Supplemental Fig. S37. Distribution of sequence identity (in percentage) calculated from multiple alignments of CDS sequences against human (a), cow (b) and sheep (c) genomes (Ensemble release 83). One thousand randomly selected 'intergenic' sequences of ~3 kb at least 5 kb distant from genes annotated by Ensembl (red circles) were used as neutral controls of conservation level. One thousand randomly selected well-annotated RefSeq genes coding sequence present in the pig reference genome (black circles) were used as positive controls of conservation level. Similar with CDS of the reference pig genome (i.e. positive controls, marked as black circles), missing sequences in ten assemblies had a distribution peak of 90% to 100% identity. CDS, coding sequence.