**Figure 7 – K-mer analysis of short-read datasets shows signs of heterozygousity within individual and populations of *H. dujardini* tardigrades.**

Modified version of Figure 1 from (Arakawa, 2016) demonstrating how heterozygousity introduces multiple peaks (one half the multiplicity of the other) within a k-mer distribution. Homozygous loci accumulate k-mer counts that are equivalent to the average sequencing depth (in this case 50X). Heterozygous loci, for which there are 2 equally represented SNPs, will accumulate k-mer counts that are approximately half the total sequencing coverage (in this case 25X). Thus, a dataset derived from a mixed population of heterozygous specimens will show a k-mer distribution with 2 peaks, one half the multiplicity of the other.