Table S1 Summary of studies presenting frequencies of mutated genes in PM-CRC

First author	Year	Ref.	Samples	Methods	*KRAS*	*BRAF*	*NRAS*	*RAS*	*TP53*	*PIK3CA*	*APC*	*SMAD4*	*GNAS*	*FBXW7*	*PTEN*	*JAK3*	Other
Gillern	2010	(26)	23	PCR	11/23												
Yaeger	2014	(32)	123	Sanger		40/123											
El-Deiry	2015	(19)	397	NGS, Sanger	191/397	25/355	2/96		19/57	13/103	19/61	9/60	3/58	5/59	1/58	1/59	*
Cremolini	2015	(33)	138	Sanger		27/138											
Kawazoe	2015	(29)	52	PCR	15/52	7/52											
Green	2015	(28)	11	Sanger	2/11	4/11											
Sasaki	2016	(23)	117	Sanger	46/100	13/47				5/58							
Fujiyoshi	2017	(30)	52	PCR	26/52	9/52											
Massalou	2017	(24)	65	PCR	28/64	7/65											
Yaeger	2018	(20)	51	NGS	29/51	9/51			38/51	7/51	29/51	15/51	1/51	4/51	3/51	3/51	**
Passot	2018	(21)	150	PCR				87/150									
Schneider	2018	(22)	378	PCR	145/378	22/378	19/378										
Morgan	2019	(27)	47	NGS	20/47	4/47	2/47										
Graf	2020	(25)	97	NGS	44/97	10/82											

The fraction of mutated samples of the total number of samples analyzed is listed for each gene studied. *, *STK11* (2/56), *CTNNB1* (2/61), *AKT1* (1/59), *HNF1A* (1/50), *SMO* (1/57), *ERBB2* (1/58). **, *STK11* (1/51), *CTNNB1* (1/51), *AKT1* (2/51), *HNF1A* (2/51), *SMO* (2/51), *ERBB2* (1/51). NGS, next generation sequencing; PCR, polymerase chain reaction.

Table S2 Summary of studies presenting frequencies of mutated genes in pseudomyxoma peritonei (PMP)

First author	Year	Ref.	Samples	Methods	*KRAS*	*GNAS*	*FAT4*	*TGFBR*	*TP53*	*SMAD3/4*
Zauber	2011	(44)	31	Sanger	31/31					
Nishikawa	2013	(45)	35	PCR	35/35	16/35				
Shetty	2013	(41)	64	PCR	37/64					
Alakus	2014	(46)	10	NGS	10/10	9/10	3/10	2/10	1/10	6/10
Singhi	2014	(39)	55	Sanger	22/55	17/55				
Liu	2014	(47)	8	NGS	3/8	2/8				
Sio	2014	(48)	10	NGS	8/10	4/10			1/8	
Green	2015	(28)	5	Sanger	2/5					
Hara	2015	(49)	16	Sanger	6/16	3/16			6/16	
Davison	2014	(40)	150	Sanger	86/150					
Nummela	2015	(50)	19	NGS	19/19	12/19			1/19	3/19
Noguchi	2015	(51)	18	NGS	14/18	8/18			4/18	3/18
Pietrantonio	2016	(42)	40	NGS	29/40	21/40			5/40	1/40
Pietrantonio	2016	(43)	15	NGS	14/15	9/15			3/15	
Saarinen	2017	(52)	9	NGS	9/9	5/9		2/9		
Pengelly	2018	(53)	5	NGS	5/5	5/5	1/5			1/5
Gleeson	2018	(55)	54	NGS, Sanger	15/31	14/19			1/19	3/19
Tokunaga	2019	(54)	66	NGS	49/66	42/66				
Graf	2020	(25)	13	NGS	7/13					

The fraction of mutated samples of the total number of samples analyzed is listed for each gene studied. NGS, next generation sequencing; PCR, polymerase chain reaction.

Table S3 Frequency of protein expression and number of patients investigated for the different proteins

Protein name	Median % positive [range]	N median [range]	Ref.
Topoisomerase 1 (TOPO1)	63 [63–76]	43 [24–66]	(54,55,64)
Excision repair cross-complementation group 1 (ERCC1)	30 [23–44]	30 [20–66]	(54,55,64)
Thymidylate synthase (TS)	13 [8–16]	45 [25–66]	(54,55,64)
Phosphate and tensin homolog (PTEN)	80 [75–98]	44 [24–66]	(54,55,64)
Methyl guanine methyl transferase (MGMT)	80 [76–95]	46 [25–66]	(54,55,64)
Ribonucleoside-diphosphate reductase large subunit (RRM1)	8 [7–9]	34 [23–44]	(55,64)
Tubulin β-3 chain (TUBB3)	31 [30–32]	18 [10–25]	(55,64)
P-glycoprotein (PGP)	89 [86–92]	37 [24–49]	(55,64)
Transducin-like enhancer protein 3 (TLE3)	22 [21–23]	22 [14–30]	(55,64)
Topoisomerase 2α (TOPO2A)	22 [22–22]	34 [23–45]	(55,64)
Secreted protein acidic and rich in cysteine (SPARC)	36 [32–40]	38 [28–47]	(55,64)
Epidermal growth factor receptor (EGFR)	82 [82–83]	17 [11–23]	(55,64)
Cyclooxygenase-2 (COX-2)	73	11	(55)
Hepatocyte growth factor receptor (cMET)	57 [50–63]	20 [12–27]	(55,64)
Mast/stem cell growth factor receptor Kit isoform 1 (cKIT)	56 [54–58]	20 [15–24]	(55,64)
Platelet-derived growth factor receptors (PDGFR)	59 [58–60]	15 [10–19]	(55,64)

References

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