SUPPLEMENTARY MATERIALS

Supplementary Table 1: FA genes ranked by aggregated carrier frequency for potentially pathogenic germline variants in the Singaporean population and 7 selected ancestry groups from gnomAD[a]

SG (n=3,523)			EAS (n=8,750)			SAS (n=15,067)			AFR (n=7,326)			NFE (n=50,621)			FIN (n=10,664)			ASJ (n=4,738)			AMR (n=16,907)		
Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)	Gene	CC	CF (per 100,000)
FANCA	35	993	*FANCA*	58	663	*FANCM*	95	631	*FANCA*	36	491	*FANCA*	636	1256	*FANCM*	288	2701	*FANCL*	68	1435	*FANCL*	206	1218
FANCM	7	199	*SLX4*	25	286	*FANCA*	89	591	*FANCD2*	27	369	*FANCL*	397	784	*FANCI*	97	910	*FANCA*	26	549	*FANCD2*	164	970
FANCD2	5	142	*ERCC4*	19	217	*FANCG*	85	564	*FANCI*	25	341	*FANCM*	360	711	*FANCA*	42	394	*FANCD2*	6	127	*FANCA*	134	793
FANCG	5	142	*FANCI*	18	206	*ERCC4*	53	352	*FANCL*	24	328	*FANCI*	168	332	*FANCL*	39	366	*XRCC2*	4	84	*FANCI*	68	402
XRCC2	4	114	*FANCM*	15	171	*FANCI*	45	299	*FANCM*	20	273	*FANCD2*	111	219	*FANCD2*	13	122	*ERCC4*	3	63	*FANCM*	48	284
SLX4	3	85	*FANCD2*	14	160	*FANCL*	40	265	*RAD51*	17	232	*ERCC4*	105	207	*ERCC4*	7	66	*FANCI*	2	42	*ERCC4*	25	148
UBE2T	3	85	*RFWD3*	9	103	*SLX4*	28	186	*ERCC4*	14	191	*FANCG*	84	166	*SLX4*	6	56	*FANCC*	1	21	*XRCC2*	23	136
FANCC	2	57	*FANCG*	8	91	*FANCD2*	23	153	*FANCC*	12	164	*FANCC*	80	158	*XRCC2*	6	56	*FANCE*	1	21	*SLX4*	20	118
FANCI	2	57	*FANCL*	7	80	*FANCC*	16	106	*FANCG*	10	137	*SLX4*	77	152	*FANCG*	4	38	*MAD2L2*	1	21	*FANCC*	14	83
FANCL	2	57	*UBE2T*	7	80	*FANCE*	13	86	*FANCF*	6	82	*XRCC2*	61	121	*FANCC*	2	19	*RFWD3*	1	21	*FANCG*	14	83
ERCC4	2	57	*FANCC*	5	57	*FANCF*	10	66	*RFWD3*	6	82	*FANCF*	40	79	*FANCF*	1	9	*FANCB*	0	0	*FANCF*	8	47
RAD51	1	28	*FANCF*	5	57	*RFWD3*	10	66	*FANCE*	5	68	*RFWD3*	29	57	*RAD51*	1	9	*FANCF*	0	0	*UBE2T*	8	47
RFWD3	1	28	*MAD2L2*	3	34	*XRCC2*	8	53	*UBE2T*	5	68	*FANCE*	21	41	*UBE2T*	1	9	*FANCG*	0	0	*RFWD3*	6	35
FANCB	0	0	*FANCE*	1	11	*RAD51*	3	20	*SLX4*	3	41	*MAD2L2*	13	26	*RFWD3*	1	9	*FANCM*	0	0	*FANCE*	4	24
FANCE	0	0	*RAD51*	1	11	*UBE2T*	3	20	*XRCC2*	2	27	*UBE2T*	11	22	*FANCB*	0	0	*SLX4*	0	0	*RAD51*	1	6
FANCF	0	0	*XRCC2*	1	11	*MAD2L2*	1	7	*MAD2L2*	2	27	*RAD51*	2	4	*FANCE*	0	0	*RAD51*	0	0	*MAD2L2*	1	6
MAD2L2	0	0	*FANCB*	0	0	*FANCB*	0	0	*FANCB*	0	0	*FANCB*	0	0	*MAD2L2*	0	0	*UBE2T*	0	0	*FANCB*	0	0
Total carriers (%, adjusted to cohort size)																							
72 (2.0%)			196 (2.2%)			522 (3.5%)			214 (2.9%)			2195 (4.3%)			508 (4.8%)			113 (2.4%)			744 (4.4%)		

[a] SG: Singaporean, EAS: East Asian, SAS: South Asian, AFR: African-American, NFE: Non-Finnish European, FIN: Finnish European, ASJ: Ashkenazi Jewish, AMR: Admixed-American, CC: Carrier count, CF: Carrier frequency.

Supplementary Table 2: Pairwise differences in proportion of germline variant carrier frequency in the 8 ancestry groups evaluated by two-tailed Fisher's exact test, with Bonferroni correction for multiple testing (448 tests)[a]

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
1	*FANCA*	SG	9.93E-03	AFR	4.91E-03	0.006	1
2	*FANCA*	SG	9.93E-03	AMR	7.93E-03	0.261	1
3	*FANCA*	SG	9.93E-03	ASJ	5.49E-03	0.041	1
4	*FANCA*	SG	9.93E-03	EAS	6.63E-03	0.085	1
5	*FANCA*	SG	9.93E-03	FIN	3.94E-03	9.00E-05	0.040
6	*FANCA*	SG	9.93E-03	NFE	1.26E-02	0.159	1
7	*FANCA*	SG	9.93E-03	SAS	5.91E-03	0.011	1
8	*FANCA*	AFR	4.91E-03	AMR	7.93E-03	0.020	1
9	*FANCA*	AFR	4.91E-03	ASJ	5.49E-03	0.615	1
10	*FANCA*	AFR	4.91E-03	EAS	6.63E-03	0.221	1
11	*FANCA*	AFR	4.91E-03	FIN	3.94E-03	0.254	1
12	*FANCA*	AFR	4.91E-03	NFE	1.26E-02	6.6E-10	2.96E-07
13	*FANCA*	AFR	4.91E-03	SAS	5.91E-03	0.570	1
14	*FANCA*	AMR	7.93E-03	ASJ	5.49E-03	0.154	1
15	*FANCA*	AMR	7.93E-03	EAS	6.63E-03	0.288	1
16	*FANCA*	AMR	7.93E-03	FIN	3.94E-03	2.60E-05	1.16E-02
17	*FANCA*	AMR	7.93E-03	NFE	1.26E-02	1.60E-07	7.17E-05
18	*FANCA*	AMR	7.93E-03	SAS	5.91E-03	0.027	1
19	*FANCA*	ASJ	5.49E-03	EAS	6.63E-03	0.652	1
20	*FANCA*	ASJ	5.49E-03	FIN	3.94E-03	0.118	1
21	*FANCA*	ASJ	5.49E-03	NFE	1.26E-02	8.50E-06	3.81E-03
22	*FANCA*	ASJ	5.49E-03	SAS	5.91E-03	1	1
23	*FANCA*	EAS	6.63E-03	FIN	3.94E-03	0.009	1
24	*FANCA*	EAS	6.63E-03	NFE	1.26E-02	3.40E-07	1.52E-04
25	*FANCA*	EAS	6.63E-03	SAS	5.91E-03	0.442	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
26	*FANCA*	FIN	3.94E-03	NFE	1.26E-02	<2.00E-16	<9.00E-14
27	*FANCA*	FIN	3.94E-03	SAS	5.91E-03	0.033	1
28	*FANCA*	NFE	1.26E-02	SAS	5.91E-03	6.10E-14	2.73E-11
29	*FANCC*	SG	5.68E-04	AFR	1.64E-03	0.251	1
30	*FANCC*	SG	5.68E-04	AMR	8.28E-04	0.414	1
31	*FANCC*	SG	5.68E-04	ASJ	2.11E-04	0.579	1
32	*FANCC*	SG	5.68E-04	EAS	5.71E-04	1	1
33	*FANCC*	SG	5.68E-04	FIN	1.88E-04	0.259	1
34	*FANCC*	SG	5.68E-04	NFE	1.58E-03	0.176	1
35	*FANCC*	SG	5.68E-04	SAS	1.06E-03	0.557	1
36	*FANCC*	AFR	1.64E-03	AMR	8.28E-04	0.575	1
37	*FANCC*	AFR	1.64E-03	ASJ	2.11E-04	0.021	1
38	*FANCC*	AFR	1.64E-03	EAS	5.71E-04	0.050	1
39	*FANCC*	AFR	1.64E-03	FIN	1.88E-04	0.001	0.627
40	*FANCC*	AFR	1.64E-03	NFE	1.58E-03	0.875	1
41	*FANCC*	AFR	1.64E-03	SAS	1.06E-03	0.326	1
42	*FANCC*	AMR	8.28E-04	ASJ	2.11E-04	0.042	1
43	*FANCC*	AMR	8.28E-04	EAS	5.71E-04	0.105	1
44	*FANCC*	AMR	8.28E-04	FIN	1.88E-04	0.001	0.582
45	*FANCC*	AMR	8.28E-04	NFE	1.58E-03	0.493	1
46	*FANCC*	AMR	8.28E-04	SAS	1.06E-03	0.749	1
47	*FANCC*	ASJ	2.11E-04	EAS	5.71E-04	0.672	1
48	*FANCC*	ASJ	2.11E-04	FIN	1.88E-04	1	1
49	*FANCC*	ASJ	2.11E-04	NFE	1.58E-03	0.015	1
50	*FANCC*	ASJ	2.11E-04	SAS	1.06E-03	0.093	1
51	*FANCC*	EAS	5.71E-04	FIN	1.88E-04	0.256	1
52	*FANCC*	EAS	5.71E-04	NFE	1.58E-03	0.020	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
53	*FANCC*	EAS	5.71E-04	SAS	1.06E-03	0.192	1
54	*FANCC*	FIN	1.88E-04	NFE	1.58E-03	5.20E-05	0.023
55	*FANCC*	FIN	1.88E-04	SAS	1.06E-03	0.005	1
56	*FANCC*	NFE	1.58E-03	SAS	1.06E-03	0.228	1
57	*FANCD2*	SG	1.42E-03	AFR	3.69E-03	0.039	1
58	*FANCD2*	SG	1.42E-03	AMR	9.70E-03	8.7E-09	3.90E-06
59	*FANCD2*	SG	1.42E-03	ASJ	1.27E-03	1	1
60	*FANCD2*	SG	1.42E-03	EAS	1.60E-03	1	1
61	*FANCD2*	SG	1.42E-03	FIN	1.22E-03	0.786	1
62	*FANCD2*	SG	1.42E-03	NFE	2.19E-03	0.450	1
63	*FANCD2*	SG	1.42E-03	SAS	1.53E-03	1	1
64	*FANCD2*	AFR	3.69E-03	AMR	9.70E-03	5.30E-07	2.37E-04
65	*FANCD2*	AFR	3.69E-03	ASJ	1.27E-03	0.013	1
66	*FANCD2*	AFR	3.69E-03	EAS	1.60E-03	0.008	1
67	*FANCD2*	AFR	3.69E-03	FIN	1.22E-03	6.20E-04	0.278
68	*FANCD2*	AFR	3.69E-03	NFE	2.19E-03	0.014	1
69	*FANCD2*	AFR	3.69E-03	SAS	1.53E-03	0.001	0.632
70	*FANCD2*	AMR	9.70E-03	ASJ	1.27E-03	1.7E-11	7.62E-09
71	*FANCD2*	AMR	9.70E-03	EAS	1.60E-03	<2.00E-16	9.12E-14
72	*FANCD2*	AMR	9.70E-03	FIN	1.22E-03	<2.00E-16	<9.00E-14
73	*FANCD2*	AMR	9.70E-03	NFE	2.19E-03	<2.00E-16	<9.00E-14
74	*FANCD2*	AMR	9.70E-03	SAS	1.53E-03	<2.00E-16	<9.00E-14
75	*FANCD2*	ASJ	1.27E-03	EAS	1.60E-03	0.815	1
76	*FANCD2*	ASJ	1.27E-03	FIN	1.22E-03	1	1
77	*FANCD2*	ASJ	1.27E-03	NFE	2.19E-03	0.244	1
78	*FANCD2*	ASJ	1.27E-03	SAS	1.53E-03	0.829	1
79	*FANCD2*	EAS	1.60E-03	FIN	1.22E-03	0.563	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
80	*FANCD2*	EAS	1.60E-03	NFE	2.19E-03	0.312	1
81	*FANCD2*	EAS	1.60E-03	SAS	1.53E-03	0.866	1
82	*FANCD2*	FIN	1.22E-03	NFE	2.19E-03	0.043	1
83	*FANCD2*	FIN	1.22E-03	SAS	1.53E-03	0.613	1
84	*FANCD2*	NFE	2.19E-03	SAS	1.53E-03	0.123	1
85	*FANCE*	SG	0	AFR	6.83E-04	0.013	1
86	*FANCE*	SG	0	AMR	2.37E-04	0.612	1
87	*FANCE*	SG	0	ASJ	2.11E-04	1	1
88	*FANCE*	SG	0	EAS	1.14E-04	1	1
89	*FANCE*	SG	0	FIN	0	1	1
90	*FANCE*	SG	0	NFE	4.15E-04	0.397	1
91	*FANCE*	SG	0	SAS	8.63E-04	0.087	1
92	*FANCE*	AFR	6.83E-04	AMR	2.37E-04	0.002	0.950
93	*FANCE*	AFR	6.83E-04	ASJ	2.11E-04	0.013	1
94	*FANCE*	AFR	6.83E-04	EAS	1.14E-04	4.90E-04	0.220
95	*FANCE*	AFR	6.83E-04	FIN	0	8.40E-06	3.76E-03
96	*FANCE*	AFR	6.83E-04	NFE	4.15E-04	2.00E-04	0.090
97	*FANCE*	AFR	6.83E-04	SAS	8.63E-04	0.101	1
98	*FANCE*	AMR	2.37E-04	ASJ	2.11E-04	1	1
99	*FANCE*	AMR	2.37E-04	EAS	1.14E-04	0.279	1
100	*FANCE*	AMR	2.37E-04	FIN	0	0.048	1
101	*FANCE*	AMR	2.37E-04	NFE	4.15E-04	1	1
102	*FANCE*	AMR	2.37E-04	SAS	8.63E-04	0.082	1
103	*FANCE*	ASJ	2.11E-04	EAS	1.14E-04	1	1
104	*FANCE*	ASJ	2.11E-04	FIN	0	0.308	1
105	*FANCE*	ASJ	2.11E-04	NFE	4.15E-04	0.717	1
106	*FANCE*	ASJ	2.11E-04	SAS	8.63E-04	0.140	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
107	*FANCE*	EAS	1.14E-04	FIN	0	0.451	1
108	*FANCE*	EAS	1.14E-04	NFE	4.15E-04	0.238	1
109	*FANCE*	EAS	1.14E-04	SAS	8.63E-04	0.014	1
110	*FANCE*	FIN	0	NFE	4.15E-04	0.023	1
111	*FANCE*	FIN	0	SAS	8.63E-04	6.50E-04	0.291
112	*FANCE*	NFE	4.15E-04	SAS	8.63E-04	0.029	1
113	*FANCF*	SG	0	AFR	8.19E-04	0.187	1
114	*FANCF*	SG	0	AMR	4.73E-04	0.366	1
115	*FANCF*	SG	0	ASJ	0	1	1
116	*FANCF*	SG	0	EAS	5.71E-04	0.331	1
117	*FANCF*	SG	0	FIN	9.38E-05	1	1
118	*FANCF*	SG	0	NFE	7.90E-04	0.111	1
119	*FANCF*	SG	0	SAS	6.64E-04	0.225	1
120	*FANCF*	AFR	8.19E-04	AMR	4.73E-04	0.382	1
121	*FANCF*	AFR	8.19E-04	ASJ	0	0.088	1
122	*FANCF*	AFR	8.19E-04	EAS	5.71E-04	0.562	1
123	*FANCF*	AFR	8.19E-04	FIN	9.38E-05	0.021	1
124	*FANCF*	AFR	8.19E-04	NFE	7.90E-04	1	1
125	*FANCF*	AFR	8.19E-04	SAS	6.64E-04	0.791	1
126	*FANCF*	AMR	4.73E-04	ASJ	0	0.214	1
127	*FANCF*	AMR	4.73E-04	EAS	5.71E-04	0.773	1
128	*FANCF*	AMR	4.73E-04	FIN	9.38E-05	0.167	1
129	*FANCF*	AMR	4.73E-04	NFE	7.90E-04	0.188	1
130	*FANCF*	AMR	4.73E-04	SAS	6.64E-04	0.490	1
131	*FANCF*	ASJ	0	EAS	5.71E-04	0.170	1
132	*FANCF*	ASJ	0	FIN	9.38E-05	1	1
133	*FANCF*	ASJ	0	NFE	7.90E-04	0.047	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
134	*FANCF*	ASJ	0	SAS	6.64E-04	0.131	1
135	*FANCF*	EAS	5.71E-04	FIN	9.38E-05	0.097	1
136	*FANCF*	EAS	5.71E-04	NFE	7.90E-04	0.676	1
137	*FANCF*	EAS	5.71E-04	SAS	6.64E-04	1	1
138	*FANCF*	FIN	9.38E-05	NFE	7.90E-04	0.007	1
139	*FANCF*	FIN	9.38E-05	SAS	6.64E-04	0.032	1
140	*FANCF*	NFE	7.90E-04	SAS	6.64E-04	0.739	1
141	*FANCG*	SG	1.42E-03	AFR	1.37E-03	1	1
142	*FANCG*	SG	1.42E-03	AMR	8.28E-04	0.355	1
143	*FANCG*	SG	1.42E-03	ASJ	0	0.014	1
144	*FANCG*	SG	1.42E-03	EAS	9.14E-04	0.539	1
145	*FANCG*	SG	1.42E-03	FIN	3.75E-04	0.048	1
146	*FANCG*	SG	1.42E-03	NFE	1.66E-03	1	1
147	*FANCG*	SG	1.42E-03	SAS	5.64E-03	3.90E-04	0.175
148	*FANCG*	AFR	1.37E-03	AMR	8.28E-04	0.265	1
149	*FANCG*	AFR	1.37E-03	ASJ	0	0.008	1
150	*FANCG*	AFR	1.37E-03	EAS	9.14E-04	0.480	1
151	*FANCG*	AFR	1.37E-03	FIN	3.75E-04	0.027	1
152	*FANCG*	AFR	1.37E-03	NFE	1.66E-03	0.643	1
153	*FANCG*	AFR	1.37E-03	SAS	5.64E-03	8.00E-07	3.58E-04
154	*FANCG*	AMR	8.28E-04	ASJ	0	0.050	1
155	*FANCG*	AMR	8.28E-04	EAS	9.14E-04	0.824	1
156	*FANCG*	AMR	8.28E-04	FIN	3.75E-04	0.225	1
157	*FANCG*	AMR	8.28E-04	NFE	1.66E-03	0.014	1
158	*FANCG*	AMR	8.28E-04	SAS	5.64E-03	1.2E-15	5.38E-13
159	*FANCG*	ASJ	0	EAS	9.14E-04	0.057	1
160	*FANCG*	ASJ	0	FIN	3.75E-04	0.319	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
161	*FANCG*	ASJ	0	NFE	1.66E-03	0.001	0.547
162	*FANCG*	ASJ	0	SAS	5.64E-03	1E-10	4.48E-08
163	*FANCG*	EAS	9.14E-04	FIN	3.75E-04	0.154	1
164	*FANCG*	EAS	9.14E-04	NFE	1.66E-03	0.107	1
165	*FANCG*	EAS	9.14E-04	SAS	5.64E-03	7.9E-10	3.54E-07
166	*FANCG*	FIN	3.75E-04	NFE	1.66E-03	5.80E-04	0.260
167	*FANCG*	FIN	3.75E-04	SAS	5.64E-03	1.9E-15	8.51E-13
168	*FANCG*	NFE	1.66E-03	SAS	5.64E-03	9.7E-15	4.35E-12
169	*FANCI*	SG	5.68E-04	AFR	3.41E-03	0.003	1
170	*FANCI*	SG	5.68E-04	AMR	4.02E-03	3.70E-04	0.166
171	*FANCI*	SG	5.68E-04	ASJ	4.22E-04	1	1
172	*FANCI*	SG	5.68E-04	EAS	2.06E-03	0.082	1
173	*FANCI*	SG	5.68E-04	FIN	9.10E-03	4.9E-10	2.20E-07
174	*FANCI*	SG	5.68E-04	NFE	3.32E-03	1.58E-03	0.708
175	*FANCI*	SG	5.68E-04	SAS	2.99E-03	0.008	1
176	*FANCI*	AFR	3.41E-03	AMR	4.02E-03	0.572	1
177	*FANCI*	AFR	3.41E-03	ASJ	4.22E-04	4.90E-04	0.220
178	*FANCI*	AFR	3.41E-03	EAS	2.06E-03	0.124	1
179	*FANCI*	AFR	3.41E-03	FIN	9.10E-03	2.80E-06	1.25E-03
180	*FANCI*	AFR	3.41E-03	NFE	3.32E-03	0.913	1
181	*FANCI*	AFR	3.41E-03	SAS	2.99E-03	0.611	1
182	*FANCI*	AMR	4.02E-03	ASJ	4.22E-04	1.40E-05	6.27E-03
183	*FANCI*	AMR	4.02E-03	EAS	2.06E-03	0.009	1
184	*FANCI*	AMR	4.02E-03	FIN	9.10E-03	2.00E-07	8.96E-05
185	*FANCI*	AMR	4.02E-03	NFE	3.32E-03	0.176	1
186	*FANCI*	AMR	4.02E-03	SAS	2.99E-03	0.131	1
187	*FANCI*	ASJ	4.22E-04	EAS	2.06E-03	0.018	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
188	*FANCI*	ASJ	4.22E-04	FIN	9.10E-03	1.80E-13	8.06E-11
189	*FANCI*	ASJ	4.22E-04	NFE	3.32E-03	8.20E-05	0.037
190	*FANCI*	ASJ	4.22E-04	SAS	2.99E-03	4.80E-04	0.215
191	*FANCI*	EAS	2.06E-03	FIN	9.10E-03	2.40E-11	1.08E-08
192	*FANCI*	EAS	2.06E-03	NFE	3.32E-03	0.049	1
193	*FANCI*	EAS	2.06E-03	SAS	2.99E-03	0.193	1
194	*FANCI*	FIN	9.10E-03	NFE	3.32E-03	9.70E-14	4.35E-11
195	*FANCI*	FIN	9.10E-03	SAS	2.99E-03	1.00E-10	4.48E-08
196	*FANCI*	NFE	3.32E-03	SAS	2.99E-03	0.568	1
197	*FANCL*	SG	5.68E-04	AFR	3.28E-03	0.005	1
198	*FANCL*	SG	5.68E-04	AMR	1.22E-02	1.40E-14	6.27E-12
199	*FANCL*	SG	5.68E-04	ASJ	1.44E-02	2.50E-14	1.12E-11
200	*FANCL*	SG	5.68E-04	EAS	8.00E-04	1	1
201	*FANCL*	SG	5.68E-04	FIN	3.66E-03	0.002	0.726
202	*FANCL*	SG	5.68E-04	NFE	7.84E-03	1.40E-09	6.27E-07
203	*FANCL*	SG	5.68E-04	SAS	2.65E-03	0.016	1
204	*FANCL*	AFR	3.28E-03	AMR	1.22E-02	9.10E-13	4.08E-10
205	*FANCL*	AFR	3.28E-03	ASJ	1.44E-02	1.90E-11	8.51E-09
206	*FANCL*	AFR	3.28E-03	EAS	8.00E-04	4.20E-04	0.188
207	*FANCL*	AFR	3.28E-03	FIN	3.66E-03	0.702	1
208	*FANCL*	AFR	3.28E-03	NFE	7.84E-03	3.00E-06	1.34E-03
209	*FANCL*	AFR	3.28E-03	SAS	2.65E-03	0.425	1
210	*FANCL*	AMR	1.22E-02	ASJ	1.44E-02	0.240	1
211	*FANCL*	AMR	1.22E-02	EAS	8.00E-04	<2.00E-16	<9.00E-14
212	*FANCL*	AMR	1.22E-02	FIN	3.66E-03	9.90E-15	4.44E-12
213	*FANCL*	AMR	1.22E-02	NFE	7.84E-03	5.10E-07	2.28E-04
214	*FANCL*	AMR	1.22E-02	SAS	2.65E-03	<2.00E-16	<9.00E-14

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
215	*FANCL*	ASJ	1.44E-02	EAS	8.00E-04	<2.00E-16	<9.00E-14
216	*FANCL*	ASJ	1.44E-02	FIN	3.66E-03	4.00E-12	1.79E-09
217	*FANCL*	ASJ	1.44E-02	NFE	7.84E-03	1.80E-05	8.06E-03
218	*FANCL*	ASJ	1.44E-02	SAS	2.65E-03	<2.00E-16	<9.00E-14
219	*FANCL*	EAS	8.00E-04	FIN	3.66E-03	3.60E-05	1.61E-02
220	*FANCL*	EAS	8.00E-04	NFE	7.84E-03	<2.00E-16	<9.00E-14
221	*FANCL*	EAS	8.00E-04	SAS	2.65E-03	0.001	0.582
222	*FANCL*	FIN	3.66E-03	NFE	7.84E-03	6.40E-07	2.87E-04
223	*FANCL*	FIN	3.66E-03	SAS	2.65E-03	0.170	1
224	*FANCL*	NFE	7.84E-03	SAS	2.65E-03	5.50E-14	2.46E-11
225	*FANCM*	SG	1.99E-03	AFR	2.73E-03	0.542	1
226	*FANCM*	SG	1.99E-03	AMR	2.84E-03	0.475	1
227	*FANCM*	SG	1.99E-03	ASJ	0	0.003	1
228	*FANCM*	SG	1.99E-03	EAS	1.71E-03	0.814	1
229	*FANCM*	SG	1.99E-03	FIN	2.70E-02	<2.00E-16	<9.00E-14
230	*FANCM*	SG	1.99E-03	NFE	7.11E-03	6.90E-05	0.031
231	*FANCM*	SG	1.99E-03	SAS	6.31E-03	8.70E-04	0.390
232	*FANCM*	AFR	2.73E-03	AMR	2.84E-03	1	1
233	*FANCM*	AFR	2.73E-03	ASJ	0	8.10E-05	0.036
234	*FANCM*	AFR	2.73E-03	EAS	1.71E-03	0.178	1
235	*FANCM*	AFR	2.73E-03	FIN	2.70E-02	<2.00E-16	<9.00E-14
236	*FANCM*	AFR	2.73E-03	NFE	7.11E-03	2.70E-06	1.21E-03
237	*FANCM*	AFR	2.73E-03	SAS	6.31E-03	3.00E-04	0.134
238	*FANCM*	AMR	2.84E-03	ASJ	0	1.10E-05	4.93E-03
239	*FANCM*	AMR	2.84E-03	EAS	1.71E-03	0.109	1
240	*FANCM*	AMR	2.84E-03	FIN	2.70E-02	<2.00E-16	<9.00E-14
241	*FANCM*	AMR	2.84E-03	NFE	7.11E-03	2.70E-11	1.21E-08

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
242	*FANCM*	AMR	2.84E-03	SAS	6.31E-03	4.50E-06	2.02E-03
243	*FANCM*	ASJ	0	EAS	1.71E-03	0.002	0.896
244	*FANCM*	ASJ	0	FIN	2.70E-02	<2.00E-16	<9.00E-14
245	*FANCM*	ASJ	0	NFE	7.11E-03	1.50E-14	6.72E-12
246	*FANCM*	ASJ	0	SAS	6.31E-03	1.10E-11	4.93E-09
247	*FANCM*	EAS	1.71E-03	FIN	2.70E-02	<2.00E-16	<9.00E-14
248	*FANCM*	EAS	1.71E-03	NFE	7.11E-03	2.20E-11	9.86E-09
249	*FANCM*	EAS	1.71E-03	SAS	6.31E-03	8.50E-08	3.81E-05
250	*FANCM*	FIN	2.70E-02	NFE	7.11E-03	<2.00E-16	<9.00E-14
251	*FANCM*	FIN	2.70E-02	SAS	6.31E-03	<2.00E-16	<9.00E-14
252	*FANCM*	NFE	7.11E-03	SAS	6.31E-03	0.314	1
253	*SLX4*	SG	8.52E-04	AFR	4.10E-04	0.397	1
254	*SLX4*	SG	8.52E-04	AMR	1.18E-03	0.785	1
255	*SLX4*	SG	8.52E-04	ASJ	0	0.078	1
256	*SLX4*	SG	8.52E-04	EAS	2.86E-03	0.036	1
257	*SLX4*	SG	8.52E-04	FIN	5.63E-04	0.699	1
258	*SLX4*	SG	8.52E-04	NFE	1.52E-03	0.494	1
259	*SLX4*	SG	8.52E-04	SAS	1.86E-03	0.252	1
260	*SLX4*	AFR	4.10E-04	AMR	1.18E-03	0.109	1
261	*SLX4*	AFR	4.10E-04	ASJ	0	0.284	1
262	*SLX4*	AFR	4.10E-04	EAS	2.86E-03	1.70E-04	0.076
263	*SLX4*	AFR	4.10E-04	FIN	5.63E-04	0.746	1
264	*SLX4*	AFR	4.10E-04	NFE	1.52E-03	0.011	1
265	*SLX4*	AFR	4.10E-04	SAS	1.86E-03	0.006	1
266	*SLX4*	AMR	1.18E-03	ASJ	0	0.012	1
267	*SLX4*	AMR	1.18E-03	EAS	2.86E-03	0.004	1
268	*SLX4*	AMR	1.18E-03	FIN	5.63E-04	0.111	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
269	*SLX4*	AMR	1.18E-03	NFE	1.52E-03	0.350	1
270	*SLX4*	AMR	1.18E-03	SAS	1.86E-03	0.147	1
271	*SLX4*	ASJ	0	EAS	2.86E-03	2.50E-05	1.12E-02
272	*SLX4*	ASJ	0	FIN	5.63E-04	0.187	1
273	*SLX4*	ASJ	0	NFE	1.52E-03	0.002	0.784
274	*SLX4*	ASJ	0	SAS	1.86E-03	6.40E-04	0.287
275	*SLX4*	EAS	2.86E-03	FIN	5.63E-04	7.80E-05	0.035
276	*SLX4*	EAS	2.86E-03	NFE	1.52E-03	0.011	1
277	*SLX4*	EAS	2.86E-03	SAS	1.86E-03	0.119	1
278	*SLX4*	FIN	5.63E-04	NFE	1.52E-03	0.009	1
279	*SLX4*	FIN	5.63E-04	SAS	1.86E-03	0.005	1
280	*SLX4*	NFE	1.52E-03	SAS	1.86E-03	0.418	1
281	*ERCC4*	SG	5.68E-04	AFR	1.91E-03	0.110	1
282	*ERCC4*	SG	5.68E-04	AMR	1.48E-03	0.303	1
283	*ERCC4*	SG	5.68E-04	ASJ	6.33E-04	1	1
284	*ERCC4*	SG	5.68E-04	EAS	2.17E-03	0.036	1
285	*ERCC4*	SG	5.68E-04	FIN	6.56E-04	1	1
286	*ERCC4*	SG	5.68E-04	NFE	2.07E-03	0.048	1
287	*ERCC4*	SG	5.68E-04	SAS	3.52E-03	0.002	0.708
288	*ERCC4*	AFR	1.91E-03	AMR	1.48E-03	0.485	1
289	*ERCC4*	AFR	1.91E-03	ASJ	6.33E-04	0.083	1
290	*ERCC4*	AFR	1.91E-03	EAS	2.17E-03	0.611	1
291	*ERCC4*	AFR	1.91E-03	FIN	6.56E-04	0.024	1
292	*ERCC4*	AFR	1.91E-03	NFE	2.07E-03	0.890	1
293	*ERCC4*	AFR	1.91E-03	SAS	3.52E-03	0.049	1
294	*ERCC4*	AMR	1.48E-03	ASJ	6.33E-04	0.176	1
295	*ERCC4*	AMR	1.48E-03	EAS	2.17E-03	0.119	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
296	*ERCC4*	AMR	1.48E-03	FIN	6.56E-04	0.068	1
297	*ERCC4*	AMR	1.48E-03	NFE	2.07E-03	0.155	1
298	*ERCC4*	AMR	1.48E-03	SAS	3.52E-03	2.40E-04	0.108
299	*ERCC4*	ASJ	6.33E-04	EAS	2.17E-03	0.018	1
300	*ERCC4*	ASJ	6.33E-04	FIN	6.56E-04	1	1
301	*ERCC4*	ASJ	6.33E-04	NFE	2.07E-03	0.025	1
302	*ERCC4*	ASJ	6.33E-04	SAS	3.52E-03	4.20E-04	0.188
303	*ERCC4*	EAS	2.17E-03	FIN	6.56E-04	0.002	0.829
304	*ERCC4*	EAS	2.17E-03	NFE	2.07E-03	0.529	1
305	*ERCC4*	EAS	2.17E-03	SAS	3.52E-03	0.148	1
306	*ERCC4*	FIN	6.56E-04	NFE	2.07E-03	0.001	0.452
307	*ERCC4*	FIN	6.56E-04	SAS	3.52E-03	5.90E-07	2.64E-04
308	*ERCC4*	NFE	2.07E-03	SAS	3.52E-03	0.002	1
309	*RAD51*	SG	2.84E-04	AFR	2.32E-03	0.011	1
310	*RAD51*	SG	2.84E-04	AMR	5.91E-05	0.315	1
311	*RAD51*	SG	2.84E-04	ASJ	0	0.426	1
312	*RAD51*	SG	2.84E-04	EAS	1.14E-04	0.492	1
313	*RAD51*	SG	2.84E-04	FIN	9.38E-05	0.435	1
314	*RAD51*	SG	2.84E-04	NFE	3.95E-05	0.236	1
315	*RAD51*	SG	2.84E-04	SAS	1.99E-04	1	1
316	*RAD51*	AFR	2.32E-03	AMR	5.91E-05	1.90E-08	8.51E-06
317	*RAD51*	AFR	2.32E-03	ASJ	0	2.50E-04	0.112
318	*RAD51*	AFR	2.32E-03	EAS	1.14E-04	1.60E-05	7.17E-03
319	*RAD51*	AFR	2.32E-03	FIN	9.38E-05	2.60E-06	1.16E-03
320	*RAD51*	AFR	2.32E-03	NFE	3.95E-05	4.10E-13	1.84E-10
321	*RAD51*	AFR	2.32E-03	SAS	1.99E-04	7.60E-06	3.40E-03
322	*RAD51*	AMR	5.91E-05	ASJ	0	1	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
323	*RAD51*	AMR	5.91E-05	EAS	1.14E-04	1	1
324	*RAD51*	AMR	5.91E-05	FIN	9.38E-05	1	1
325	*RAD51*	AMR	5.91E-05	NFE	3.95E-05	1	1
326	*RAD51*	AMR	5.91E-05	SAS	1.99E-04	0.195	1
327	*RAD51*	ASJ	0	EAS	1.14E-04	1	1
328	*RAD51*	ASJ	0	FIN	9.38E-05	1	1
329	*RAD51*	ASJ	0	NFE	3.95E-05	1	1
330	*RAD51*	ASJ	0	SAS	1.99E-04	0.579	1
331	*RAD51*	EAS	1.14E-04	FIN	9.38E-05	1	1
332	*RAD51*	EAS	1.14E-04	NFE	3.95E-05	0.472	1
333	*RAD51*	EAS	1.14E-04	SAS	1.99E-04	0.658	1
334	*RAD51*	FIN	9.38E-05	NFE	3.95E-05	0.535	1
335	*RAD51*	FIN	9.38E-05	SAS	1.99E-04	0.411	1
336	*RAD51*	NFE	3.95E-05	SAS	1.99E-04	0.053	1
337	*UBE2T*	SG	8.52E-04	AFR	6.83E-04	0.720	1
338	*UBE2T*	SG	8.52E-04	AMR	4.73E-04	0.416	1
339	*UBE2T*	SG	8.52E-04	ASJ	0	0.078	1
340	*UBE2T*	SG	8.52E-04	EAS	8.00E-04	1	1
341	*UBE2T*	SG	8.52E-04	FIN	9.38E-05	0.050	1
342	*UBE2T*	SG	8.52E-04	NFE	2.17E-04	0.058	1
343	*UBE2T*	SG	8.52E-04	SAS	1.99E-04	0.086	1
344	*UBE2T*	AFR	6.83E-04	AMR	4.73E-04	0.550	1
345	*UBE2T*	AFR	6.83E-04	ASJ	0	0.164	1
346	*UBE2T*	AFR	6.83E-04	EAS	8.00E-04	1	1
347	*UBE2T*	AFR	6.83E-04	FIN	9.38E-05	0.044	1
348	*UBE2T*	AFR	6.83E-04	NFE	2.17E-04	0.042	1
349	*UBE2T*	AFR	6.83E-04	SAS	1.99E-04	0.124	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
350	*UBE2T*	AMR	4.73E-04	ASJ	0	0.214	1
351	*UBE2T*	AMR	4.73E-04	EAS	8.00E-04	0.414	1
352	*UBE2T*	AMR	4.73E-04	FIN	9.38E-05	0.167	1
353	*UBE2T*	AMR	4.73E-04	NFE	2.17E-04	0.109	1
354	*UBE2T*	AMR	4.73E-04	SAS	1.99E-04	0.235	1
355	*UBE2T*	ASJ	0	EAS	8.00E-04	0.105	1
356	*UBE2T*	ASJ	0	FIN	9.38E-05	1	1
357	*UBE2T*	ASJ	0	NFE	2.17E-04	0.615	1
358	*UBE2T*	ASJ	0	SAS	1.99E-04	1	1
359	*UBE2T*	EAS	8.00E-04	FIN	9.38E-05	0.027	1
360	*UBE2T*	EAS	8.00E-04	NFE	2.17E-04	0.011	1
361	*UBE2T*	EAS	8.00E-04	SAS	1.99E-04	0.044	1
362	*UBE2T*	FIN	9.38E-05	NFE	2.17E-04	0.705	1
363	*UBE2T*	FIN	9.38E-05	SAS	1.99E-04	0.647	1
364	*UBE2T*	NFE	2.17E-04	SAS	1.99E-04	1	1
365	*XRCC2*	SG	1.14E-03	AFR	2.73E-04	0.092	1
366	*XRCC2*	SG	1.14E-03	AMR	1.36E-03	1	1
367	*XRCC2*	SG	1.14E-03	ASJ	8.44E-04	0.730	1
368	*XRCC2*	SG	1.14E-03	EAS	1.14E-04	0.026	1
369	*XRCC2*	SG	1.14E-03	FIN	5.63E-04	0.278	1
370	*XRCC2*	SG	1.14E-03	NFE	1.21E-03	1	1
371	*XRCC2*	SG	1.14E-03	SAS	5.31E-04	0.259	1
372	*XRCC2*	AFR	2.73E-04	AMR	1.36E-03	0.015	1
373	*XRCC2*	AFR	2.73E-04	ASJ	8.44E-04	0.219	1
374	*XRCC2*	AFR	2.73E-04	EAS	1.14E-04	0.595	1
375	*XRCC2*	AFR	2.73E-04	FIN	5.63E-04	0.485	1
376	*XRCC2*	AFR	2.73E-04	NFE	1.21E-03	0.021	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
377	*XRCC2*	AFR	2.73E-04	SAS	5.31E-04	0.514	1
378	*XRCC2*	AMR	1.36E-03	ASJ	8.44E-04	0.488	1
379	*XRCC2*	AMR	1.36E-03	EAS	1.14E-04	8.60E-04	0.385
380	*XRCC2*	AMR	1.36E-03	FIN	5.63E-04	0.056	1
381	*XRCC2*	AMR	1.36E-03	NFE	1.21E-03	0.615	1
382	*XRCC2*	AMR	1.36E-03	SAS	5.31E-04	0.019	1
383	*XRCC2*	ASJ	8.44E-04	EAS	1.14E-04	0.055	1
384	*XRCC2*	ASJ	8.44E-04	FIN	5.63E-04	0.509	1
385	*XRCC2*	ASJ	8.44E-04	NFE	1.21E-03	0.657	1
386	*XRCC2*	ASJ	8.44E-04	SAS	5.31E-04	0.497	1
387	*XRCC2*	EAS	1.14E-04	FIN	5.63E-04	0.138	1
388	*XRCC2*	EAS	1.14E-04	NFE	1.21E-03	9.90E-04	0.444
389	*XRCC2*	EAS	1.14E-04	SAS	5.31E-04	0.168	1
390	*XRCC2*	FIN	5.63E-04	NFE	1.21E-03	0.075	1
391	*XRCC2*	FIN	5.63E-04	SAS	5.31E-04	1	1
392	*XRCC2*	NFE	1.21E-03	SAS	5.31E-04	0.022	1
393	*MAD2L2*	SG	0	AFR	2.73E-04	0.092	1
394	*MAD2L2*	SG	0	AMR	5.91E-05	0.004	1
395	*MAD2L2*	SG	0	ASJ	2.11E-04	0.171	1
396	*MAD2L2*	SG	0	EAS	3.43E-04	0.110	1
397	*MAD2L2*	SG	0	FIN	0	0.004	1
398	*MAD2L2*	SG	0	NFE	2.57E-04	0.022	1
399	*MAD2L2*	SG	0	SAS	6.64E-05	0.006	1
400	*MAD2L2*	AFR	2.73E-04	AMR	5.91E-05	0.219	1
401	*MAD2L2*	AFR	2.73E-04	ASJ	2.11E-04	1	1
402	*MAD2L2*	AFR	2.73E-04	EAS	3.43E-04	1	1
403	*MAD2L2*	AFR	2.73E-04	FIN	0	0.166	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
404	*MAD2L2*	AFR	2.73E-04	NFE	2.57E-04	1	1
405	*MAD2L2*	AFR	2.73E-04	SAS	6.64E-05	0.251	1
406	*MAD2L2*	AMR	5.91E-05	ASJ	2.11E-04	0.390	1
407	*MAD2L2*	AMR	5.91E-05	EAS	3.43E-04	0.118	1
408	*MAD2L2*	AMR	5.91E-05	FIN	0	1	1
409	*MAD2L2*	AMR	5.91E-05	NFE	2.57E-04	0.213	1
410	*MAD2L2*	AMR	5.91E-05	SAS	6.64E-05	1	1
411	*MAD2L2*	ASJ	2.11E-04	EAS	3.43E-04	1	1
412	*MAD2L2*	ASJ	2.11E-04	FIN	0	0.308	1
413	*MAD2L2*	ASJ	2.11E-04	NFE	2.57E-04	1	1
414	*MAD2L2*	ASJ	2.11E-04	SAS	6.64E-05	0.421	1
415	*MAD2L2*	EAS	3.43E-04	FIN	0	0.092	1
416	*MAD2L2*	EAS	3.43E-04	NFE	2.57E-04	0.720	1
417	*MAD2L2*	EAS	3.43E-04	SAS	6.64E-05	0.144	1
418	*MAD2L2*	FIN	0	NFE	2.57E-04	0.143	1
419	*MAD2L2*	FIN	0	SAS	6.64E-05	1	1
420	*MAD2L2*	NFE	2.57E-04	SAS	6.64E-05	0.213	1
421	*RFWD3*	SG	2.84E-04	AFR	8.19E-04	0.440	1
422	*RFWD3*	SG	2.84E-04	AMR	3.55E-04	1	1
423	*RFWD3*	SG	2.84E-04	ASJ	2.11E-04	1	1
424	*RFWD3*	SG	2.84E-04	EAS	1.03E-03	0.299	1
425	*RFWD3*	SG	2.84E-04	FIN	9.38E-05	0.435	1
426	*RFWD3*	SG	2.84E-04	NFE	5.73E-04	0.720	1
427	*RFWD3*	SG	2.84E-04	SAS	6.64E-04	0.702	1
428	*RFWD3*	AFR	8.19E-04	AMR	3.55E-04	0.204	1
429	*RFWD3*	AFR	8.19E-04	ASJ	2.11E-04	0.258	1
430	*RFWD3*	AFR	8.19E-04	EAS	1.03E-03	0.798	1

No.	Gene	Ancestry group 1	Cohort size-normalized carrier frequency (Ancestry group 1)	Ancestry group 2	Cohort size-normalized carrier frequency (Ancestry group 2)	Unadjusted p-value	Bonferroni-corrected p-value
431	*RFWD3*	AFR	8.19E-04	FIN	9.38E-05	0.021	1
432	*RFWD3*	AFR	8.19E-04	NFE	5.73E-04	0.441	1
433	*RFWD3*	AFR	8.19E-04	SAS	6.64E-04	0.790	1
434	*RFWD3*	AMR	3.55E-04	ASJ	2.11E-04	1	1
435	*RFWD3*	AMR	3.55E-04	EAS	1.03E-03	0.052	1
436	*RFWD3*	AMR	3.55E-04	FIN	9.38E-05	0.261	1
437	*RFWD3*	AMR	3.55E-04	NFE	5.73E-04	0.334	1
438	*RFWD3*	AMR	3.55E-04	SAS	6.64E-04	0.317	1
439	*RFWD3*	ASJ	2.11E-04	EAS	1.03E-03	0.181	1
440	*RFWD3*	ASJ	2.11E-04	FIN	9.38E-05	0.521	1
441	*RFWD3*	ASJ	2.11E-04	NFE	5.73E-04	0.512	1
442	*RFWD3*	ASJ	2.11E-04	SAS	6.64E-04	0.478	1
443	*RFWD3*	EAS	1.03E-03	FIN	9.38E-05	0.007	1
444	*RFWD3*	EAS	1.03E-03	NFE	5.73E-04	0.164	1
445	*RFWD3*	EAS	1.03E-03	SAS	6.64E-04	0.349	1
446	*RFWD3*	FIN	9.38E-05	NFE	5.73E-04	0.050	1
447	*RFWD3*	FIN	9.38E-05	SAS	6.64E-04	0.032	1
448	*RFWD3*	NFE	5.73E-04	SAS	6.64E-04	0.703	1

[a] Adjusted p value threshold of <0.05 is considered significant event. SG: Singaporean, EAS: East Asian, SAS: South Asian, AFR: African-American, NFE: Non-Finnish European, FIN: Finnish European, ASJ: Ashkenazi Jewish, AMR: Admixed-American/Latino.

Supplementary Table 3: Alleles with highest frequencies for each of the investigated 17 FA genes across the 8 ancestry groups[a]

Gene	SG			EAS			SAS			AFR			NFE			FIN			ASJ			AMR		
	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF
FANCA	c.3068A>G (p.Glu1023Gly)	12	1.70E-03	c.3068A>G (p.Glu1023Gly)	19	1.07E-03	c.1874G>C (p.Cys625Ser)	35	1.16E-03	c.1874G>C (p.Cys625Ser)	10	6.81E-04	c.1874G>C (p.Cys625Ser)	393	3.85E-03	c.1874G>C (p.Cys625Ser)	25	1.17E-03	c.65G>A (p.Trp22*)	12	1.67E-03	c.1874G>C (p.Cys625Ser)	57	1.67E-03
	c.1777-1G>C	5	7.10E-04	c.1777-1G>C	6	3.39E-04	c.539_540dup (p.Ala181Lysfs*12)	4	1.31E-04	c.190-2A>T	4	2.69E-04	c.1115_1118del (p.Val372Alafs*42)	15	1.46E-04	c.3349-1G>A	11	7.04E-04	c.1874G>C (p.Cys625Ser)	12	1.26E-03	c.1549C>T (p.Arg517Trp)	17	4.96E-04
	c.1840C>T (p.Pro614Ser)	2	2.84E-04	c.1874G>A (p.Cys625Tyr)	5	2.83E-04	c.2639G>A (p.Arg880Gln)	3	9.83E-05	c.2291G>A (p.Arg764Gln)	2	1.65E-04	c.2807A>G (p.Glu936Gly)	15	1.46E-04	c.3391A>G (p.Thr1131Ala)	2	1.23E-04				c.3536C>G (p.Pro1179Arg)	4	1.18E-04
				c.987_990del (p.His330Alafs*4)	4	2.26E-04	c.1561C>T (p.Leu521Phe)	3	9.83E-05				c.100A>T (p.Lys34*)	13	1.27E-04							c.1226-2A>G	4	1.17E-04
													c.862G>T (p.Glu288*)	13	1.27E-04									
FANCC	*			*			c.1642C>T (p.Arg548*)	4	1.31E-04	c.360del (p.His120Glnfs*24)	3	2.02E-04	c.67del (p.Asp23Ilefs*23)	28	2.73E-04	*			*			c.487_490del (p.Glu163Ilefs*30)	5	1.46E-04
							c.520C>T (p.Arg174*)	3	9.83E-05	c.355_358del (p.Ser119Ilefs*24)	3	2.02E-04	c.553C>T (p.Arg185*)	11	1.07E-04							c.673G>T (p.Glu225*)	3	9.26E-05
							c.1533+1G>C	2	6.55E-05	c.1663C>T (p.Arg555*)	2	1.35E-04	c.1642C>T (p.Arg548*)	6	5.84E-05									
										c.521+1G>A	2	1.34E-04	c.1663C>T (p.Arg555*)	3	2.92E-05									
FANCD2	c.2376G>C (p.Trp792Cys)	2	2.84E-04	c.3692T>C (p.Phe1231Ser)	4	2.26E-04	c.1844del (p.Gln615Argfs*24)	3	9.83E-05	c.990-1G>A	7	4.89E-04	c.2715+1G>A	27	2.63E-04	c.2715+1G>A	9	4.16E-04	c.1222C>T (p.Arg408*)	3	3.13E-04	c.2273G>C (p.Cys758Ser)	112	3.27E-03
				c.1318C>T (p.Gln440*)	2	1.13E-04	c.1656+1G>A	2	6.55E-05	c.1279-2A>G	5	3.36E-04	c.2273G>C (p.Cys758Ser)	13	1.27E-04				c.491+1G>A	2	2.09E-04	c.2444G>A (p.Arg815Gln)	20	5.84E-04
				c.2376G>C (p.Trp792Cys)	2	1.13E-04				c.2776C>T (p.Arg926*)	2	1.34E-04	c.2444G>A (p.Arg815Gln)	9	8.77E-05							c.3185A>C (p.Tyr1062Ser)	4	1.17E-04
										c.236T>G (p.Leu79Arg)	2	1.34E-04												
FANCE	Nil			*			c.350_351del (p.Val117Alafs*11)	2	6.55E-05	c.940C>T (p.Gln314*)	2	1.34E-04	c.1383+2T>G	10	9.78E-05	Nil			*			c.355C>T (p.Gln119*)	2	5.84E-05
							c.1510-1G>A	2	6.55E-05															

Gene	SG			EAS			SAS			AFR			NFE			FIN			ASJ			AMR		
	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF
FANCF	Nil			c.235G>T (p.Gly79*)	2	1.13 E-04	c.484_485del (p.Leu162Aspfs*103)	7	2.29 E-04	c.484_485del (p.Leu162Aspfs*103)	2	1.40 E-04	c.1087C>T (p.Gln363*)	10	9.73 E-05	*			Nil			c.1087C>T (p.Gln363*)	6	1.75 E-04
				c.167del (p.Thr56Argfs*25)	2	1.13 E-04				c.230_252del (p.Val77Glyfs*6)	2	1.35 E-04	c.484_485del (p.Leu162Aspfs*103)	8	7.82 E-05									
													c.351_397del (p.Gly120Profs*17)	3	2.94 E-05									
													c.690del (p.Gly231Glufs*7)	3	2.96 E-05									
FANCG	c.1656dup (p.His553Serfs*14)	2	2.84 E-04	c.307+1G>C	6	3.39 E-04	c.366G>C (p.Trp122Cys)	68	2.23 E-03	c.1852_1853del (p.Lys618Valfs*3)	5	3.36 E-04	c.366G>C (p.Trp122Cys)	17	1.66 E-04	c.1183_1192del (p.Glu395Trpfs*5)	2	1.02 E-04	Nil			c.1077-2A>G	3	8.76 E-05
							c.448T>C (p.Trp150Arg)	3	9.83 E-05				c.1183_1192del (p.Glu395Trpfs*5)	9	8.83 E-05							c.1642C>T (p.Arg548*)	2	5.85 E-05
							c.1761-2A>C	2	6.55 E-05				c.1158dup (p.Ser387Leufs*9)	5	5.50 E-05									
							c.1652_1655del (p.Tyr551Phefs*7)	2	6.56 E-05				c.1144-1G>T	5	4.99 E-05									
							c.1044_1057del (p.His348Glnfs*25)	2	6.55 E-05															
FANCI	*			c.2889+2T>C	2	1.13 E-04	c.1890+6_1890+7insATGTAAAA	6	1.97 E-04	c.1840C>T (p.Arg614*)	2	1.34 E-04	c.1264G>A (p.Gly422Arg)	23	2.24 E-04	c.2957_2969del (p.Val986Alafs*39)	64	2.96 E-03	*			c.3473G>T (p.Cys1158Phe)	21	6.13 E-04
				c.3187-2A>G	2	1.13 E-04	c.3007-1G>C	6	1.97 E-04	c.3116del (p.Tyr1039Leufs*22)	2	1.34 E-04	c.3255T>G (p.Cys1085Trp)	20	1.95 E-04	c.3041G>A (p.Cys1014Tyr)	22	1.02 E-03				c.3493del (p.Asp1165Thrfs*34)	13	3.79 E-04
							c.3853C>T (p.Arg1285*)	5	1.64 E-04	c.1322T>G (p.Leu441Trp)	2	1.34 E-04	c.1412C>G (p.Pro471Arg)	9	8.77 E-05	c.3645C>G (p.Tyr1215*)	2	9.25 E-05				c.3604G>C (p.Gly1202Arg)	7	2.04 E-04
							c.2456+1G>A	3	9.83 E-05	c.3734G>T (p.Arg1245Leu)	2	1.34 E-04	c.3041G>A (p.Cys1014Tyr)	7	6.81 E-05	c.1668_1669del (p.Gln557Valfs*24)	2	9.25 E-05				c.998C>A (p.Ser333*)	4	1.36 E-04
													c.3466G>C (p.Gly1156Arg)	7	6.81 E-05	c.1804C>T (p.Arg602*)	2	9.25 E-05				c.3622_3623del (p.Leu1208Valfs*11)	4	1.17 E-04

Gene	SG			EAS			SAS			AFR			NFE			FIN			ASJ			AMR		
	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF
FANCL	*			*			c.1096_1099dup (p.Thr367Asnfs*13)	22	7.23E-04	c.1096_1099dup (p.Thr367Asnfs*13)	11	7.65E-04	c.1096_1099dup (p.Thr367Asnfs*13)	345	3.39E-03	c.1096_1099dup (p.Thr367Asnfs*13)	39	1.82E-03	c.1096_1099dup (p.Thr367Asnfs*13)	64	6.72E-03	c.1096_1099dup (p.Thr367Asnfs*13)	182	5.34E-03
							c.676C>T (p.Arg226Cys)	3	9.83E-05	c.296_297del (p.Gln99Argfs*17)	4	2.69E-04	c.677G>A (p.Arg226His)	5	4.87E-05				c.89C>A (p.Ser30*)	2	2.09E-04	c.1051_1052del (p.Ser351Phefs*2)	17	4.96E-04
							c.982C>T (p.Gln328*)	2	6.56E-05	c.680G>C (p.Arg227Thr)	2	1.34E-04	c.641T>C (p.Leu214Pro)	4	3.89E-05							c.217-2A>G	2	5.85E-05
										c.1103dup (p.Leu368Phefs*11)	2	1.39E-04	c.378del (p.Val127Cysfs*12)	3	2.93E-05									
													c.274-2A>G	3	2.93E-05									
FANCM	c.1015del (p.Asp339Ilefs*18)	2	2.84E-04	c.1718G>A (p.Arg573Gln)	4	2.26E-04	c.4318-1G>A	19	6.24E-04	c.5791C>T (p.Arg1931*)	6	4.03E-04	c.5101C>T (p.Gln1701*)	111	1.08E-03	c.5101C>T (p.Gln1701*)	178	8.23E-03	Nil			c.5791C>T (p.Arg1931*)	12	3.50E-04
				c.1655T>C (p.Ile552Thr)	2	1.13E-04	c.5339_5340insT (p.Lys1780Asnfs*4)	16	5.24E-04	c.5101C>T (p.Gln1701*)	2	1.34E-04	c.5791C>T (p.Arg1931*)	106	1.03E-03	c.5791C>T (p.Arg1931*)	97	4.48E-03				c.4820G>A (p.Cys1607Tyr)	9	2.64E-04
							c.5340+1_5340+2insAATCACTG	16	5.25E-04	c.3628C>T (p.Gln1210*)	2	1.35E-04	c.1597C>T (p.Arg533Cys)	60	5.84E-04	c.1491dup (p.Gln498Thrfs*7)	5	2.31E-04				c.2260C>T (p.Arg754*)	5	1.46E-04
							c.5791C>T (p.Arg1931*)	8	2.62E-04	c.5364_5367dup (p.Thr1790*)	2	1.34E-04	c.1972C>T (p.Arg658*)	11	1.07E-04	c.1597C>T (p.Arg533Cys)	4	1.85E-04				c.5101C>T (p.Gln1701*)	4	1.17E-04
							c.2040_2041del (p.Leu680Phefs*6)	8	2.62E-04	c.5530del (p.Gln1844Lysfs*2)	2	1.34E-04	c.1491dup (p.Gln498Thrfs*7)	5	4.87E-05	c.4025_4026del (p.Ser1342*)	2	9.29E-05				c.4637T>G (p.Leu1546*)	3	9.16E-05
SLX4	c.4693dup (p.Gln1565Profs*16)	2	2.84E-04	c.4693dup (p.Gln1565Profs*16)	7	3.96E-04	c.4921dup (p.Val1641Glyfs*15)	5	1.64E-04	*			c.5242C>T (p.Gln1748*)	6	5.86E-05	c.5242C>T (p.Gln1748*)	2	9.414E-05	Nil			c.1129C>T (p.Gln377*)	4	1.17E-04
				c.4996C>T (p.Arg1666*)	3	1.70E-04	c.1163+2T>A	3	9.83E-05				c.4089_4090del (p.Asp1365Profs*26)	5	4.88E-05							c.2314_2327del (p.Ser772Valfs*5)	2	5.88E-05
				c.5248del (p.Ala1750Argfs*7)	2	1.13E-04	c.2137C>T (p.Arg713*)	2	6.57E-05				c.2808_2809del (p.Ala938Thrfs*7)	5	4.87E-05							c.5154-1G>A	2	5.87E-05
							c.4996C>T (p.Arg1666*)	2	6.55E-05				c.4259dup (p.Ile1421Asnfs*4)	3	3.07E-05							c.2700G>A (p.Trp900*)	2	5.84E-05

Gene	SG			EAS			SAS			AFR			NFE			FIN			ASJ			AMR		
	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF
							c.2387_2388del (p.Glu796Glyfs*30)	2	6.55E-05															
ERCC4	*			c.2169C>A (p.Cys723*)	7	3.96E-04	c.521G>A (p.Gly174Asp)	13	4.26E-04	c.579G>A (p.Trp193*)	4	2.68E-04	c.1765C>T (p.Arg589Trp)	8	7.96E-05	c.1293del (p.Leu432Tyrfs*2)	2	9.26E-05	c.1376C>A (p.Ser459*)	2	2.09E-04	c.1765C>T (p.Arg589Trp)	5	1.46E-04
				c.458G>A (p.Arg153His)	3	1.70E-04	c.1882_1885del (p.Glu628Leufs*6)	8	2.62E-04	c.1765C>T (p.Arg589Trp)	3	2.02E-04	c.938T>C (p.Leu313Pro)	7	6.82E-05							c.1765C>G (p.Arg589Gly)	3	8.76E-05
				c.2219G>A (p.Arg740His)	2	1.13E-04	c.822G>A (p.Trp274*)	3	9.83E-05	c.314G>C (p.Gly105Ala)	2	1.34E-04	c.875G>A (p.Arg292Gln)	6	5.85E-05							c.2177G>A (p.Arg726His)	3	8.76E-05
							c.395T>C (p.Leu132Ser)	3	9.83E-05				c.989A>C (p.Asp330Ala)	6	5.85E-05							c.2078G>T (p.Ser693Ile)	2	5.84E-05
							c.2176C>A (p.Arg726Ser)	3	9.83E-05				c.2219G>A (p.Arg740His)	5	4.87E-05									
RAD51	*			*			*			c.823C>T (p.Arg275*)	16	1.07E-03	*			*			Nil			*		
UBE2T	c.368dup (p.Leu124Alafs*4)	2	2.84E-04	c.529_533del (p.Ser177Thrfs*18)	2	1.13E-04	*			c.205C>T (p.Arg69*)	3	2.02E-04	c.32T>G (p.Leu11Arg)	5	4.89E-05	*			Nil			c.109C>T (p.Gln37*)	3	8.76E-05
																						c.208T>G (p.Phe70Val)	2	5.84E-05
XRCC2	*			*			*			*			c.450C>G (p.Ser150Arg)	14	1.36E-04	c.190C>T (p.Arg64*)	2	9.54E-05	c.643C>T (p.Arg215*)	2	2.09E-04	c.450C>G (p.Ser150Arg)	7	2.04E-04
													c.96del (p.Phe32Leufs*30)	11	1.07E-04	c.764T>G (p.Leu255*)	2	9.25E-05				c.378_381del (p.Leu126Phefs*7)	5	1.46E-04
													c.643C>T (p.Arg215*)	7	6.82E-05							c.39+2T>A	3	8.76E-05
													c.350dup (p.Leu117Phefs*6)	4	3.99E-05							c.109dup (p.Ser37Phefs*6)	2	5.88E-05
													c.398T>C (p.Leu133Pro)	4	3.90E-05									
MAD2L2	Nil			*			*			*			c.427+2T>A	5	4.88E-05	Nil			*			*		
													c.-3_1dup (p.Met1?)	2	2.22E-05									

Gene	SG			EAS			SAS			AFR			NFE			FIN			ASJ			AMR		
	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF	Variant	AC	AF
RFWD3	*			*			*			*			c.1990C>T (p.Arg664*)	3	2.92 E-05	*			*			c.1673G>A (p.Gly558Glu)	2	5.85 E-05
													c.582del (p.Thr195Leufs*45)	2	1.95 E-05									
													c.1126dup (p.Ser376Phefs*13)	2	1.95 E-05									

[a] Up to top 5 predicted pathogenic variants are listed for each gene. Variants with allele count of 1 are not listed. *: No recurrent variants identified, only variants with allele count of 1, AC: allele count, AF: allele frequency, Nil: no predicted pathogenic variant identified for the gene. SG: Singaporean, EAS: East Asian, SAS: South Asian, AFR: African-American, NFE: Non-Finnish European, FIN: Finnish European, ASJ: Ashkenazi Jewish, AMR: Admixed-American/Latino.

Supplementary Table 4: Proportion of total unique variants (adjusted to cohort size) and private variants in each FA gene across ancestry groups[a]

Gene	SG				EAS				SAS				AFR			
	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)
FANCA	19	539	16	84%	25	286	18	72%	44	292	36	82%	20	273	14	70%
FANCC	2	57	2	100%	5	57	5	100%	10	66	7	70%	6	82	2	33%
FANCD2	4	114	3	75%	9	103	6	67%	20	133	18	90%	15	205	11	73%
FANCE	0	0	0	0	1	11	1	100%	11	73	9	82%	4	55	3	75%
FANCF	0	0	0	0	3	34	1	33%	4	27	3	75%	4	55	2	50%
FANCG	4	114	3	75%	3	34	2	67%	13	86	8	62%	6	82	5	83%
FANCI	2	57	2	100%	16	183	14	88%	25	166	17	68%	21	287	17	81%
FANCL	2	57	2	100%	7	80	7	100%	16	106	13	81%	9	123	5	56%
FANCM	6	170	5	83%	11	126	9	82%	20	133	11	55%	11	150	6	55%
SLX4	2	57	1	50%	16	183	13	81%	19	126	14	74%	3	41	3	100%
ERCC4	2	57	2	100%	10	114	7	70%	23	153	13	57%	8	109	5	63%
RAD51	1	28	1	100%	1	11	1	100%	3	20	3	100%	2	27	1	50%
UBE2T	2	57	1	50%	6	69	5	83%	3	20	3	100%	3	41	2	67%
XRCC2	4	114	4	100%	1	11	1	100%	8	53	8	100%	2	27	2	100%
MAD2L2	0	0	0	0	3	34	3	100%	1	7	1	100%	2	27	2	100%
RFWD3	1	28	1	100%	9	103	9	100%	10	66	10	100%	6	82	6	100%

Gene	NFE				FIN				ASJ				AMR			
	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)	Total unique variants	Adjusted fraction of unique variants (per 100,000)	No. private variants	Fraction of private variants (%)
FANCA	112	221	78	70%	7	66	4	57%	4	84	2	50%	38	236	22	58%
FANCC	30	59	20	67%	2	19	2	100%	1	21	1	100%	8	50	6	75%
FANCD2	52	103	40	77%	5	47	4	80%	3	63	1	33%	23	143	15	65%
FANCE	12	24	11	92%	0	0	0	0	1	21	1	100%	3	19	2	67%
FANCF	18	36	12	67%	1	9	1	100%	0	0	0	0	3	19	2	67%
FANCG	32	63	18	56%	3	28	2	67%	0	0	0	0	11	68	9	82%
FANCI	66	130	42	64%	10	94	5	50%	2	42	2	100%	21	130	13	62%
FANCL	34	67	22	65%	1	9	0	0	4	84	2	50%	8	50	5	63%
FANCM	53	105	36	68%	7	66	2	29%	0	0	0	0	18	112	11	61%
SLX4	52	103	40	77%	5	47	4	80%	0	0	0	0	14	87	10	71%
ERCC4	56	111	37	66%	6	56	5	83%	2	42	1	50%	16	99	12	75%
RAD51	2	4	2	100%	1	9	1	100%	0	0	0	0	1	6	1	100%
UBE2T	7	14	6	86%	1	9	1	100%	0	0	0	0	5	31	3	60%
XRCC2	18	36	8	44%	4	38	2	50%	3	63	2	67%	10	62	6	60%
MAD2L2	8	16	6	75%	0	0	0	0	1	21	1	100%	1	6	1	100%
RFWD3	25	49	22	88%	1	9	1	1	1	21	1	100%	5	31	4	80%

[a] Private variants are defined as variants that occurred in only single individual within the ancestry group. SG: Singaporean, EAS: East Asian, SAS: South Asian, AFR: African-American, NFE: Non-Finnish European, FIN: Finnish European, ASJ: Ashkenazi Jewish, AMR: Admixed-American/Latino.

Supplementary Table 5: Carrier frequency of potentially pathogenic germline variants identified in White (non-Hispanic) racial subset of patients from the selected TCGA cohorts

TCGA cohort	TCGA-BRCA		TCGA-HNSC		TCGA-LUAD		TCGA-LUSC		TCGA-OV		TCGA-UCEC		TCGA-UCS	
Individuals with germline data	693		430		385		343		381		363		43	
	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*
FANCA	12	1.73%	8	1.86%	6	1.56%	6	1.75%	4	1.05%	2	0.55%	0	0
FANCB	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FANCC	1	0.14%	2	0.47%	0	0	1	0.29%	0	0	0	0	0	0
FANCD2	3	0.43%	1	0.23%	1	0.26%	1	0.29%	2	0.52%	0	0	0	0
FANCE	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FANCF	0	0	0	0	1	0.26%	0	0	0	0	1	0.28%	0	0
FANCG	0	0	2	0.47%	1	0.26%	2	0.58%	1	0.26%	1	0.28%	1	2.33%
FANCI	2	0.29%	2	0.47%	2	0.52%	0	0	0	0	2	0.55%	0	0
FANCL	5	0.72%	2	0.47%	4	1.04%	2	0.58%	6	1.57%	2	0.55%	0	0
FANCM	9	1.30%	3	0.70%	2	0.52%	1	0.29%	0	0	1	0.28%	0	0
SLX4	1	0.14%	0	0	0	0	0	0	0	0	2	0.55%	0	0
ERCC4	0	0	1	0.23%	0	0	0	0	0	0	0	0	0	0
RAD51	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UBE2T	0	0	0	0	0	0	0	0	1	0.26%	0	0	0	0
XRCC2	4	0.58%	0	0	1	0.26%	0	0	0	0	0	0	0	0
MAD2L2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RFWD3	0	0.00%	0	0	0	0	1	0.29%	0	0	0	0	0	0

*Carrier frequency is normalized to number of cases with available germline data. TCGA-BRCA: breast invasive carcinoma, TCGA-HNSC: head and neck squamous cell carcinoma, TCGA-LUAD: lung adenocarcinoma, TCGA-LUSC: lung squamous cell carcinoma, TCGA-OV: ovarian serous cystadenocarcinoma, TCGA-UCEC: uterine corpus endometrial carcinoma, TCGA-UCS: uterine carcinosarcoma

Supplementary Table 6: Pairwise differences in proportion of germline variant carrier frequency in the 6 TCGA cohorts evaluated by two-tailed Fisher's exact test, with Bonferroni correction for multiple testing (195 tests)[a]

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
1	*FANCA*	BRCA	1.73E-02	HNSC	1.86E-02	1	1
2	*FANCA*	BRCA	1.73E-02	LUAD	1.56E-02	1	1
3	*FANCA*	BRCA	1.73E-02	LUSC	1.75E-02	1	1
4	*FANCA*	BRCA	1.73E-02	OV	1.05E-02	0.44	1
5	*FANCA*	BRCA	1.73E-02	UCEC	5.51E-03	0.16	1
6	*FANCA*	HNSC	1.86E-02	LUAD	1.56E-02	0.79	1
7	*FANCA*	HNSC	1.86E-02	LUSC	1.75E-02	1	1
8	*FANCA*	HNSC	1.86E-02	OV	1.05E-02	0.39	1
9	*FANCA*	HNSC	1.86E-02	UCEC	5.51E-03	0.12	1
10	*FANCA*	LUAD	1.56E-02	LUSC	1.75E-02	1	1
11	*FANCA*	LUAD	1.56E-02	OV	1.05E-02	0.75	1
12	*FANCA*	LUAD	1.56E-02	UCEC	5.51E-03	0.29	1
13	*FANCA*	LUSC	1.75E-02	OV	1.05E-02	0.53	1
14	*FANCA*	LUSC	1.75E-02	UCEC	5.51E-03	0.17	1
15	*FANCA*	OV	1.05E-02	UCEC	5.51E-03	0.69	1
16	*FANCC*	BRCA	1.44E-03	HNSC	4.65E-03	0.56	1
17	*FANCC*	BRCA	1.44E-03	LUAD	0	1	1
18	*FANCC*	BRCA	1.44E-03	LUSC	2.92E-03	0.55	1
19	*FANCC*	BRCA	1.44E-03	OV	0	1	1
20	*FANCC*	BRCA	1.44E-03	UCEC	0	1	1
21	*FANCC*	HNSC	4.65E-03	LUAD	0	0.50	1
22	*FANCC*	HNSC	4.65E-03	LUSC	2.92E-03	1	1
23	*FANCC*	HNSC	4.65E-03	OV	0	0.50	1
24	*FANCC*	HNSC	4.65E-03	UCEC	0	0.50	1
25	*FANCC*	LUAD	0	LUSC	2.92E-03	0.47	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
26	*FANCC*	LUAD	0	OV	0	1	1
27	*FANCC*	LUAD	0	UCEC	0	1	1
28	*FANCC*	LUSC	2.92E-03	OV	0	0.47	1
29	*FANCC*	LUSC	2.92E-03	UCEC	0	0.49	1
30	*FANCC*	OV	0	UCEC	0	1	1
31	*FANCD2*	BRCA	4.33E-03	HNSC	2.33E-03	1	1
32	*FANCD2*	BRCA	4.33E-03	LUAD	2.60E-03	1	1
33	*FANCD2*	BRCA	4.33E-03	LUSC	2.92E-03	1	1
34	*FANCD2*	BRCA	4.33E-03	OV	5.25E-03	1	1
35	*FANCD2*	BRCA	4.33E-03	UCEC	0	0.56	1
36	*FANCD2*	HNSC	2.33E-03	LUAD	2.60E-03	1	1
37	*FANCD2*	HNSC	2.33E-03	LUSC	2.92E-03	1	1
38	*FANCD2*	HNSC	2.33E-03	OV	5.25E-03	0.60	1
39	*FANCD2*	HNSC	2.33E-03	UCEC	0	1	1
40	*FANCD2*	LUAD	2.60E-03	LUSC	2.92E-03	1	1
41	*FANCD2*	LUAD	2.60E-03	OV	5.25E-03	0.62	1
42	*FANCD2*	LUAD	2.60E-03	UCEC	0	1	1
43	*FANCD2*	LUSC	2.92E-03	OV	5.25E-03	1	1
44	*FANCD2*	LUSC	2.92E-03	UCEC	0	0.49	1
45	*FANCD2*	OV	5.25E-03	UCEC	0	0.50	1
46	*FANCF*	BRCA	0	HNSC	0	1	1
47	*FANCF*	BRCA	0	LUAD	2.60E-03	0.36	1
48	*FANCF*	BRCA	0	LUSC	0	1	1
49	*FANCF*	BRCA	0	OV	0	1	1
50	*FANCF*	BRCA	0	UCEC	2.75E-03	0.34	1
51	*FANCF*	HNSC	0	LUAD	2.60E-03	0.47	1
52	*FANCF*	HNSC	0	LUSC	0	1	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
53	*FANCF*	HNSC	0	OV	0	1	1
54	*FANCF*	HNSC	0	UCEC	2.75E-03	0.46	1
55	*FANCF*	LUAD	2.60E-03	LUSC	0	1	1
56	*FANCF*	LUAD	2.60E-03	OV	0	1	1
57	*FANCF*	LUAD	2.60E-03	UCEC	2.75E-03	1	1
58	*FANCF*	LUSC	0	OV	0	1	1
59	*FANCF*	LUSC	0	UCEC	2.75E-03	1	1
60	*FANCF*	OV	0	UCEC	2.75E-03	0.49	1
61	*FANCG*	BRCA	0	HNSC	4.65E-03	0.15	1
62	*FANCG*	BRCA	0	LUAD	2.60E-03	0.36	1
63	*FANCG*	BRCA	0	LUSC	5.83E-03	0.11	1
64	*FANCG*	BRCA	0	OV	2.62E-03	0.35	1
65	*FANCG*	BRCA	0	UCEC	2.75E-03	0.34	1
66	*FANCG*	HNSC	4.65E-03	LUAD	2.60E-03	1	1
67	*FANCG*	HNSC	4.65E-03	LUSC	5.83E-03	1	1
68	*FANCG*	HNSC	4.65E-03	OV	2.62E-03	1	1
69	*FANCG*	HNSC	4.65E-03	UCEC	2.75E-03	1	1
70	*FANCG*	LUAD	2.60E-03	LUSC	5.83E-03	0.60	1
71	*FANCG*	LUAD	2.60E-03	OV	2.62E-03	1	1
72	*FANCG*	LUAD	2.60E-03	UCEC	2.75E-03	1	1
73	*FANCG*	LUSC	5.83E-03	OV	2.62E-03	0.61	1
74	*FANCG*	LUSC	5.83E-03	UCEC	2.75E-03	0.61	1
75	*FANCG*	OV	2.62E-03	UCEC	2.75E-03	1	1
76	*FANCI*	BRCA	2.89E-03	HNSC	4.65E-03	0.64	1
77	*FANCI*	BRCA	2.89E-03	LUAD	5.19E-03	0.62	1
78	*FANCI*	BRCA	2.89E-03	LUSC	0	1	1
79	*FANCI*	BRCA	2.89E-03	OV	0	0.54	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
80	*FANCI*	BRCA	2.89E-03	UCEC	5.51E-03	0.61	1
81	*FANCI*	HNSC	4.65E-03	LUAD	5.19E-03	1	1
82	*FANCI*	HNSC	4.65E-03	LUSC	0	0.51	1
83	*FANCI*	HNSC	4.65E-03	OV	0	0.50	1
84	*FANCI*	HNSC	4.65E-03	UCEC	5.51E-03	1	1
85	*FANCI*	LUAD	5.19E-03	LUSC	0	0.50	1
86	*FANCI*	LUAD	5.19E-03	OV	0	0.50	1
87	*FANCI*	LUAD	5.19E-03	UCEC	5.51E-03	1	1
88	*FANCI*	LUSC	0	OV	0	1	1
89	*FANCI*	LUSC	0	UCEC	5.51E-03	0.50	1
90	*FANCI*	OV	0	UCEC	5.51E-03	0.24	1
91	*FANCL*	BRCA	7.22E-03	HNSC	4.65E-03	0.71	1
92	*FANCL*	BRCA	7.22E-03	LUAD	1.04E-02	0.73	1
93	*FANCL*	BRCA	7.22E-03	LUSC	5.83E-03	1	1
94	*FANCL*	BRCA	7.22E-03	OV	1.57E-02	0.21	1
95	*FANCL*	BRCA	7.22E-03	UCEC	5.51E-03	1	1
96	*FANCL*	HNSC	4.65E-03	LUAD	1.04E-02	0.43	1
97	*FANCL*	HNSC	4.65E-03	LUSC	5.83E-03	1	1
98	*FANCL*	HNSC	4.65E-03	OV	1.57E-02	0.16	1
99	*FANCL*	HNSC	4.65E-03	UCEC	5.51E-03	1	1
100	*FANCL*	LUAD	1.04E-02	LUSC	5.83E-03	0.69	1
101	*FANCL*	LUAD	1.04E-02	OV	1.57E-02	0.54	1
102	*FANCL*	LUAD	1.04E-02	UCEC	5.51E-03	0.69	1
103	*FANCL*	LUSC	5.83E-03	OV	1.57E-02	0.29	1
104	*FANCL*	LUSC	5.83E-03	UCEC	5.51E-03	1	1
105	*FANCL*	OV	1.57E-02	UCEC	5.51E-03	0.29	1
106	*FANCM*	BRCA	1.30E-02	HNSC	6.98E-03	0.39	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
107	*FANCM*	BRCA	1.30E-02	LUAD	5.19E-03	0.35	1
108	*FANCM*	BRCA	1.30E-02	LUSC	2.92E-03	0.18	1
109	*FANCM*	BRCA	1.30E-02	OV	0	0.03	1
110	*FANCM*	BRCA	1.30E-02	UCEC	2.75E-03	0.18	1
111	*FANCM*	HNSC	6.98E-03	LUAD	5.19E-03	1	1
112	*FANCM*	HNSC	6.98E-03	LUSC	2.92E-03	0.63	1
113	*FANCM*	HNSC	6.98E-03	OV	0	0.25	1
114	*FANCM*	HNSC	6.98E-03	UCEC	2.75E-03	0.63	1
115	*FANCM*	LUAD	5.19E-03	LUSC	2.92E-03	1	1
116	*FANCM*	LUAD	5.19E-03	OV	0	0.50	1
117	*FANCM*	LUAD	5.19E-03	UCEC	2.75E-03	1	1
118	*FANCM*	LUSC	2.92E-03	OV	0	0.47	1
119	*FANCM*	LUSC	2.92E-03	UCEC	2.75E-03	1	1
120	*FANCM*	OV	0	UCEC	2.75E-03	0.49	1
121	*SLX4*	BRCA	1.44E-03	HNSC	0	1	1
122	*SLX4*	BRCA	1.44E-03	LUAD	0	1	1
123	*SLX4*	BRCA	1.44E-03	LUSC	0	1	1
124	*SLX4*	BRCA	1.44E-03	OV	0	1	1
125	*SLX4*	BRCA	1.44E-03	UCEC	5.51E-03	0.27	1
126	*SLX4*	HNSC	0	LUAD	0	1	1
127	*SLX4*	HNSC	0	LUSC	0	1	1
128	*SLX4*	HNSC	0	OV	0	1	1
129	*SLX4*	HNSC	0	UCEC	5.51E-03	0.21	1
130	*SLX4*	LUAD	0	LUSC	0	1	1
131	*SLX4*	LUAD	0	OV	0	1	1
132	*SLX4*	LUAD	0	UCEC	5.51E-03	0.24	1
133	*SLX4*	LUSC	0	OV	0	1	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
134	*SLX4*	LUSC	0	UCEC	5.51E-03	0.50	1
135	*SLX4*	OV	0	UCEC	5.51E-03	0.24	1
136	*ERCC4*	BRCA	0	HNSC	2.33E-03	0.38	1
137	*ERCC4*	BRCA	0	LUAD	0	1	1
138	*ERCC4*	BRCA	0	LUSC	0	1	1
139	*ERCC4*	BRCA	0	OV	0	1	1
140	*ERCC4*	BRCA	0	UCEC	0	1	1
141	*ERCC4*	HNSC	2.33E-03	LUAD	0	1	1
142	*ERCC4*	HNSC	2.33E-03	LUSC	0	1	1
143	*ERCC4*	HNSC	2.33E-03	OV	0	1	1
144	*ERCC4*	HNSC	2.33E-03	UCEC	0	1	1
145	*ERCC4*	LUAD	0	LUSC	0	1	1
146	*ERCC4*	LUAD	0	OV	0	1	1
147	*ERCC4*	LUAD	0	UCEC	0	1	1
148	*ERCC4*	LUSC	0	OV	0	1	1
149	*ERCC4*	LUSC	0	UCEC	0	1	1
150	*ERCC4*	OV	0	UCEC	0	1	1
151	*UBE2T*	BRCA	0	HNSC	0	1	1
152	*UBE2T*	BRCA	0	LUAD	0	1	1
153	*UBE2T*	BRCA	0	LUSC	0	1	1
154	*UBE2T*	BRCA	0	OV	2.62E-03	0.35	1
155	*UBE2T*	BRCA	0	UCEC	0	1	1
156	*UBE2T*	HNSC	0	LUAD	0	1	1
157	*UBE2T*	HNSC	0	LUSC	0	1	1
158	*UBE2T*	HNSC	0	OV	2.62E-03	0.47	1
159	*UBE2T*	HNSC	0	UCEC	0	1	1
160	*UBE2T*	LUAD	0	LUSC	0	1	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
161	*UBE2T*	LUAD	0	OV	2.62E-03	0.50	1
162	*UBE2T*	LUAD	0	UCEC	0	1	1
163	*UBE2T*	LUSC	0	OV	2.62E-03	1	1
164	*UBE2T*	LUSC	0	UCEC	0	1	1
165	*UBE2T*	OV	2.62E-03	UCEC	0	1	1
166	*XRCC2*	BRCA	5.77E-03	HNSC	0	0.30	1
167	*XRCC2*	BRCA	5.77E-03	LUAD	2.60E-03	0.66	1
168	*XRCC2*	BRCA	5.77E-03	LUSC	0	0.31	1
169	*XRCC2*	BRCA	5.77E-03	OV	0	0.30	1
170	*XRCC2*	BRCA	5.77E-03	UCEC	0	0.31	1
171	*XRCC2*	HNSC	0	LUAD	2.60E-03	0.47	1
172	*XRCC2*	HNSC	0	LUSC	0	1	1
173	*XRCC2*	HNSC	0	OV	0	1	1
174	*XRCC2*	HNSC	0	UCEC	0	1	1
175	*XRCC2*	LUAD	2.60E-03	LUSC	0	1	1
176	*XRCC2*	LUAD	2.60E-03	OV	0	1	1
177	*XRCC2*	LUAD	2.60E-03	UCEC	0	1	1
178	*XRCC2*	LUSC	0	OV	0	1	1
179	*XRCC2*	LUSC	0	UCEC	0	1	1
180	*XRCC2*	OV	0	UCEC	0	1	1
181	*RFWD3*	BRCA	0	HNSC	0	1	1
182	*RFWD3*	BRCA	0	LUAD	0	1	1
183	*RFWD3*	BRCA	0	LUSC	2.92E-03	0.33	1
184	*RFWD3*	BRCA	0	OV	0	1	1
185	*RFWD3*	BRCA	0	UCEC	0	1	1
186	*RFWD3*	HNSC	0	LUAD	0	1	1
187	*RFWD3*	HNSC	0	LUSC	2.92E-03	0.44	1

No.	Gene	TCGA group 1	Cohort size-normalized carrier frequency (TCGA group 1)	TCGA group 2	Cohort size-normalized carrier frequency (TCGA group 2)	Unadjusted p-value	Bonferroni-adjusted p-value
188	*RFWD3*	HNSC	0	OV	0	1	1
189	*RFWD3*	HNSC	0	UCEC	0	1	1
190	*RFWD3*	LUAD	0	LUSC	2.92E-03	0.47	1
191	*RFWD3*	LUAD	0	OV	0	1	1
192	*RFWD3*	LUAD	0	UCEC	0	1	1
193	*RFWD3*	LUSC	2.92E-03	OV	0	0.47	1
194	*RFWD3*	LUSC	2.92E-03	UCEC	0	0.49	1
195	*RFWD3*	OV	0	UCEC	0	1	1

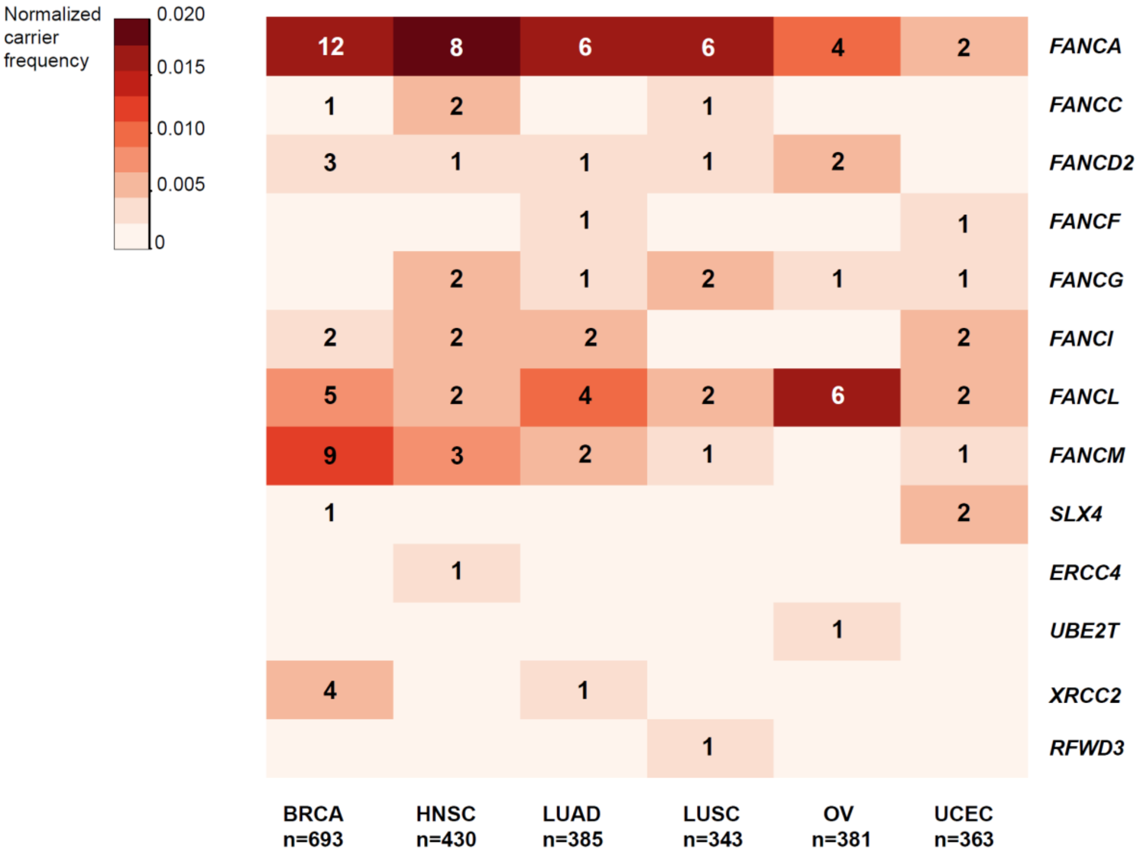
[a] Adjusted p value threshold of <0.05 is considered significant event. BRCA: breast invasive carcinoma, HNSC: head and neck squamous cell carcinoma, LUAD: lung adenocarcinoma, LUSC: lung squamous cell carcinoma, OV: ovarian serous cystadenocarcinoma, UCEC: uterine corpus endometrial carcinoma. The uterine carcinosarcoma (UCS) cohort was not included due to the lack of germline variant carriers.

Supplementary Table 7: Carrier frequency of potentially pathogenic somatic variants identified in White (non-Hispanic) racial subset of patients without known POLE/POLD1 somatic driver mutations from the selected TCGA cohorts[a]

TCGA cohort	TCGA-BRCA		TCGA-HNSC		TCGA-LUAD		TCGA-LUSC		TCGA-OV		TCGA-UCEC		TCGA-UCS	
No. patients	721		431		386		344		488		337		43	
	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*	No. carriers	Carrier frequency*
FANCA	2	0.28%	3	0.70%	4	1.04%	7	2.03%	4	0.82%	6	1.78%	0	0
FANCB	3	0.42%	2	0.46%	2	0.52%	4	1.16%	1	0.20%	3	0.89%	1	2.33%
FANCC	0	0	2	0.46%	0	0	2	0.58%	1	0.20%	1	0.30%	0	0
FANCD2	5	0.69%	5	1.16%	1	0.26%	5	1.45%	4	0.82%	7	2.08%	0	0
FANCE	0	0	0	0	2	0.52%	1	0.29%	4	0.82%	7	2.08%	0	0
FANCF	1	0.14%	1	0.23%	1	0.26%	5	1.45%	1	0.20%	0	0	0	0
FANCG	3	0.42%	0	0	2	0.52%	2	0.58%	1	0.20%	4	1.19%	0	0
FANCI	4	0.55%	6	1.39%	5	1.30%	5	1.45%	3	0.61%	10	2.97%	0	0
FANCL	1	0.14%	1	0.23%	0	0	2	0.58%	2	0.41%	1	0.30%	0	0
FANCM	1	0.14%	6	1.39%	15	3.89%	11	3.20%	3	0.61%	8	2.37%	1	2.33%
SLX4	4	0.55%	4	0.93%	4	1.04%	5	1.45%	12	2.46%	10	2.97%	0	0
ERCC4	3	0.42%	3	0.70%	6	1.55%	3	0.87%	4	0.82%	12	3.56%	0	0
RAD51	1	0.14%	1	0.23%	0	0	1	0.29%	1	0.20%	2	0.59%	0	0
UBE2T	0	0	0	0	2	0.52%	1	0.29%	0	0	1	0.30%	0	0
XRCC2	2	0.28%	1	0.23%	4	1.04%	1	0.29%	0	0	2	0.59%	0	0
MAD2L2	0	0	0	0	1	0.26%	0	0	3	0.61%	2	0.59%	0	0
RFWD3	1	0.14%	3	0.70%	2	0.52%	2	0.58%	1	0.20%	1	0.30%	0	0

[a] Fisher's exact test for pairwise comparisons with Bonferroni correction did not indicate any statistically significant events ($p<0.05$ considered significant event). *Carrier frequency is normalized to number of cases with available somatic data. TCGA-BRCA: breast invasive carcinoma, TCGA-HNSC: head and neck squamous cell carcinoma, TCGA-LUAD: lung adenocarcinoma, TCGA-LUSC: lung squamous cell carcinoma, TCGA-OV: ovarian serous cystadenocarcinoma, TCGA-UCEC: uterine corpus endometrial carcinoma, TCGA-UCS: uterine carcinosarcoma

Supplementary Figure 1: Frequency of potentially pathogenic germline variant carriers in FA genes for 6 TCGA cancer cohorts. Color gradient is scaled to carrier frequency adjusted to cohort size. Numbers within the matrix indicate the number of variant carriers. Color map is not clustered by row or column. Fisher's exact test for statistical significance was performed with Bonferroni-correction of p-values applied for multiple testing (195 tests) but no significant events were identified (p <0.05 considered significant event, see Supplementary Table 6 for pairwise p-values). n: number of individuals with germline data. BRCA: breast invasive carcinoma, HNSC: head and neck squamous cell carcinoma, LUAD: lung adenocarcinoma, LUSC: lung squamous cell carcinoma, OV: ovarian serous cystadenocarcinoma, UCEC: uterine corpus endometrial carcinoma.



BRCA n=693	HNSC n=430	LUAD n=385	LUSC n=343	OV n=381	UCEC n=363	
12	8	6	6	4	2	*FANCA*
1	2		1			*FANCC*
3	1	1	1	2		*FANCD2*
		1			1	*FANCF*
	2	1	2	1	1	*FANCG*
2	2	2			2	*FANCI*
5	2	4	2	6	2	*FANCL*
9	3	2	1		1	*FANCM*
1					2	*SLX4*
	1					*ERCC4*
				1		*UBE2T*
4		1				*XRCC2*
			1			*RFWD3*