

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:03:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506336.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_SRR1506336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:03:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,367,703
Mapped reads	10,589,518 / 79.22%
Unmapped reads	2,778,185 / 20.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	184,991 / 1.38%
Read min/max/mean length	30 / 94 / 94.5
Duplicated reads (estimated)	1,530,899 / 11.45%
Duplication rate	10.52%
Clipped reads	7,074,278 / 52.92%

2.2. ACGT Content

Number/percentage of A's	230,625,119 / 28.17%
Number/percentage of C's	148,115,240 / 18.09%
Number/percentage of T's	236,742,694 / 28.92%
Number/percentage of G's	202,920,693 / 24.79%
Number/percentage of N's	179,142 / 0.02%
GC Percentage	42.88%

2.3. Coverage

Mean	0.2645

Standard Deviation	1.6186
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2.4. Mapping Quality

Mean Mapping Quality	47.5
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2.5. Mismatches and indels

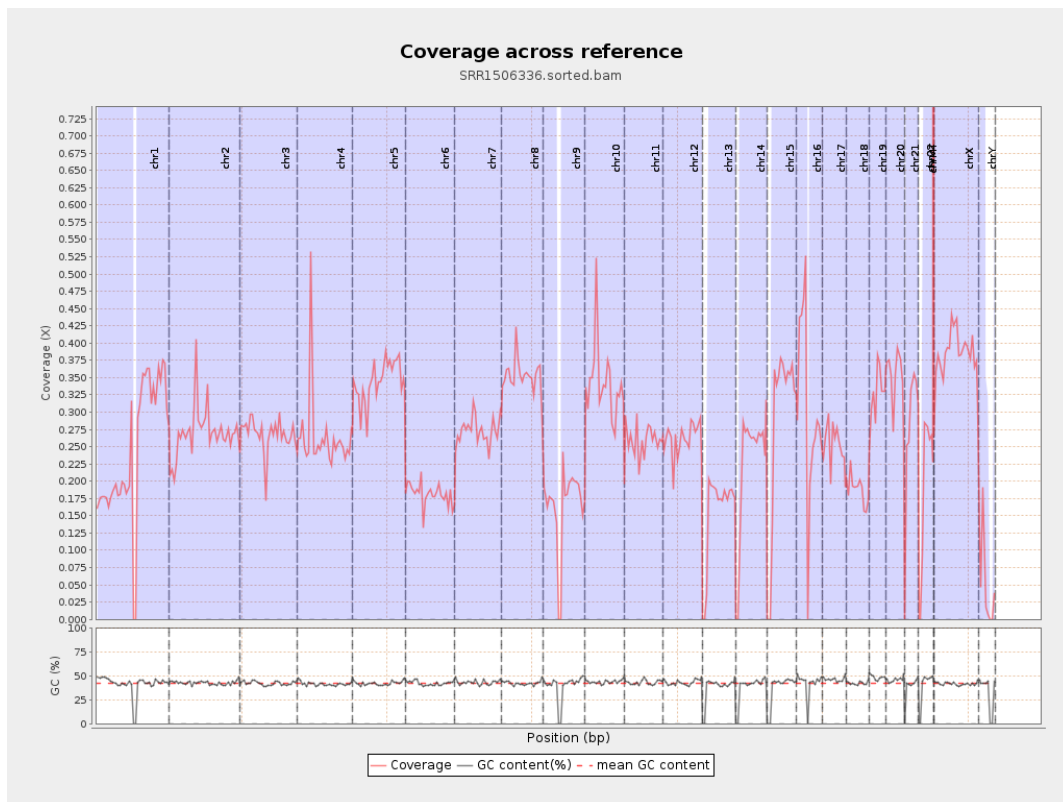
General error rate	0.76%
Mismatches	6,091,338
Insertions	67,565
Mapped reads with at least one insertion	0.62%
Deletions	177,045
Mapped reads with at least one deletion	1.64%
Homopolymer indels	43.93%

2.6. Chromosome stats

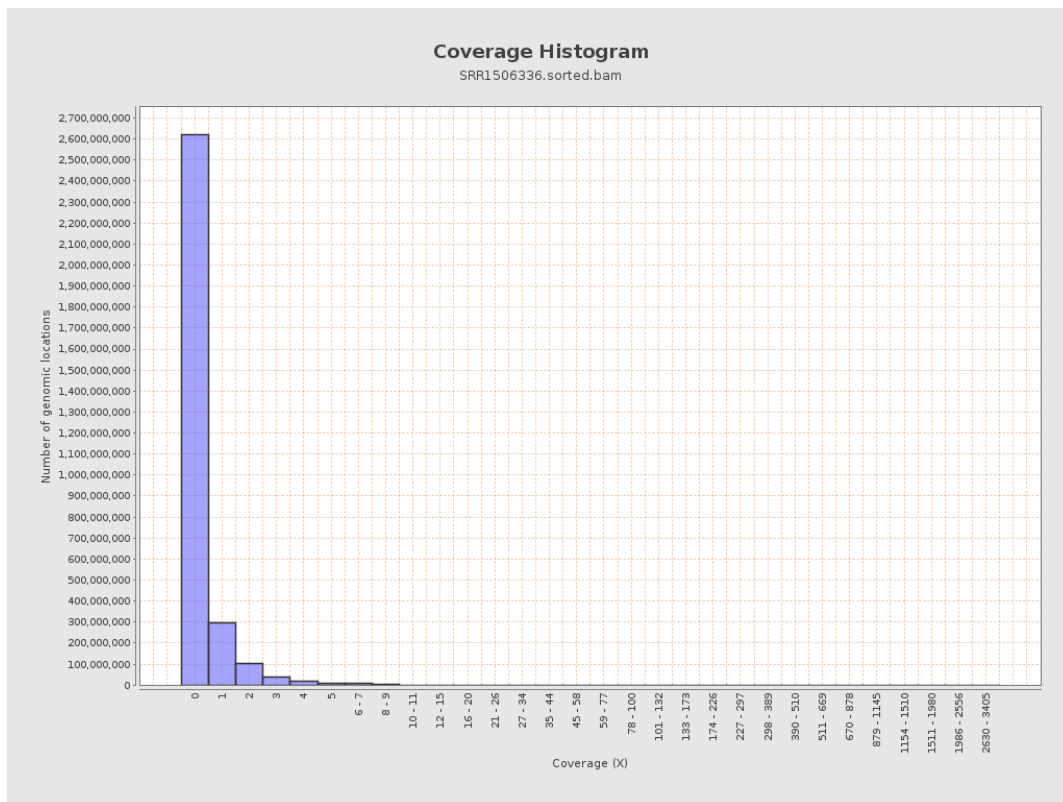
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	60778405	0.2438	2.8132
chr2	243199373	65773240	0.2704	1.7618
chr3	198022430	52959234	0.2674	0.8079
chr4	191154276	50166467	0.2624	1.43
chr5	180915260	62251926	0.3441	0.9482
chr6	171115067	31023104	0.1813	0.7973
chr7	159138663	43547040	0.2736	1.9261

chr8	146364022	51689129	0.3532	2.6819
chr9	141213431	23067455	0.1634	1.4593
chr10	135534747	46363265	0.3421	1.8957
chr11	135006516	34939594	0.2588	1.49
chr12	133851895	34862897	0.2605	0.9381
chr13	115169878	17759568	0.1542	0.5943
chr14	107349540	23887198	0.2225	0.8614
chr15	102531392	29586117	0.2886	0.8964
chr16	90354753	27791414	0.3076	1.2099
chr17	81195210	20450321	0.2519	0.9838
chr18	78077248	14664880	0.1878	2.5554
chr19	59128983	19513824	0.33	2.0634
chr20	63025520	22035292	0.3496	1.0516
chr21	48129895	13472175	0.2799	1.2561
chr22	51304566	9652469	0.1881	0.7104
chrMT	16571	120803	7.29	5.6198
chrX	155270560	59657553	0.3842	1.1992
chrY	59373566	2916943	0.0491	1.6274

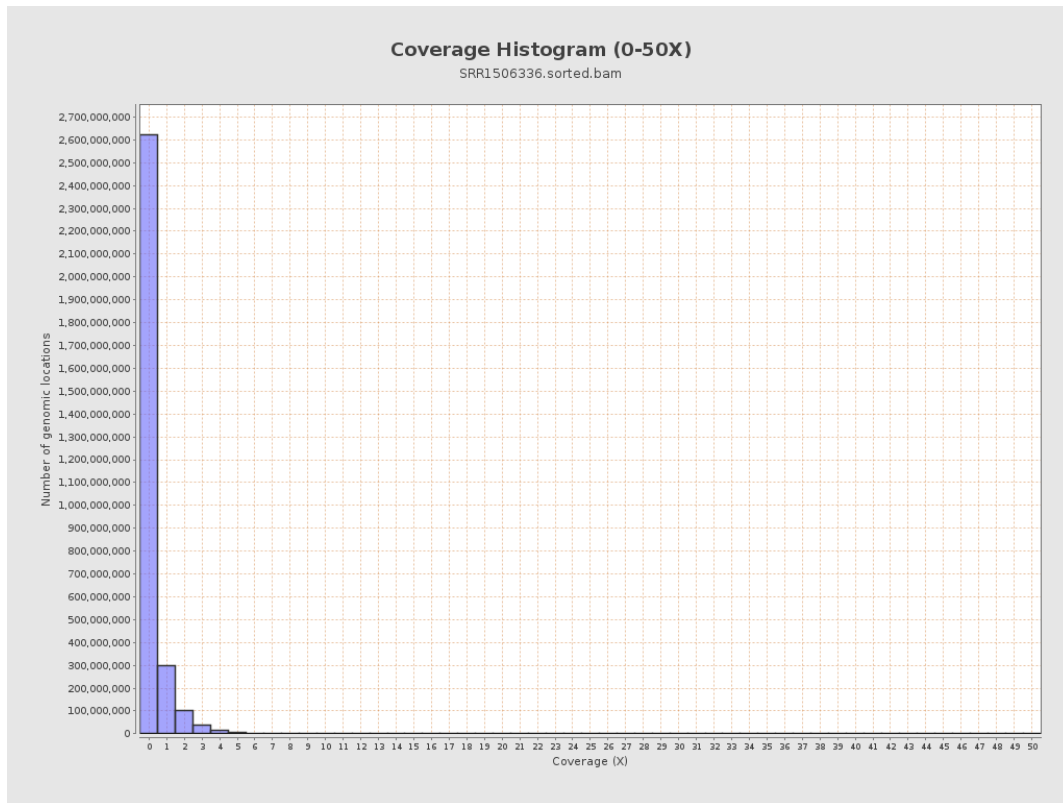
3. Results : Coverage across reference



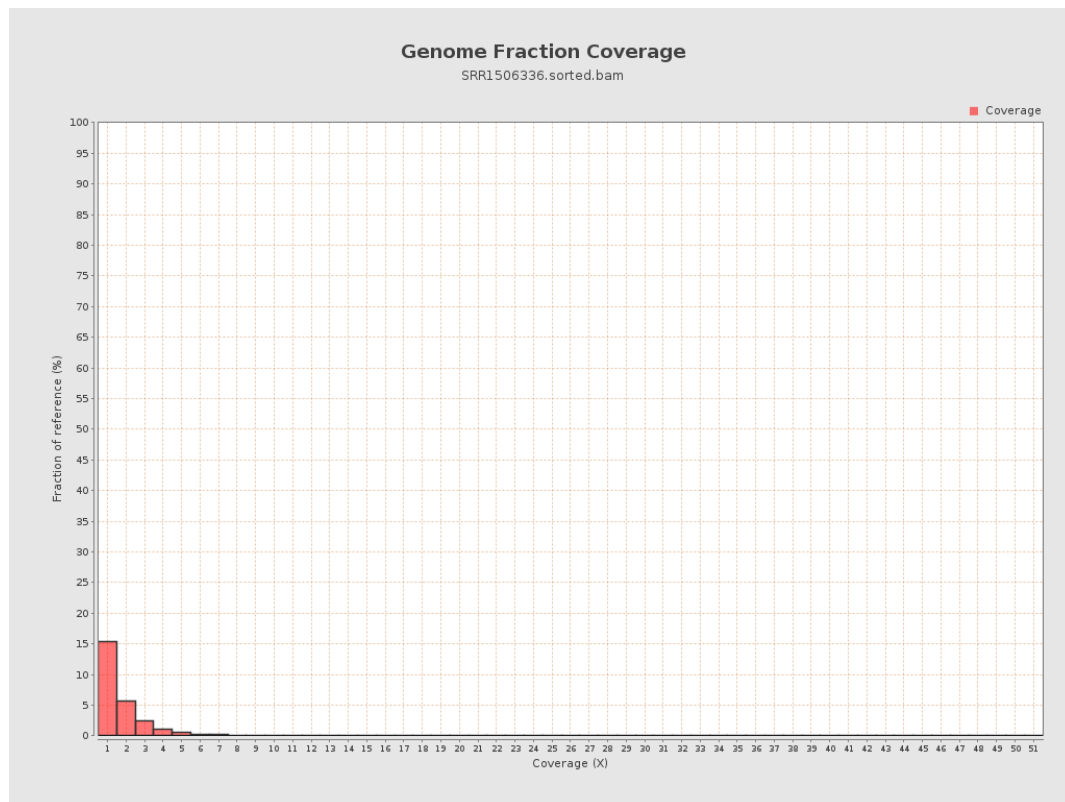
4. Results : Coverage Histogram



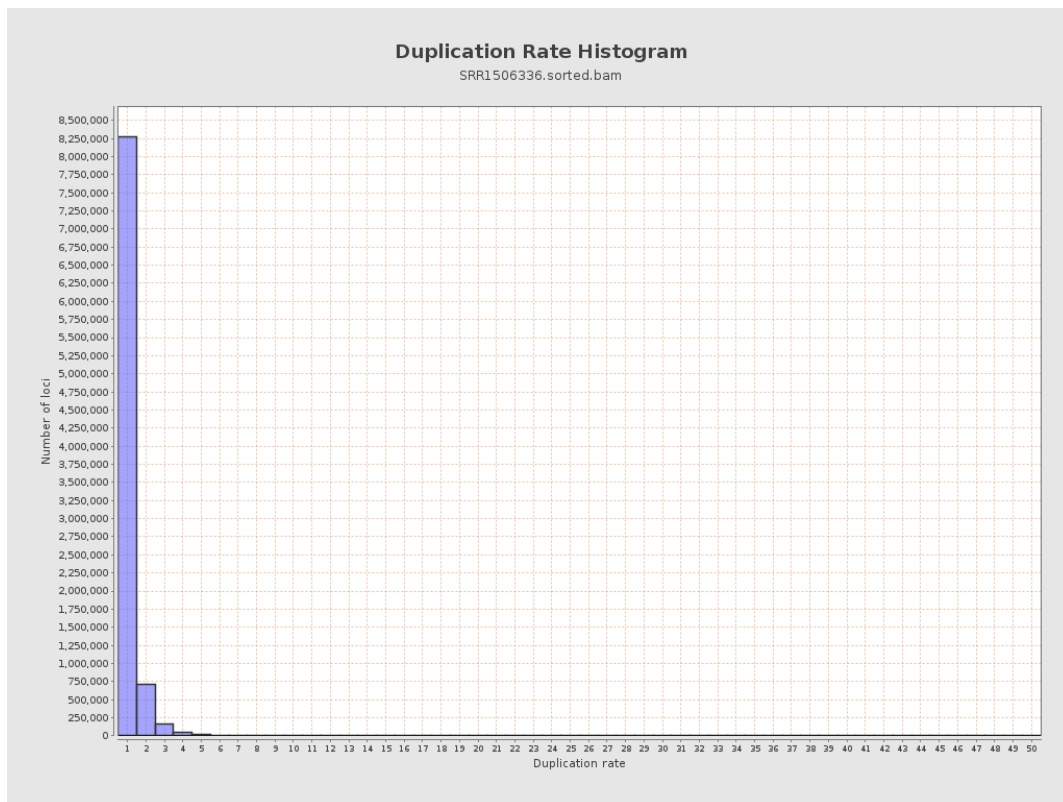
5. Results : Coverage Histogram (0-50X)



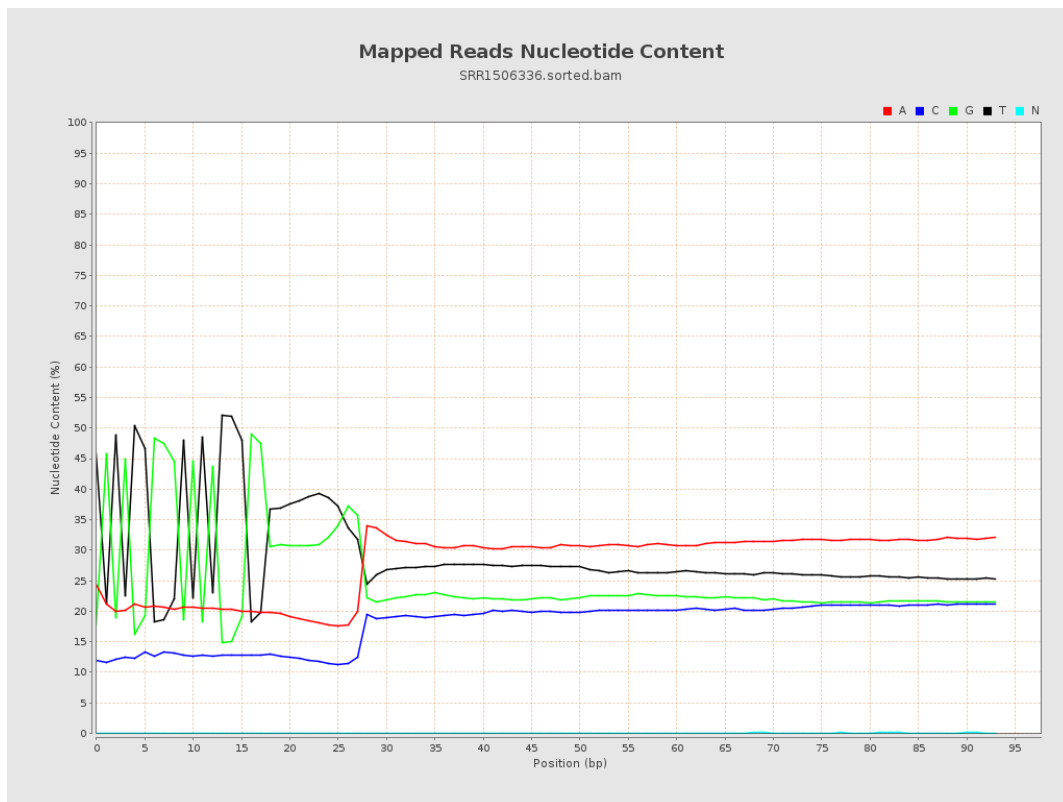
6. Results : Genome Fraction Coverage



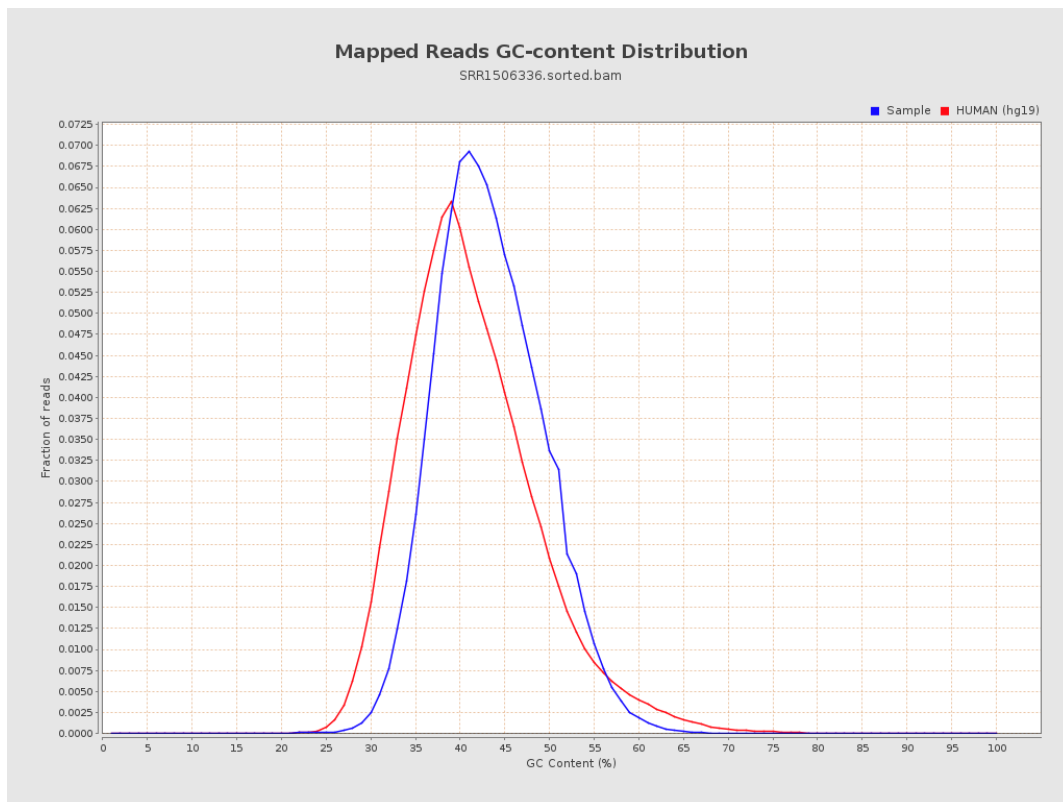
7. Results : Duplication Rate Histogram



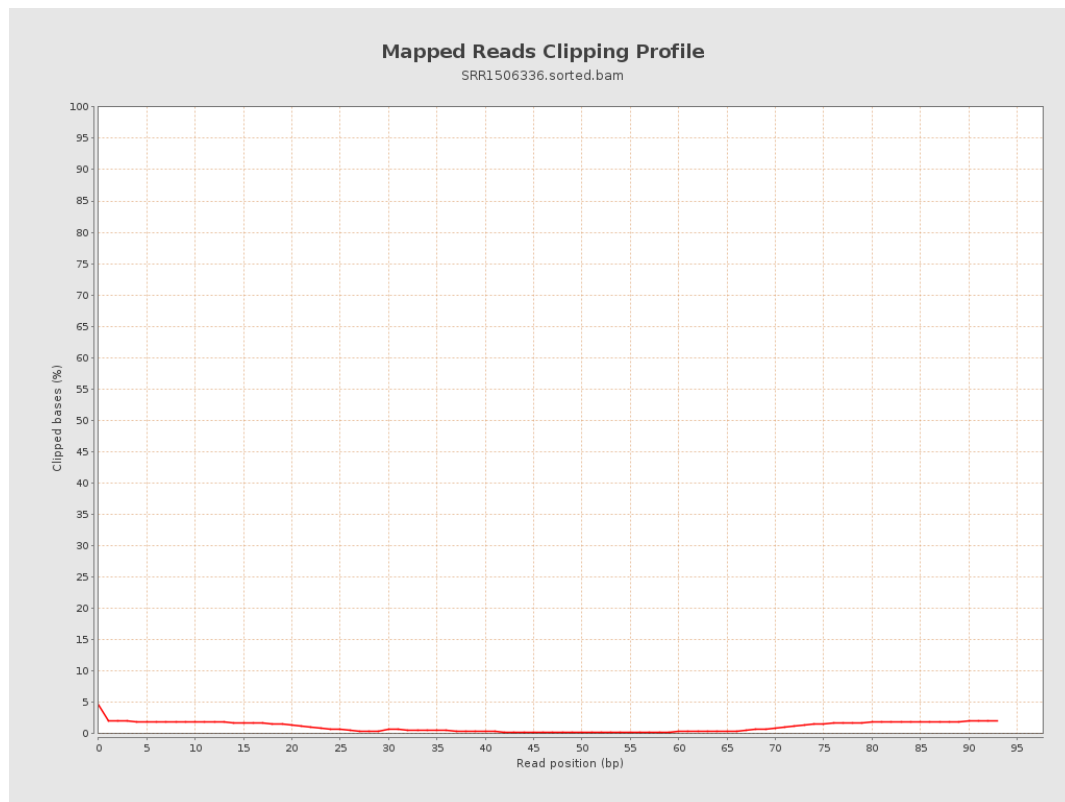
8. Results : Mapped Reads Nucleotide Content



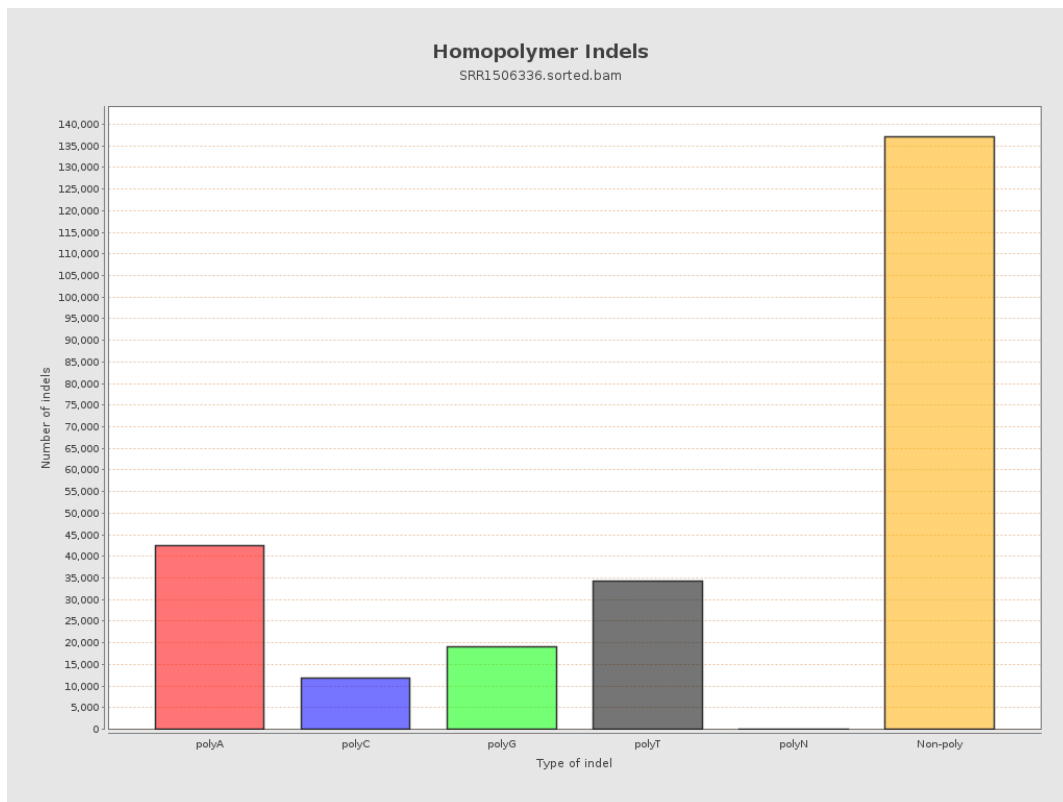
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

