

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:05:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068149.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_SRR6068149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:05:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,526,916
Mapped reads	4,172,897 / 92.18%
Unmapped reads	354,019 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,494 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,237,479 / 27.34%
Duplication rate	20.31%
Clipped reads	2,530,027 / 55.89%

2.2. ACGT Content

Number/percentage of A's	68,294,581 / 26.07%
Number/percentage of C's	45,957,059 / 17.54%
Number/percentage of T's	86,422,447 / 32.99%
Number/percentage of G's	61,285,077 / 23.39%
Number/percentage of N's	29,092 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0847

Standard Deviation	0.7981
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2.4. Mapping Quality

Mean Mapping Quality	45.99
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2.5. Mismatches and indels

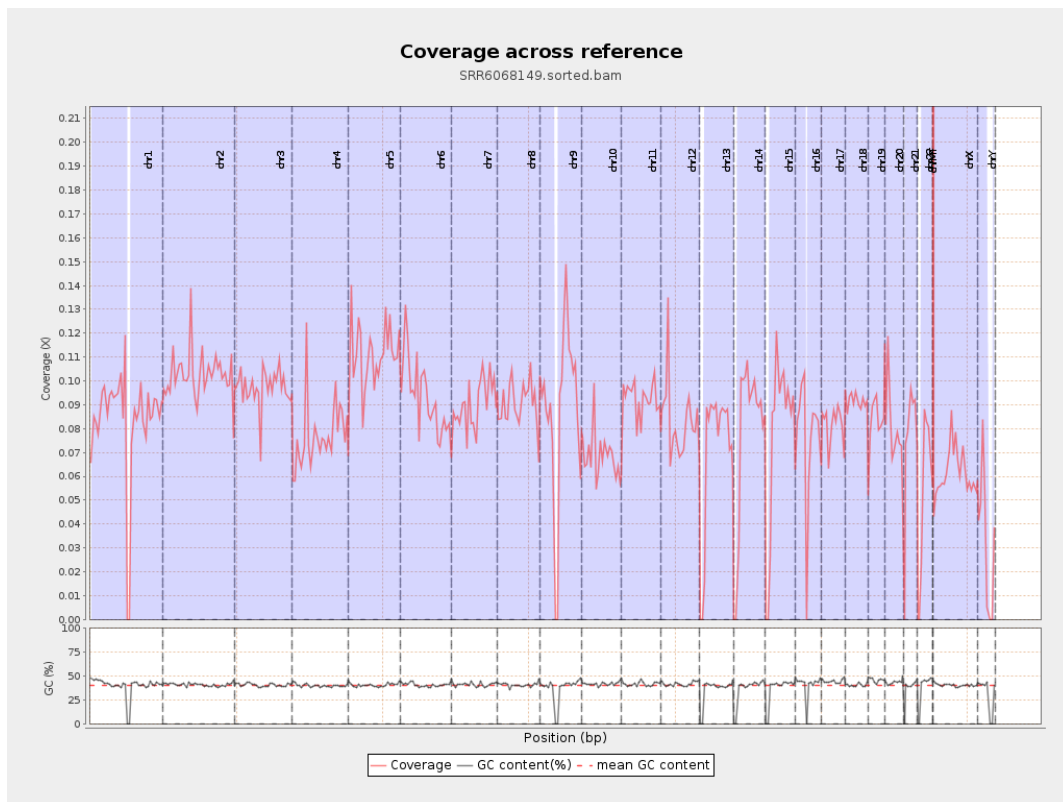
General error rate	0.64%
Mismatches	1,645,629
Insertions	17,646
Mapped reads with at least one insertion	0.42%
Deletions	71,559
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.94%

2.6. Chromosome stats

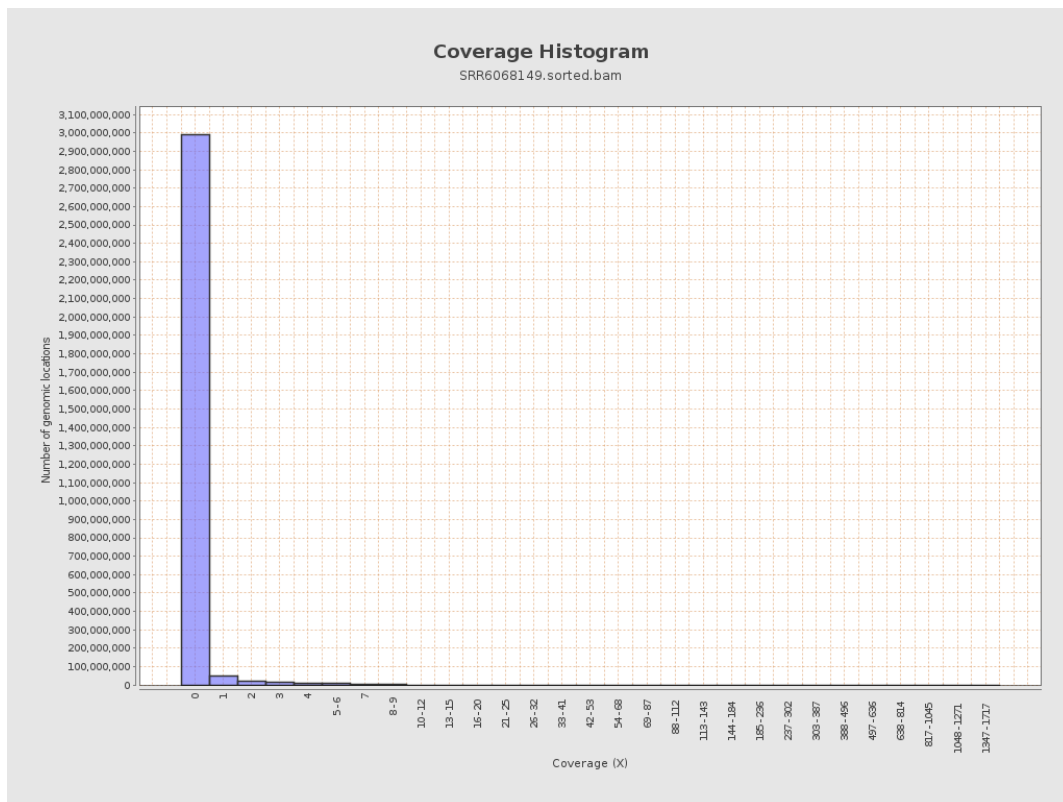
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20822573	0.0835	1.1808
chr2	243199373	25018937	0.1029	1.0783
chr3	198022430	19222589	0.0971	0.647
chr4	191154276	14763751	0.0772	0.6228
chr5	180915260	20058348	0.1109	0.6795
chr6	171115067	15910083	0.093	0.7013
chr7	159138663	14346746	0.0902	0.8119

chr8	146364022	13227712	0.0904	1.1907
chr9	141213431	12384458	0.0877	0.7211
chr10	135534747	9289964	0.0685	0.6696
chr11	135006516	12439667	0.0921	0.7809
chr12	133851895	11136644	0.0832	0.5975
chr13	115169878	8080267	0.0702	0.5567
chr14	107349540	8482071	0.079	0.601
chr15	102531392	7881213	0.0769	0.6026
chr16	90354753	6784257	0.0751	0.5779
chr17	81195210	6671386	0.0822	0.6194
chr18	78077248	7145134	0.0915	1.1466
chr19	59128983	5022162	0.0849	0.8588
chr20	63025520	5051262	0.0801	0.6038
chr21	48129895	3703243	0.0769	0.6075
chr22	51304566	2757064	0.0537	0.4829
chrMT	16571	373371	22.5316	16.8381
chrX	155270560	9566637	0.0616	0.5333
chrY	59373566	1977633	0.0333	0.4096

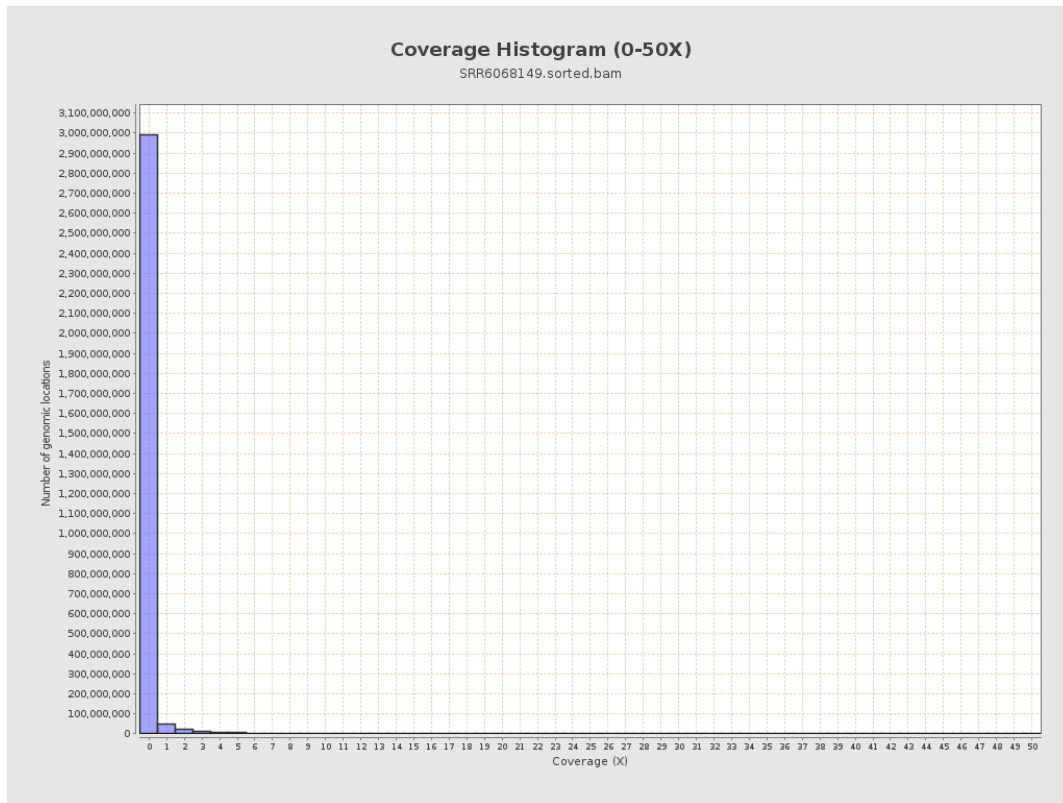
3. Results : Coverage across reference



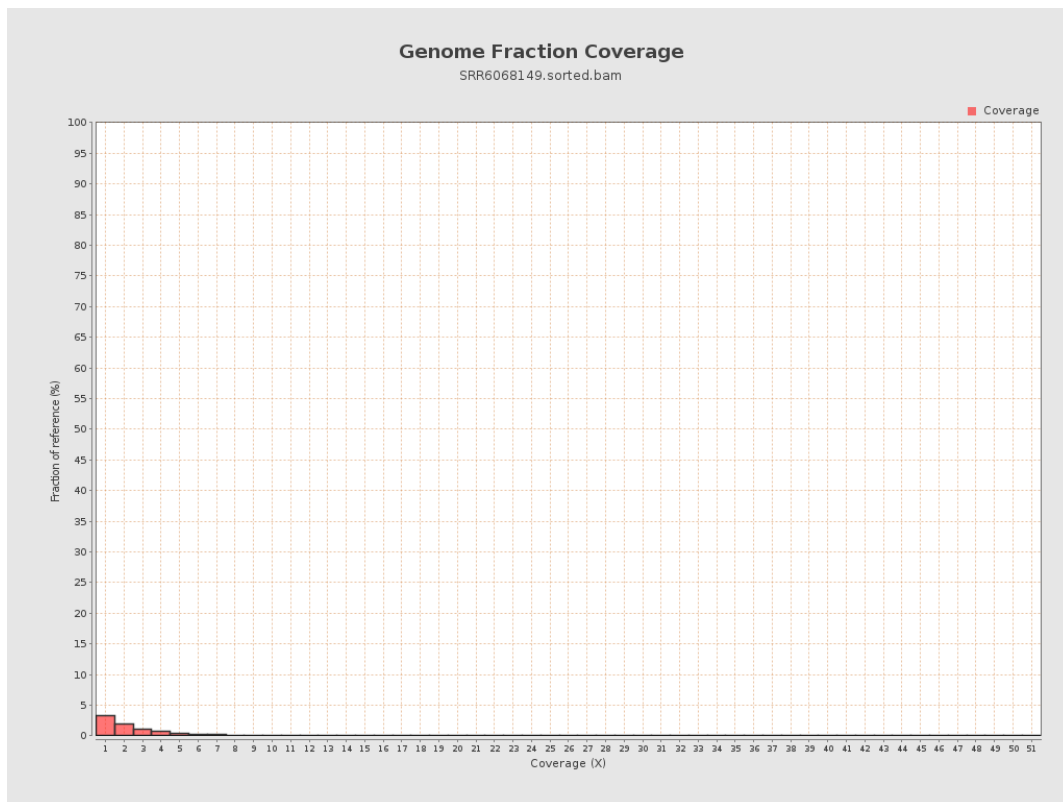
4. Results : Coverage Histogram



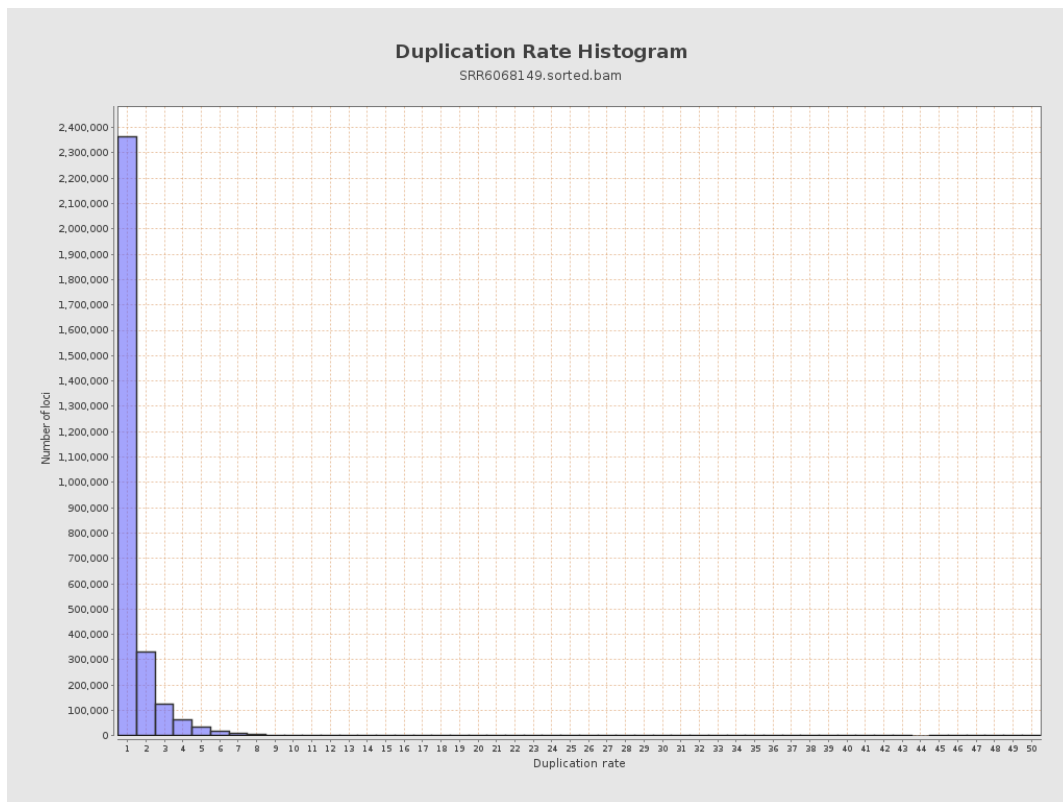
5. Results : Coverage Histogram (0-50X)



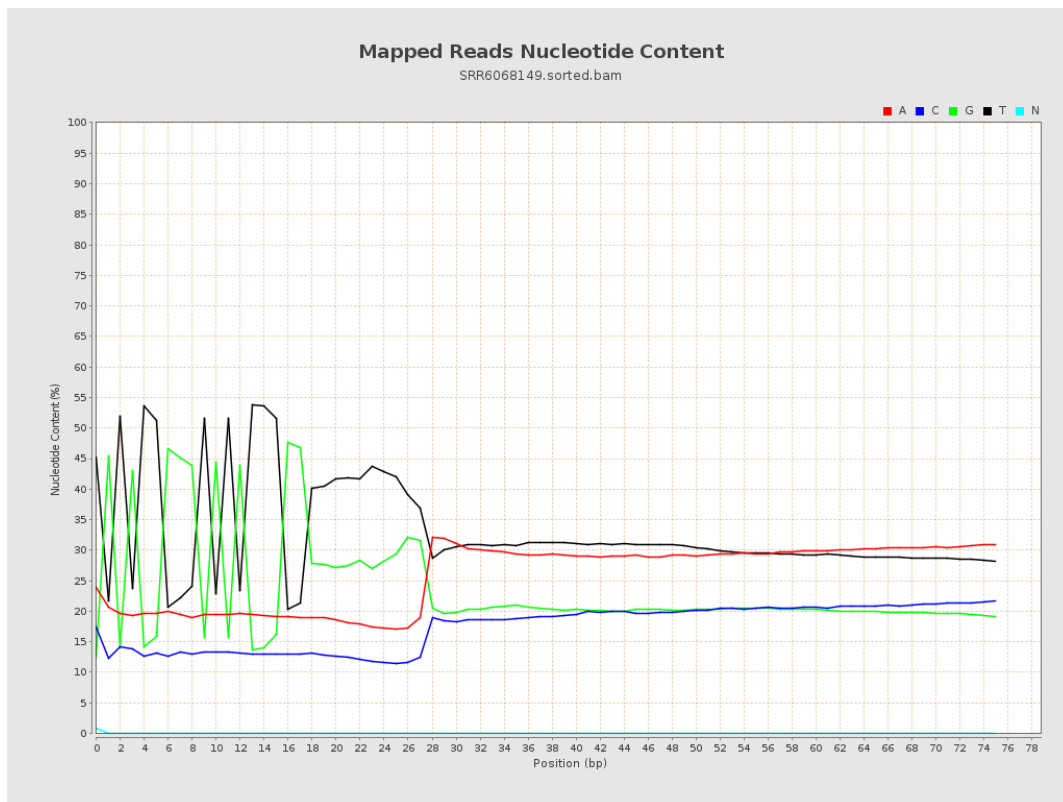
6. Results : Genome Fraction Coverage



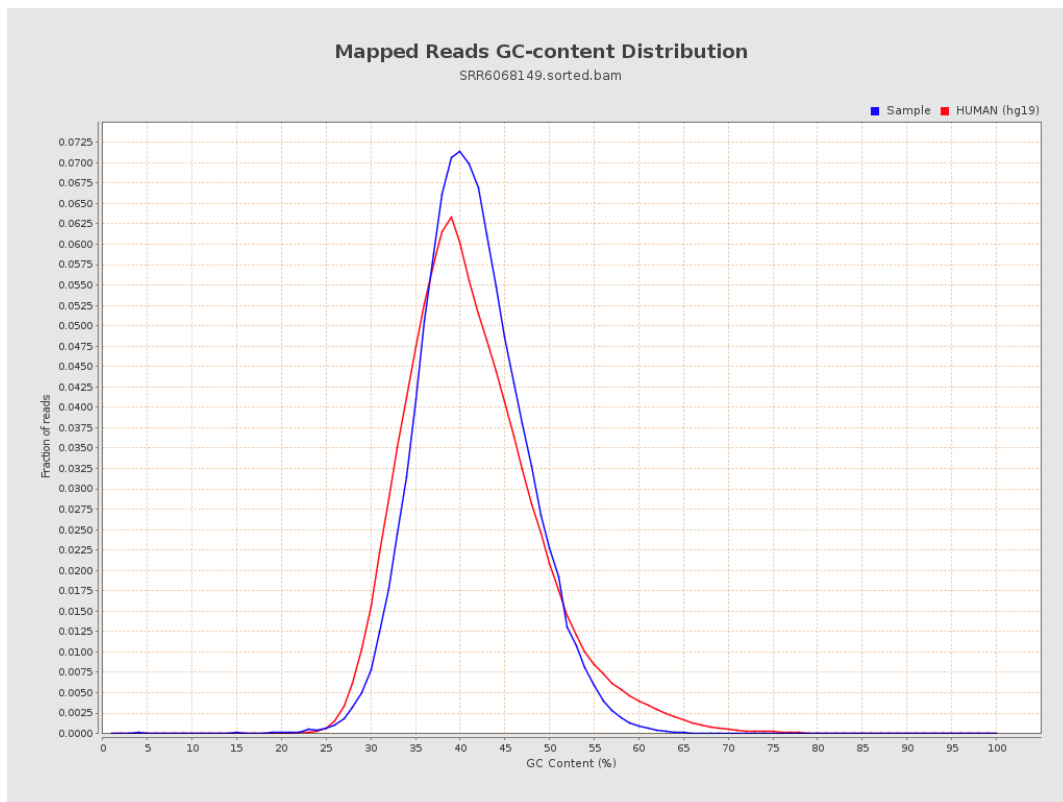
7. Results : Duplication Rate Histogram



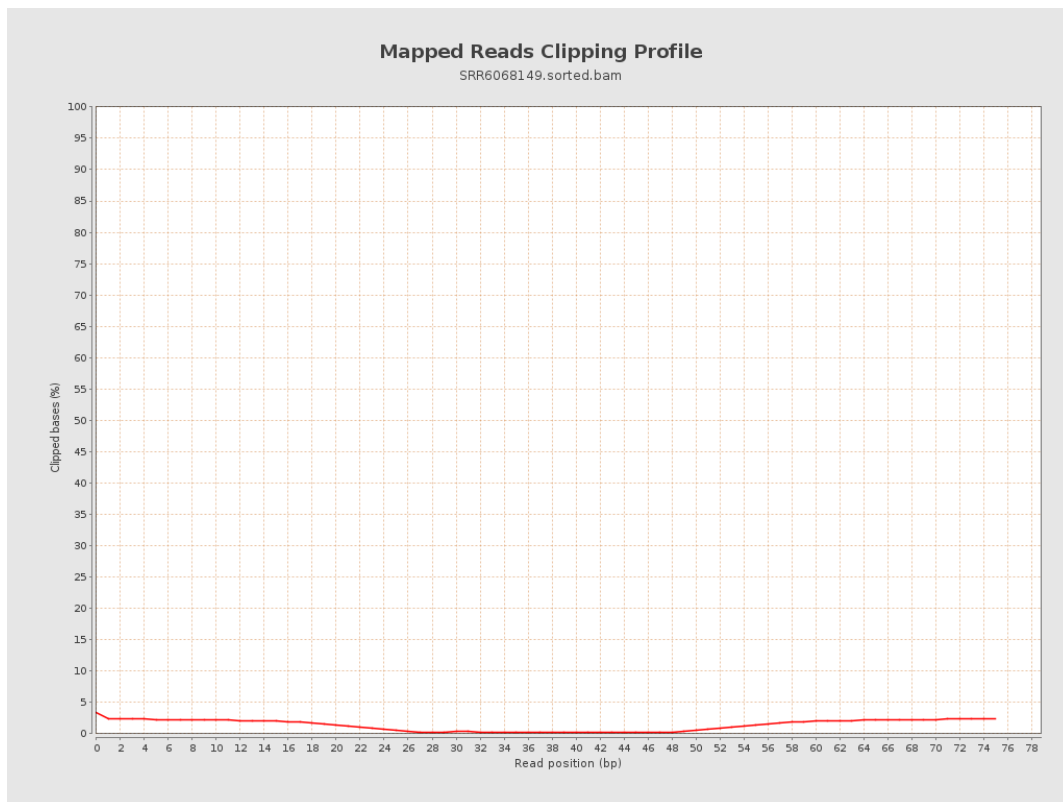
8. Results : Mapped Reads Nucleotide Content



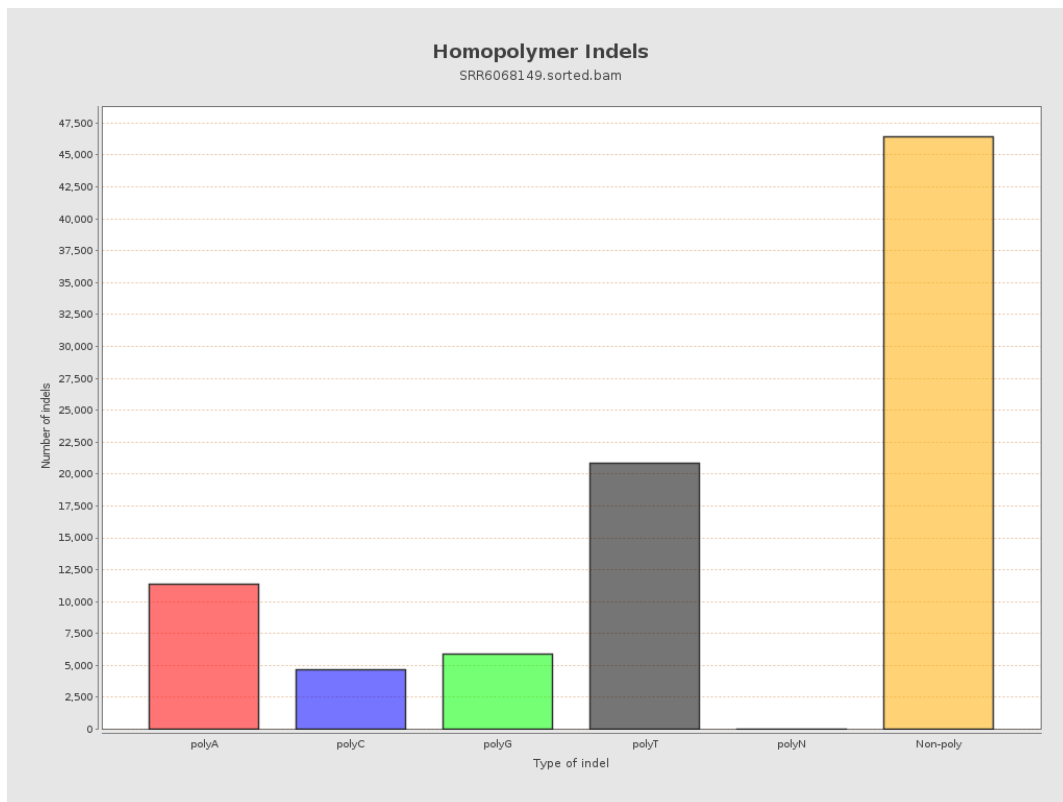
9. Results : Mapped Reads GC-content Distribution



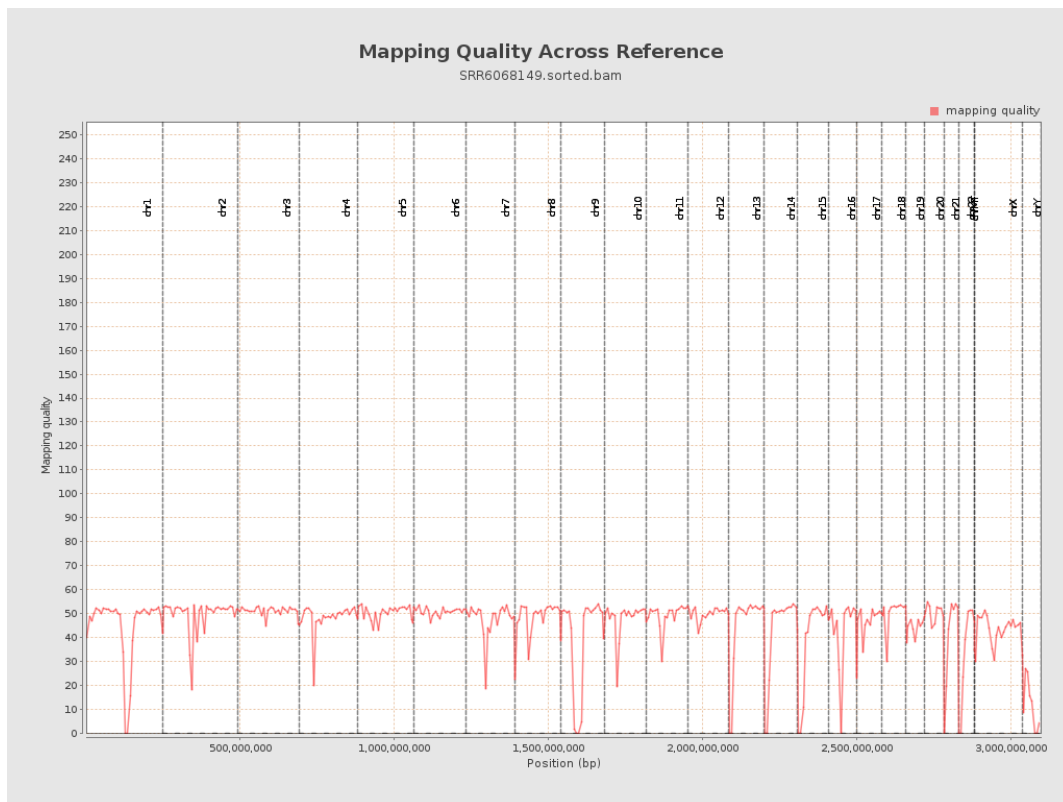
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

