Supplementary Table 1 *APC* mutational data from the COSMIC database

Amino acid change	Nucleotide mutation	Relative mutation distribution in carcinomas, *n* (%)	Absolute mutation frequency in carcinomas, %
p.Q1291*	c.3871C>T	7 (0.68)	0.25
p.T1301fs*15	c.3900_3901insT	0 (0)	0
p.L1302fs*3	c.3903delC	1 (0.10)	0.04
p.I1304fs*4	c.3912delA	1 (0.10)	0.04
p.E1306*	c.3916G>T	8 (0.78)	0.29
p.E1309fs*4	c.3921_3925delAA AAG	44 (4.30)	1.59
p.E1309*	c.3925G>T	12 (1.17)	0.43
p.K1310*	c.3928A>T	2 (0.20)	0.07
p.S1315*	c.3944C>A	4 (0.39)	0.14
p.E1317Q	*c.3949G>C*	2 (0.20)	0.07
p.V1320fs*11	c.3957_3958insT	0 (0)	0
p.E1322*	c.3964G>T	7 (0.68)	0.25
p.R1331*	c.3991A>T	2 (0.20)	0.07
p.Q1338*	c.4012C>T	12 (1.17)	0.43
p.S1344*	c.4031C>A	0 (0)	0
p.E1353*	c.4057G>T	6 (0.59)	0.22
p.S1356*	c.4067C>G	3 (0.29)	0.11
p.Q1367*	c.4099C>T	14 (1.37)	0.51
p.Q1378fs*7	c.4131_4132insT	0 (0)	0
p.Q1378*	c.4132C>T	11 (1.07)	0.40
p.E1397fs*1	c.4184_4185insT	0 (0)	0
p.S1400*	c.4199C>A	3 (0.29)	0.11
p.Q1406fs*11	c.4216_4217insCGT TC	0 (0)	0
p.Q1406*	c.4216C>T	6 (0.59)	0.22
p.E1408*	c.4222G>T	5 (0.49)	0.18

	c.4232_4238delGTG		
p.S1411fs*1	GAAT	0 (0)	0
p.S1411fs*4	c.4233delT	6 (0.59)	0.22
p.V1414fs*5	c.4241delT	0 (0)	0
p.G1416fs*3	c.4247delG	1 (0.10)	0.04
	c.4259_4272delCCC		
p.P1420fs*2	AGTGATCTTCC	0 (0)	0
p.S1421fs*52	c.4263delT	2 (0.20)	0.07
p.Q1429*	c.4285C>T	8 (0.78)	0.29
p.T1430fs*43	c.4287delC	0 (0)	0
	c.4294_4314delCAC		
	C		
	AAGCAGAAGTA		
p.P1432fs*35	AAAC	0 (0)	0
p.T1438fs*35	c.4312delA	4 (0.39)	0.14
p.T1438fs*35	c.4313delC	0 (0)	0
p.P1439fs*34	c.4316delC	1 (0.10)	0.04
p.P1441fs*32	c.4322delC	0 (0)	0
p.P1442P	*c.4326T>A*	2 (0.20)	0.07
p.T1445fs*28	c.4333delA	0 (0)	0
p.T1445fs*28	c.4334delC	0 (0)	0
p.R1450*	c.4348C>T	60 (5.86)	2.17
p.E1461*	c.4381G>T	1 (0.10)	0.04
p.E1461fs*7	c.4382_4383insA	0 (0)	0
p.S1465fs*3	c.4386_4387delGA	19 (1.86)	0.69
p.K1462fs*10	c.4386delG	0 (0)	0
p.P1483S	*c.4447C>T*	0 (0)	0
p.A1485T	*c.4453G>A*	0 (0)	0
	c.4460_4464delCTT		
p.T1487fs*27	TA	0 (0)	0
p.L1488fs*19	c.4464delA	4 (0.39)	0.14

p.H1490fs*17	c.4469_4470insTA	0 (0)	0
p.A1492fs*22	c.4473_4474insT	2 (0.20)	0.07
p.E1494fs*13	c.4480delG	3 (0.29)	0.11
p.G1499R	*c.4495G>A*	0 (0)	0
other mutations within MCR (1286-1513)		477 (46.59)	17.24
Total mutants (MCR)		740 (72.27)	26.75
Total mutants (COSMIC)		1024 (100)	37.01

Supplementary Table 2 *BRAF* mutational data from the COSMIC database

Amino acid change	Nucleotide mutation	Relative mutation distribution in carcinomas, *n* (%)	Absolute mutation frequency in carcinomas, %
p.D594G	c.1781A>G	11 (0.37)	0.04
p.V600E	c.1799T>A	2862 (97.38)	10.05
p.V600M	c.1798G>A	1 (0.03)	0
p.K601E	c.1801A>G	4 (0.14)	0.01
Total mutants (SEQUENOM)		2878 (97.92)	10.10
Total mutants (COSMIC)		2940 (100)	10.32

Supplementary Table 3 *KRAS* mutational data from the COSMIC database

Amino acid change	Nucleotide mutation	Relative mutation distribution in carcinomas, *n* (%)	Absolute mutation frequency in carcinomas, %
p.G12C	c.34G>T	600 (7.99)	2.84
p.G12S	c.34G>A	448 (5.97)	2.12
p.G12R	c.34G>C	88 (1.17)	0.42
p.G12D	c.35G>A	2551 (33.97)	12.06
p.G12V	c.35G>T	1588 (21.15)	7.51
p.G12A	c.35G>C	493 (6.56)	2.33
p.G13D	c.38G>A	1444 (19.23)	6.83
p.G13A	c.38G>C	7 (0.09)	0.03
p.G13V	c.38G>T	9 (0.12)	0.04
p.G13G	c.39C>A	2 (0.03)	0.01
p.G13G	c.39C>G	1 (0.01)	0
p.G13G	c.39C>T	0 (0)	0
p.A59T	c.175G>A	1 (0.01)	0
p.Q61K	c.181C>A	4 (0.05)	0.05
p.Q61E	c.181C>G	1 (0.01)	0.01
p.Q61L	c.182A>T	11 (0.15)	0.15
p.Q61R	c.182A>G	6 (0.08)	0.08
p.Q61P	c.182A>C	0 (0)	0
p.Q61H	c.183A>C	24 (0.32)	0.32
p.Q61H	c.183A>T	15 (0.20)	0.20
p.A146T	c.436G>A	20 (0.27)	0.09
p.A146P	c.436G>C	2 (0.03)	0.01
Total codon 12		5768 (76.81)	27.28
Total codon 13		1463 (19.48)	6.91
Total codon 61		61 (0.81)	0.81
Total codon 146		22 (0.30)	0.10
Total mutants (SEQUENOM)		7306 (97.28)	34.54

Total mutants (COSMIC)	7511 (100)	35.51

Supplementary Table 4 *NRAS* mutational data from the COSMIC database

Amino acid Change	Nucleotide mutation	Relative mutation distribution in carcinomas, *n* (%)	Absolute mutation frequency in carcinomas, %
p.G12C	c.34G>T	2 (12.50)	0.31
p.G12S	c.34G>A	1 (6.25)	0.16
p.G12R	c.34G>C	0 (0)	0
p.G13R	c.37G>C	1 (6.25)	0.16
p.G13S	c.37G>A	0 (0)	0
p.G13C	c.37G>T	0 (0)	0
p.Q61K	c.181C>A	0 (0)	0
p.Q61E	c.181C>G	0 (0)	0
p.Q61R	c.182A>G	6 (37.50)	0.93
p.Q61P	c.182A>C	0 (0)	0
p.Q61L	c.182A>T	1 (6.25)	0.16
p.Q61H	c.183A>C	0 (0)	0
p.Q61Q	c.183A>G	0 (0)	0
p.Q61H	c.183A>T	0 (0)	0
Total codon 12		3 (18.75)	0.47
Total codon 13		1 (6.25)	0.16
Total codon 61		7 (43.75)	1.09
Total mutants (SEQUENOM)		11 (68.75)	1.71
Total mutants (COSMIC)		16 (100)	2.48

Supplementary Table 5 *PIKCA3* mutational data from the COSMIC database

Amino acid change	Nucleotide mutation	Relative mutation distribution in carcinomas, *n* (%)	Absolute mutation frequency in carcinomas, %
p.G12D	c.35G>A	1 (0.16)	0.02
p.R38H	c.113G>A	3 (0.47)	0.07
p.E81K	c.241G>A	1 (0.16)	0.02
p.R88Q	c.263G>A	6 (0.95)	0.13
p.R93W	c.277C>T	3 (0.47)	0.07
p.G106V	c.317G>T	3 (0.47)	0.07
p.R108H	c.323G>A	4 (0.63)	0.63
p.G118D	c.353G>A	3 (0.47)	0.47
p.P134S	c.400C>T	1 (0.16)	0.02
p.S158L	c.473C>T	1 (0.16)	0.02
p.H160N	c.478C>A	1 (0.16)	0.02
p.K179T	c.536A>C	1 (0.16)	0.02
p.K184E	c.550A>G	1 (0.16)	0.02
p.N345K	c.1035T>A	3 (0.47)	0.07
p.C420R	c.1258T>C	5 (0.79)	0.11
p.P539R	c.1616C>G	1 (0.16)	0.02
p.E542K	c.1624G>A	100 (15.80)	2.17
p.E542Q	c.1624G>C	2 (0.32)	0.04
p.E545K	c.1633G>A	179 (28.28)	3.88
p.Q546K	c.1636C>A	25 (3.95)	0.54
p.Q546E	c.1636C>G	3 (0.47)	0.07
p.H701P	c.2102A>C	0 (0)	0
p.C901F	c.2702G>T	1 (0.16)	0.02
p.M1004I	c.3012G>T	1 (0.16)	0.02
p.G1007R	G3019C	1 (0.16)	0.02
p.H1047Y	c.3139C>T	9 (1.42)	0.20

p.H1047R	c.3140A>G	121 (19.12)	2.62
p.H1047L	c.3140A>T	22 (3.48)	0.48
p.G1049S	c.3145G>A	0 (0)	0
p.G1049R	c.3145G>C	16 (2.53)	0.35
exon 9		310 (49.43)	6.72
exon 20		170 (26.87)	3.69
Total mutants (SEQUENOM)		515 (81.36)	11.17
Total mutants (COSMIC)		633 (100)	13.73