

## Supplemental Table 1

**Cox regression modeling was performed to examine the relationship between NUAK1 transcript expression<sup>ϕ</sup> and overall survival**

Cohort	Univariate Modeling				Multivariate Modeling †			
	N	HR	95% CI	p	N <sup>1</sup>	aHR	95% CI	p
Discovery ¥	1262	1.229	1.147-1.316	4.2E-09	1262	1.19	1.118-1.283	3.03E-07
Validation Ψ	174	2.039	1.094-3.801	0.025	174	1.029	3.46	0.04

N: number of patients, HR (hazard ratio), CI (confidence interval), aHR (stage adjusted hazard ratio).

ϕ NUAK1 transcript expression was evaluated as a continuous variable with HR and 95 CI as well as aHR and 95% CI calculated per unit increase in transcript expression level.

† Multivariate Cox modeling adjusted for stage at diagnosis.

¥ Discovery cohorts with Affymetrix derived transcript data for NUAK1 from Bonome<sup>13</sup>, Denkert<sup>14</sup>, Dressman<sup>15</sup>, Mok<sup>17</sup>, Tothill<sup>18</sup>, Mateescu<sup>16</sup> and TCGA<sup>3</sup>.

Ψ Validation cohort with Agilent derived transcript data for NUAK1 from Konecny<sup>19</sup>.