

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:48:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237809.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_SRR6237809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:48:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,221,608
Mapped reads	1,863,632 / 83.89%
Unmapped reads	357,976 / 16.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,297 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	52,005 / 2.34%
Duplication rate	1.7%
Clipped reads	1,088,532 / 49%

2.2. ACGT Content

Number/percentage of A's	31,460,348 / 26.83%
Number/percentage of C's	23,286,907 / 19.86%
Number/percentage of T's	34,197,433 / 29.16%
Number/percentage of G's	28,227,427 / 24.07%
Number/percentage of N's	104,231 / 0.09%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0379

Standard Deviation	0.3701
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2.4. Mapping Quality

Mean Mapping Quality	40.96
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2.5. Mismatches and indels

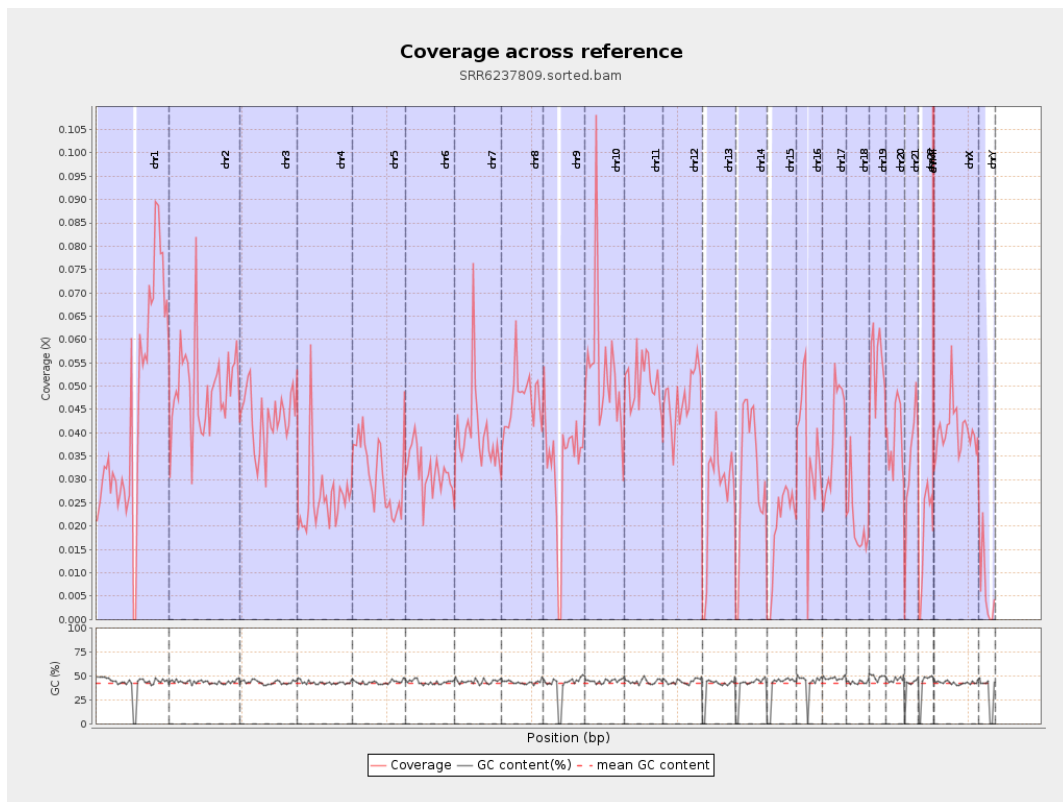
General error rate	0.82%
Mismatches	937,985
Insertions	10,432
Mapped reads with at least one insertion	0.55%
Deletions	31,527
Mapped reads with at least one deletion	1.67%
Homopolymer indels	44.18%

2.6. Chromosome stats

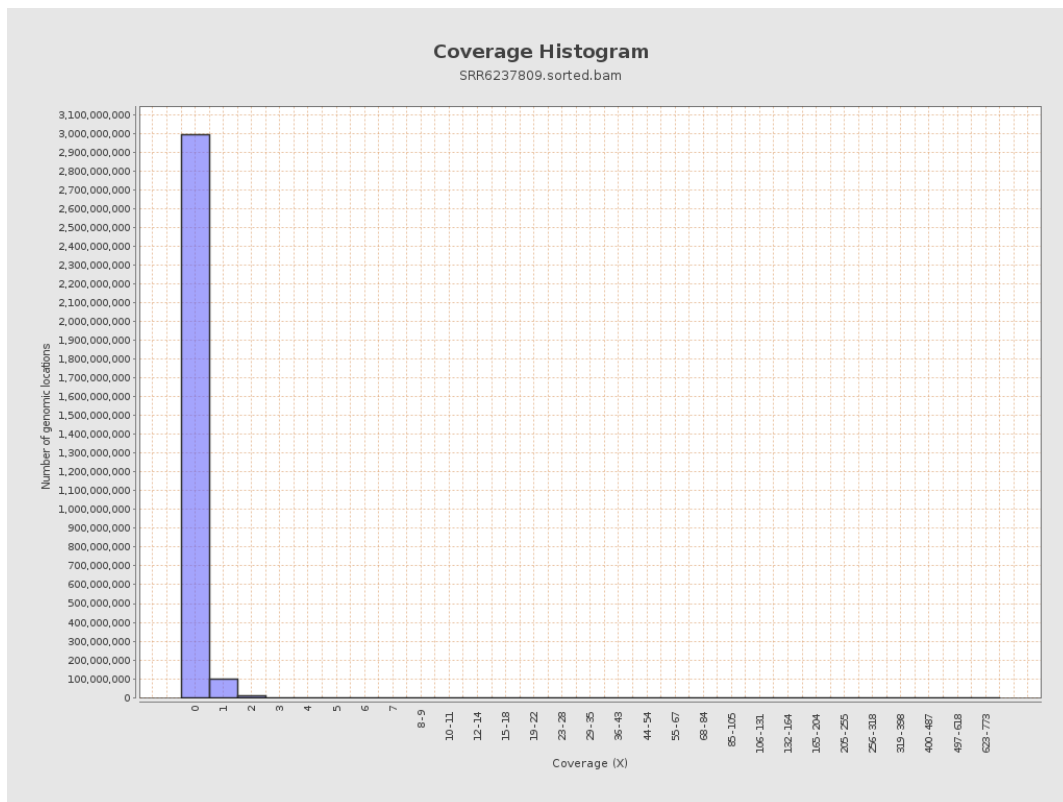
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11107006	0.0446	0.6844
chr2	243199373	12014775	0.0494	0.4211
chr3	198022430	8554831	0.0432	0.234
chr4	191154276	4909120	0.0257	0.2337
chr5	180915260	5640304	0.0312	0.1912
chr6	171115067	5421399	0.0317	0.2407
chr7	159138663	6392506	0.0402	0.5449

chr8	146364022	6856402	0.0468	0.3274
chr9	141213431	4602826	0.0326	0.3205
chr10	135534747	7178328	0.053	0.5574
chr11	135006516	6849521	0.0507	0.3719
chr12	133851895	6324864	0.0473	0.2395
chr13	115169878	3108518	0.027	0.1752
chr14	107349540	3341967	0.0311	0.2277
chr15	102531392	1997360	0.0195	0.1501
chr16	90354753	3278710	0.0363	0.2514
chr17	81195210	3218585	0.0396	0.262
chr18	78077248	1605979	0.0206	0.5365
chr19	59128983	3232681	0.0547	0.5059
chr20	63025520	2430049	0.0386	0.2289
chr21	48129895	1619668	0.0337	0.2454
chr22	51304566	935514	0.0182	0.1438
chrMT	16571	47488	2.8657	2.4303
chrX	155270560	6279107	0.0404	0.256
chrY	59373566	382529	0.0064	0.1852

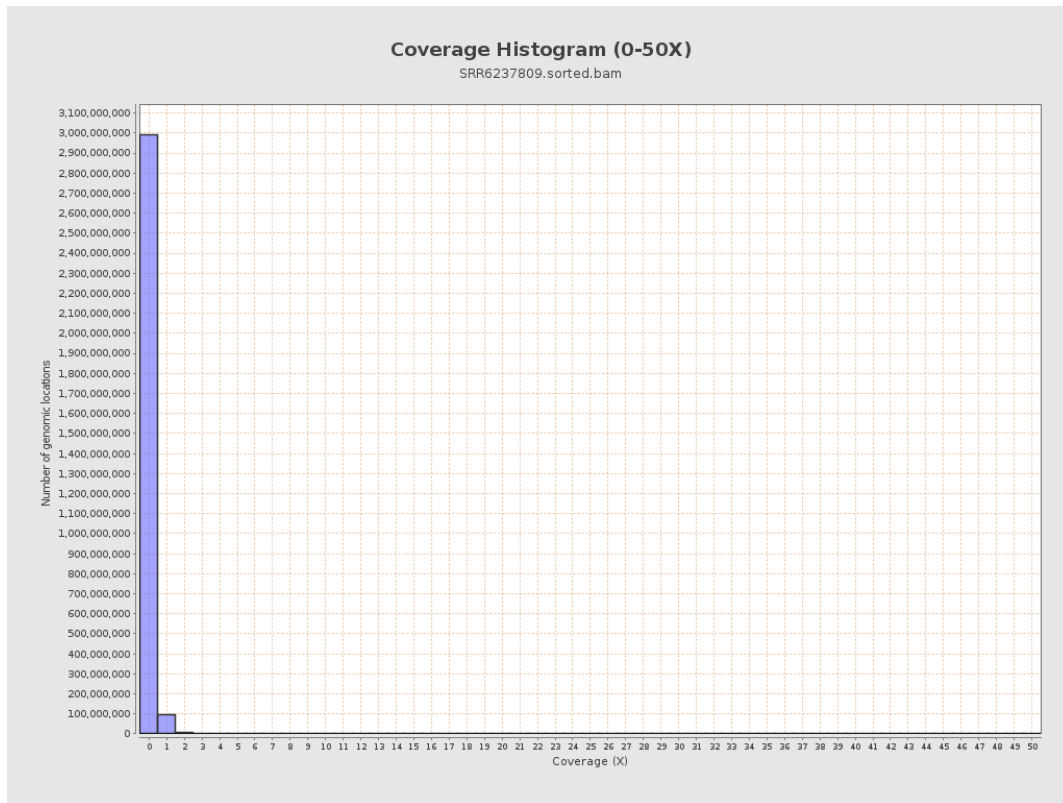
3. Results : Coverage across reference



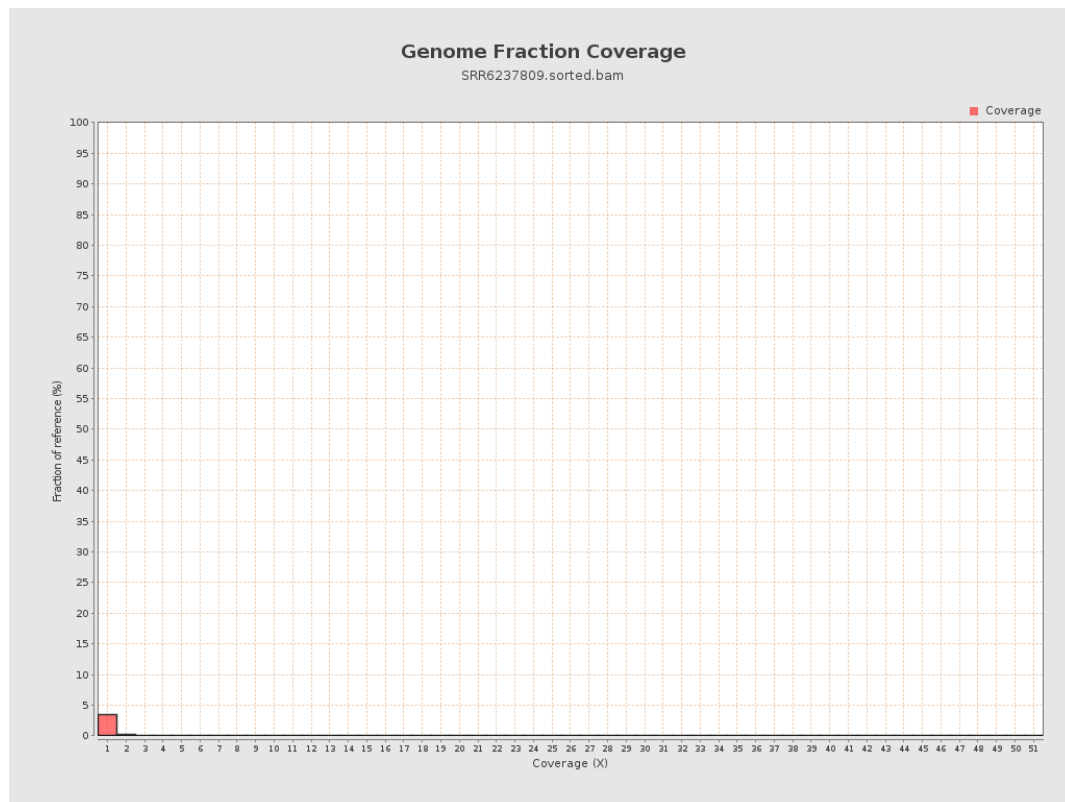
4. Results : Coverage Histogram



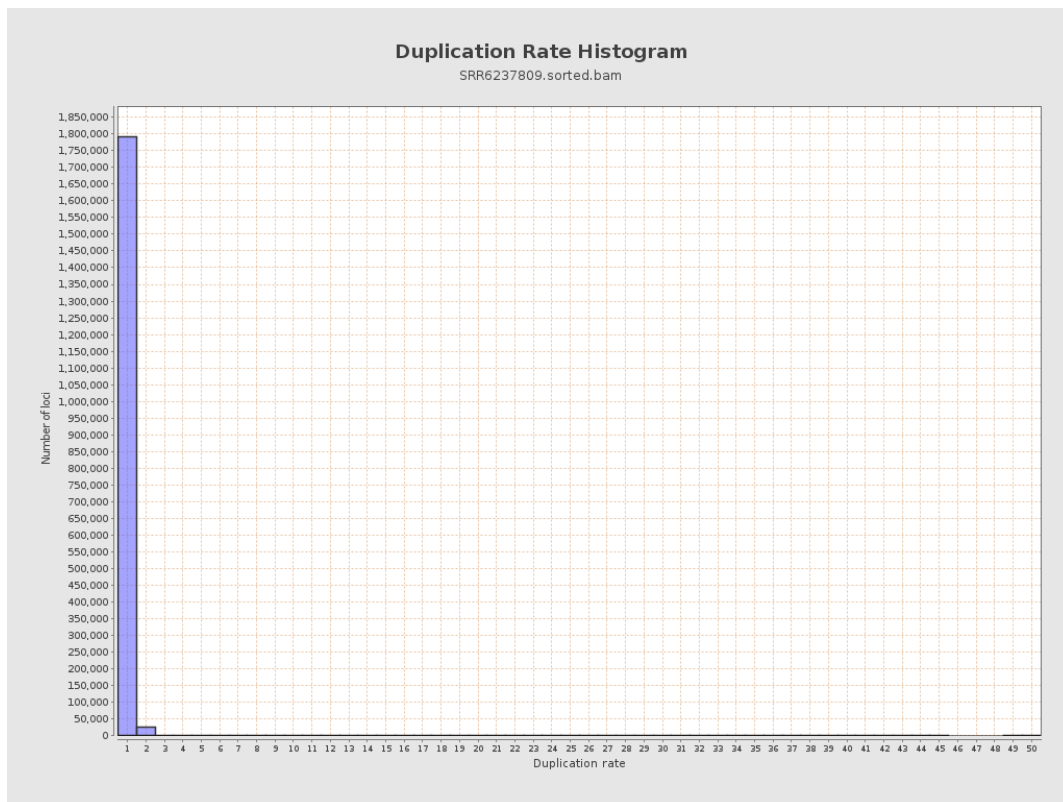
5. Results : Coverage Histogram (0-50X)



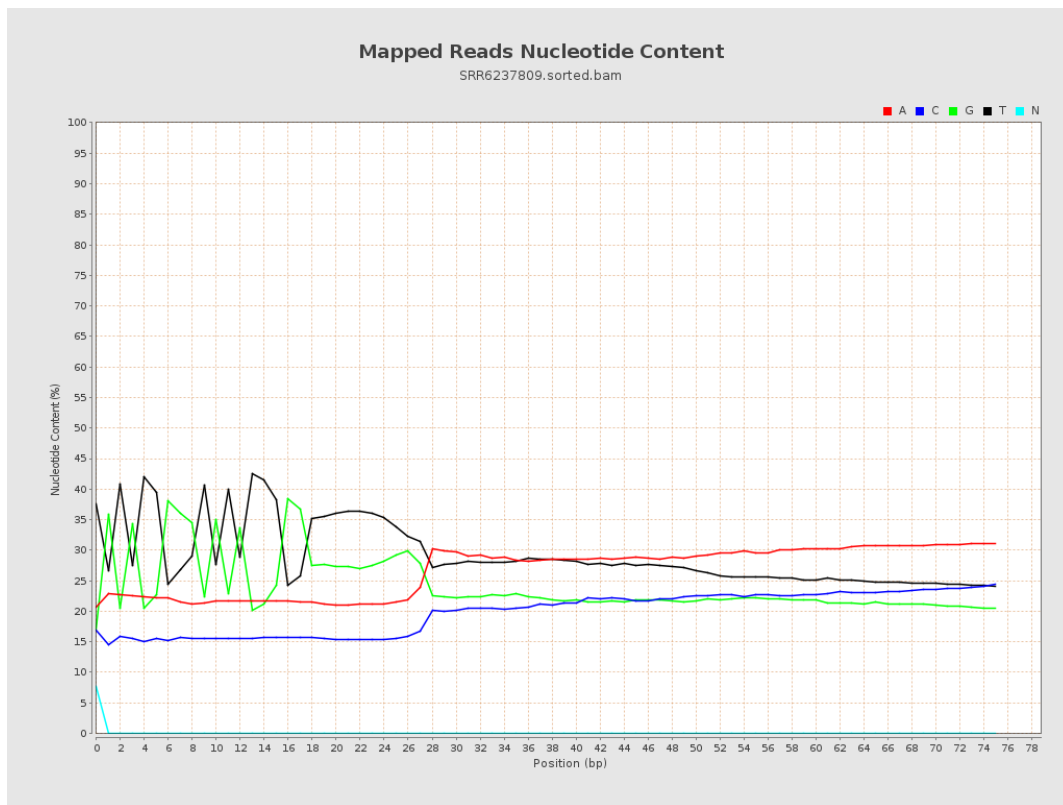
6. Results : Genome Fraction Coverage



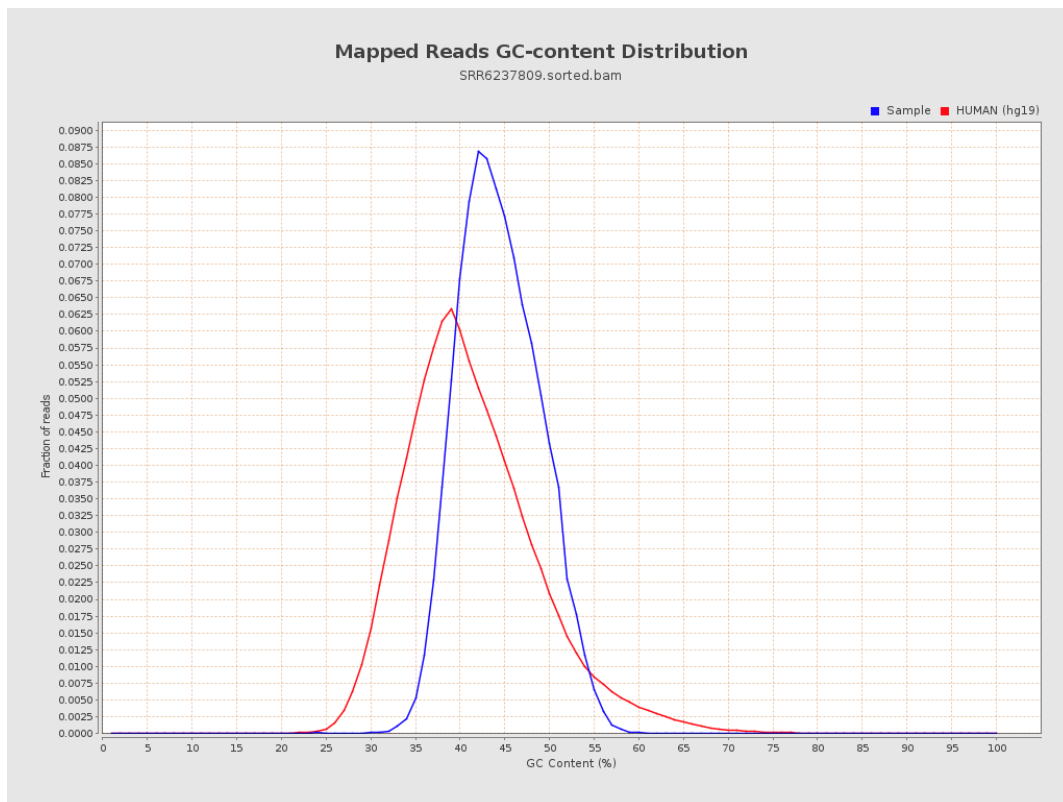
7. Results : Duplication Rate Histogram



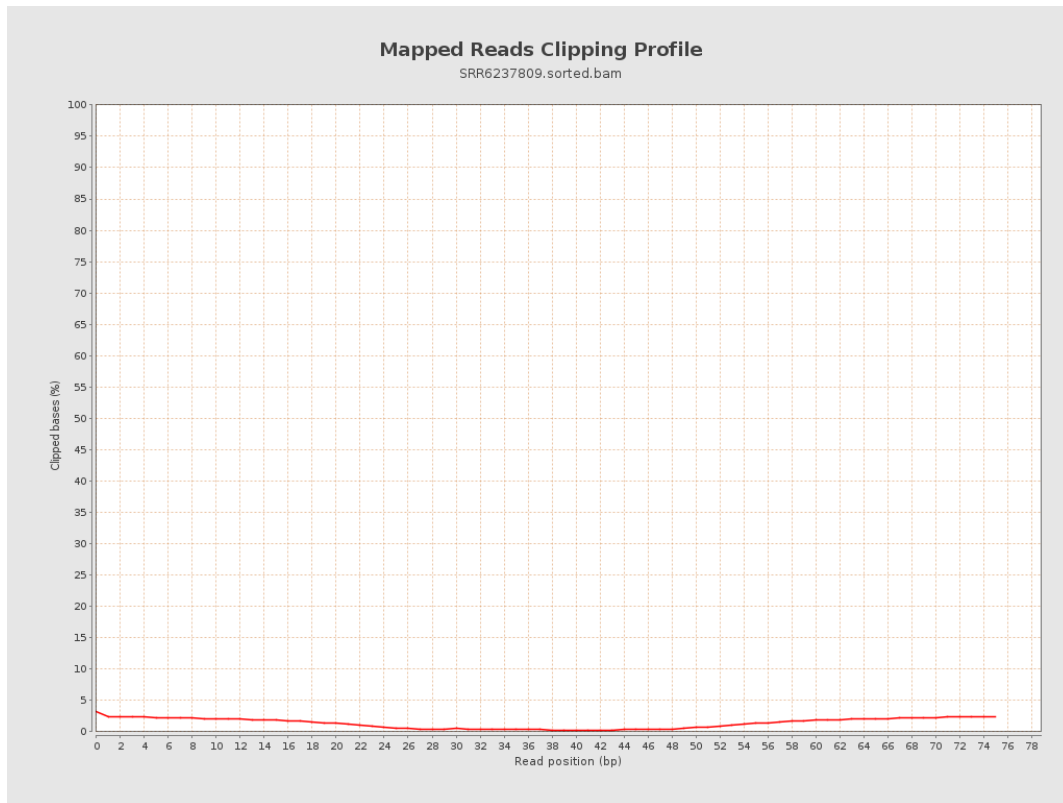
8. Results : Mapped Reads Nucleotide Content



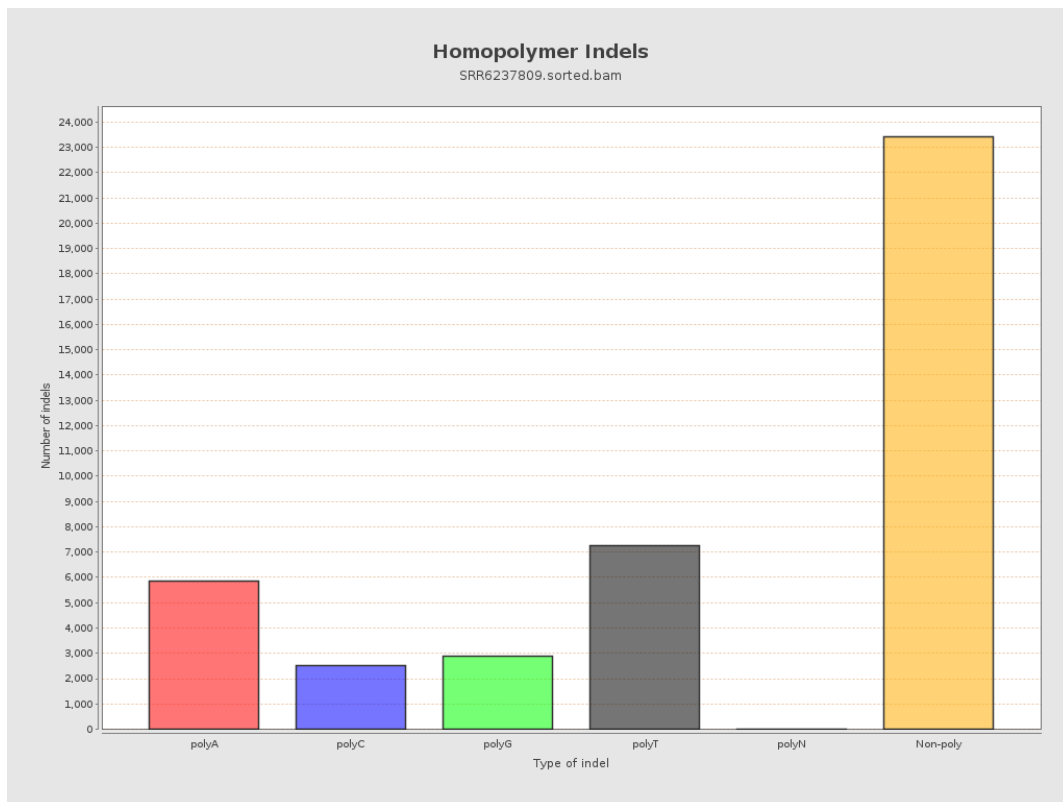
9. Results : Mapped Reads GC-content Distribution



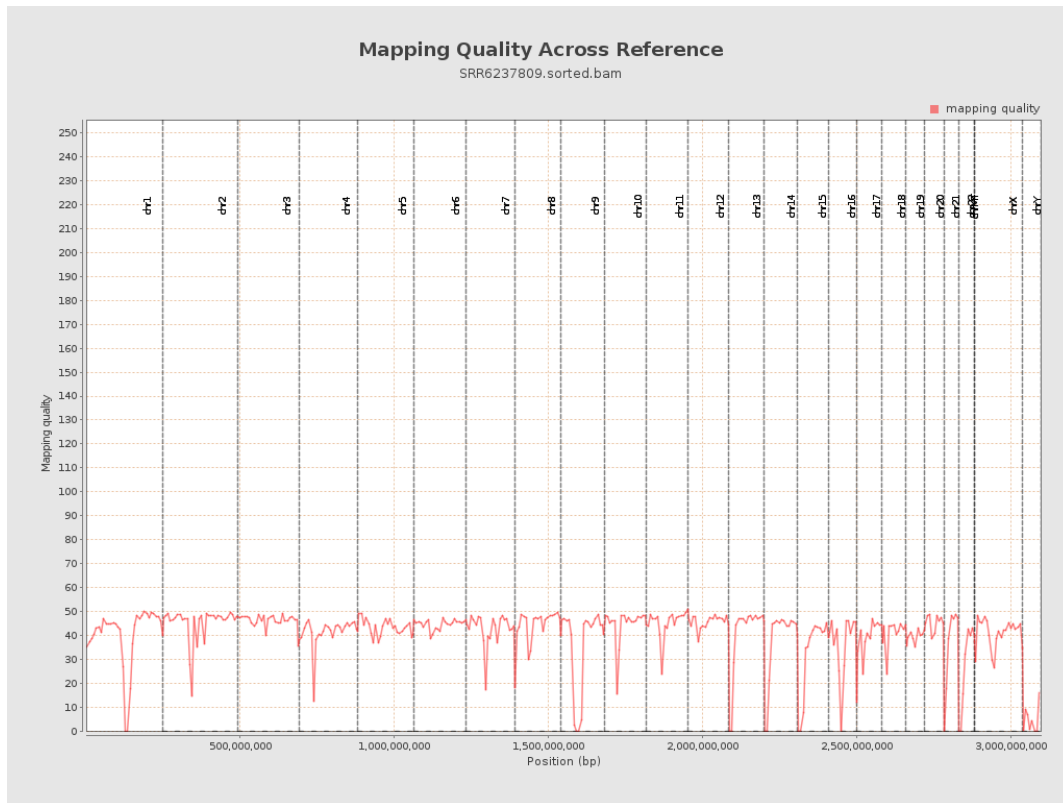
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

