

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:57:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013333.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_SRR6013333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:57:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,482,282
Mapped reads	1,008,822 / 68.06%
Unmapped reads	473,460 / 31.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,699 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	156,214 / 10.54%
Duplication rate	11.99%
Clipped reads	665,300 / 44.88%

2.2. ACGT Content

Number/percentage of A's	16,190,576 / 26.02%
Number/percentage of C's	11,650,736 / 18.73%
Number/percentage of T's	19,510,821 / 31.36%
Number/percentage of G's	14,854,135 / 23.88%
Number/percentage of N's	6,874 / 0.01%
GC Percentage	42.6%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2768
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2.4. Mapping Quality

Mean Mapping Quality	42.69
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2.5. Mismatches and indels

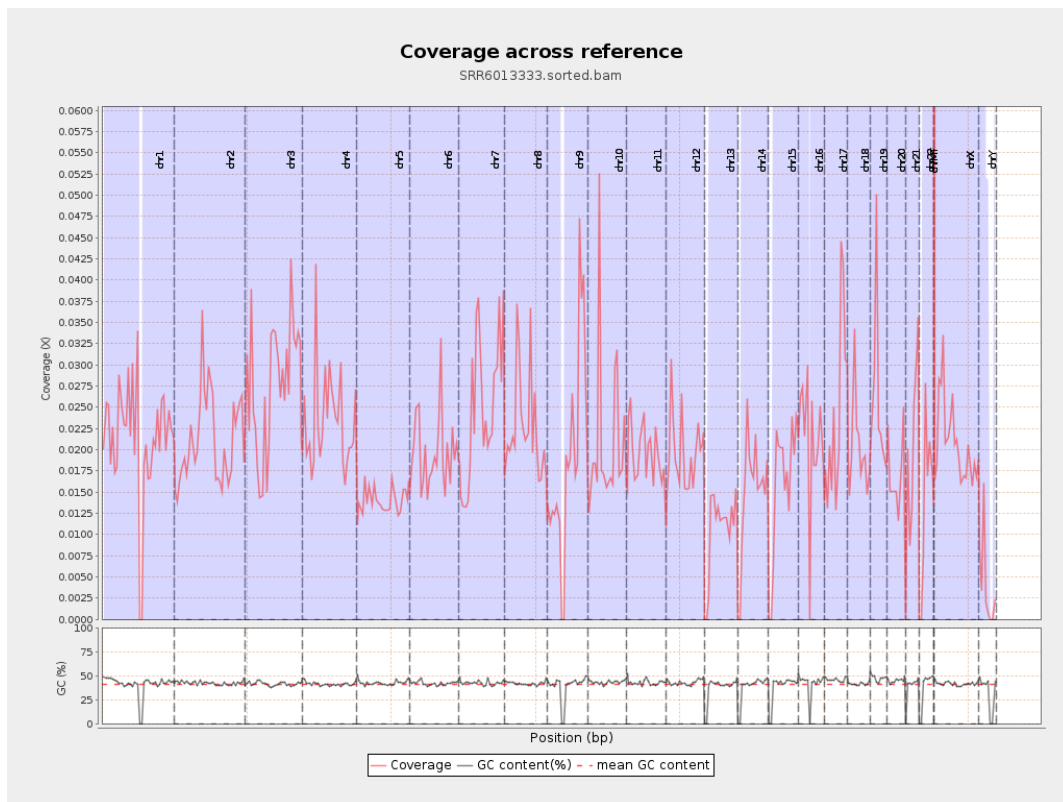
General error rate	0.91%
Mismatches	555,842
Insertions	4,622
Mapped reads with at least one insertion	0.45%
Deletions	20,544
Mapped reads with at least one deletion	2%
Homopolymer indels	42.86%

2.6. Chromosome stats

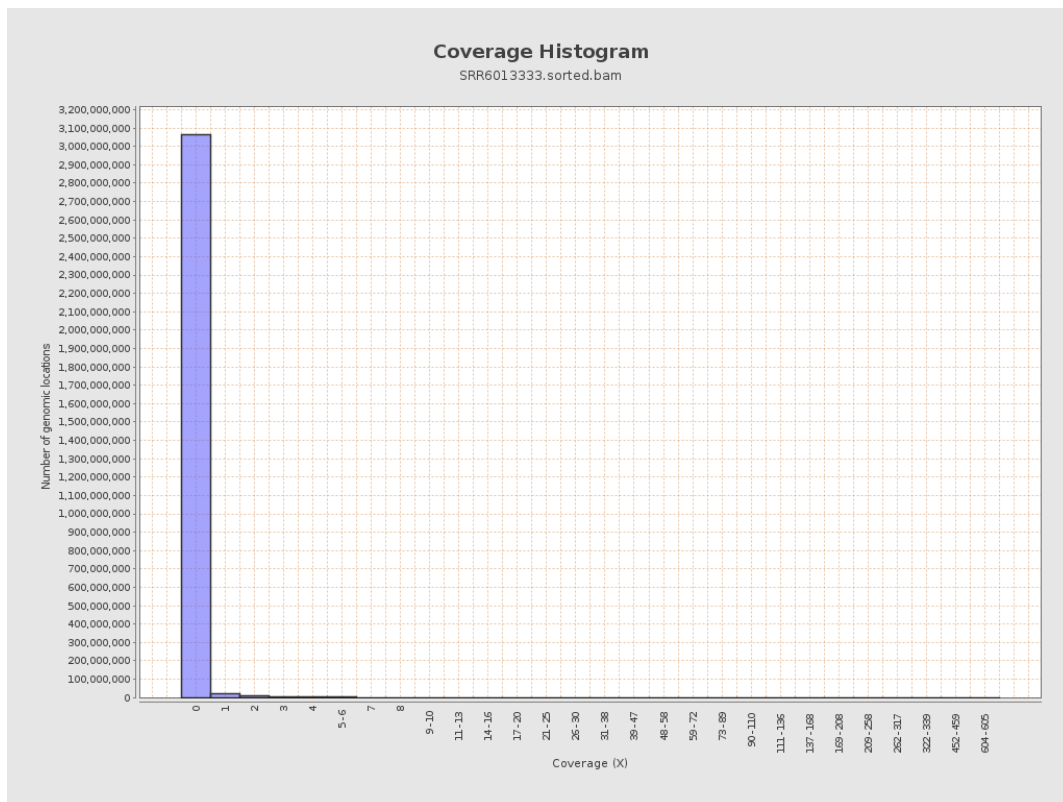
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5302780	0.0213	0.3497
chr2	243199373	5171957	0.0213	0.3657
chr3	198022430	5472578	0.0276	0.2813
chr4	191154276	4453175	0.0233	0.2701
chr5	180915260	2548041	0.0141	0.1913
chr6	171115067	3343148	0.0195	0.2551
chr7	159138663	3934576	0.0247	0.3085

chr8	146364022	3340804	0.0228	0.2791
chr9	141213431	2698636	0.0191	0.2411
chr10	135534747	2801892	0.0207	0.3567
chr11	135006516	2688136	0.0199	0.2469
chr12	133851895	2607977	0.0195	0.2312
chr13	115169878	1218659	0.0106	0.1672
chr14	107349540	1631079	0.0152	0.2046
chr15	102531392	1636754	0.016	0.2066
chr16	90354753	1898369	0.021	0.2507
chr17	81195210	1990109	0.0245	0.2693
chr18	78077248	1557037	0.0199	0.3018
chr19	59128983	1536677	0.026	0.3224
chr20	63025520	1056328	0.0168	0.2128
chr21	48129895	942854	0.0196	0.2511
chr22	51304566	725813	0.0141	0.1926
chrMT	16571	213747	12.8989	10.3097
chrX	155270560	3243742	0.0209	0.2407
chrY	59373566	234145	0.0039	0.143

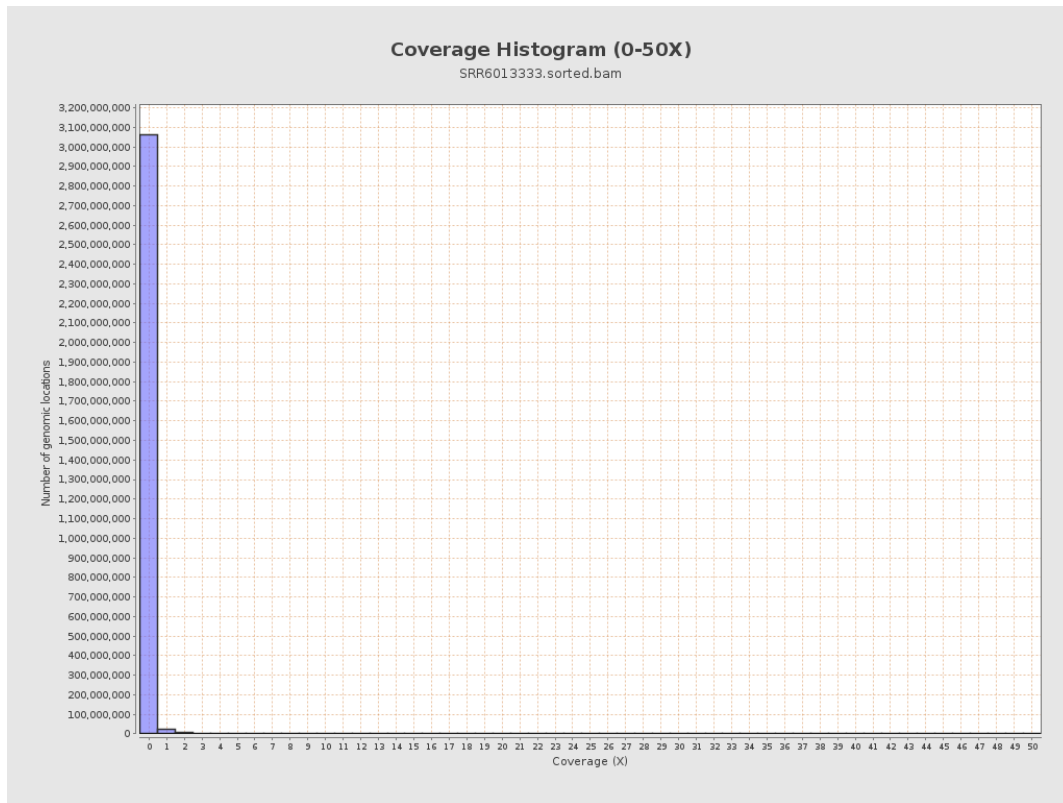
3. Results : Coverage across reference



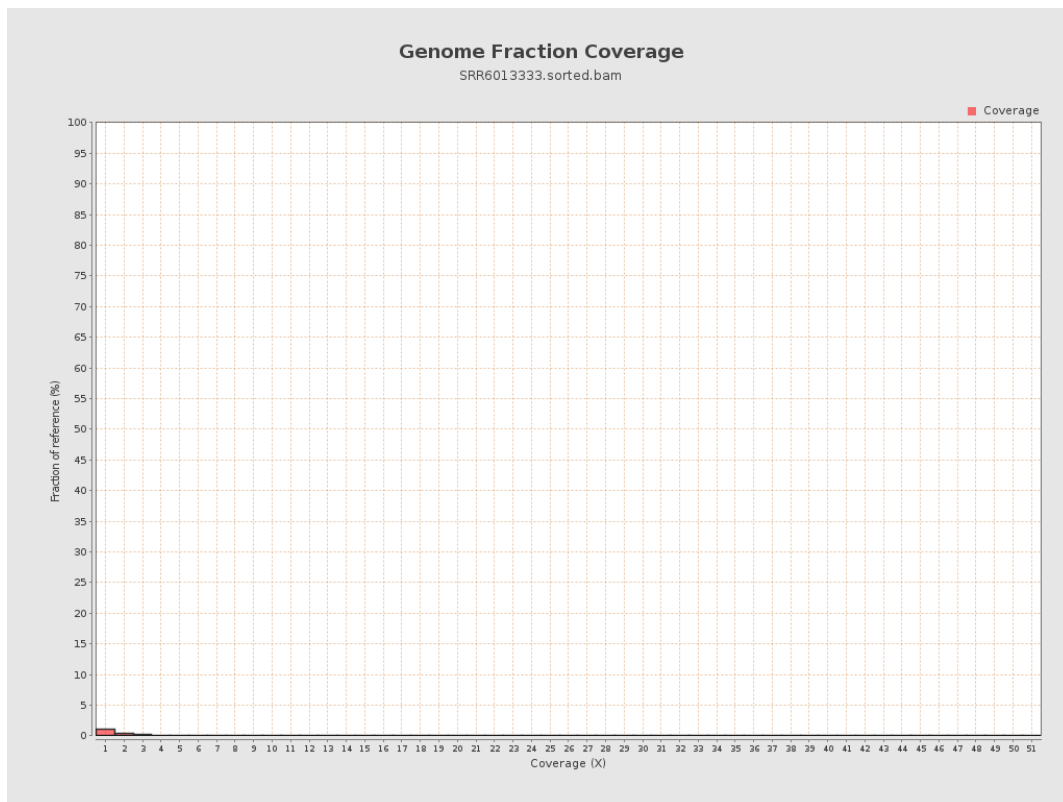
4. Results : Coverage Histogram



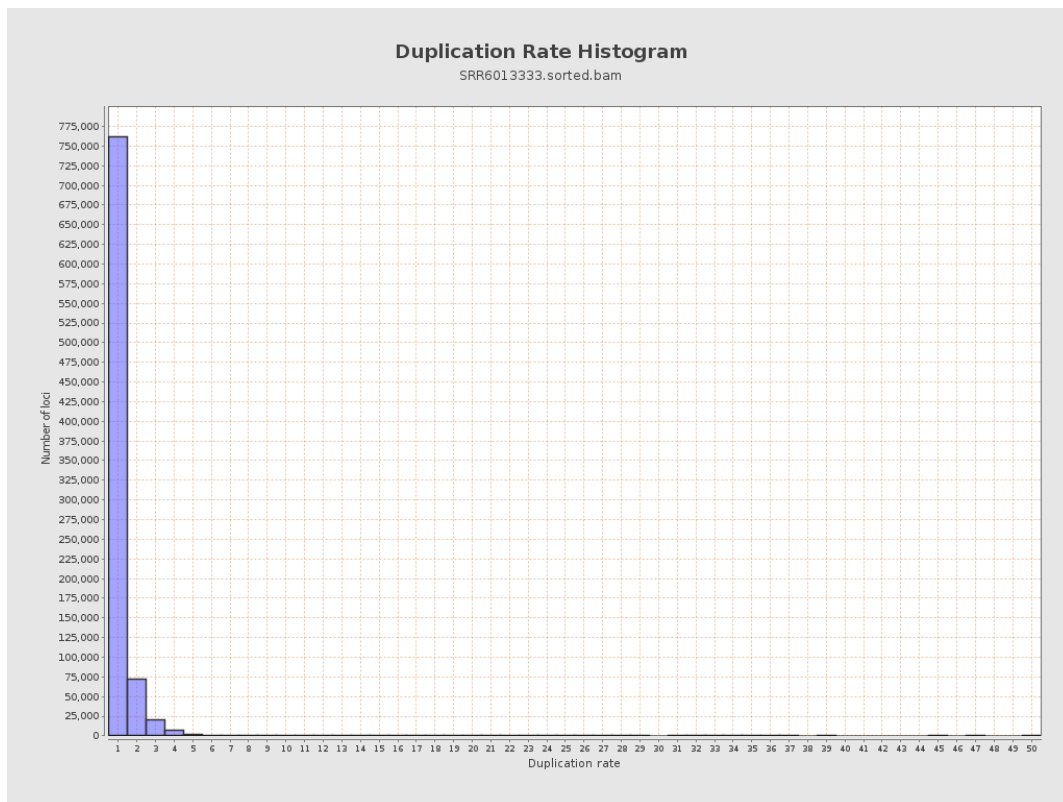
5. Results : Coverage Histogram (0-50X)



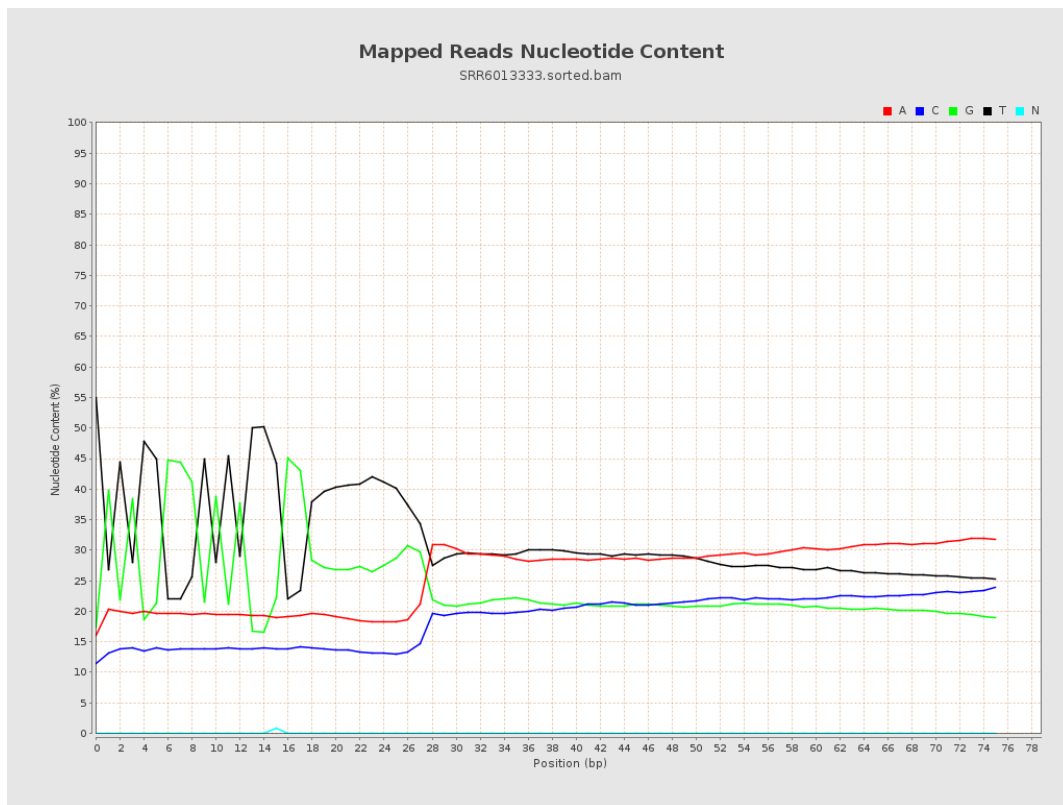
6. Results : Genome Fraction Coverage



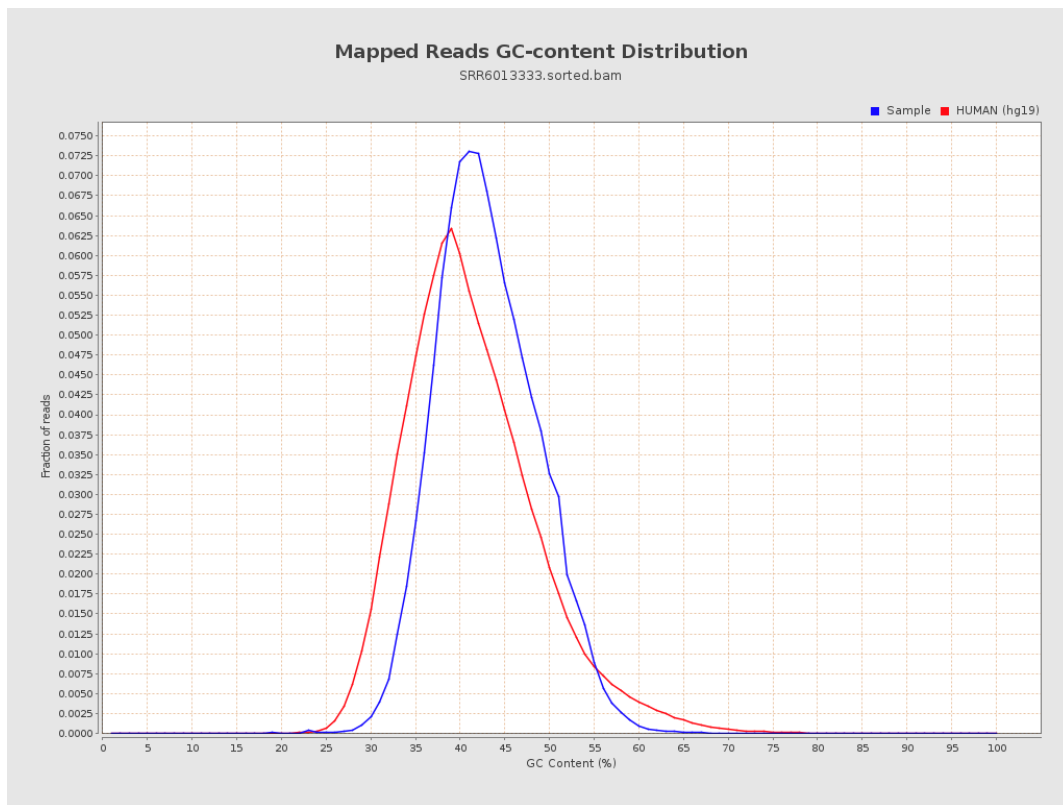
7. Results : Duplication Rate Histogram



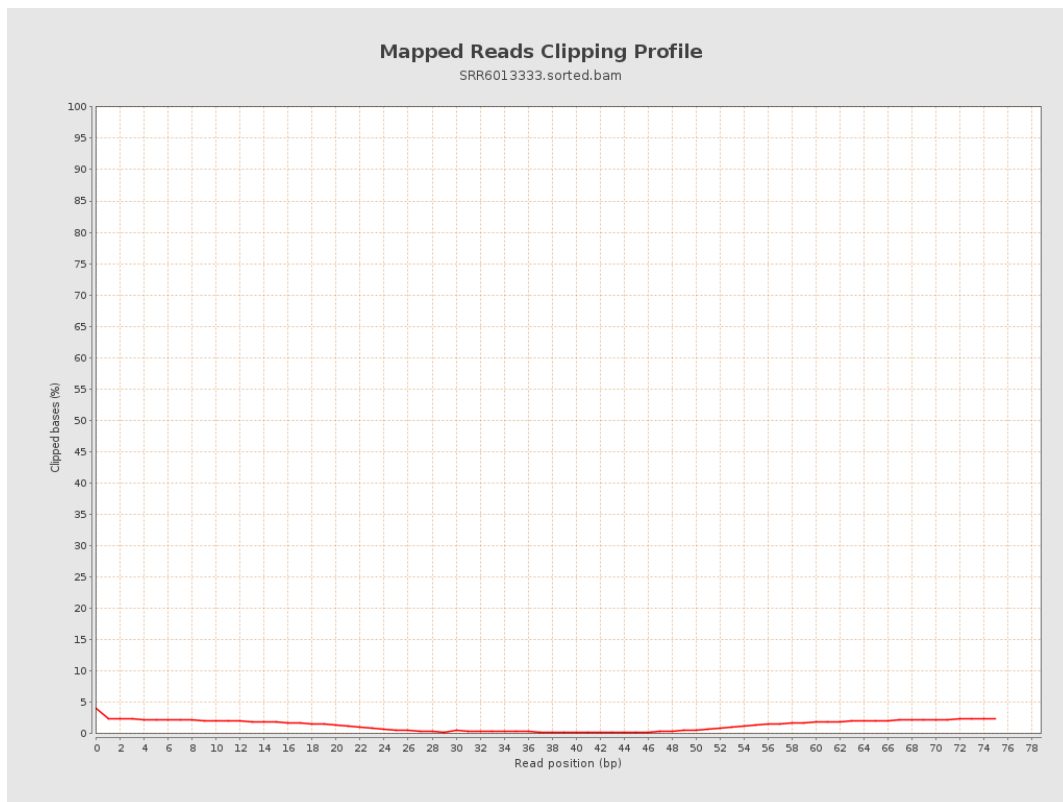
8. Results : Mapped Reads Nucleotide Content



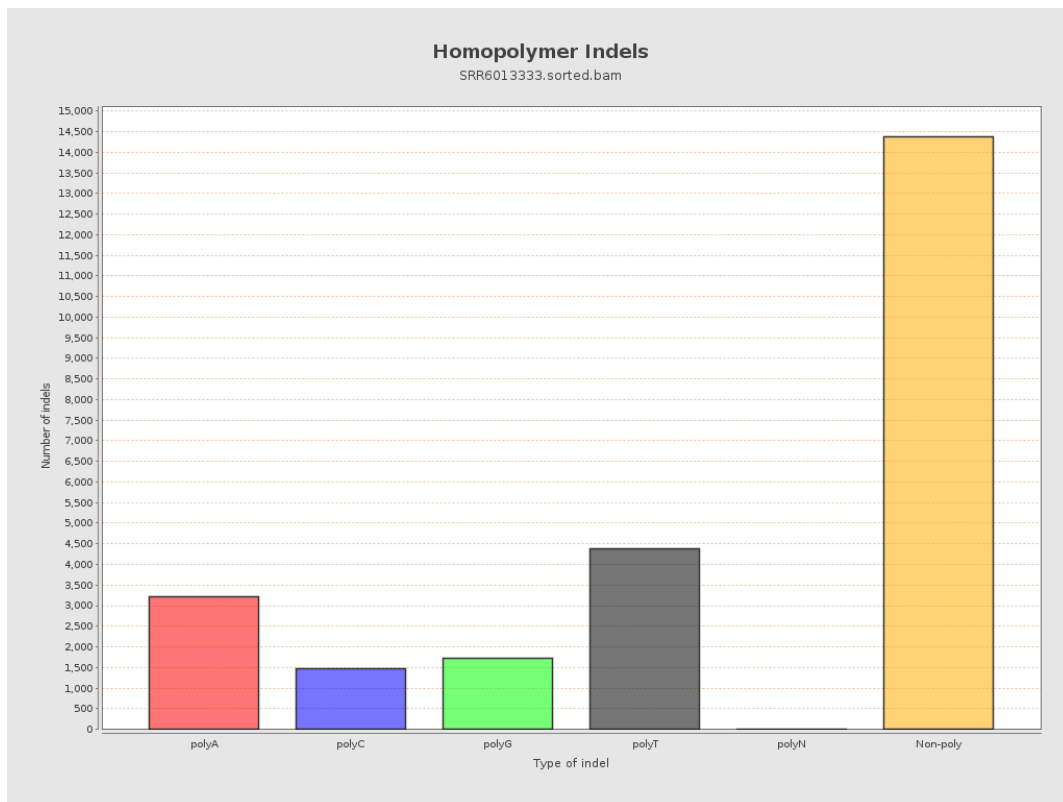
9. Results : Mapped Reads GC-content Distribution



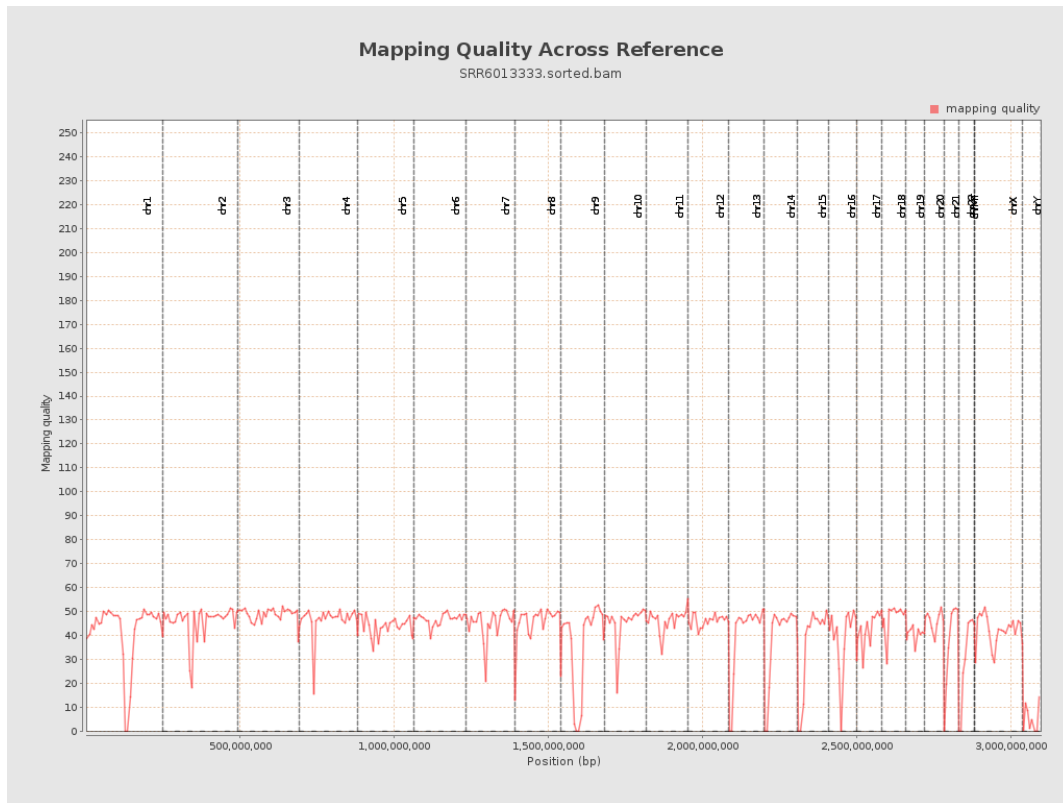
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

