Table S3. Description of Candidate Germline Variants from Multiplexed, Panel Sequencing of FIGC

Position GRCh38									Frequency Cohorts (nr patients)				Frequency 1000Genomes							
Chr	Coordinate	Patient Genotype	Gene	Transcript ID	cDNA	Type of Variant/Location	Protein	Impact	FIGC (n=50)	HDGC (n=17)	Sporadic GC (n=47)	Variation ID	TSI (n=107)	FIN (n=99)	GBR (n=91)	IBS (n=107)	Global AF	EUR AF	EAS AF	gnomAD
13	32337410	C/G	***BRCA2***	NM_000059.3	c.3055C>G	Missense	p.Leu1019Val	Moderate	1	0	0	rs55638633	1	0	0	0	2,00E-04	1,00E-03	0,00E+00	2,00E-04
1	45331485	G/T	***MUTYH***	NM_001048171.1	c.1216C>A	Missense	p.Leu420Met	Moderate	1	0	0	rs144079536	0	0	0	0	2,00E-04	1,00E-03	0,00E+00	2,00E-04
11	108289671	C/T	***ATM***	NM_000051.3	c.4306C>T	Missense	p.His1436Tyr	Moderate	1	0	0	rs544891616	1	0	0	0	2,00E-04	1,00E-03	0,00E+00	3,26E-05
8	16155081	C/T	***MSR1***	NM_138715.2	c.881G>A	Missense	Gly294Glu	Moderate	1	0	0	rs41440349	0	0	0	0	3,99E-04	0,00E+00	0,00E+00	4,00E-04
8	16168606	G/T	***MSR1***	NM_138715.2	c.482C>A	Missense	p.Thr161Asn	Moderate	1	0	0	rs76147566	1	0	0	0	3,99E-04	1,00E-03	1,00E-03	4,00E-04
22	44726610	C/T	***PRR5***	NM_001017528.2	c.271C>T	Missense	p.Arg91Trp	Moderate	1	0	0	rs201344303	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
2	189795860	C/T	***PMS1***	NM_000534.4	c.224C>T	Missense	p.Thr75Ile	Moderate	1	0	0	rs61756360	0	0	0	0	3,99E-04	0,00E+00	0,00E+00	4,00E-04
10	87965825	C/T	***PTEN***	NM_000314.6	c.*353C>T	3'UTR		Modifier	1	0	0	rs181234898	0	0	0	0	4,99E-03	1,00E-03	7,90E-03	5,00E-03
10	87966260	T/C	***PTEN***	NM_000314.6	c.*788T>C	3'UTR		Modifier	1	0	0	rs138309082	0	0	0	0	4,99E-03	1,00E-03	7,90E-03	5,00E-03
10	87967174	G/A	***PTEN***	NM_000314.6	c.*1702G>A	3'UTR		Modifier	1	0	0	rs150265244	0	0	0	0	4,99E-03	1,00E-03	7,90E-03	5,00E-03
10	87967417	G/A	***PTEN***	NM_000314.6	c.*1945G>A	3'UTR		Modifier	1	0	0	rs567800059	0	0	0	0	4,99E-03	1,00E-03	7,90E-03	5,00E-03
10	87967645	C/T	***PTEN***	NM_000314.6	c.*2173C>T	3'UTR		Modifier	1	0	0	rs186996550	0	0	0	0	7,99E-04	0,00E+00	0,00E+00	8,00E-04
1	27355895	C/T	***MAP3K6***	NM_004672.4	c.3711+131G>A	3'UTR		Modifier	1	0	0	rs554613210	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
10	86924090	C/T	***BMPR1A***	NM_004329.2	c.*371C>T	3'UTR		Modifier	35	0	0	rs550209042	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
3	36993862	C/T	***MLH1***	NM_001167617	c.-202C>T	5'UTR		Modifier	1	0	0	rs561267247	0	0	0	0	2,00E-04	0,00E+00	1,00E-03	2,00E-04
22	44676975	G/A	***PRR5***	NM_001017528.2	c.-11+8170G>A	5'UTR			1	0	0	rs552907174	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
5	112775612	T/A	***APC***	NM_000038.5	c.423-17T>A	Intronic		Modifier	1	0	0	rs534684461	0	0	0	0	3,19E-03	1,00E-03	6,00E-03	3,20E-03
5	147828151	T/A	***SPINK1***	NM_003122.4	c.88-23A>T	Intronic		Modifier	1	0	0	rs199929811	0	0	0	0	3,99E-04	2,00E-03	0,00E+00	4,00E-04
18	51048865	G/A	***SMAD4***	NM_005359.5	c.424+5G>A	Intronic		Low	1	0	0	rs200772603	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
10	86899915	G/A	***BMPR1A***	NM_004329.2	c.430+25G>A	Intronic		Modifier	1	0	0	rs200416589	1	0	0	0	2,80E-03	1,00E-03	0,00E+00	2,80E-03
10	87925641	G/A	***PTEN***	NM_000314.6	c.209+84G>A	Intronic		Modifier	1	0	0	rs185262832	0	0	0	0	4,99E-03	1,00E-03	7,90E-03	5,00E-03
1	27362613	C/T	***MAP3K6***	NM_004672.4	c.1255+28G>A	Intronic		Modifier	1	0	0	rs538360379	1	0	0	0	2,00E-04	1,00E-03	0,00E+00	2,00E-04
2	47791206	T/C	***MSH6***	NM_000179.2	c.457+83T>C	Intronic		Modifier	1	0	0	rs150046242	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
18	51049362	G/C	***SMAD4***	NM_005359.5	c.454+38G>C	Intronic		Modifier	1	0	0	rs201924714	0	0	0	0	2,00E-04	0,00E+00	0,00E+00	2,00E-04
16	86512849	C/T	***FOXF1***	NM_001451.2	c.980-76C>T	Intronic		Modifier	2	0	0	rs139488479	1	0	0	0	3,99E-04	1,00E-03	0,00E+00	4,00E-04
11	108280904	G/T	***ATM***	NM_000051.3	c.3403-91G>T	Intronic		Modifier	1	0	0	rs372950664	1	0	0	0	7,99E-04	1,00E-03	0,00E+00	8,00E-04
7	117666855	C/T	***CFTR***	NM_000492.3	c.4243-53C>T	Intronic		Modifier	1	0	0	rs185664216	1	0	0	0	4,59E-03	1,00E-03	0,00E+00	4,60E-03
7	142751675	G/C	***PRSS1***	NM_002769.4	c.201-99G>C	Intronic		Modifier	1	0	0	rs530207004	1	0	0	0	2,00E-04	1,00E-03	0,00E+00	2,00E-04
7	142750586	C/T	***PRSS1***	NM_002769.4	c.72C>T	Synonymous	p.Ile24=	Low	3	0	0	rs372637371	0	0	0	0	3,99E-04	0,00E+00	2,00E-03	4,00E-04
17	43097246	G/A	***BRCA1***	NM_007294.3	c.591C>T	Synonymous	p.Cys197=	Low	1	0	0	rs1799965	1	0	0	0	3,99E-04	2,00E-03	0,00E+00	4,00E-04
10	86919293	C/T	***BMPR1A***	NM_004329.2	c.990C>T	Synonymous	p.Ala330=	Low	1	0	0	rs199808362	1	0	0	0	2,00E-04	1,00E-03	0,00E+00	2,00E-04

VUS - Variants of Uncertain Significance; NA - Not Available; na - not applicable

							COSMIC	
ExAC	ClinVar clinical significance (variation ID)	Selected for Sanger Validation	Validated by Sanger sequencing	SIFT	PolyPhen	FATHMM	ID	Detected as Somatic in:
1,26E-04	Benign, Likely Benign (37817)	No	na	Tolerated	Benign	NA	NA	NA
5,73E-04	VUS (41752)	Yes	Yes	Deleterious	Benign	NA	NA	NA
5,06E-05	VUS (187606)	Yes	Yes	Deleterious	Benign	NA	NA	NA
7,01E-04	NA	Yes	Yes	Deleterious	Probably damaging	NA	NA	NA
3,54E-04	NA	Yes	Yes	Tolerated	Benign	NA	NA	NA
6,98E-05	NA	Yes	Yes	Deleterious	Probably damaging	NA	NA	NA
6,22E-04	NA	Yes	Yes	Deleterious	Probably damaging	Pathogenic (score 0.99)	COSM6198026	Gastric Cancer
NA	Likely Benign (301429)	Yes	Yes			NA	NA	NA
NA	Likely Benign (301440)	Yes	Yes			NA	NA	NA
NA	Likely Benign (301472)	Yes	Yes			NA	NA	NA
NA	Likely Benign (301475)	Yes	Yes			NA	NA	NA
NA	Likely Benign (301482)	Yes	Yes			NA	NA	NA
NA	NA	Yes	Yes			NA	NA	NA
NA	NA	Yes	No			NA	NA	NA
NA	NA	Yes	Yes			NA	NA	NA
NA	NA	Yes	Yes			NA	NA	NA
1,43E-03	Likely benign (217981)	No	na			NA	NA	NA
2,51E-03	Benign, Likely Benign (239508)	No	na			NA	NA	NA
2,08E-04	VUS (127950)	Yes	Yes			NA	NA	NA
1,73E-03	NA	No	na			NA	NA	NA
NA	NA	No	na			NA	NA	NA
1,32E-05	NA	No	na			NA	NA	NA
NA	NA	No	na			NA	NA	NA
2,05E-04	NA	No	na			NA	NA	NA
NA	NA	No	na			NA	NA	NA
NA	NA	No	na			NA	NA	NA
NA	NA	No	na			NA	NA	NA
NA	NA	Yes	Yes			NA	NA	NA
1,74E-03	NA	No	na			NA	NA	NA
1,54E-03	Benign, Likely Benign (55642)	No	na			Pathogenic (score 0.80)	COSM5020112	Haemangioblastoma
4,07E-06	Likely Benign (184817)	No	na			NA	COSM1559326, COSM35609	Glioma