

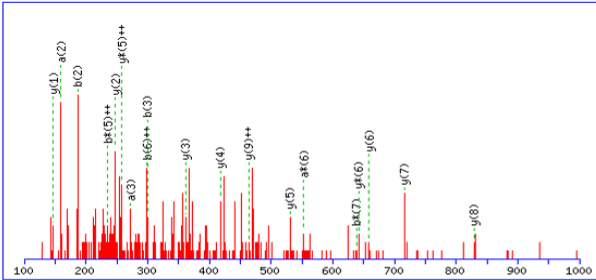
# Supplemental Figure S1A

Peak ID: 1740

MS/MS Fragmentation of **SVLGQLGITK**

Found in **gi|24438**, alpha-1-antitrypsin (aa 268-394) [Homo sapiens]

Match to Query 6: 1014.645800 from(508.330176,2+)



Monoisotopic mass of neutral peptide Mr(calc): 1014.6073

Ions Score: 15 Expect: 47

Matches (**Bold**): 19/92 fragment ions using 81 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	60.0444	30.5258			88.0393	44.5233			S					10
2	<b>159.1128</b>	80.0600			<b>187.1077</b>	94.0575			V	928.5826	<b>464.7949</b>	911.5560	456.2817	9
3	<b>272.1969</b>	136.6021			<b>300.1918</b>	150.5995			L	<b>829.5142</b>	415.2607	812.4876	406.7475	8
4	329.2183	165.1128			357.2132	179.1103			G	<b>716.4301</b>	358.7187	699.4036	350.2054	7
5	457.2769	229.1421	440.2504	220.6288	485.2718	243.1395	468.2453	<b>234.6263</b>	Q	<b>659.4087</b>	330.2080	<b>642.3821</b>	321.6947	6
6	570.3610	285.6841	<b>553.3344</b>	277.1709	598.3559	<b>299.6816</b>	581.3293	291.1683	L	<b>531.3501</b>	266.1787	514.3235	<b>257.6654</b>	5
7	627.3824	314.1949	610.3559	305.6816	655.3774	328.1923	<b>638.3508</b>	319.6790	G	<b>418.2660</b>	209.6366	401.2395	201.1234	4
8	740.4665	370.7369	723.4400	362.2236	768.4614	384.7343	751.4349	376.2211	I	<b>361.2445</b>	181.1259	344.2180	172.6126	3
9	841.5142	421.2607	824.4876	412.7475	869.5091	435.2582	852.4825	426.7449	T	<b>248.1605</b>	124.5839	231.1339	116.0706	2
10									K	<b>147.1128</b>	74.0600	130.0863	65.5468	1

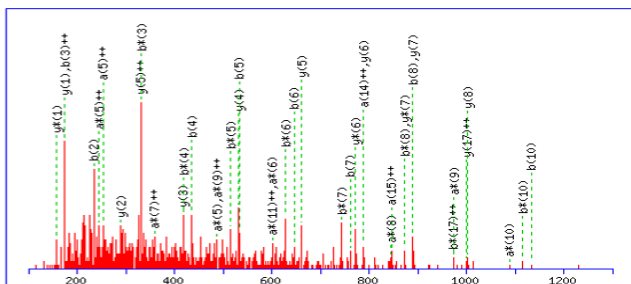
Matched peptides shown in **Bold Red**

1 THDIITKFLE NEDRRSASLH LPKLSITGTY DLK**SVLGQLG** ITKVFSNGAD  
 51 LSGVTEEAPL KLSKAVHKAV LTIDEKGTGA AGAMFLEAIP MSIPPEVKFN  
 101 KPFVFLMIEQ NTKSPLFMGK VVNPTQK

# Supplemental Figure S1B

Peak ID: 11165

MS/MS Fragmentation of **HPNSPLDEENLTQENQDR**  
 Found in **gj|443345**, Chain A, Alpha1 Antichymotrypsin  
 Match to Query 2: 2134.980774 from(712.667534,3+)



Monoisotopic mass of neutral peptide Mr(calc): 2134.9515  
 Ions Score: 28 Expect: 0.93  
 Matches (**Bold**): 41/196 fragment ions using 64 most intense peaks

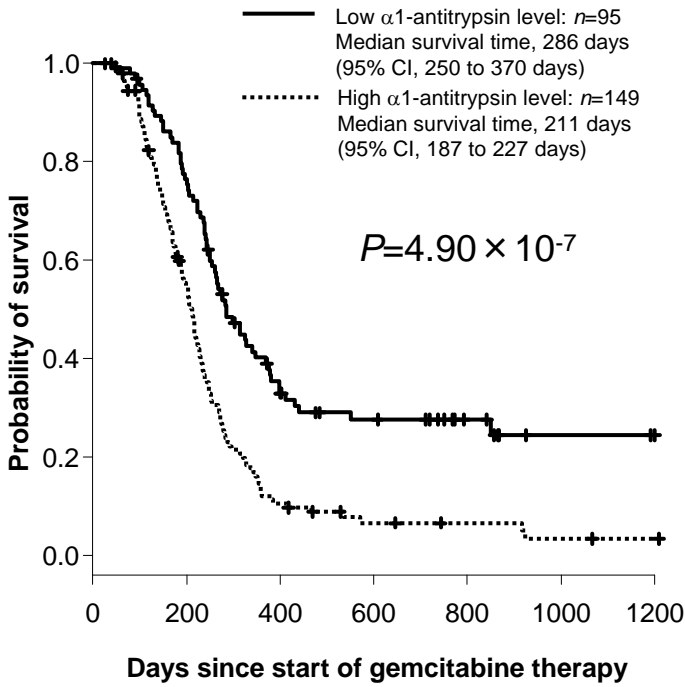
#	a	a <sup>++</sup>	a <sup>+</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>+</sup>	y <sup>+++</sup>	#
1	110.0713	55.5393			138.0662	69.5367			<b>H</b>					<b>18</b>
2	207.1240	104.0657			<b>235.1190</b>	118.0631			<b>P</b>	1998.8999	<b>999.9536</b>	1981.8734	991.4403	<b>17</b>
3	321.1670	161.0871	304.1404	152.5738	349.1619	<b>175.0846</b>	<b>332.1353</b>	166.5713	<b>N</b>	1901.8472	951.4272	1884.8206	942.9139	<b>16</b>
4	408.1990	204.6031	391.1724	196.0899	<b>436.1939</b>	218.6006	<b>419.1674</b>	210.0873	<b>S</b>	1787.8042	894.4058	1770.7777	885.8925	<b>15</b>
5	505.2518	<b>253.1295</b>	<b>488.2252</b>	<b>244.6162</b>	<b>533.2467</b>	267.1270	<b>516.2201</b>	258.6137	<b>P</b>	1700.7722	850.8897	1683.7456	842.3765	<b>14</b>
6	618.3358	309.6715	<b>601.3093</b>	301.1583	<b>646.3307</b>	323.6690	<b>629.3042</b>	315.1557	<b>L</b>	1603.7194	802.3634	1586.6929	793.8501	<b>13</b>
7	733.3628	367.1850	716.3362	<b>358.6717</b>	<b>761.3577</b>	381.1825	<b>744.3311</b>	372.6692	<b>D</b>	1490.6354	745.8213	1473.6088	737.3080	<b>12</b>
8	862.4054	431.7063	<b>845.3788</b>	423.1930	<b>890.4003</b>	445.7038	<b>873.3737</b>	437.1905	<b>E</b>	1375.6084	688.3079	1358.5819	679.7946	<b>11</b>
9	991.4479	496.2276	<b>974.4214</b>	<b>487.7143</b>	1019.4429	510.2251	1002.4163	501.7118	<b>E</b>	1246.5658	623.7866	1229.5393	615.2733	<b>10</b>
10	1105.4909	553.2491	<b>1088.4643</b>	544.7358	<b>1133.4858</b>	567.2465	<b>1116.4592</b>	558.7333	<b>N</b>	1117.5232	559.2653	1100.4967	550.7520	<b>9</b>
11	1218.5749	609.7911	1201.5484	<b>601.2778</b>	1246.5699	623.7886	1229.5433	615.2753	<b>L</b>	<b>1003.4803</b>	502.2438	986.4538	493.7305	<b>8</b>
12	1319.6226	660.3149	1302.5961	651.8017	1347.6175	674.3124	1330.5910	665.7991	<b>T</b>	<b>890.3963</b>	445.7018	<b>873.3697</b>	437.1885	<b>7</b>
13	1447.6812	724.3442	1430.6546	715.8310	1475.6761	738.3417	1458.6496	729.8284	<b>Q</b>	<b>789.3486</b>	395.1779	<b>772.3220</b>	386.6646	<b>6</b>
14	1576.7238	<b>788.8655</b>	1559.6972	780.3523	1604.7187	802.8630	1587.6922	794.3497	<b>E</b>	<b>661.2900</b>	<b>331.1486</b>	644.2634	322.6354	<b>5</b>
15	1690.7667	<b>845.8870</b>	1673.7402	837.3737	1718.7616	859.8845	1701.7351	851.3712	<b>N</b>	<b>532.2474</b>	266.6273	515.2209	258.1141	<b>4</b>
16	1818.8253	909.9163	1801.7987	901.4030	1846.8202	923.9137	1829.7937	915.4005	<b>Q</b>	<b>418.2045</b>	209.6059	401.1779	201.0926	<b>3</b>
17	1933.8522	967.4298	1916.8257	958.9165	1961.8472	981.4272	1944.8206	<b>972.9139</b>	<b>D</b>	<b>290.1459</b>	145.5766	273.1193	137.0633	<b>2</b>
18									<b>R</b>	<b>175.1190</b>	88.0631	<b>158.0924</b>	79.5498	<b>1</b>

Matched peptides shown in **Bold Red**

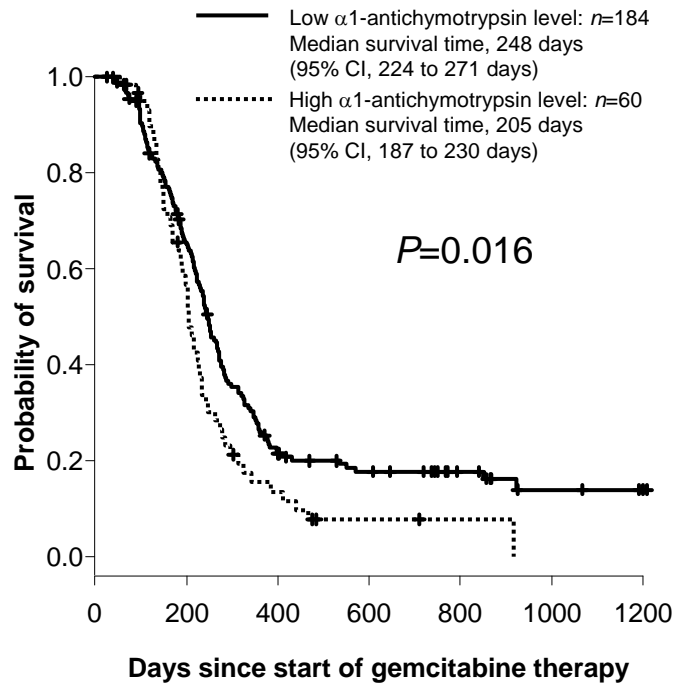
**1 HPNSPLDEEN LTQENQDRGT** HVDLGLASAN VDFAFSLYKQ LVLKAPDKNV  
**51 IFSPLSISTA** LAFLSLGAHN TTLTEILKGL KFNLTETSEA EIHQSFQHLL  
**101 RTLNQSSDEL** QLMSGNAMFV KEQLSLLDRF TEDAKRLYGS EAFATDFQDS  
**151 AAAKKLINDY** VKNGTRGKIT DLIKDLDSQT MMVLVNYIFF KAKWEMPFDP  
**201 QDTHQSRFYL** SKKKWVMVPM MSLHHLTIPY FRDEELSCV VELKYTGNAS  
**251 ALFILPDQDK** MEEVEAMLLP ETLKRWRDSL EFREIGELYL PKFSISRDN  
**301 LNDILLQLGI** EEAFYSKADL SGITGARNLA VSQVVKAVL DVFEEGTEAS  
**351 AATAVKITLL**

# Supplemental Figure S2

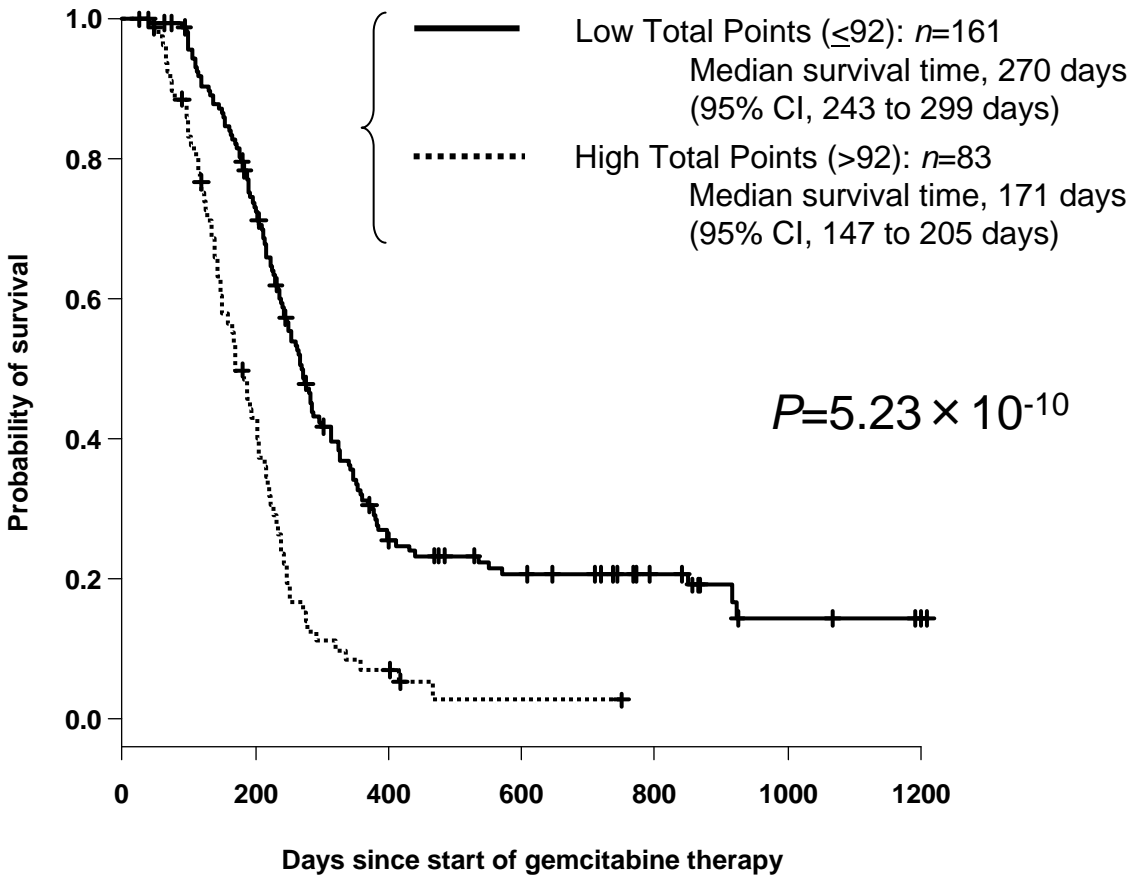
## A



## B



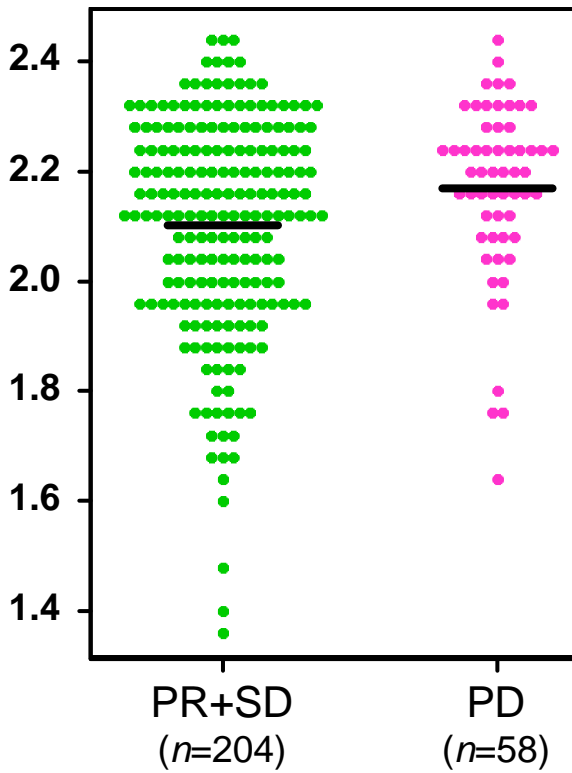
## C



# Supplemental Figure S3

**A**

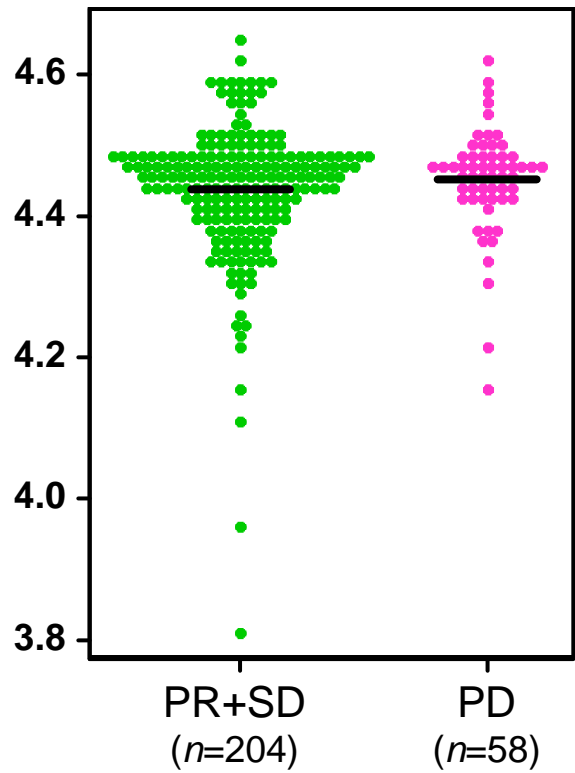
$\alpha$ 1-Antitrypsin



$P=0.020$

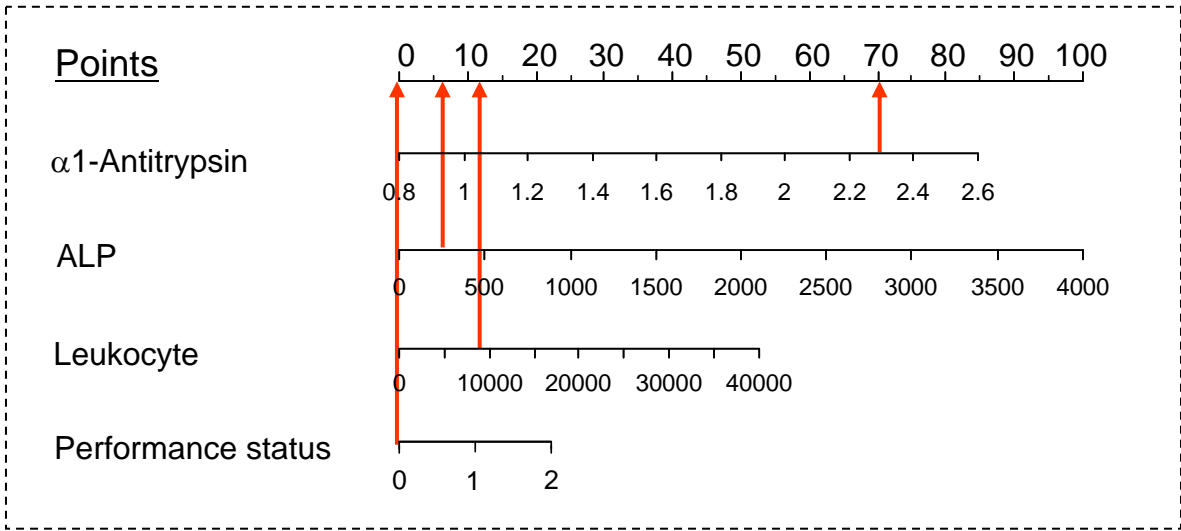
**B**

$\alpha$ 1-Antichymotrypsin

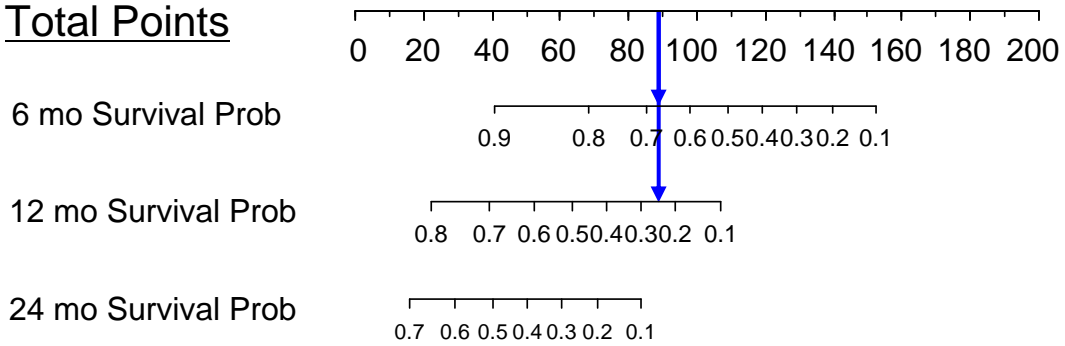


$P=0.312$

# Supplemental Figure S4



## Total Points



## LEGENDS FOR SUPPLEMENTAL FIGURES ONLINE

### Supplemental Figure S1 online

MS/MS spectra and database search results of two representative MS peaks [ID 1740 (A) and ID 11165 (B)] identified as being derived from  $\alpha$ 1-antitrypsin and  $\alpha$ 1-antichymotrypsin, respectively. Peptides that matched the amino acid sequences in the database are highlighted in red.

### Supplemental Figure S2 online

Kaplan-Meier plots of overall survival in relation to  $\alpha$ 1-antitrypsin (A),  $\alpha$ 1-antichymotrypsin (B) data, and Total Point score (C) in 244 samples that were not used in the 2DICAL analysis.

### Supplemental Figure S3 online

Plasma/serum levels of  $\alpha$ 1-antitrypsin and  $\alpha$ 1-antichymotrypsin according to tumor response (RECIST guideline). Horizontal lines represent the average levels. Forty-two patients whose tumor response was not evaluable were excluded. PR, partial response; SD, stable disease; PD, progressive disease.

### Supplemental Figure S4 online

First, draw a vertical line (*red*) upward to the Points row (*top*) to obtain the number of points for each variable (*top*). Then, total the points and drop a vertical line (*blue*) from the Total Points row to obtain the estimated probability (Prob) of survival 6, 12, and 24 months (mo) after gemcitabine treatment (*bottom*). This particular patient was estimated to have no chance of surviving more than 24 months using the current gemcitabine treatment.