

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 14:47:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153329.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_SRR1153329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 14:47:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	111,367,544
Mapped reads	109,336,091 / 98.18%
Unmapped reads	2,031,453 / 1.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	545,674 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	51,980,295 / 46.67%
Duplication rate	32.92%
Clipped reads	14,314,642 / 12.85%

2.2. ACGT Content

Number/percentage of A's	2,742,887,130 / 25.81%
Number/percentage of C's	2,570,234,581 / 24.19%
Number/percentage of T's	2,775,165,189 / 26.11%
Number/percentage of G's	2,535,884,498 / 23.86%
Number/percentage of N's	2,740,526 / 0.03%
GC Percentage	48.05%

2.3. Coverage

Mean	3.4334

Standard Deviation	24.7194
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2.4. Mapping Quality

Mean Mapping Quality	49.65
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2.5. Mismatches and indels

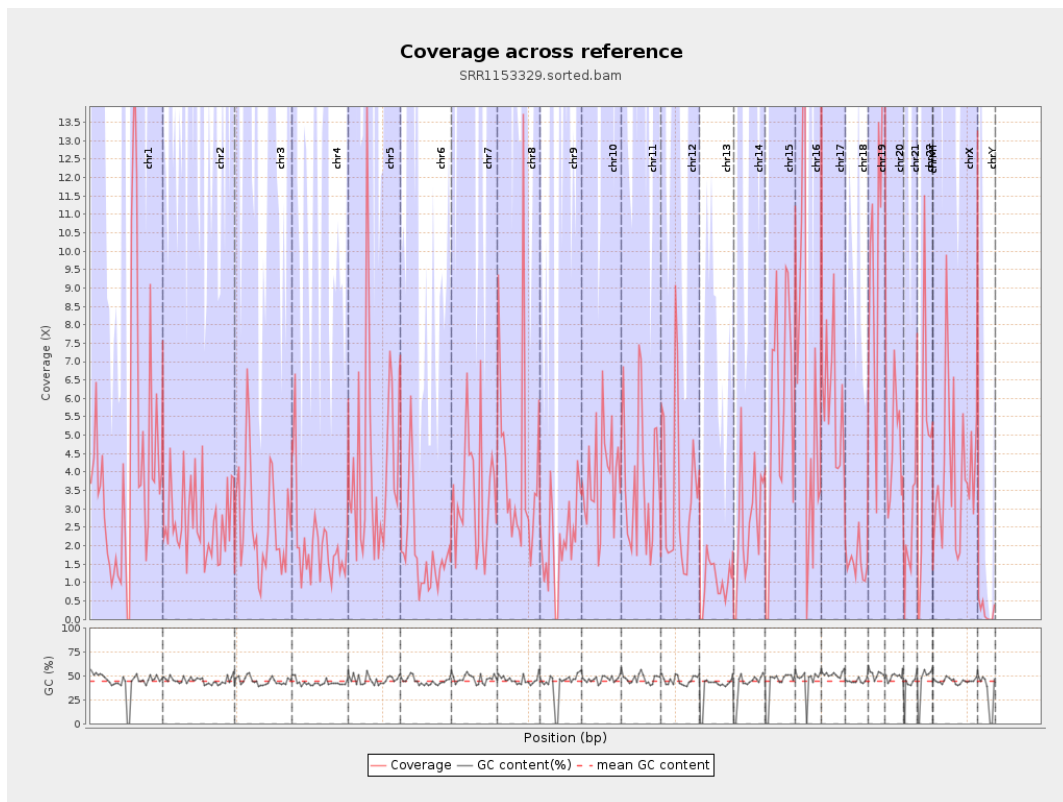
General error rate	0.39%
Mismatches	40,589,299
Insertions	593,223
Mapped reads with at least one insertion	0.53%
Deletions	777,895
Mapped reads with at least one deletion	0.7%
Homopolymer indels	44.42%

2.6. Chromosome stats

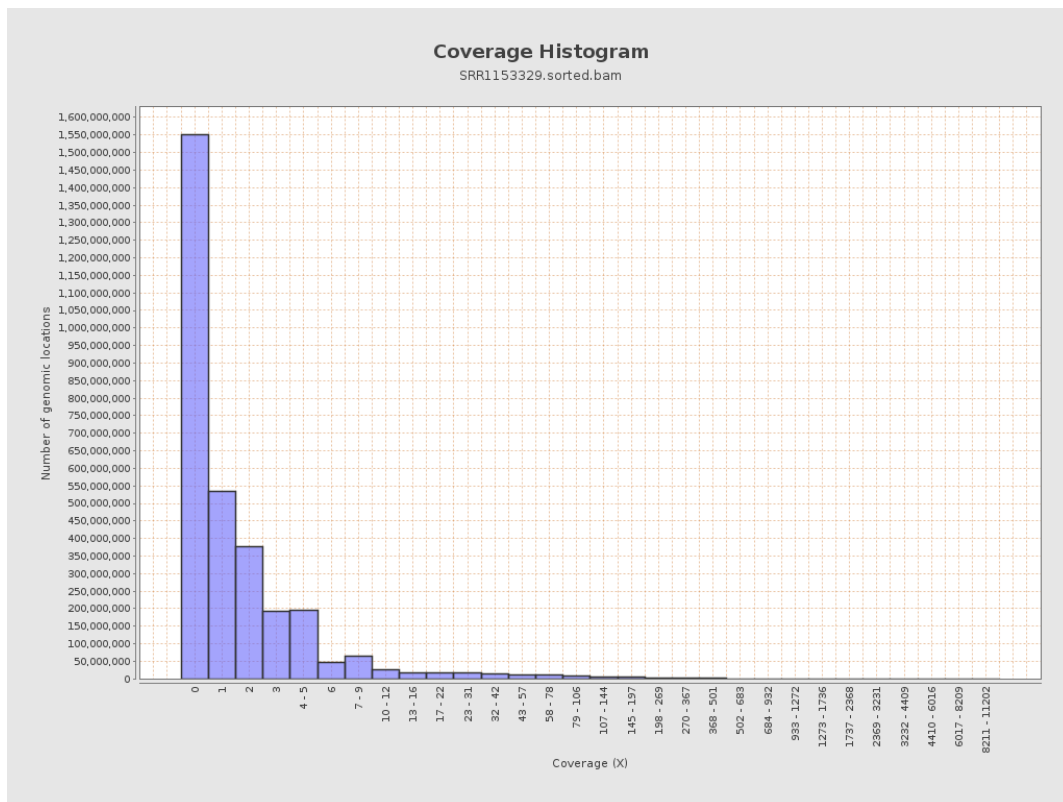
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1010628430	4.0547	24.1509
chr2	243199373	646356339	2.6577	13.1368
chr3	198022430	524552900	2.649	13.2016
chr4	191154276	390906204	2.045	15.3891
chr5	180915260	759379172	4.1974	56.256
chr6	171115067	301970500	1.7647	10.2099
chr7	159138663	545705165	3.4291	23.064

chr8	146364022	599506018	4.096	39.1916
chr9	141213431	293217676	2.0764	11.498
chr10	135534747	520852177	3.8429	19.5224
chr11	135006516	505708877	3.7458	17.5623
chr12	133851895	469876381	3.5104	17.2648
chr13	115169878	119374909	1.0365	6.3786
chr14	107349540	278740334	2.5966	14.0548
chr15	102531392	559466915	5.4565	28.4647
chr16	90354753	571988862	6.3305	36.9136
chr17	81195210	483070911	5.9495	26.9204
chr18	78077248	119258101	1.5274	8.0658
chr19	59128983	617505295	10.4434	41.2701
chr20	63025520	299879663	4.7581	22.1139
chr21	48129895	134162166	2.7875	24.7365
chr22	51304566	233111285	4.5437	25.7879
chrMT	16571	21831	1.3174	1.8168
chrX	155270560	630736784	4.0622	21.2447
chrY	59373566	12650930	0.2131	7.6

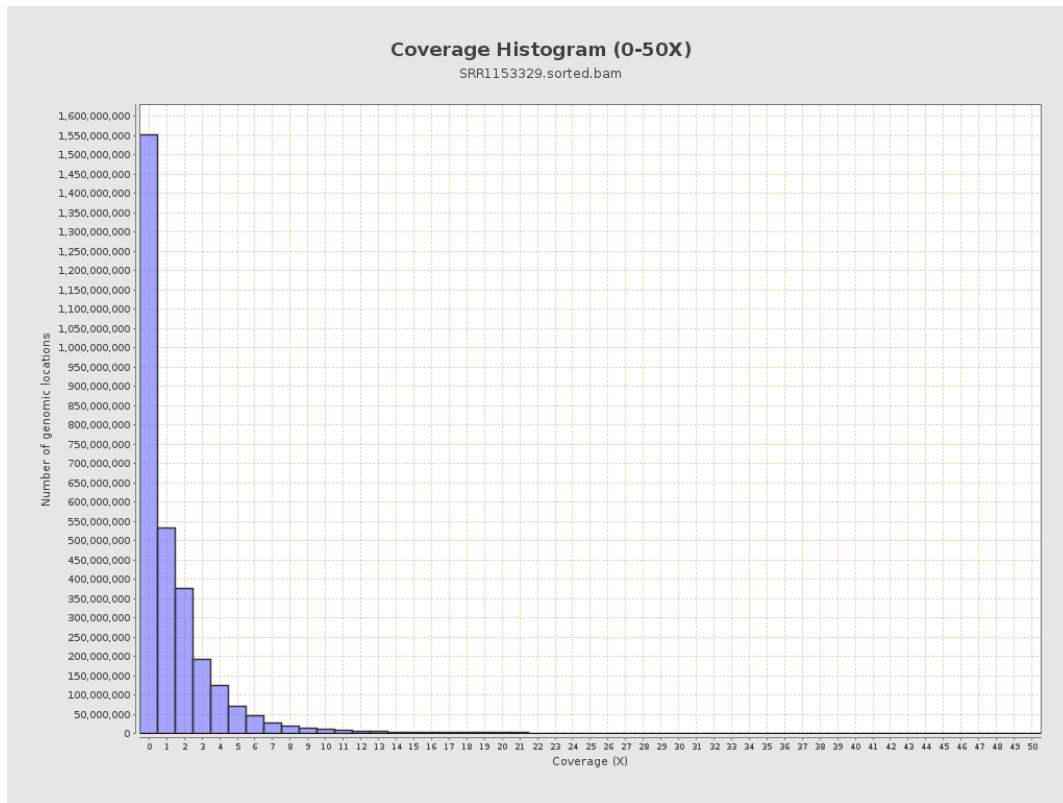
3. Results : Coverage across reference



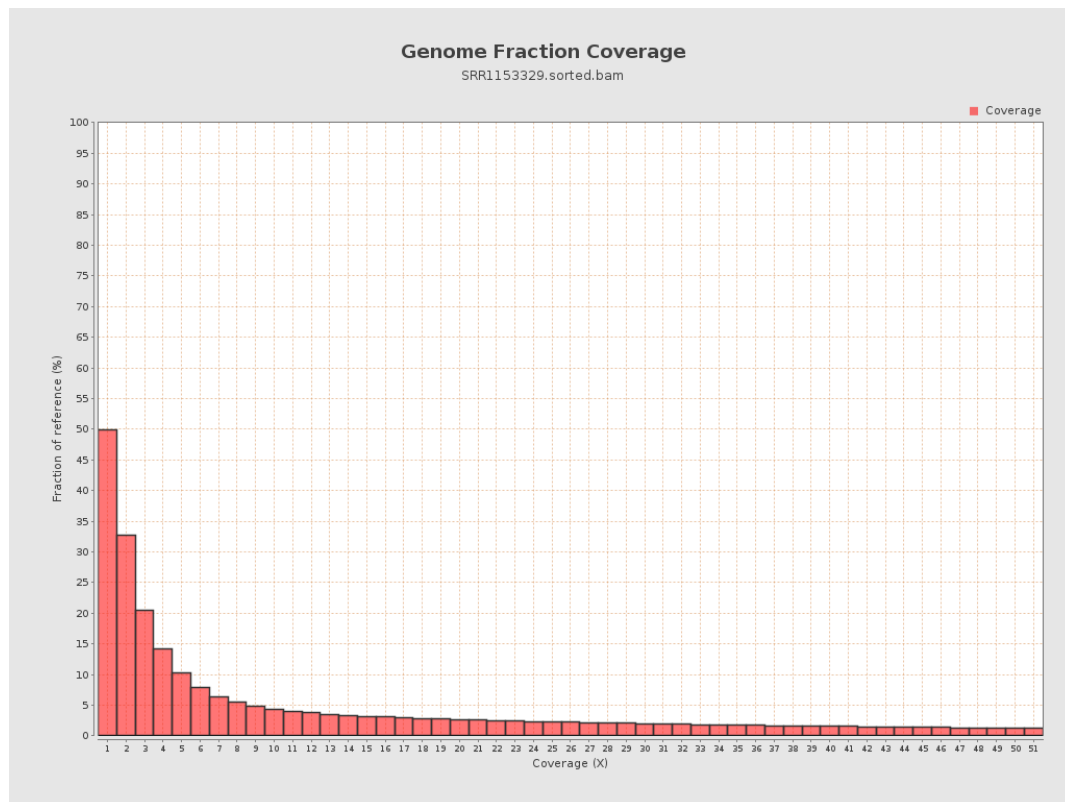
4. Results : Coverage Histogram



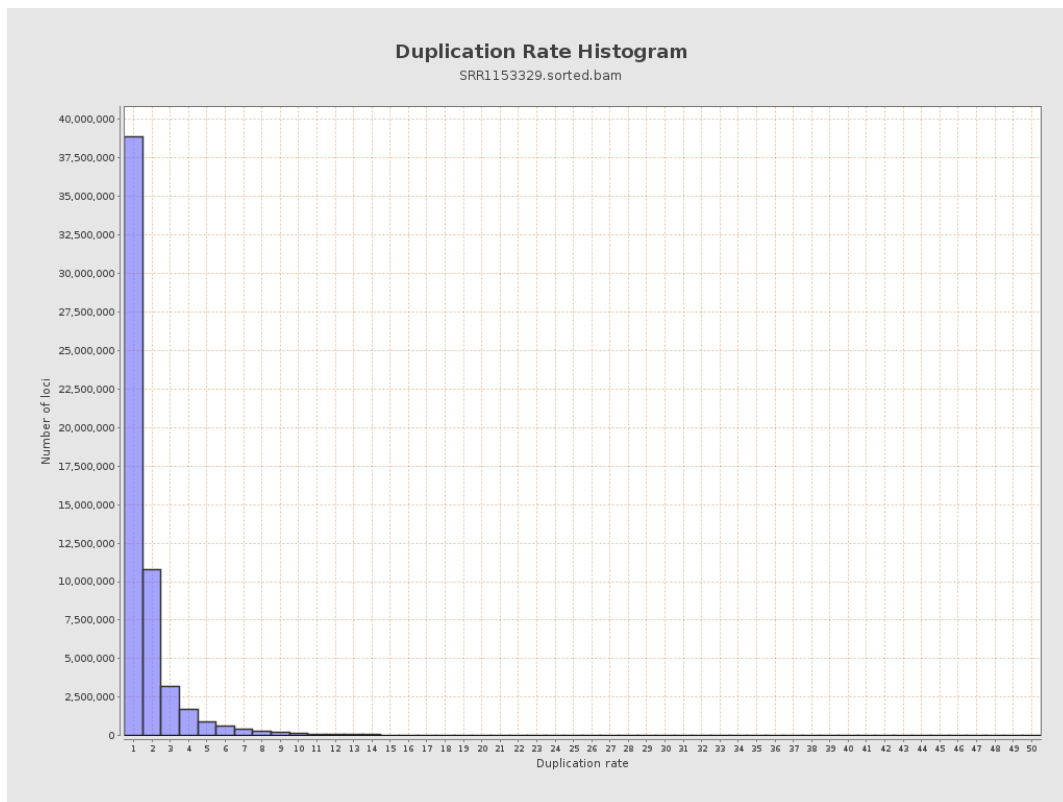
5. Results : Coverage Histogram (0-50X)



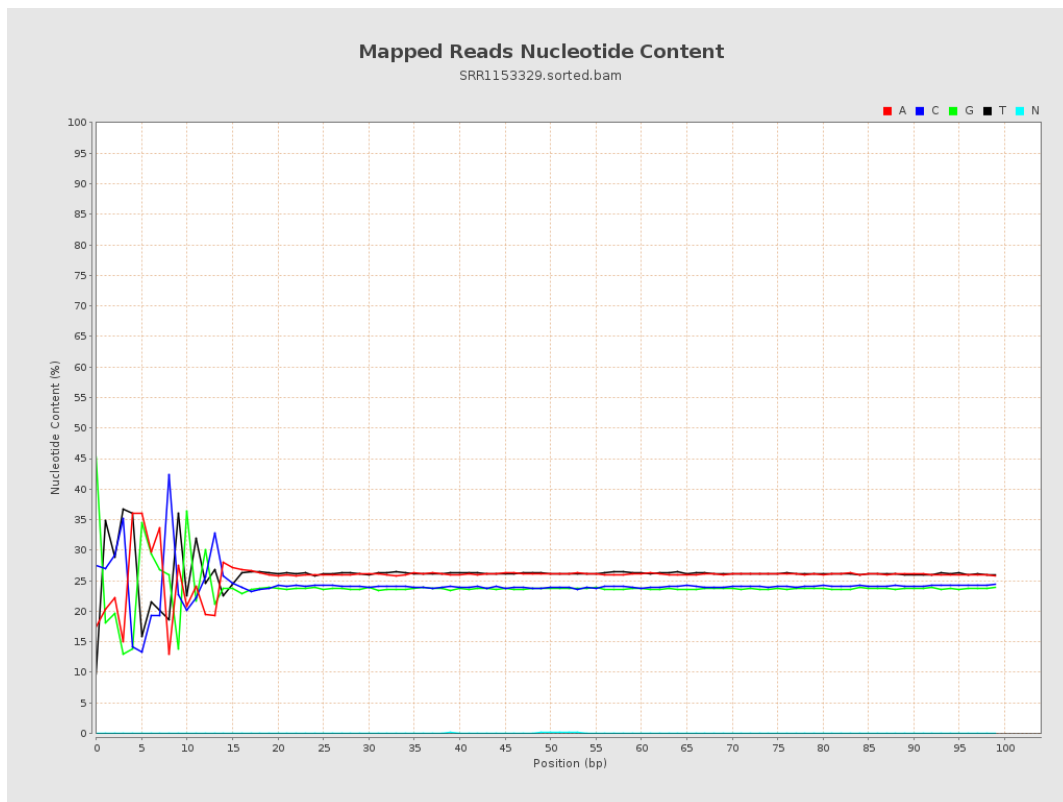
6. Results : Genome Fraction Coverage



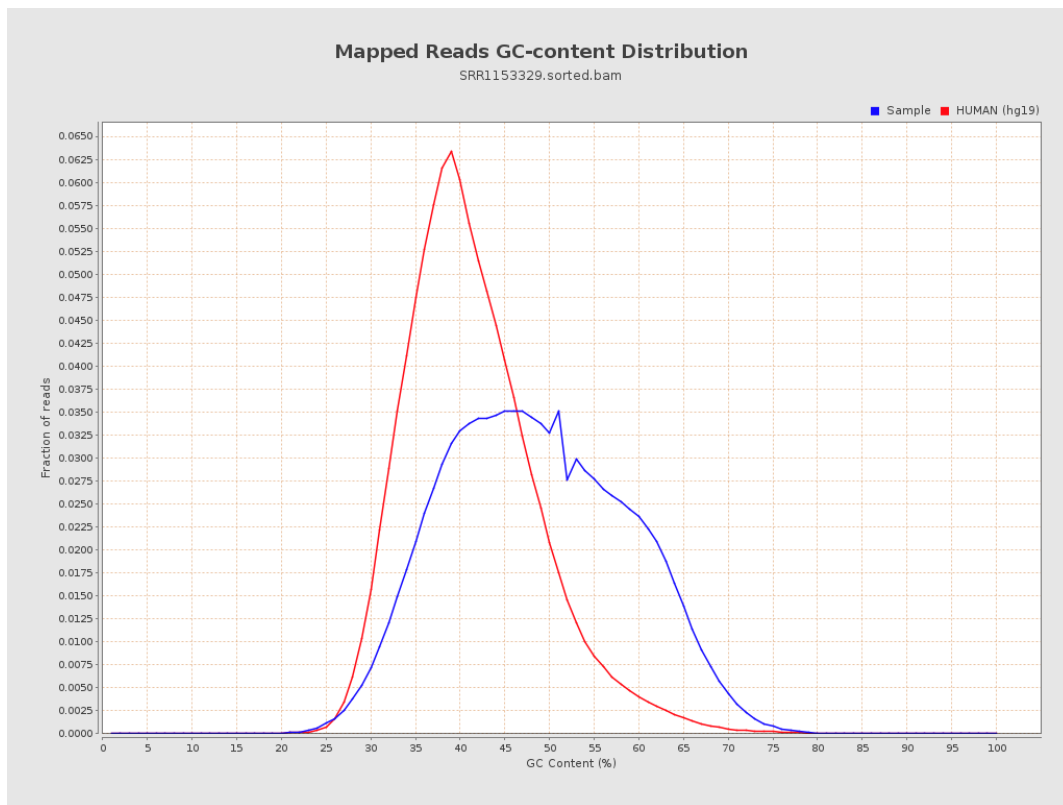
7. Results : Duplication Rate Histogram



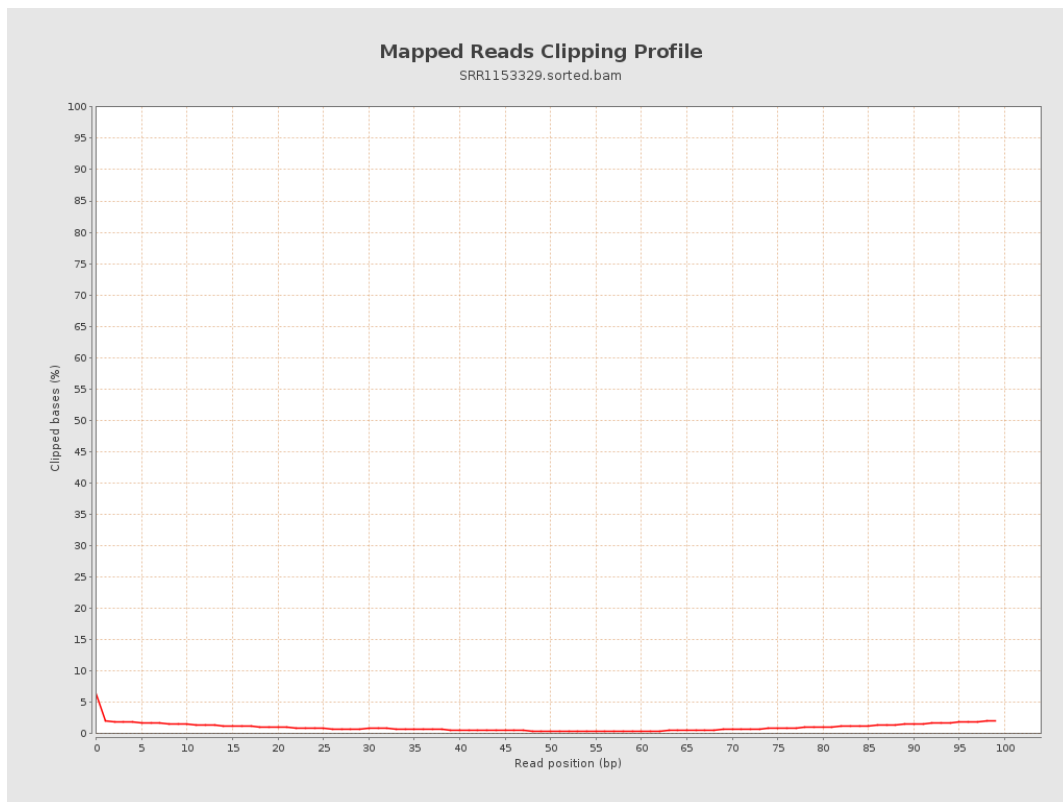
8. Results : Mapped Reads Nucleotide Content



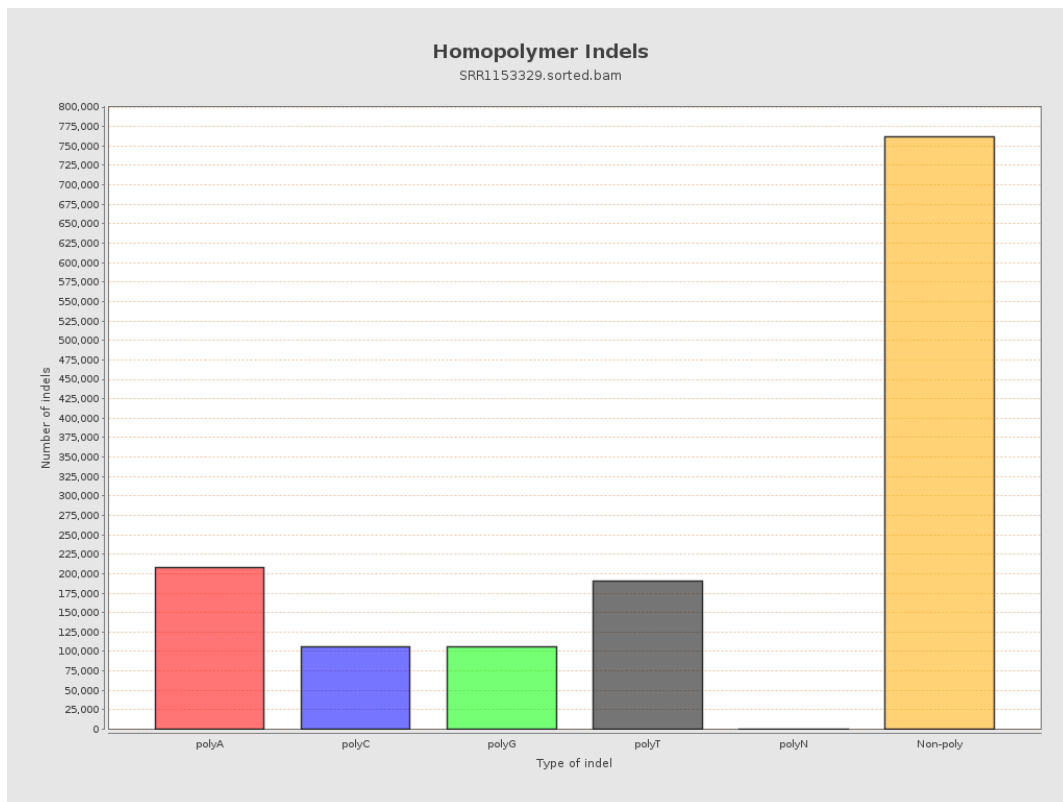
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

