

**Table S3.** Top 15 significant results of multivariate cox regression analysis

<b>Gene.name</b>	<b>Hazard.Ratio</b>	<b>p.value</b>
<i>IL20RB</i>	0.024058797	<0.001
<i>MYEOV</i>	0.011066403	<0.001
<i>ANKRD57</i>	0.027997057	<0.001
<i>FAM83A</i>	0.028973563	0.001
<i>HIST1H2BK</i>	0.023579432	0.001
<i>PLAU</i>	0.052454276	0.001
<i>C11orf34</i>	0.040479933	0.002
<i>EXTL1</i>	0.008051021	0.003
<i>SPATA21</i>	0.052794781	0.003
<i>SMG6</i>	0.021086653	0.005
<i>FCRLA</i>	0.040093744	0.006
<i>MAP4K5</i>	0.148089138	0.006
<i>SLC39A2</i>	0.038290701	0.007
<i>CAPN2</i>	0.009838279	0.007
<i>EVC</i>	5.350443069	0.008

P-value corrected for multiple tests using the Benjamini–Hochberg method. The hazard ratio (HR) of the COX model shown. The HR is relative, and sites with value > 1 and < 1 are considered to be associated with poor and good prognosis, respectively.