

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:50:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237848.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_SRR6237848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:50:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,908,265
Mapped reads	1,394,531 / 73.08%
Unmapped reads	513,734 / 26.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,054 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	101,740 / 5.33%
Duplication rate	4.87%
Clipped reads	957,355 / 50.17%

2.2. ACGT Content

Number/percentage of A's	23,175,369 / 27.2%
Number/percentage of C's	15,099,986 / 17.72%
Number/percentage of T's	25,959,414 / 30.47%
Number/percentage of G's	20,894,539 / 24.52%
Number/percentage of N's	69,622 / 0.08%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2996
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2.4. Mapping Quality

Mean Mapping Quality	42.2
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2.5. Mismatches and indels

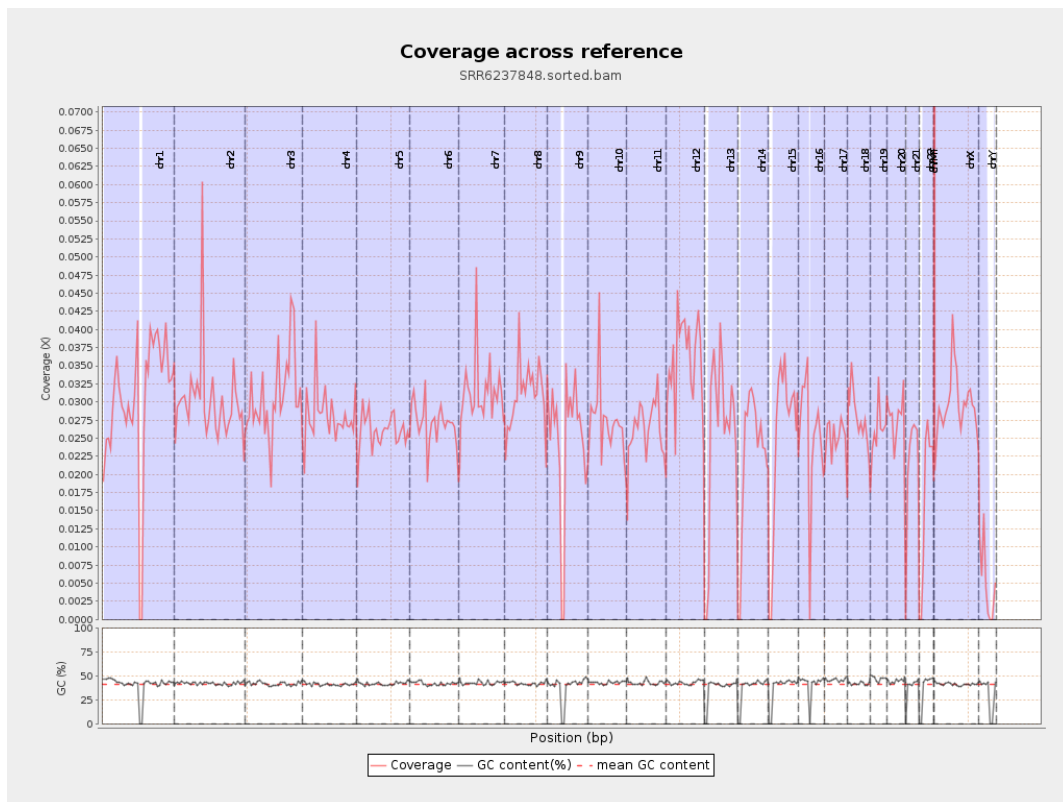
General error rate	1.1%
Mismatches	923,211
Insertions	8,501
Mapped reads with at least one insertion	0.61%
Deletions	37,912
Mapped reads with at least one deletion	2.68%
Homopolymer indels	48.49%

2.6. Chromosome stats

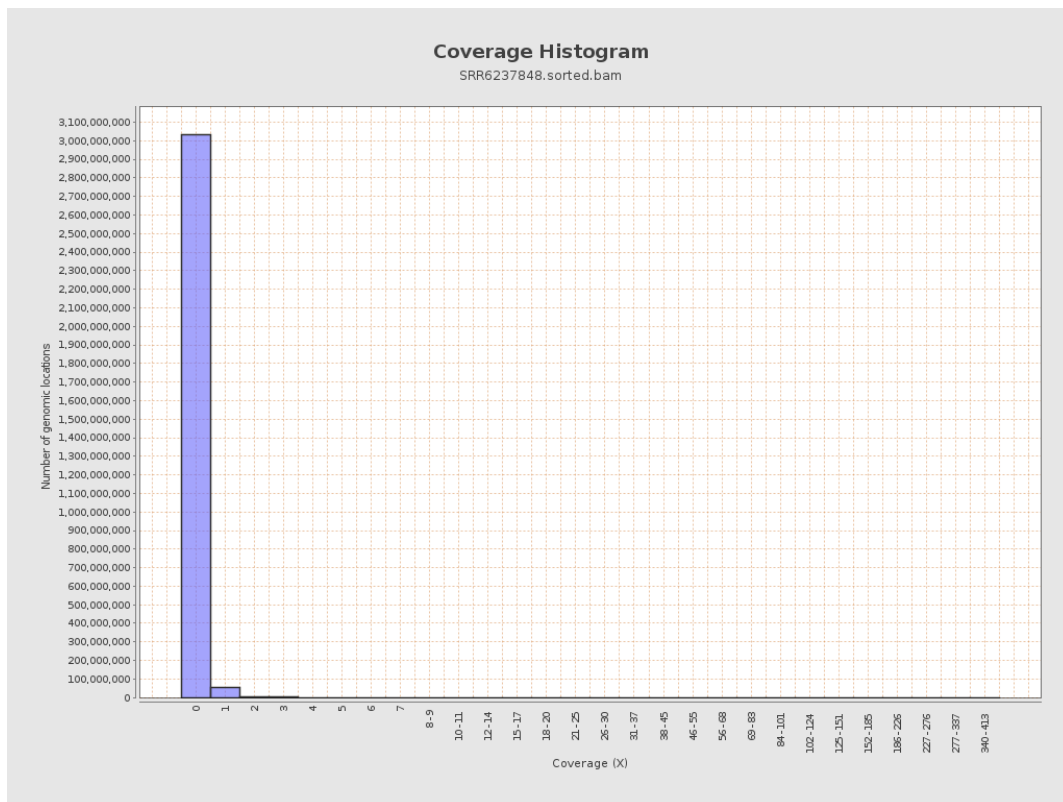
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7539247	0.0302	0.3582
chr2	243199373	7328667	0.0301	0.3951
chr3	198022430	6065581	0.0306	0.2544
chr4	191154276	5352653	0.028	0.238
chr5	180915260	4725149	0.0261	0.22
chr6	171115067	4616937	0.027	0.2538
chr7	159138663	4980881	0.0313	0.4407

chr8	146364022	4511770	0.0308	0.3257
chr9	141213431	3492439	0.0247	0.3089
chr10	135534747	3695866	0.0273	0.281
chr11	135006516	3567966	0.0264	0.3479
chr12	133851895	4793679	0.0358	0.2767
chr13	115169878	2924715	0.0254	0.2341
chr14	107349540	2429823	0.0226	0.2347
chr15	102531392	2580697	0.0252	0.2271
chr16	90354753	2253808	0.0249	0.2463
chr17	81195210	2024531	0.0249	0.2361
chr18	78077248	2181261	0.0279	0.4451
chr19	59128983	1551309	0.0262	0.2884
chr20	63025520	1723372	0.0273	0.2378
chr21	48129895	1060607	0.022	0.2229
chr22	51304566	876464	0.0171	0.182
chrMT	16571	55771	3.3656	3.6875
chrX	155270560	4627321	0.0298	0.2585
chrY	59373566	299513	0.005	0.1206

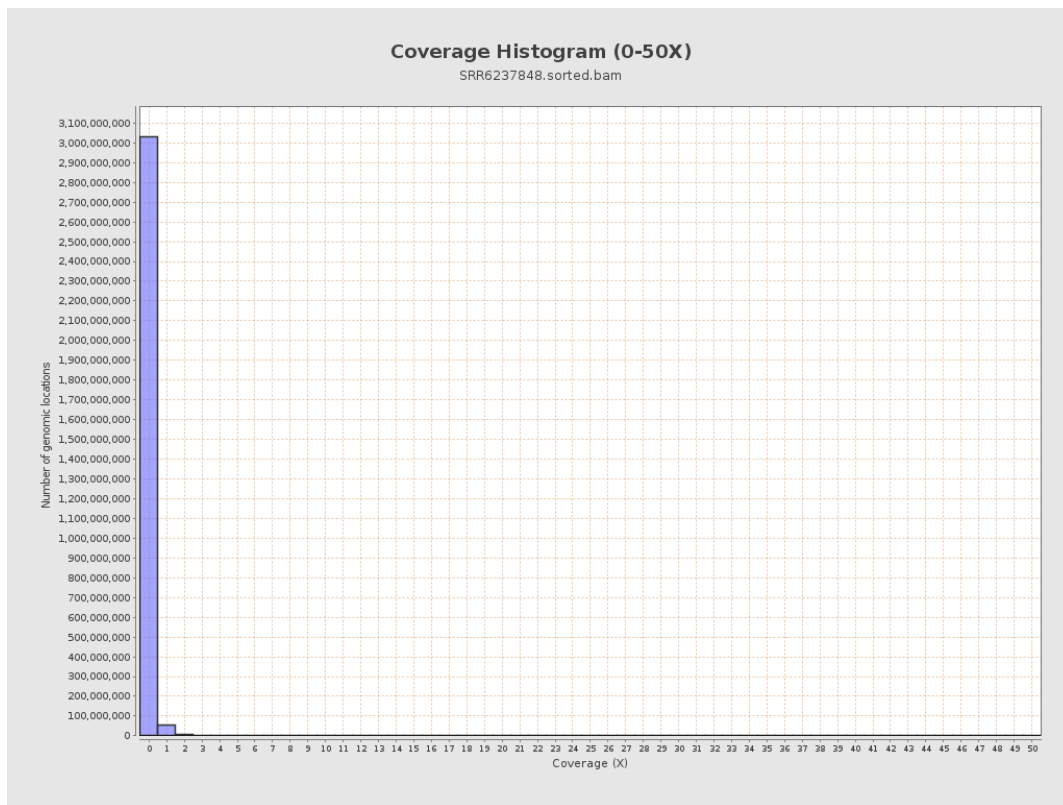
3. Results : Coverage across reference



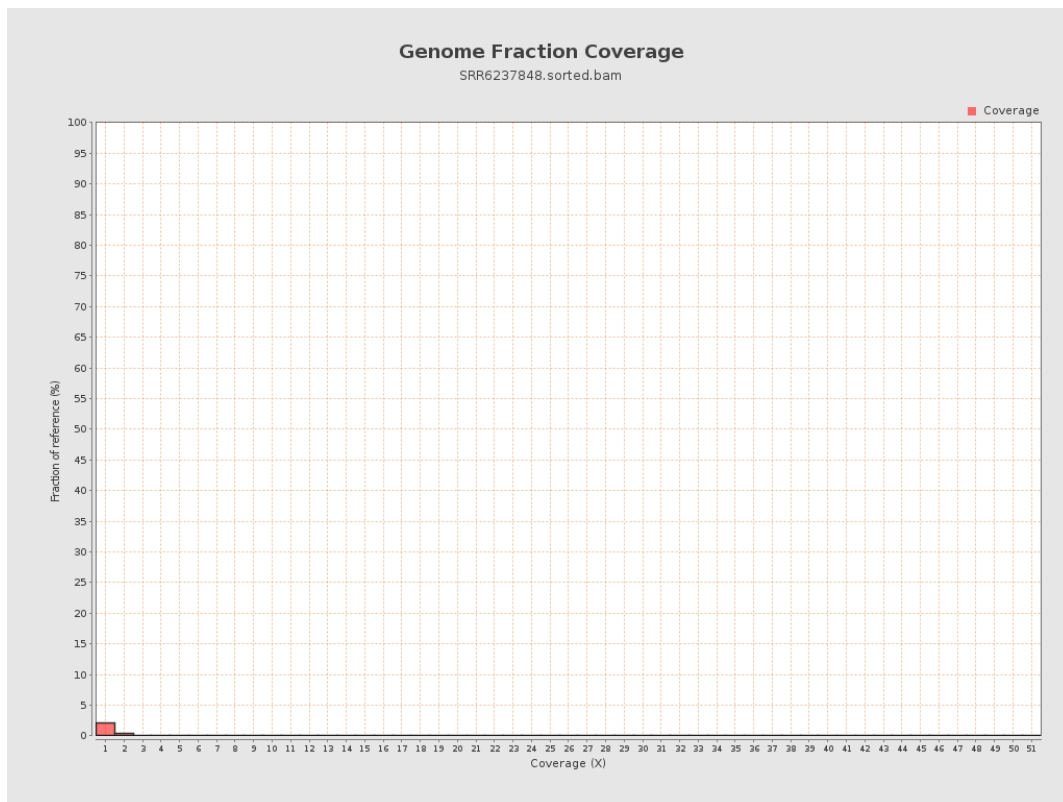
4. Results : Coverage Histogram



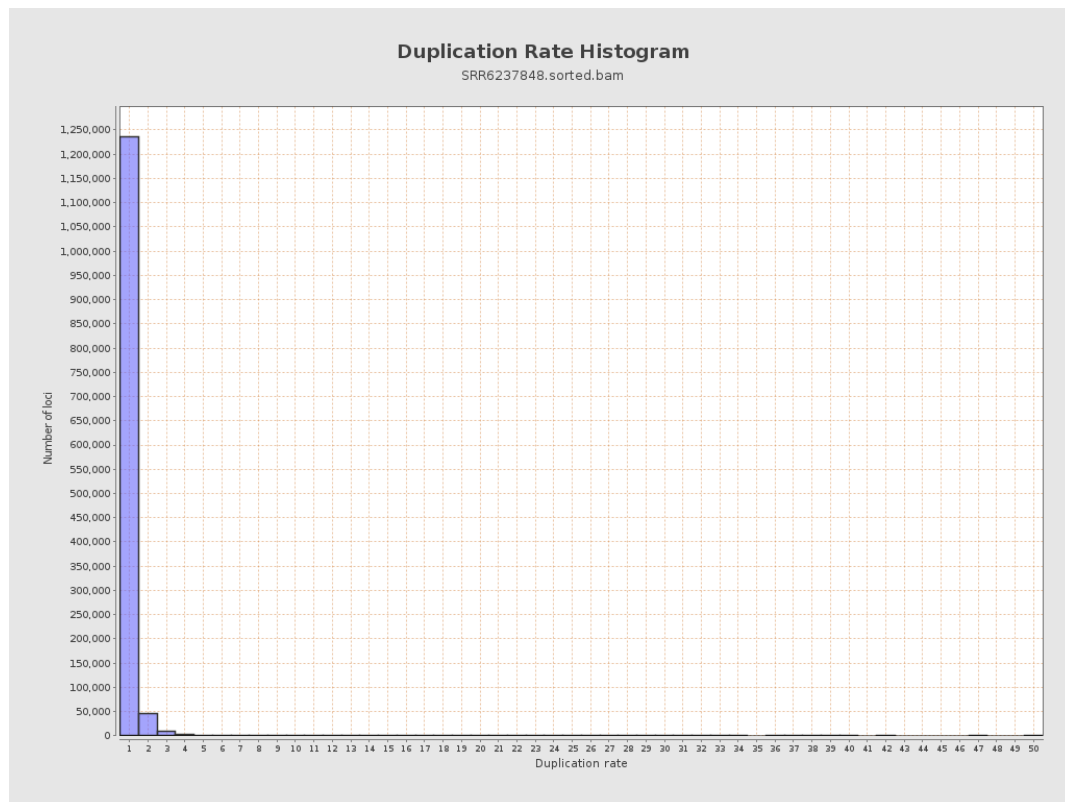
5. Results : Coverage Histogram (0-50X)



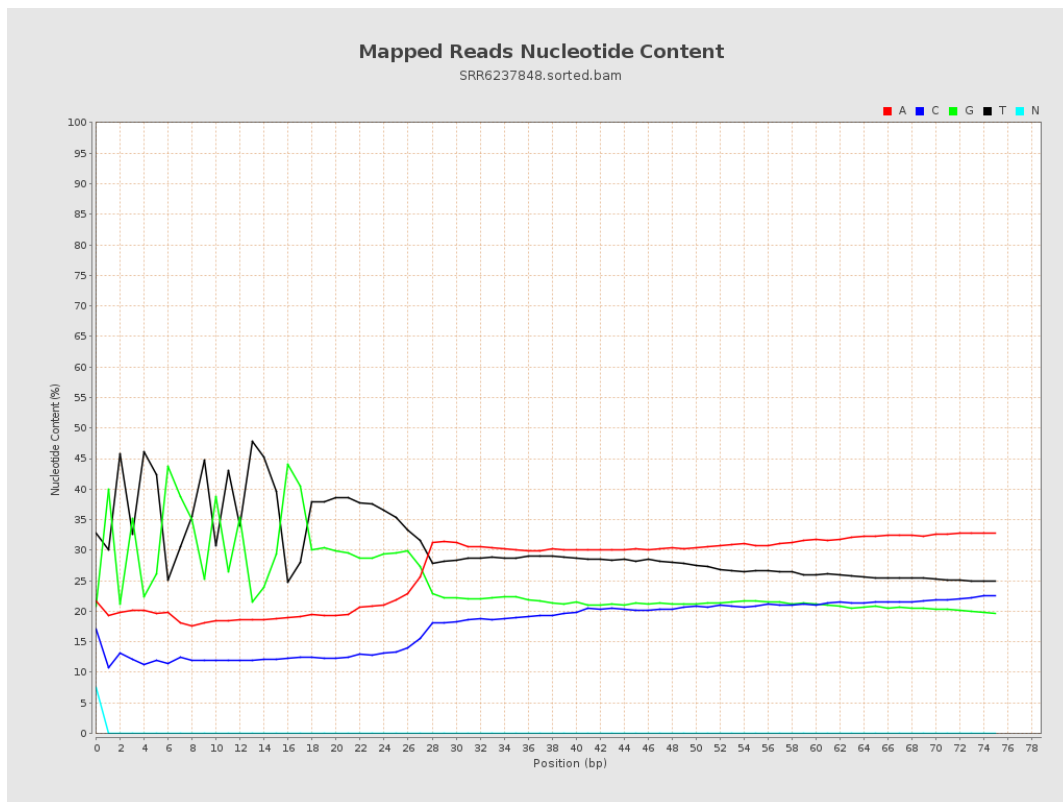
6. Results : Genome Fraction Coverage



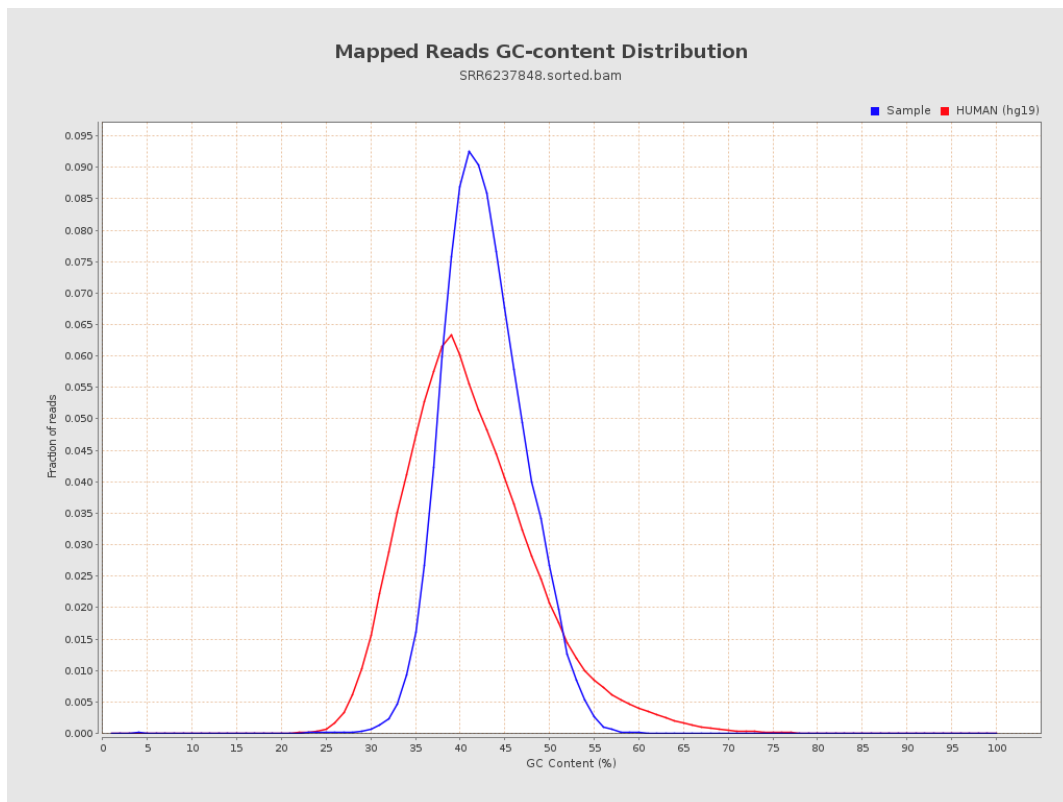
7. Results : Duplication Rate Histogram



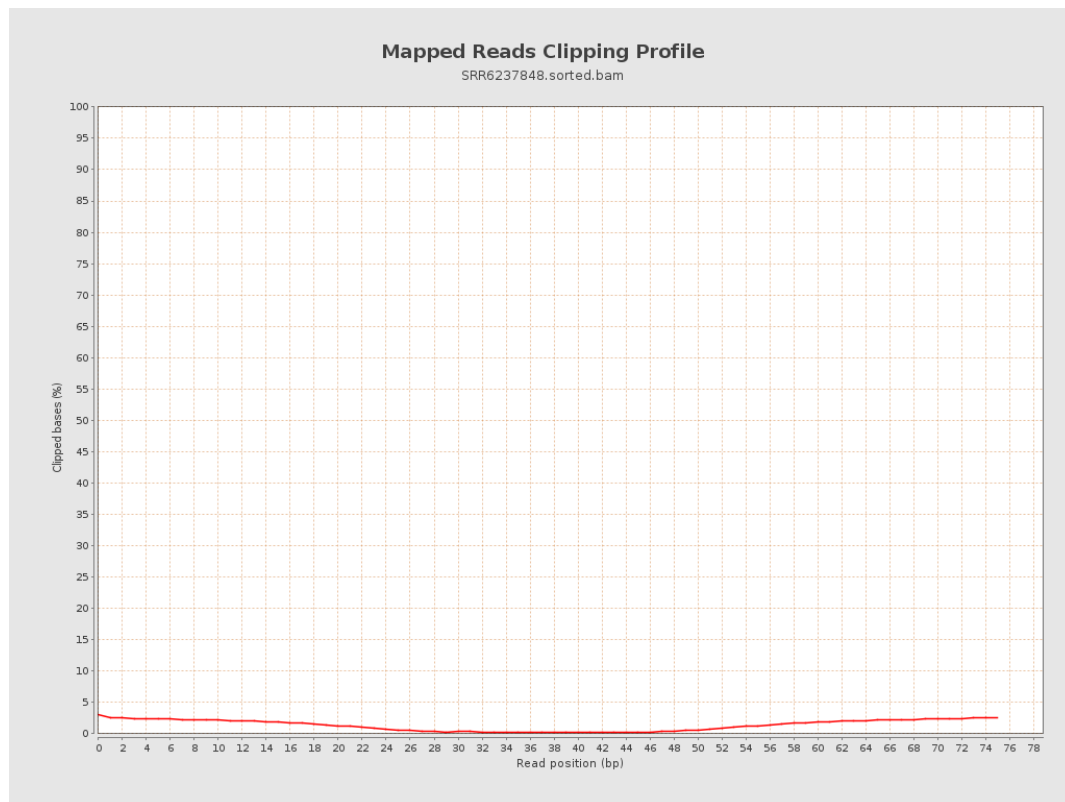
8. Results : Mapped Reads Nucleotide Content



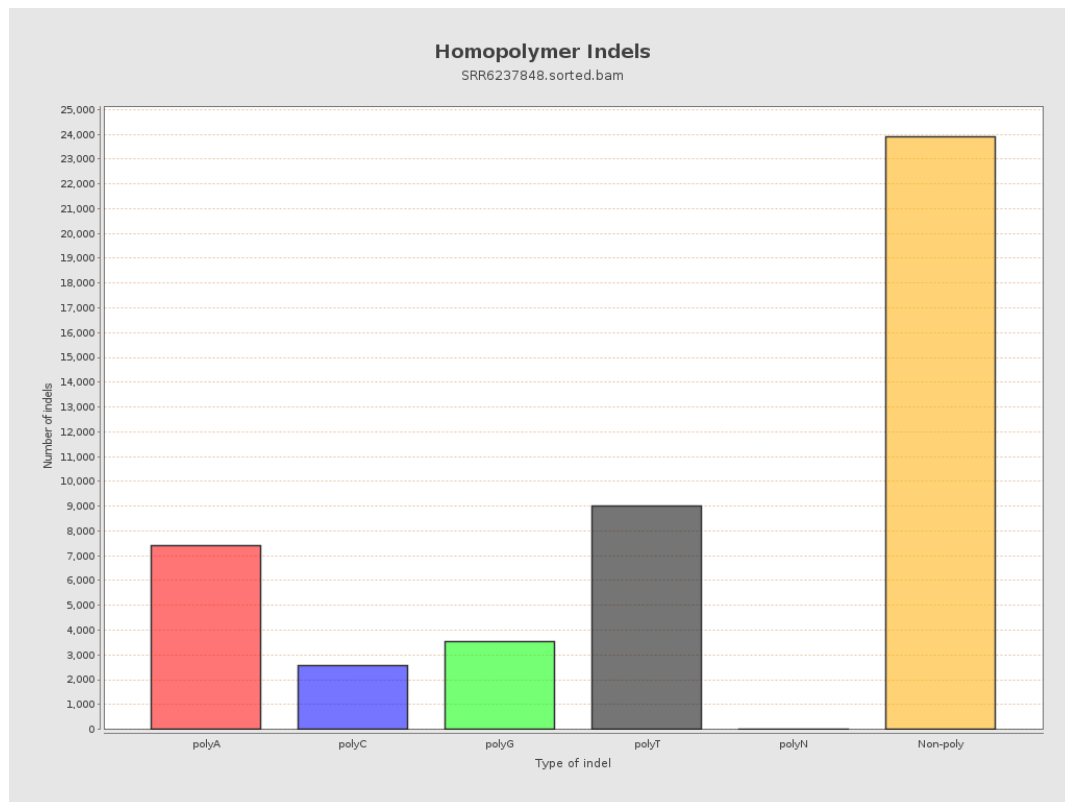
9. Results : Mapped Reads GC-content Distribution



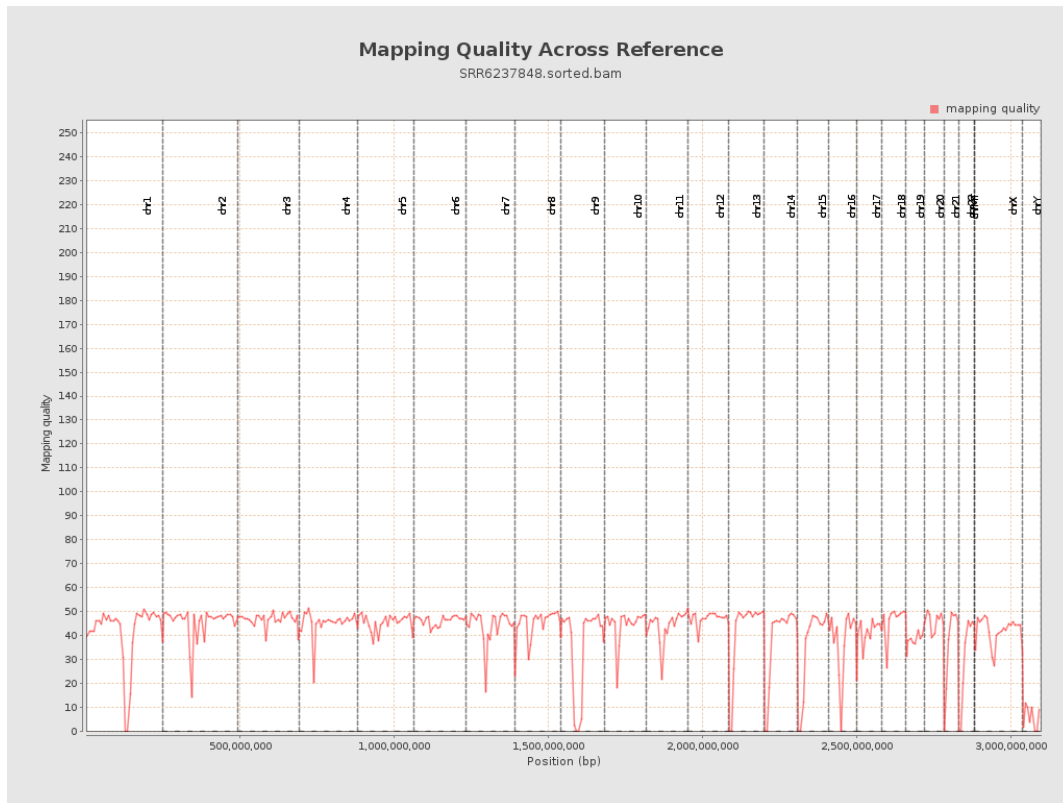
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

