

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013238.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_SRR6013238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:29:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,633,965
Mapped reads	1,479,659 / 90.56%
Unmapped reads	154,306 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,121 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	57,379 / 3.51%
Duplication rate	2.75%
Clipped reads	648,099 / 39.66%

2.2. ACGT Content

Number/percentage of A's	27,860,316 / 28.15%
Number/percentage of C's	18,197,499 / 18.39%
Number/percentage of T's	31,311,898 / 31.64%
Number/percentage of G's	21,572,966 / 21.8%
Number/percentage of N's	21,354 / 0.02%
GC Percentage	40.19%

2.3. Coverage

Mean	0.032

Standard Deviation	0.3682
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2.4. Mapping Quality

Mean Mapping Quality	44.84
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2.5. Mismatches and indels

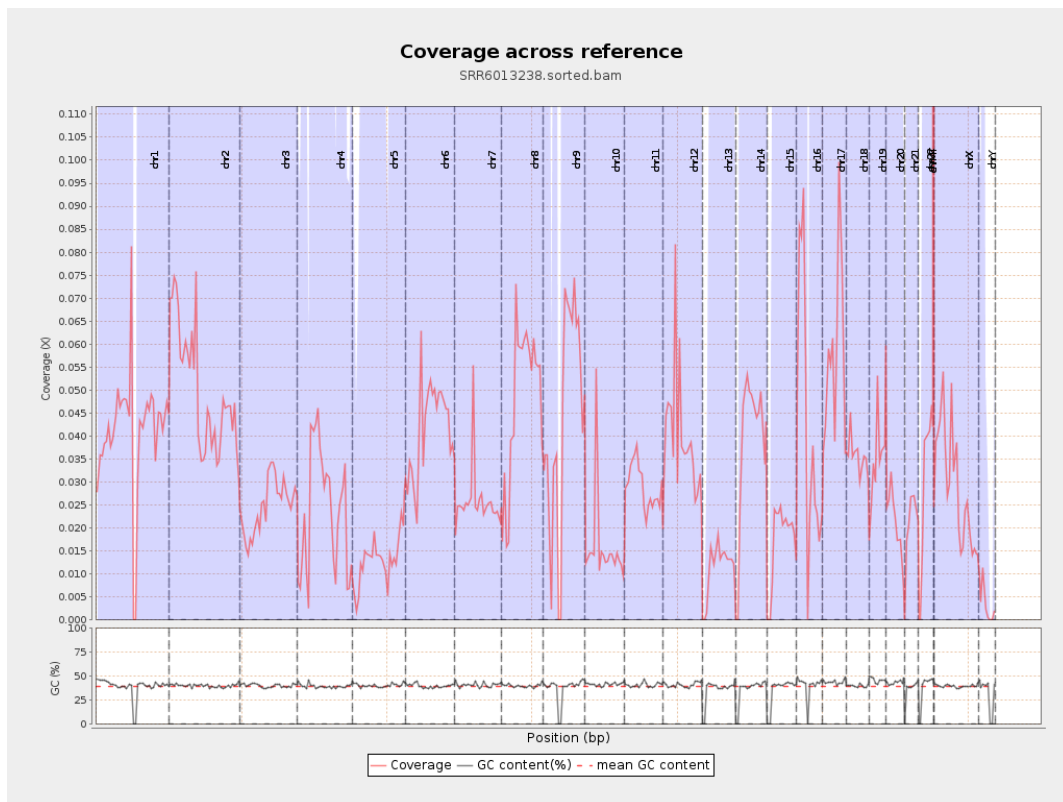
General error rate	0.83%
Mismatches	810,583
Insertions	7,747
Mapped reads with at least one insertion	0.52%
Deletions	24,701
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.98%

2.6. Chromosome stats

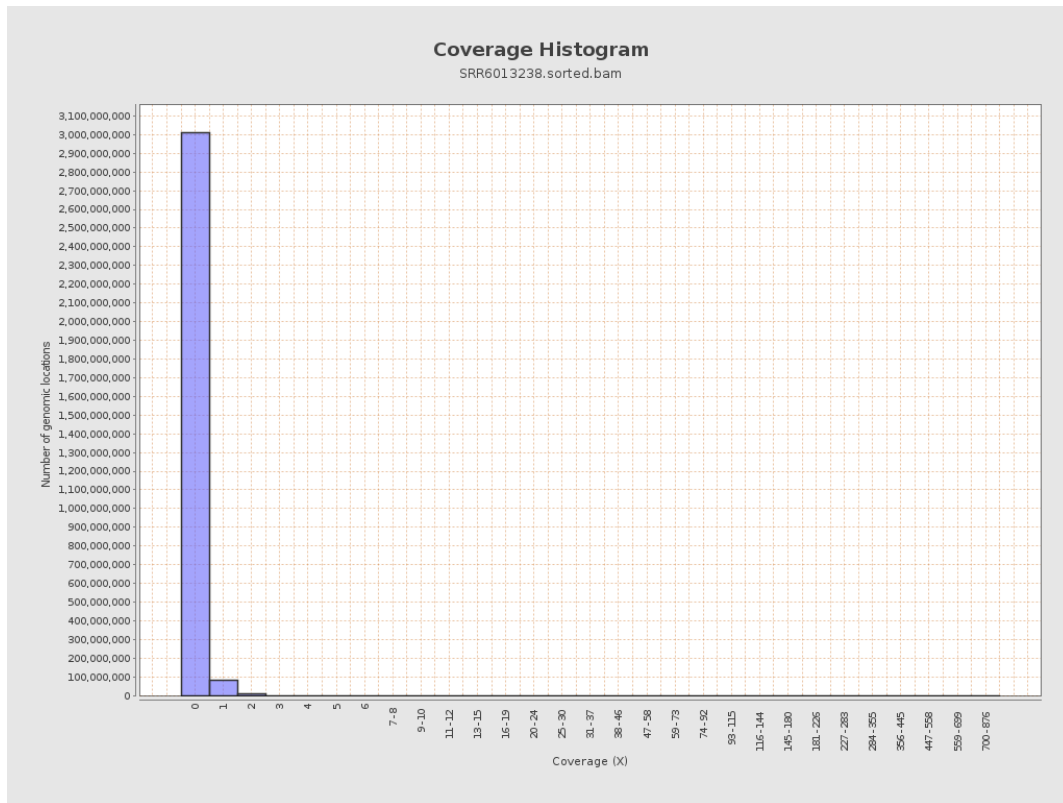
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10230055	0.041	0.7824
chr2	243199373	12200232	0.0502	0.4188
chr3	198022430	4880789	0.0246	0.1726
chr4	191154276	4439991	0.0232	0.1899
chr5	180915260	2359607	0.013	0.1272
chr6	171115067	7100268	0.0415	0.3045
chr7	159138663	4117589	0.0259	0.4623

chr8	146364022	7042996	0.0481	0.3578
chr9	141213431	6170137	0.0437	0.3454
chr10	135534747	2105616	0.0155	0.3579
chr11	135006516	3865981	0.0286	0.2489
chr12	133851895	5317113	0.0397	0.2233
chr13	115169878	1293662	0.0112	0.1144
chr14	107349540	4182364	0.039	0.2366
chr15	102531392	1788747	0.0174	0.1426
chr16	90354753	3862464	0.0427	0.259
chr17	81195210	4636233	0.0571	0.2936
chr18	78077248	2781867	0.0356	0.6511
chr19	59128983	2113064	0.0357	0.6041
chr20	63025520	1338254	0.0212	0.1623
chr21	48129895	1000848	0.0208	0.1841
chr22	51304566	1489123	0.029	0.1852
chrMT	16571	32040	1.9335	1.7582
chrX	155270560	4459371	0.0287	0.2117
chrY	59373566	198555	0.0033	0.1151

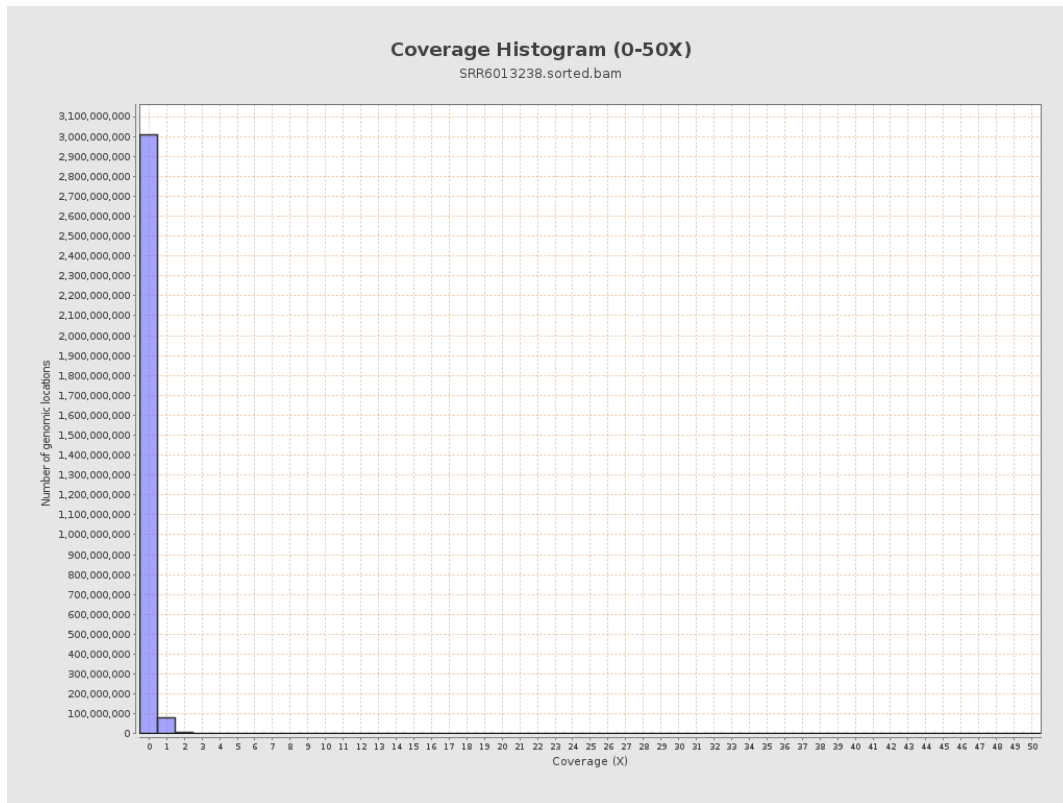
3. Results : Coverage across reference



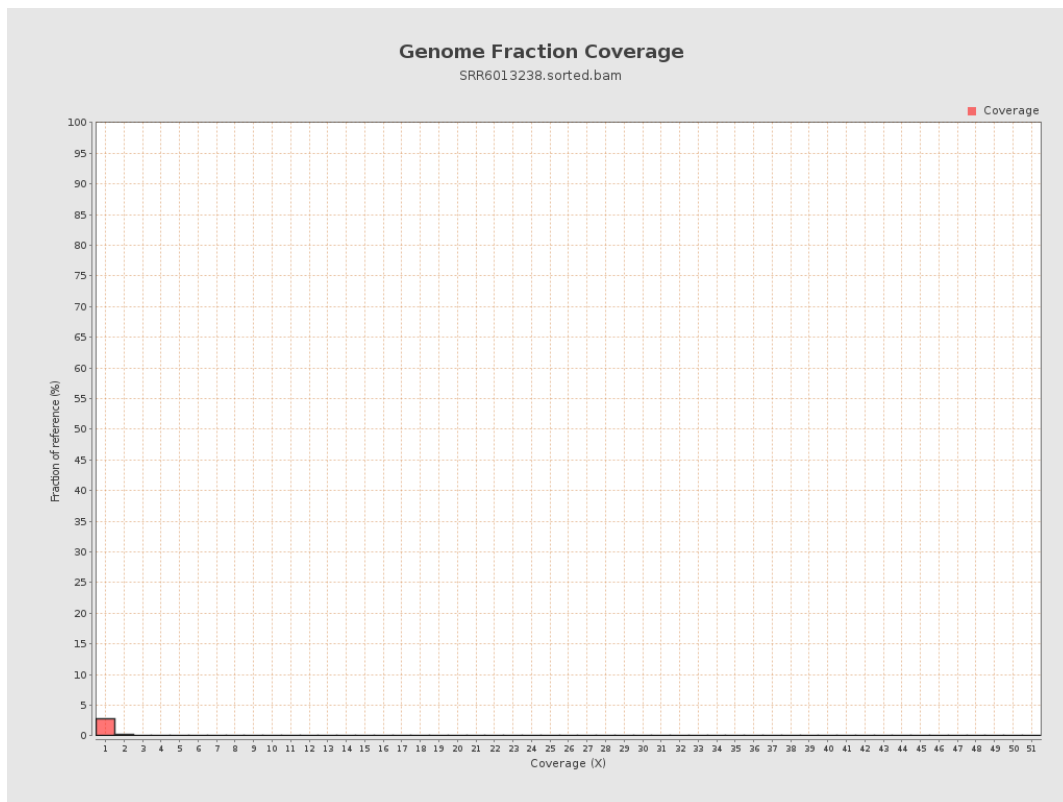
4. Results : Coverage Histogram



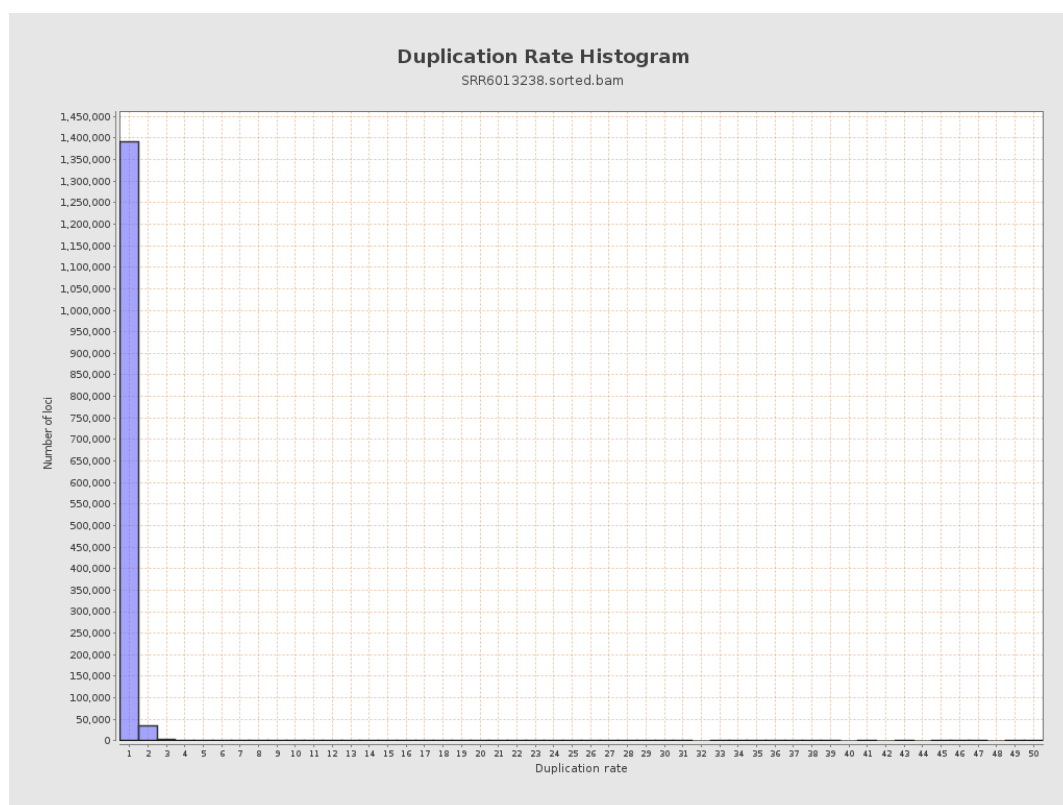
5. Results : Coverage Histogram (0-50X)



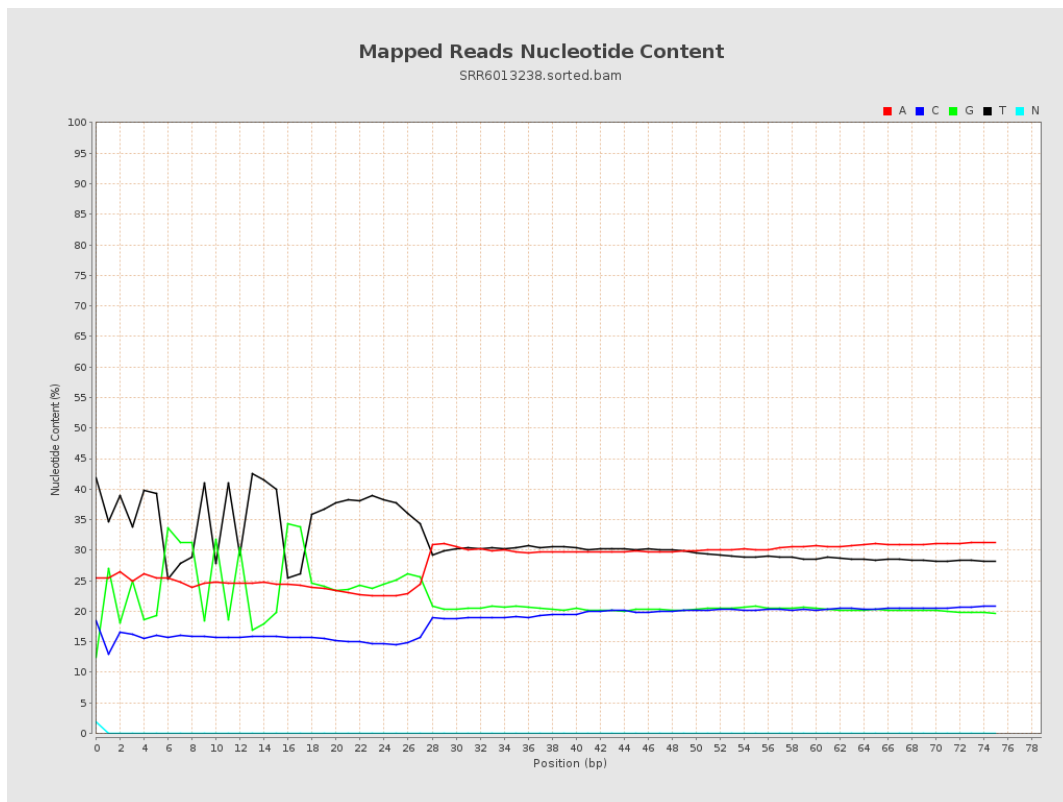
6. Results : Genome Fraction Coverage



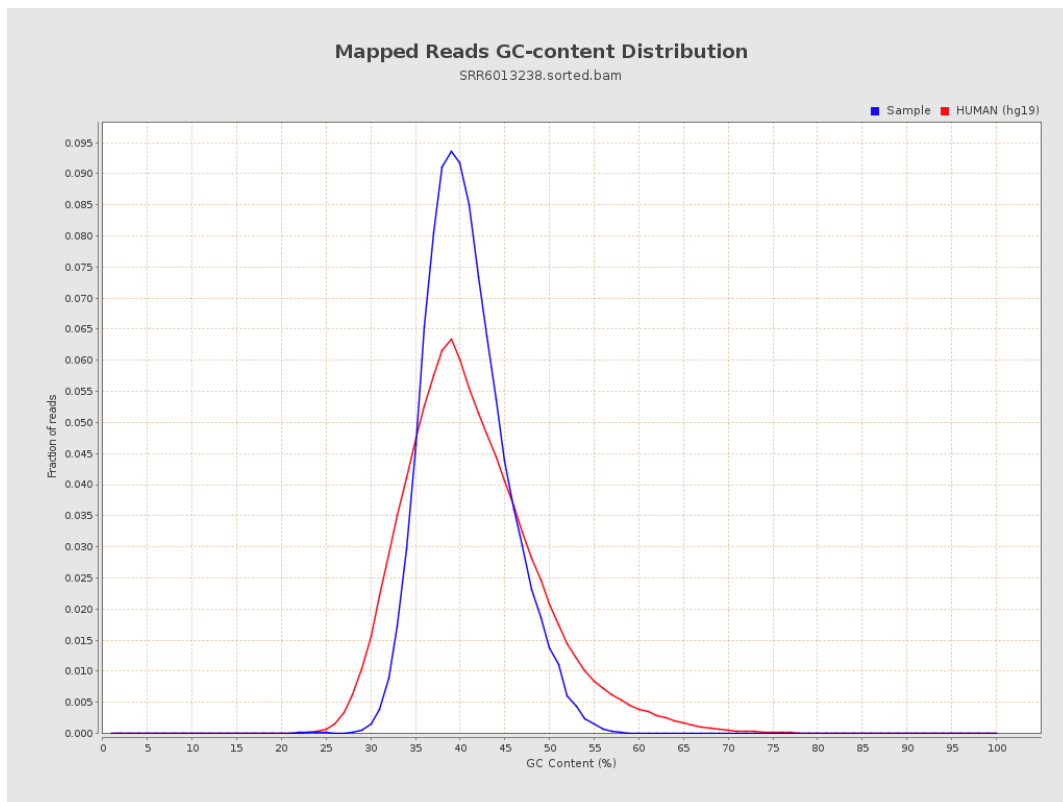
7. Results : Duplication Rate Histogram



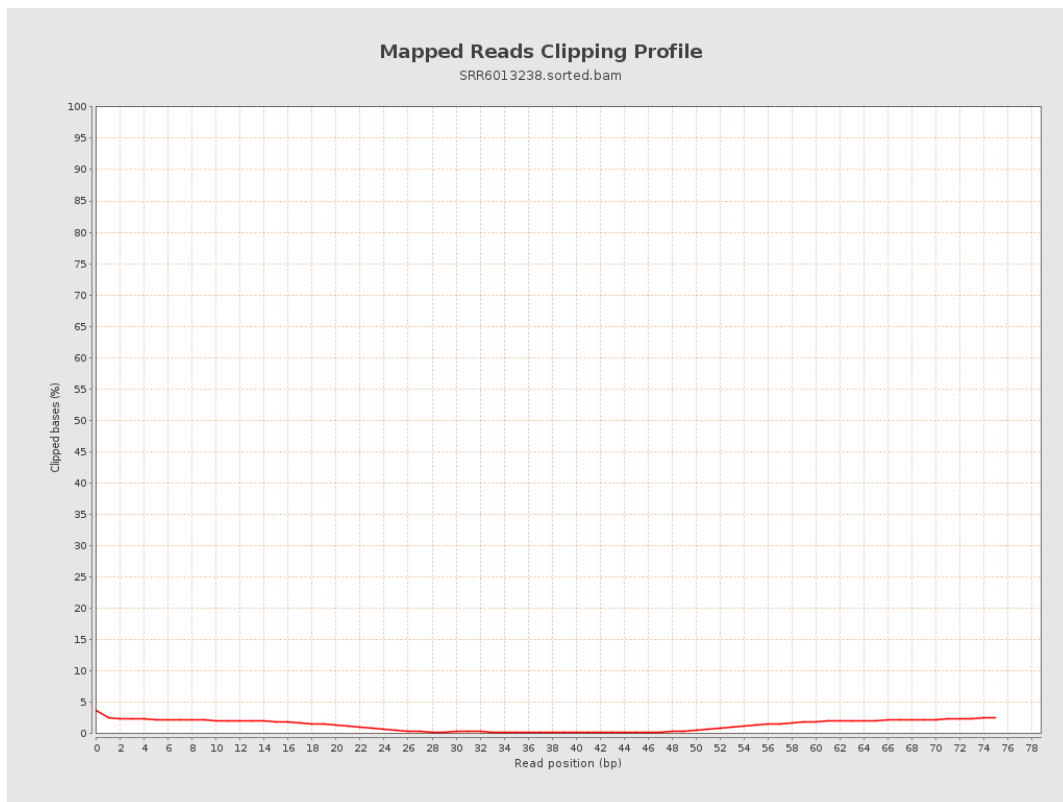
8. Results : Mapped Reads Nucleotide Content



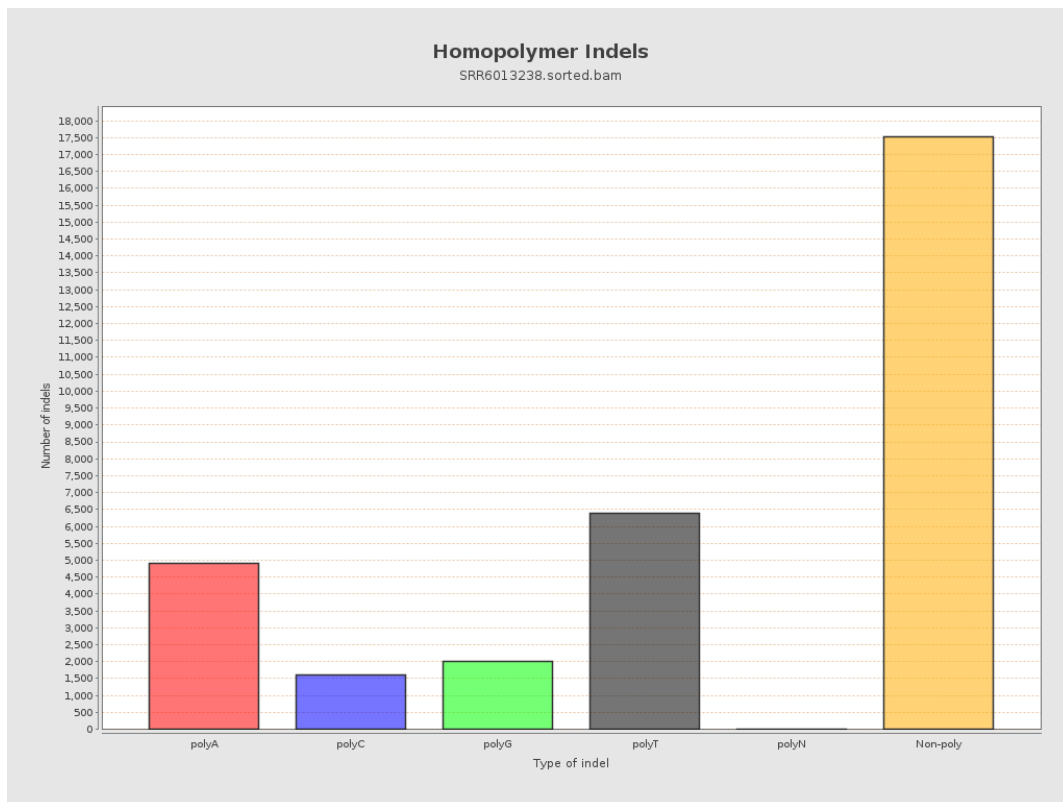
9. Results : Mapped Reads GC-content Distribution



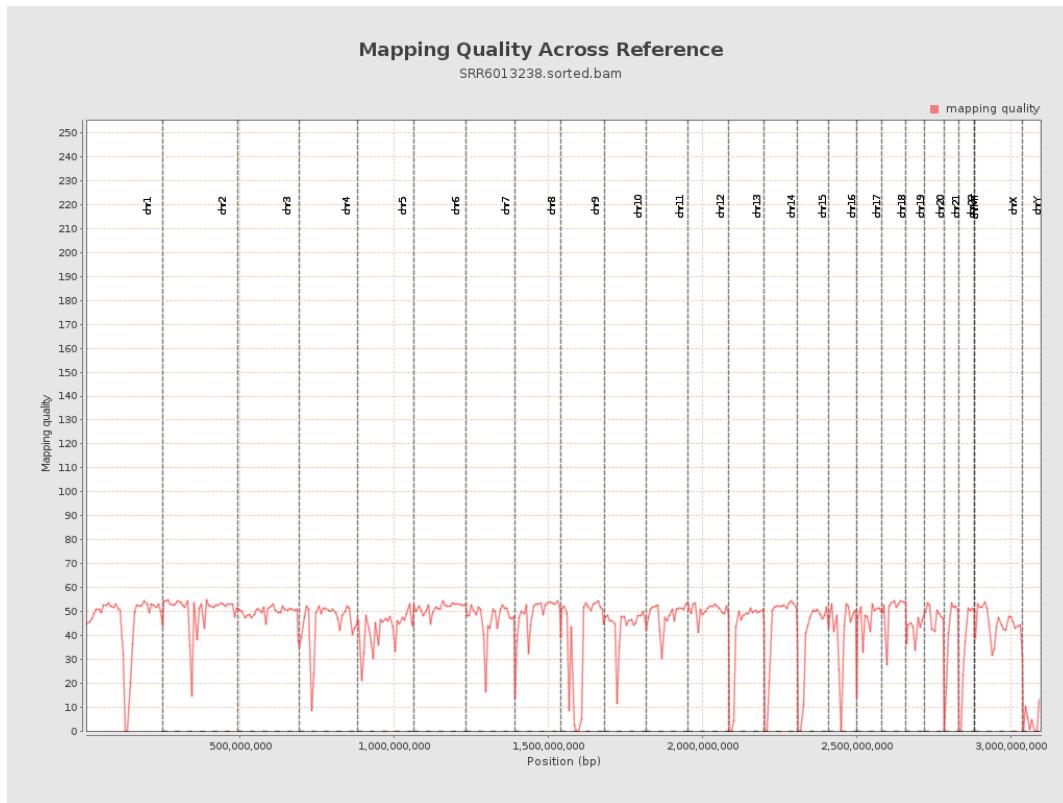
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

