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SF3B4_K562_rep02_chr10_74769646_74769837_-
UPF1_K562_rep02_chr11_767761_767968_-
UPF1_K562_rep02_chr1_184761013_184761202_-
UPF1_K562_rep02_chr1T_44641237_44641419_+
RPS5_K562_rep02_chr10_7848527_7848745_+
QKI_HepG2_rep02_chr4_74061623_74061810_-
QKI_HepG2_rep02_chr3_9947860_9948044_+
XRCC6_K562_rep01_chr1_160982345_160982534_-
UPF1_K562_rep01_chr1_19543369_19543504_-
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# B



A horizontal bar chart showing the distribution of 24 chromosomes (chr1 to chrY) across a genomic scale from 0 Mb to 250 Mb. Each chromosome is represented by a dark gray bar with vertical cyan lines indicating specific genomic features. The bars are arranged in descending order of length, with chr1 being the longest and chrY being the shortest. The x-axis is labeled with 0 Mb, 50 Mb, 100 Mb, 150 Mb, 200 Mb, and 250 Mb.

Detailed description of Figure 1: This bar chart displays the detection ratio for 100 different repeat classes in the human genome. The vertical axis (y-axis) represents the 'Detection ratio' from 0.0 to 1.0. The horizontal axis (x-axis) lists the 'Repeat class' categories. A red line at the bottom of the chart indicates the 'Total repeat count (hg19)' for each class, with a corresponding scale on the right ranging from 0 to 150,000. The bars show that many repeat classes have a detection ratio between 0.1 and 0.4, while a few, such as CGTAA and CTTAA, have ratios near 1.0. The total repeat count for most classes is below 50,000, but some classes like A and G have counts exceeding 100,000.

Repeat class	Detection ratio (approx.)	Total repeat count (hg19) (approx.)
(AATAG)n	0.15	10,000
(ACATG)n	0.12	10,000
(AGTGG)n	0.15	10,000
(ACTGG)n	0.12	10,000
(AGTAG)n	0.18	10,000
(ATGAG)n	0.55	10,000
(ATTGG)n	0.20	10,000
(CAAA)n	0.40	10,000
(CAAAA)n	0.15	10,000
(CAAAAC)n	0.35	10,000
(CAAAAT)n	0.35	10,000
(CAACG)n	1.00	10,000
(CAAG)n	0.15	10,000
(CAAGC)n	0.18	10,000
(CAAGT)n	0.55	10,000
(CAAT)n	0.18	10,000
(CACA)n	0.15	10,000
(CAGT)n	0.22	10,000
(CAGTT)n	0.20	10,000
(CAGTG)n	0.25	10,000
(CAT)n	0.10	10,000
(CATAA)n	0.38	10,000
(CATAC)n	0.50	10,000
(CATGG)n	0.20	10,000
(CATTT)n	0.25	10,000
(CCAA)n	0.20	10,000
(CCAT)n	0.15	10,000
(CGA)n	0.28	10,000
(CGAA)n	0.80	10,000
(CGG)n	0.35	10,000
(CGGAA)n	0.65	10,000
(CGTAA)n	1.00	10,000
(CTAA)n	0.40	10,000
(CTAAAT)n	0.40	10,000
(CTTAA)n	0.35	10,000
(CTTAG)n	0.50	10,000
(CTTGG)n	0.15	10,000
(CTTTG)n	0.10	10,000
(GAA)n	0.25	10,000
(GAAA)n	0.15	10,000
(GAAAA)n	0.15	10,000
(GAGAA)n	0.15	10,000
(GGAA)n	0.15	10,000
(GGAGAA)n	0.15	10,000
(GGGAA)n	0.15	10,000
(GGGAAAT)n	0.38	10,000
(GTTG)n	0.28	10,000
(TAA)n	0.45	10,000
(TAAAT)n	0.28	10,000
(TAAATAT)n	0.30	10,000
(TAAAG)n	0.10	10,000
(TAAAGAT)n	0.42	10,000
(TATTG)n	0.25	10,000
(TCCCC)n	0.15	10,000
(TCCCG)n	0.10	10,000
(TCCG)n	0.25	10,000
(TCTG)n	0.20	10,000
(TCTTA)n	0.45	10,000
(TTA)n	0.40	10,000
(TTAA)n	0.35	10,000
(TTAAAT)n	0.58	10,000
(TTACG)n	0.35	10,000
(TTATG)n	0.40	10,000
(TTCC)n	0.15	10,000
(TTCCC)n	0.10	10,000
(TTCCCG)n	0.10	10,000
(TTCCG)n	0.50	10,000
(TTCTC)n	0.15	10,000
(TTCTCC)n	0.40	10,000
(TTG)n	0.20	10,000
(TTGG)n	0.10	10,000
(TTTAA)n	0.28	10,000
(TTTAAAT)n	0.35	10,000
(TTTAG)n	0.42	10,000
(TTTC)n	0.20	10,000
(TTTCG)n	0.15	10,000
(TTTGG)n	0.30	10,000
(TTTTA)n	0.15	10,000
(TTTTAT)n	0.28	10,000
(TTTTG)n	0.15	10,000
(TTTTT)n	0.15	10,000
(TTTTTT)n	0.15	10,000
Aluab	0.85	10,000
Aluao	0.75	10,000
Aluaj	0.75	10,000
Alu4	0.75	10,000
AluSC	0.95	10,000
AluSC8	0.95	10,000
AluSC9	0.95	10,000
AluSC8	0.95	10,000
AluSC9	0.95	10,000
AluSC7	0.95	10,000
AluSp	0.95	10,000
AluSq	0.95	10,000
AluSq10	0.55	10,000
AluSq2	0.95	10,000
AluSq4	0.95	10,000
AluSx	0.85	10,000
AluSx1	0.95	10,000
AluSx3	0.95	10,000
AluSx4	0.95	10,000
AluSx2	0.95	10,000
AluSx5	0.95	10,000
AluY	0.95	10,000
AluY5	0.95	10,000
AluY58	0.80	10,000
AluYb8	0.95	10,000
AluYb9	0.95	10,000
AluYc	0.70	10,000
AluYc3	0.85	10,000
AluYc5		