



**Figure 6.** Epigenomic features of *N. crassa* genome. The genomic distributions of H3K9me3 (orange), HP1 (yellow), 5-methylcytosine (green), H3K27me3 (medium blue), and H3K4me3 (dark blue) are displayed for each of *N. crassa*'s seven linkage groups (OR74A NC10 sequence assembly, <http://www.broadinstitute.org/annotation/genome/neurospora/MultiHome.html>) using the Integrative Genomics Viewer (<http://www.broadinstitute.org/igv>) (Jamieson et al. 2013; MR Rountree and EU Selker, unpubl.). Base composition is shown at the top of each linkage group as the moving average of %GC (red) calculated for 500-bp windows in 100-bp steps, whereas the positions of predicted genes (purple) and repeats (black) are indicated below. The predicted gene file was downloaded from The Broad Institute (<http://www.broadinstitute.org/annotation/genome/neurospora>) and repeats were determined using the RepeatMasker program (<http://www.repeatmasker.org>).