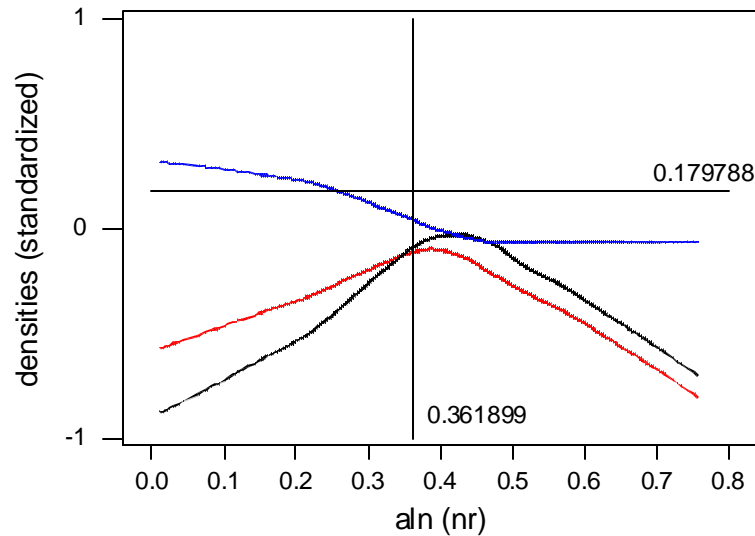


Fig 1: genome-wide



Densities of young alus and old alus are standardized to eliminate genome-wide level and variation scale effects.

Red: lowess (smooth. param 0.5) for stand. dens. of young alus

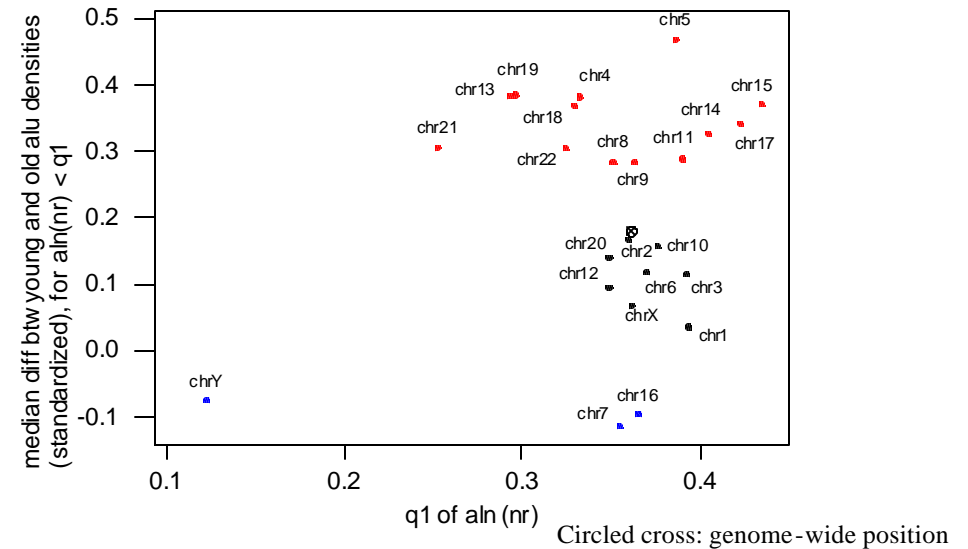
Black: lowess (smooth. param 0.5) for stand. dens. of old alus

Blue: lowess (smooth. param 0.5) for difference between the stand. dens.'s of young and old alus.

The vertical line at 0.361899 marks the genome-wide first quartile of $\ln(nr)$; windows with $\ln(nr)$ below this quartile are considered as low conservation windows.

The horizontal line at 0.179788 marks the median difference between standardized densities for low conservation windows. This represents a measure of alu depletion in low conservation regions. The blue lowess curve and the positive value of this median show the depletion in a robust fashion.

Fig 2: by chromosome

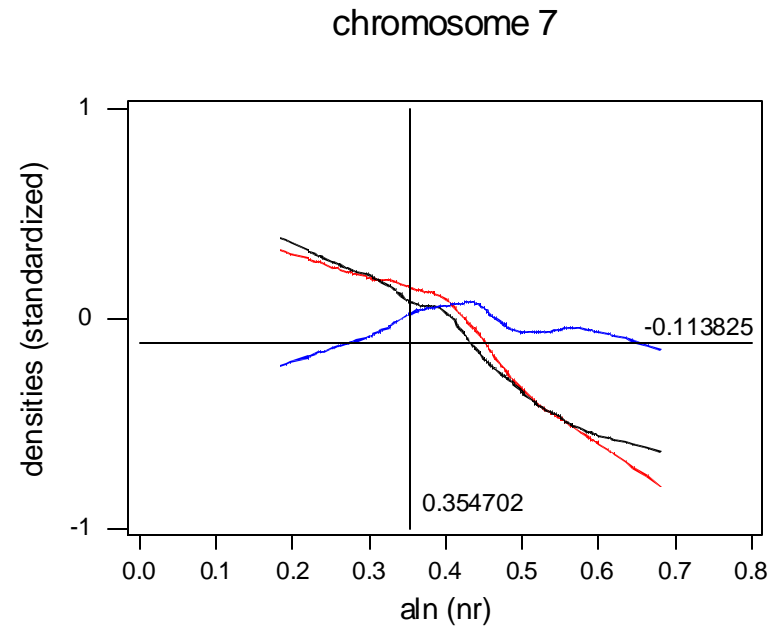
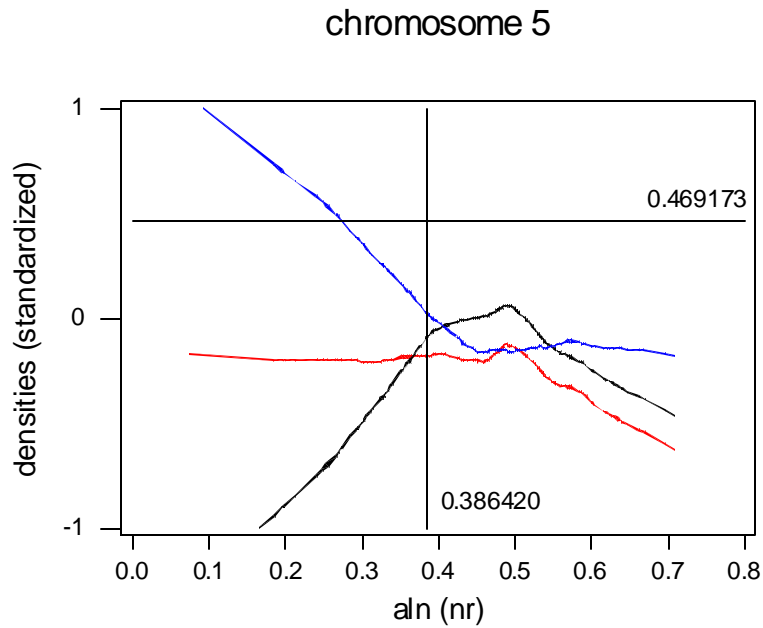


To eliminate chromosome-specific level and variation scale effects, the densities of young alus and old alus are standardized within each chromosome.

To give a chromosome-specific definition of low conservation, the first quartile of $\ln(nr)$ is calculated for each chromosome -- horizontal axis Fig 2.

Thus, a chromosome-specific measure of alu depletion in low conservation regions is obtained as the median difference between (chromosome) standardized densities for windows with $\ln(nr)$ below the (chromosome) first quartile -- vertical axis Fig 2.

Each point in Fig 2 is equivalent to the crossing of the vertical and horizontal lines in Fig 1, but relative to a single chromosome. Chromosomes differ in terms of how low low conservation is (spread along horizontal axis). Moreover, they differ and CLUSTER in terms of the chromosome-specific measure of alu depletion in low conservation regions (spread along vertical axis, color coding).



Depletion of alus in low-conservation regions varies dramatically from chromosome to chromosome. Above are the two extreme cases of chromosome 5 and 7 (the first quartile of $\text{aln}(\text{nr})$ is similar for these two chromosomes, and similar to the overall one, but the median difference between young and old alus (standardized) densities are very different. For chromosome 7, the difference curve (blue lowess) is actually negative at low conservation levels; here the preferential depletion of alus seems to occur at intermediate $\text{aln}(\text{nr})$ ranges, with old alus surviving best at very low or very high ranges.

Fig 3: genome-wide

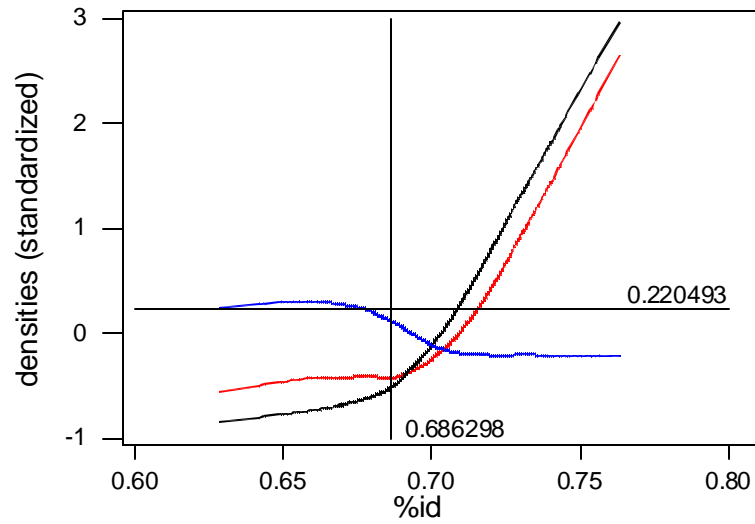
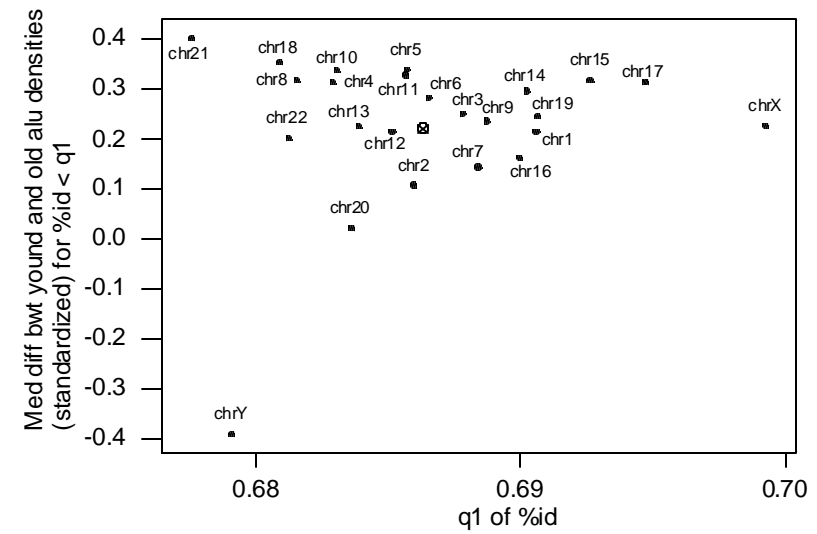


Fig 4: by chromosome



Same analysis as in Fig 1 and 2, using %id instead of aln (nr) as a proxy for conservation

chrom	Med(st_y-o)aln<q1all	chrom	Med(st_y-o) %id<q1all
chr16	-0.501285	chr19	-0.274254
chr7	-0.349424	chr20	-0.122031
chr20	-0.235145	chr16	-0.077257
chr19	-0.040428	chrX	0.104103
chr3	0.029504	chr8	0.117399
chrX	0.034775	chr10	0.131177
chr1	0.053943	chr2	0.149068
chr12	0.084225	chr12	0.180716
chr10	0.096978	chr7	0.191264
chr6	0.130448	chr3	0.196086
chr8	0.139342	chrY	0.218464
chr2	0.149068	chr15	0.230783
chr22	0.216599	chr6	0.232123
chr11	0.246723	chr18	0.244980
chrY	0.286886	chr14	0.247846
chr14	0.290423	chr13	0.258840
chr13	0.316795	chr11	0.275871
chr17	0.323615	chr5	0.278113
chr4	0.329252	chr9	0.291835
chr18	0.333645	chr1	0.331505
chr5	0.341634	chr4	0.337322
chr9	0.359201	chr22	0.437368
chr15	0.649117	chr17	0.469381
chr21	0.663078	chr21	0.631367

USING A COMMON STANDARDIZATION AND DEFINITION OF LOW CONSERVATION:

In this table, instead of computing the standardization of young and old alu densities, and the first quartile of aln(nr) and %id, within each chromosome, one refers to the genome-wide standardization, and to the genome-wide quartiles.

Thus, for each chromosome, the measure of alu depletion in low conservation regions is the median difference between young and old alu densities (standardized **overall**) for windows in the chromosome with aln(nr), or %id, below the first **overall** quartile.

0.179788

0.220493