

## Supplemental Table 2

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

Cohort	Univariate Modeling				Multivariate Modeling †			
	N	HR	95% CI	p	N	aHR	95% CI	p
Discovery ¥	802	1.134	1.048-1.227	0.0018	802	1.09	1.006-1.182	0.036

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>. Progression-free survival data was not available for the Validation cohort (Konecny<sup>19</sup>).