

## SUPPLEMENTARY MATERIALS

### Supplementary Files

Please browse Full Text version to see the data of Supplementary Files 1–9.

**Supplementary File 1.** TCGA *KEAP1*-mutated LUAD patient samples ID from Xena browser and ID of TCGA *KEAP1*-mutated patient samples that have both DNA methylation and gene expression data

**Supplementary File 2.** Discovery dataset (30 *KEAP1*-mutated vs 155 WT), Validation dataset (30 *KEAP1*-mutated vs 155 WT), and the third dataset (30 *KEAP1*-mutated vs 32 normal) patients ID.

**Supplementary File 3.** Differentially-methylated CpG sites from the discovery dataset (30 *KEAP1*-mutated vs 155 WT) with *p*-value cutoff of  $< 0.05$  (BH-FDR adjustment), and a delta  $\beta$ -value cutoff of  $> |0.2|$ .

**Supplementary File 4.** Differentially-methylated CpG sites from the third dataset (*KEAP1*-mutated vs Normal with delta  $\beta$ -value  $> |0.2|$  and *p*-value  $< 0.05$  (BH-FDR adjustment)).

**Supplementary File 5.** *insilico*-predicted NRF2 binding sites (AREs) in the promoter regions of 11 differentially-methylated genes using LASAGNA-Search 2.0 web tool.

**Supplementary File 6.** Differentially-expressed genes from the discovery dataset (30 *KEAP1*-mutated vs 155 WT) with *p*-value  $< 0.05$  (BH-FDR adjustment).

**Supplementary File 7.** List of genes that shows both differential methylation and gene expression with *p*-value  $< 0.05$  between *KEAP1*-mutated vs WT LUAD patient samples.

**Supplementary File 8.** Differentially-methylated CpG sites from the validation dataset (30 *KEAP1*-mutated vs 155 WT) with *p*-value cutoff of  $< 0.05$  (BH-FDR adjustment), and a delta  $\beta$ -value cutoff of  $> |0.2|$ .

**Supplementary File 9.** List of differentially-expressed genes between *KEAP1*-mutated vs WT from Linkedomics database.

**Supplementary Table 1. Chromosomal distribution of differentially-methylated CpG sites between *KEAP1*-mutated and wild-type LUAD samples.**

Hypo methylated CpG sites		Hyper methylated CpG sites	
Chromosome Number	Number of CpG sites	Chromosome Number	Number of CpG sites
1	8	1	1
2	6	2	-
3	1	3	-
4	2	4	-
5	6	5	1
6	4	6	1
7	3	7	-
8	18	8	-
9	3	9	-
10	6	10	1
11	2	11	3
12	10	12	1
13	3	13	2
14	6	14	-
15	1	15	-
16	12	16	2
17	4	17	1
18	2	18	4
19	1	19	-
20	6	20	-
21	1	21	4
22	-	22	-

**Supplementary Table 2. Chromosomal distribution of differentially methylated CpG sites between *KEAP1*-mutated LUAD and normal samples.**

<b>Hypo methylated CpG sites</b>		<b>Hyper methylated CpG sites</b>	
<b>Chromosome Number</b>	<b>Number of CpG sites</b>	<b>Chromosome Number</b>	<b>Number of CpG sites</b>
<b>1</b>	1457	<b>1</b>	1063
<b>2</b>	1044	<b>2</b>	1010
<b>3</b>	341	<b>3</b>	473
<b>4</b>	364	<b>4</b>	594
<b>5</b>	884	<b>5</b>	720
<b>6</b>	641	<b>6</b>	885
<b>7</b>	1102	<b>7</b>	751
<b>8</b>	1050	<b>8</b>	503
<b>9</b>	208	<b>9</b>	127
<b>10</b>	994	<b>10</b>	532
<b>11</b>	1002	<b>11</b>	453
<b>12</b>	697	<b>12</b>	478
<b>13</b>	320	<b>13</b>	310
<b>14</b>	646	<b>14</b>	367
<b>15</b>	466	<b>15</b>	284
<b>16</b>	767	<b>16</b>	274
<b>17</b>	670	<b>17</b>	468
<b>18</b>	136	<b>18</b>	180
<b>19</b>	461	<b>19</b>	426
<b>20</b>	373	<b>20</b>	216
<b>21</b>	165	<b>21</b>	45
<b>22</b>	207	<b>22</b>	85