

Table SI. Top 20 enriched GO biological processes gene sets in *ZNF750*-high compared with *ZNF750*-low samples from patients with esophageal squamous cell carcinoma analyzed by Gene Set Enrichment Analysis.

Name	Size	ES	NES	NOM P-value	FDR q-value
GO_CORNIFICATION	112	0.8319	4.4650	<0.0001	<0.0001
GO_KERATINIZATION	223	0.6540	3.9010	<0.0001	<0.0001
GO_KERATINOCYTE_DIFFERENTIATION	300	0.6192	3.7104	<0.0001	<0.0001
GO_EPIDERMAL_CELL_DIFFERENTIATION	355	0.5940	3.6131	<0.0001	<0.0001
GO_REGULATION_OF_WATER_LOSS_VIA_SKIN	27	0.8685	3.3703	<0.0001	<0.0001
GO_WATER_HOMEOSTASIS	75	0.6655	3.3606	<0.0001	<0.0001
GO_EPIDERMIS_DEVELOPMENT	462	0.5510	3.3594	<0.0001	<0.0001
GO_SKIN_DEVELOPMENT	415	0.5476	3.3050	<0.0001	<0.0001
GO_MULTIVESICULAR_BODY_ORGANIZATION	31	0.7468	3.0552	<0.0001	<0.0001
GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	29	0.7720	3.0516	<0.0001	<0.0001
GO_ENDOSOME_ORGANIZATION	79	0.5982	3.0306	<0.0001	<0.0001
GO_PEPTIDE_CROSS_LINKING	33	0.7531	3.0066	<0.0001	<0.0001
GO_VIRION_ASSEMBLY	39	0.6685	2.8334	<0.0001	<0.0001
GO_EXTRACELLULAR_VESICLE_BIOGENESIS	22	0.7483	2.7696	<0.0001	<0.0001
GO_ENDOSOMAL_TRANSPORT	227	0.4829	2.7670	<0.0001	<0.0001
GO_CELL_CELL_JUNCTION_ORGANIZATION	188	0.4741	2.7617	<0.0001	<0.0001
GO_REGULATION_OF_EPIDERMIS_DEVELOPMENT	85	0.5275	2.6916	<0.0001	<0.0001
GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	51	0.6069	2.6861	<0.0001	<0.0001
GO_MULTIVESICULAR_BODY_SORTING_PATHWAY	34	0.6439	2.6840	<0.0001	<0.0001
GO_ADHERENS_JUNCTION_ORGANIZATION	65	0.5715	2.6769	<0.0001	<0.0001

GO, Gene Ontology; *ZNF750*, zinc finger protein 750; Size, number of genes in the geneset; ES, enrichment score; NES, normalized enrichment score; NOM, nominal; FDR, false discovery rate.

Table SII. Top 20 enriched genes in the GO_KERATINOCYTE_DIFFERENTIATION and the GO_EPIDERMAL_CELL_DIFFERENTIATION gene sets in *ZNF750*-high compared with *ZNF750*-low samples from patients with esophageal squamous cell carcinoma analyzed by Gene Set Enrichment Analysis.

A, GO_KERATINOCYTE_DIFFERENTIATION

No.	Symbol	Rank in gene list	Rank metric score	Running ES
1	CERS3	2	0.853	0.0134
2	JUP	7	0.801	0.0259
3	SPRR1B	22	0.715	0.0370
4	TMEM79	23	0.713	0.0482
5	DSG3	24	0.712	0.0594
6	SPRR2E	35	0.690	0.0701
7	SPRR2A	37	0.683	0.0808
8	KRT80	40	0.667	0.0913
9	SPRR2D	51	0.649	0.1014
10	EVPL	61	0.639	0.1113
11	TGM1	83	0.618	0.1206
12	PERP	85	0.617	0.1303
13	ANXA1	87	0.615	0.1400
14	GRHL1	92	0.611	0.1496
15	TGM5	107	0.596	0.1587
16	DSP	113	0.585	0.1678
17	IVL	115	0.583	0.1770
18	ZFP36	140	0.568	0.1855
19	KRT6A	141	0.568	0.1945
20	SPRR1A	144	0.565	0.2033

B, GO_EPIDERMAL_CELL_DIFFERENTIATION

No.	Symbol	Rank in gene list	Rank metric score	Running ES
1	CERS3	2	0.853	0.0113
2	JUP	7	0.801	0.0218
3	OVOL1	8	0.796	0.0323
4	SPRR1B	22	0.715	0.0416
5	TMEM79	23	0.713	0.0510
6	DSG3	24	0.712	0.0604
7	SULT2B1	30	0.699	0.0696
8	SPRR2E	35	0.690	0.0787
9	SPRR2A	37	0.683	0.0877
10	KRT80	40	0.667	0.0965
11	SPRR2D	51	0.649	0.1049
12	EVPL	61	0.639	0.1132
13	KLF4	71	0.626	0.1214
14	TGM1	83	0.618	0.1293
15	PERP	85	0.617	0.1375
16	ANXA1	87	0.615	0.1456
17	GRHL1	92	0.611	0.1536
18	TGM5	107	0.596	0.1613
19	DSP	113	0.585	0.1689
20	IVL	115	0.583	0.1767

GO, Gene Ontology; *ZNF750*, zinc finger protein 750; ES, enrichment score.

Table SIII. Top 20 enriched GO biological process gene sets in *ZNF750*-upregulated KYSE180 cells analyzed by TopFunn.

ID	Name	P-value	q-value FDR B&H	q-value Bonferroni
GO:0070268	Cornification	1.26x10 ⁻¹³	4.48x10 ⁻¹⁰	5.44x10 ⁻¹⁰
GO:1903575	Cornified envelope assembly	2.22x10 ⁻¹³	4.48x10 ⁻¹⁰	1.05x10 ⁻⁹
GO:0008544	Epidermis development	7.79x10 ⁻¹³	1.05x10 ⁻⁹	5.80x10 ⁻⁸
GO:0071709	Membrane assembly	1.02x10 ⁻¹¹	1.03x10 ⁻⁸	9.17x10 ⁻⁸
GO:0044091	Membrane biogenesis	2.07x10 ⁻¹¹	1.67x10 ⁻⁸	1.16x10 ⁻⁷
GO:0031424	Keratinization	8.77x10 ⁻¹¹	5.90x10 ⁻⁸	2.09x10 ⁻⁷
GO:0007009	Plasma membrane organization	1.09x10 ⁻¹⁰	6.28x10 ⁻⁸	7.75x10 ⁻⁷
GO:0030855	Epithelial cell differentiation	2.51x10 ⁻¹⁰	1.27x10 ⁻⁷	2.89x10 ⁻⁶
GO:0043588	Skin development	2.90x10 ⁻¹⁰	1.30x10 ⁻⁷	3.69x10 ⁻⁶
GO:0009913	Epidermal cell differentiation	4.90x10 ⁻¹⁰	1.81x10 ⁻⁷	1.43x10 ⁻⁵
GO:0030216	Keratinocyte differentiation	4.93x10 ⁻¹⁰	1.81x10 ⁻⁷	3.08x10 ⁻⁵
GO:0060429	Epithelium development	1.97x10 ⁻⁹	6.63x10 ⁻⁷	3.40x10 ⁻⁵
GO:0018149	Peptide cross-linking	2.41x10 ⁻⁸	7.49x10 ⁻⁶	3.51x10 ⁻⁵
GO:0001944	Vasculature development	2.05x10 ⁻⁷	5.91x10 ⁻⁵	4.00x10 ⁻⁵
GO:0001568	Blood vessel development	3.05x10 ⁻⁷	8.20x10 ⁻⁵	1.10x10 ⁻⁴
GO:0010466	Negative regulation of peptidase activity	5.61x10 ⁻⁷	1.41x10 ⁻⁴	4.16x10 ⁻⁴
GO:1901342	Regulation of vasculature development	1.29x10 ⁻⁶	3.06x10 ⁻⁴	5.65x10 ⁻⁴
GO:0048514	Blood vessel morphogenesis	4.28x10 ⁻⁶	9.52x10 ⁻⁴	2.56x10 ⁻³
GO:0072359	Circulatory system development	4.48x10 ⁻⁶	9.52x10 ⁻⁴	3.21x10 ⁻³
GO:0035239	Tube morphogenesis	5.86x10 ⁻⁶	1.18x10 ⁻³	3.51x10 ⁻³

GO, Gene Ontology; *ZNF750*, zinc finger protein 750; FDR, false discovery rate; B&H, Benjamini-Hochberg method.