Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 17:07:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163155.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_SRR1163155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 17:07:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	82,847,166
Mapped reads	80,571,754 / 97.25%
Unmapped reads	2,275,412 / 2.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	366,776 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	41,947,159 / 50.63%
Duplication rate	41.55%
Clipped reads	7,758,629 / 9.36%

2.2. ACGT Content

Number/percentage of A's	1,983,808,355 / 25.02%
Number/percentage of C's	1,975,841,860 / 24.92%
Number/percentage of T's	1,989,972,219 / 25.1%
Number/percentage of G's	1,965,167,880 / 24.79%
Number/percentage of N's	13,701,800 / 0.17%
GC Percentage	49.71%

2.3. Coverage

Mean	2.5614

Standard Deviation	30.0127

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

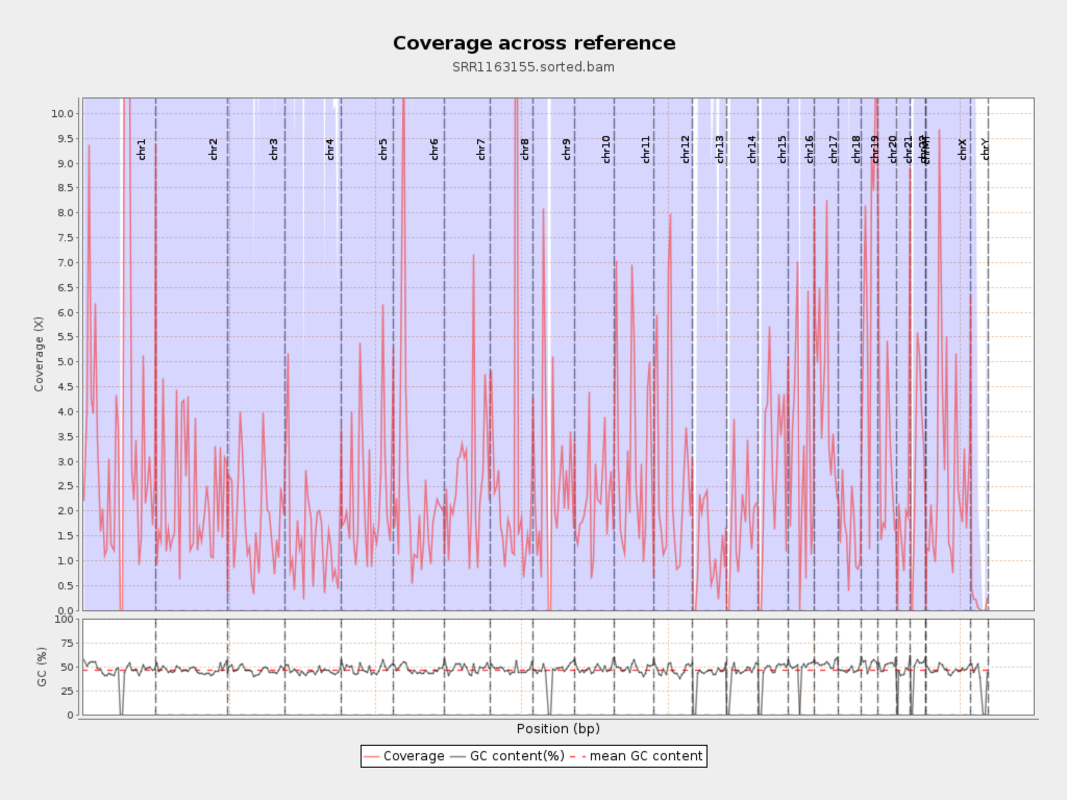
General error rate	0.65%
Mismatches	50,353,483
Insertions	553,399
Mapped reads with at least one insertion	0.68%
Deletions	405,159
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.76%

2.6. Chromosome stats

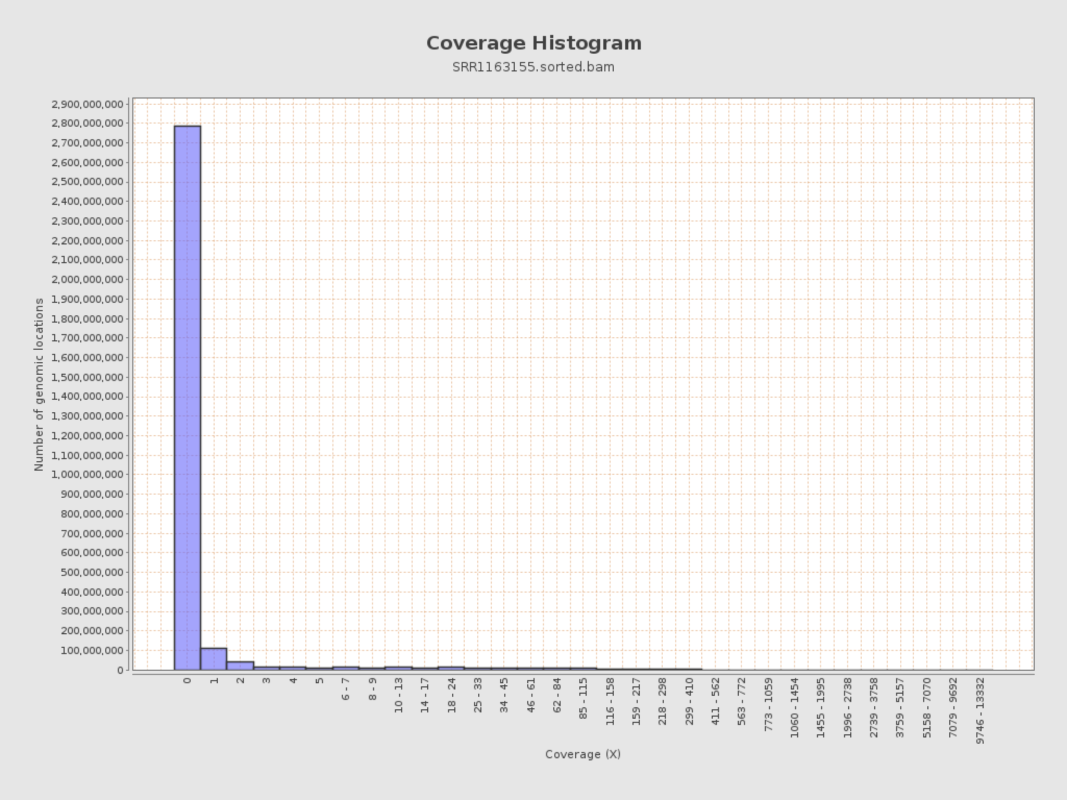
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	925664331	3.7138	35.348
chr2	243199373	541564331	2.2268	23.0589
chr3	198022430	365454597	1.8455	19.3776
chr4	191154276	291452470	1.5247	22.2467
chr5	180915260	431388633	2.3845	35.0856
chr6	171115067	406225554	2.374	28.2432
chr7	159138663	422183386	2.6529	27.2657

chr8	146364022	413193961	2.8231	59.425
chr9	141213431	354285941	2.5089	30.8939
chr10	135534747	296601417	2.1884	21.2564
chr11	135006516	415623378	3.0785	28.4638
chr12	133851895	392553355	2.9327	26.6977
chr13	115169878	132840904	1.1534	13.7803
chr14	107349540	189810672	1.7682	17.9144
chr15	102531392	292344719	2.8513	24.7089
chr16	90354753	277827161	3.0748	26.8167
chr17	81195210	365735321	4.5044	31.1589
chr18	78077248	121547189	1.5568	16.7945
chr19	59128983	410363720	6.9401	45.9401
chr20	63025520	174799238	2.7735	26.3496
chr21	48129895	108989922	2.2645	50.7085
chr22	51304566	156832024	3.0569	31.1671
chrMT	16571	576	0.0348	0.22
chrX	155270560	434124283	2.7959	31.114
chrY	59373566	8030374	0.1353	7.5675

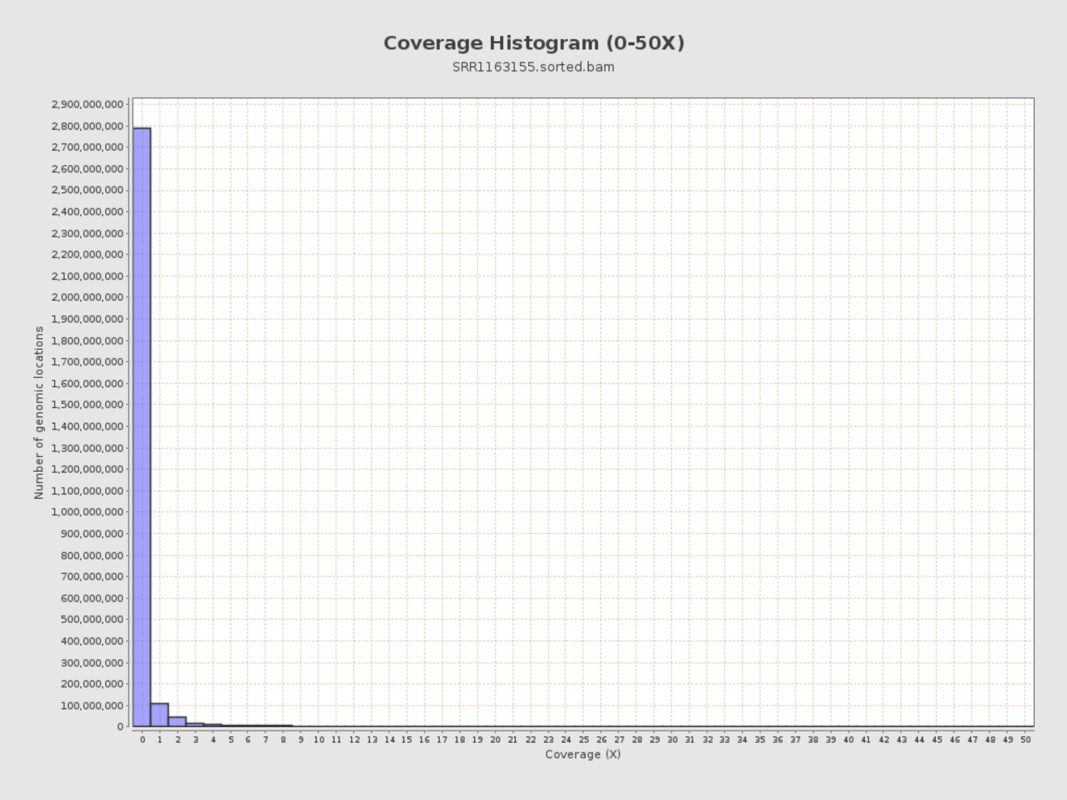
3. Results : Coverage across reference



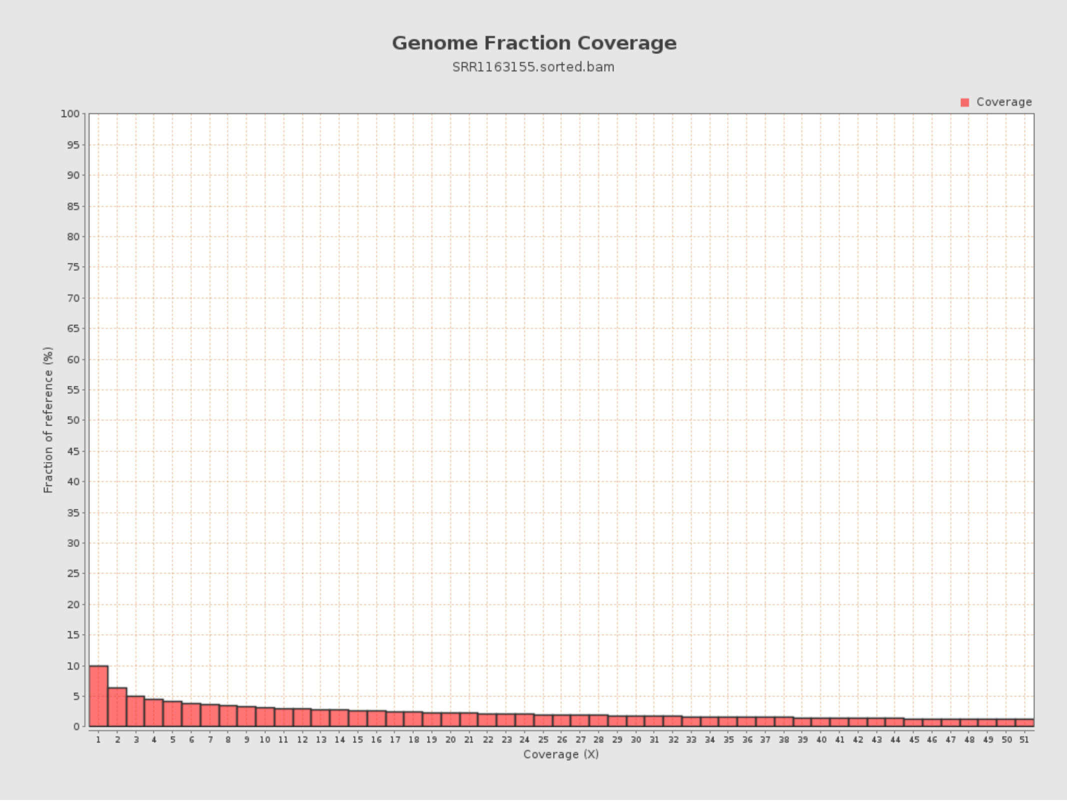
4. Results : Coverage Histogram



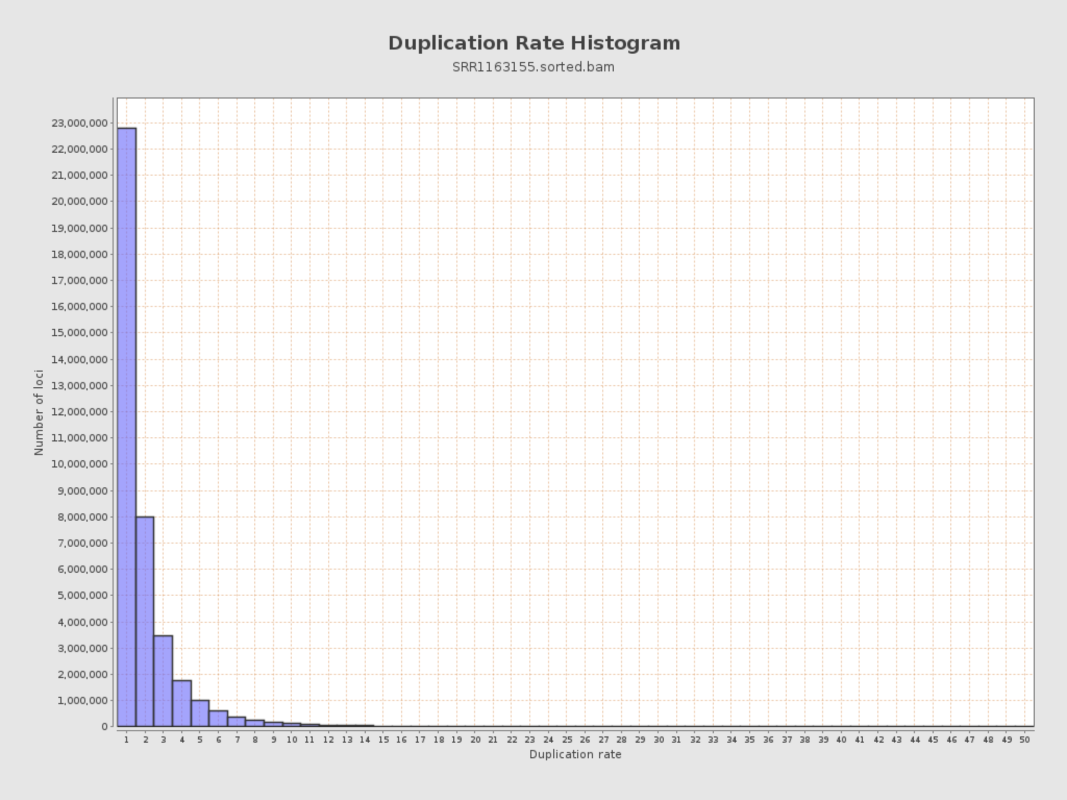
5. Results : Coverage Histogram (0-50X)



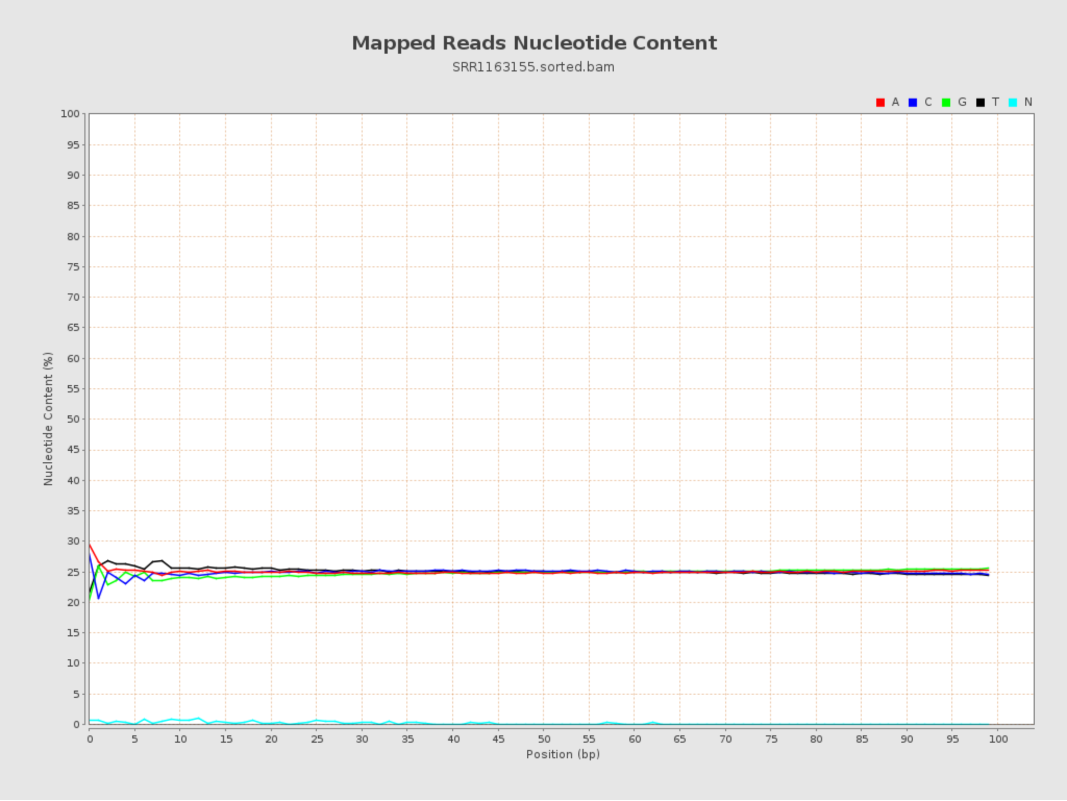
6. Results : Genome Fraction Coverage



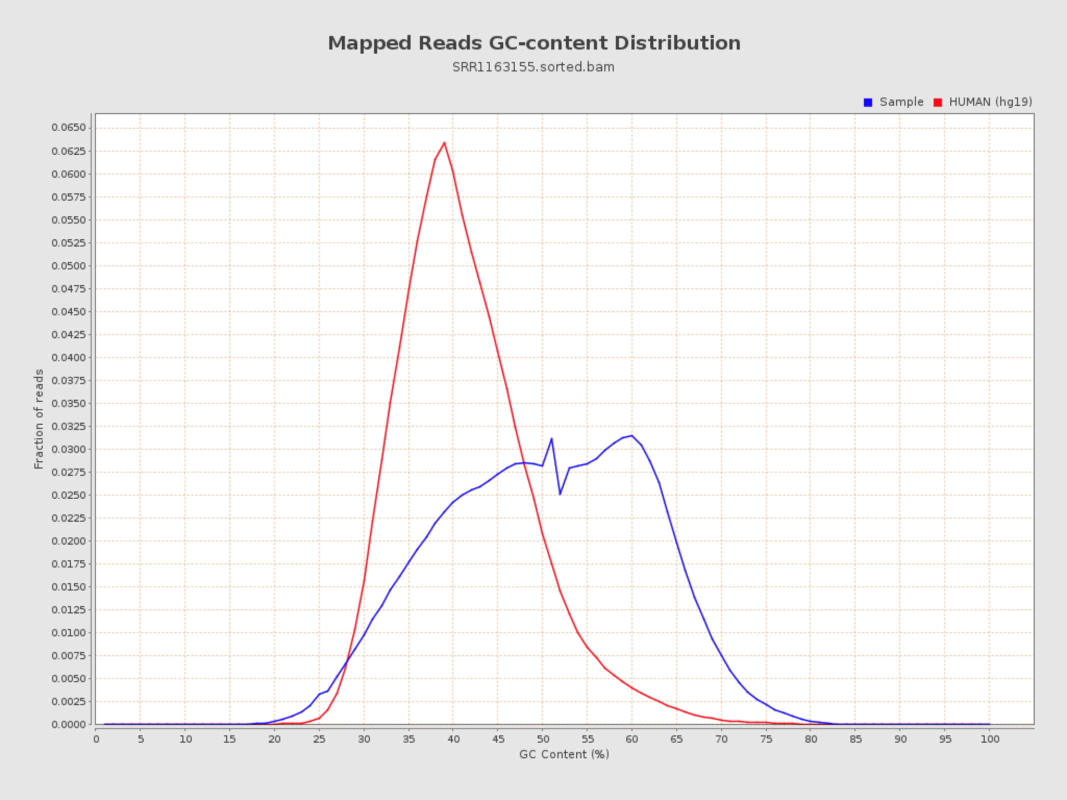
7. Results : Duplication Rate Histogram



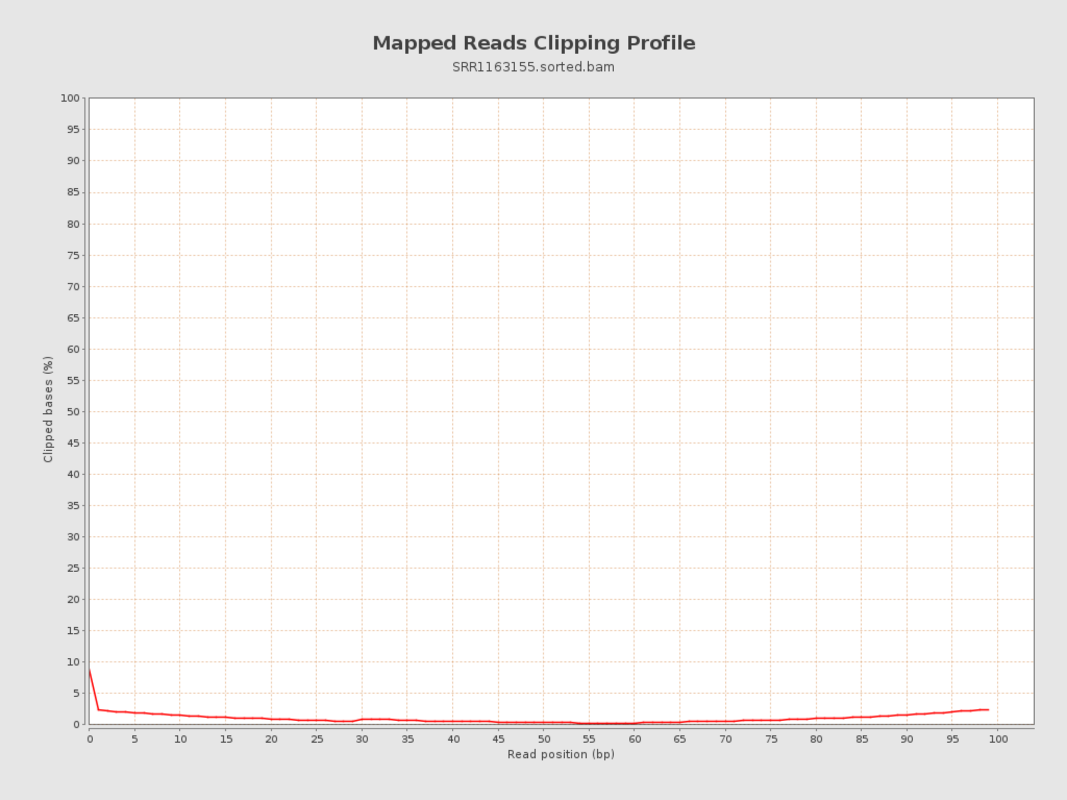
8. Results : Mapped Reads Nucleotide Content



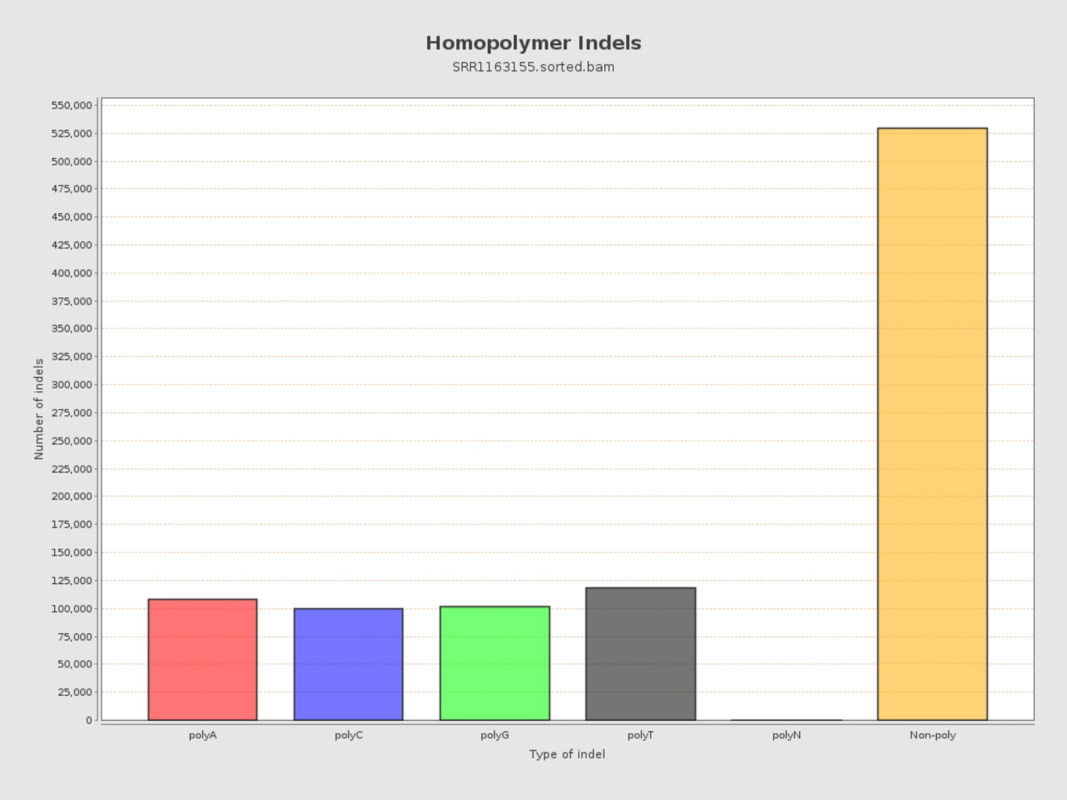
9. Results : Mapped Reads GC-content Distribution



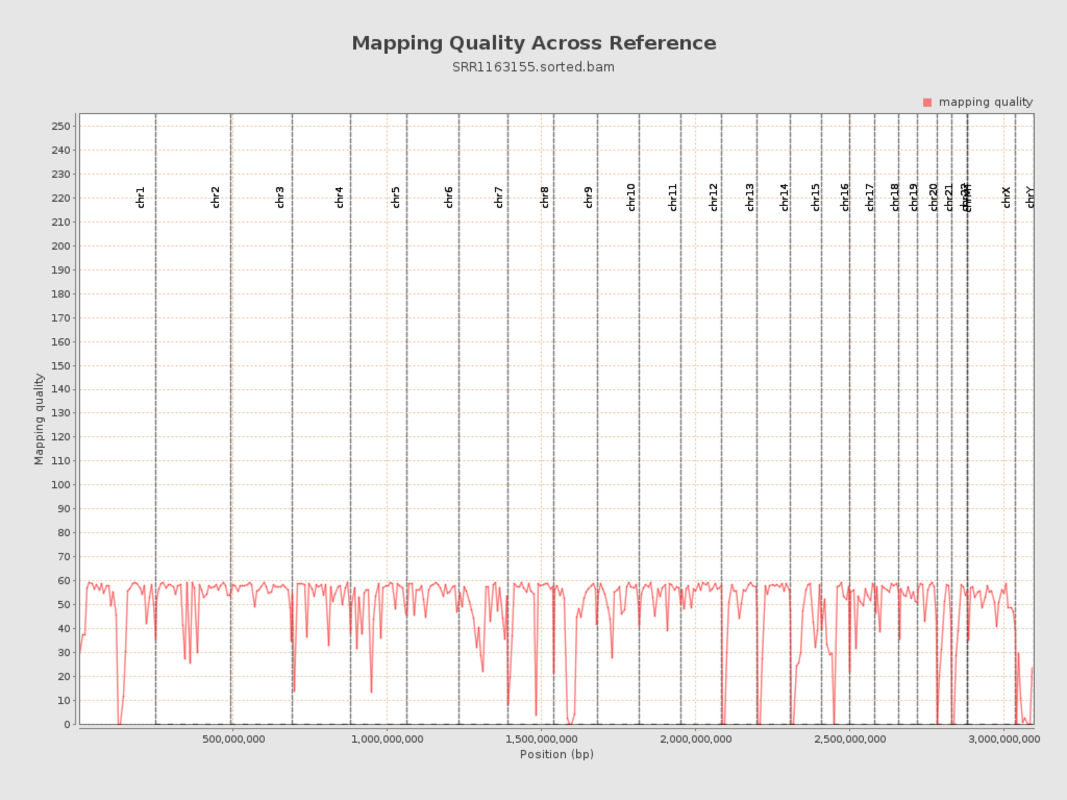
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram