

# Table S1

Tumor Type	Origin of Samples	Number of Samples	Type of Array	Method of DNA Extraction	Mode of Validation	Notes
Esophageal Adenocarcinoma	University of Pittsburgh, U.S.A.	112	SNP6.0	Salt precipitation	>70% tumor content by pathological review	7q21 amplification frequency in these data was previously reported (Ismail A, et al. 2011)
	University of Michigan, U.S.A.	74	250K Styl	Phenol Chloroform	>70% tumor content by pathological review	Frequency of <i>GATA6</i> amplification in these data was previously reported (Lin L, et al. 2012)
	<b>Total</b>	<b>186</b>				
Gastric Adenocarcinoma	University of Siena	97	SNP6.0	Salt Precipitation	>80% tumor content by pathological review	Pathological examination excluded these cases as esophageal or GEJ
	Massachusetts General Hospital, U.S.A.	9	250K Styl	Salt Precipitation	>70% tumor content by pathological review	
	University of North Carolina, U.S.A.	4	250K Styl	Salt Precipitation	>70% tumor content by pathological review	
<b>Total</b>	<b>110</b>					
Colorectal Carcinoma	Vall d'Hebron Hospital, Barcelona	62	SNP6.0	Salt Precipitation	>70% tumor content by pathological review	
	Brigham and Women's Hospital, U.S.A.	46	250K Styl	Salt precipitation	>70% tumor content by pathological review	Data described previously (Firestein R, et al. 2008)
	Genomics Collaborative Incorporated	43	250K Styl	Salt precipitation	>70% tumor content by pathological review	Data described previously (Firestein R, et al. 2008)
	Massachusetts General Hospital, U.S.A.	25	250K Styl	Salt precipitation	>70% tumor content by pathological review	Data described previously (Firestein R, et al. 2008)
	Vall d'Hebron Hospital, Barcelona	9	250K Styl	Salt precipitation	>70% tumor content by pathological review	Data described previously (Firestein R, et al. 2008)
	Brigham and Women's Hospital, U.S.A.	5	250K Styl	Salt Precipitation	>70% tumor content by pathological review	
<b>Total</b>	<b>190</b>					

Table S2-A

### Significant amplifications in colorectal adenocarcinomas

<b>Cytoband</b>	<b>Residual q-value</b>	<b>Peak Boundaries (Mb)</b>	<b>Number of Genes in Peak</b>	<b>Candidate Target(s)</b>
17q12	7.39E-07	34.97-35.52	20	<i>ERBB2</i>
8q24.21	2.15E-06	128.50-128.83	2	<i>MYC</i>
13q12.2	5.24E-05	27.13-27.33	2	<i>CDK8*</i>
8p12	6.09E-03	38.26-38.46	3	<i>FGFR1</i>
18q11.2	9.21E-03	18.52-18.97	2	<i>GATA6</i>

\* denotes gene is adjacent to peak

Table S2-B

## Significant amplifications in gastric adenocarcinomas

<b>Cytoband</b>	<b>Residual q-value</b>	<b>Peak Boundaries (Mb)</b>	<b>Number of Genes in Peak</b>	<b>Candidate Target(s)</b>
19q12	1.16E-18	34.95-35.10	1	<i>CCNE1</i>
17q12	5.88E-17	34.97-35.24	10	<i>ERBB2</i>
8q24.21	1.19E-16	128.51-128.64	1	<i>MYC</i>
1q42.3	5.80E-06	23.31-23.34	4	
8p23.1	1.07E-05	11.41-11.77	5	<i>GATA4</i>
18q11.2	2.73E-05	17.74-18.05	1	<i>GATA6</i>
11q13.3	3.71E-05	68.43-70.10	17	<i>CCND1, FGF3, FGF4, FGF19</i>
12p12.1	4.83E-05	25.01-25.78	6	<i>KRAS</i>
6p21.1	5.01E-05	43.79-44.01	2	<i>VEGFA</i>
3q27.1	8.33E-04	185.71-186.17	3	<i>EPHB3</i>
1p36.22	8.79E-04	10.54-10.92	2	
12q15	2.71E-03	65.90-69.27	23	<i>MDM2, FRS2</i>
7p11.2	5.22E-03	54.84-55.28	1	<i>EGFR</i>
11q13.4	5.38E-03	73.89-74.04	1	

Table S2-C

### Significant amplifications in esophageal adenocarcinomas

Cytoband	Residual q-value	Peak Boundaries (Mb)	Number of Genes in Peak	Candidate Target(s)
12p12.1	5.13E-47	25.23-25.34	3	<i>KRAS</i>
18q11.2	5.10E-30	17.95-18.16	1	<i>GATA6</i>
8p23.1	2.07E-28	11.41-11.71	4	<i>GATA4</i>
19q12	1.44E-18	34.94-35.10	1	<i>CCNE1</i>
7q21.2	1.93E-18	92.32-92.50	1	<i>CDK6*</i>
11q13.2	5.61E-18	68.97-69.49	5	<i>CCND1, FGF3, FGF4, FGF19</i>
17q12	2.09E-16	34.97-35.27	10	<i>ERBB2</i>
17q21.2	2.95E-14	37.02-37.21	7	
7p11.2	2.24E-13	54.92-55.40	1	<i>EGFR</i>
8q24.21	2.76E-12	128.47-128.91	5	<i>MYC</i>
6p21.1	8.44E-12	43.32-43.46	4	<i>VEGFA*</i>
9p13.3	8.51E-08	35.47-35.93	25	
13q13.1	3.05E-07	32.28-33.33	3	
7q22.1	5.52E-07	99.13-99.84	32	
7q31.2	2.20E-05	115.92-116.42	7	<i>MET</i>
12q15	3.96E-05	65.56-68.50	20	<i>MDM2</i>
7q34	1.16E-04	141.92-142.26	4	<i>EPHB6</i>
6q23.3	1.53E-04	135.32-135.87	5	<i>MYB</i>
10q22.2	3.88E-04	75.00-75.80	16	
1q21.3	8.38E-04	146.23-152.37	167	<i>MCL1</i>
10q26.12	1.47E-03	122.75-123.91	4	<i>FGFR2</i>
3q26.2	2.14E-03	170.20-173.76	27	<i>PRKCι</i>
18q11.2	2.21E-03	21.70-22.46	4	
13q14.11	2.38E-03	40.27-40.83	10	
11p14.2	5.25E-03	27.04-27.57	5	

\* denotes gene is adjacent to peak

Table S3

**Significant amplifications  
(comparing gut adenocarcinomas to all other cancer types)**

Restricted to Gut Adenocarcinomas		Restricted to All Other Cancers		Restricted to All Other Cancers		Observed in All Cancers	
<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>
1p36.22		1p32.1	<i>JUN</i>	8q24.3		1q21.2	<i>MCL1</i>
1q42.3		1p34.2		12q14.1	<i>CDK4</i>	6p21.1	<i>VEGFA</i>
3q26.31		1p36.33		12q14.2		6q23.3	<i>MYB</i>
3q27.1	<i>EPHB3</i>	1q23.2		12q14.3		7p11.2	<i>EGFR</i>
7q21.2	<i>CDK6</i>	1q24.3		12q21.1		8p12	<i>FGFR1</i>
7q22.1		1q32.1		12q21.2		8q24.21	<i>MYC</i>
7q31.2	<i>MET</i>	1q44	<i>AKT3</i>	12q21.31		11q13.2	<i>CCND1</i>
7q34	<i>EPHB6</i>	2p24.3	<i>MYCN</i>	12q21.33		11q14.1	
8p23.1	<i>GATA4</i>	3q26.2		12q23.1		12p12.1	<i>KRAS</i>
9p13.3		3q26.33	<i>SOX2</i>	13q34		12q15	<i>MDM2</i>
10q22.2		5p13.2		14q13.3		15q26.1	<i>IGF1R</i>
10q26.12	<i>FGFR2</i>	5p15.2		17q11.2		17q12	<i>ERBB2</i>
11p14.2		5p15.33	<i>TERT</i>	17q21.33		19q12	<i>CCNE1</i>
13q13.1		5q35.3		17q23.1		20q13.2	
13q14.11		6q21		17q24.2			
13q22.1		8p11.21		17q25.1	<i>CDK3</i>		
17q21.2		8p12		19q13.12			
17q24.3		8q21.13		20q11.22			
18q11.2	<i>GATA6</i>	8q22.3		20q13.33	<i>MYT1</i>		
		8q23.3		22q11.21	<i>CRKL</i>		

Table S4-A

## Significant deletions in colorectal adenocarcinomas

Cytoband	Residual q-value	Peak Boundaries (Mb)	Number of Genes in		Candidate Target(s)
			Peak	Peak	
16p13.3	9.23E-50	5.06-7.71	2		<i>A2BP1</i>
3p14.2	1.32E-43	58.98-61.52	1		<i>FHIT</i>
20p12.1	9.34E-22	14.21-15.99	2		<i>MACROD2</i>
6q26	4.22E-11	161.61-163.13	1		<i>PARK2</i>
1p36.11	2.95E-09	18.58-29.38	180		<i>ARID1A</i>
4q22.1	1.77E-06	91.37-93.49	2		<i>FAM190A</i>
5q22.2	1.77E-06	110.88-113.74	12		<i>APC</i>
5q21.1	6.25E-06	100.16-102.24	4		
5q11.2	2.30E-05	58.18-59.84	3		<i>PDE4D</i>
16q23.1	2.60E-05	76.69-78.21	2		<i>WWOX</i>
10q23.31	8.67E-05	89.57-90.10	2		<i>PTEN</i>
10q25.2	2.54E-04	114.15-115.82	11		<i>CASP7</i>
1p13.2	4.18E-04	112.32-116.32	35		
10q11.23	1.42E-03	52.31-53.77	5		
4q35.1	2.51E-03	179.06-189.20	39		<i>CASP3</i>
18q21.2	6.59E-03	46.17-48.13	6		<i>SMAD4</i>

Table S4-B

## Significant deletions in esophageal adenocarcinomas

Cytoband	Residual q-value	Peak Boundaries (Mb)	Number of Genes in	
			Peak	Candidate Target(s)
3p14.2	9.51E-211	58.96-61.52	2	<i>FHIT</i>
16q23.1	5.07E-129	76.69-78.21	3	<i>WWOX</i>
9p21.3	6.40E-59	21.85-22.01	3	<i>CDKN2A</i>
5q11.2	1.48E-18	58.30-59.83	3	<i>PDE4D</i>
6p25.3	3.42E-18	1.54-2.57	2	
20p12.1	2.99E-14	14.21-15.99	2	<i>MACROD2</i>
4q22.1	2.57E-13	91.37-93.49	2	<i>FAM190A</i>
18q21.2	1.24E-09	46.77-46.97	1	<i>SMAD4</i>
21q22.12	7.38E-07	35.03-35.35	2	<i>RUNX1</i>
9p24.1	9.14E-07	7.78-12.71	3	<i>PTPRD</i>
6q26	1.05E-05	161.61-163.13	2	<i>PARK2</i>
2q33.2	2.43E-05	204.53-206.27	1	
21q11.2	6.12E-05	1.00-16.26	17	
1q44	1.49E-04	243.92-244.78	1	
8p23.3	5.68E-04	1.00-1.45	6	
7q32.1	8.77E-04	123.45-142.24	145	
7q36.3	2.02E-03	147.74-158.82	95	
1p36.11	3.87E-03	25.64-31.02	89	<i>ARID1A</i>
4q35.1	4.51E-03	179.06-185.55	14	<i>CASP3</i>
11q22.3	6.00E-03	105.46-112.34	50	<i>ATM</i>
11q25	8.17E-03	120.54-134.45	111	

Table S4-C

## Significant deletions in gastric adenocarcinomas

<b>Cytoband</b>	<b>Residual q-value</b>	<b>Peak Boundaries (Mb)</b>	<b>Number of Genes in Peak</b>	<b>Candidate Target(s)</b>
3p14.2	5.28E-60	58.98-61.52	1	<i>FHIT</i>
16q23.1	2.16E-26	76.69-78.21	2	<i>WWOX</i>
20p12.1	2.31E-14	14.21-15.9	2	<i>MACROD2</i>
5q11.2	2.26E-12	58.30-59.84	3	<i>PDE4D</i>
9p24.1	6.95E-11	7.78-12.71	3	<i>PTPRD</i>
4q22.1	1.36E-07	91.37-93.49	2	<i>FAM190A</i>
6p25.3	1.44E-06	1.54-2.57	2	
6q26	2.20E-03	161.61-163.13	1	<i>PARK2</i>

Table S5

**Significant deletions  
(comparing gut adenocarcinomas to all other cancer types)**

Restricted to Gut Adenocarcinomas		Restricted to All Other Cancers		Restricted to All Other Cancers		Observed in All Cancers	
<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>	<i>Peak</i>	<i>Candidate</i>
1p13.2		1p13.3		11q25		3p14.2	<i>FHIT</i>
1p36.11		1p36.31		12p13.2		4q22.1	<i>FAM190A</i>
1q44		1q42.3		12q24.33		4q35.2	<i>CASP3</i>
2q33.2		2p25.3		13q12.11		5q11.2	<i>PDE4D</i>
3p26.2		2q22.1		13q14.11		5q22.2	<i>APC</i>
4q35.1		2q37.1		13q14.2	<i>RB1</i>	6q26	<i>PARK2</i>
5q15		2q37.3		15q11.2		7q36.3	<i>PTPRN2</i>
6p25.3		3p26.3		15q15.1		9p21.3	<i>CDKN2A</i>
8p23.3		6q16.1		16p11.2		9p24.1	<i>PTPRD</i>
10q11.23		7q34		16q24.3		10q23.31	<i>PTEN</i>
12q21.2		8p21.2		17p13.1	<i>TP53</i>	11q23.2	<i>ATM</i>
17p12		8p23.2	<i>CSMD1</i>	17q11.2		16p13.3	<i>A2BP1</i>
18q21.2	<i>SMAD4</i>	9p13.2	<i>PAX5</i>	18q23		16q23.1	<i>WWOX</i>
21q22.12	<i>RUNX1</i>	9p24.3		19p13.3		20p12.1	<i>MACROD2</i>
21q22.3		10p15.3		19q13.32		21q11.2	
		10q26.3		20p13			
		11p15.5		22q11.23			
				22q13.31			

Table S6-A

## Significant amplifications (across all gut adenocarcinomas) in SNP6 Data

Cytoband	Residual q-value	Peak Boundaries (Mb)	Number of Genes in Peak	Candidate Target(s) (Bold designates therapeutic target)
<i>Gut Adenocarcinomas</i>				
12p12.1	9.61E-35	25.24-25.34	2	<i>KRAS</i>
17q12	9.48E-26	35.06-35.16	7	<b>ERBB2</b>
18q11.2	1.46E-24	17.96-18.04	1	<i>GATA6</i>
8q24.21	1.81E-19	128.54-128.84	2	<i>MYC</i>
11q13.2	2.99E-18	68.98-69.49	5	<i>CCND1</i>
19q12	2.10E-17	35.00-35.04	1	<i>CCNE1</i>
8p23.1	4.02E-17	11.30-11.75	7	<i>GATA4</i>
7q21.2	7.55E-16	91.56-92.48	12	<b>CDK6</b>
6p21.1	2.41E-15	43.80-43.93	1	<b>VEGFA</b>
7q34	2.57E-13	142.03-142.09	1	[ <i>PRSS1</i> ]
17q21.2	1.30E-08	37.13-37.16	1	<i>HAP1</i>
12q15	4.44E-07	65.95-68.34	19	<i>MDM2</i>
7q22.1	7.58E-07	98.44-98.82	6	
9p13.3	1.20E-06	35.59-35.76	13	
17q21.2	4.87E-06	36.16-36.24	6	
7p11.2	9.45E-06	54.72-55.38	2	<b>EGFR</b>
10q22.2	1.44E-05	75.07-75.45	13	
20q13.2	7.81E-05	51.62-51.97	2	
1q42.3	5.30E-04	233.06-233.32	1	[ <i>TOMM20</i> ]
13q22.1	1.83E-03	72.48-73.07	2	<i>KLF5</i>
1p36.22	2.41E-03	10.60-10.99	3	
17q24.3	2.61E-03	67.87-67.97	1	[ <i>SLC39A11</i> ]
10q26.13	3.05E-03	122.79-123.82	4	<b>FGFR2</b>
3q27.1	3.16E-03	185.73-186.16	3	<i>EPHB3</i>
18q11.2	6.31E-03	19.91-19.94	1	<b>TTC39C</b>
8q11.1*	7.78E-03	47.52-47.56	1	[ <i>BEYLA</i> ]
2q21.2*	8.33E-03	132.77-132.83	1	[ <i>NCRNA0016</i> ]

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\*unique to SNP6.0

[ ] denotes adjacent to peak

Table S6-B

Significant deletions (across all gut adenocarcinomas) with SNP6 Data

Cytoband	Residual q-value	Peak Boundaries (Mb)	Number of Genes in Peak	Candidate Target(s)
<i>Gut Adenocarcinomas</i>				
3p14.2	1.48E-181	59.01-61.52	1	<i>FHIT</i>
16q23.1	1.19E-99	76.69-78.19	1	<i>WWOX</i>
9p21.3	3.39E-45	21.86-21.99	2	<i>CDKN2A</i>
20p12.1	2.62E-44	14.25-15.98	2	<i>MACROD2</i>
5q11.2	1.51E-40	58.30-59.82	3	<i>PDE4D</i>
4q22.1	3.88E-38	91.37-93.46	2	<i>FAM190A</i>
6p25.3	1.32E-25	15.54-25.69	2	
7q31.1*	9.08E-25	110.51-111.16	1	<i>LRRN3</i>
6q26	1.39E-18	161.61-163.07	1	<i>PARK2</i>
21q22.12	3.54E-09	35.03-35.34	2	<i>RUNX1</i>
3q26.31*	2.87E-08	175.48-178.22	1	<i>NAALADL2</i>
16p13.3	2.64E-07	50.86-77.04	1	<i>A2BP1</i>
18q21.2	3.16E-07	46.77-46.96	1	<i>SMAD4</i>
1q44	5.95E-07	243.93-244.77	1	<i>SMYD3</i>
9p24.1	5.51E-06	7.79-12.68	2	<i>PTPRD</i>
7q36.3	2.67E-05	157.06-158.03	4	
2q33.2	4.46E-05	204.53-206.27	1	<i>PARD3B</i>
4q35.2	2.43E-04	183.33-191.27	49	<i>CASP3</i>
21q11.2	2.62E-04	14.59-15.26	2	
1p36.11	3.05E-04	25.77-31.02	88	<i>ARID1A</i>
10q23.31	4.25E-04	89.30-90.02	5	<i>PTEN</i>
8p23.3	1.36E-03	1.00-1.70	7	
1p13.1*	3.46E-03	103.84-144.10	168	
21q22.3	5.64E-03	41.14-46.94	98	
1p33*	7.42E-03	48.97-50.29	1	
5q22.2	8.73E-03	89.89-121.40	92	<i>APC</i>
11q25*	9.46E-03	120.56-134.45	111	

2

\*unique to SNP6.0