

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237600.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_SRR6237600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:59:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,545,262
Mapped reads	1,255,253 / 81.23%
Unmapped reads	290,009 / 18.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,224 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	71,061 / 4.6%
Duplication rate	3.86%
Clipped reads	772,840 / 50.01%

2.2. ACGT Content

Number/percentage of A's	20,188,452 / 25.61%
Number/percentage of C's	14,441,848 / 18.32%
Number/percentage of T's	24,104,971 / 30.58%
Number/percentage of G's	20,040,151 / 25.42%
Number/percentage of N's	57,265 / 0.07%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2779
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2.4. Mapping Quality

Mean Mapping Quality	39.8
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2.5. Mismatches and indels

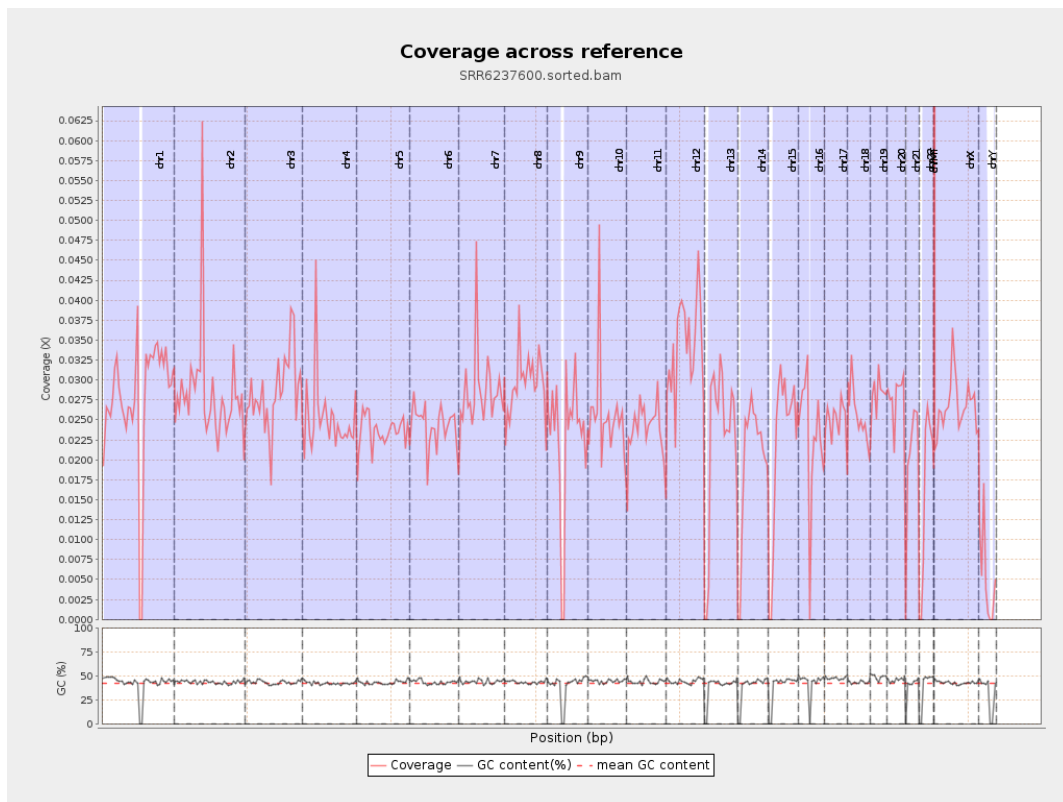
General error rate	1%
Mismatches	771,881
Insertions	7,444
Mapped reads with at least one insertion	0.59%
Deletions	27,790
Mapped reads with at least one deletion	2.19%
Homopolymer indels	46.52%

2.6. Chromosome stats

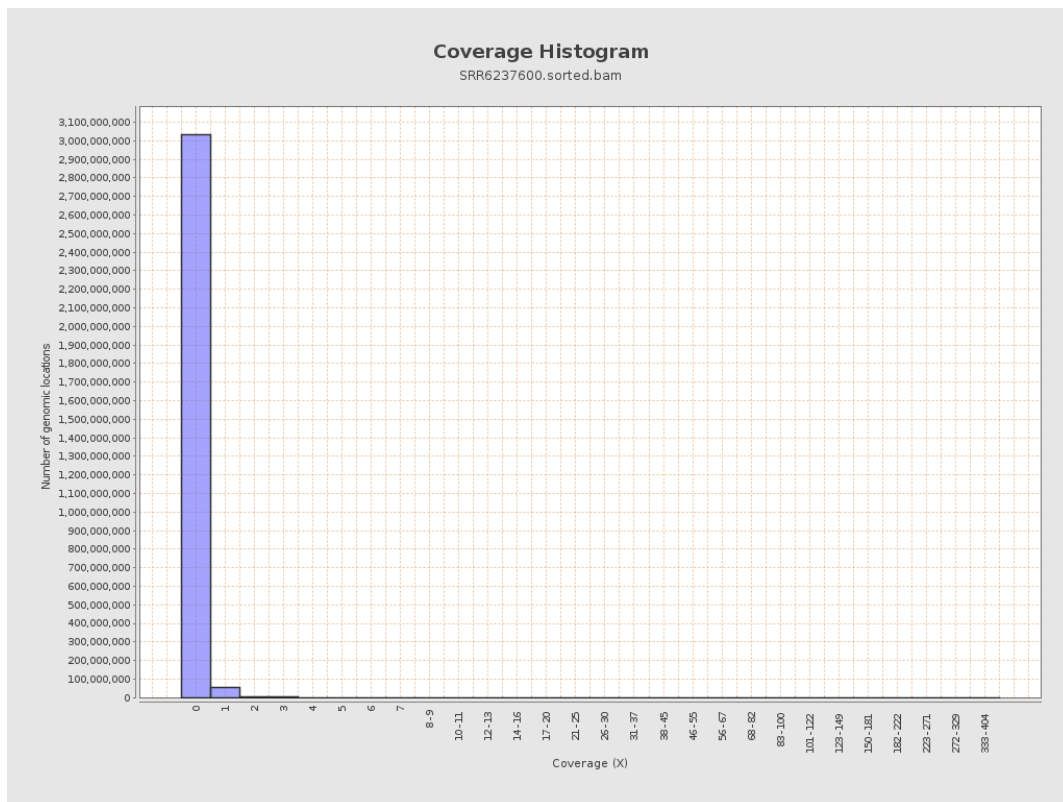
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6899231	0.0277	0.3618
chr2	243199373	6866615	0.0282	0.3954
chr3	198022430	5624570	0.0284	0.2122
chr4	191154276	4791927	0.0251	0.218
chr5	180915260	4293776	0.0237	0.1895
chr6	171115067	4149860	0.0243	0.2114
chr7	159138663	4540554	0.0285	0.4121

chr8	146364022	4314485	0.0295	0.2671
chr9	141213431	3201030	0.0227	0.2982
chr10	135534747	3448960	0.0254	0.2844
chr11	135006516	3262643	0.0242	0.2973
chr12	133851895	4596999	0.0343	0.2409
chr13	115169878	2586501	0.0225	0.1906
chr14	107349540	2135555	0.0199	0.2134
chr15	102531392	2274000	0.0222	0.1941
chr16	90354753	2056282	0.0228	0.2155
chr17	81195210	2032202	0.025	0.218
chr18	78077248	2000469	0.0256	0.418
chr19	59128983	1674222	0.0283	0.2948
chr20	63025520	1728584	0.0274	0.2126
chr21	48129895	1000565	0.0208	0.2008
chr22	51304566	850393	0.0166	0.1643
chrMT	16571	58724	3.5438	3.4503
chrX	155270560	4180907	0.0269	0.2279
chrY	59373566	309539	0.0052	0.138

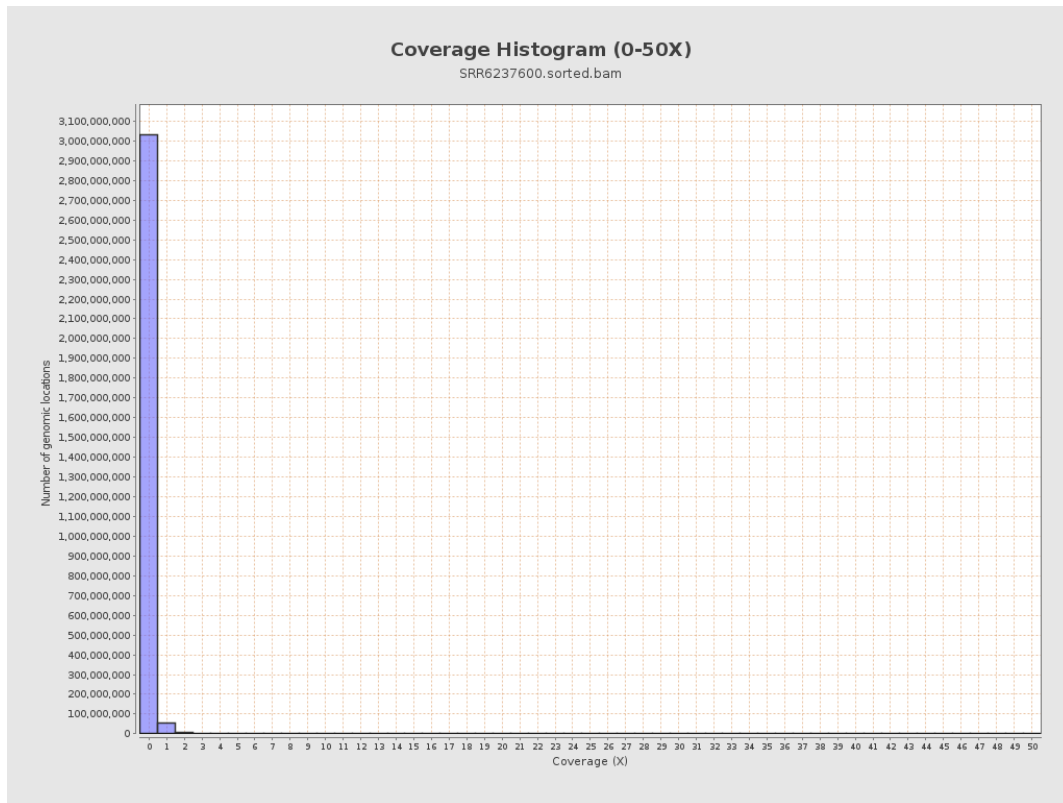
3. Results : Coverage across reference



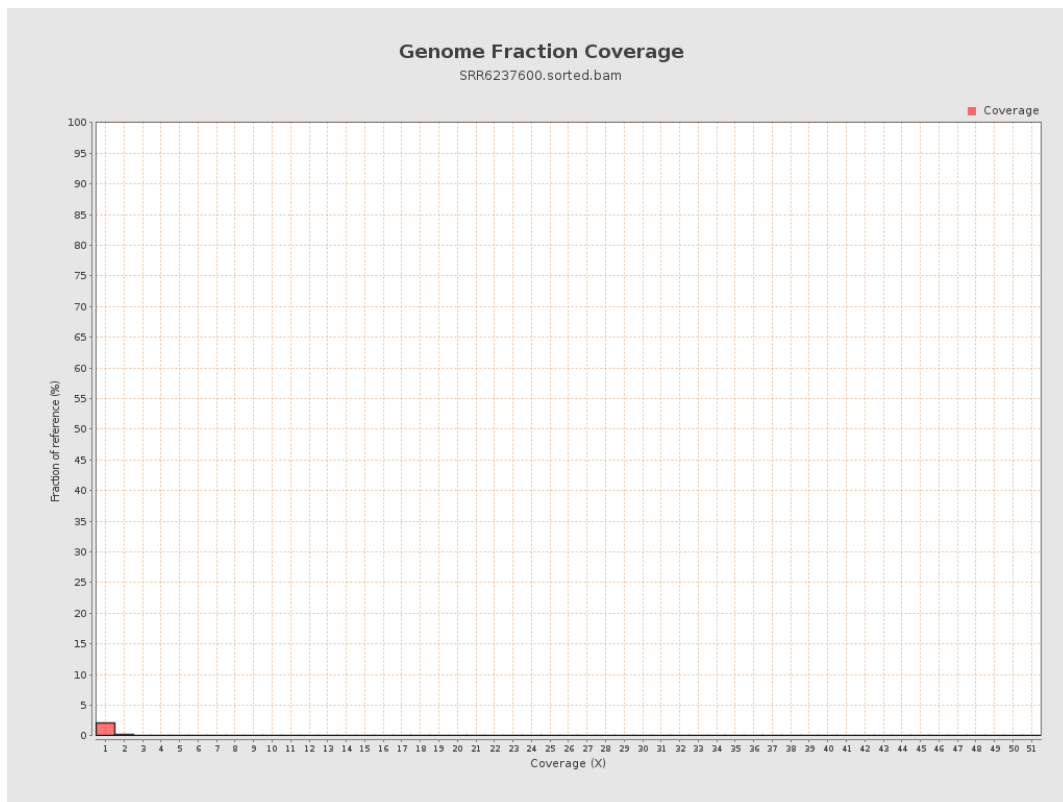
4. Results : Coverage Histogram



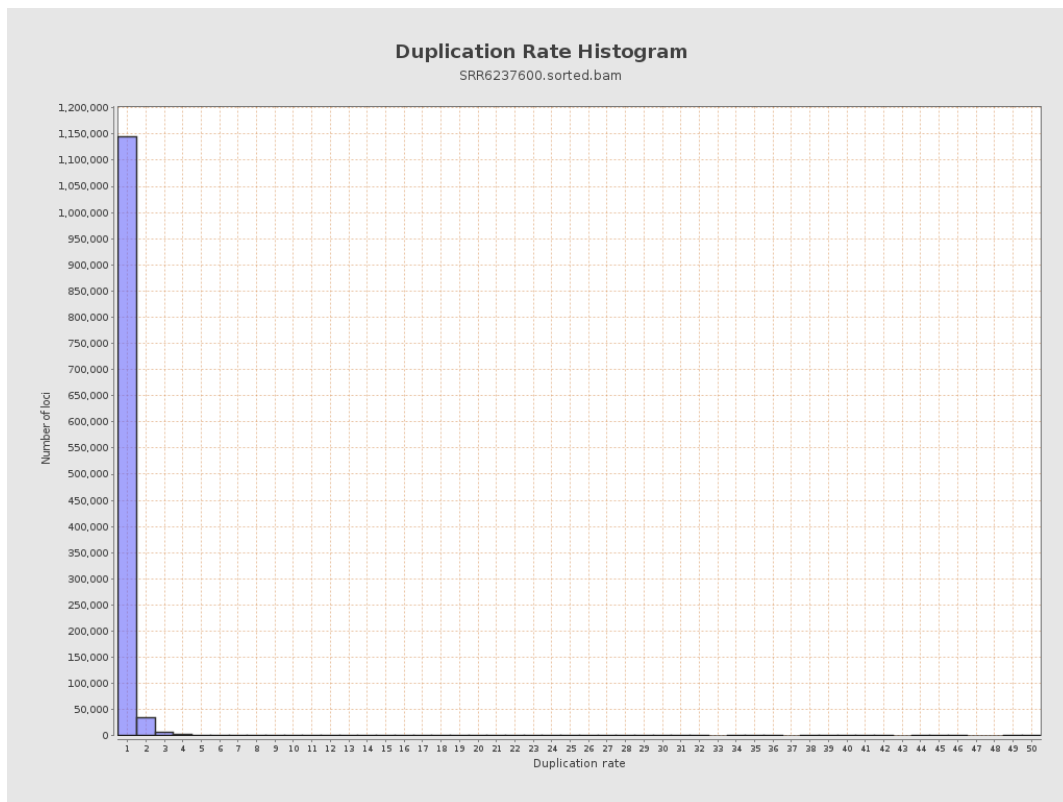
5. Results : Coverage Histogram (0-50X)



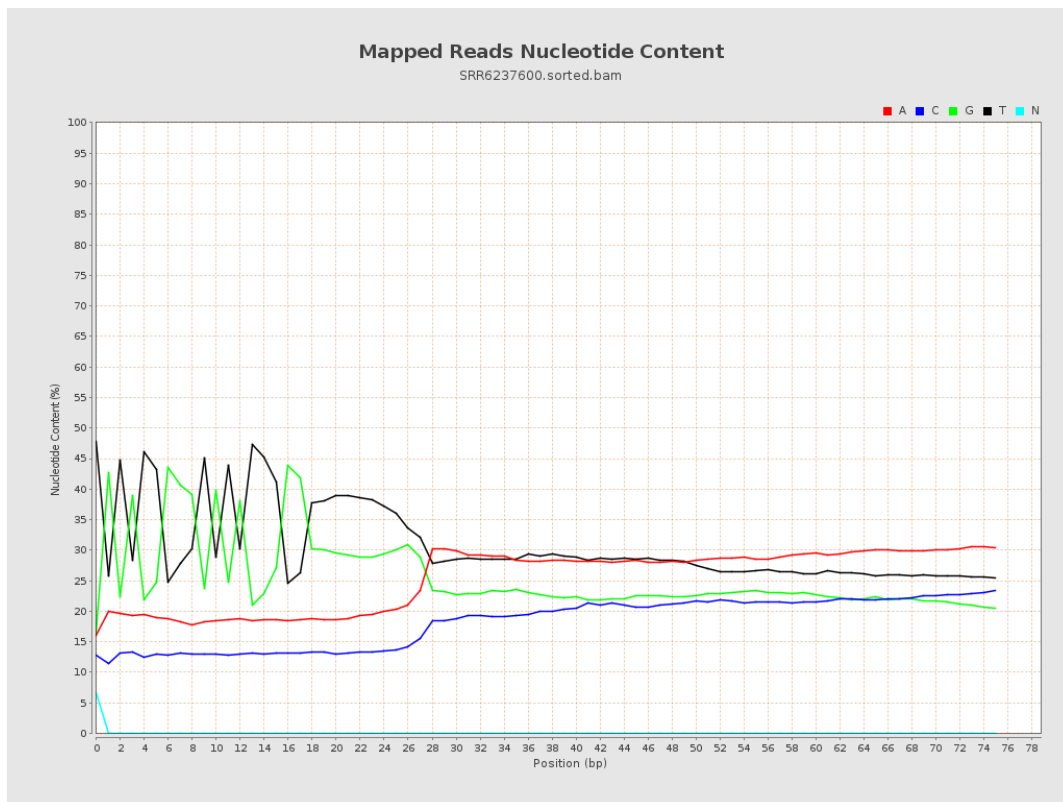
6. Results : Genome Fraction Coverage



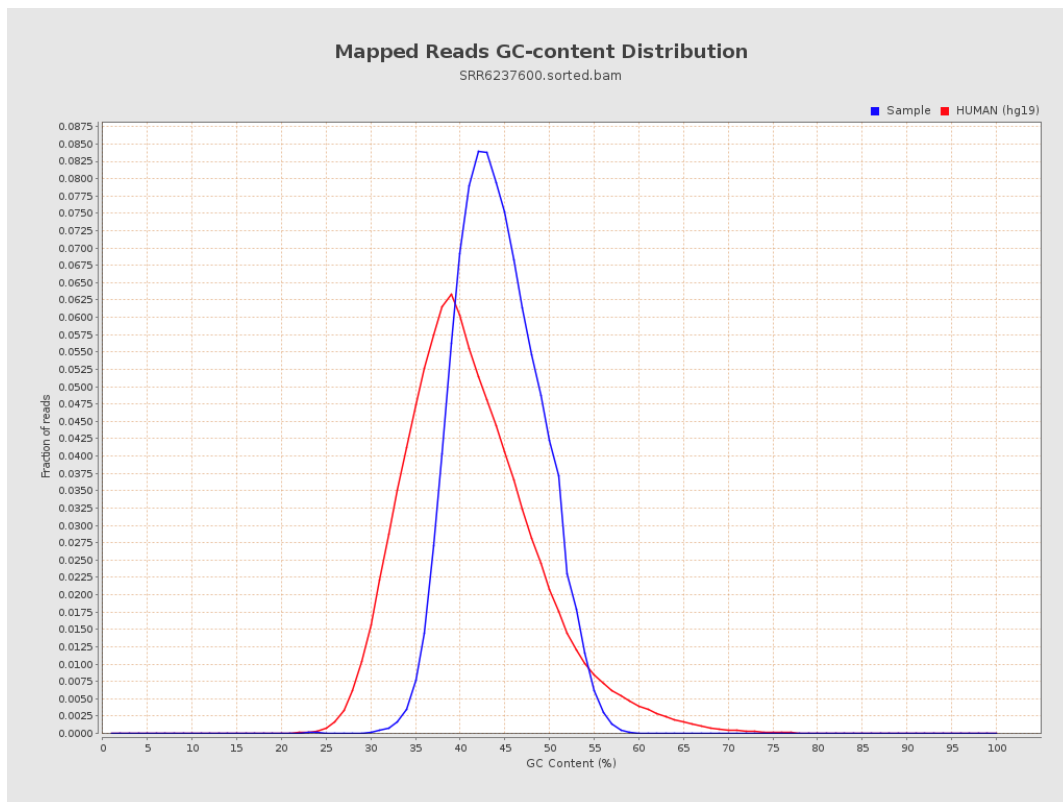
7. Results : Duplication Rate Histogram



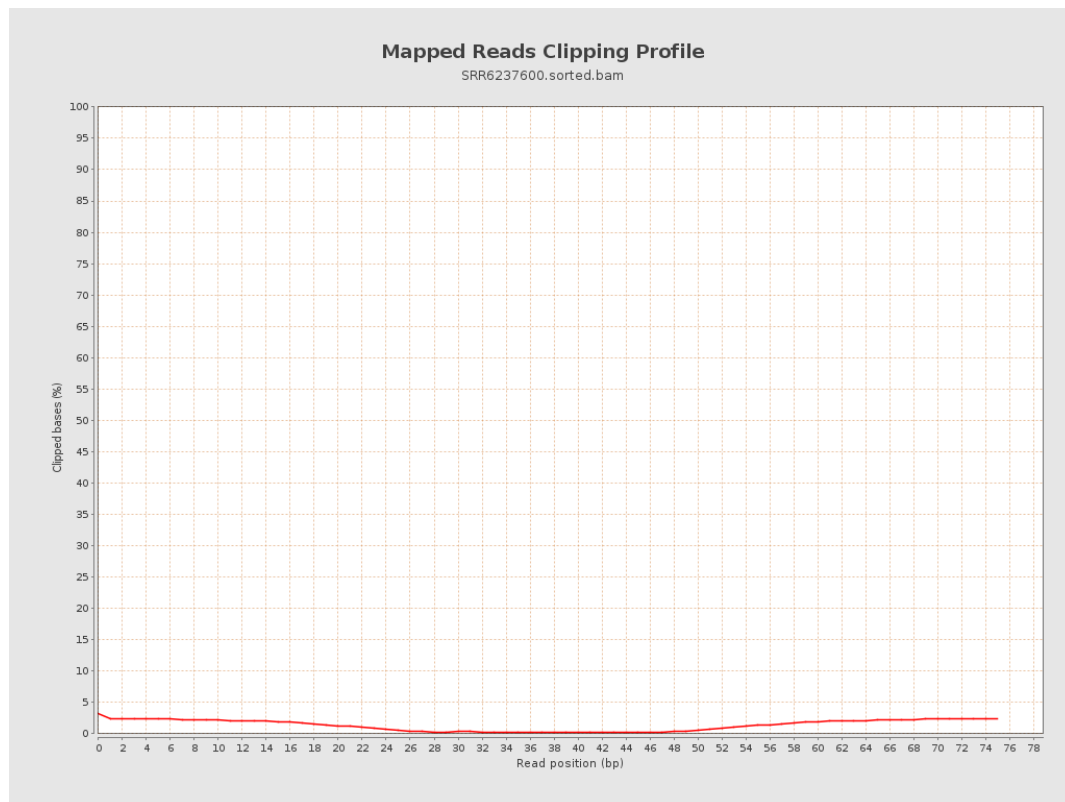
8. Results : Mapped Reads Nucleotide Content



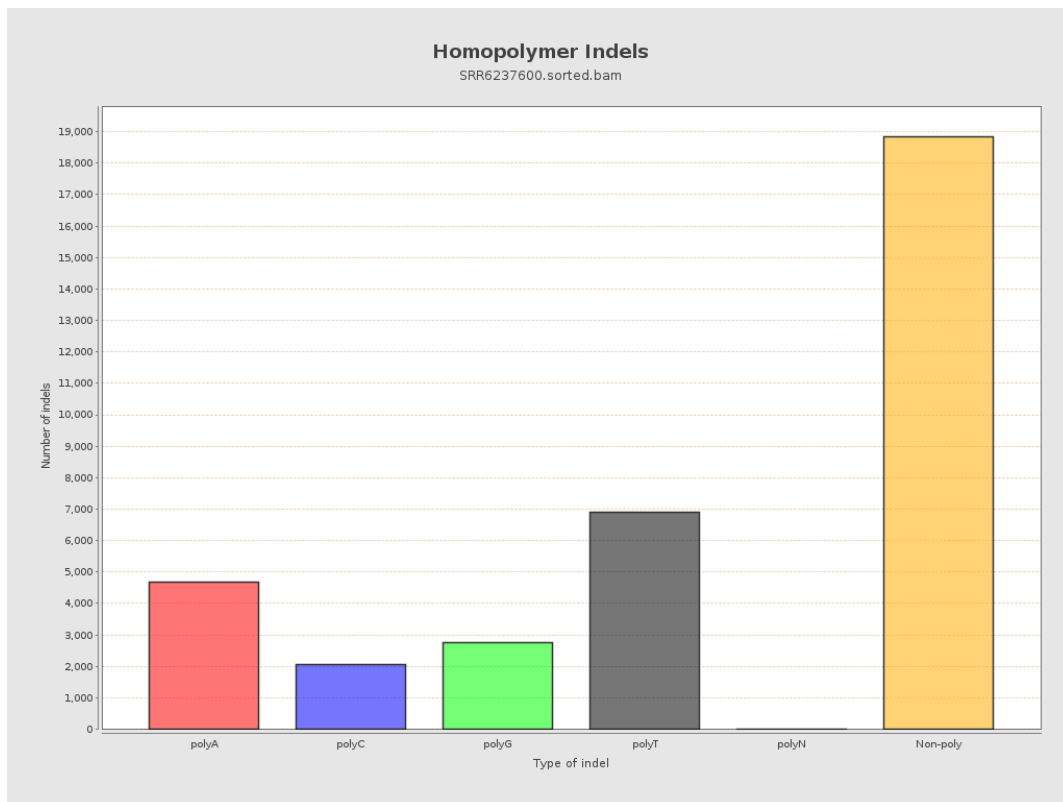
9. Results : Mapped Reads GC-content Distribution



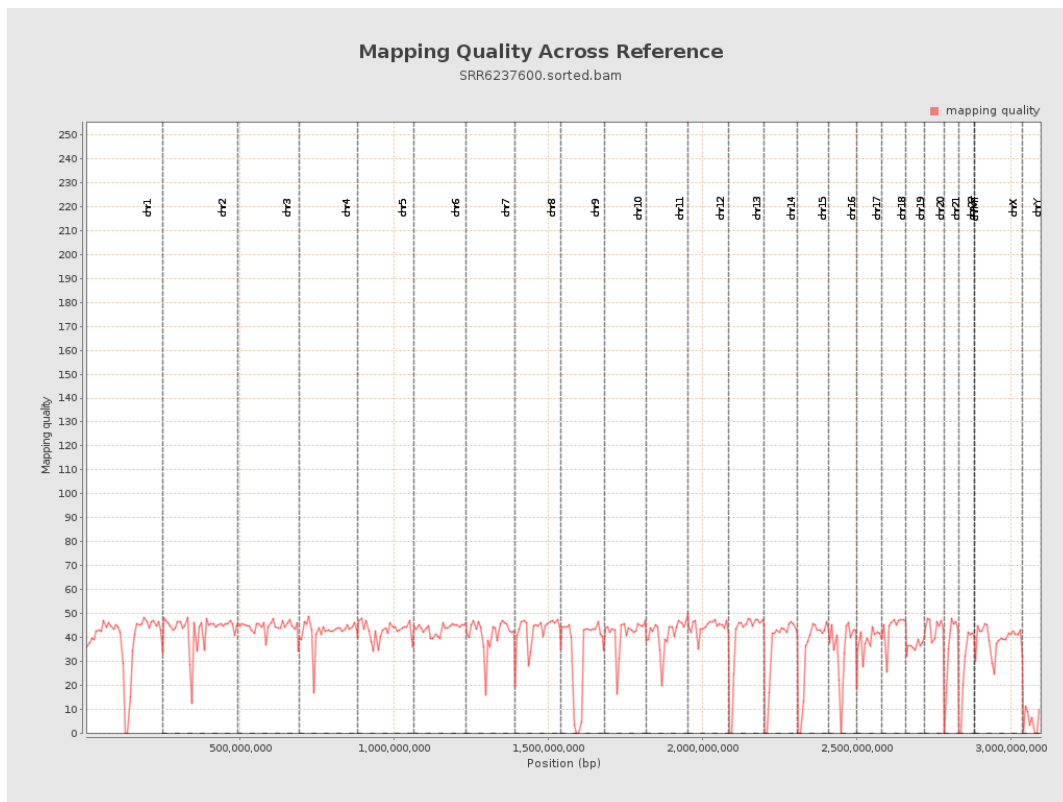
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

