Figure S1. Association of SLC39A family genes with disease-free survival of patients with liver cancer determined using Gene Expression Profiling Interactive Analysis. (A) SLC39A1, (B) SLC39A2, (C) SLC39A3, (D) SLC39A4, (E) SLC39A5, (F) SLC39A6, (G) SLC39A7, (H) SLC39A8, (I) SLC39A9, (J) SLC39A10, (K) SLC39A11, (L) SLC39A12, (M) SLC39A13 and (N) SLC39A14. P1 and P2 represent the P-value prior to and after curve crossing, respectively, and P represents the P-value for the whole graphs. Mean differences were considered statistically significant when P<0.05. SLC, solute carrier; H, high; L, low.
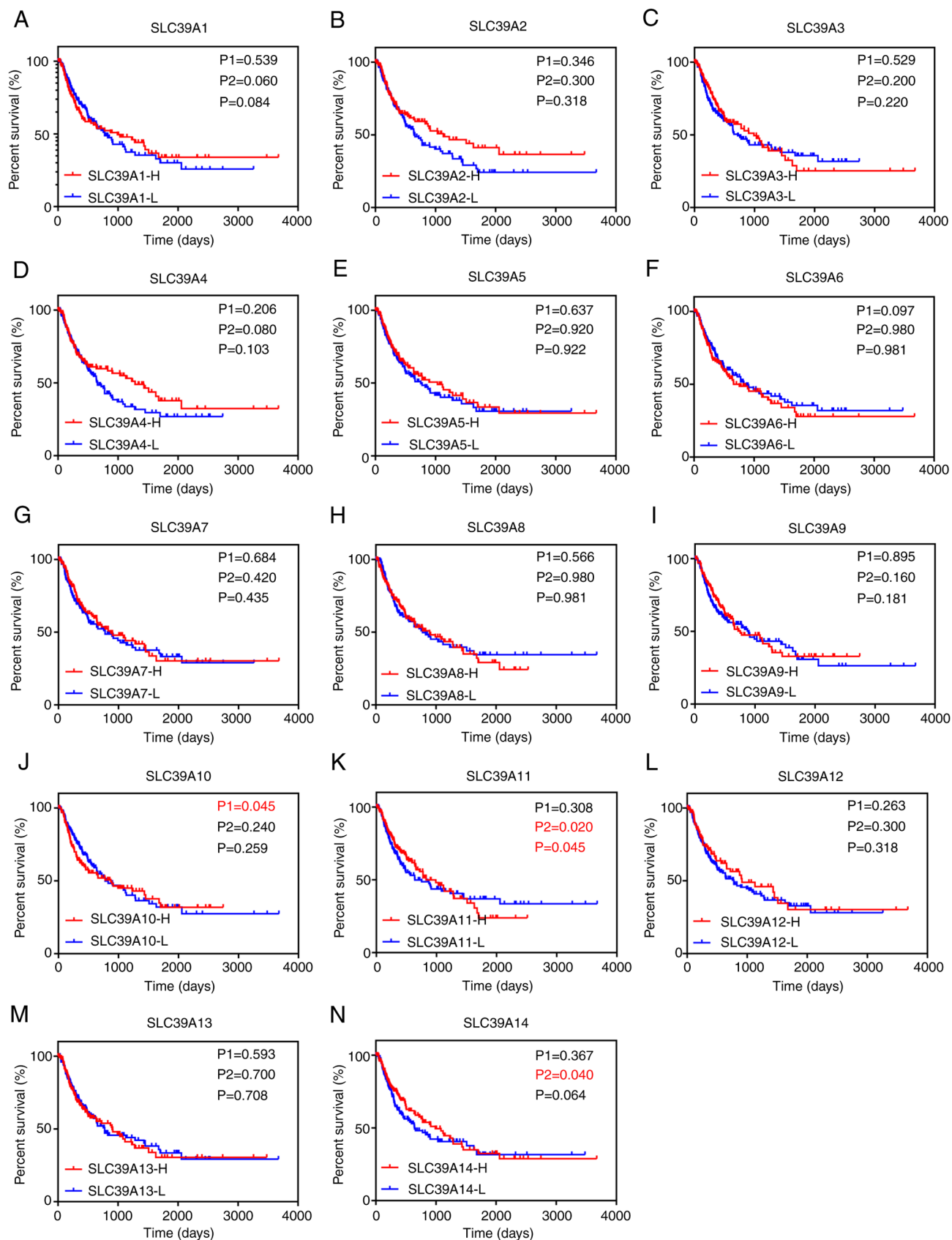
Figure S2. Relevant statistical analysis. (A) Immunohistochemistry scores were calculated to determine the expression of SLC39A6 in tumor and the corresponding noncancerous tissues. (B) Semi-quantification of western blot experiments of HepG2 and Hep3B cells transfected with si-NC and si-SLC39A6. (C) The relative colony numbers of HepG2 and Hep3B cells in colony formation assays. (D) OS of SLC39A6 in patients with liver cancer with different sex using The Cancer Genome Atlas database. (E) The bodyweight of the animals over the course of the experiment. Mean differences were considered statistically significant when P<0.05. *P<0.05, **P<0.01. SLC, solute carrier; ns, no significance; si-SLC39A6, small inhibitory RNA targeting SLC39A6; si-NC, negative control small inhibitory RNA; OS, overall survival; sh-SLC39A6, short hairpin RNA targeting SLC39A6; NC, negative control.