

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:05:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237602.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_SRR6237602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:05:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,915,796
Mapped reads	1,587,963 / 82.89%
Unmapped reads	327,833 / 17.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,255 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	73,892 / 3.86%
Duplication rate	3.16%
Clipped reads	933,921 / 48.75%

2.2. ACGT Content

Number/percentage of A's	25,815,773 / 25.55%
Number/percentage of C's	19,467,465 / 19.27%
Number/percentage of T's	30,352,961 / 30.04%
Number/percentage of G's	25,372,675 / 25.11%
Number/percentage of N's	24,262 / 0.02%
GC Percentage	44.38%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.3064
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2.4. Mapping Quality

Mean Mapping Quality	39.47
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2.5. Mismatches and indels

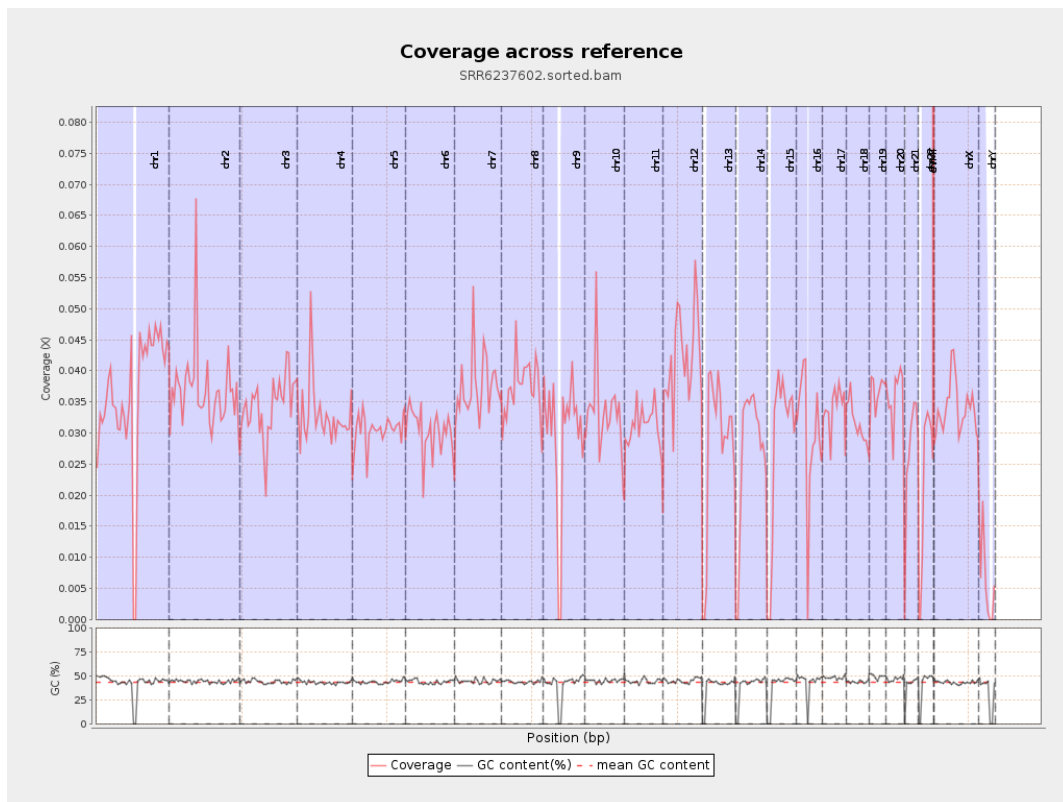
General error rate	0.93%
Mismatches	922,746
Insertions	9,598
Mapped reads with at least one insertion	0.6%
Deletions	34,268
Mapped reads with at least one deletion	2.13%
Homopolymer indels	45.88%

2.6. Chromosome stats

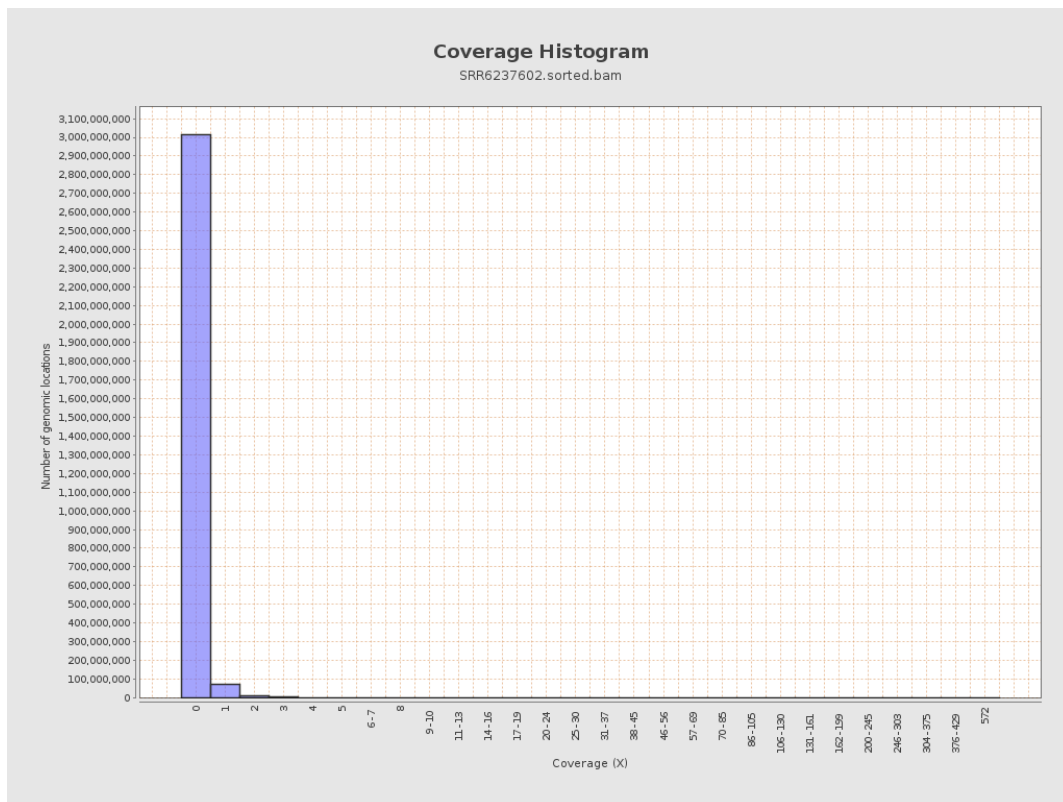
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9002636	0.0361	0.3889
chr2	243199373	8982621	0.0369	0.4406
chr3	198022430	6779860	0.0342	0.2319
chr4	191154276	6248563	0.0327	0.2459
chr5	180915260	5526247	0.0305	0.2121
chr6	171115067	5193454	0.0304	0.2395
chr7	159138663	5986940	0.0376	0.4464

chr8	146364022	5437465	0.0372	0.2973
chr9	141213431	4111065	0.0291	0.3207
chr10	135534747	4507764	0.0333	0.313
chr11	135006516	4181611	0.031	0.3202
chr12	133851895	5693879	0.0425	0.2674
chr13	115169878	3188642	0.0277	0.2087
chr14	107349540	2893626	0.027	0.2336
chr15	102531392	2911425	0.0284	0.2212
chr16	90354753	2716080	0.0301	0.2468
chr17	81195210	2749295	0.0339	0.2465
chr18	78077248	2472171	0.0317	0.4583
chr19	59128983	2161535	0.0366	0.3214
chr20	63025520	2225963	0.0353	0.2429
chr21	48129895	1300699	0.027	0.231
chr22	51304566	1111695	0.0217	0.186
chrMT	16571	85962	5.1875	4.532
chrX	155270560	5259627	0.0339	0.2604
chrY	59373566	361342	0.0061	0.1514

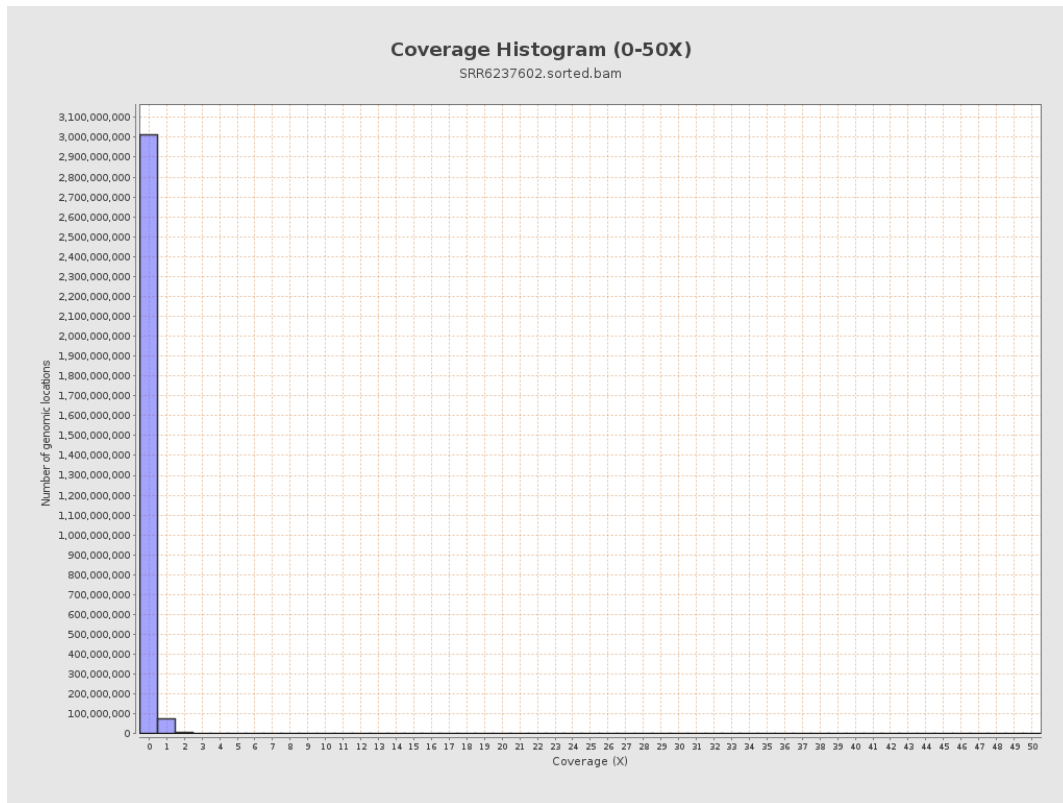
3. Results : Coverage across reference



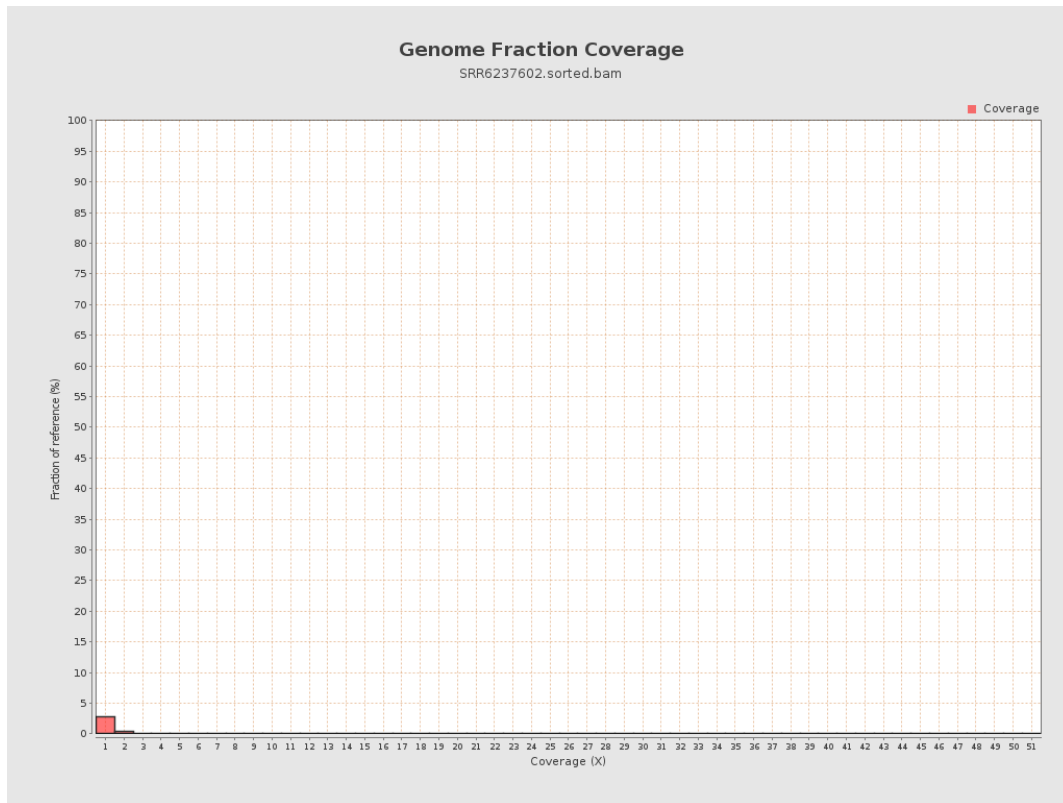
4. Results : Coverage Histogram



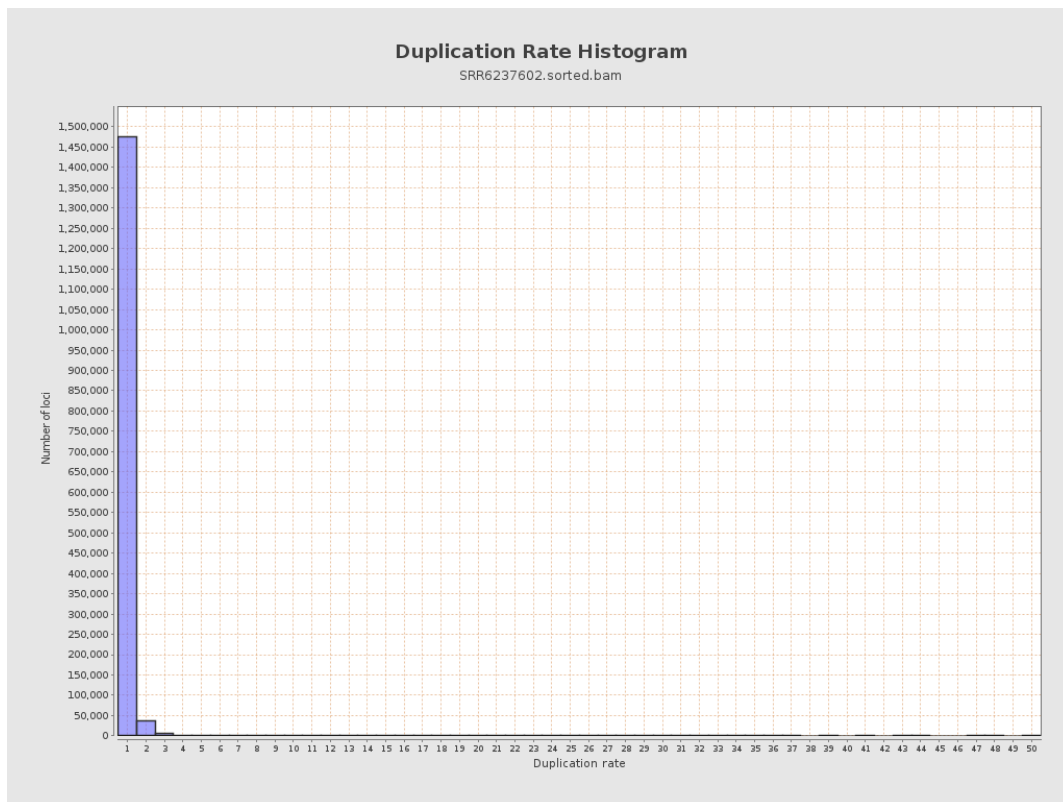
5. Results : Coverage Histogram (0-50X)



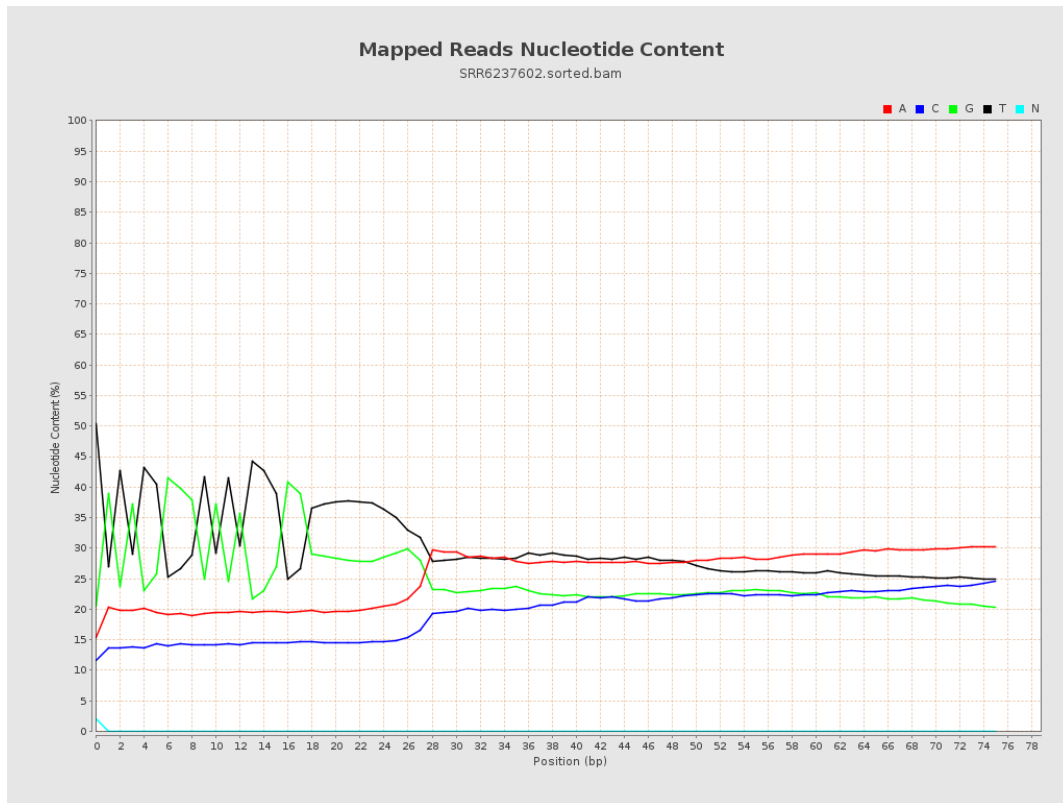
6. Results : Genome Fraction Coverage



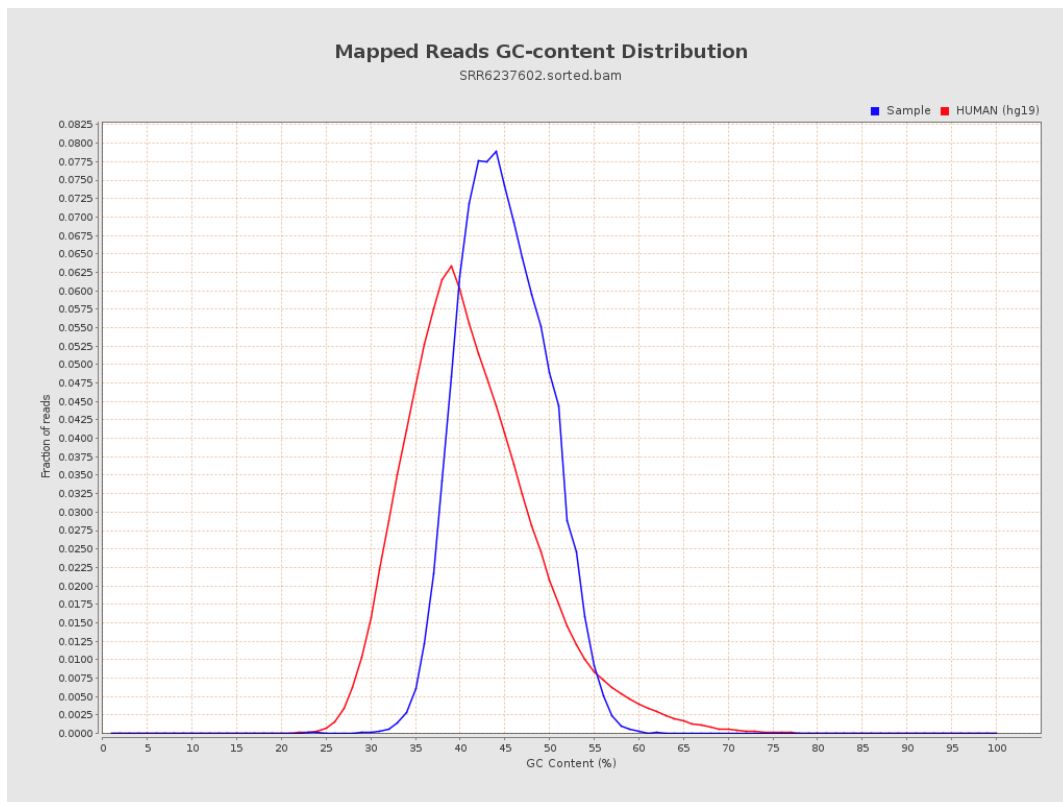
7. Results : Duplication Rate Histogram



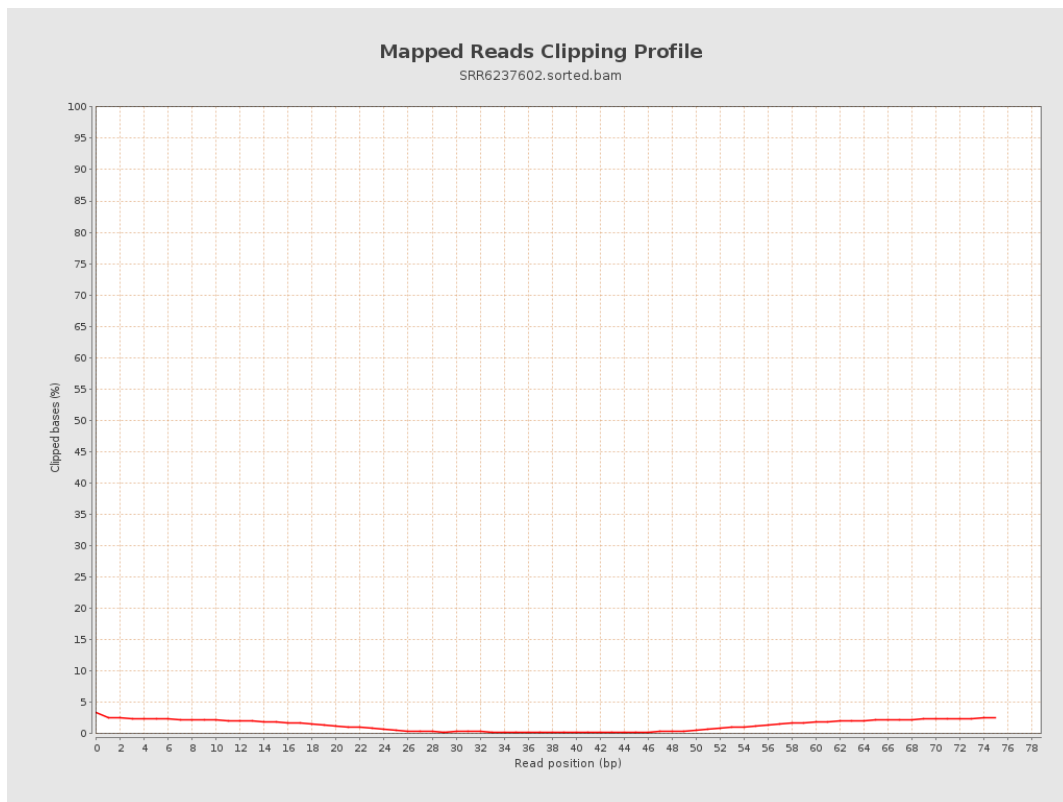
8. Results : Mapped Reads Nucleotide Content



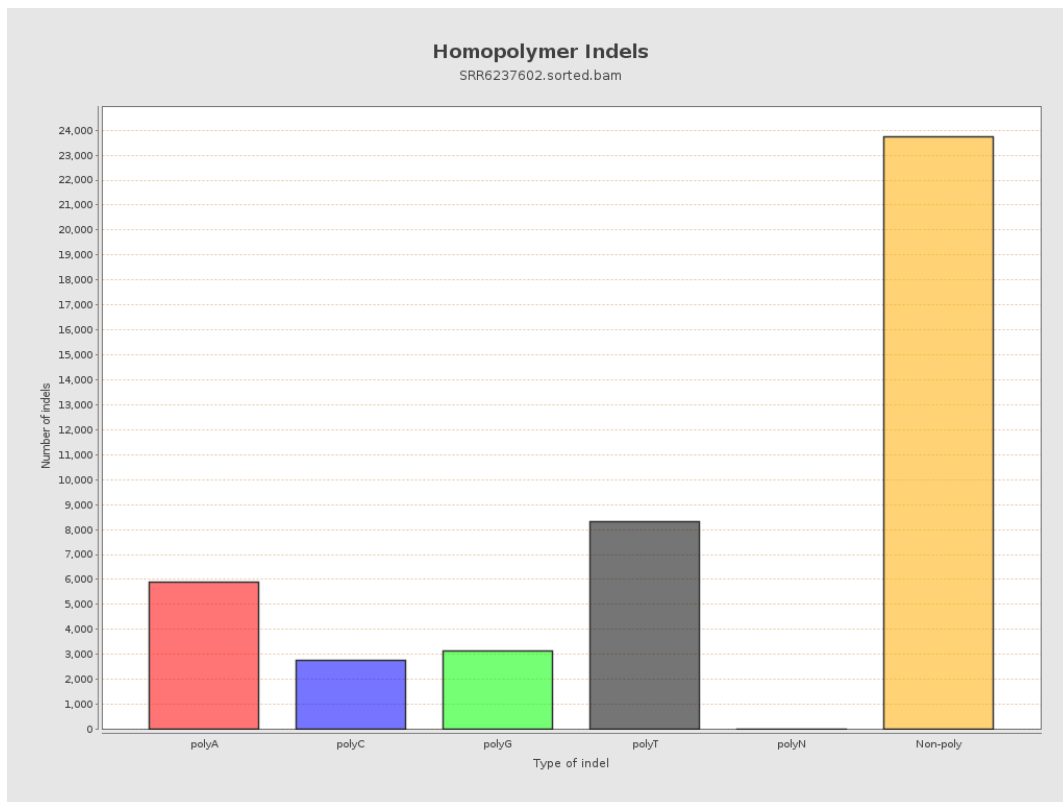
9. Results : Mapped Reads GC-content Distribution



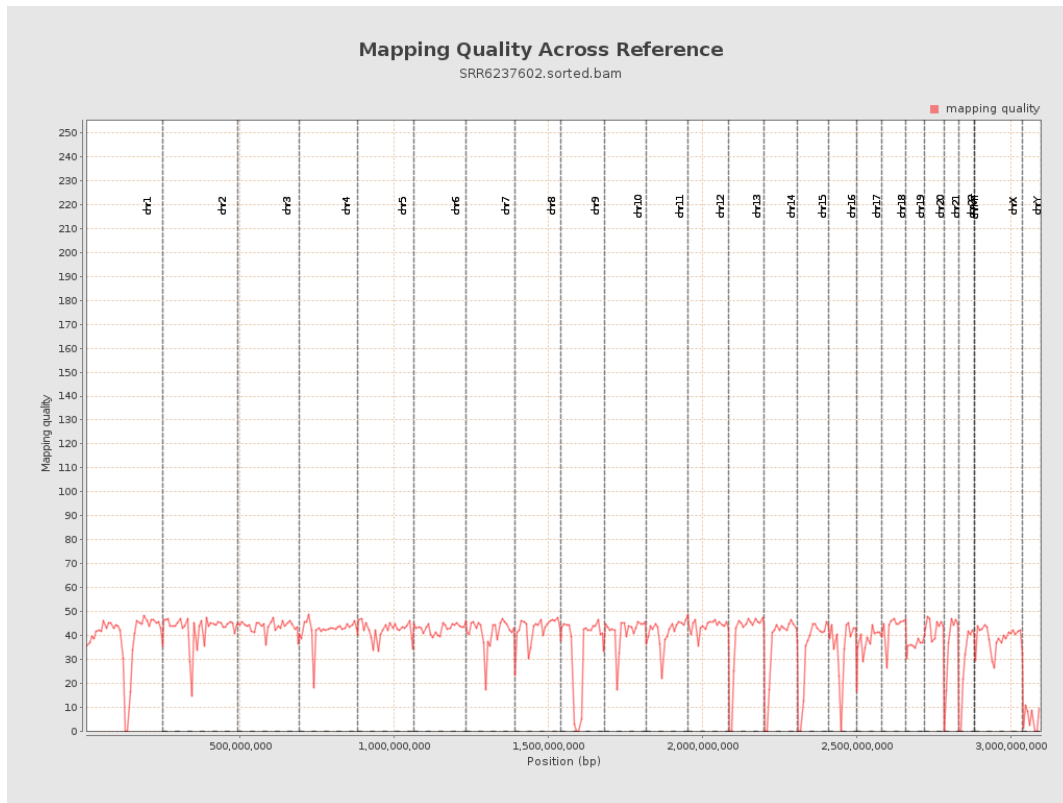
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

