

Supplemental Table 1

DNA polymerases		Correlation with MKI-67		Transcription cluster	Relapse Free Survival				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value		Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values
POLA1	Replication	0.2333	0.0298	4	7.943	27.8	0.0046	0.0201	8.234	54.4	0.2806	0.2826
POLA2	Replication	0.601	1.11E-09	3	8.421	85.2	0.0004	0.0053	8.604	79.7	1.11E-08	6.03E-08
POLD1	Replication / repair	0.697	1.42E-13	3	9.09	72.2	0.0277	0.0516	9.09	55.7	1.81E-09	1.29E-08
POLD2	Replication / repair	0.2601	0.01513	4	11.79	77.8	0.0006	0.0069	11.64	59.5	1.84E-05	4.10E-05
POLD3	Replication / repair	0.5597	2.29E-08	3	8.267	88.9	0.0274	0.0516	8.081	72.1	7.57E-06	1.89E-05
POLD4	Replication / repair	-0.2499	0.0197	1	11.06	81.5	0.0204	0.0428	9.785	11.4	0.0003	0.0006
POLE	Replication / repair	0.431	3.36E-05	3	9.588	74.1	0.1009	0.1172	9.842	78.5	0.0003	0.0005
POLE2	Replication / repair	0.7138	2.07E-14	3	4.891	68.5	0.0015	0.0125	6.211	75.9	1.92E-08	8.73E-08
POLE3	Replication / repair	0.4681	5.48E-06	4	10.3	44.4	0.0001	0.0032	10.5	45.6	0.0001	0.0002
POLE4	Replication / repair	0.2168	0.04387	4	8.512	18.5	0.0319	0.0538	9.55	73.4	0.0052	0.0075
POLB	Replication / repair	0.0238	0.8268	4	7.692	9.3	0.1461	0.1629	8.705	77.2	0.0010	0.0018
POLG	Mitochondrial DNA replication	0.2232	0.0379	4	9.568	46.3	0.0038	0.0190	9.893	53.2	0.0001	0.0002
POLG2	Mitochondrial DNA replication	0.1385	0.2010	2	7.394	88.9	0.0058	0.0234	7.27	87.3	0.0240	0.0303
POLL	Replication / repair	-0.06111	0.5738	1	9.842	81.5	0.0128	0.0352	9.327	45.6	0.1071	0.1165
POLM	Replication / repair	-0.1761	0.1029	1	8.136	11.1	0.0336	0.0544	8.087	12.7	0.1581	0.1629
POLQ	Replication / repair	0.7578	0.0000	3	6.071	68.5	0.0039	0.0190	6.25	57.0	9.49E-09	5.38E-08
POLN	Translesion DNA synthesis	-0.2193	0.04144	1	4.365	20.4	0.0020	0.0123	3.837	15.2	1.95E-05	4.27E-05
REV3L	Translesion DNA synthesis	0.149	0.1685	2	8.224	29.6	0.1252	0.1408	9.295	86.1	0.0024	0.0039
MAD2L2	Translesion DNA synthesis	0.4611	7.86E-06	3	9.38	88.9	0.0259	0.0503	9.438	79.7	2.12E-10	1.81E-09
REV1	Translesion DNA synthesis	0.2021	0.0606	1	9.479	44.4	0.0122	0.0352	10.22	77.2	7.64E-06	1.89E-05
POLK	Translesion DNA synthesis	-0.1658	0.1250	1	9.145	29.6	0.0008	0.0075	8.899	26.6	1.26E-05	2.90E-05
POLH	Translesion DNA synthesis	0.3561	0.0007	4	9.01	48.1	0.0397	0.0623	9.362	73.4	0.0829	0.0924
POLI	Translesion DNA synthesis	-0.003165	0.9768	1	8.54	53.7	0.0565	0.0768	8.058	26.6	0.0583	0.0677

G1/S checkpoint		Correlation with MKI-67		Transcription cluster	Time to relapse				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value		Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values
CDK2	CDK and their regulators	0.6564	9.18E-12	3	9.233	64.8	0.0527	0.0731	9.526	63.3	2.36E-07	8.22E-07
CDK4	CDK and their regulators	0.1335	0.2178	4	12.63	68.5	0.2822	0.2864	11.29	10.1	0.2477	0.2533
CDK6	CDK and their regulators	0.1239	0.2529	2	10.63	79.6	5.12E-08	6.97E-06	10.74	69.6	1.79E-05	4.05E-05
CDKN2A	CDK and their regulators	0.2599	0.0152	4	7.55	31.5	0.0848	0.1041	10.29	87.3	3.72E-05	7.90E-05
CDKN2B	CDK and their regulators	0.1209	0.2645	2	7.09	29.6	0.0031	0.0169	8.264	75.9	0.0025	0.0039
CDKN2C	CDK and their regulators	0.3	0.0049	4	9.428	37.0	0.0258	0.0503	10.85	88.6	0.0156	0.0204
CDKN2D	CDK and their regulators	0.4078	9.45E-05	4	8.713	18.5	0.0334	0.0544	10.39	74.7	0.0003	0.0006
CDKN1A	CDK and their regulators	-0.2559	0.0169	1	11.32	11.1	0.0117	0.0352	10.07	10.1	8.60E-06	2.09E-05
CDKN1B	CDK and their regulators	-0.05606	0.6059	1	11.36	66.7	0.1775	0.1916	10.52	15.2	0.0822	0.0924
CDKN1C	CDK and their regulators	-0.2749	0.0101	1	8.325	48.1	0.0759	0.0973	10.03	73.4	0.0282	0.0349
CCND1	CDK and their regulators	0.02788	0.7976	1	12.53	87.0	0.0266	0.0510	12.66	81.0	0.0038	0.0056
CCND2	CDK and their regulators	-0.3974	0.0001	1	13.99	77.8	0.0129	0.0352	10.13	12.7	4.62E-06	1.26E-05
CCND3	CDK and their regulators	-0.09043	0.4048	1	12.23	24.1	0.0896	0.1060	12.55	45.6	0.0010	0.0017
CCNE1	CDK and their regulators	0.3751	0.0004	3	9.74	74.1	0.0208	0.0428	9.923	73.4	0.0022	0.0037
HDAC1	pRb1 pathway	0.1997	0.0639	4	11.03	48.1	0.0164	0.0399	10.31	12.7	0.0102	0.0140
HDAC2	pRb1 pathway	0.2628	0.0141	4	10.66	51.9	0.0399	0.0623	11.28	79.7	0.0006	0.0011
HDAC3	pRb1 pathway	-0.01198	0.9123	2	10.81	72.2	0.3039	0.3039	11	86.1	0.0665	0.0767
RB1	pRb1 pathway	-0.1955	0.0698	1	9.334	13.0	0.0076	0.0285	9.899	29.1	0.0556	0.0652
RBL1	pRb1 pathway	0.4255	0.0000	4	5.371	20.4	0.0185	0.0419	6.364	54.4	0.0111	0.0150
RBL2	pRb1 pathway	-0.3227	0.0024	1	10.19	16.7	0.0115	0.0352	10.1	26.6	2.85E-05	6.15E-05
E2F1	pRb1 pathway	0.5798	5.55E-09	3	9.458	63.0	0.0321	0.0538	9.533	58.2	3.31E-07	1.10E-06
E2F2	pRb1 pathway	0.8433	0	3	5.708	64.8	0.0003	0.0047	6.172	55.7	2.23E-07	7.99E-07
E2F3	pRb1 pathway	0.1764	0.1024	2	9.201	87.0	0.0130	0.0352	7.804	11.4	0.1264	0.1364
E2F4	pRb1 pathway	0.1165	0.2827	1	10.96	61.1	0.0217	0.0440	10.77	40.5	0.1294	0.1375
E2F5	pRb1 pathway	0.08457	0.4360	2	5.532	20.4	0.0411	0.0636	7.213	84.8	0.0107	0.0146
TFDP1	pRb1 pathway	0.5205	2.89E-07	4	9.222	46.3	0.0012	0.0109	9.832	63.3	1.19E-07	4.64E-07
TFDP2	pRb1 pathway	-0.007805	0.9428	2	8.354	72.2	0.0049	0.0209	7.35	13.9	0.1284	0.1375

DNA replication		Correlation with MKI-67		Transcription cluster	Time to relapse				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value		Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values
CDC6	Pre-replication complex	0.6909	2.78E-13	3	6.618	18.5	0.1153	0.1317	8.232	67.1	4.36E-11	4.56E-10
CDT1	Pre-replication complex	0.799	0	3	7.727	53.7	6.87E-06	0.0003	8.636	58.2	1.39E-08	7.29E-08
GMNN	Pre-replication complex formation	0.5515	4.02E-08	3	9.023	79.6	0.0188	0.0419	9.418	81.0	4.90E-06	1.27E-05
ORC1L	Pre-replication complex	0.8265	0	3	4.27	35.2	0.0179	0.0419	5.709	65.8	2.33E-12	4.53E-11
ORC2L	Pre-replication complex	0.137	0.2056	2	8.245	77.8	0.0040	0.0190	8.577	84.8	2.69E-05	5.91E-05
ORC3L	Pre-replication complex	-0.09642	0.3742	1	8.879	13.0	0.0869	0.1055	10.12	87.3	0.1356	0.1418
ORC4L	Pre-replication complex	-0.05241	0.6296	2	8.576	29.6	0.0104	0.0352	9.099	75.9	0.0518	0.0612
ORC5L	Pre-replication complex	0.1365	0.2076	2	8.235	16.7	0.2891	0.2912	9.51	88.6	0.0043	0.0063
ORC6L	Pre-replication complex	0.5775	6.56E-09	3	6.859	31.5	0.1595	0.1764	7.249	39.2	6.61E-05	0.0001
MCM2	Pre-replication complex	0.6644	4.22E-12	3	8.327	33.3	0.0182	0.0419	9.538	68.4	9.34E-08	3.74E-07
MCM3	Pre-replication complex	0.6724	1.91E-12	3	10.71	64.8	0.0007	0.0073	10.84	67.1	1.28E-06	3.95E-06
MCM4	Pre-replication complex	0.5926	2.13E-09	3	10.35	87.0	6.92E-05	0.0024	9.63	51.9	0.0019	0.0032
MCM5	Pre-replication complex	0.7685	0	3	8.481	20.4	0.0135	0.0353	9.854	72.2	3.84E-12	6.54E-11
MCM6	Pre-replication complex	0.7319	2.22E-15	3	9.488	74.1	0.0182	0.0419	9.835	70.9	9.45E-12	1.07E-10
MCM7	Pre-replication complex	0.7683	0	3	9.544	31.5	0.0724	0.0937	10.64	68.4	1.59E-08	7.71E-08
CDC7	Initiation of DNA replication	0.7383	8.88E-16	3	7.835	87.0	0.0388	0.0621	7.224	59.5	5.03E-09	3.26E-08
CDC45	Initiation of DNA replication	0.8867	0	3	4.76	38.9	0.0001	0.0032	6.869	64.6	1.92E-12	4.36E-11
DBF4	Initiation of DNA replication	0.5082	6.02E-07	4	8.057	85.2	0.0019	0.0125	8.242	78.5	2.65E-08	1.16E-07
MCM10	Initiation of DNA replication	0.8755	0	3	3.969	27.8	0.0077	0.0285	6.271	69.6	3.03E-14	1.37E-12
GIN51	Initiation of DNA replication	0.6637	4.55E-12	3	8.318	85.2	0.0330	0.0544	7.97	64.6	1.34E-07	5.06E-07
GIN52	Initiation of DNA replication	0.6816	7.40E-13	3	6.921	31.5	0.0534	0.0733	9.17	86.1	6.73E-11	6.53E-10
GIN53	Initiation of DNA replication	0.01906	0.8609	1	9.355	57.4	0.0819	0.1032	8.902	41.8	0.0024	0.0038
GIN54	Initiation of DNA replication	0.6338	7.28E-11	3	6.987	57.4	0.0018	0.0125	7.365	59.5	1.72E-06	5.21E-06

WDHD1	Initiation of DNA replication	0.6982	1.24E-13	3	5.919	24.1	0.0308	0.0531	7.529	74.7	3.07E-06	8.89E-06
FEN1	DNA replication	0.6892	3.32E-13	3	8.774	38.9	0.0002	0.0040	9.846	74.7	6.69E-09	3.96E-08
LIG1	DNA replication	0.623	1.83E-10	3	9.923	79.6	0.0153	0.0378	9.923	65.8	2.05E-07	7.52E-07
PCNA	DNA replication	0.4114	8.12E-05	3	10.7	38.9	0.0462	0.0675	11.09	55.7	0.0295	0.0361
RFC1	DNA replication	0.007875	0.9423	1	9.625	7.4	0.0478	0.0684	10.95	83.5	0.0792	0.0898
RPA1	DNA replication	0.04381	0.6869	2	10.38	44.4	0.0286	0.0522	9.82	12.7	0.0791	0.0898
RPA2	DNA replication	0.283	0.0080	4	10.17	85.2	0.0142	0.0357	10.36	82.3	0.0240	0.0303
RPA3	DNA replication	0.2234	0.0377	4	9.632	85.2	0.1721	0.1873	9.647	87.3	0.0014	0.0024
RPA4	DNA replication	0.1688	0.1182	2	1.198	46.3	0.2508	0.2584	2.079	88.6	0.1499	0.1556
TICRR	DNA replication	0.7778	0	3	5.99	79.6	0.0021	0.0130	6.736	68.4	5.71E-12	8.63E-11
TOP1	Topoisomerase	-0.03081	0.7769	1	10.86	25.9	0.0090	0.0314	10.55	19.0	0.0146	0.0195
TOP2A	Topoisomerase	0.9284	0	3	7.097	20.4	0.0194	0.0419	9.946	69.6	6.80E-12	9.25E-11

S phase checkpoint		Correlation with MKI-67			Time to relapse				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value	Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values	
ATR	ATR + Rad17-9-1-1 DNA damage sensors	0.06289	0.5627	1	10.57	85.2	0.0423	0.0644	10.38	70.9	0.1355	0.1418
ATRIP	ATR + Rad17-9-1-1 DNA damage sensors	-0.07991	0.4618	2	8.318	87.0	0.0932	0.1093	7.658	31.6	0.2645	0.2684
HUS1	ATR + Rad17-9-1-1 DNA damage sensors	-0.02332	0.8302	1	7.75	13.0	0.0044	0.0200	8.911	72.2	0.0361	0.0430
RAD1	ATR + Rad17-9-1-1 DNA damage sensors	0.3105	0.003495	4	10.01	70.4	0.0016	0.0125	9.695	46.8	0.0269	0.0336
RAD17	ATR + Rad17-9-1-1 DNA damage sensors	-0.132	0.2229	1	9.195	25.9	0.0477	0.0684	9.471	49.4	0.0005	0.0008
RAD9A	ATR + Rad17-9-1-1 DNA damage sensors	0.2789	0.009017	4	8.111	50.0	0.0126	0.0352	8.014	35.4	0.0034	0.0051
RFC2	ATR + Rad17-9-1-1 DNA damage sensors	0.6268	1.33E-10	3	9.459	88.9	0.0884	0.1060	9.473	79.7	1.45E-08	7.29E-08
RFC3	ATR + Rad17-9-1-1 DNA damage sensors	0.5021	8.58E-07	4	9.388	88.9	0.0019	0.0125	8.922	58.2	2.72E-06	8.03E-06
RFC4	ATR + Rad17-9-1-1 DNA damage sensors	0.586	3.51E-09	3	7.382	24.1	0.0656	0.0867	8.651	79.7	5.18E-08	2.20E-07
RFC5	ATR + Rad17-9-1-1 DNA damage sensors	0.5417	7.68E-08	3	7.937	25.9	0.0583	0.0785	8.392	51.9	0.0001	0.0002
ATM	ATM - MRN DNA damage sensors	-0.2387	0.02613	1	9.833	57.4	0.0596	0.0795	9.661	40.5	0.0977	0.1071
MRE11A	ATM - MRN DNA damage sensors	0.2121	0.04879	4	7.697	46.3	0.0503	0.0713	8.425	88.6	0.0026	0.0040
NBN	ATM - MRN DNA damage sensors	-0.04222	0.6977	1	9.129	9.3	0.0034	0.0179	10.39	79.7	0.0175	0.0225
RAD50	ATM - MRN DNA damage sensors	-0.2698	0.01162	1	9.881	22.2	0.0193	0.0419	10.93	75.9	0.0097	0.0135
BRCA1	ATM/ATR pathways mediators	0.642	3.49E-11	3	7.582	83.3	0.0060	0.0234	6.558	53.2	9.16E-06	2.15E-05
CLSPN	ATM/ATR pathways mediators	0.7709	0	3	3.101	42.6	0.2338	0.2427	5.216	79.7	3.17E-10	2.54E-09
TIMELESS	ATM/ATR pathways mediators	0.6557	9.78E-12	3	9.175	48.1	0.2204	0.2306	10.03	79.7	6.22E-15	4.23E-13
TIPIN	ATM/ATR pathways mediators	0.1816	0.09256	4	5.981	40.7	0.2053	0.2181	6.53	70.9	0.0054	0.0077
TOPBP1	ATM/ATR pathways mediators	0.4434	1.88E-05	4	8.456	24.1	0.0435	0.0644	8.661	32.9	0.0016	0.0027
CHEK1	ATM and ATR pathways regulated kinases	0.6022	1.00E-09	3	7.724	85.2	4.35E-07	2.96E-05	7.784	79.7	3.27E-06	9.26E-06
CHEK2	ATM and ATR pathways regulated kinases	0.642	3.49E-11	3	7.582	77.8	0.0060	0.0234	6.558	45.6	9.16E-06	2.15E-05
H2AFX	ATM and ATR pathways effector	0.5574	2.69E-08	3	10.27	85.2	0.0111	0.0352	10.3	72.2	1.11E-16	1.51E-14
TP53	ATM and ATR pathways effector	-0.06086	0.5754	1	10.02	79.6	0.0002	0.0040	10.13	84.8	0.0019	0.0032
MDC1	ATM and ATR pathways effector	0.4496	1.39E-05	4	8.99	44.4	0.0142	0.0357	8.658	22.8	0.0044	0.0064
TP53BP1	ATM and ATR pathways effector	-0.09276	0.3927	1	9.333	11.1	0.1691	0.1855	10.16	57.0	0.0168	0.0217

Stalled forks restart by remodelling / DSB repair		Correlation with MKI-67			Time to relapse				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value	Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values	
BLM	Helicase	0.6556	9.96E-12	3	5.692	87.0	0.1234	0.1399	5.692	68.4	1.33E-09	1.00E-08
BRIP1	Helicase	0.581	5.06E-09	3	3.968	22.2	0.2589	0.2647	5.658	72.2	0.0032	0.0049
FANCM	Helicase	0.4251	4.41E-05	4	7.034	61.1	0.0030	0.0168	7.204	67.1	0.0003	0.0006
SMARCA1	Helicase	0.146	0.1773	2	8.843	35.2	0.0205	0.0428	9.37	81.0	0.0152	0.0200
WRN	Helicase	0.118	0.2763	2	8.697	83.3	0.0303	0.0529	7.163	13.9	0.3214	0.3214
EXO1	Exonuclease / Recruitment to DSBs	0.8979	0	3	4.96	46.3	0.0017	0.0125	7.003	72.2	7.86E-13	2.14E-11
BRCA2	Recruitment to DSBs	0.6932	0.0000	3	3.64	18.5	0.0850	0.1041	5.991	69.6	1.23E-06	3.90E-06
FANCD2	Recruitment to DSBs	0.635	0.0000	3	7.814	87.0	0.0111	0.0352	7.431	63.3	1.85E-08	8.69E-08
RAD51	Recruitment to DSBs	0.8551	0	3	4.375	37.0	0.0028	0.0164	6.877	75.9	1.72E-10	1.56E-09
RAD51C	Recruitment to DSBs	0.271	0.0113	4	7.916	37.0	0.0429	0.0644	8.124	58.2	0.0016	0.0027
RAD51L3	Recruitment to DSBs	0.2801	0.0087	4	7.396	87.0	0.0523	0.0731	7.465	82.3	0.0071	0.0099
RMI2	Recruitment to DSBs	0.6815	7.53E-13	3	7.648	38.9	0.0006	0.0069	8.75	59.5	2.54E-09	1.73E-08
XRCC2	Recruitment to DSBs	0.6583	7.65E-12	3	4.88	42.6	0.2102	0.2216	5.494	68.4	3.63E-06	1.01E-05
MCM8	Interstrand crosslink repair	0.2491	0.0202	4	7.916	63.0	0.1046	0.1205	8.631	87.3	0.0034	0.0051
MCM9	Interstrand crosslink repair	-0.2139	0.0468	1	3.633	14.8	0.0289	0.0522	5.356	86.1	0.0300	0.0364
PARP1	Interstrand crosslink repair	0.3815	0.0003	4	10.26	20.4	0.0433	0.0644	11.14	67.1	7.65E-07	2.48E-06
RMI1	Interstrand crosslink repair	0.2378	0.0267	2	9.486	77.8	0.0082	0.0293	9.164	64.6	0.0322	0.0387
TOP3A	DNA end processing by MRE11	0.2494	0.0200	4	8.308	24.1	0.0788	0.1002	9.098	86.1	0.0034	0.0051
GEN1	Holliday junction dissolution	0.4515	1.27E-05	3	8.202	85.2	0.2007	0.2149	8.259	79.7	4.72E-06	1.26E-05
XRCC3	Holliday junction dissolution	0.5689	1.21E-08	3	7.472	55.6	0.0897	0.1060	7.874	64.6	6.29E-08	2.59E-07
MUS81	Holliday junction resolution	0.1526	0.1582	4	8.886	66.7	0.0834	0.1040	8.951	59.5	4.94E-06	1.27E-05
EME1	Holliday junction resolution	0.6979	1.28E-13	3	4.216	29.6	0.0245	0.0490	5.389	60.8	5.75E-09	3.56E-08
FAN1	Holliday junction resolution / Interstrand crosslink repair	-0.08815	0.4167	1	9.192	83.3	0.0708	0.0926	8.769	51.9	0.09213984	0.1018782

dNTP synthesis		Correlation with MKI-67			Time to relapse				Overall Survival			
Gene	Cellular process	Correl. Coef	P-value	Cutoff	Percentile	P-value	Adj P-values	Cutoff	Percentile	P-value	Adj P-values	
RRM1	Ribonucleotide reductase	0.5658	1.50E-08	4	10.1	63	0.0292	0.0522	10.3	60.7	2.51E-07	8.53E-07
RRM2	Ribonucleotide reductase	0.9112	0	3	6.59	40.7	0.0124	0.0352	9.619	78.5	7.69E-12	9.51E-11
RRM2B	Ribonucleotide reductase	-0.1183	0.2751	1	10.89	70.4	0.0296	0.0523	9.512	17.8	0.0004	0.0007

MKI67	Indicator of cell proliferation	-	-	3	6.762	31.5	0.0134	0.0353	9.709	70.9	1.54E-13	5.25E-12
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