

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:02:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230336.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_SRR6230336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:02:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,179,059
Mapped reads	1,624,753 / 74.56%
Unmapped reads	554,306 / 25.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,818 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	121,099 / 5.56%
Duplication rate	5.76%
Clipped reads	756,603 / 34.72%

2.2. ACGT Content

Number/percentage of A's	29,281,321 / 27.28%
Number/percentage of C's	19,023,026 / 17.73%
Number/percentage of T's	35,133,465 / 32.74%
Number/percentage of G's	23,676,828 / 22.06%
Number/percentage of N's	202,418 / 0.19%
GC Percentage	39.79%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.4122
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2.4. Mapping Quality

Mean Mapping Quality	46.16
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2.5. Mismatches and indels

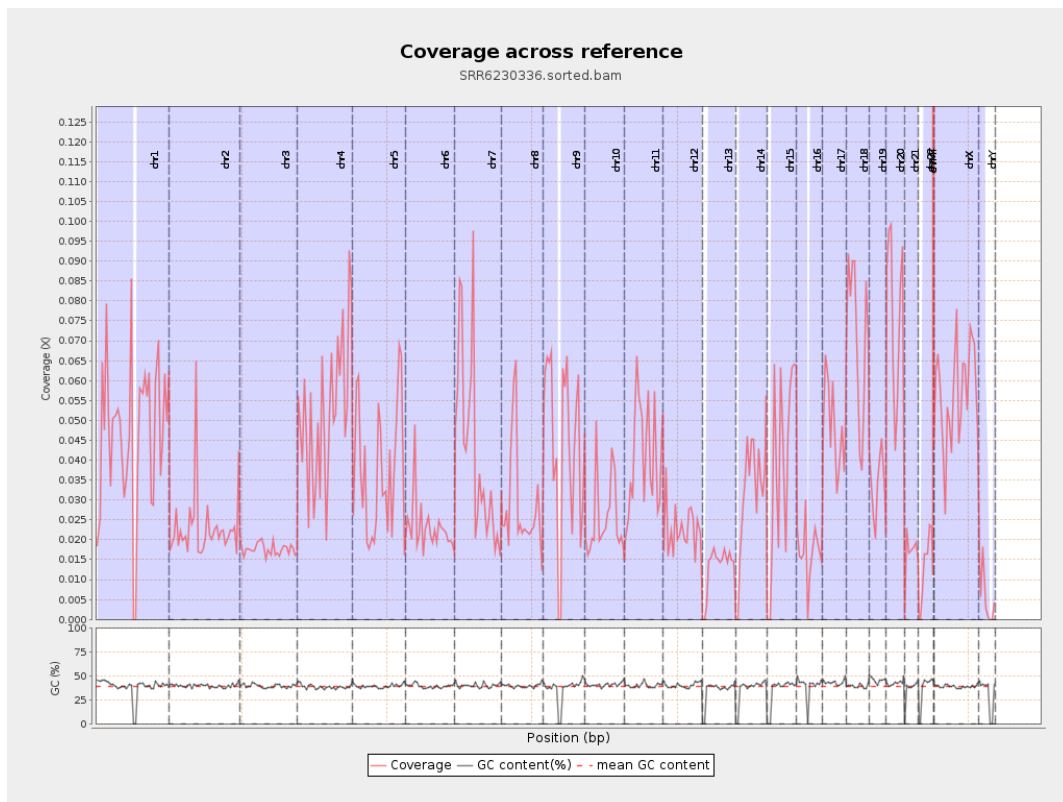
General error rate	1.05%
Mismatches	1,110,225
Insertions	10,257
Mapped reads with at least one insertion	0.63%
Deletions	29,525
Mapped reads with at least one deletion	1.8%
Homopolymer indels	48.24%

2.6. Chromosome stats

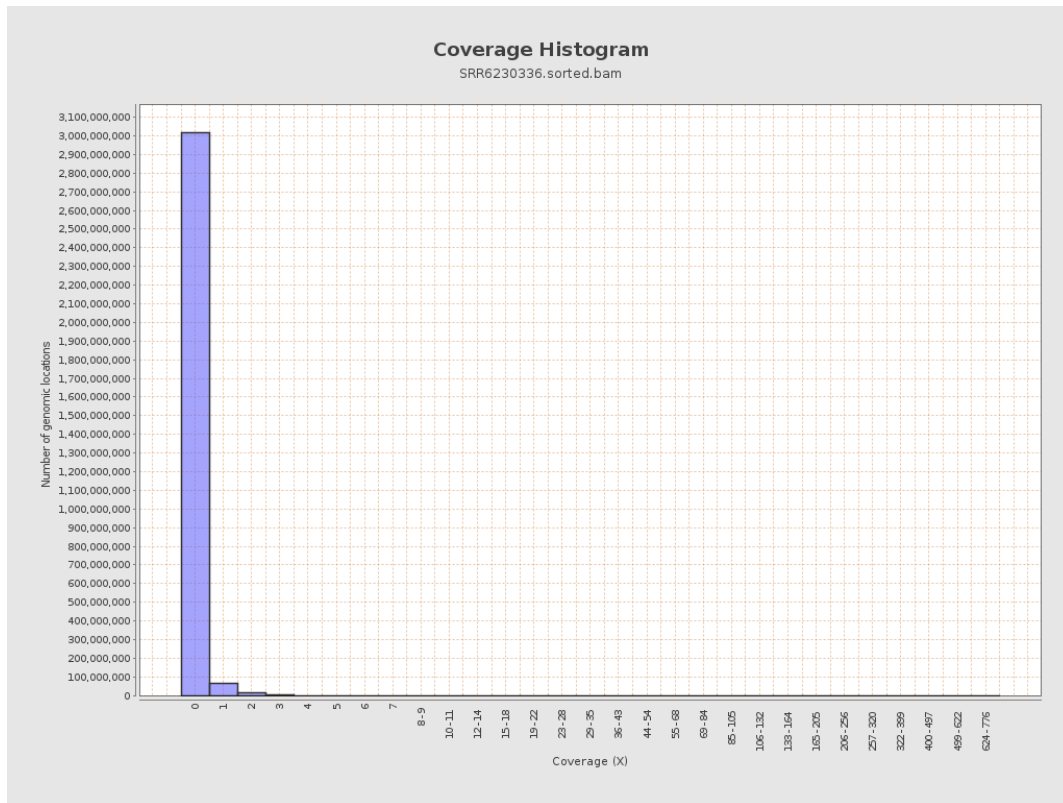
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11522073	0.0462	0.6935
chr2	243199373	5623843	0.0231	0.5092
chr3	198022430	3507628	0.0177	0.1663
chr4	191154276	9969233	0.0522	0.3216
chr5	180915260	6744695	0.0373	0.244
chr6	171115067	3909475	0.0228	0.2181
chr7	159138663	6589597	0.0414	0.7867

chr8	146364022	4145599	0.0283	0.5445
chr9	141213431	6230045	0.0441	0.43
chr10	135534747	3371723	0.0249	0.3098
chr11	135006516	5445684	0.0403	0.3702
chr12	133851895	3004094	0.0224	0.1973
chr13	115169878	1491047	0.0129	0.1406
chr14	107349540	3354838	0.0313	0.2365
chr15	102531392	4036135	0.0394	0.2485
chr16	90354753	1530791	0.0169	0.1821
chr17	81195210	3879679	0.0478	0.3198
chr18	78077248	5491333	0.0703	0.5305
chr19	59128983	1968401	0.0333	0.4755
chr20	63025520	4809044	0.0763	0.3509
chr21	48129895	803675	0.0167	0.2107
chr22	51304566	690687	0.0135	0.1426
chrMT	16571	170109	10.2655	6.3061
chrX	155270560	8757940	0.0564	0.3306
chrY	59373566	318116	0.0054	0.1753

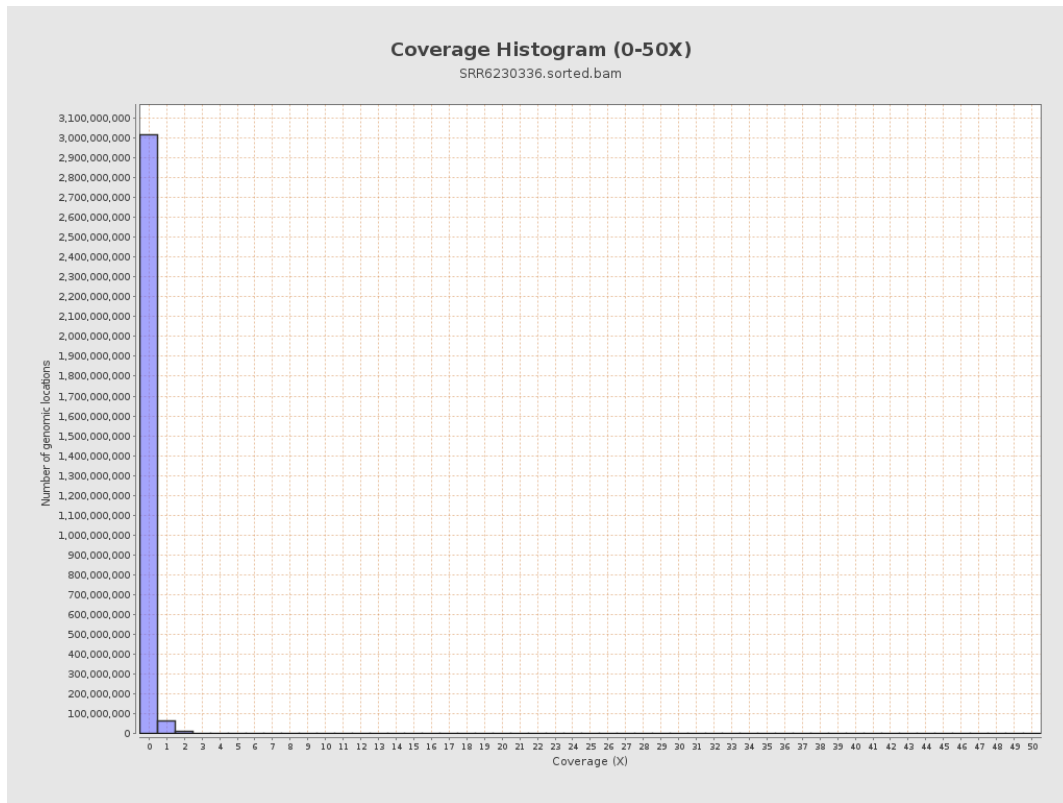
3. Results : Coverage across reference



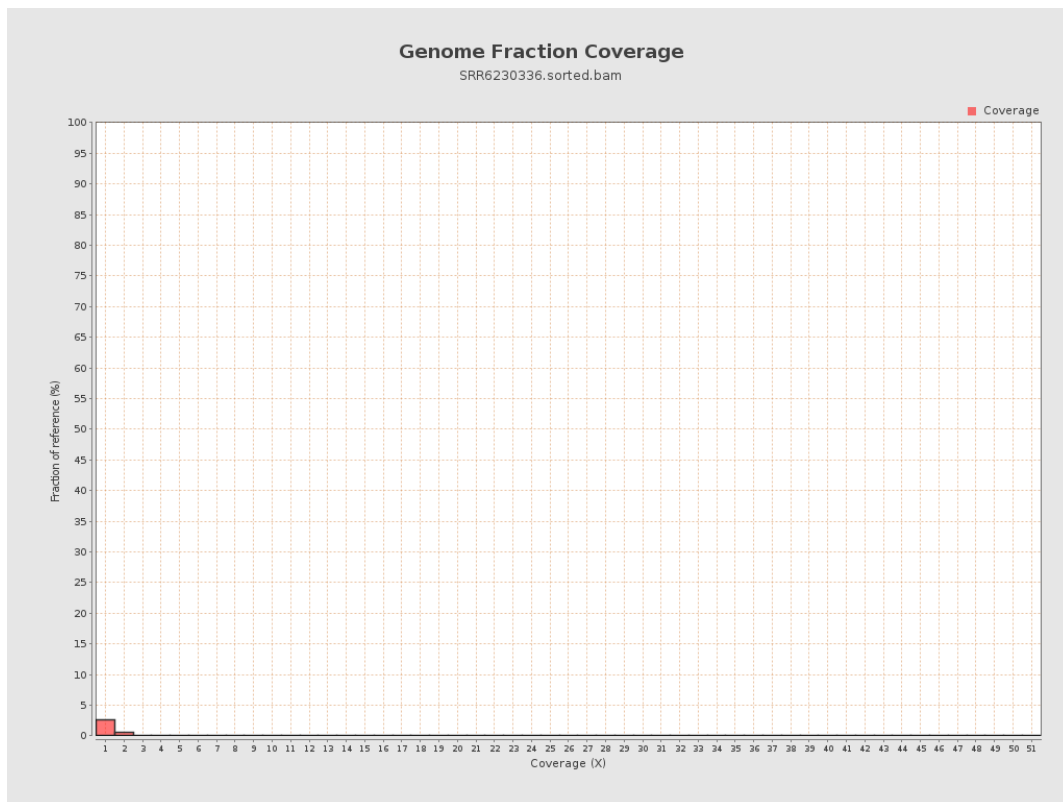
4. Results : Coverage Histogram



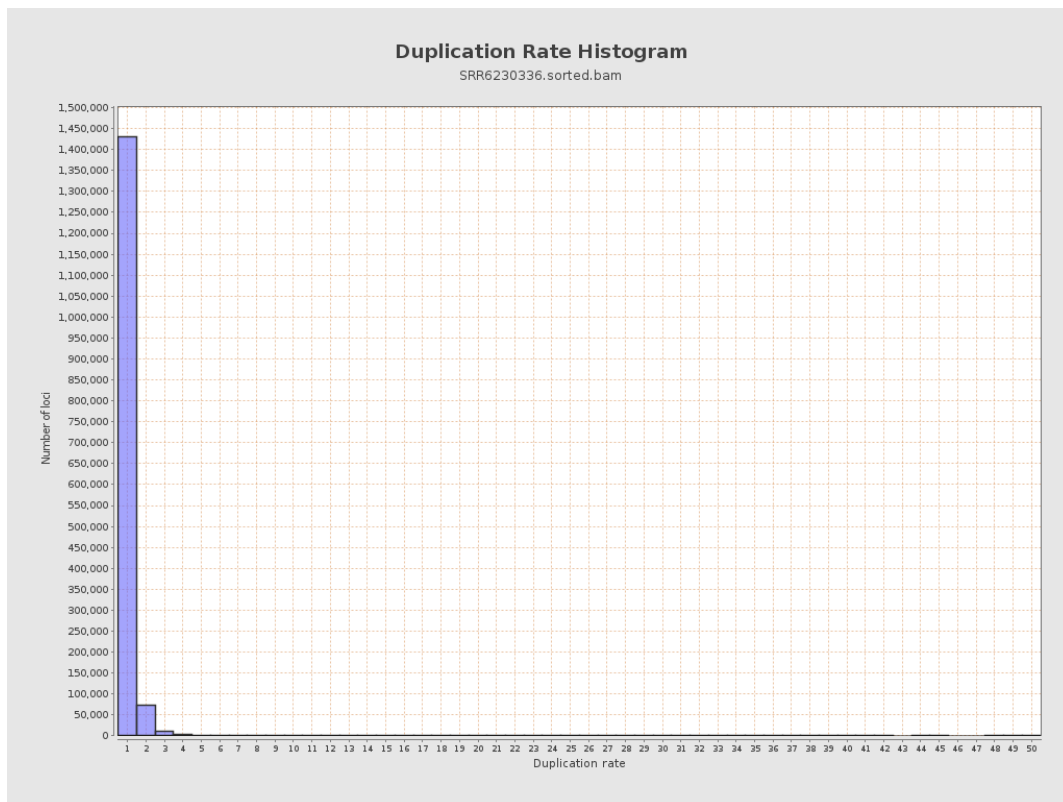
5. Results : Coverage Histogram (0-50X)



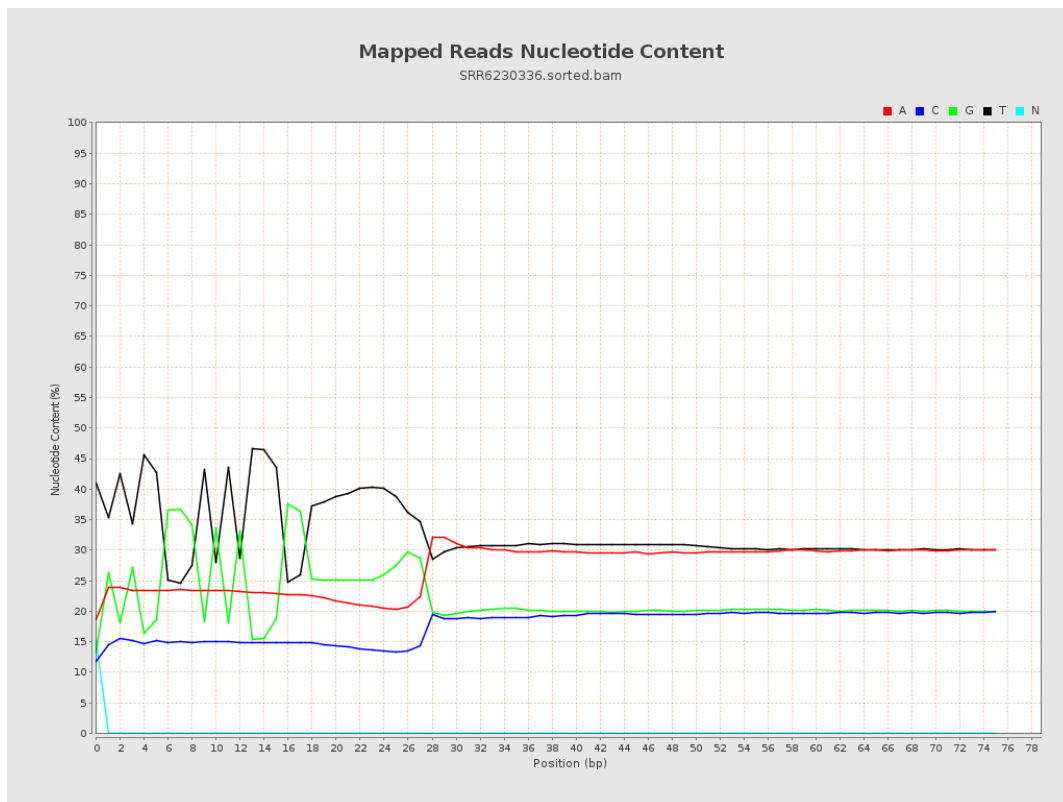
6. Results : Genome Fraction Coverage



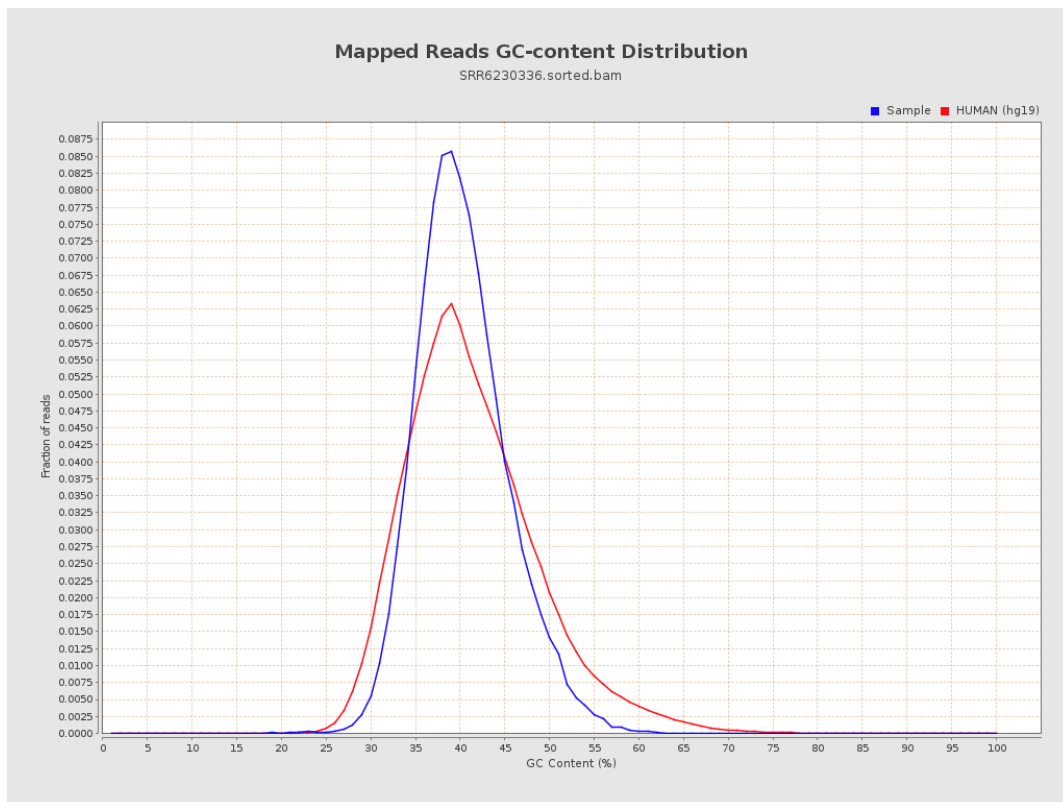
7. Results : Duplication Rate Histogram



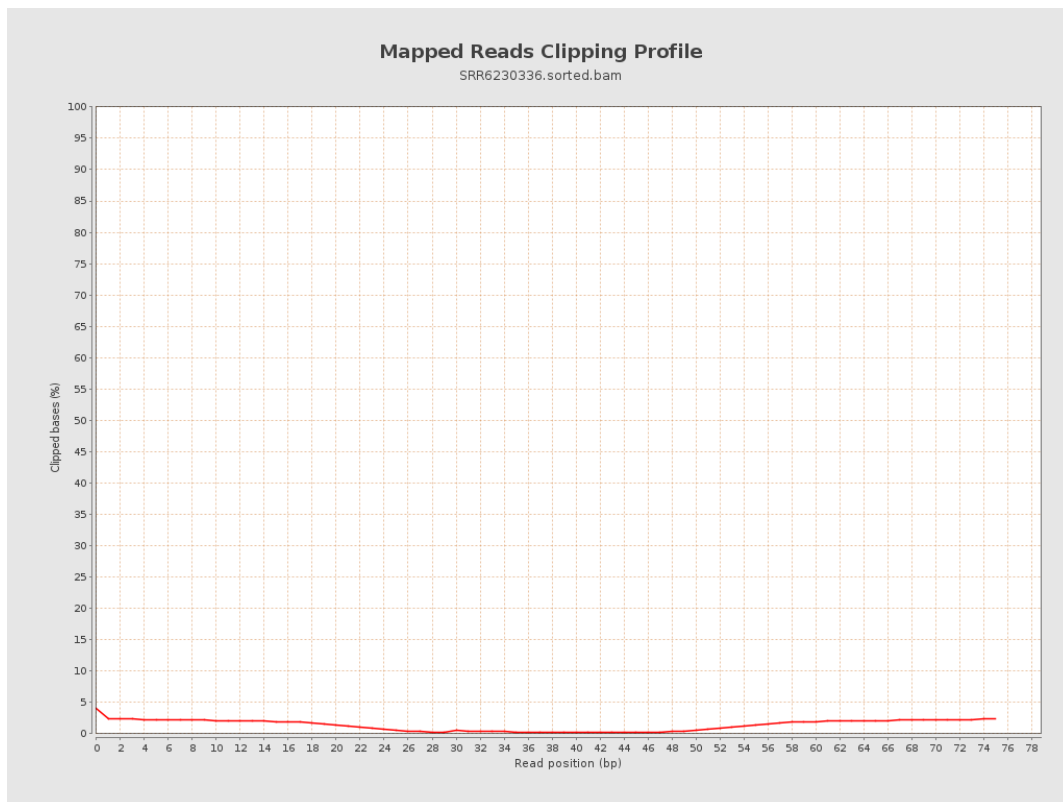
8. Results : Mapped Reads Nucleotide Content



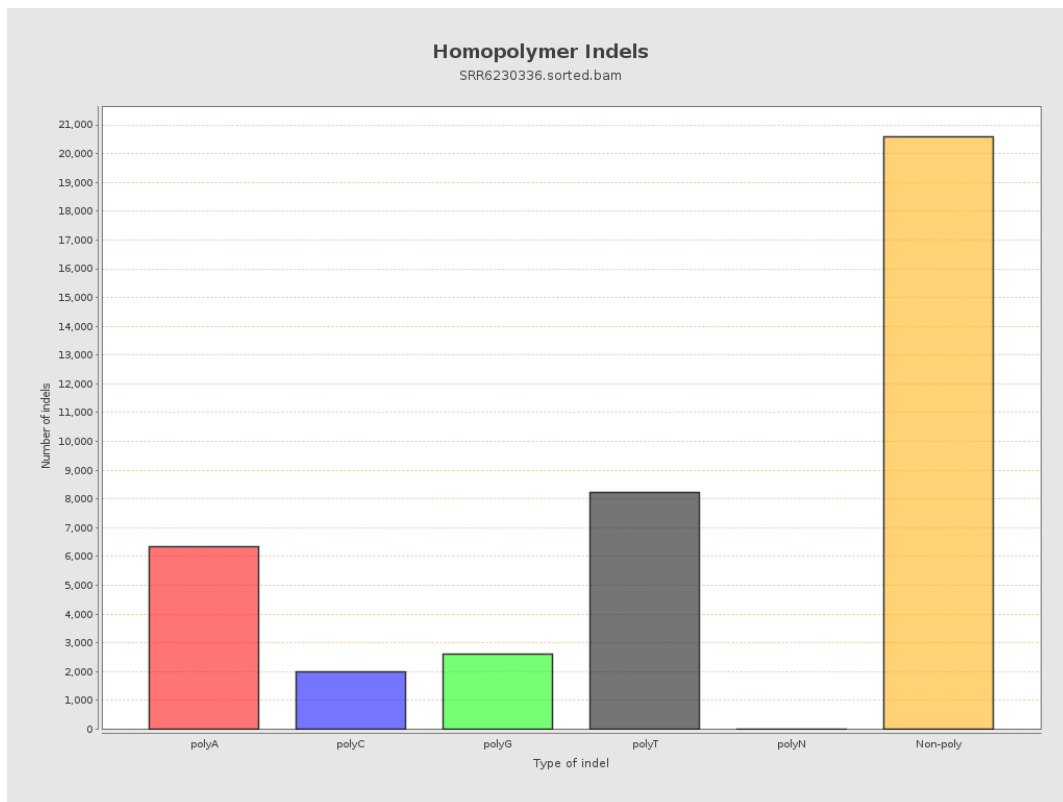
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

