

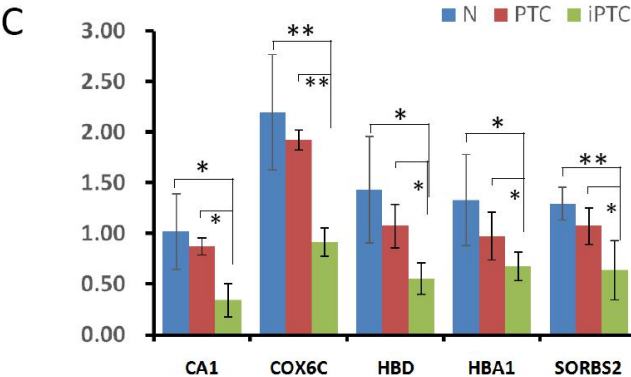
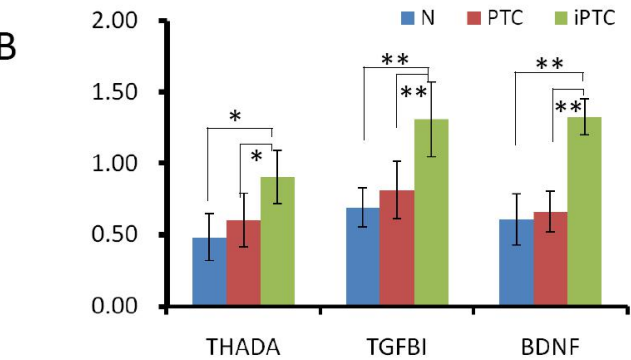
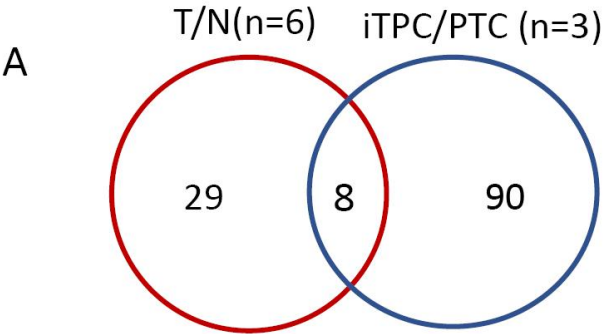
**Figure S1.** Differential expressed genes(DEPs) tumorigenesis (in situ) and invasion process. A. analysis of DEPs from tumor (iPTC and PTC) and invasion process and found 8 common genes. specific DEPs in situ and invasion process were 29 and 90, respectively. B-C. 3 upregulated (B) and 5 downregulated (C) genes common to in situ and invasion process. \*and \*\* represent p-value < 0.01 and 0.05, respectively. D. GO and KEGG analysis of DEPs in iPTC/PTC process were carried out by only gProfiler.

**Figure S2.** Five genes including FHL1, TPO, SLC26A7, HGD and COL23A1 showed significant OS on THCA from UALCAN website(<http://ualcan.path.uab.edu/index.html>)

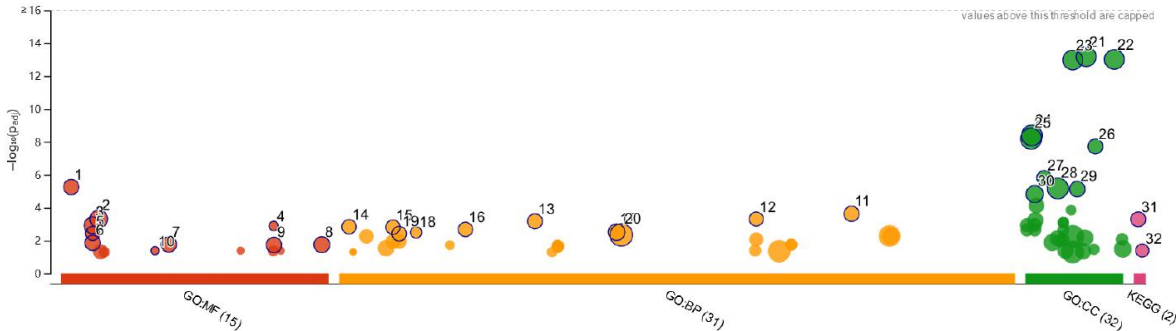
**Figure S3.** Three genes including FHL1, TPO and ADH1B showed significant OS on THCA from GEPIA website (<http://gepia.cancer-pku.cn/>)

**Figure S4.** Association of 10 DEPs with clinical staging and metastasis. TCGA database indicated the nodal metastasis (left) and staging (right) for up- and downregulated genes in thyroid tissues compared to the normal tissues. Staging dataset contains normal tissues (n=59), N0 (n=230) and N1 (n=58). Nodal metastasis data including normal tissue (n=59), stage 1 (n=284), stage 2 (n=52), stage 3 (n=112) and stage 4 (n=55). P values were calculated by online tools.

Fig S1



**D**



ID	Source	Term ...	Term Name	Padj (query_1)
1	GO:MF	GO:0003735	structural constituent of ribosome	5.527 × 10 <sup>-6</sup>
2	GO:MF	GO:0005198	structural molecule activity	4.797 × 10 <sup>-4</sup>
3	GO:MF	GO:0004857	enzyme inhibitor activity	1.176 × 10 <sup>-3</sup>
4	GO:MF	GO:0000228	phosphatidylcholine-sterol O-acyltransferase activ...	1.273 × 10 <sup>-3</sup>
5	GO:MF	GO:0004867	serine-type endopeptidase inhibitor activity	3.592 × 10 <sup>-3</sup>
6	GO:MF	GO:0004866	endopeptidase inhibitor activity	1.371 × 10 <sup>-2</sup>
7	GO:MF	GO:0003044	peptidase inhibitor activity	1.699 × 10 <sup>-2</sup>
8	GO:MF	GO:1901681	sulfur compound binding	1.754 × 10 <sup>-2</sup>
9	GO:MF	GO:0061135	endopeptidase regulator activity	1.822 × 10 <sup>-2</sup>
10	GO:MF	GO:0018636	phenanthrene 9,10-monooxygenase activity	4.103 × 10 <sup>-2</sup>
11	GO:BP	GO:0140053	mitochondrial gene expression	2.342 × 10 <sup>-4</sup>
12	GO:BP	GO:0070126	mitochondrial translational termination	4.811 × 10 <sup>-6</sup>
13	GO:BP	GO:0032543	mitochondrial translation	6.619 × 10 <sup>-4</sup>
14	GO:BP	GO:0001523	retinoid metabolic process	1.416 × 10 <sup>-3</sup>
15	GO:BP	GO:0006415	translational termination	1.512 × 10 <sup>-5</sup>
16	GO:BP	GO:0016101	diterpenoid metabolic process	2.080 × 10 <sup>-3</sup>
17	GO:BP	GO:0043687	post-translational protein modification	3.008 × 10 <sup>-3</sup>
18	GO:BP	GO:0007597	blood coagulation, intrinsic pathway	3.146 × 10 <sup>-3</sup>
19	GO:BP	GO:0006721	terpenoid metabolic process	3.761 × 10 <sup>-3</sup>
20	GO:BP	GO:0044237	cellular metabolic process	4.477 × 10 <sup>-3</sup>
21	GO:CC	GO:0070062	extracellular exosome	6.612 × 10 <sup>-14</sup>
22	GO:CC	GO:1903561	extracellular vesicle	9.644 × 10 <sup>-14</sup>
23	GO:CC	GO:0043230	extracellular organelle	1.046 × 10 <sup>-13</sup>
24	GO:CC	GO:0005615	extracellular space	3.996 × 10 <sup>-9</sup>
25	GO:CC	GO:0005576	extracellular region	6.347 × 10 <sup>-9</sup>
26	GO:CC	GO:0072562	blood microparticle	1.888 × 10 <sup>-8</sup>
27	GO:CC	GO:0015934	large ribosomal subunit	1.502 × 10 <sup>-6</sup>
28	GO:CC	GO:0031982	vesicle	6.675 × 10 <sup>-6</sup>
29	GO:CC	GO:0044391	ribosomal subunit	7.406 × 10 <sup>-6</sup>
30	GO:CC	GO:0005759	mitochondrial matrix	1.473 × 10 <sup>-5</sup>
31	KEGG	KEGG:03010	Ribosome	5.026 × 10 <sup>-4</sup>
32	KEGG	KEGG:04979	Cholesterol metabolism	4.016 × 10 <sup>-2</sup>

Fig S2

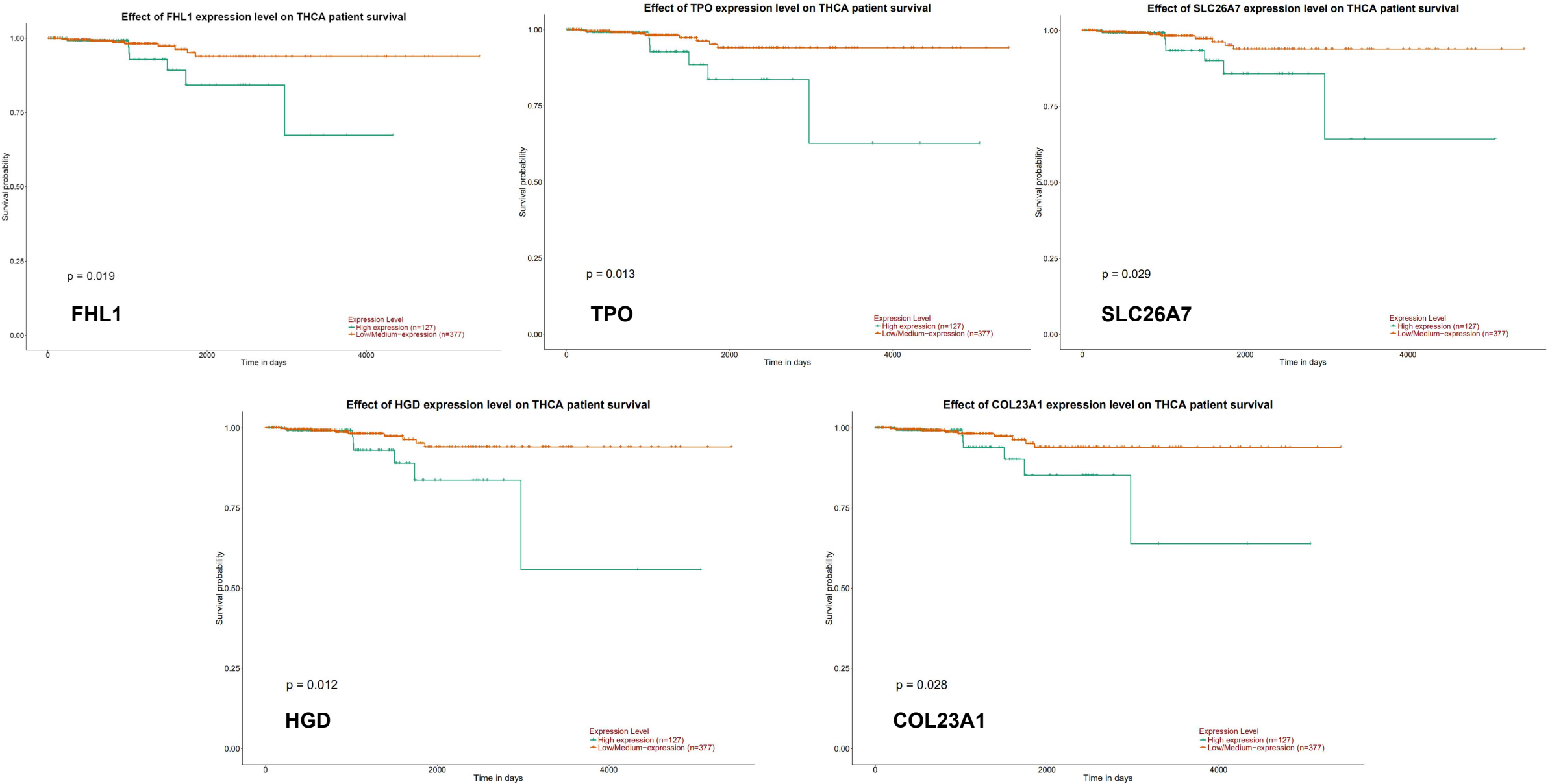


Fig S3

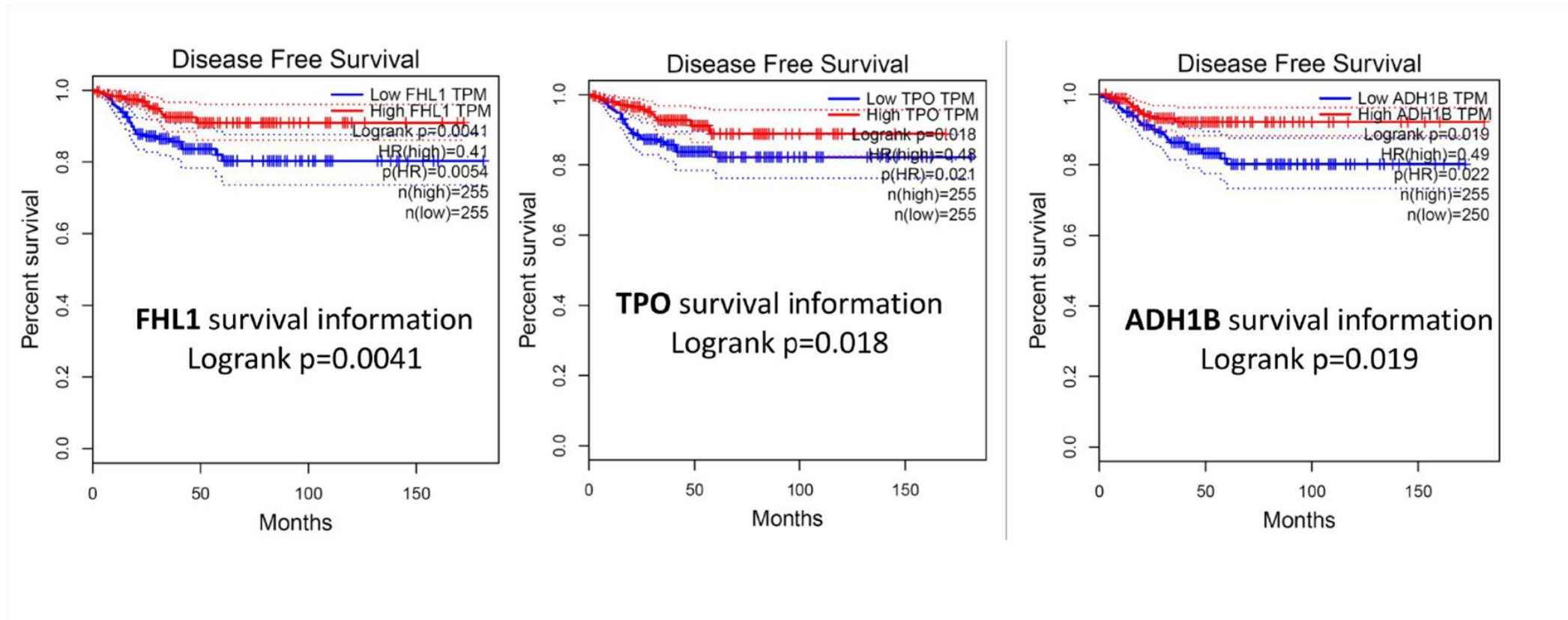


Fig S4

