

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:24:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013300.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_SRR6013300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:24:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,072,991
Mapped reads	2,772,166 / 90.21%
Unmapped reads	300,825 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,639 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	94,628 / 3.08%
Duplication rate	2.03%
Clipped reads	1,435,108 / 46.7%

2.2. ACGT Content

Number/percentage of A's	49,776,111 / 27.68%
Number/percentage of C's	34,922,156 / 19.42%
Number/percentage of T's	53,722,843 / 29.87%
Number/percentage of G's	41,402,679 / 23.02%
Number/percentage of N's	19,910 / 0.01%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0581

Standard Deviation	0.5674
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2.4. Mapping Quality

Mean Mapping Quality	43.21
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2.5. Mismatches and indels

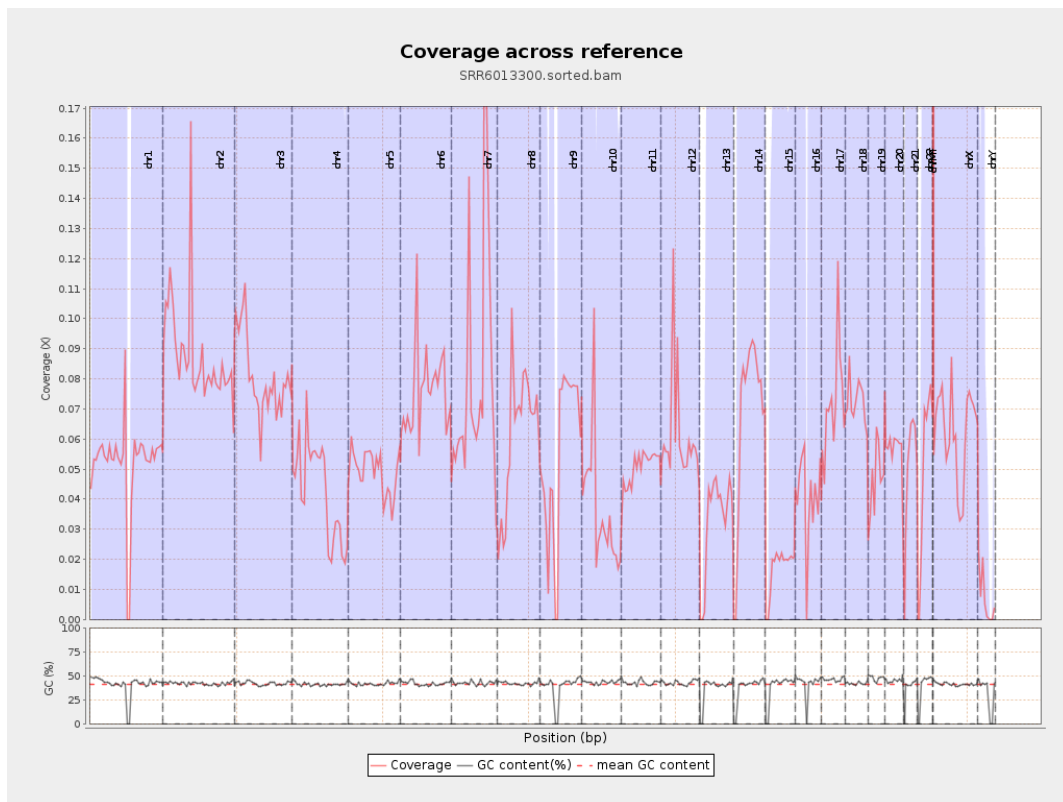
General error rate	0.8%
Mismatches	1,412,643
Insertions	13,326
Mapped reads with at least one insertion	0.48%
Deletions	48,019
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.07%

2.6. Chromosome stats

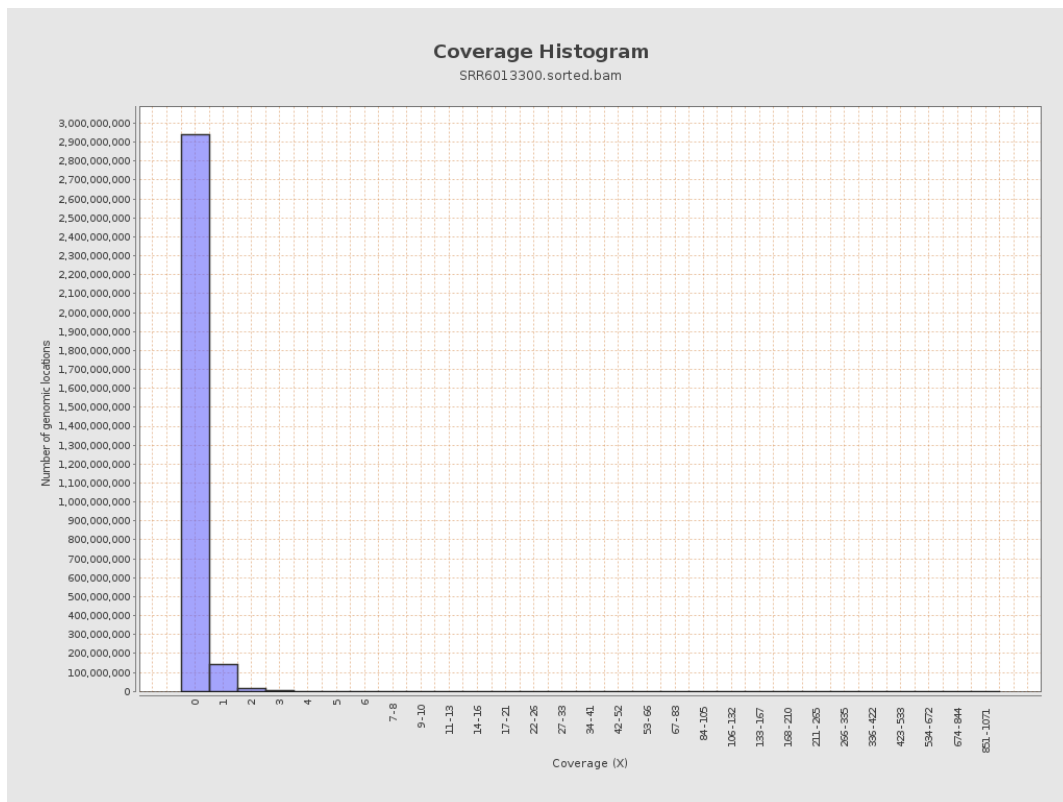
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12987603	0.0521	0.8068
chr2	243199373	21362999	0.0878	0.7679
chr3	198022430	16023997	0.0809	0.3144
chr4	191154276	8255917	0.0432	0.2742
chr5	180915260	8885521	0.0491	0.2472
chr6	171115067	13089059	0.0765	0.5254
chr7	159138663	12905564	0.0811	1.2656

chr8	146364022	8972045	0.0613	0.4494
chr9	141213431	7686173	0.0544	0.5331
chr10	135534747	4839265	0.0357	0.5775
chr11	135006516	6813146	0.0505	0.4281
chr12	133851895	8174387	0.0611	0.2854
chr13	115169878	3833131	0.0333	0.1988
chr14	107349540	7435219	0.0693	0.3419
chr15	102531392	1698213	0.0166	0.1632
chr16	90354753	3660201	0.0405	0.2958
chr17	81195210	5910529	0.0728	0.3416
chr18	78077248	5684883	0.0728	1.1102
chr19	59128983	2844042	0.0481	0.6311
chr20	63025520	3590914	0.057	0.2743
chr21	48129895	2379868	0.0494	0.2856
chr22	51304566	2538463	0.0495	0.2445
chrMT	16571	162210	9.7888	5.714
chrX	155270560	9781542	0.063	0.3485
chrY	59373566	413036	0.007	0.1983

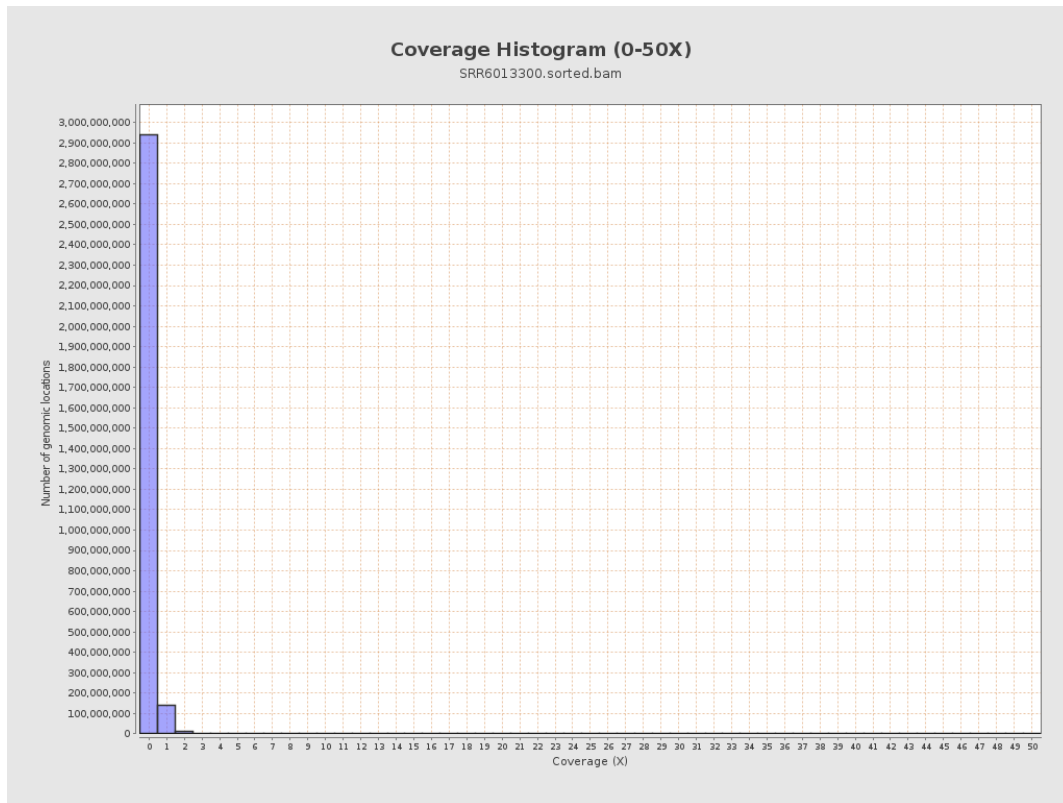
3. Results : Coverage across reference



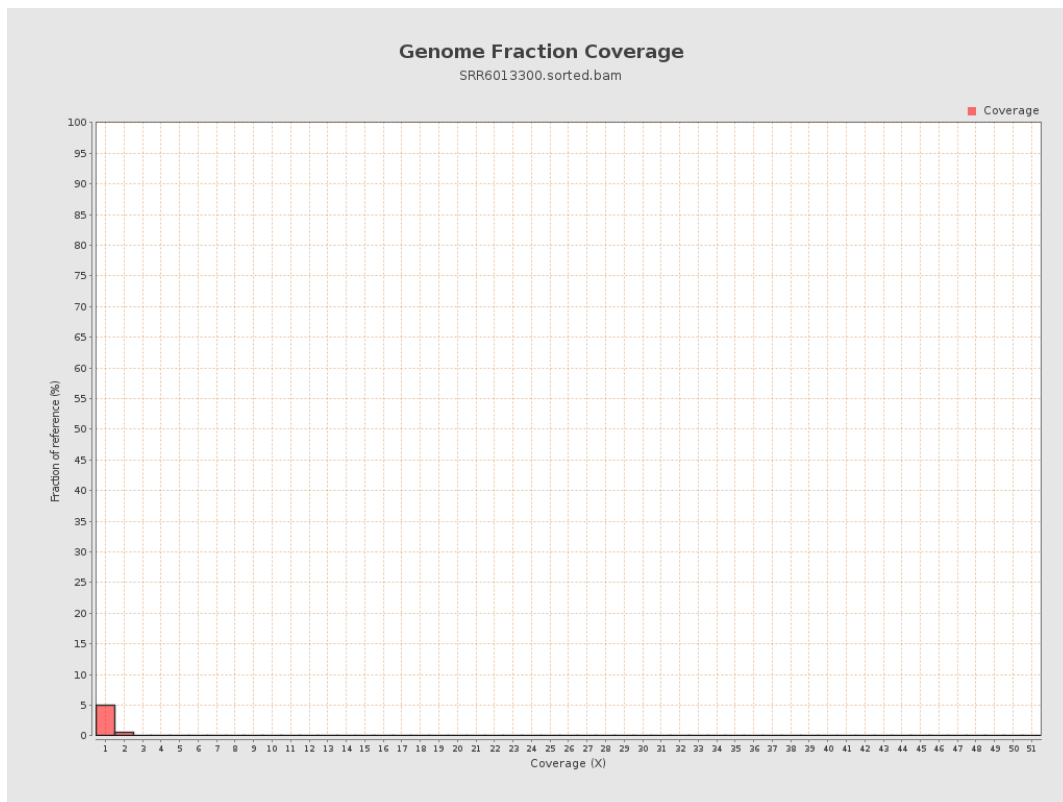
4. Results : Coverage Histogram



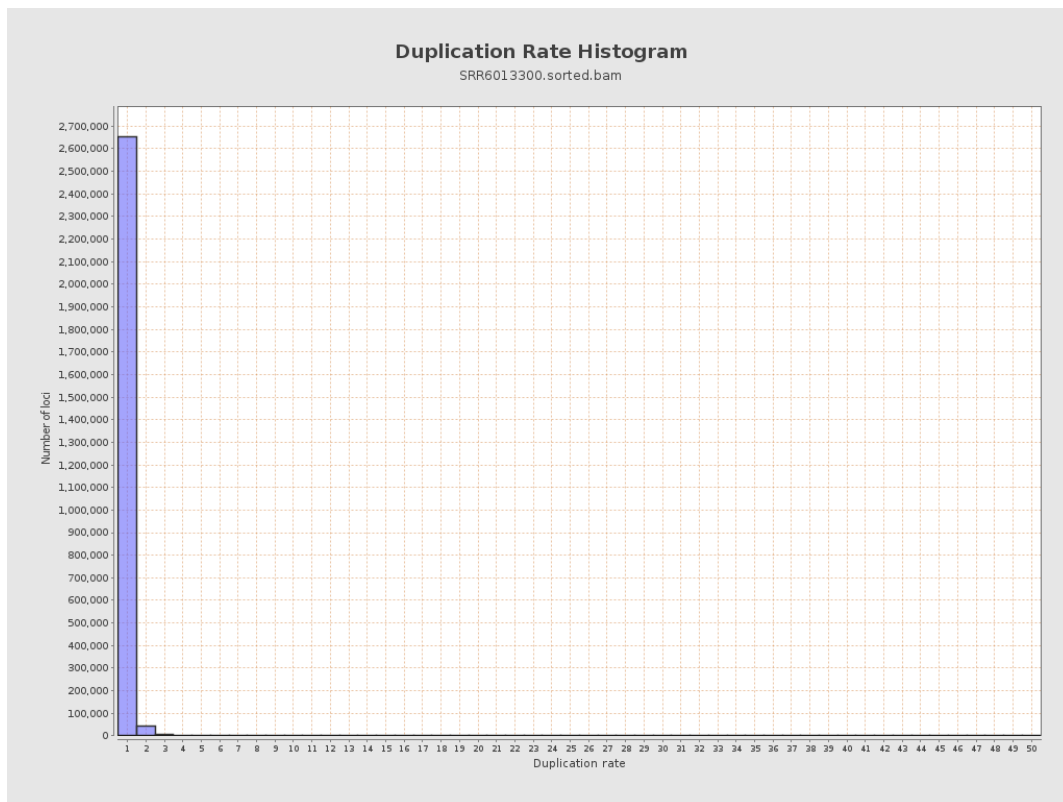
5. Results : Coverage Histogram (0-50X)



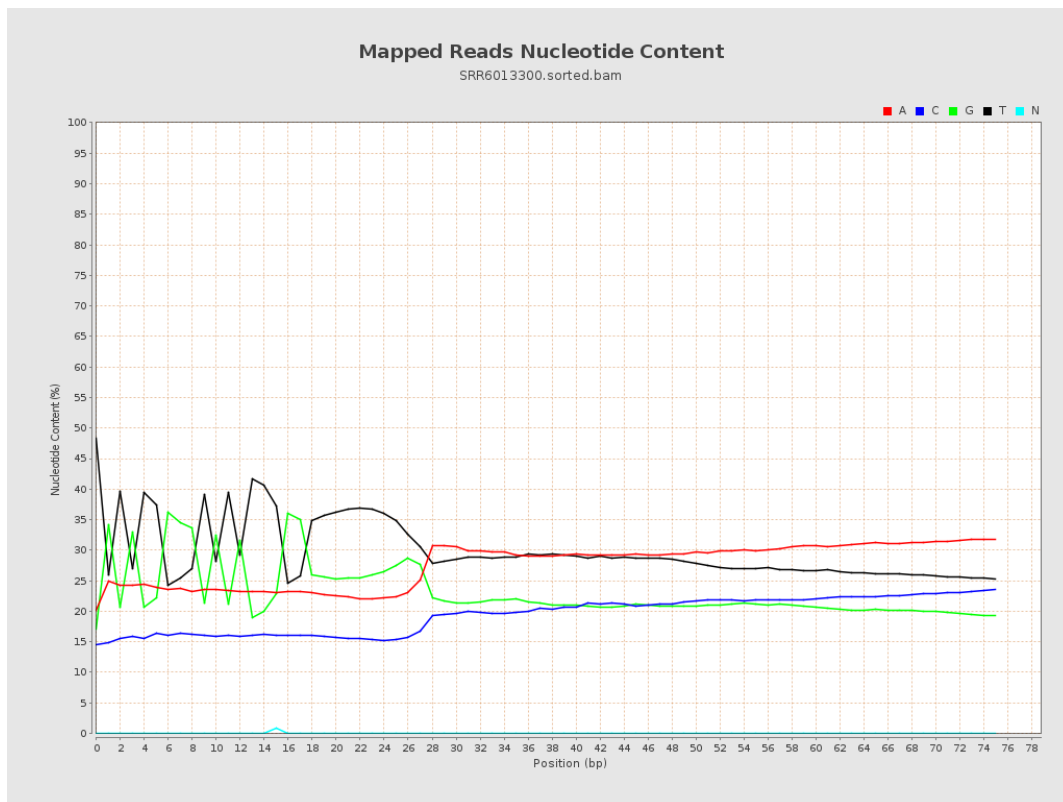
6. Results : Genome Fraction Coverage



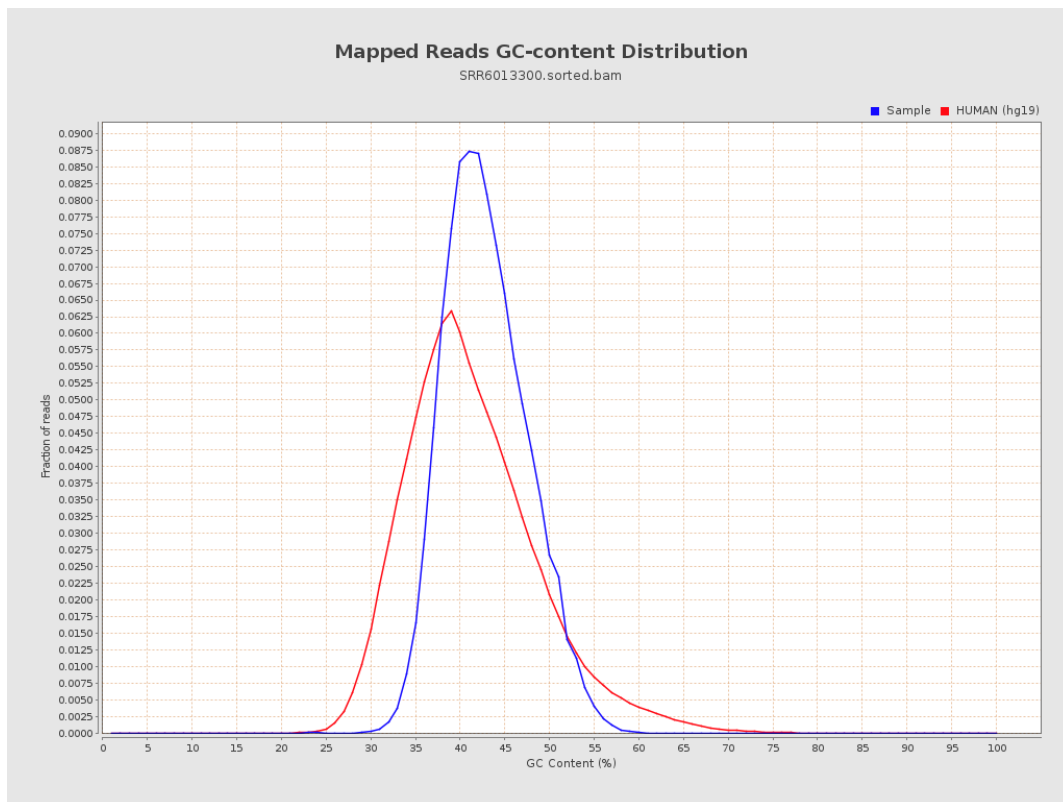
7. Results : Duplication Rate Histogram



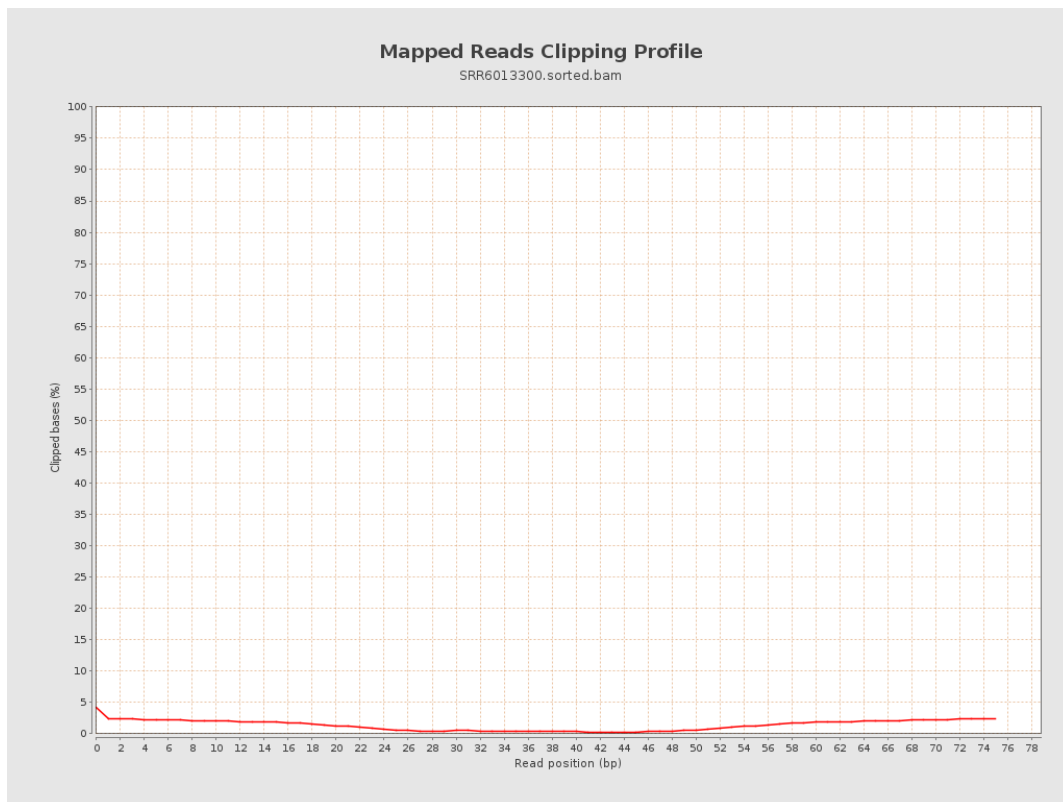
8. Results : Mapped Reads Nucleotide Content



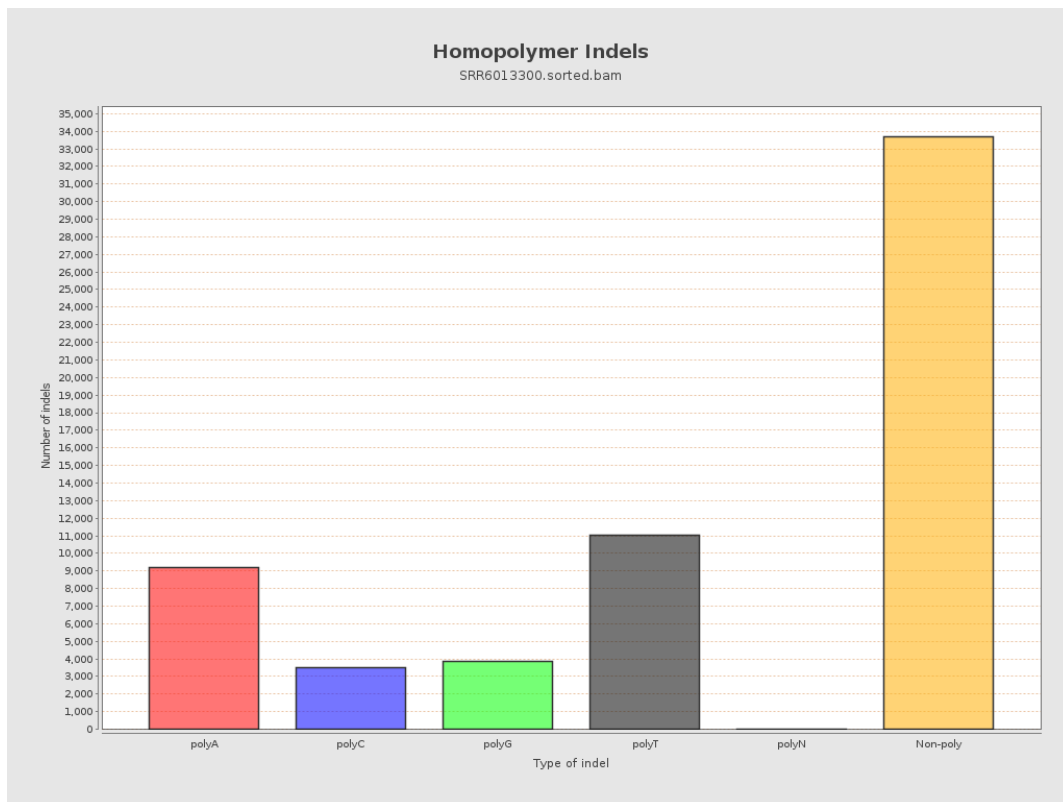
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

