Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 18:42:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536745.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_SRR536745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 18:42:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,832,078
Mapped reads	15,292,702 / 81.21%
Unmapped reads	3,539,376 / 18.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	335 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	114,948 / 0.61%
Duplication rate	0.74%
Clipped reads	250,519 / 1.33%

2.2. ACGT Content

Number/percentage of A's	239,941,395 / 31.47%
Number/percentage of C's	140,991,432 / 18.49%
Number/percentage of T's	238,441,021 / 31.27%
Number/percentage of G's	143,087,372 / 18.77%
Number/percentage of N's	16,443 / 0%
GC Percentage	37.26%

2.3. Coverage

Mean	0.2463

Standard Deviation	0.556

2.4. Mapping Quality

Mean Mapping Quality	47.52

2.5. Mismatches and indels

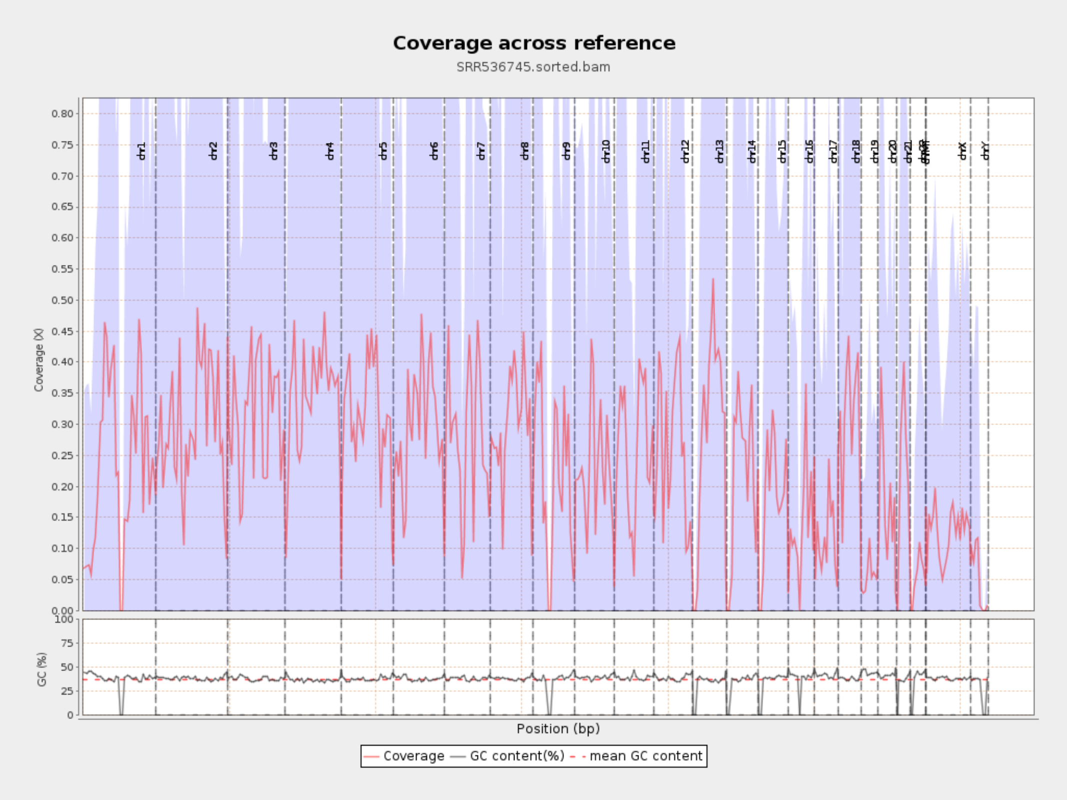
General error rate	0.35%
Mismatches	2,585,348
Insertions	50,660
Mapped reads with at least one insertion	0.33%
Deletions	39,939
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.05%

2.6. Chromosome stats

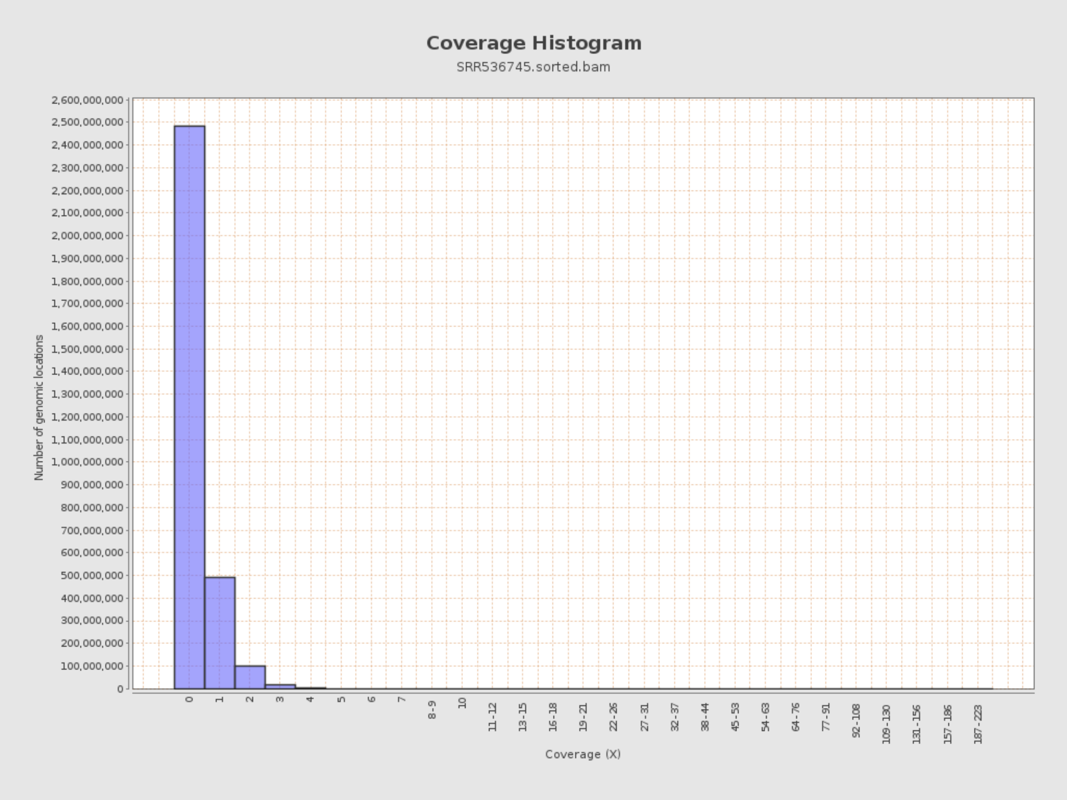
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57989945	0.2327	0.5438
chr2	243199373	72380349	0.2976	0.6074
chr3	198022430	62877249	0.3175	0.6218
chr4	191154276	66371385	0.3472	0.6413
chr5	180915260	56450788	0.312	0.6111
chr6	171115067	51894161	0.3033	0.6019
chr7	159138663	43896189	0.2758	0.5853

chr8	146364022	44177991	0.3018	0.6007
chr9	141213431	31999420	0.2266	0.5382
chr10	135534747	31696594	0.2339	0.525
chr11	135006516	34993142	0.2592	0.5643
chr12	133851895	34335802	0.2565	0.5609
chr13	115169878	34036956	0.2955	0.6044
chr14	107349540	23723105	0.221	0.524
chr15	102531392	18672866	0.1821	0.4736
chr16	90354753	12303510	0.1362	0.5258
chr17	81195210	9366744	0.1154	0.3753
chr18	78077248	24804398	0.3177	0.6155
chr19	59128983	3398826	0.0575	0.2554
chr20	63025520	11583570	0.1838	0.4761
chr21	48129895	10108843	0.21	0.5245
chr22	51304566	2889465	0.0563	0.2543
chrMT	16571	2787	0.1682	0.4153
chrX	155270560	19576187	0.1261	0.3714
chrY	59373566	3014187	0.0508	0.2441

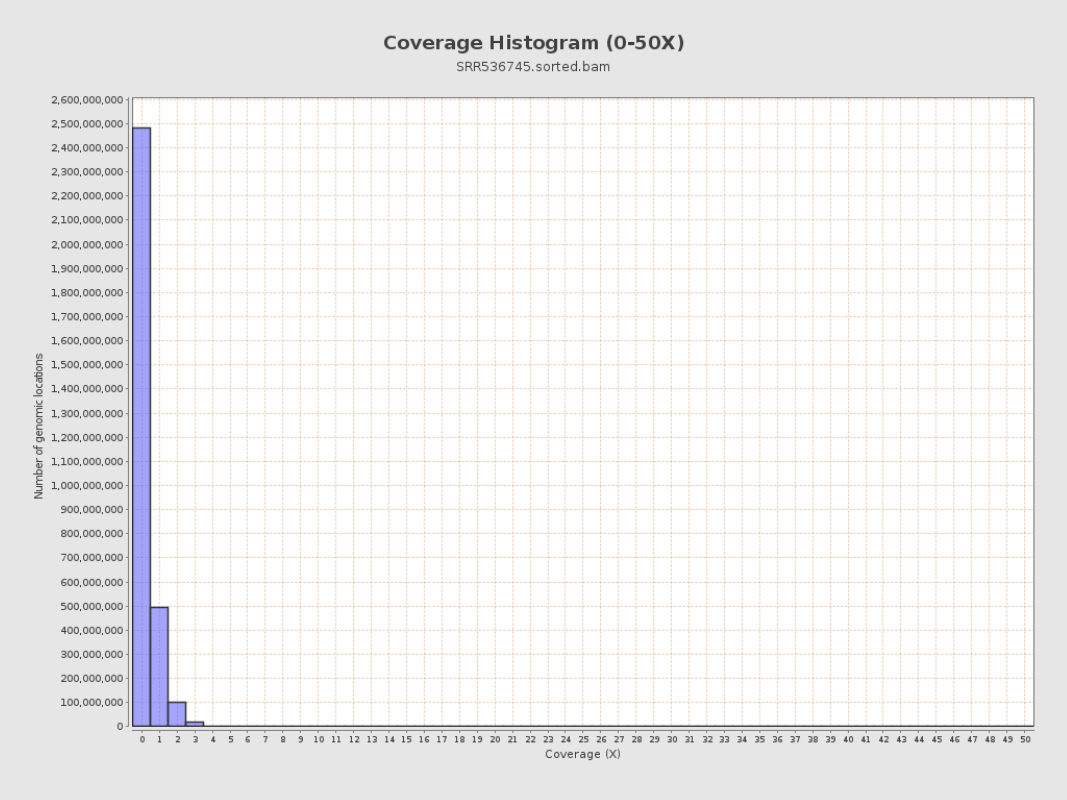
3. Results : Coverage across reference



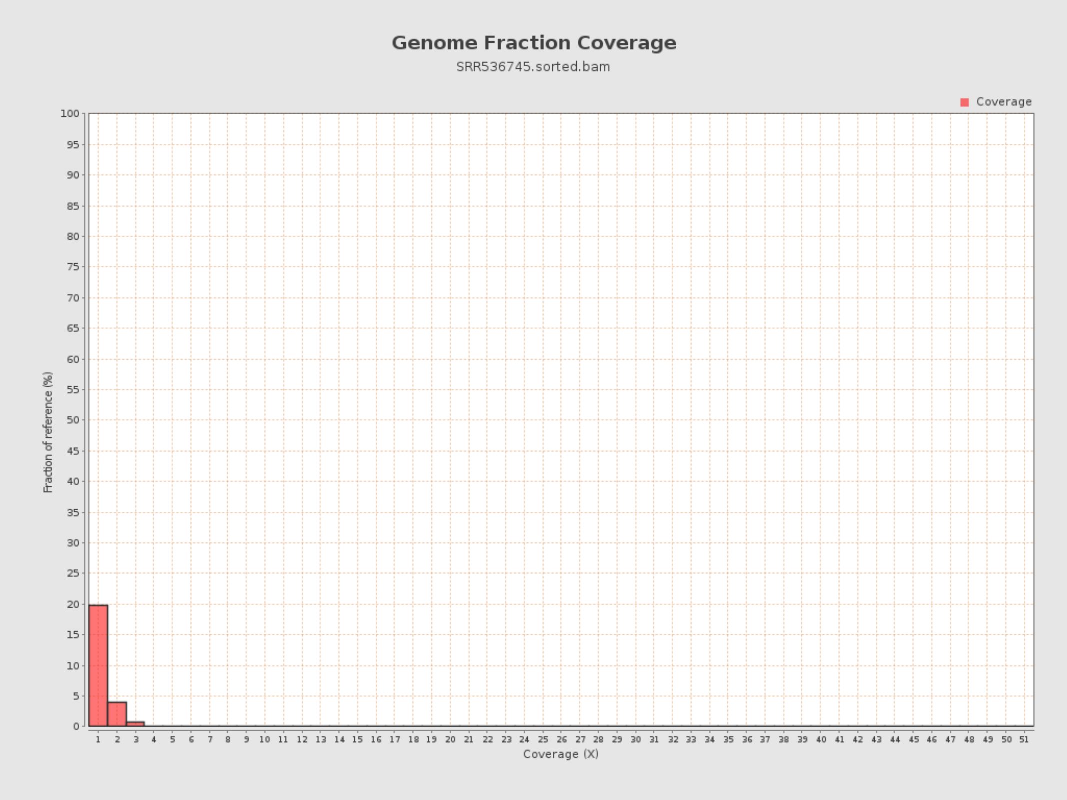
4. Results : Coverage Histogram



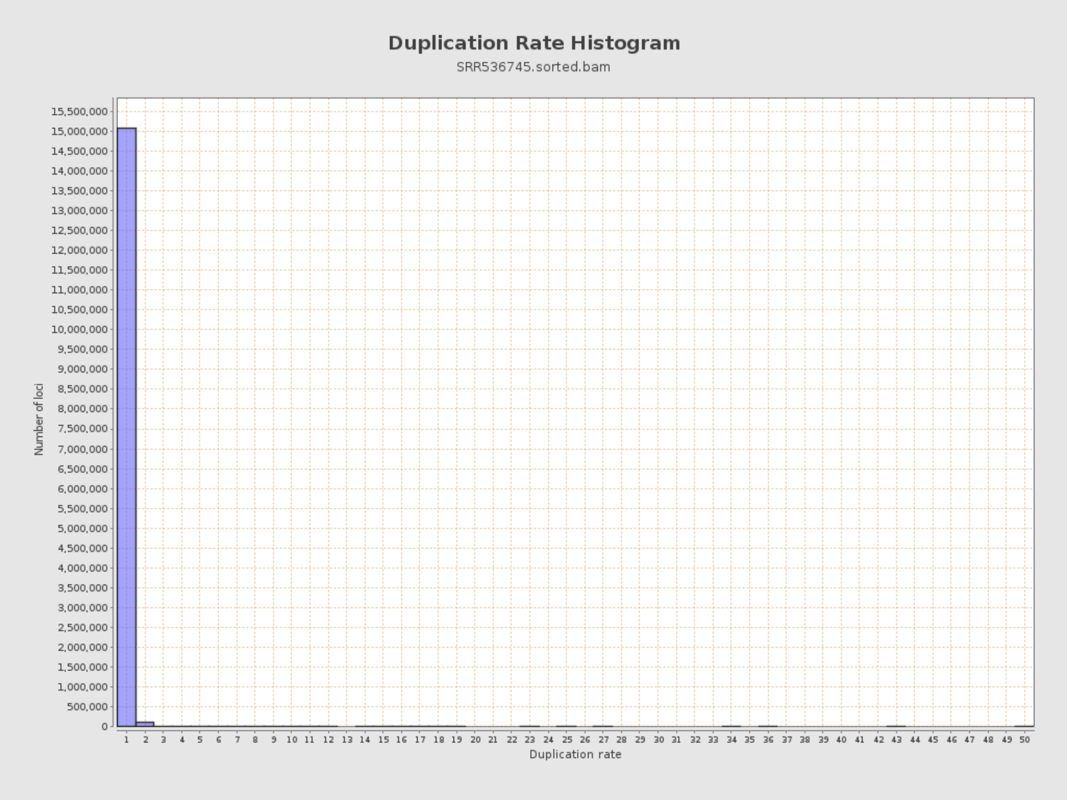
5. Results : Coverage Histogram (0-50X)



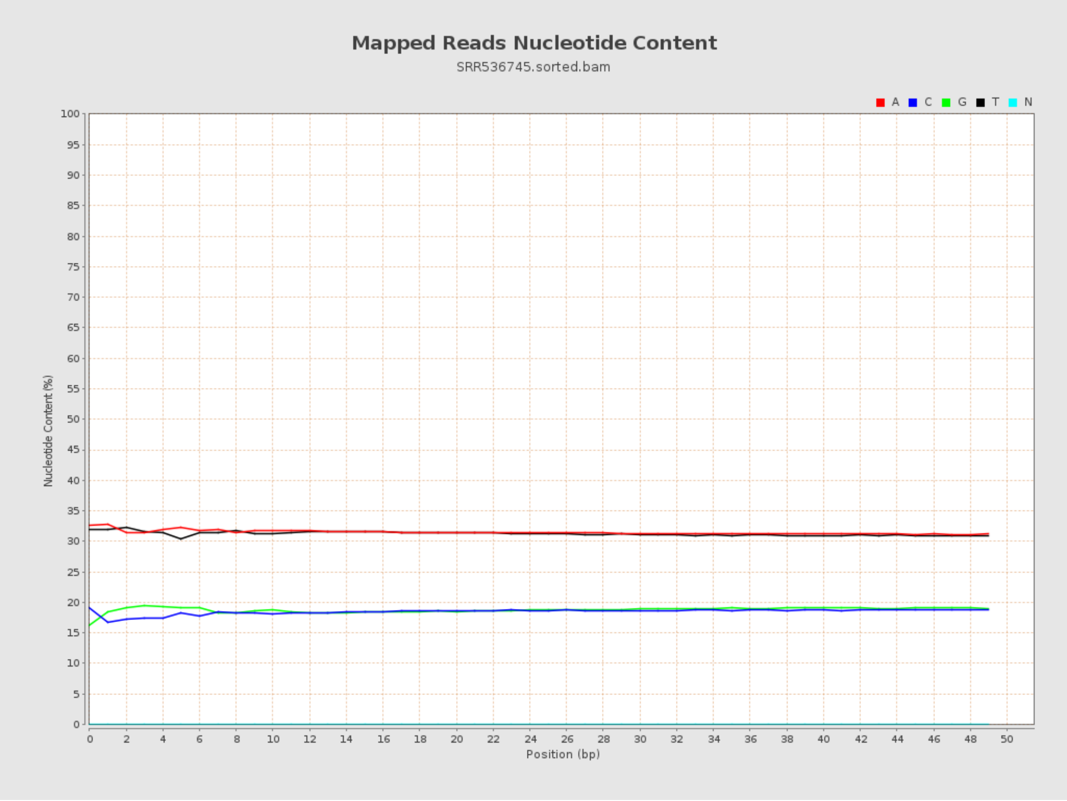
6. Results : Genome Fraction Coverage



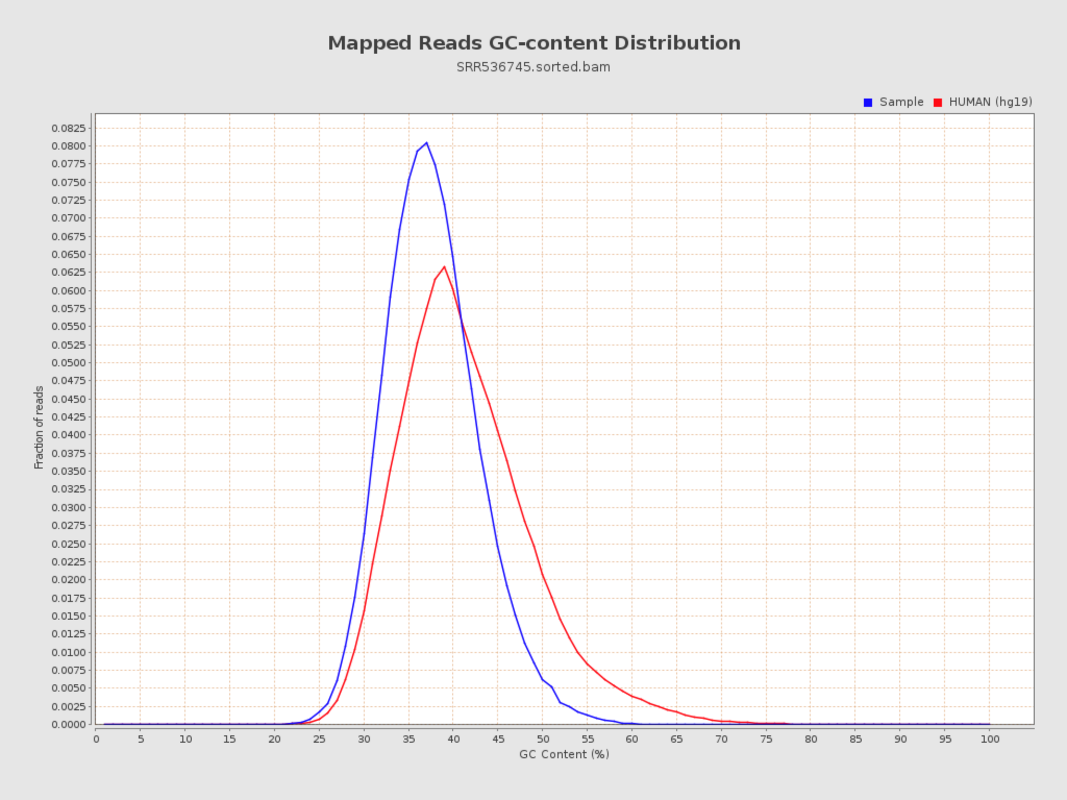
7. Results : Duplication Rate Histogram



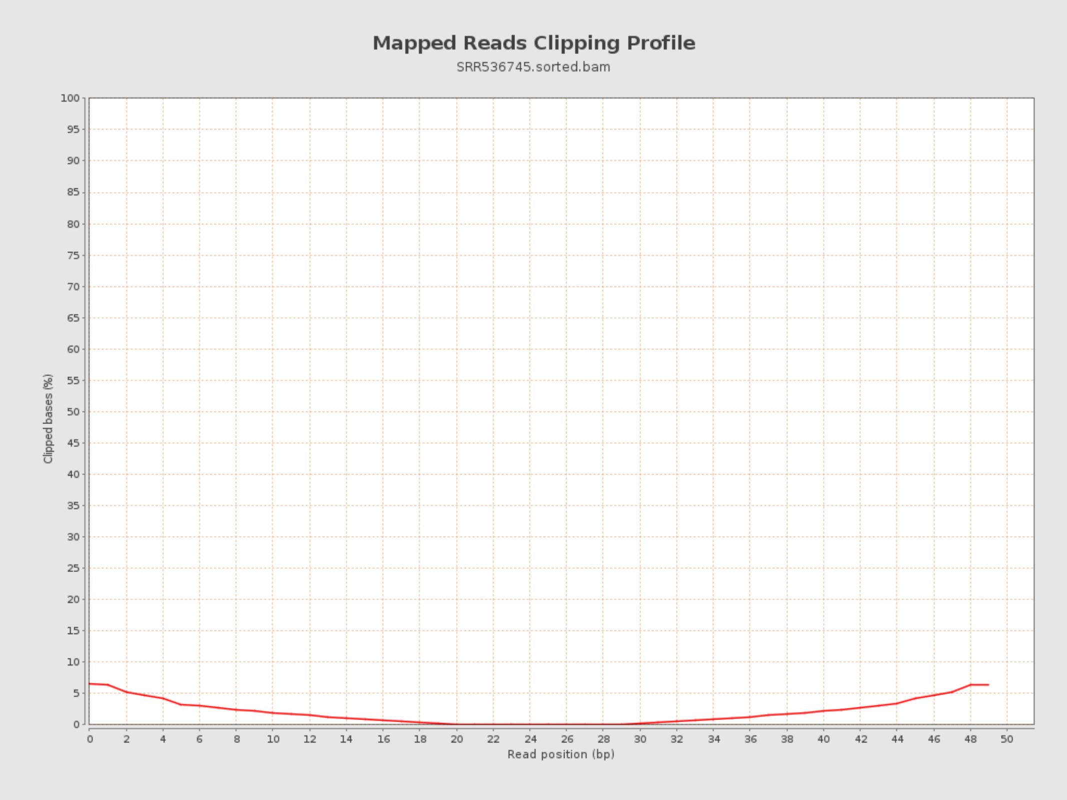
8. Results : Mapped Reads Nucleotide Content



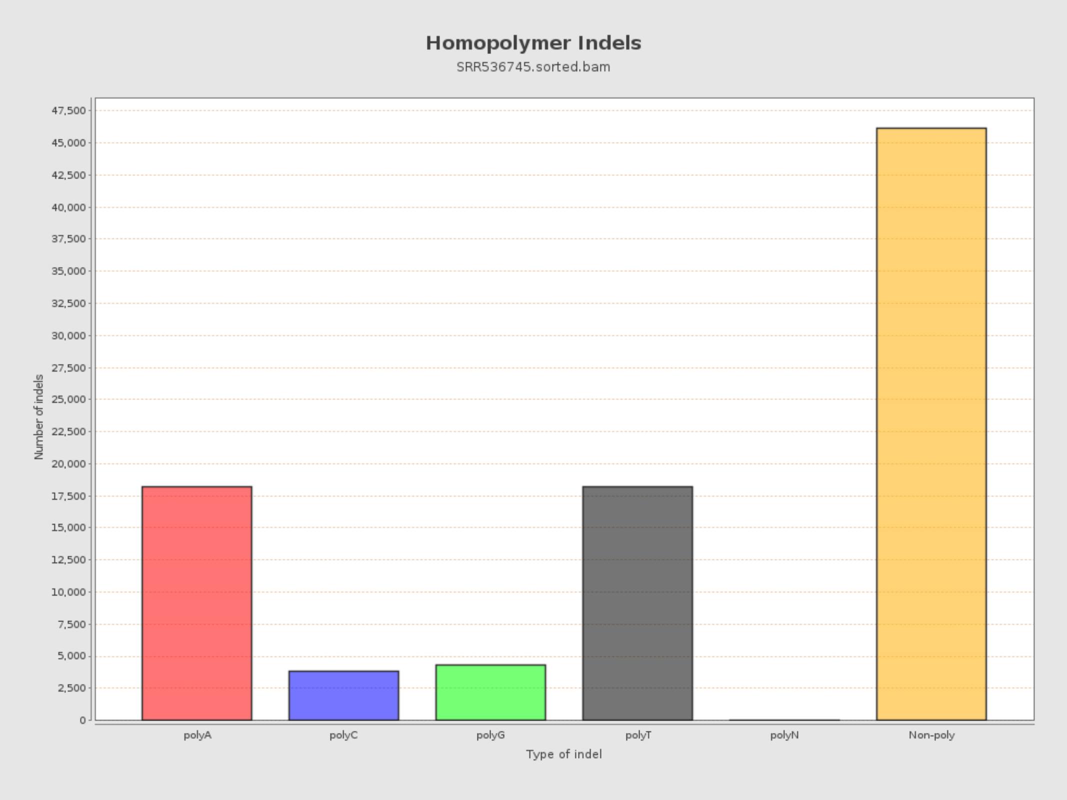
9. Results : Mapped Reads GC-content Distribution



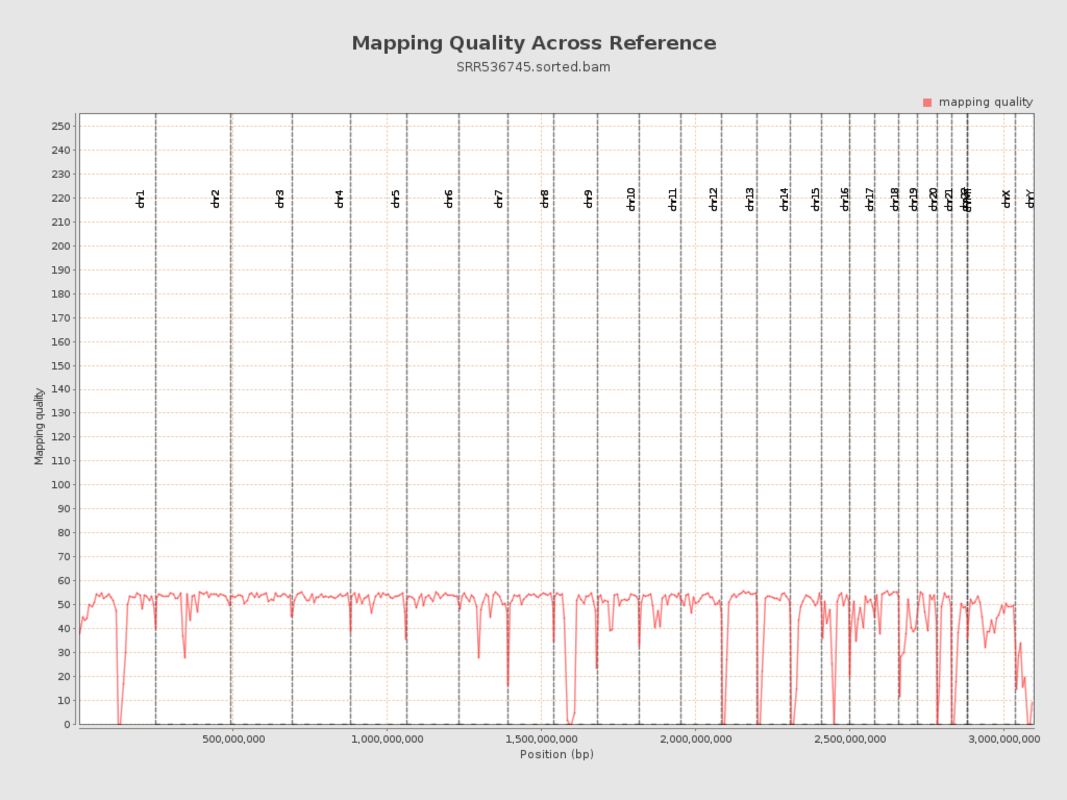
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram