

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:21:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240225.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_SRR6240225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:21:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,909,012
Mapped reads	2,399,234 / 82.48%
Unmapped reads	509,778 / 17.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,575 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	318,653 / 10.95%
Duplication rate	9.8%
Clipped reads	1,150,545 / 39.55%

2.2. ACGT Content

Number/percentage of A's	45,786,655 / 28.8%
Number/percentage of C's	29,407,432 / 18.49%
Number/percentage of T's	50,492,168 / 31.75%
Number/percentage of G's	33,306,864 / 20.95%
Number/percentage of N's	15,233 / 0.01%
GC Percentage	39.44%

2.3. Coverage

Mean	0.0514

Standard Deviation	0.6381
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2.4. Mapping Quality

Mean Mapping Quality	46.22
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2.5. Mismatches and indels

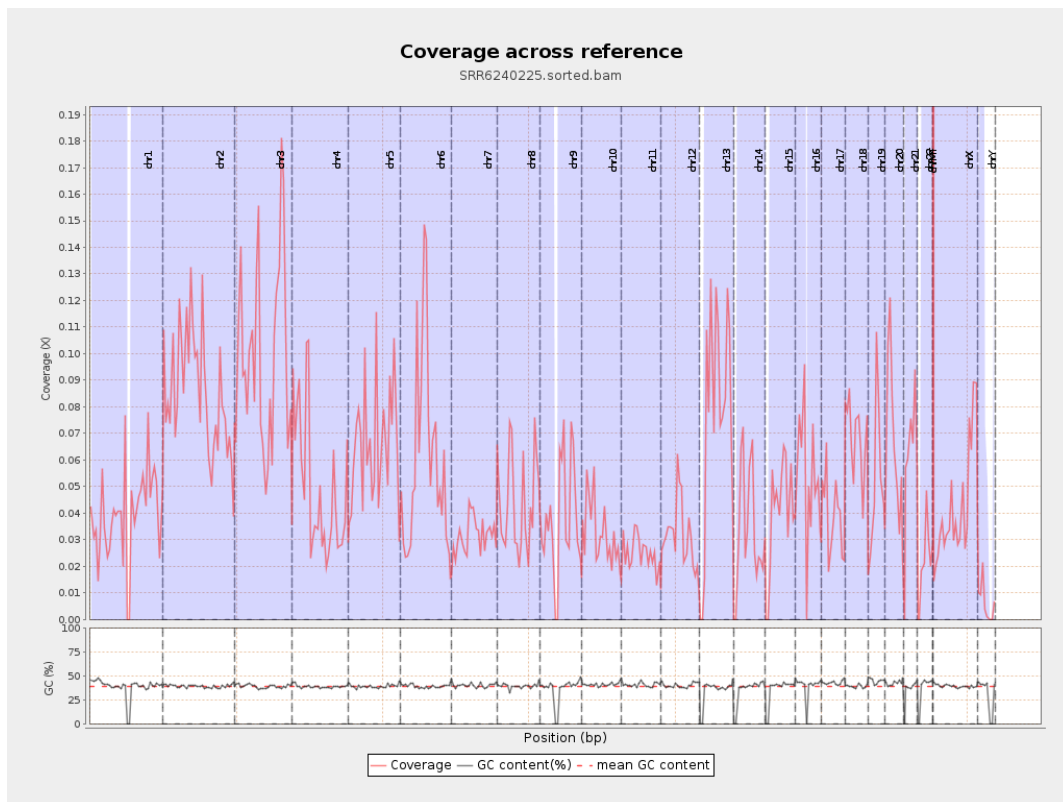
General error rate	0.84%
Mismatches	1,315,652
Insertions	12,004
Mapped reads with at least one insertion	0.5%
Deletions	41,182
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.36%

2.6. Chromosome stats

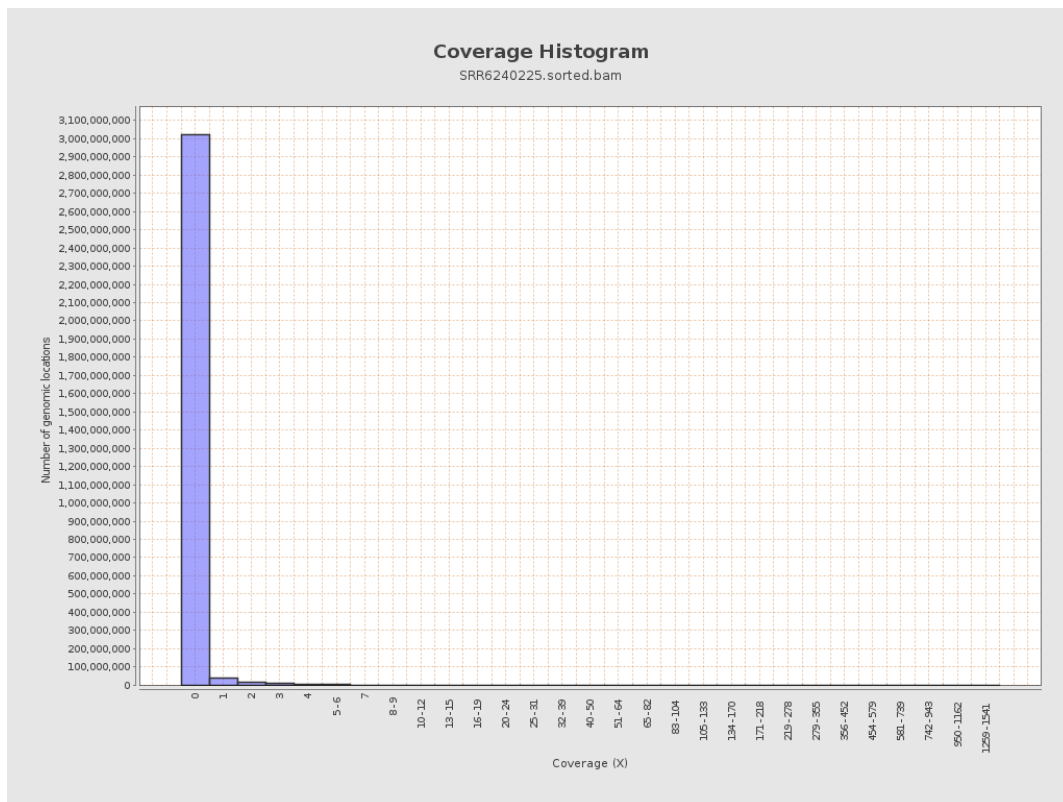
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9791421	0.0393	1.0374
chr2	243199373	20932591	0.0861	0.8068
chr3	198022430	19693054	0.0994	0.6026
chr4	191154276	9491916	0.0497	0.4303
chr5	180915260	11682693	0.0646	0.4942
chr6	171115067	10195753	0.0596	0.6125
chr7	159138663	4980888	0.0313	0.4232

chr8	146364022	6338120	0.0433	1.0585
chr9	141213431	5447344	0.0386	0.5661
chr10	135534747	4415828	0.0326	0.427
chr11	135006516	3358347	0.0249	0.412
chr12	133851895	4276571	0.032	0.3379
chr13	115169878	9096525	0.079	0.546
chr14	107349540	3565115	0.0332	0.3721
chr15	102531392	4120261	0.0402	0.3861
chr16	90354753	4738524	0.0524	0.4868
chr17	81195210	3241416	0.0399	0.4126
chr18	78077248	5276078	0.0676	1.24
chr19	59128983	3121768	0.0528	0.7506
chr20	63025520	4294924	0.0681	0.5205
chr21	48129895	3010949	0.0626	0.4883
chr22	51304566	1126895	0.022	0.2685
chrMT	16571	28480	1.7187	2.3507
chrX	155270560	6477585	0.0417	0.4291
chrY	59373566	377168	0.0064	0.1779

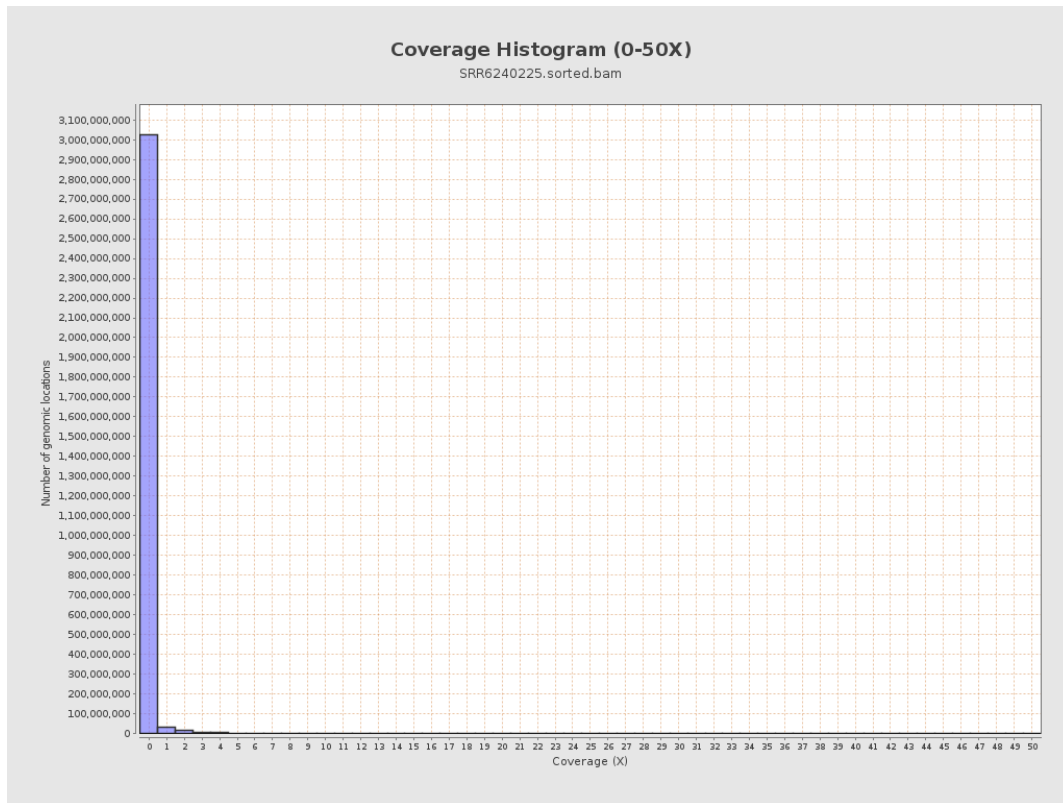
3. Results : Coverage across reference



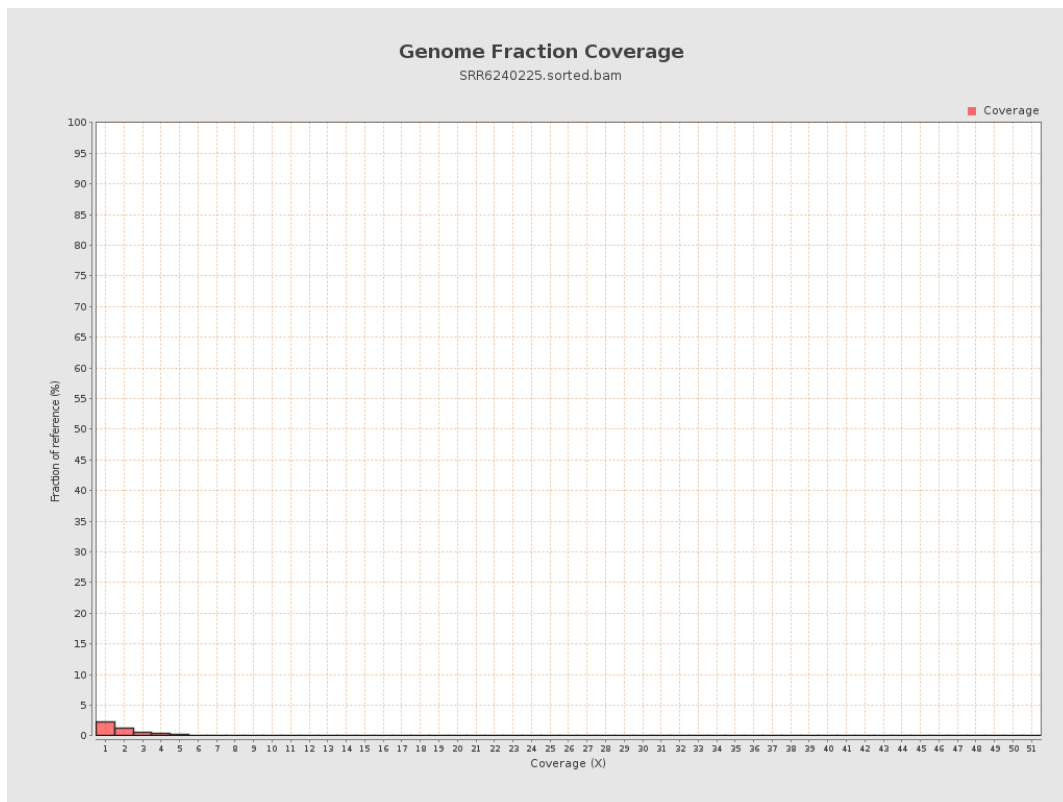
4. Results : Coverage Histogram



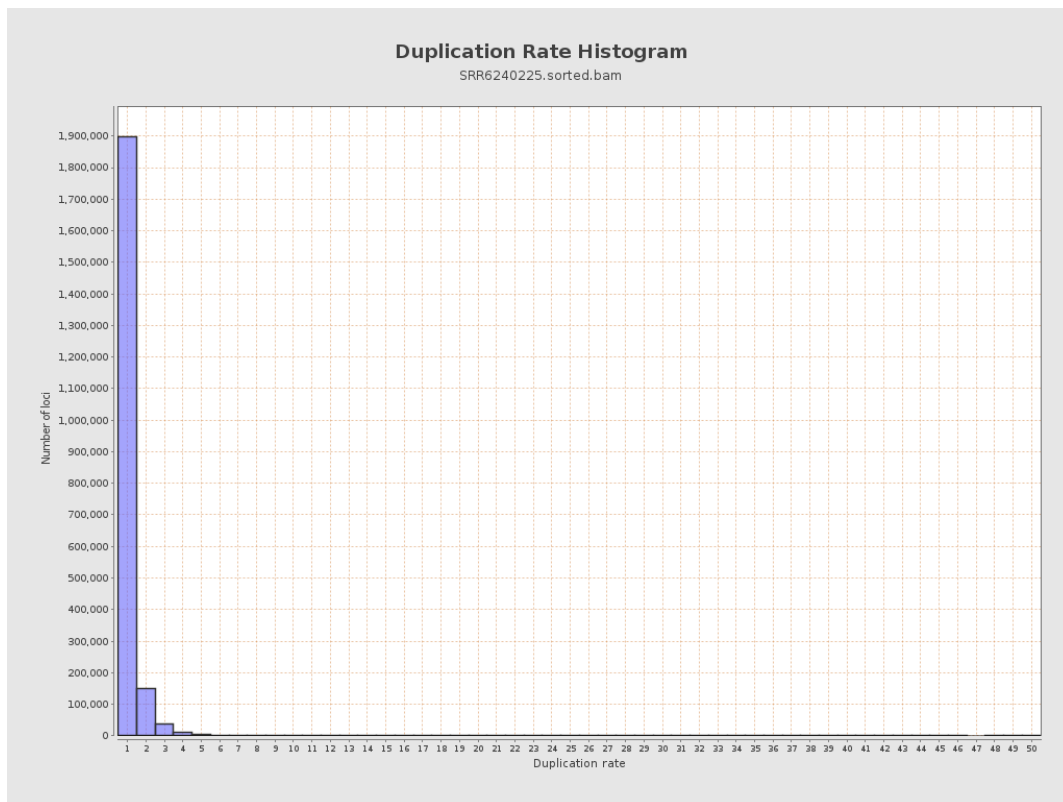
5. Results : Coverage Histogram (0-50X)



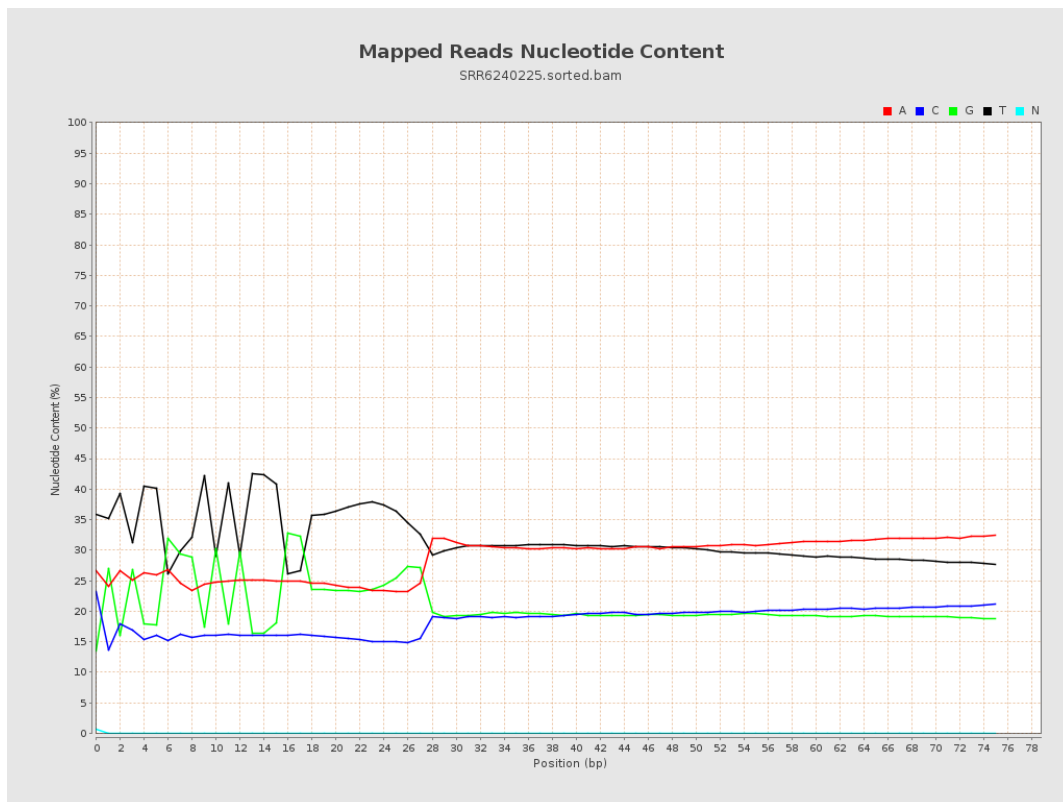
6. Results : Genome Fraction Coverage



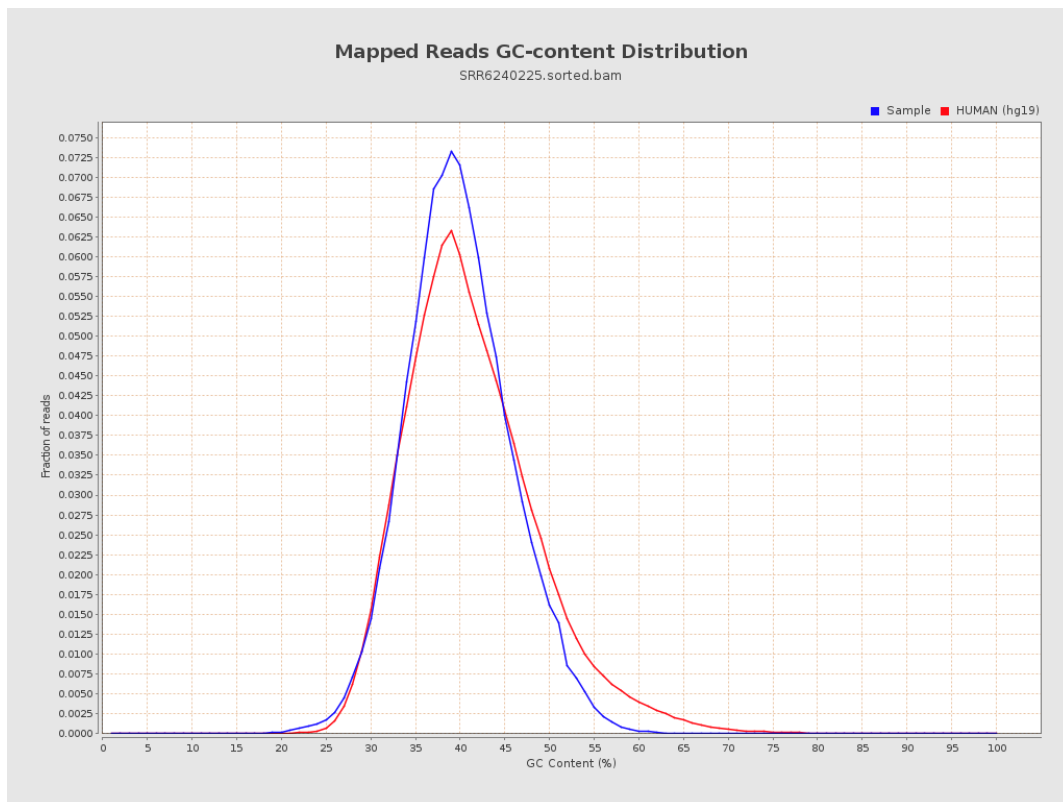
7. Results : Duplication Rate Histogram



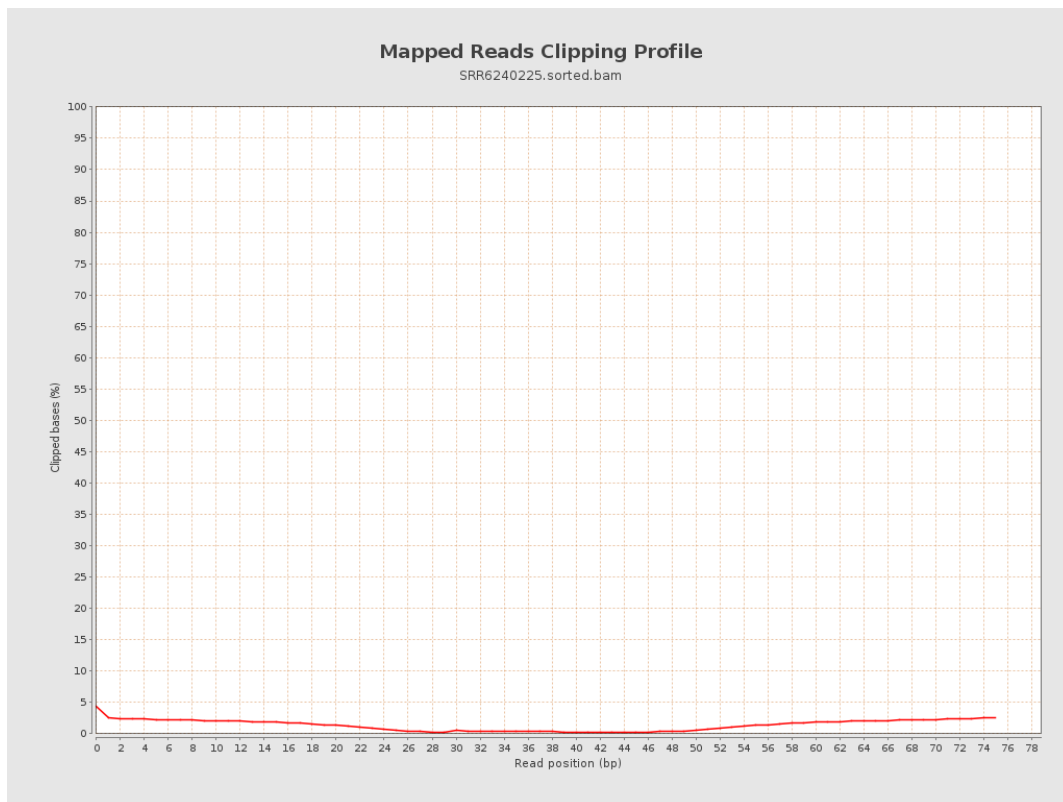
8. Results : Mapped Reads Nucleotide Content



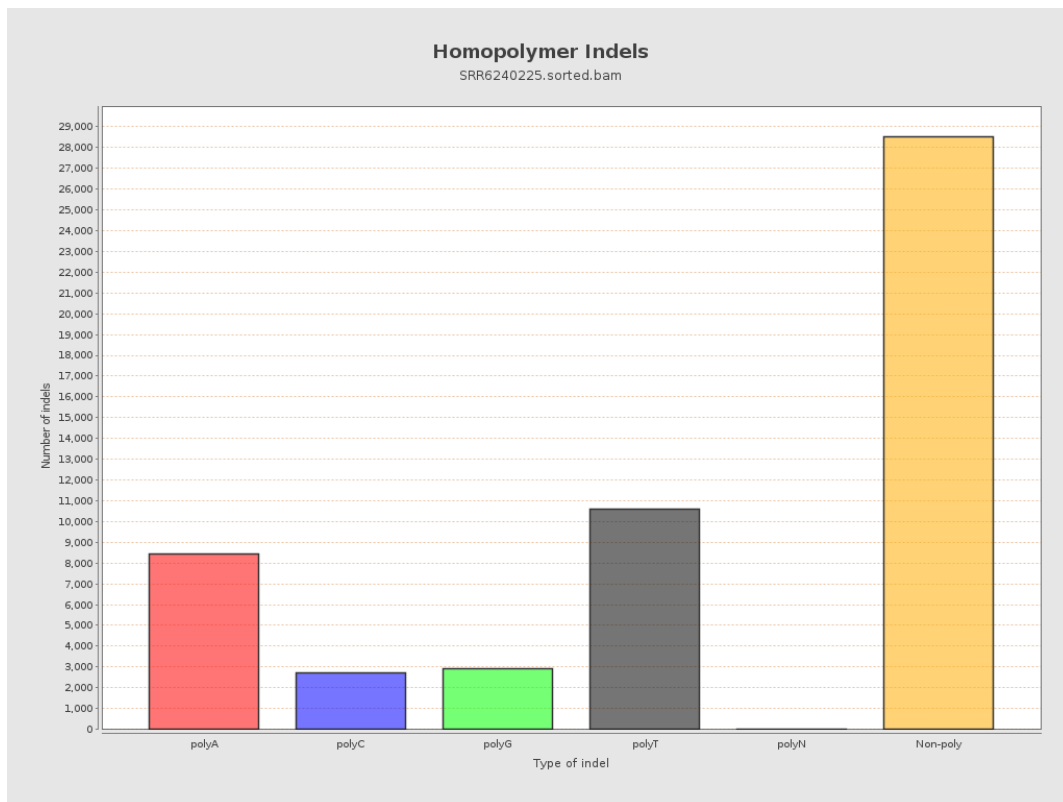
9. Results : Mapped Reads GC-content Distribution



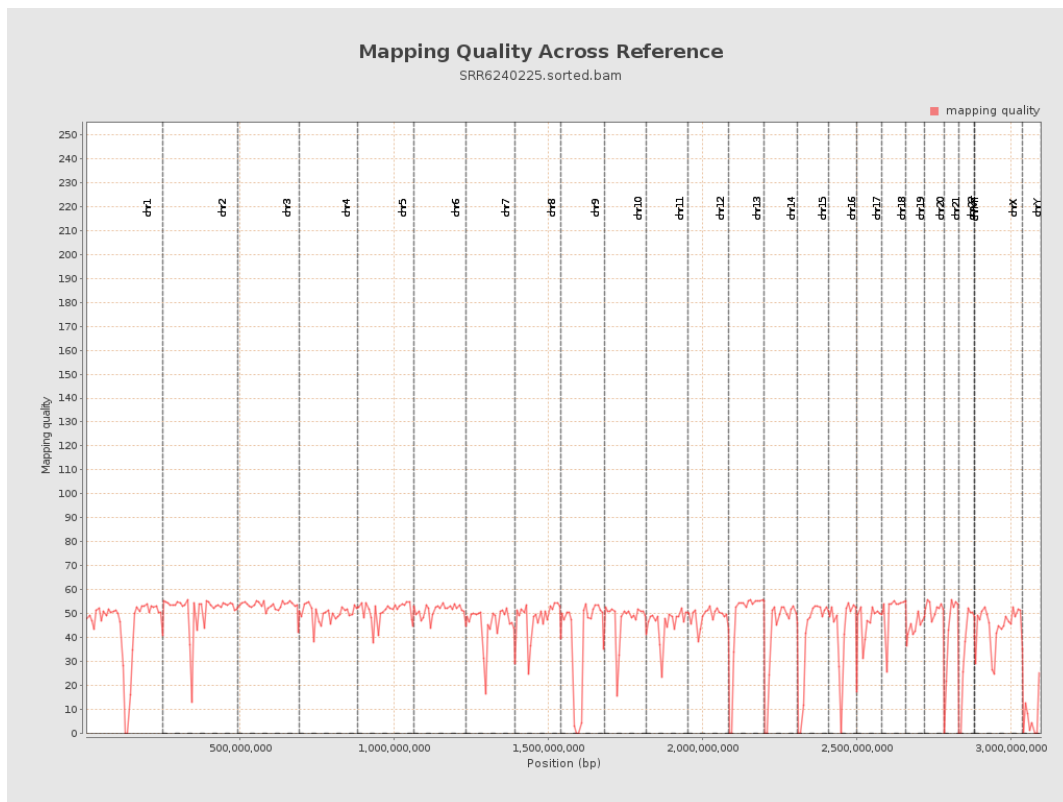
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

