

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:40:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237789.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_SRR6237789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:40:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,622,921
Mapped reads	2,379,762 / 90.73%
Unmapped reads	243,159 / 9.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,312 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	100,503 / 3.83%
Duplication rate	2.45%
Clipped reads	1,256,954 / 47.92%

2.2. ACGT Content

Number/percentage of A's	39,764,428 / 25.76%
Number/percentage of C's	30,427,666 / 19.71%
Number/percentage of T's	45,838,321 / 29.7%
Number/percentage of G's	38,281,027 / 24.8%
Number/percentage of N's	37,214 / 0.02%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.5605
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2.4. Mapping Quality

Mean Mapping Quality	40
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2.5. Mismatches and indels

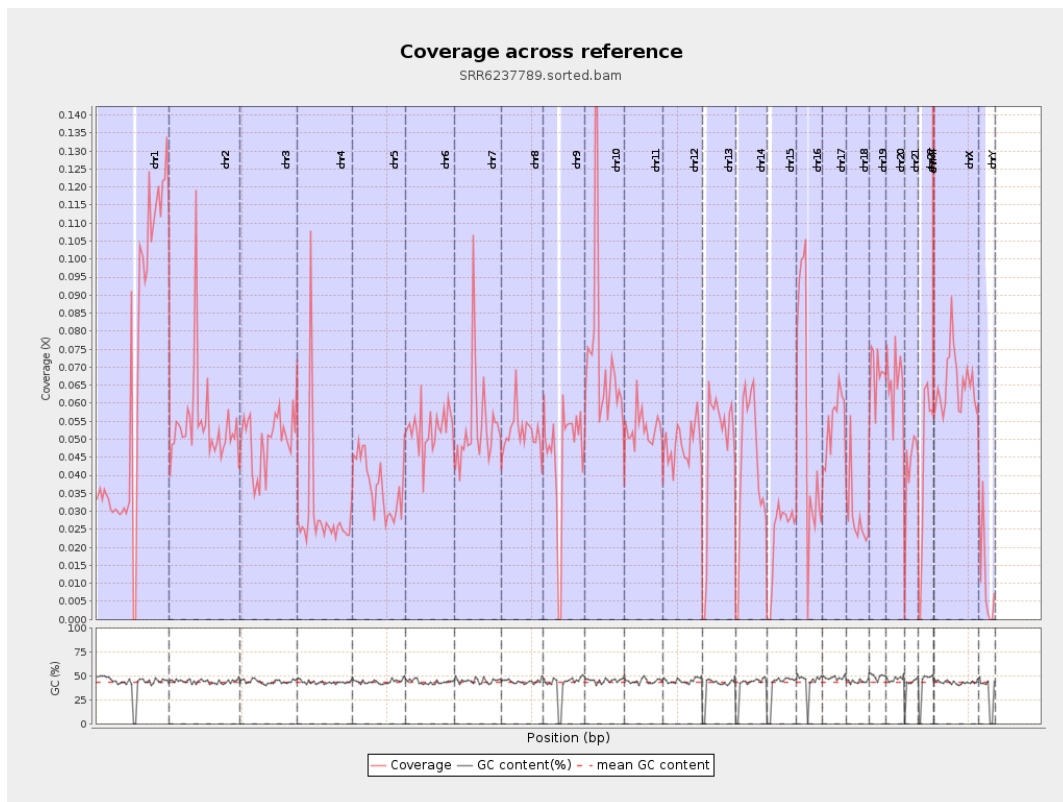
General error rate	0.88%
Mismatches	1,332,004
Insertions	14,155
Mapped reads with at least one insertion	0.59%
Deletions	46,430
Mapped reads with at least one deletion	1.93%
Homopolymer indels	43.97%

2.6. Chromosome stats

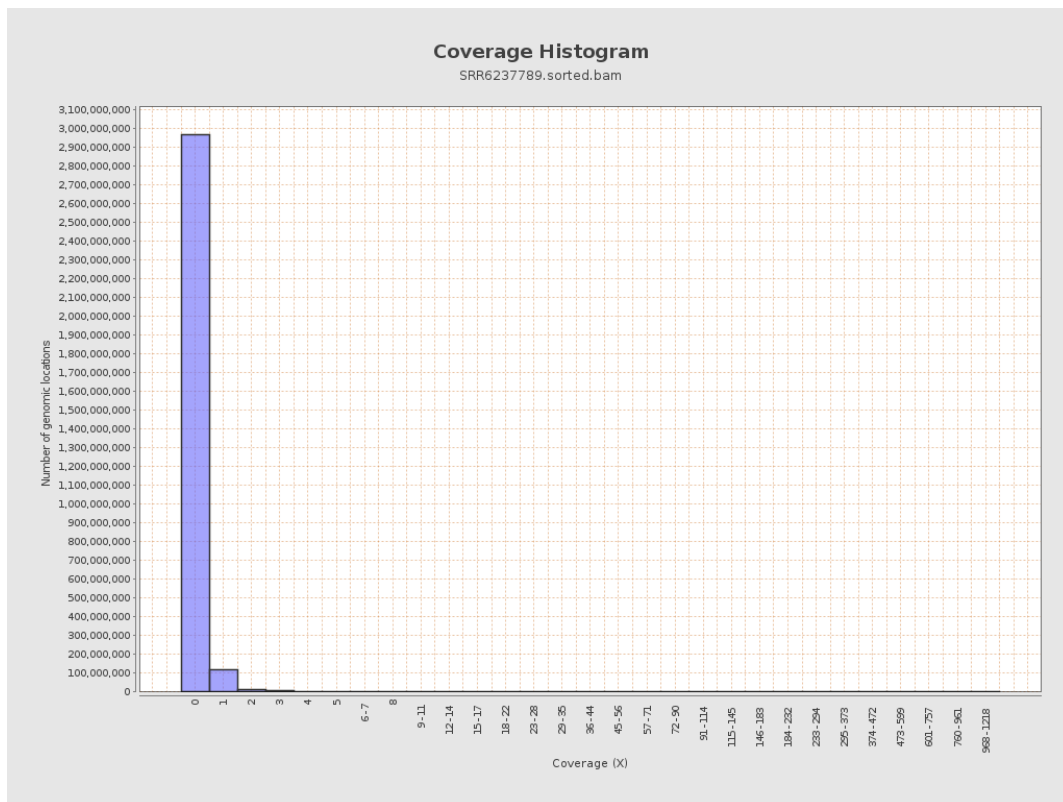
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16388190	0.0657	1.0687
chr2	243199373	13202293	0.0543	0.6372
chr3	198022430	9837827	0.0497	0.2872
chr4	191154276	5516863	0.0289	0.3623
chr5	180915260	6736800	0.0372	0.2216
chr6	171115067	9017599	0.0527	0.3391
chr7	159138663	8605785	0.0541	0.7599

chr8	146364022	7576528	0.0518	0.3807
chr9	141213431	6403190	0.0453	0.4814
chr10	135534747	9803831	0.0723	0.9857
chr11	135006516	7100955	0.0526	0.4623
chr12	133851895	6536974	0.0488	0.2557
chr13	115169878	5464612	0.0474	0.2445
chr14	107349540	4567880	0.0426	0.2899
chr15	102531392	2374043	0.0232	0.1737
chr16	90354753	4957854	0.0549	0.3749
chr17	81195210	4431318	0.0546	0.3541
chr18	78077248	2247227	0.0288	0.8861
chr19	59128983	4028035	0.0681	0.8077
chr20	63025520	4160468	0.066	0.3286
chr21	48129895	2010656	0.0418	0.3394
chr22	51304566	2195862	0.0428	0.2364
chrMT	16571	484930	29.2638	20.0744
chrX	155270560	10144149	0.0653	0.3443
chrY	59373566	634856	0.0107	0.3526

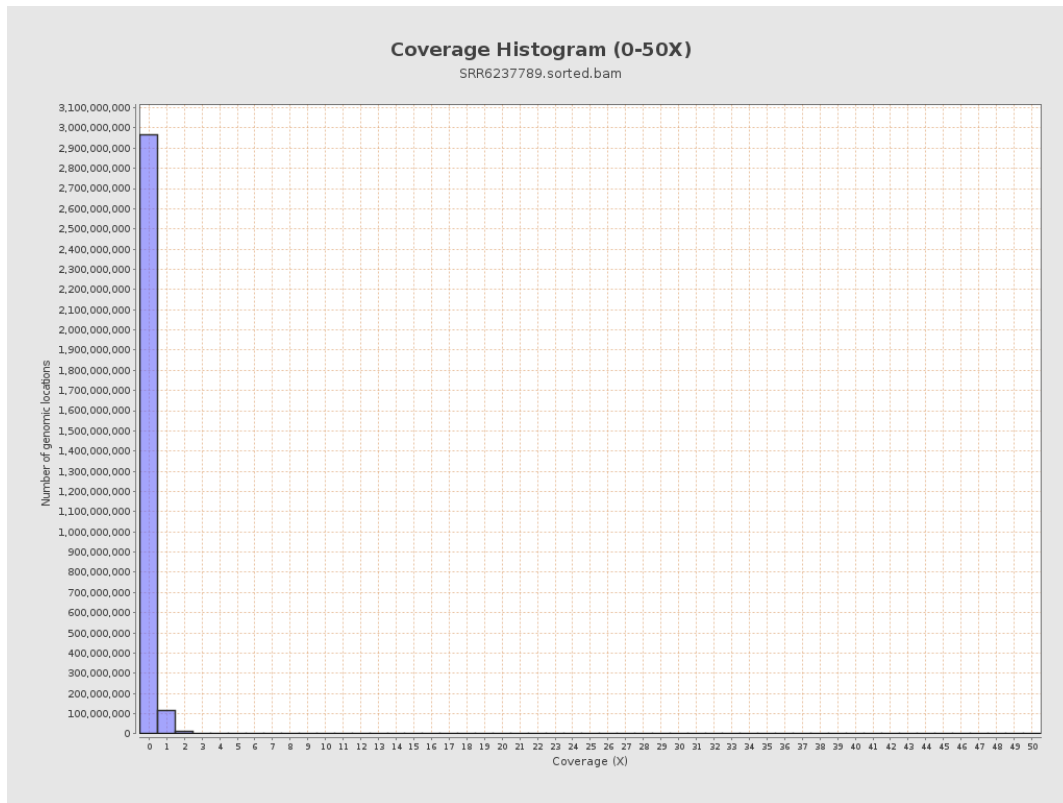
3. Results : Coverage across reference



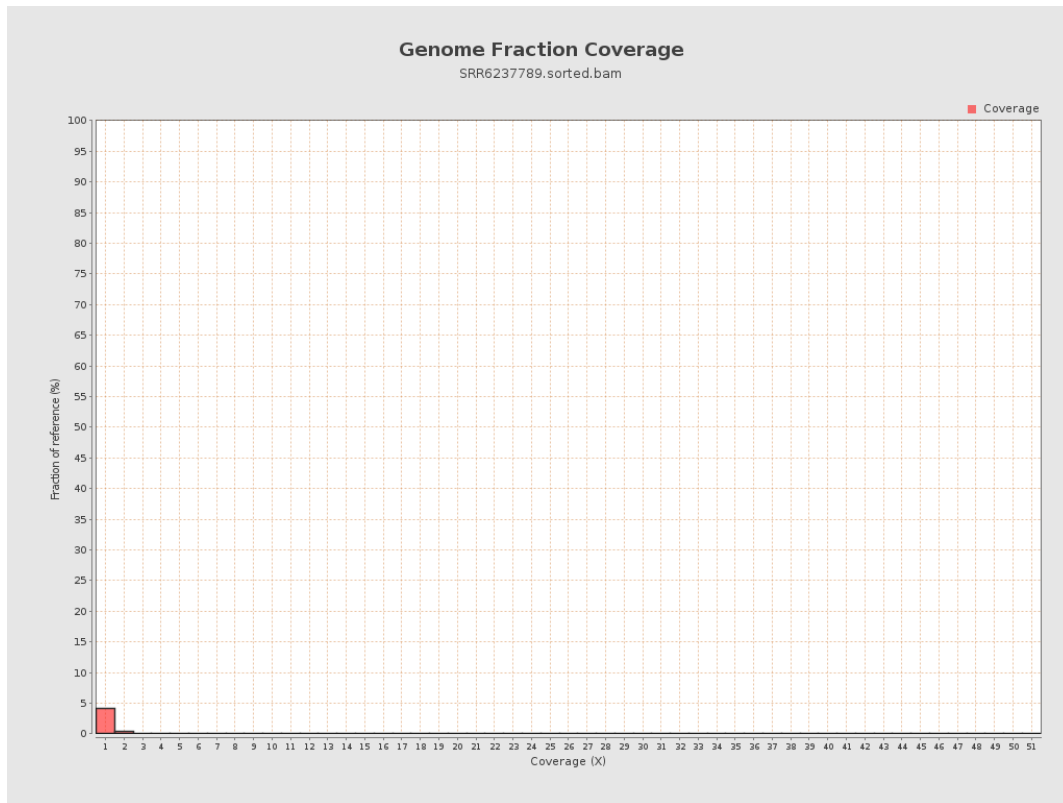
4. Results : Coverage Histogram



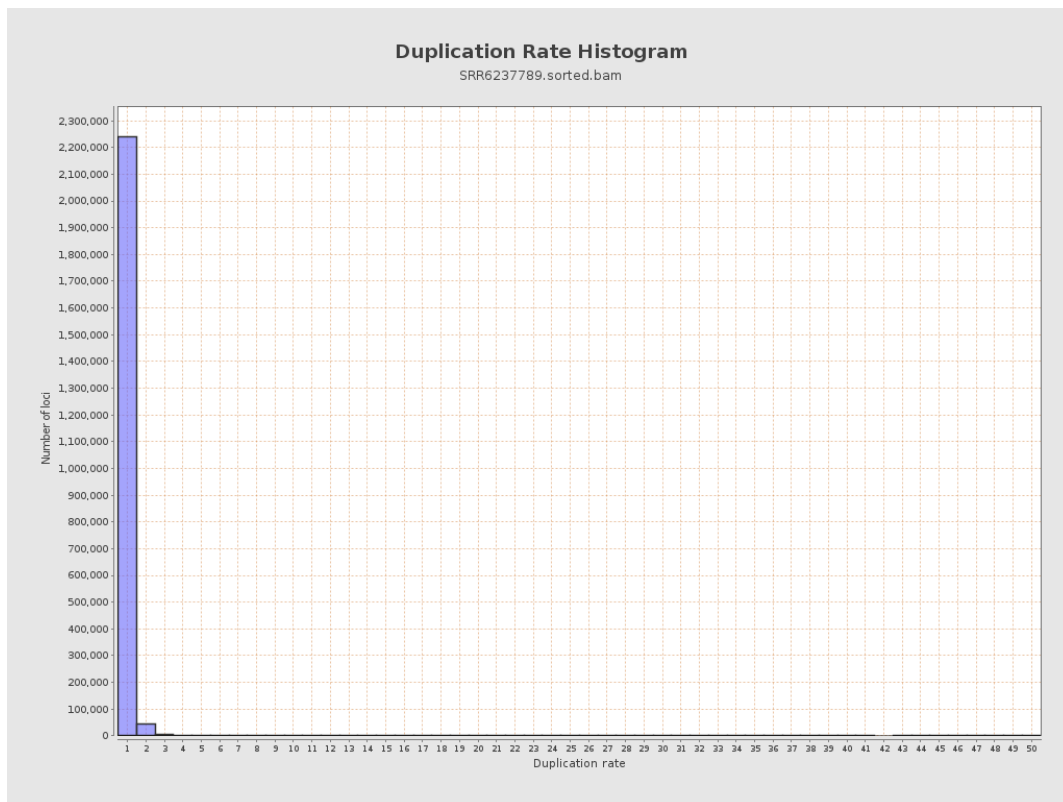
5. Results : Coverage Histogram (0-50X)



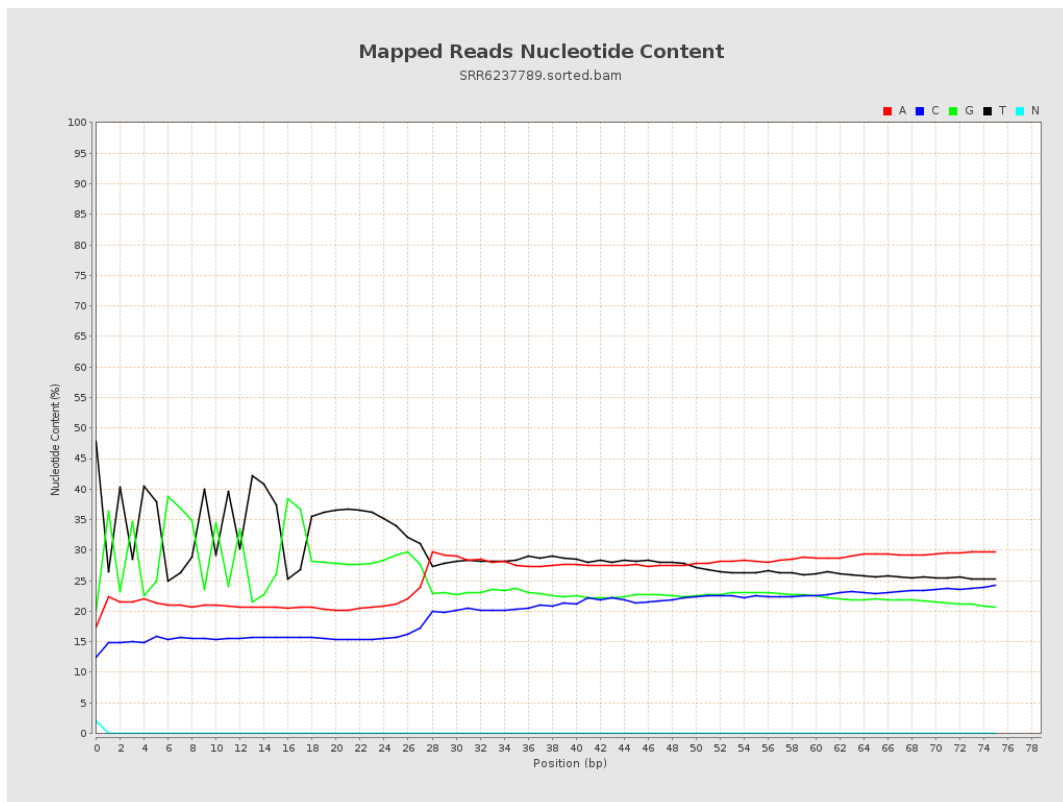
6. Results : Genome Fraction Coverage



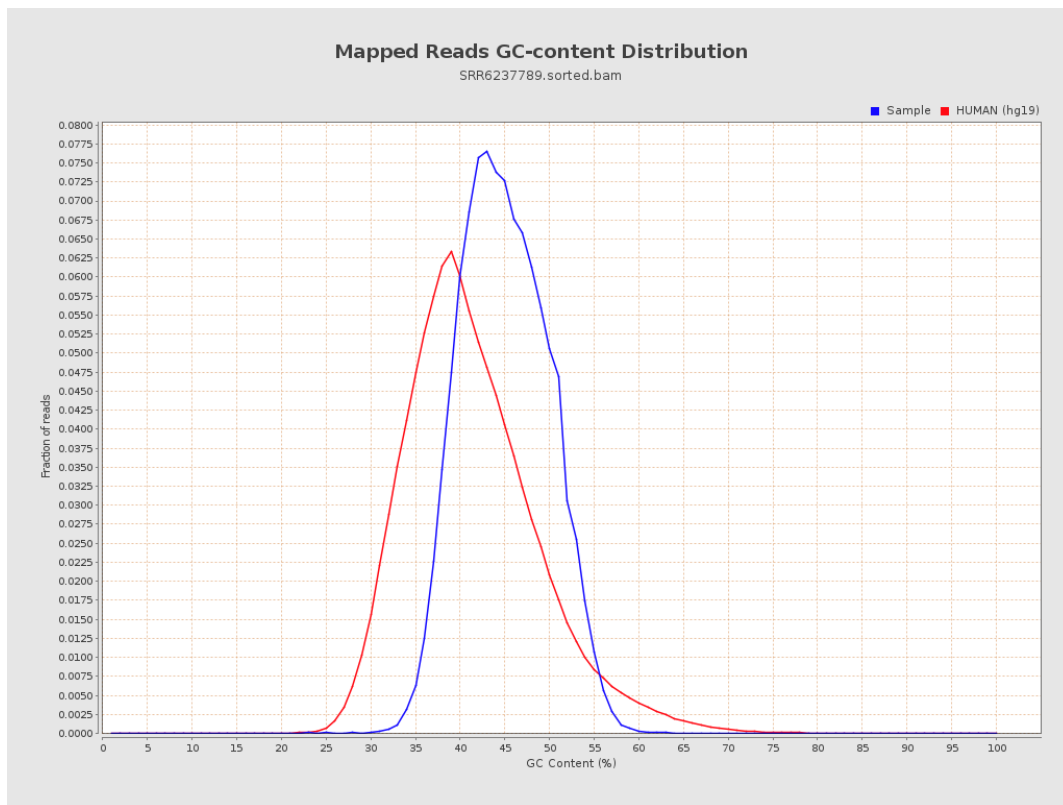
7. Results : Duplication Rate Histogram



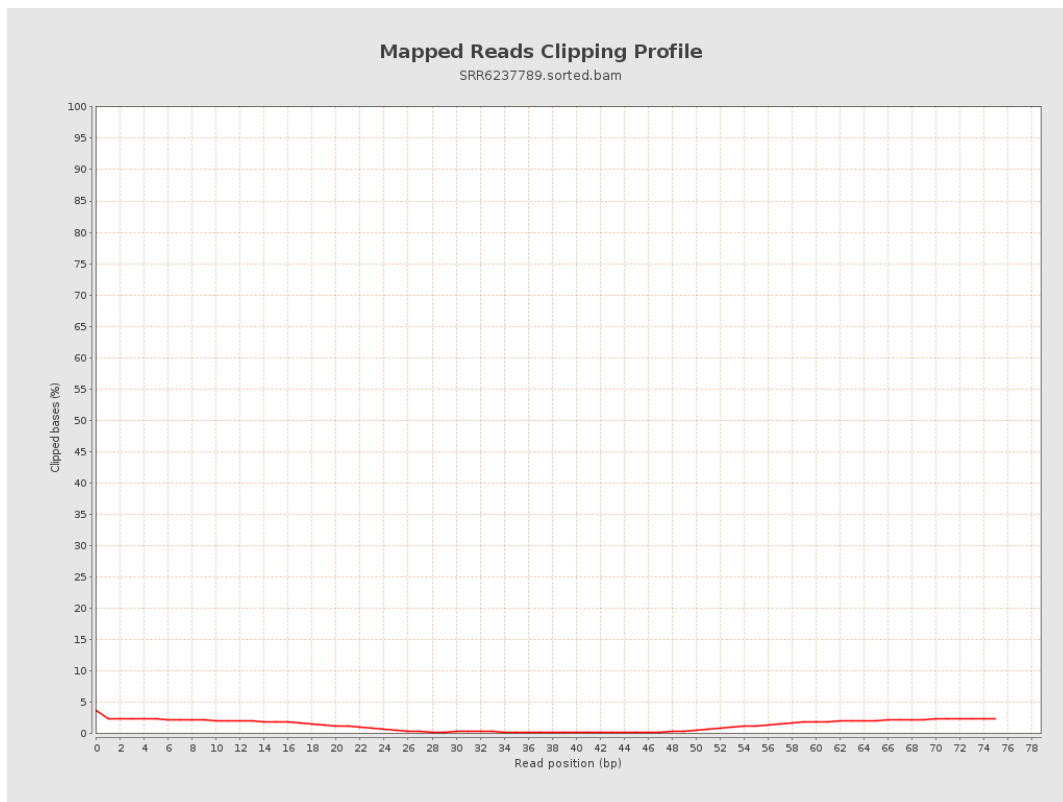
8. Results : Mapped Reads Nucleotide Content



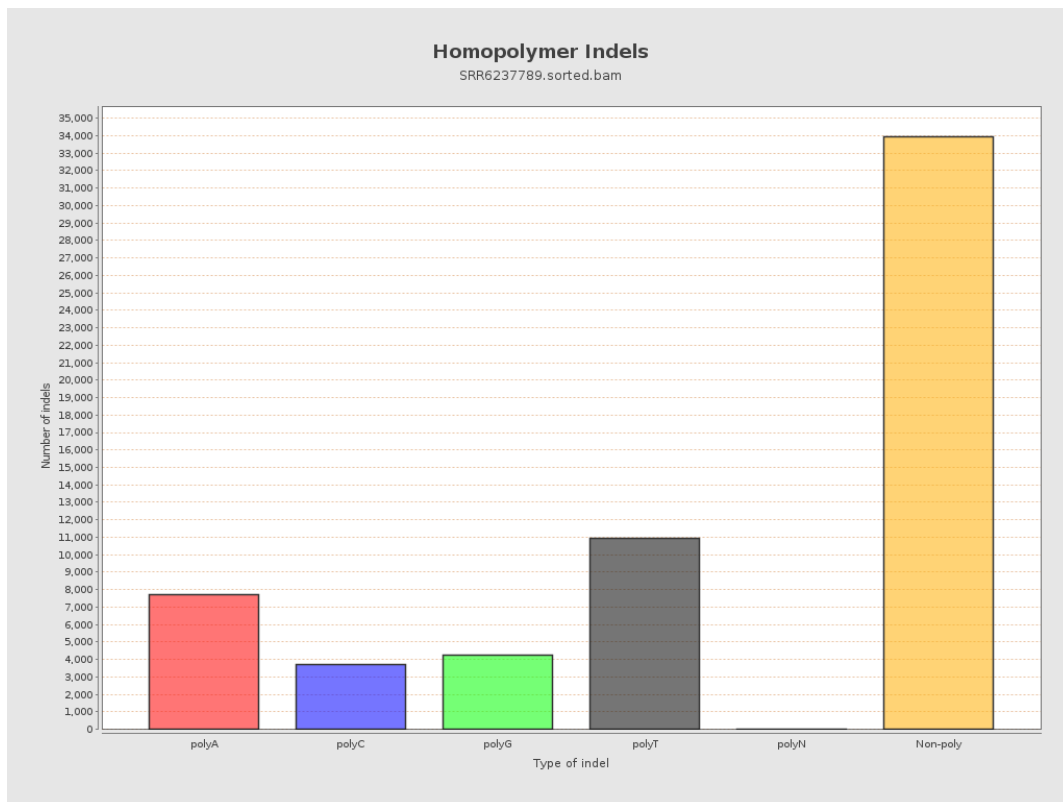
9. Results : Mapped Reads GC-content Distribution



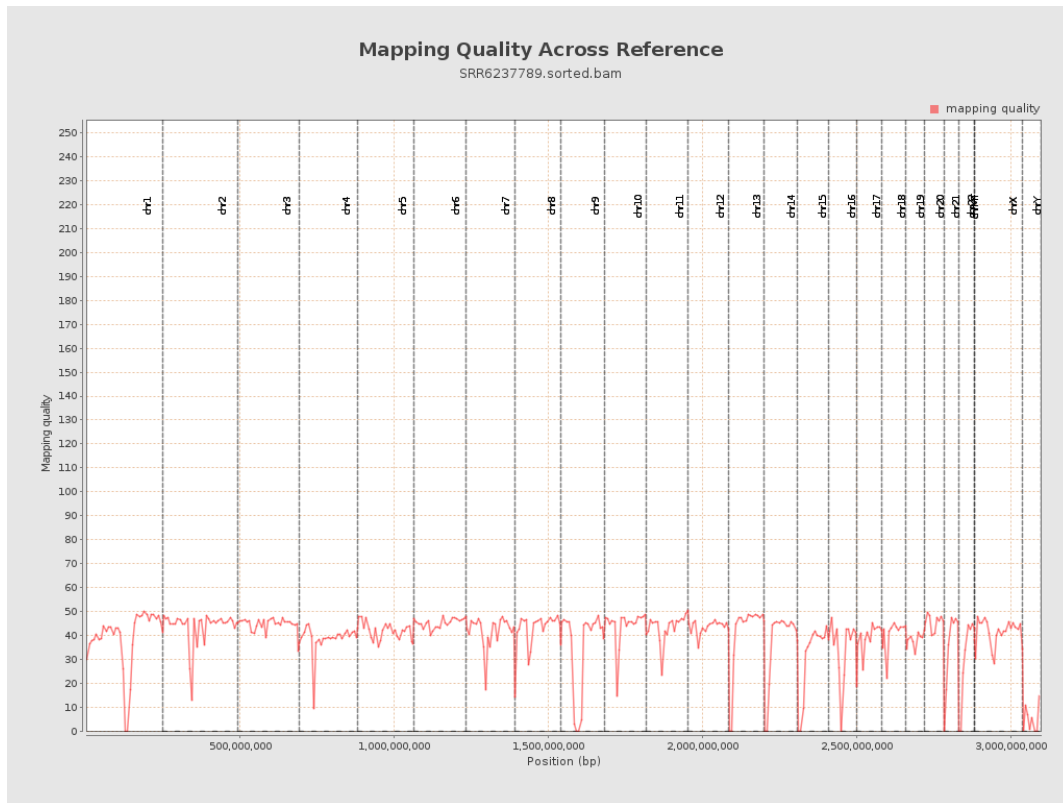
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

