

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 19:24:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514758.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_SRR5514758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 19:24:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,420,432
Mapped reads	57,374,682 / 94.96%
Unmapped reads	3,045,750 / 5.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,078,765 / 13.37%
Read min/max/mean length	30 / 100 / 104.59
Duplicated reads (estimated)	45,654,916 / 75.56%
Duplication rate	46.77%
Clipped reads	27,225,734 / 45.06%

2.2. ACGT Content

Number/percentage of A's	1,715,597,060 / 31.37%
Number/percentage of C's	1,023,431,848 / 18.71%
Number/percentage of T's	1,685,358,133 / 30.81%
Number/percentage of G's	1,044,653,959 / 19.1%
Number/percentage of N's	376,610 / 0.01%
GC Percentage	37.81%

2.3. Coverage

Mean	1.768

Standard Deviation	61.2232
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2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Mismatches and indels

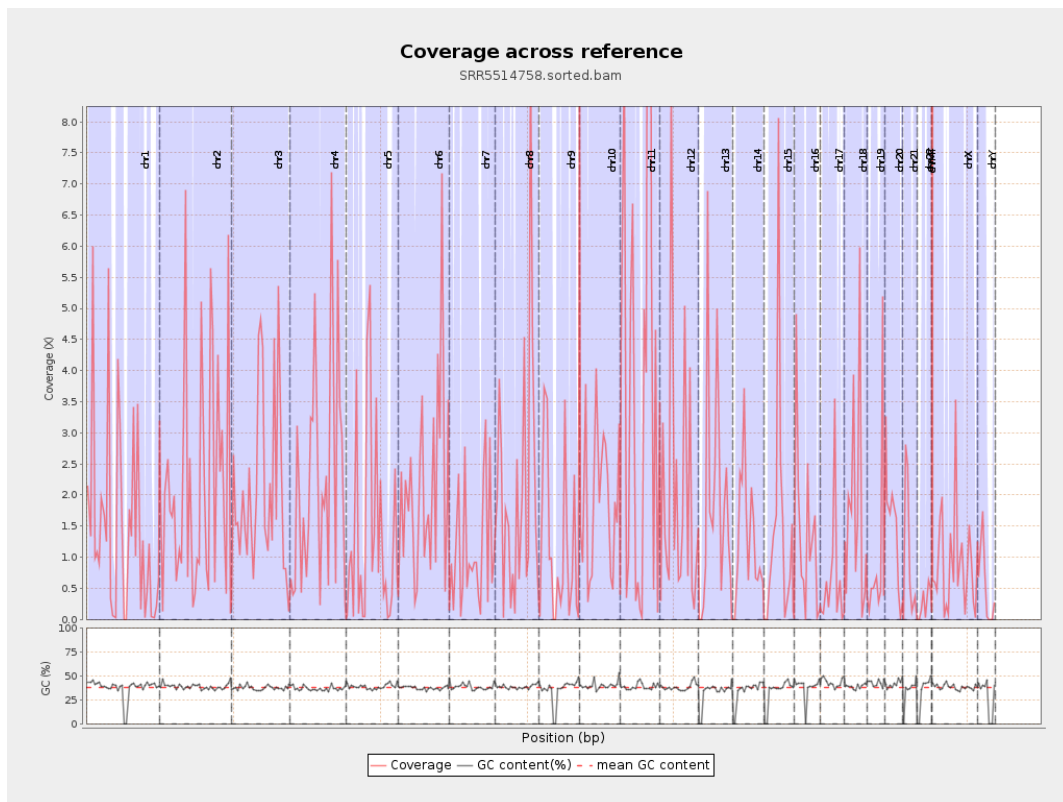
General error rate	0.63%
Mismatches	29,038,783
Insertions	3,546,228
Mapped reads with at least one insertion	5.92%
Deletions	1,361,175
Mapped reads with at least one deletion	2.23%
Homopolymer indels	52.25%

2.6. Chromosome stats

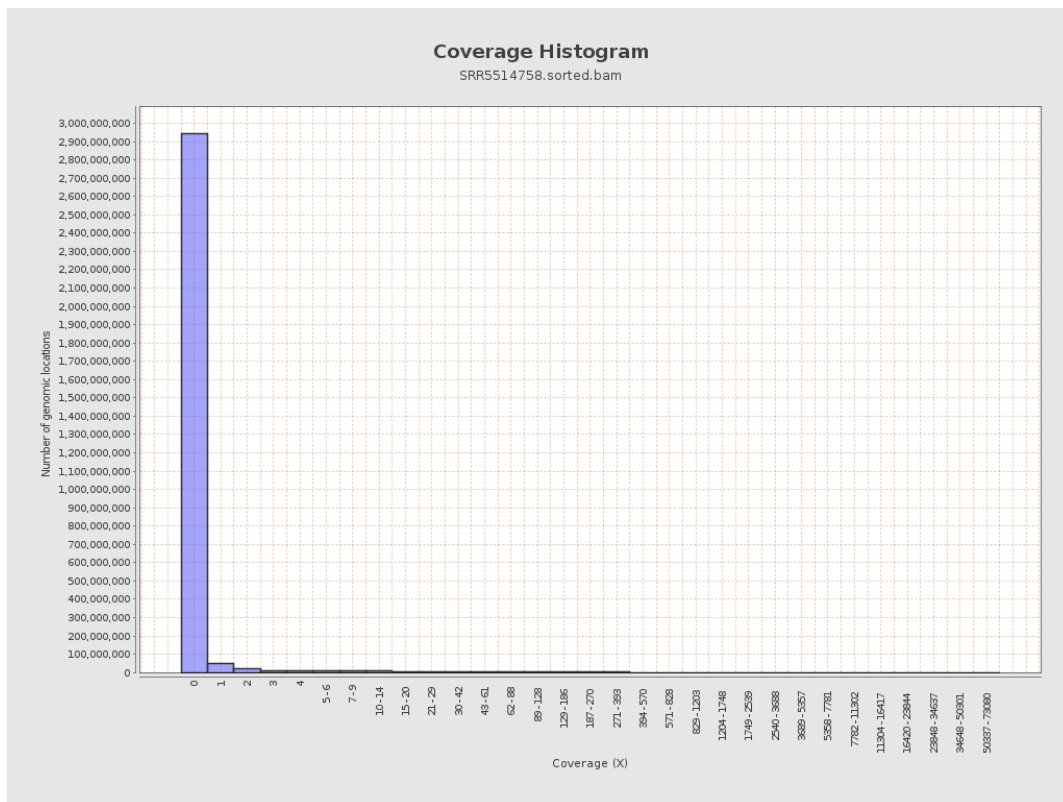
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	371233121	1.4894	69.1207
chr2	243199373	522443014	2.1482	43.6737
chr3	198022430	415727429	2.0994	33.3112
chr4	191154276	438495639	2.2939	93.7686
chr5	180915260	233369118	1.2899	26.1719
chr6	171115067	358730379	2.0964	41.4346
chr7	159138663	176455955	1.1088	21.5496

chr8	146364022	309025826	2.1114	38.3488
chr9	141213431	168859329	1.1958	26.783
chr10	135534747	256490001	1.8924	72.1564
chr11	135006516	553831816	4.1023	44.5739
chr12	133851895	257822258	1.9262	29.3575
chr13	115169878	217915674	1.8921	31.8671
chr14	107349540	139895402	1.3032	25.8786
chr15	102531392	149392580	1.457	27.627
chr16	90354753	115910823	1.2828	31.3485
chr17	81195210	54628254	0.6728	14.841
chr18	78077248	140077494	1.7941	48.8538
chr19	59128983	61661727	1.0428	118.0943
chr20	63025520	93350459	1.4812	44.845
chr21	48129895	49944513	1.0377	18.7071
chr22	51304566	13812430	0.2692	11.1004
chrMT	16571	202446389	12,216.9084	11,178.1599
chrX	155270560	137135279	0.8832	19.5182
chrY	59373566	34452897	0.5803	15.0768

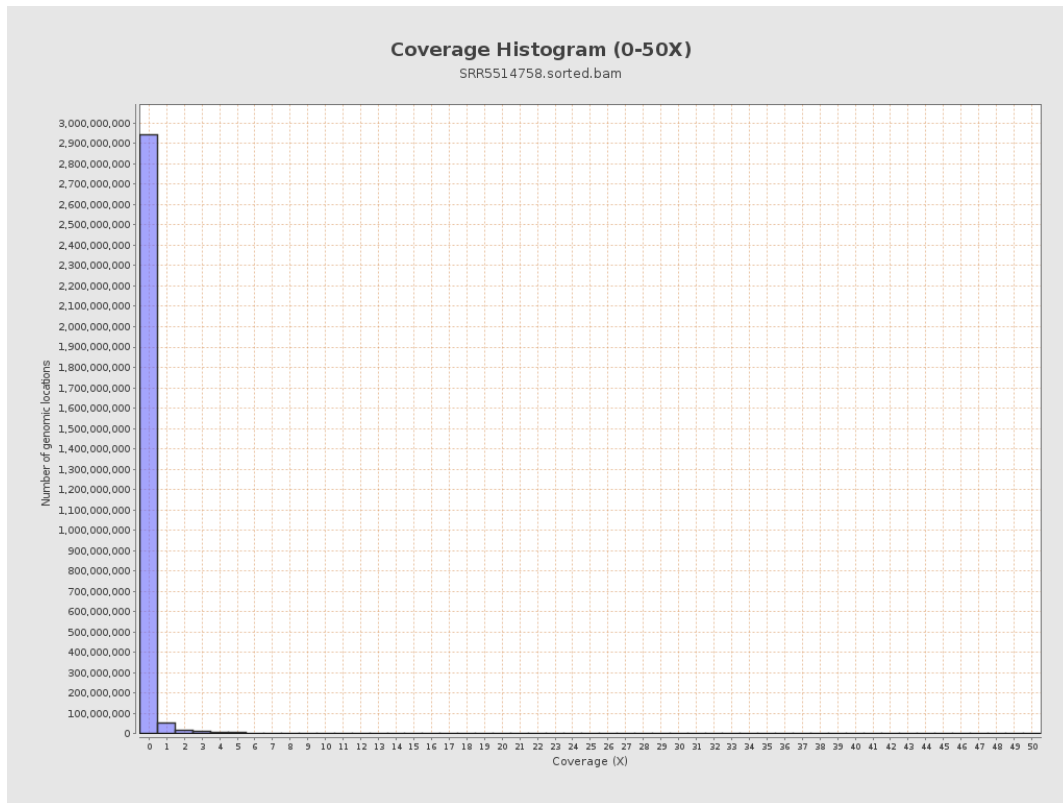
3. Results : Coverage across reference



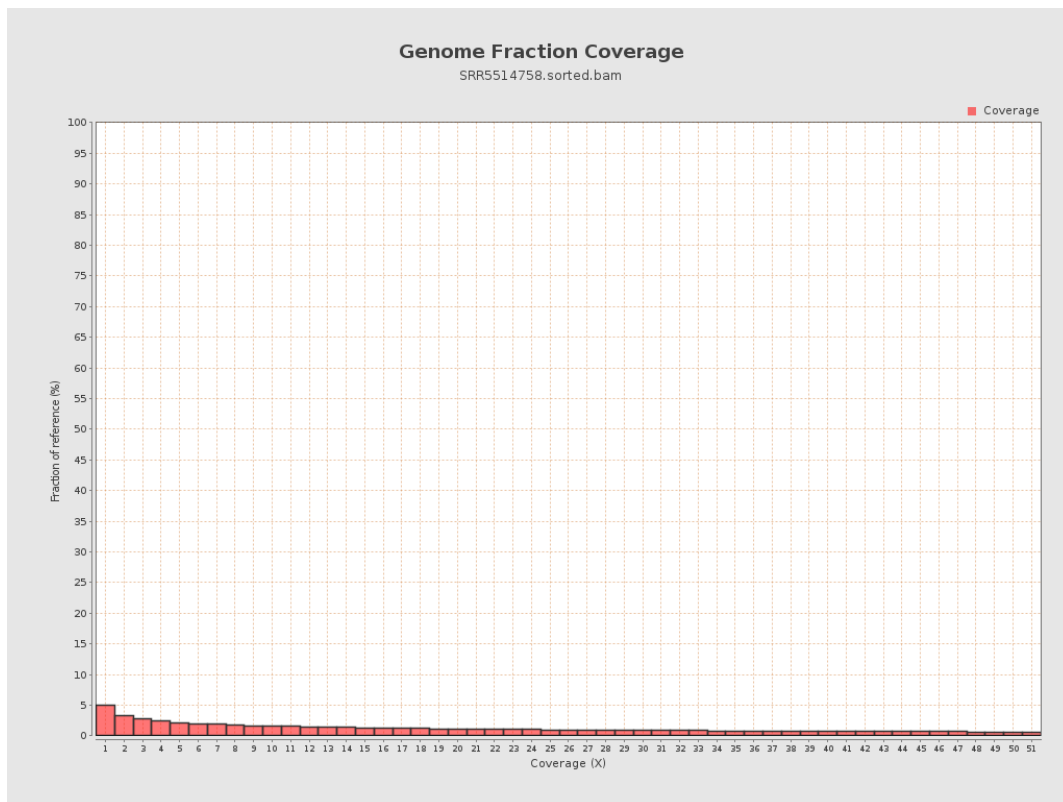
4. Results : Coverage Histogram



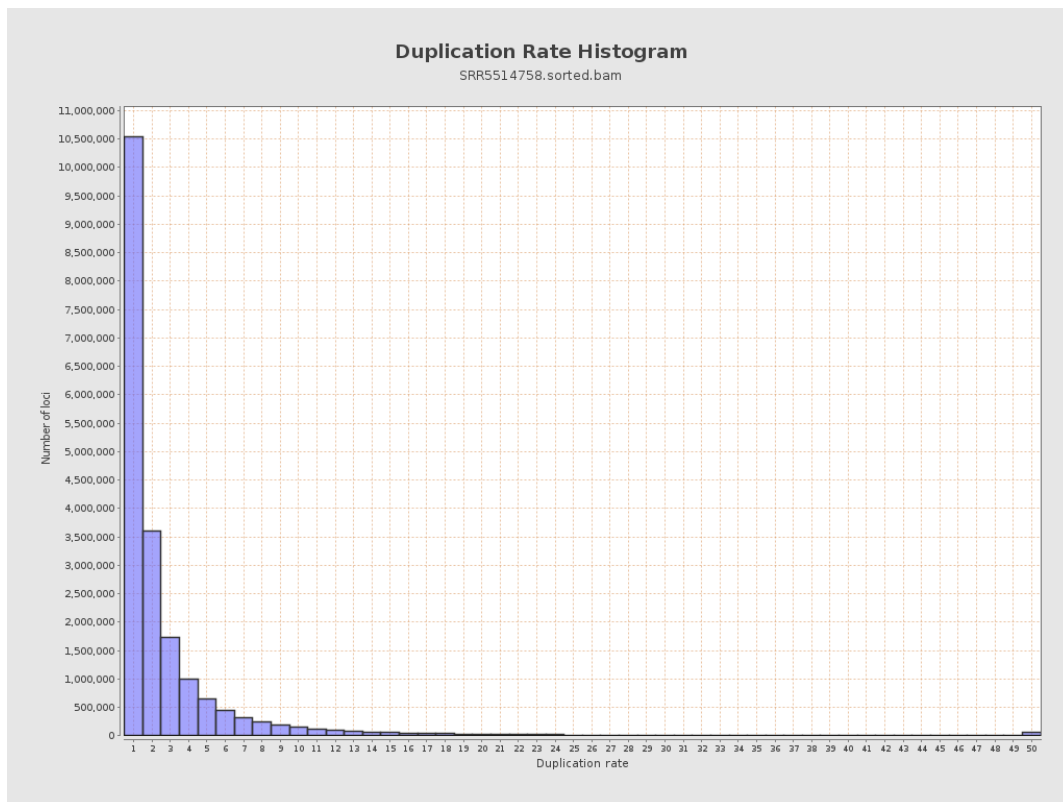
5. Results : Coverage Histogram (0-50X)



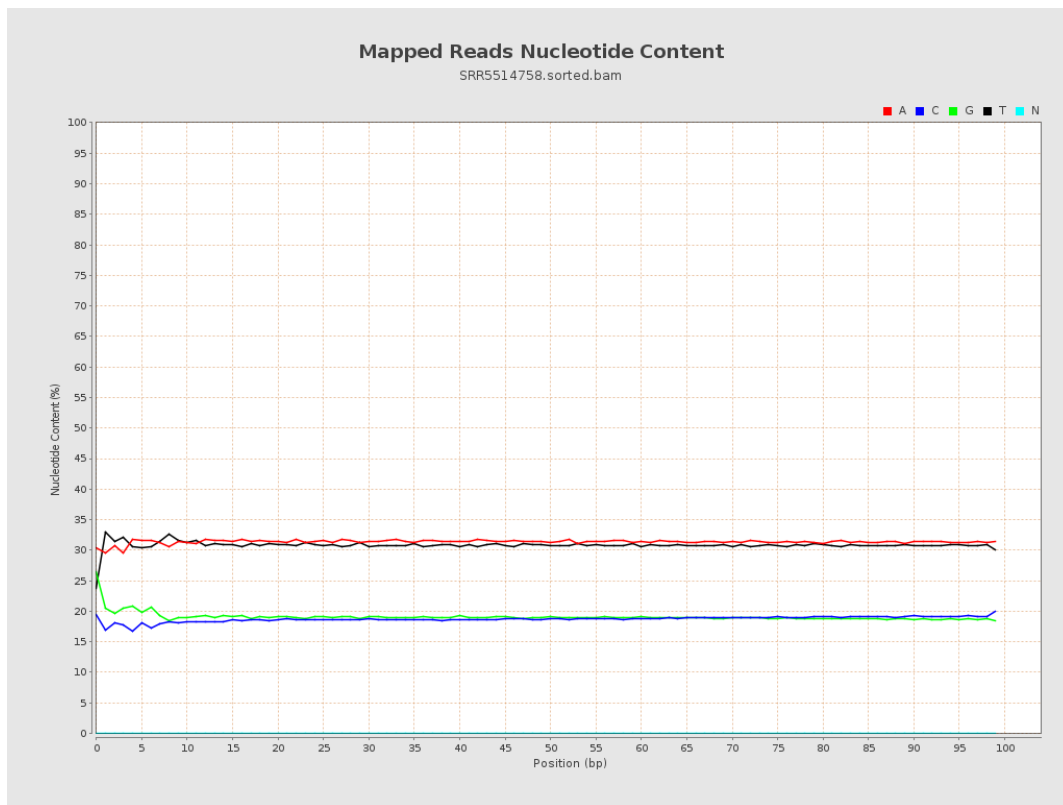
6. Results : Genome Fraction Coverage



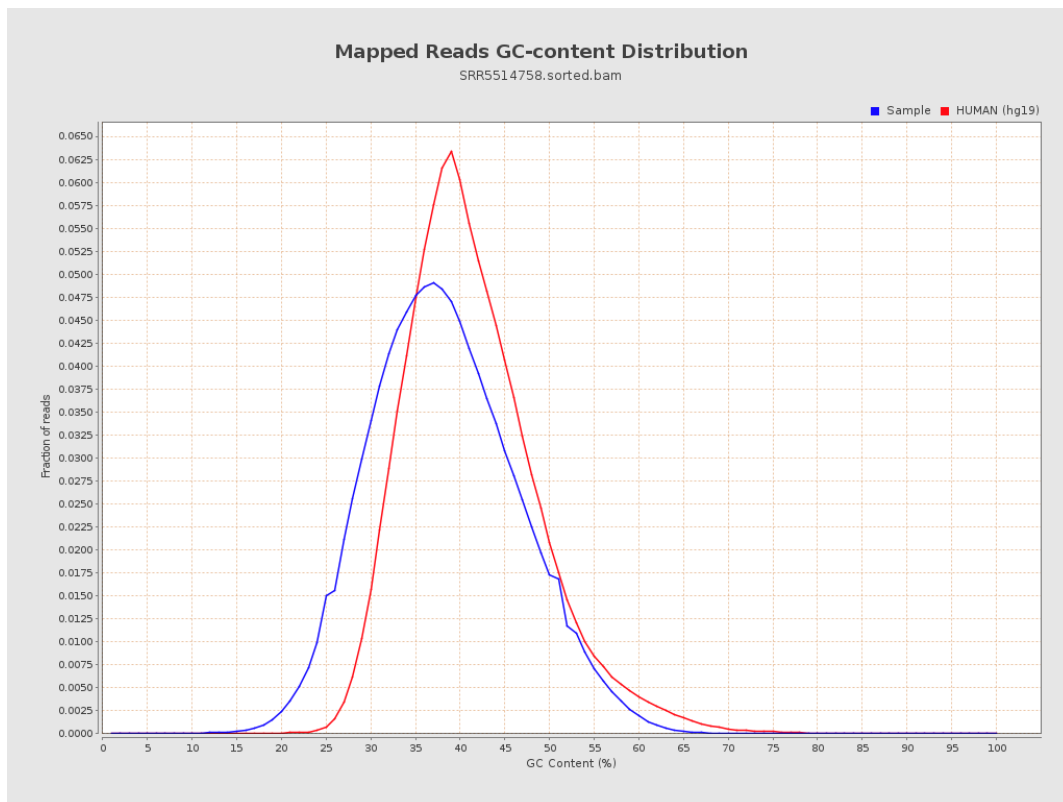
7. Results : Duplication Rate Histogram



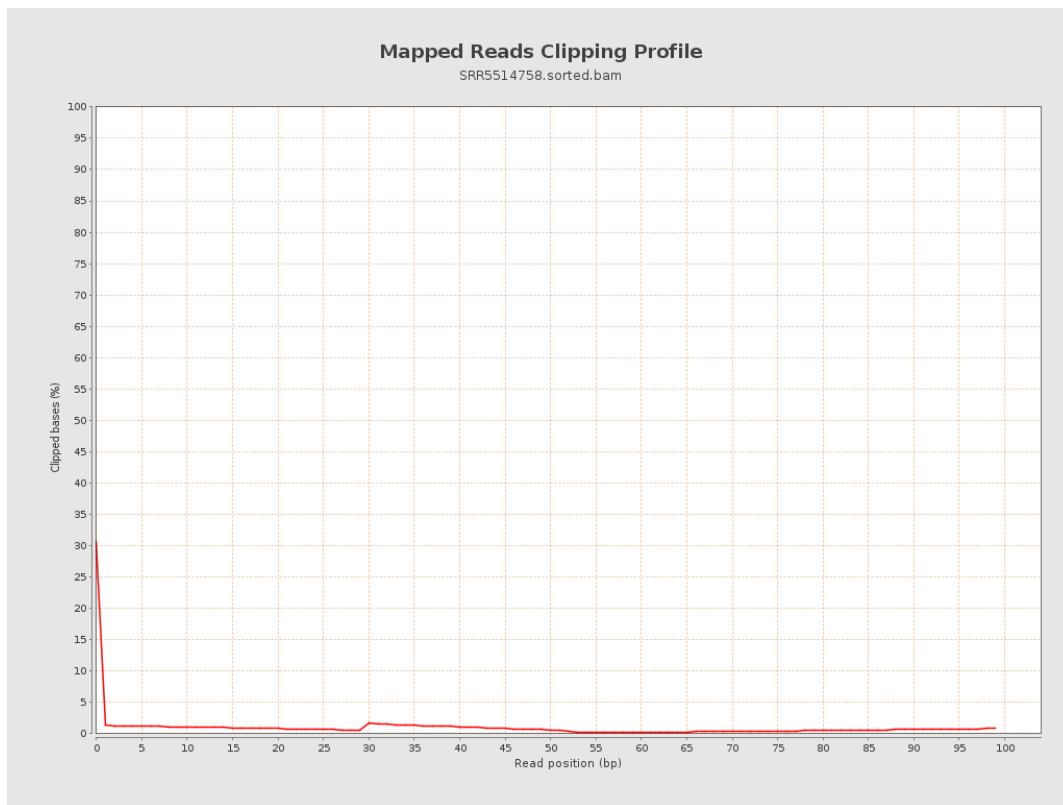
8. Results : Mapped Reads Nucleotide Content



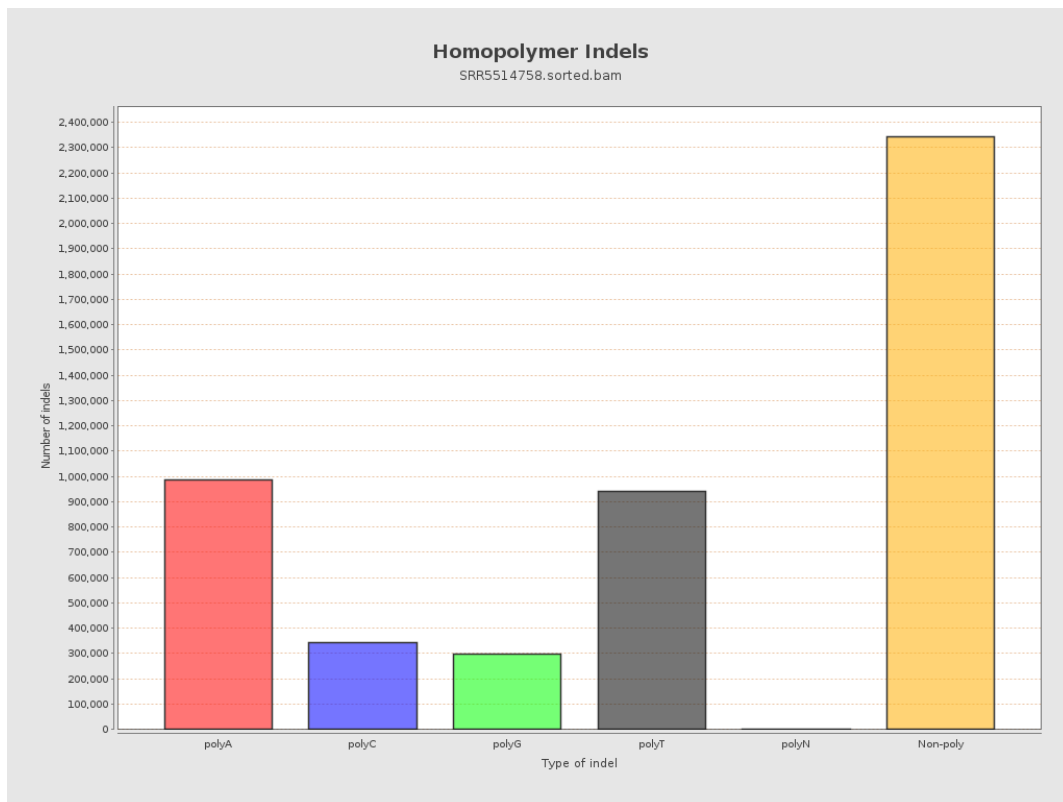
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

