

1 **Supplementary Materials:**

2 **Fig. S1.** Representative images for (A) normal hepatocyte, (B) steatosis, (C) Hyperplasia, (D)  
3 Dysplasia, and (E,F) HCC in transgenic zebrafish.

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5 **Fig. S2.** Pathways analysis for the differential expressed genes in [*HBx,src*], and [*HBx,src,p53*<sup>-/+</sup>]  
6 <sup>+/+</sup>] transgenic zebrafish following oligo-fucoidan treatment. (A) Enriched pathways of oligo-  
7 fucoidan upregulated genes. (B) Enriched pathways of oligo-fucoidan downregulated genes..

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9 **Fig. S3.** Upstream regulator analysis using IPA for the differential expressed genes in  
10 [*HBx,src*], and [*HBx,src,p53*<sup>-/+</sup>] transgenic zebrafish following oligo-fucoidan treatment. (A)  
11 Clustering of the upstream regulators identified by IPA for the [*HBx,src,p53*<sup>-/+</sup>]-DIO transgenic  
12 fish compare to NOR (DIO-batch2), [*HBx,src*]-DIO+OF compare to DIO (DIO-batch1), and  
13 [*HBx,src,p53*<sup>-/+</sup>]-DIO+OF compare to DIO (DIO-batch2). (B-E) The upstream regulators  
14 predicted by IPA including *MYCN*, *KRAS*, *TGFB1* and *STK1* which were predicted induced  
15 by DIO (as shown in orange), and repressed by OF (as shown in blue) together they either  
16 upregulates the downstream genes (as shown in red) or inhibit the downstream genes (as shown  
17 in green) in [*HBx,src,p53*<sup>-/+</sup>] transgenic fish.

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