Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:52:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506122.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_SRR1506122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:52:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,123,670
Mapped reads	6,636,621 / 72.74%
Unmapped reads	2,487,049 / 27.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	107,720 / 1.18%
Read min/max/mean length	30 / 94 / 94.42
Duplicated reads (estimated)	1,583,516 / 17.36%
Duplication rate	14.16%
Clipped reads	3,900,532 / 42.75%

2.2. ACGT Content

Number/percentage of A's	140,886,207 / 26.64%
Number/percentage of C's	100,781,894 / 19.06%
Number/percentage of T's	154,678,376 / 29.25%
Number/percentage of G's	132,474,586 / 25.05%
Number/percentage of N's	70,770 / 0.01%
GC Percentage	44.1%

2.3. Coverage

Mean	0.1709

Standard Deviation	1.3072

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

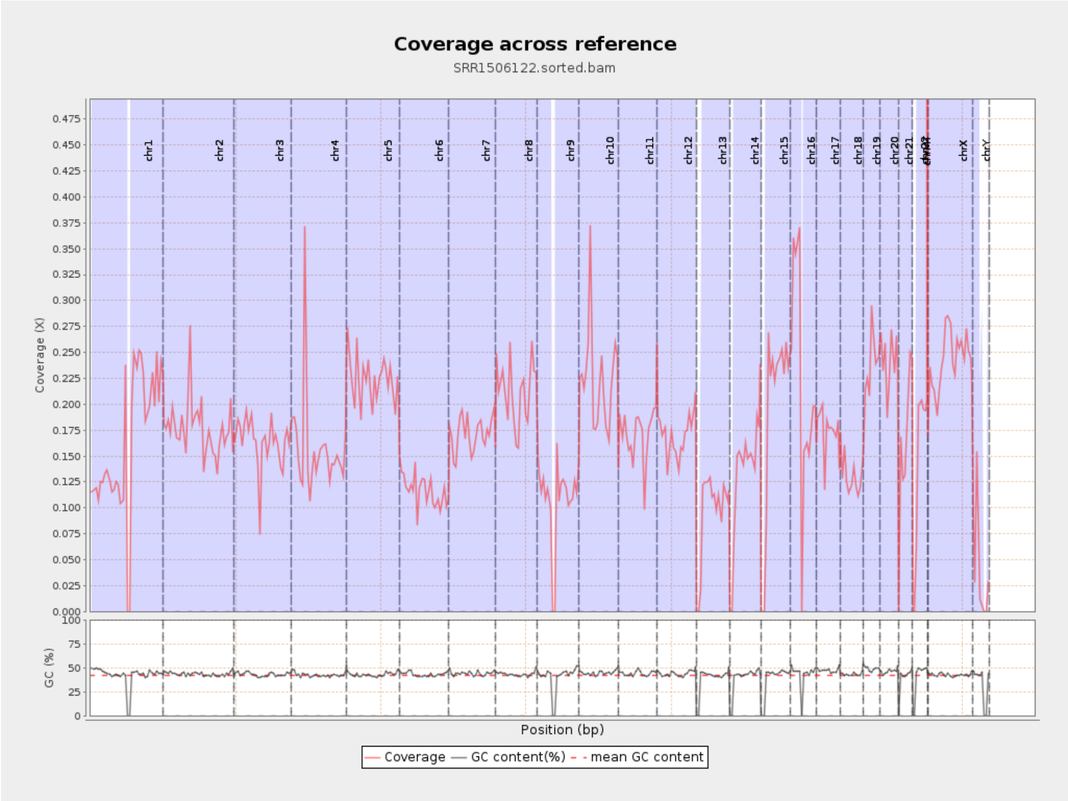
General error rate	0.85%
Mismatches	4,392,601
Insertions	45,009
Mapped reads with at least one insertion	0.66%
Deletions	105,561
Mapped reads with at least one deletion	1.56%
Homopolymer indels	42.09%

2.6. Chromosome stats

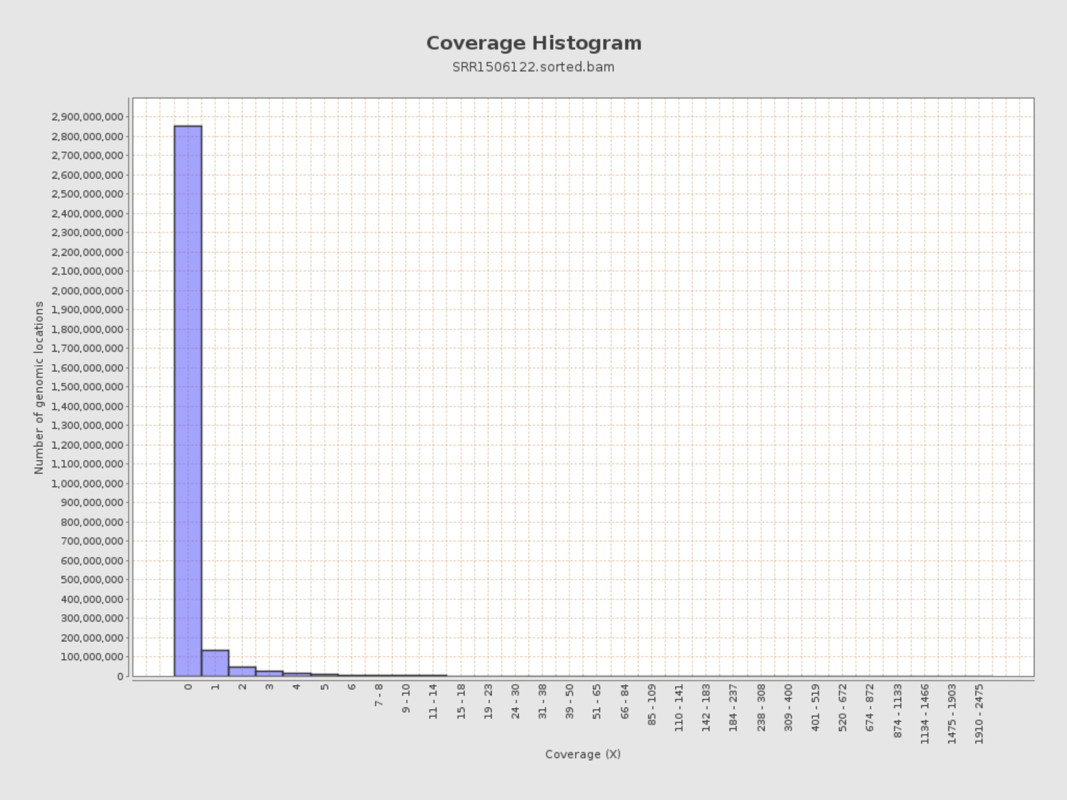
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40194908	0.1613	2.4095
chr2	243199373	42949362	0.1766	1.3996
chr3	198022430	32430271	0.1638	0.7871
chr4	191154276	29762856	0.1557	1.2297
chr5	180915260	40420146	0.2234	0.9886
chr6	171115067	19994085	0.1168	0.7518
chr7	159138663	27204737	0.1709	1.1895

chr8	146364022	31075059	0.2123	1.2726
chr9	141213431	14989001	0.1061	1.1287
chr10	135534747	30340331	0.2239	1.6396
chr11	135006516	23048884	0.1707	1.2209
chr12	133851895	22617741	0.169	0.8508
chr13	115169878	10969773	0.0952	0.6133
chr14	107349540	14038115	0.1308	0.8199
chr15	102531392	20126687	0.1963	0.8986
chr16	90354753	20426549	0.2261	1.1811
chr17	81195210	14146537	0.1742	0.9847
chr18	78077248	10150236	0.13	1.9086
chr19	59128983	14085489	0.2382	1.8207
chr20	63025520	15184486	0.2409	1.1109
chr21	48129895	8032331	0.1669	1.2
chr22	51304566	7034351	0.1371	0.8626
chrMT	16571	161696	9.7578	7.3761
chrX	155270560	37565707	0.2419	1.0876
chrY	59373566	2162478	0.0364	1.3936

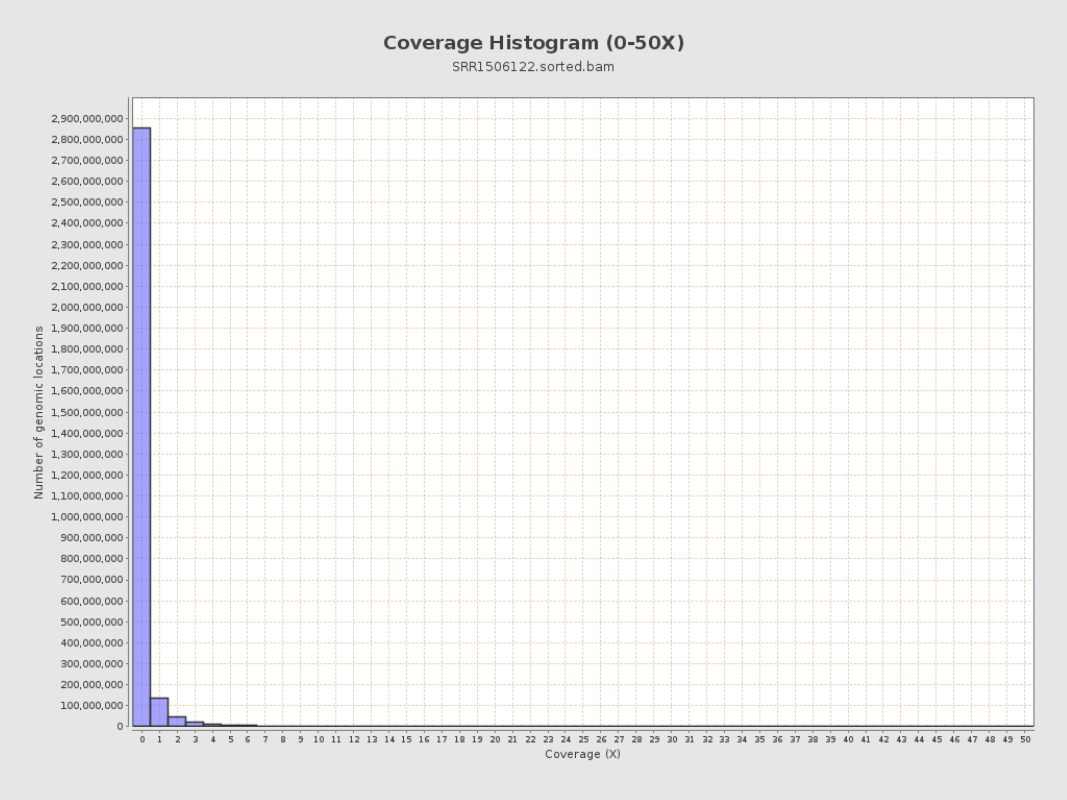
3. Results : Coverage across reference



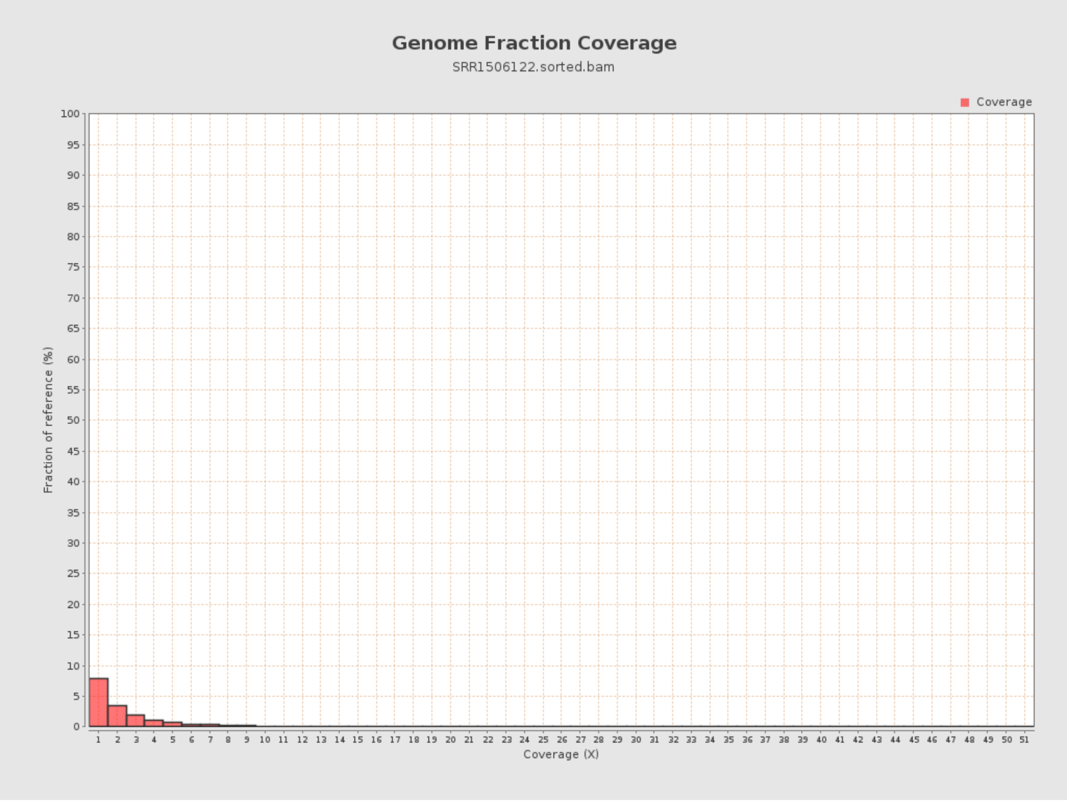
4. Results : Coverage Histogram



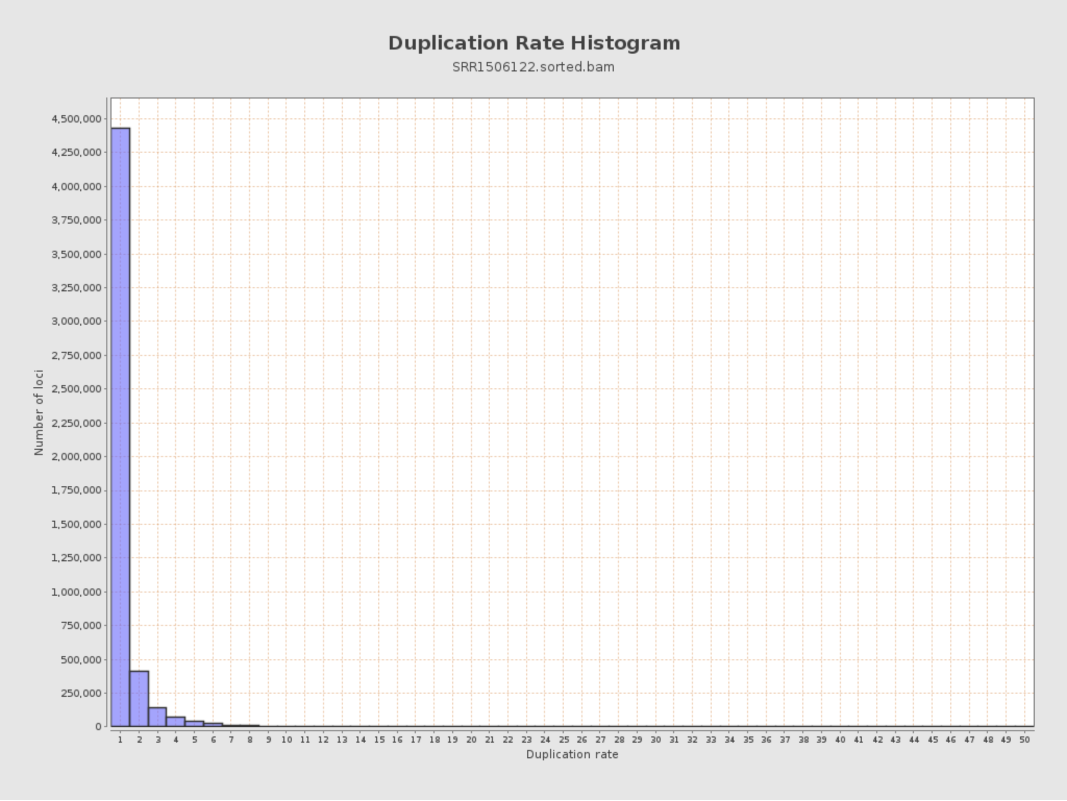
5. Results : Coverage Histogram (0-50X)



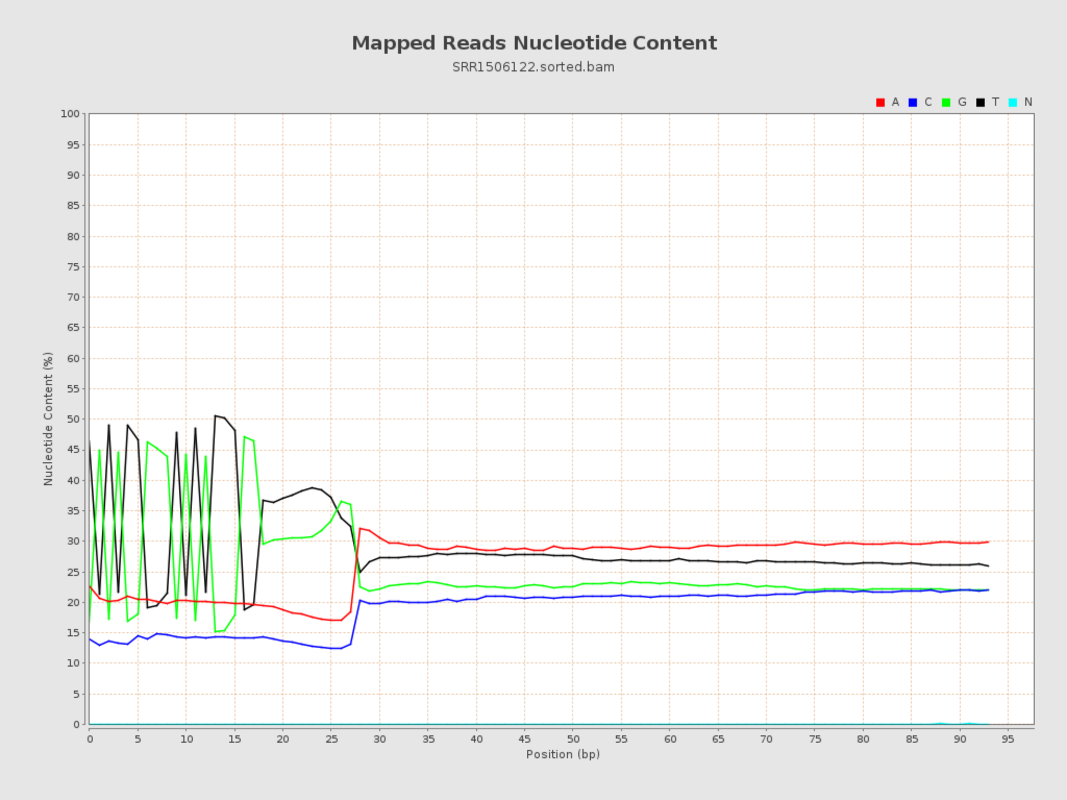
6. Results : Genome Fraction Coverage



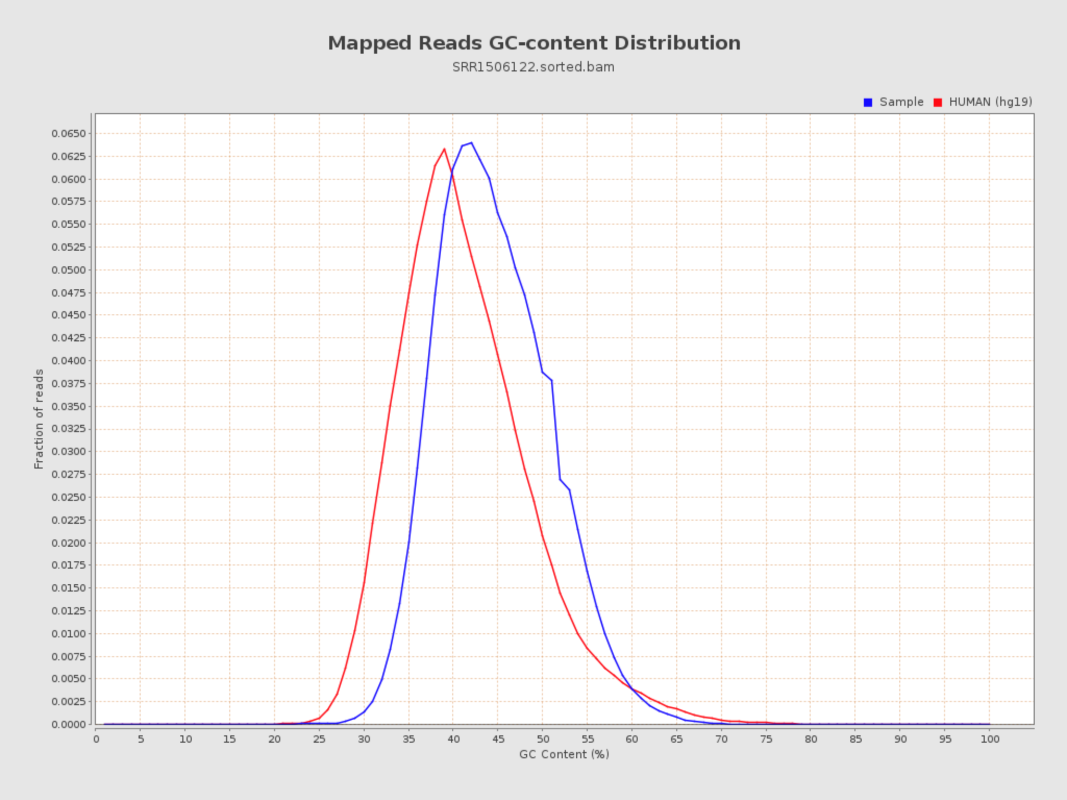
7. Results : Duplication Rate Histogram



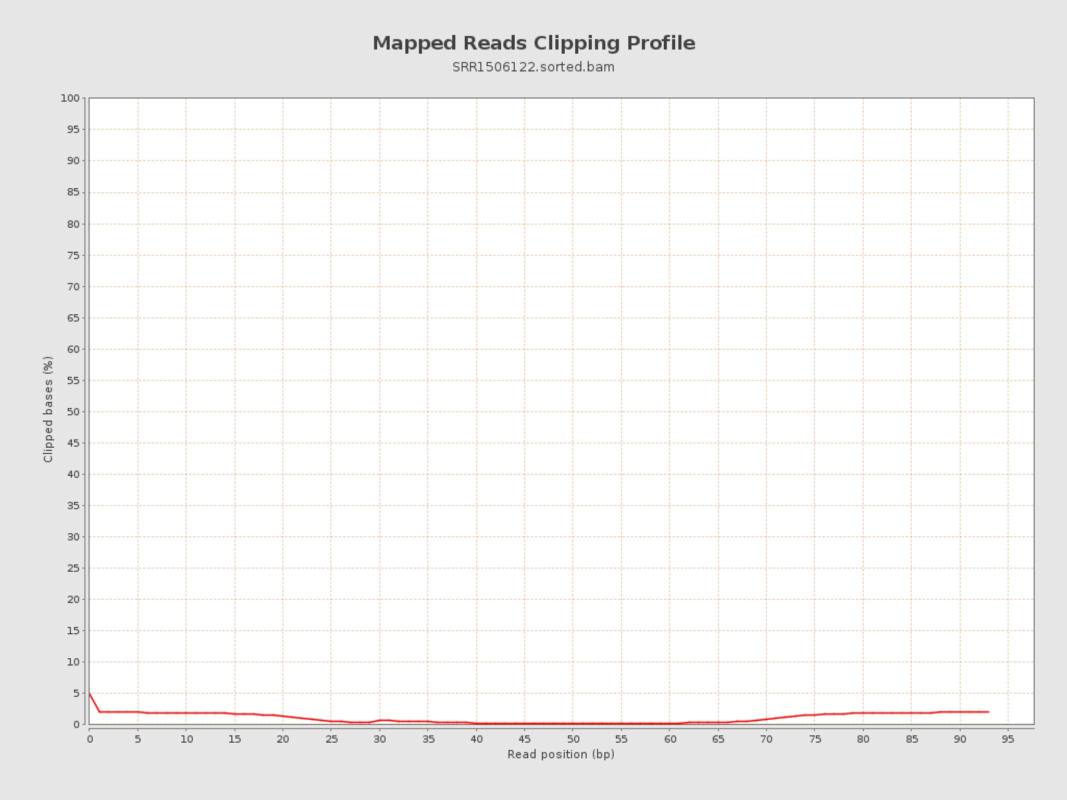
8. Results : Mapped Reads Nucleotide Content



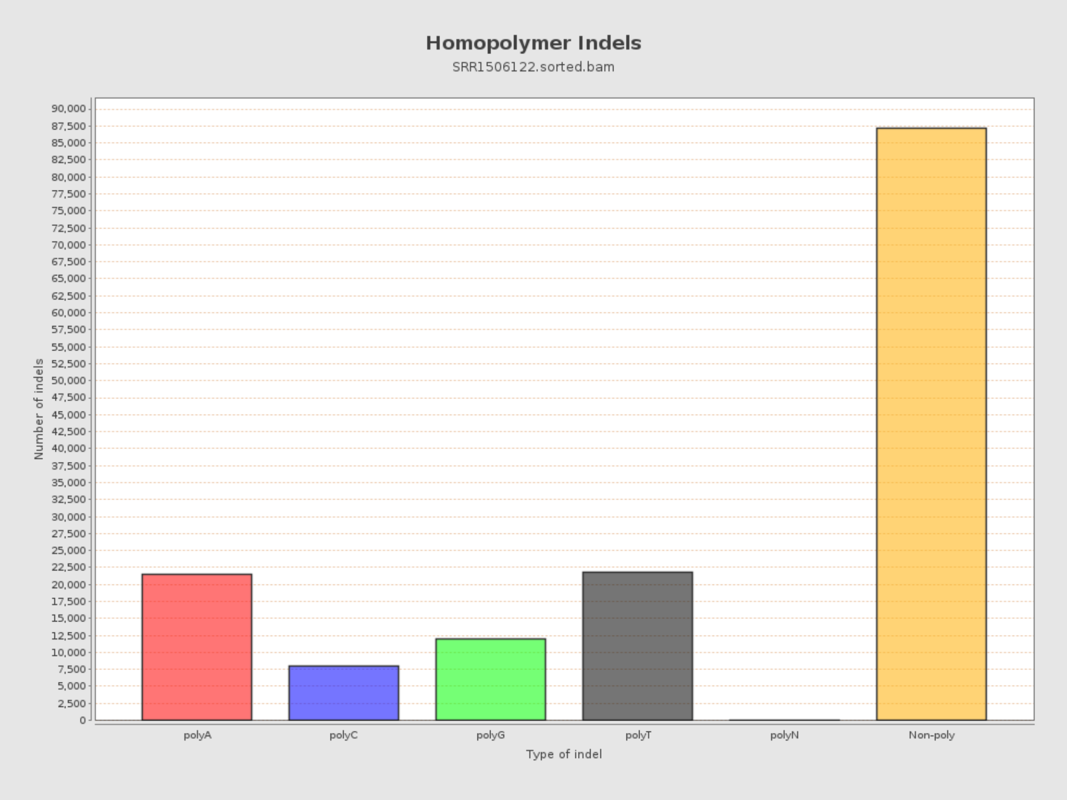
9. Results : Mapped Reads GC-content Distribution



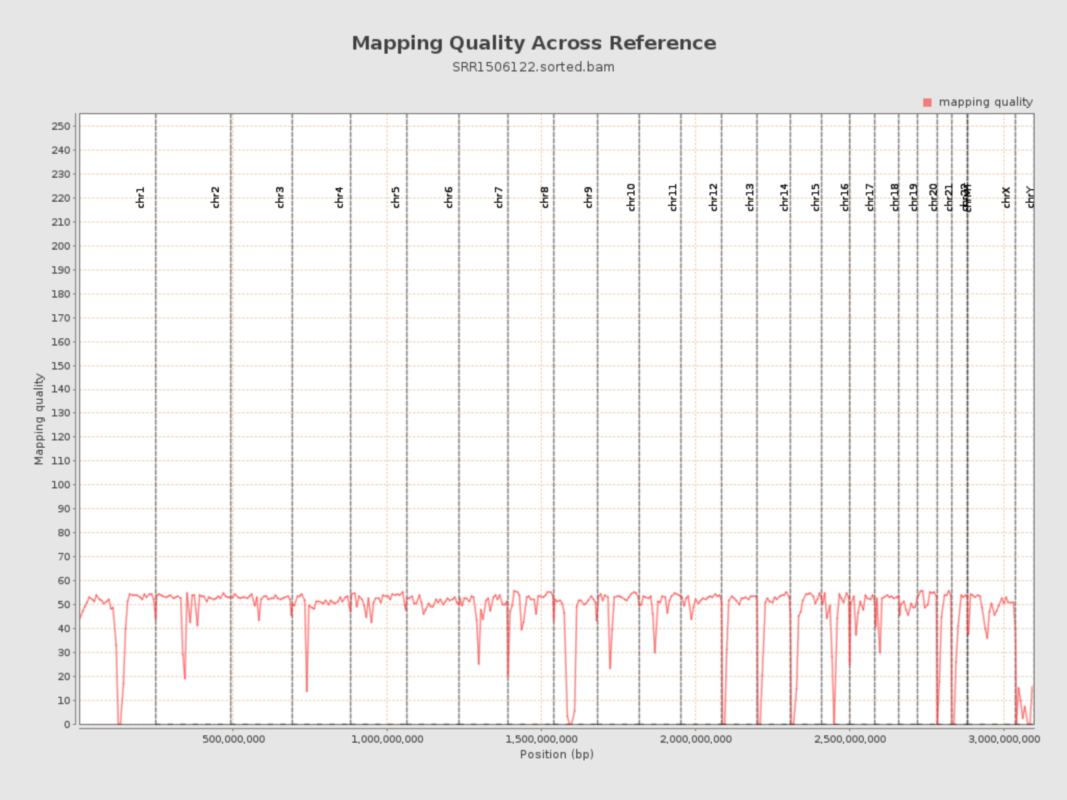
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram