

An oncogenic role for Four-jointed Box 1 (FJX1) in nasopharyngeal carcinoma

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Supplementary Tables

Supplementary Table 1. STR profile of TW04 with a match of $\geq 80.0\%$ to HeLa D98-AH2 clone.

Type	Test Sample	Closest Match
Cell Line	TW04	D98-AH2
Database	-	DSMZ
TH01	6,7,9	7
D21S11	27,30	N/A
D5S818	11,12	11,12
D13S317	10,12	N/A
D7S820	10,12	12
D16S539	9,10	9,10
CSF1PO	10,11	9,10,11
Amelogenin	X	X
vWA	14,16	16,18
TPOX	8,12	8,12
Match to Test Sample		80.00%

Supplementary Table 2. Histological characteristics of non-malignant nasopharyngeal tissue samples.

Sample	Histology
NP 3	Nasopolyps
NP 4	Nasopharyngitis
NP 5	Normal epithelium
NP 6	Synovial sarcoma
NP 7	Nasopharyngitis
NP 8	Nasopharyngitis
NP 9	Nasopharyngitis
NP 10	Nasopharyngitis
NP 11	Adenoid
NP 12	Nasopharyngitis
NP 13	Lymphoid hyperplasia and rhinosinusitis

Supplementary Table 3. Correlation between FJX1 expression and clinicopathological characteristics of NPC tissue samples.

Characteristics	FJX1 expression	<i>p</i> -value
<i>T category</i>		
T1	3/6 (50%)	0.948
T2	8/19 (42%)	
T3	4/12 (33%)	
T4	3/6 (50%)	
<i>N category</i>		
N0	5/12 (42%)	0.841
N1	4/6 (67%)	
N2	9/23 (39%)	
N3	0/2 (0%)	
<i>Stage</i>		
I	2/3 (67%)	0.526
II	4/7 (57%)	
III	9/24 (38%)	
IV	3/9 (33%)	

Supplementary Figure Legends

Figure S1. Transcriptomic levels of FJX1 in cancer. (a) Previous microarray analysis (GSE13597) showed that the mRNA level of FJX1 transcript is increased in NPC biopsies and NPC cell lines compared to normal nasopharynx tissue, suggesting FJX1 as a potential biomarker for NPC. (b) FJX1 mRNA levels also reported being elevated in head and neck cancer patients when comparing RNAseq data of 43 cancer tissues with matched normal samples from the TCGA database.

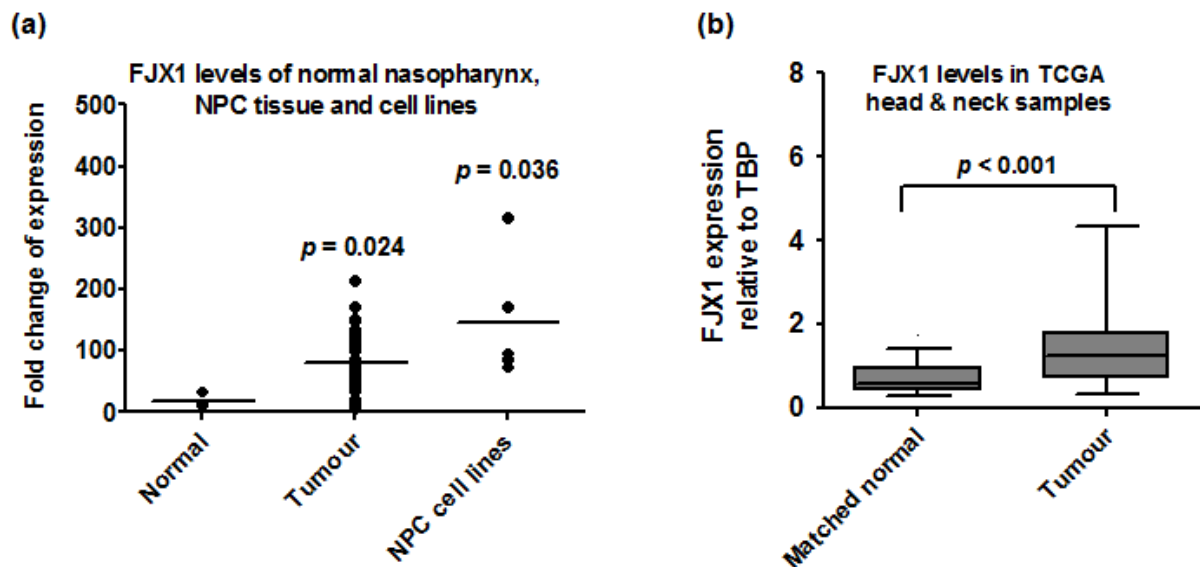


Figure S2. FJX1:V5 overexpression in HeLa/T cell was confirmed using V5 antibody. Three bands with different molecular weight of FJX1 protein in was detected in Western blotting.

