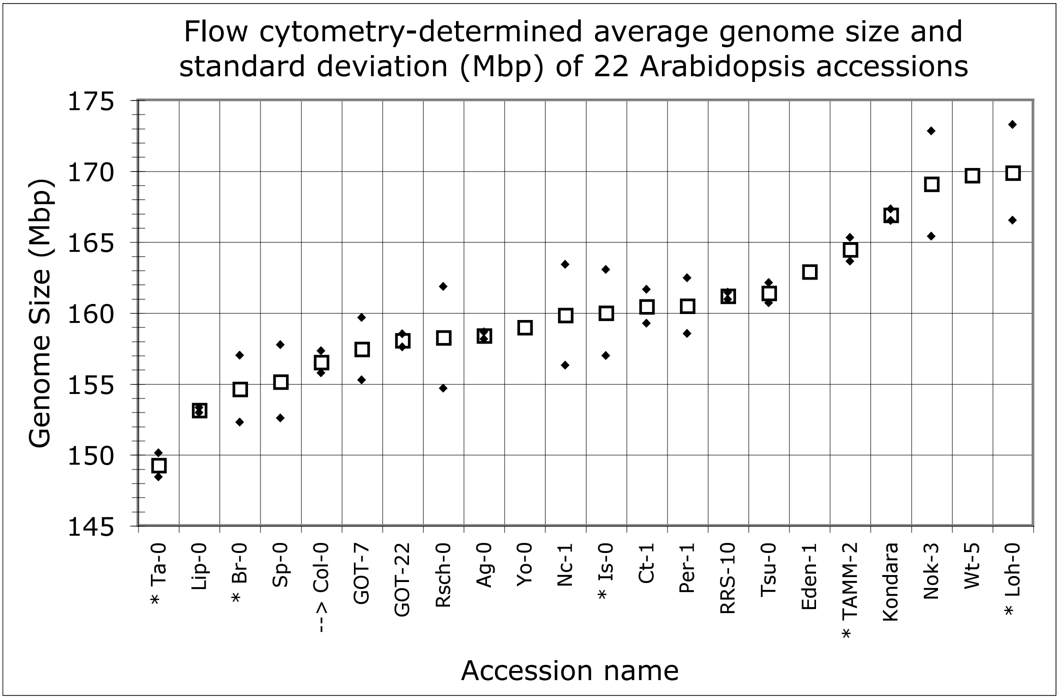

GS_figure. Mean genome size in millions of base pairs (Mbp) of 22 *Arabidopsis thaliana* accessions, measured using flow cytometry. Values are shown by a square marker; where more than one individual was measured the standard deviation of the separate means is given by diamond markers. Accessions selected for more detailed genome size measurement and assessment of repeat array size are marked with asterisks; the sequenced accession Col-0 is noted with an arrow.