

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:27:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR23117299.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_SRR23117299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR23117299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:27:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR23117299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,765,350
Mapped reads	1,684,715 / 95.43%
Unmapped reads	80,635 / 4.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,860 / 0.56%
Read min/max/mean length	25 / 585 / 262.4
Duplicated reads (estimated)	785,321 / 44.49%
Duplication rate	33.55%
Clipped reads	1,694,573 / 95.99%

2.2. ACGT Content

Number/percentage of A's	116,582,193 / 29.6%
Number/percentage of C's	80,512,155 / 20.44%
Number/percentage of T's	115,924,566 / 29.44%
Number/percentage of G's	80,786,824 / 20.51%
Number/percentage of N's	0 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.1275

Standard Deviation	1.7581
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2.4. Mapping Quality

Mean Mapping Quality	53.75
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2.5. Mismatches and indels

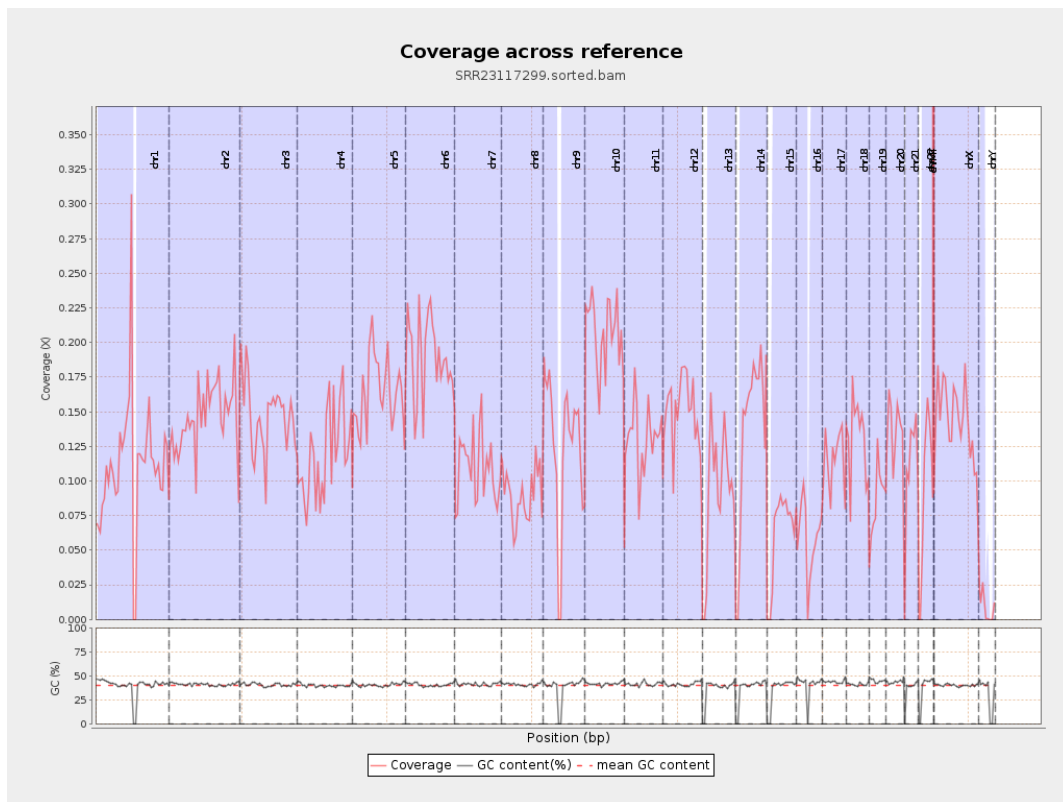
General error rate	0.87%
Mismatches	1,963,582
Insertions	1,285,915
Mapped reads with at least one insertion	35%
Deletions	615,858
Mapped reads with at least one deletion	25.07%
Homopolymer indels	33.13%

2.6. Chromosome stats

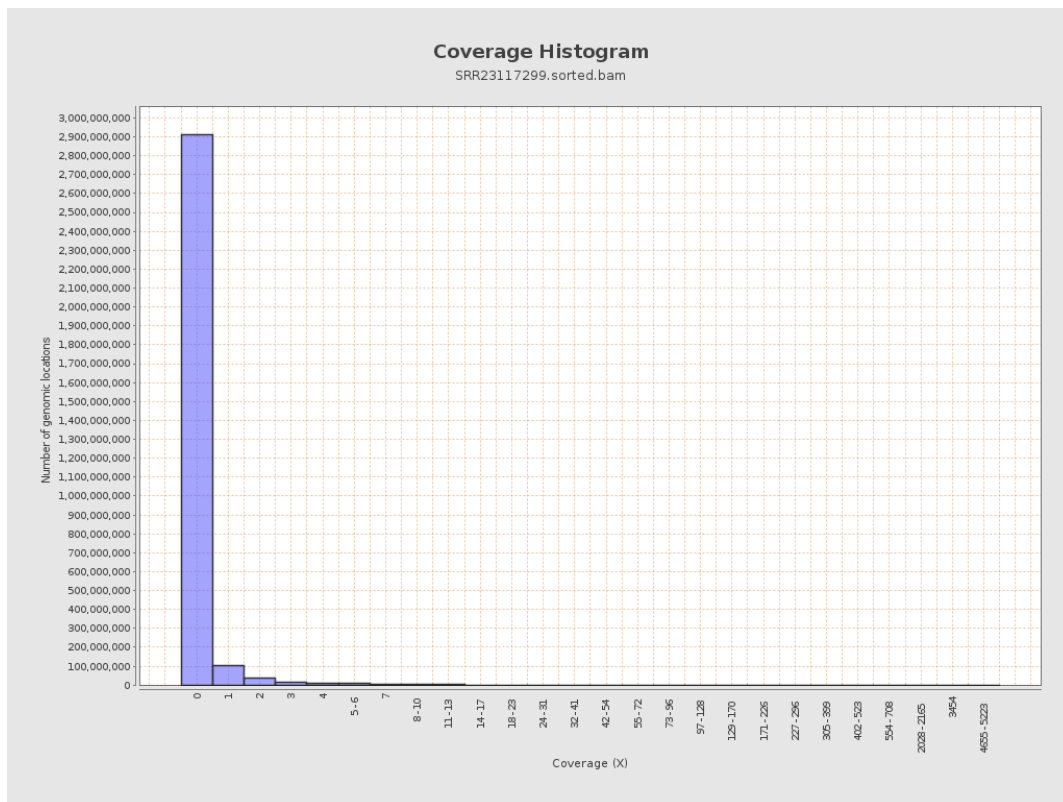
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27824125	0.1116	5.1967
chr2	243199373	35523679	0.1461	0.7857
chr3	198022430	29257037	0.1477	0.7573
chr4	191154276	22437082	0.1174	0.7691
chr5	180915260	29668968	0.164	0.8158
chr6	171115067	32382376	0.1892	0.9074
chr7	159138663	17517665	0.1101	2.696

chr8	146364022	13202683	0.0902	0.5502
chr9	141213431	17737583	0.1256	0.7297
chr10	135534747	28233852	0.2083	1.2424
chr11	135006516	17676846	0.1309	0.7107
chr12	133851895	20114699	0.1503	0.7766
chr13	115169878	10450613	0.0907	0.5698
chr14	107349540	14597052	0.136	0.7613
chr15	102531392	6422747	0.0626	0.4409
chr16	90354753	5411303	0.0599	0.7673
chr17	81195210	9202327	0.1133	0.6994
chr18	78077248	10269983	0.1315	0.7878
chr19	59128983	5173936	0.0875	1.1343
chr20	63025520	8511978	0.1351	0.8342
chr21	48129895	5282397	0.1098	0.8771
chr22	51304566	4726108	0.0921	0.6668
chrMT	16571	217406	13.1197	30.8131
chrX	155270560	22221924	0.1431	0.7396
chrY	59373566	513910	0.0087	0.5292

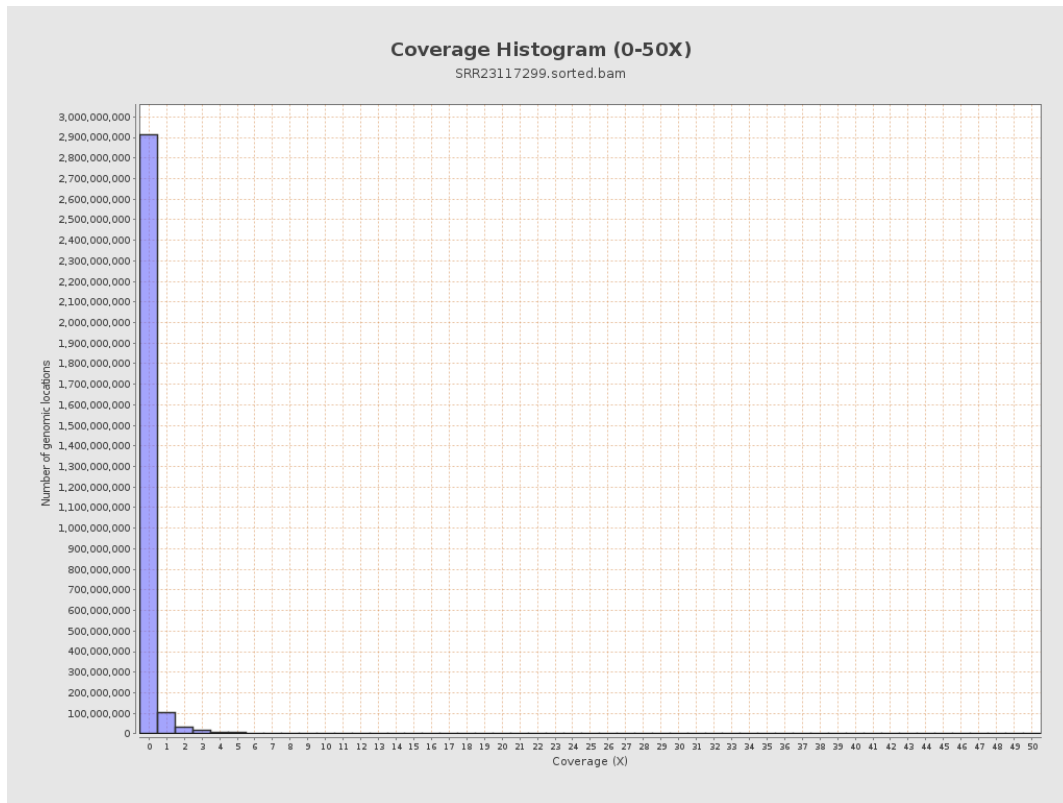
3. Results : Coverage across reference



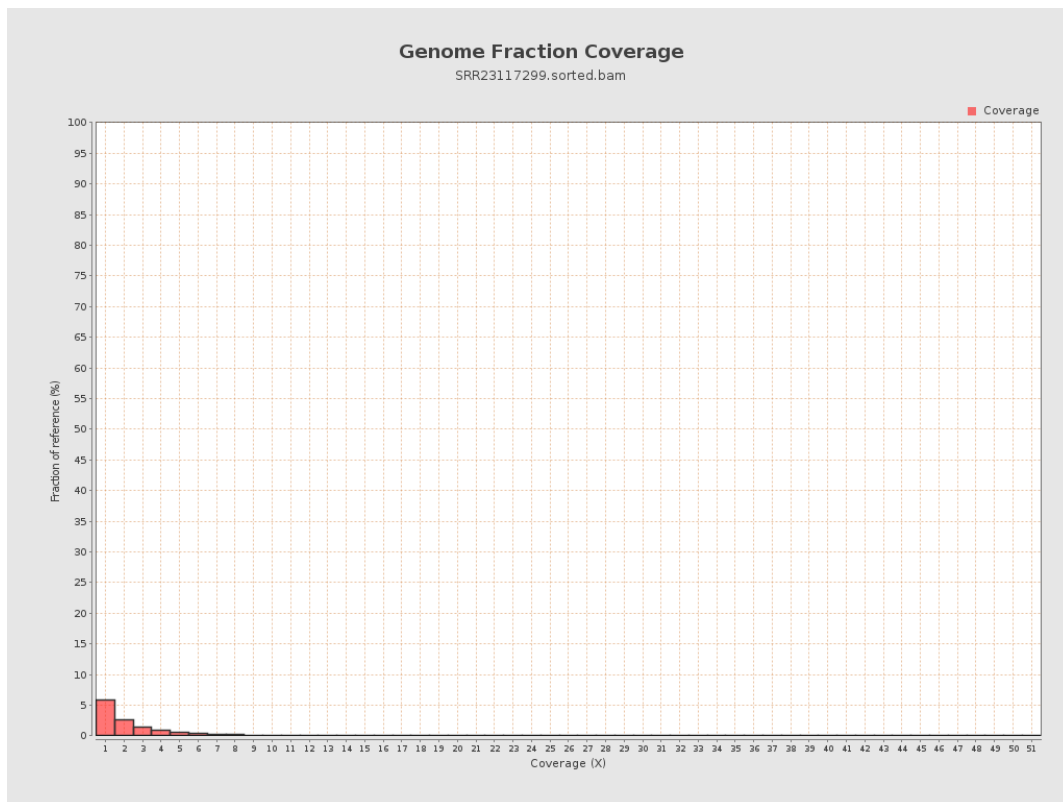
4. Results : Coverage Histogram



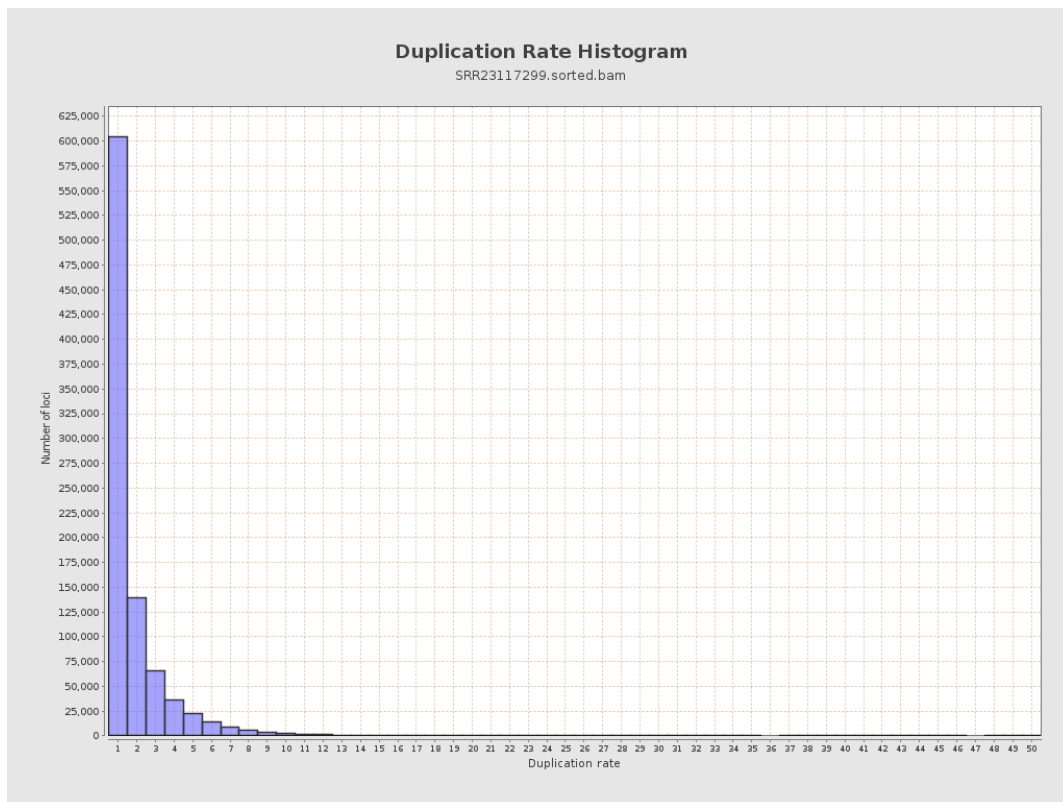
5. Results : Coverage Histogram (0-50X)



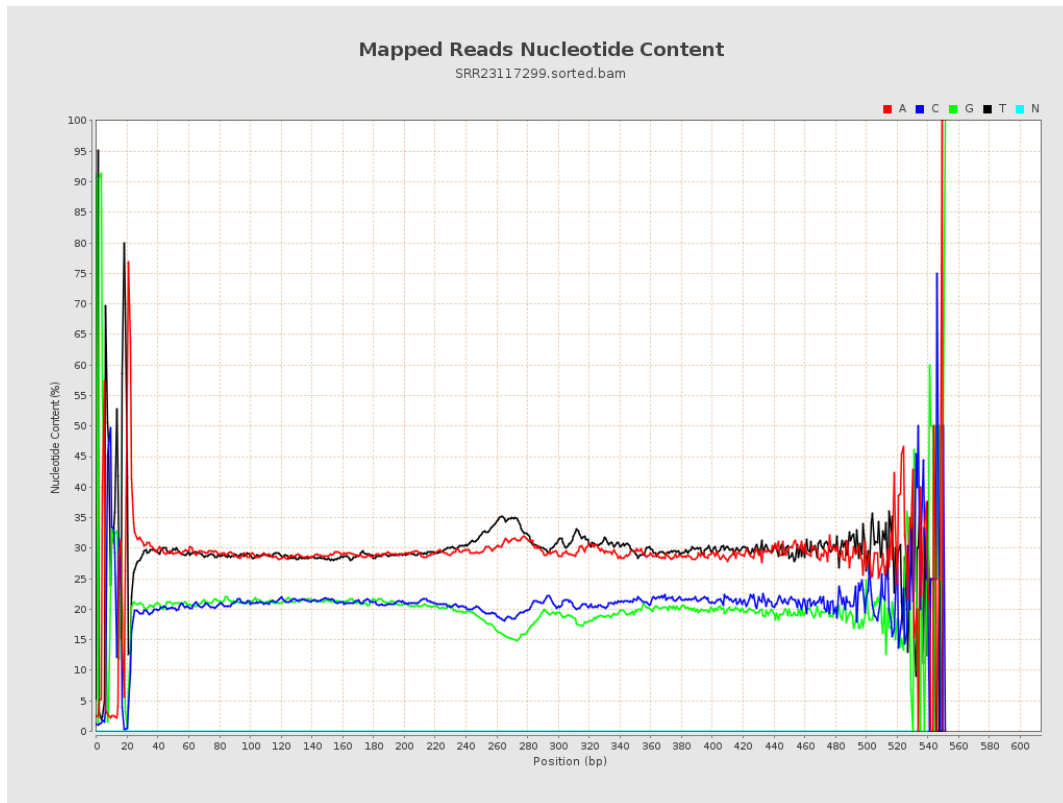
6. Results : Genome Fraction Coverage



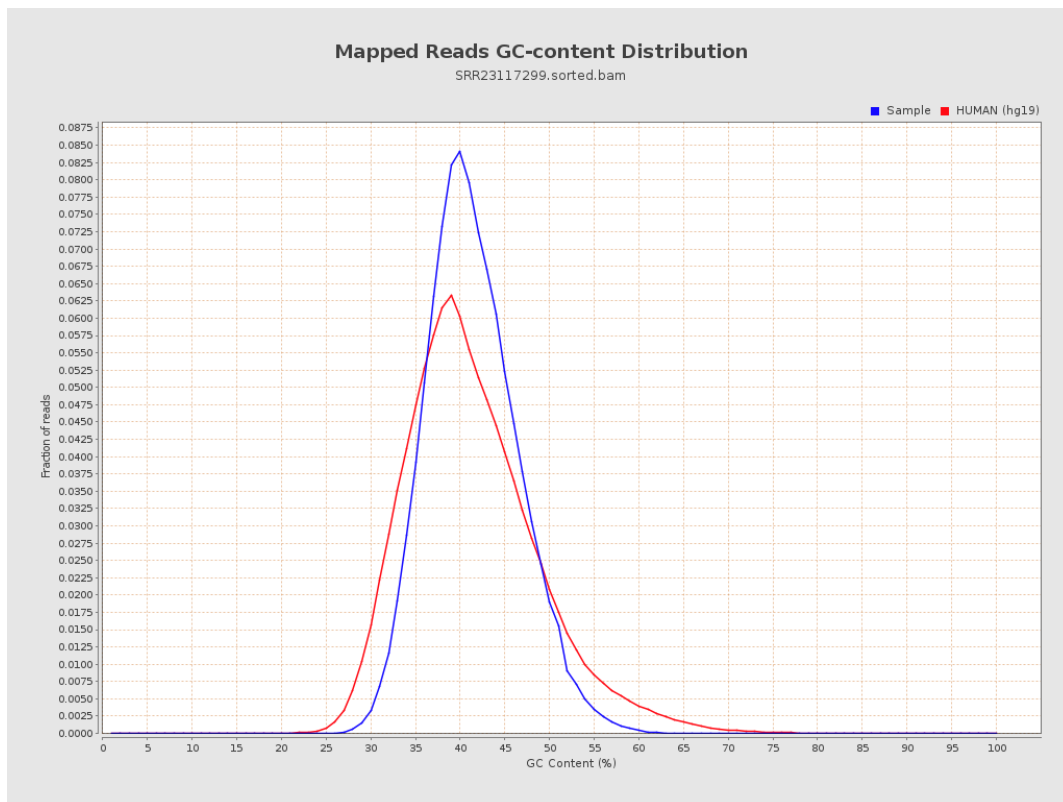
7. Results : Duplication Rate Histogram



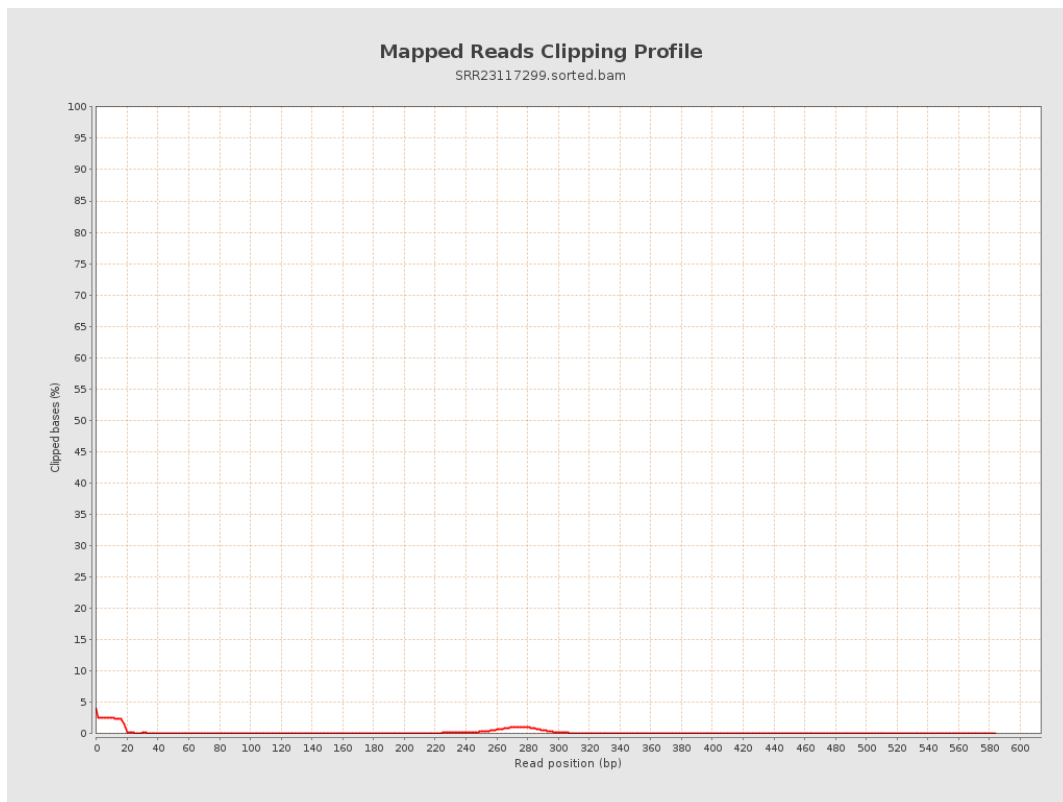
8. Results : Mapped Reads Nucleotide Content



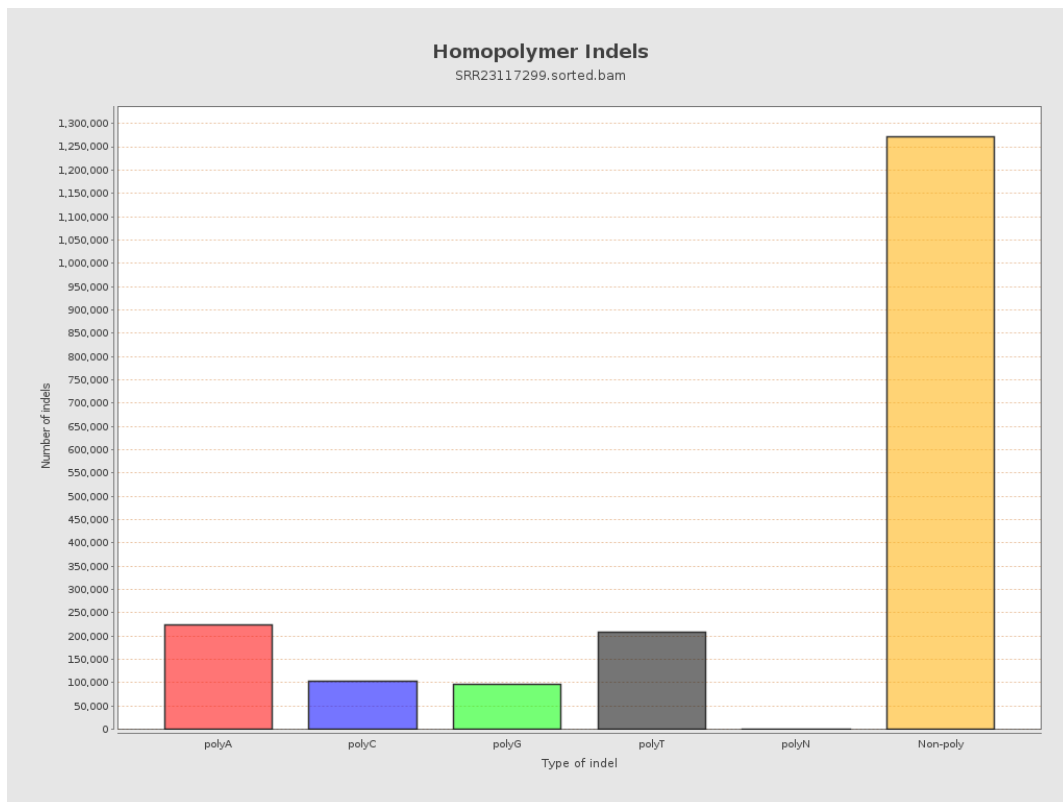
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

