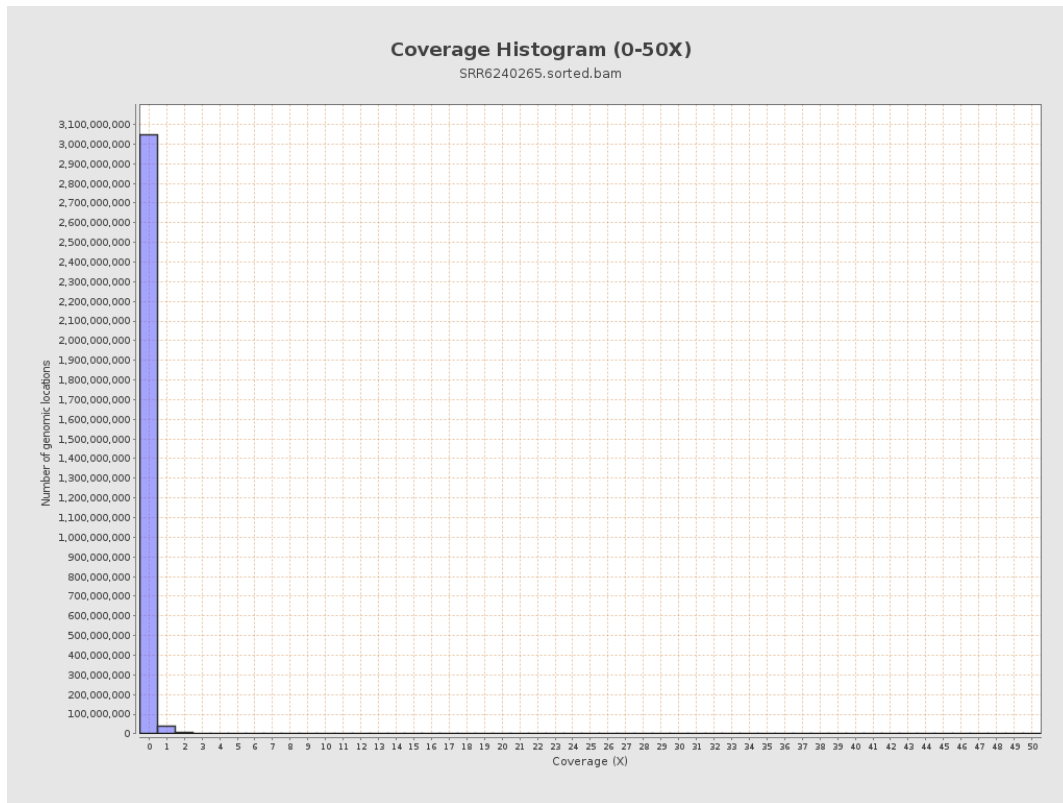
3. Results : Coverage across reference



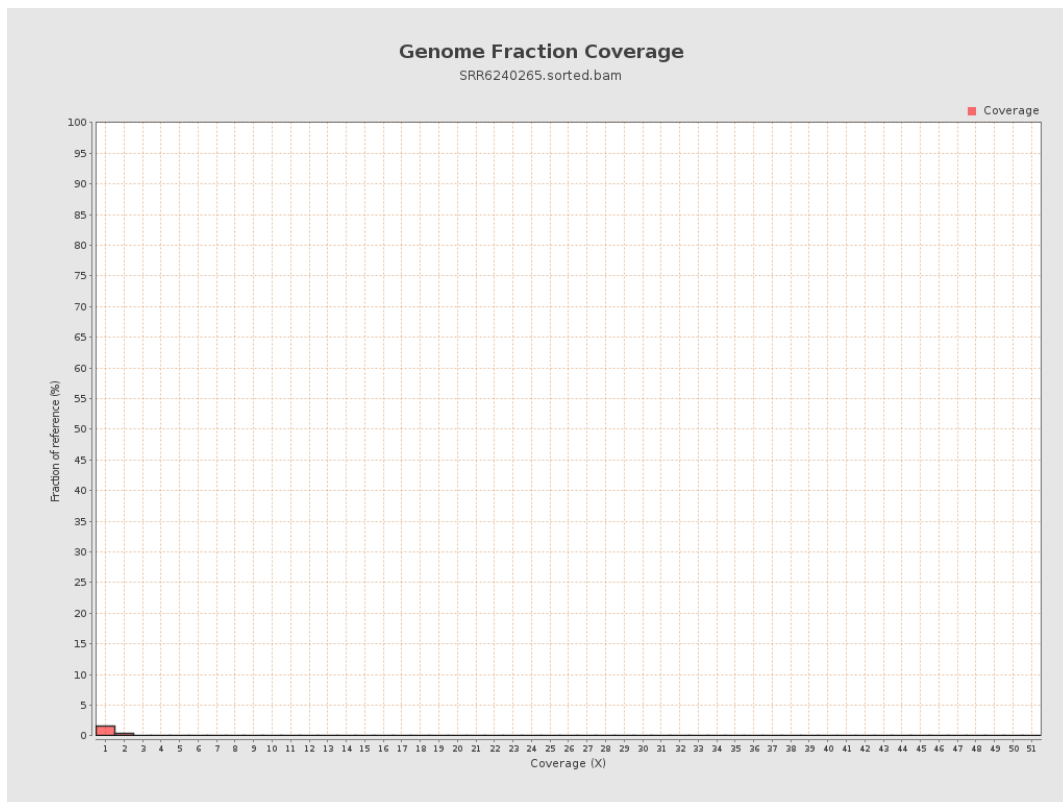
4. Results : Coverage Histogram



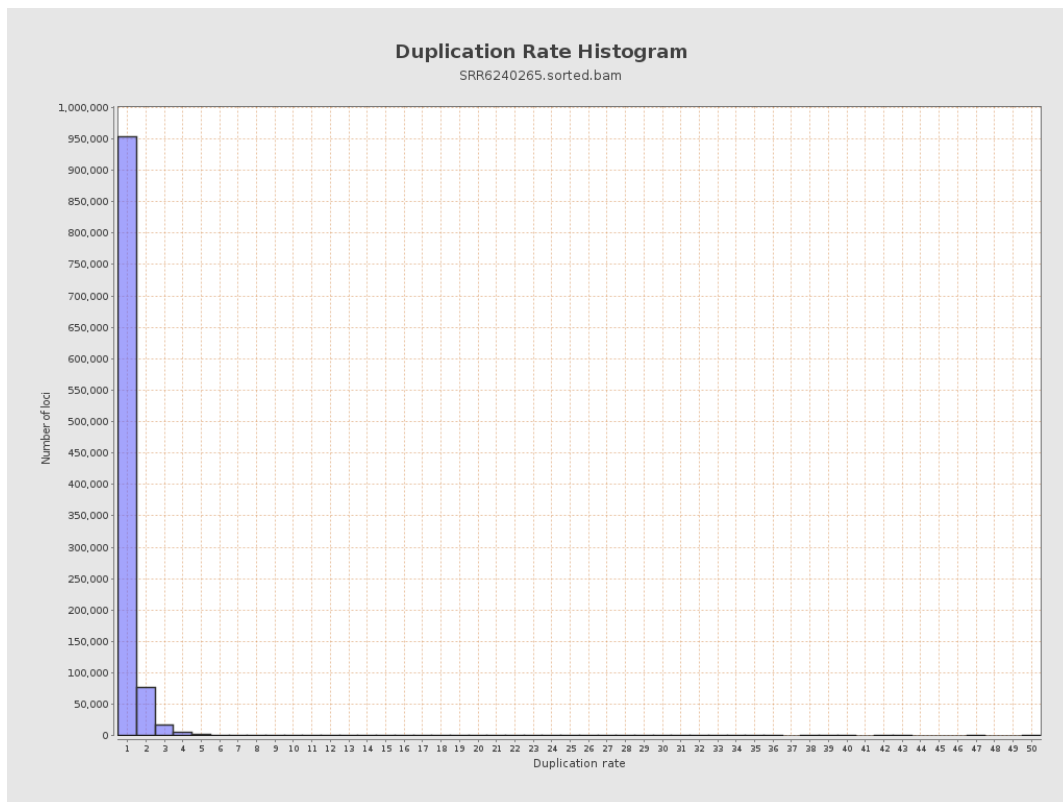
5. Results : Coverage Histogram (0-50X)



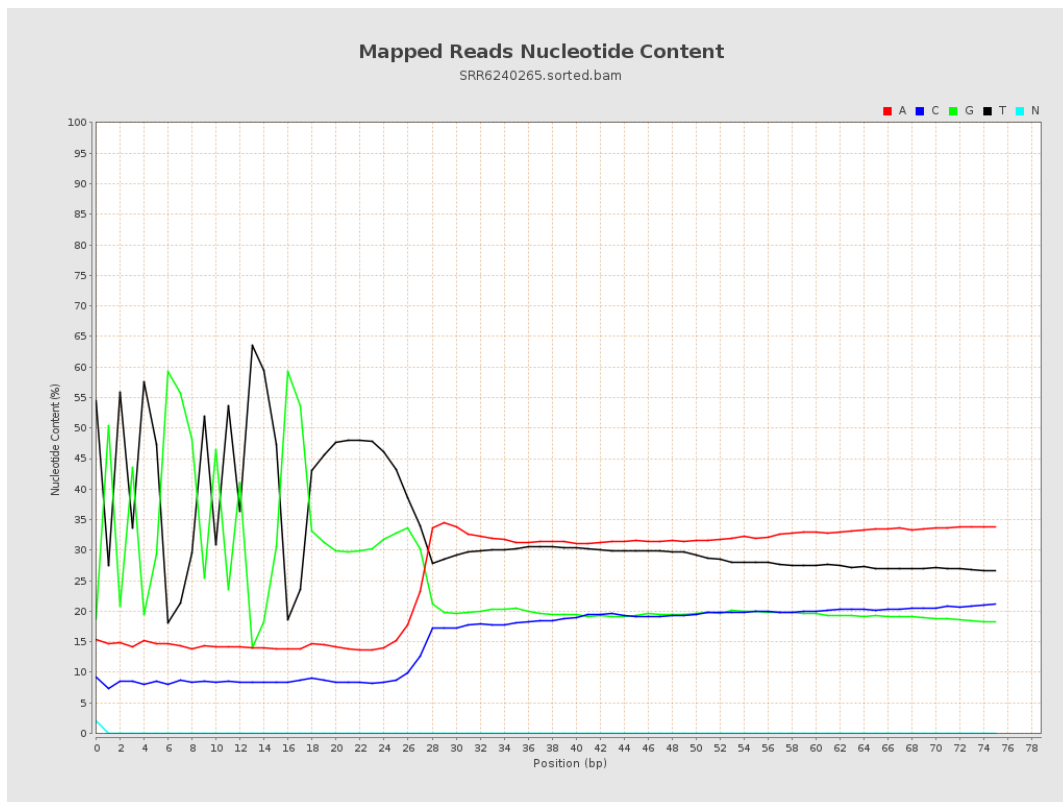
6. Results : Genome Fraction Coverage



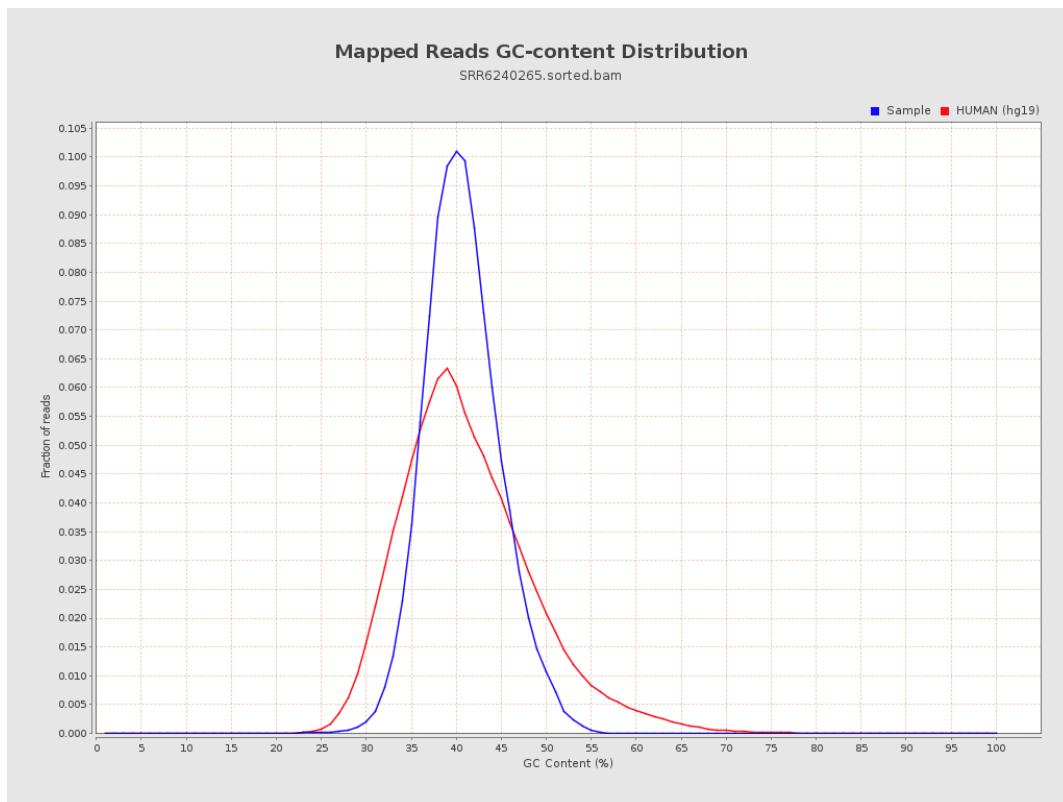
7. Results : Duplication Rate Histogram



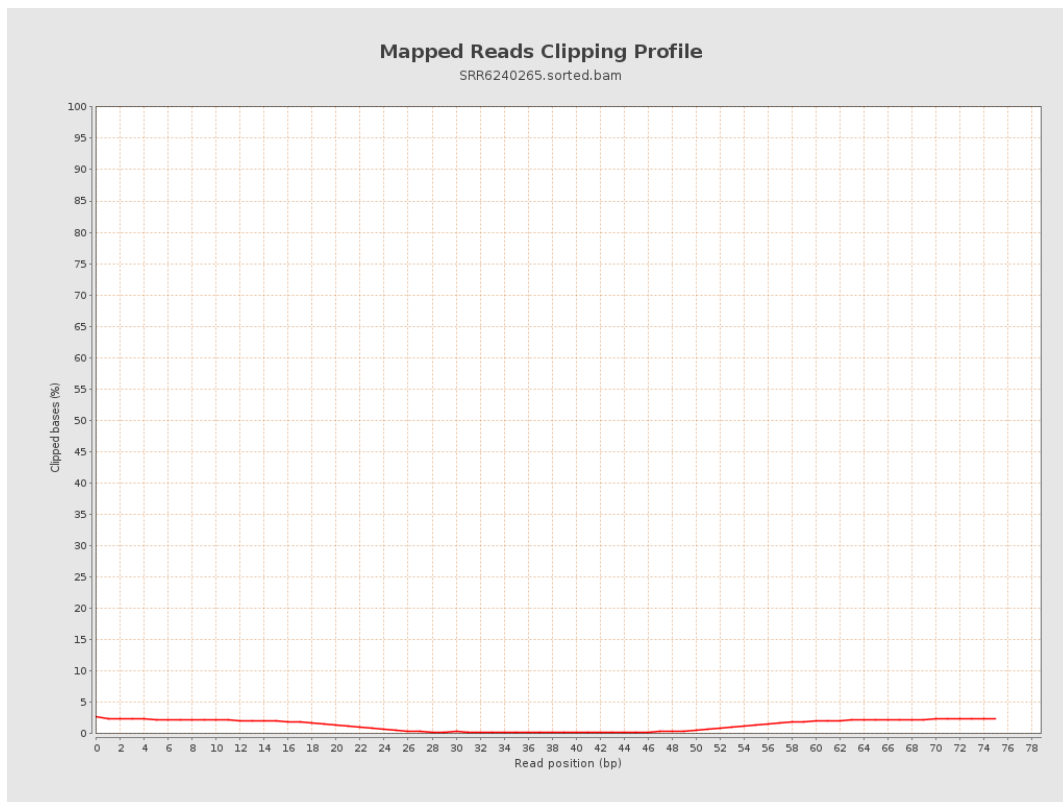
8. Results : Mapped Reads Nucleotide Content



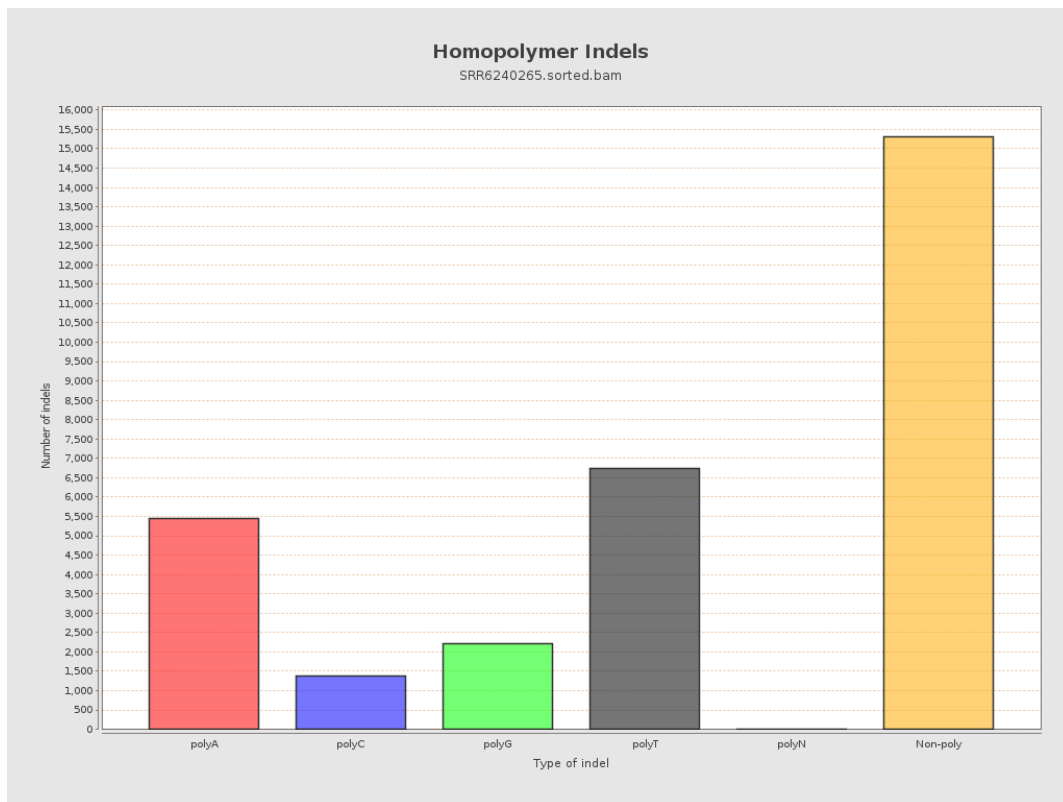
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

