**Figure S5:** Comparison of the p-values from the exact permutational test, the exact conditional test, the asymptotic conditional approximation (as implemented in the `survdiff` package in R), and the asymptotic permutational approximation for cancer datasets COADREAD, GBM, KIRC, LUSC, OV, UCEC. (a,b,c,d,e,f): Each data point represents a gene, and the p-values computed using the exact permutational test and the p-values from R `survdiff` for the gene are shown. (g,h,i,k,l): Each data point represents a gene, and the p-values computed using the exact permutational test and the exact conditional test for the gene are shown. (m,n,o,p,q,r): Each data point represents a gene, and the p-values computed using the exact permutational test and the asymptotic permutational test for the gene are shown.