



Figure S2. the consensus sequences comparison of T4-like phages and *Acinetobacter baumannii* phage IME-AB2. T4-like phage IME08, IME09, IME-EC1 were assumed aspartially permuted genome and *Acinetobacter baumannii* phage IME-AB2 was assumed as completely permuted circular genome which without any evident HFSs.