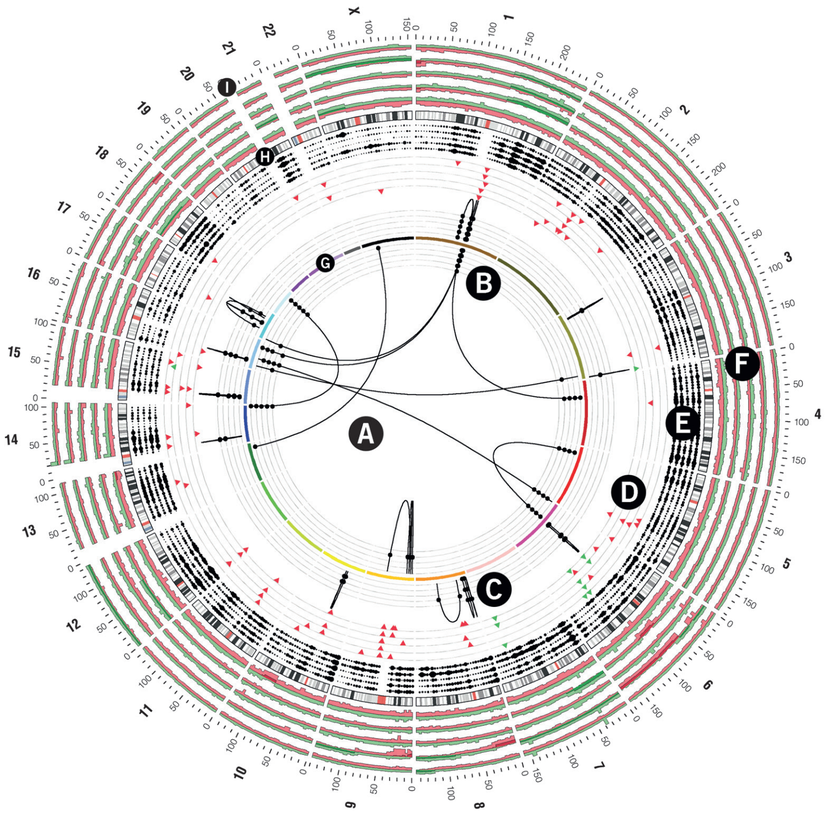

Figure 1. A whole-genome view of structural changes in five follicular lymphoma tumor samples observed using restriction digest fingerprints and Affymetrix Mapping 500k arrays. Chromosomes 1–22 and X are represented by circularly arranged ideograms (*H*), demarcated by a megabase scale on the *outer* rim of the figure (*I*). A stylized and color-coded instance of each ideogram is found in track *G*. (*B*–*F*) Data tracks comprise five concentric rings, each corresponding to a different sample. Translocations are shown in track *A* as curves that connect regions brought into adjacency by the rearrangement. Each curve is associated with a specific sample by circular glyphs in track *B* attached to the sample's ring. Track *C* shows inversions by curves pointing outward from the center. Large-scale deletions and insertions are shown as red and green triangular glyphs, respectively, in track *D*. The density of small-scale indels is shown in track *E*, where the size of the circular glyph for each 5-Mb region is proportional to the number of events in the region. Copy number information for each of the five samples is shown in track *F*, which comprises five concentric rings of histograms. Each histogram in track *F* shows the average copy number value across 1000 probes, as well as the minimum and maximum three-probe average within each 1000-probe subset (see Fig. 5 for details).

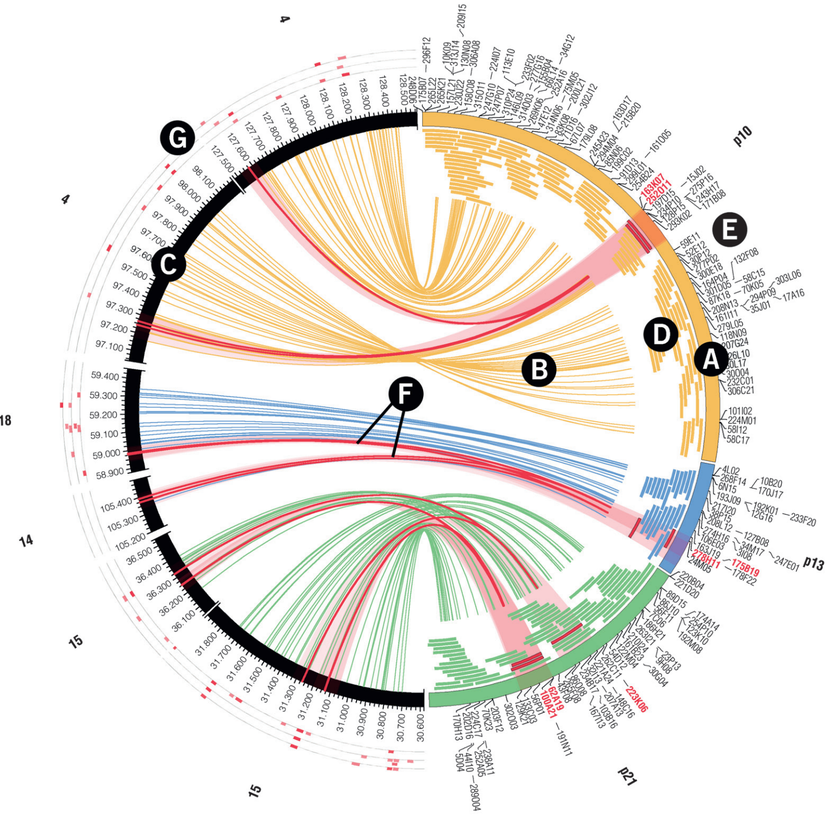

Figure 2. Ordered clone structure of three fingerprint map contigs (colored segments at *right* of figure; *A*) from three follicular lymphoma tumor samples. Fingerprint-based alignments for each clone are shown as curves (*B*) from the middle of the clone to the corresponding genomic region (*C*). Fingerprinted clones are represented as tiles in track *D*, with clone names shown in track *E*. Clones that have multiple alignments to distant genomic regions are highlighted in red (e.g., 175B19 in sample 13). The alignments and extent of these clones on the map contig and genomic region are similarly highlighted (*F*). Small-scale indels detected by fingerprints in each of the three samples are shown in track *G* in three concentric rings. The glyphs used for the small-scale indels are magnified to be discernable (events are too small to directly show at this scale) and proportional to the size of the indel.

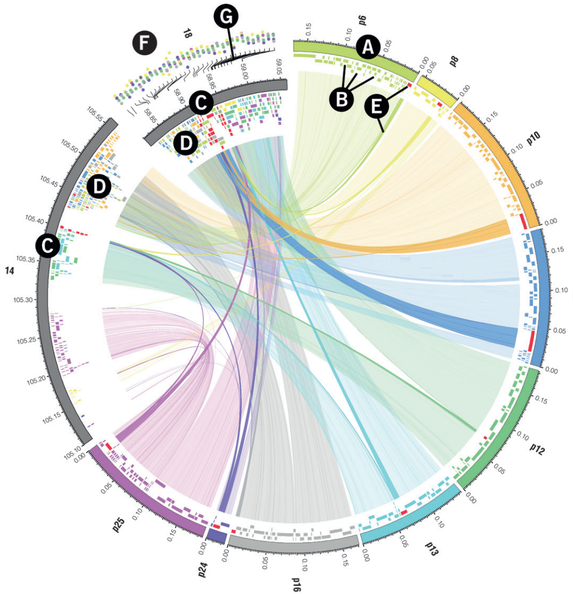

Figure 3. Alignment of short-read Illumina assemblies of BAC clones capturing the t(14;18) translocation in nine distinct follicular lymphoma tumor samples. Each BAC assembly is represented by a colored segment (*A*), and its individual sequence contigs are represented as tiles (*B*). Ribbons inside the image connect the sequence contigs within the BAC assembly to their alignments on the reference assembly (*C*) on chromosomes 14 (105.1–105.56 Mb) and 18 (58.83–59.06 Mb). The position of the contig alignments on the reference assembly is shown as tiles in track *D*, and assigned the same color as the corresponding BAC. Sequence contigs that capture a translocation are highlighted in red (*E*) and have their alignment ribbons strongly colored, and these alignments are shown in red in track *D*. Affymetrix probe values for each of the nine samples are shown in track *F* as a scatterplot, using the same color scheme as for the BAC segments, with the radial position of the glyph proportional to the copy number value. The probe position within this region of chromosome 18 is not uniform, and a connector track (*G*) is used to relate the original probe positions to a uniformly distributed layout in track *F*.

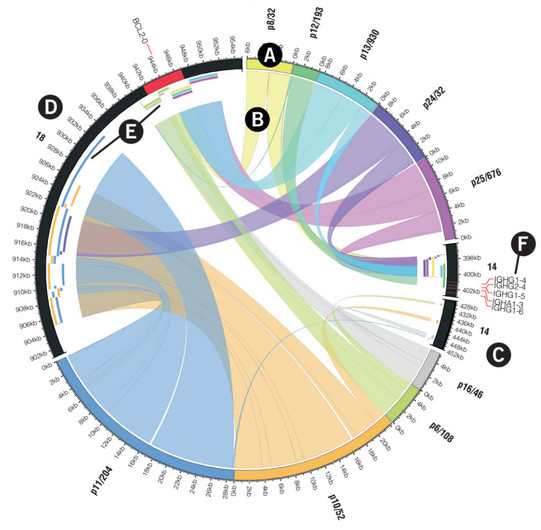

Figure 4. Detailed sequence alignments of sequence contigs from nine follicular lymphoma tumor samples (see Fig. 3, track C) that were found to span translocations. Each of the contigs is represented by a colored segment (*A*) with a label that encodes the patient and contig number (e.g., "p25/676" refers to patient 25, sequence contig 676). Sequence alignments of the contig are shown as ribbons (*B*) to regions of chromosome 14 (*C*, 105.396–105.403 Mb and 105.436–105.452 Mb) and chromosome 18 (*D*, 58.901–58.955 Mb). The extent of each alignment is shown as tiles in track *E*, colored after the corresponding sequence contig. Gene exons in the vicinity are labeled in track *F* and suffixed with their order within the gene (e.g., BCL2-0 is the first exon, BCL2-1 the next, etc.).

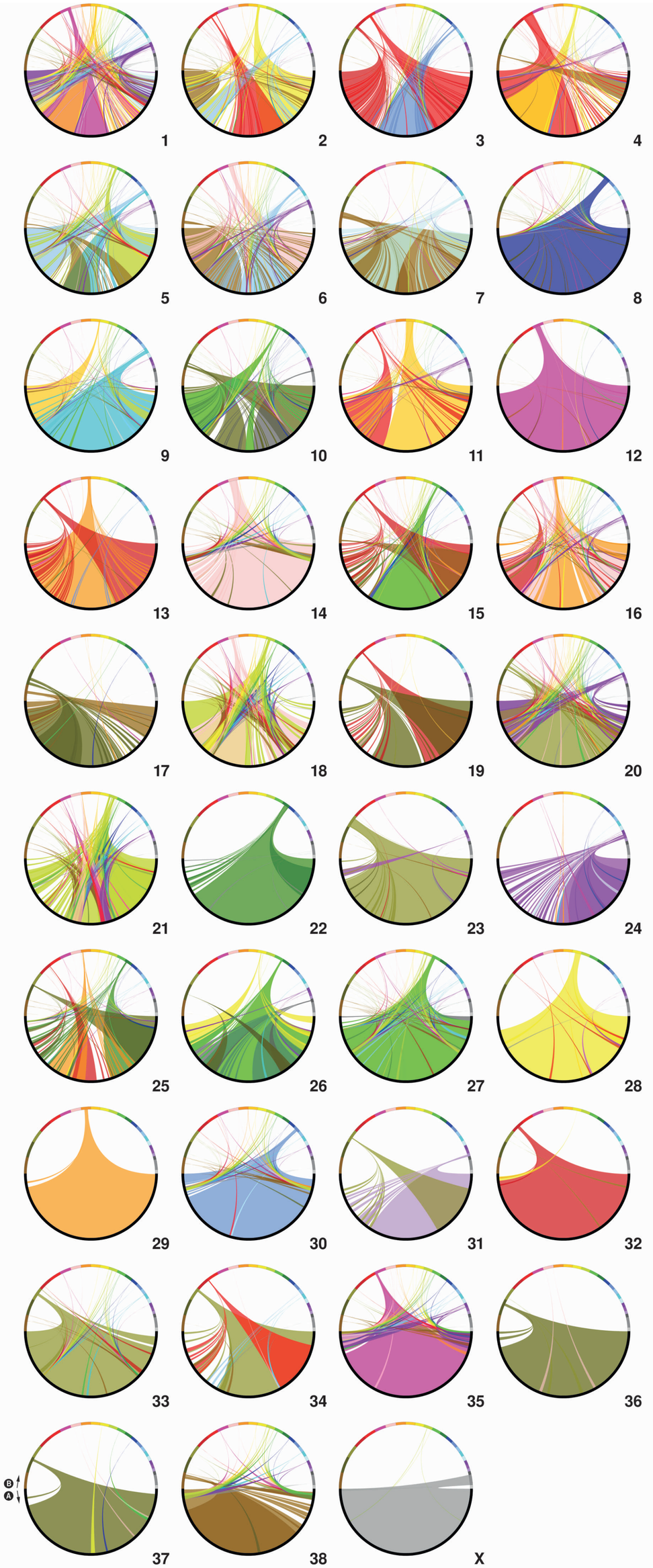

Figure 8. Whole-genome profile of conserved synteny between dog (chromosomes 1–38, X) and human (chromosomes 1–22, X, Y) genomes. Each of the 39 images in the panel shows sequence similarity between a single dog chromosome (*A*, expanded to fill the *bottom* half of the image and progressing *counterclockwise* from the 9 o'clock position) and the entire human genome (*B*, scaled to fill the *top* half of the image, and progressing *clockwise* from the 9 o'clock position). Sequence similarity was derived from gapped alignments of dog and human sequence assemblies. Adjacent alignments were grouped into bundles (see Methods), which are shown as ribbons colored by the target human chromosome according to the color key (1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X).