

**Table 2 – Association between Bethesda category and molecular mutation on USFNA**

<b>Mutation</b>	<b>Bethesda III/IV (n=241)</b>	<b>Bethesda V/VI (n=210)</b>	<b>Chi-Square Test</b>
<b><i>BRAF V600E</i></b>	1.7% (4)	44.3% (93)	P < 0.0001
<b><i>TERT</i></b>	2.1% (5)	1% (2)	P = 0.35
<b><i>RAS</i>-type</b>	31.1% (75)	11.9% (25)	P < 0.0001
<b>Copy Number Alterations</b>	8.7% (21)	1% (2)	P = 0.0002
<b><i>RET</i></b>	0	1% (2)	P = 0.12
<b><i>EIF1AX</i></b>	4.1% (10)	0.5% (1)	P = 0.01
<b><i>GEP</i></b>	7.5% (18)	0	P = 0.0001
<b>No Mutation</b>	46.9% (113)	40.5% (85)	P = 0.17

USFNA: Ultrasound-guided fine needle aspiration.