For the Venn bar plots:

Probabilistic set overlap relations between each taxon were calculated with bootstrapping for the Deep and Shallow groups. Samples and their individual read depths were computationally resampled to simulate the probabilities of rediscovering the same relationship between groups and across taxa had the sample collection and sequencing been performed again. Proportions associated with the bars colored in red or blue represent the probabilities of that taxa being rediscovered only in the Deep or Shallow groups, respectively. Proportions associated with purple, represent the probabilities of a taxon being rediscovered in both (Shallow ∩ Deep) groups. The proportions associated with bars colored in black, represent the probability that the taxon may not be discovered (Deep ∩ Shallow)' again due to its low abundance in both groups of samples. In the figure, taxa are sorted first by decreasing probability of overlap, then by decreasing probability of being recovered only in Deep, and then by increasing probability of being recovered only in Shallow.

For the numbers in the last page:

To summarize the overall taxonomic overlap relationships among all taxa discovered in both the Deep and Shallow groups, for each taxa the set category (only in Deep, only in Shallow, in both, or in neither) with the greatest probability was chosen to represent that taxa's most likely resampling outcome. Probabilities for each of the four set categories were estimated computationally with bootstrapping by resampling both the samples and their respective read depths. Taxa associated with neither groups, may potentially not be recovered again due to their low abundance, if the experiment were performed again with the same number of samples and sequencing depth. Note that additional low abundance taxa may be recovered to replace these if the samples were recollected.