1. **What was the total amount of raw sequence data generated (in gigabases)?**
   26.8 Gb

2. **What's the name of the software program that the investigators used to assemble the genome?**
   Celera assembler

3. **What are "axenic" cultures?**
   Culture that have no contamination from other organisms.

4. **In their PCR testing, where Boothby et al. tested cases when a non-metazoan gene (something from a bacterium or fungus) was near a metazoan gene in their assembly, how many times was the PCR product the correct size?**
   58 out of 59, which is 98.3%.

5. **How many contigs from the PacBio assembly failed to match the Illumina assembly?**
   4,440 contigs.
   A total of 4,440 (10.72%) of the PacBio contigs, making up 7.91% of the assembled sequence, do not have direct homologous matches in the Illumina assembly.

6. **How large was the genome of the tardigrade H. dujardini estimated to be, based on flow cytometry?**
   110Mb.
   Using propidium iodide flow cytometry, we estimated the genome of H. dujardini to be ~110 Mb, similar to a previous estimate.

7. **In the nHd.2.3 assembly, how many scaffolds had either no genes or only bacterial genes?**
   195 scaffolds, 1.5 Mb.
   Some scaffolds (195 spanning 1.5 Mb) had only bacterial or no genes and were very likely to be contamination.

8. **In their nHd.2.3 assembly, how many genes did the authors find, as an upper bound, for the number of "hard" candidates for horizontal gene transfer?**
   196 genes.
   Most of these (196, 0.9% of all genes) had expression >0.1 tpm (Fig. 3D) and are an upper bound of "hard" candidates for fHGT.

9. **How many of the PCR products from Boothby et al. were determined not to assess HGT because they only probed relationships between bacterial genes?**
   49 products.
   We found no expression of the 49 bacterial–bacterial junction loci, supporting assignment as contaminants rather than examples of fHGT.