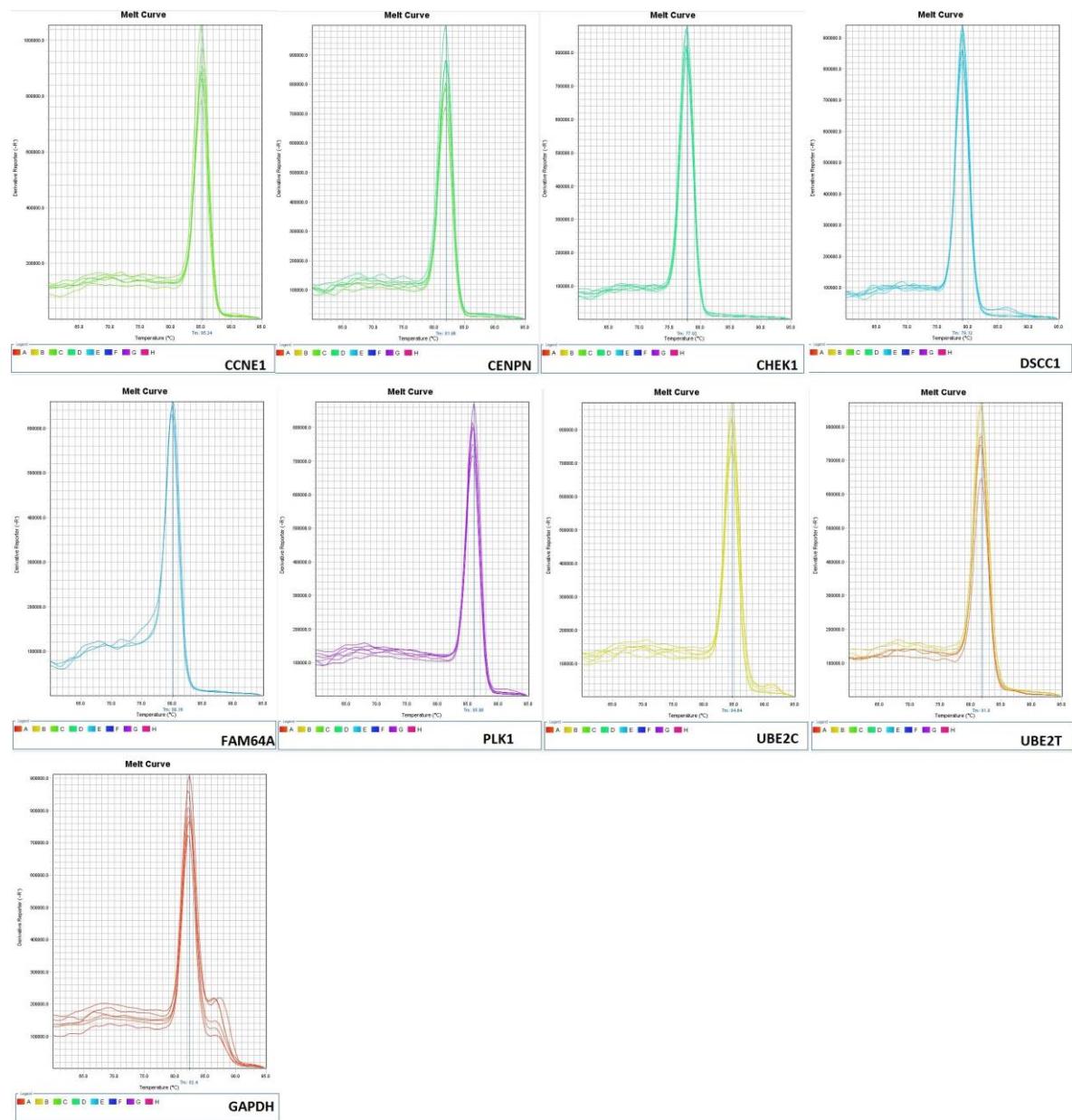


**Supple Figure 1.** The clustering was based on the expression data of DEGs, which contained 373 Luminal A (white), 177 Luminal B (blue), 65 Her2 positive (red) and 130 Basal like (green) subtype samples.



**Supple Figure 2.** The melting curves for hub genes in qRT-PCR.

**Table 1.** The primer sequences (5' to 3') used for gene amplification.

<b>Gene</b>	<b>Upstream primer(5'-3')</b>	<b>Downstream primer(5'-3')</b>
CCNE1	GGAAGAGGAAGGCAAACGTG	GCAATAATCCGAGGCTTGCA
CENPN	TGAGGAGTGAGACTGCAGGA	CCCAGGCCTTCAGGATTGTT
CHEK1	ATATGAAGCGTGCCCTAGACT	TGCCTATGTCTGGCTTATTCTG
PLK1	GCTTGCCAAGTGCTTCGAG	AATCCTACGACGTGCTGGTG
DSCC1	TCCATATGAAGGACCTGACAGT	CCGAGTTCCCTGAAGGCATGT
FAM64A	GCAGACTTGAACCGTTGCTG	TGTTGGTGAGGCATGCTGAT
UBE2C	AGCAGCTGGAACAAACCAA	AAGACGACACAAGGACAGGC
UBE2T	ATGTTAGCCACAGAGCCACC	GGTGTGTTGGCTCCACCTAA
GAPDH	AGGGCTGCTTTAACTCTGGT	CCCCACTTGATTTGGAGGGA