

Additional data file 2

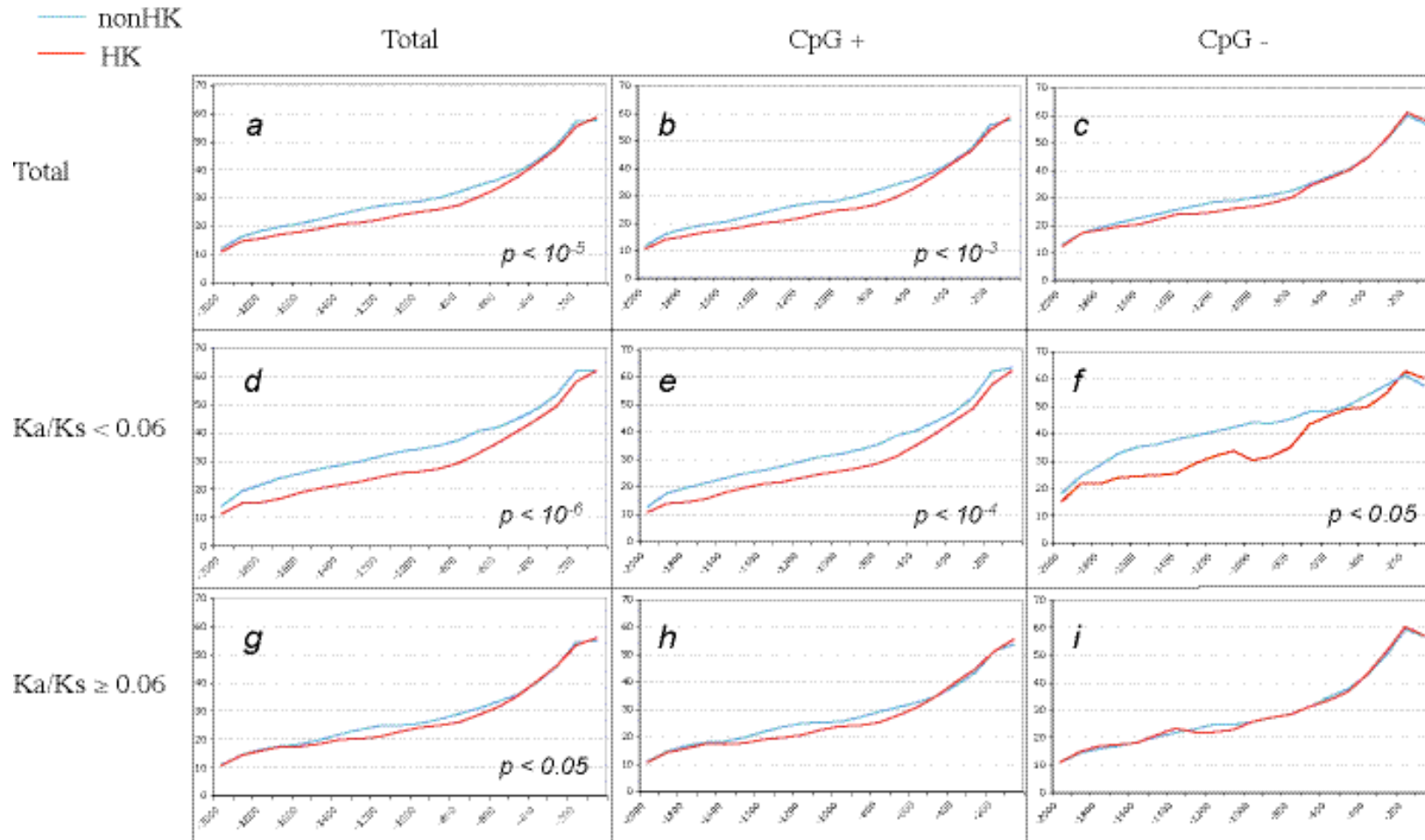


Figure S1. Promoter sequence conservation in housekeeping (HK) and non-housekeeping (non-HK) genes. Expression breadth estimated from Gene Atlas (GNF1H) data. The X-axis shows 100 nucleotide bins along 2Kb upstream of the TSS. The Y-axis shows percent conservation $((1 - d_{SM}) \cdot 100)$. Genes were grouped according to the presence or absence of a CpG island and Ka/Ks values. Significant p-values ($p < 0.05$) are indicated.

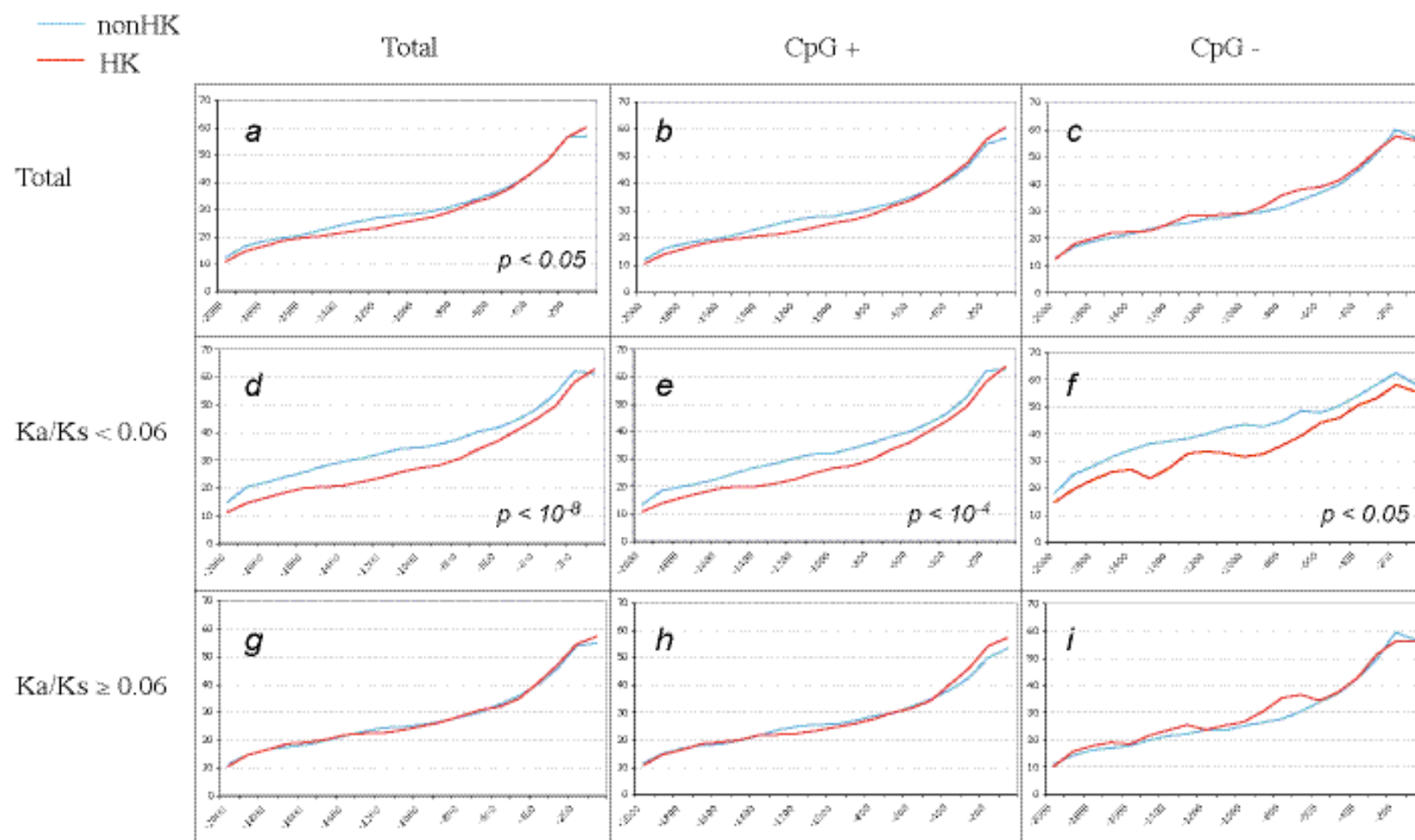


Figure S2. Promoter sequence conservation in housekeeping (HK) and non-housekeeping (non-HK) genes. Expression breadth estimated from eVOC anatomical systems data. The X-axis shows 100 nucleotide bins along 2Kb upstream of the TSS. The Y-axis shows percent conservation ($(1 - d_{SM}) \cdot 100$). Genes were grouped according to the presence or absence of a CpG island and Ka/Ks values. Significant p-values ($p < 0.05$) are indicated.

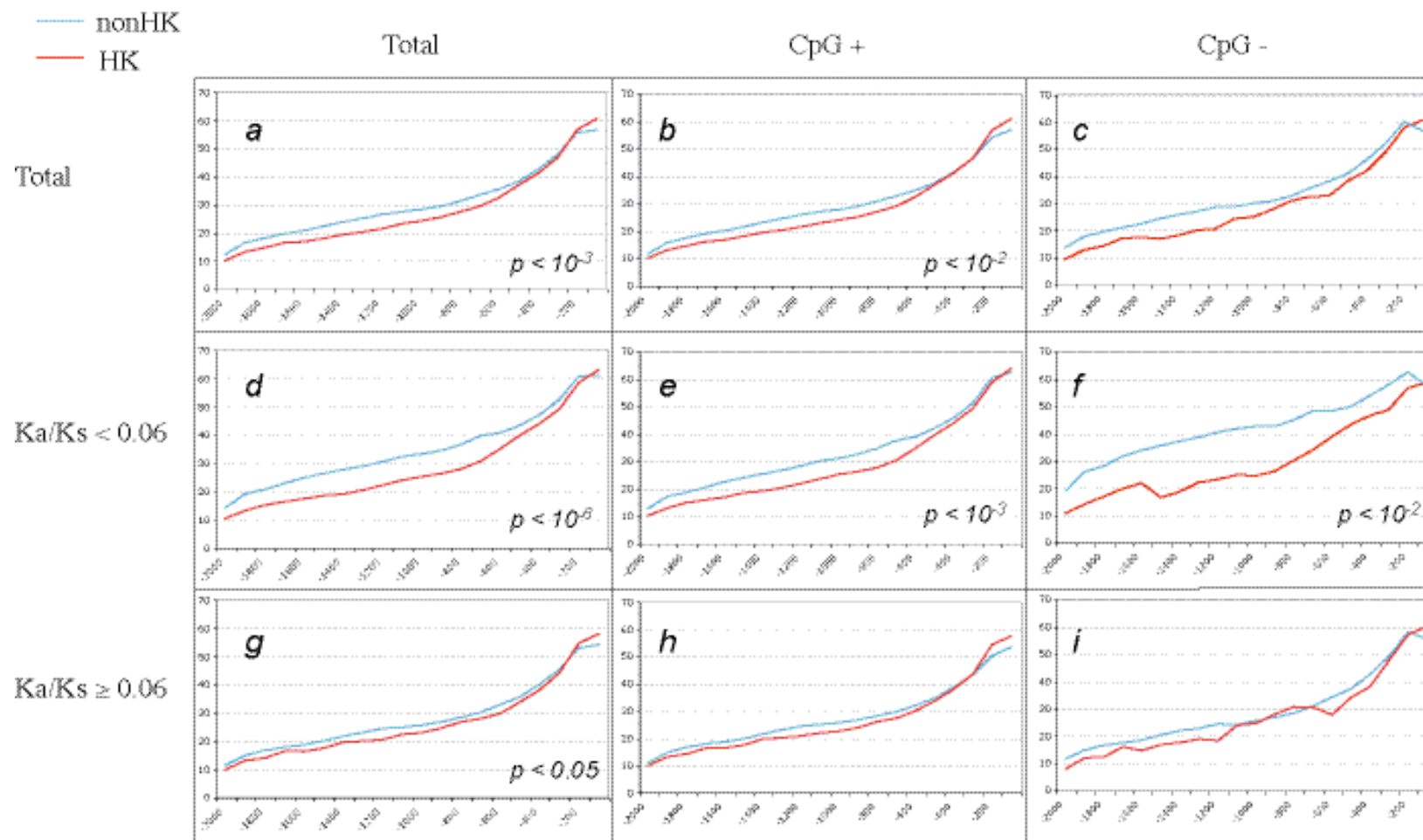


Figure S3. Promoter sequence conservation in housekeeping (HK) and non-housekeeping (non-HK) genes. Expression breadth estimated from eVOC cell types data. The X-axis shows 100 nucleotide bins along 2Kb upstream of the TSS. The Y-axis shows percent conservation $((1 - d_{SM}) \cdot 100)$. Genes were grouped according to the presence or absence of a CpG island and Ka/Ks values. Significant p-values ($p < 0.05$) are indicated.