NCBI gene symbol	Target seq 1	Target seq 2
POLE2	TTCCGTGAAGACTTAGTAAAT	TACCGAATGCCTCTGCATAAA
MPG	CCTGTACGTGTACATCATTTA	CACCGCCAGCCGTGTCCTCAA
NFKBIL2	AACCACCTTTACGAGGACCTA	CTGGGTAGTGCTTTCCAAGAT
CA14	CGGGATCTCTCCTTAGGATAA	GTGGGTGAGACTAAGAATATA
TGFB2	TGGATGCGGCCTATTGCTTTA	CAGGTATTGATGGCACCTCCA
PRPF19	AAGTACATTGCGGAGAATGGT	CCCGGCCATTCTGAAAGCTTT
TERF2	TGGGCTATGTAGGCAGGTTAA	AAGGAACTTAGTCTGTTATGA
HIST1H1E	CTCGCTCACGCTTGCCTTCAA	AGCGGCGAAGAAGCCCAAGAA
DNAJC5	CTGCTGCTGCGGGAAGTGTAA	CGCCAACCTTAGAATCATGAA
EXO1	CAGATGTAGCACGTAATTCAA	ATGGATGTACTTTACCTTCTA
BTG2	CAGGCCTGTCTCTCCTATTAA	CTCGAGTTTCCCAAACCGAAT
POLB	TACGAGTTCATCCATCAATTT	CAGGTTGTGGAGCAGTTACAA
ALKBH2	CACGGACGTGTTGCAGTGATA	ATGGACAGATTCCTGGTGAAA
XAB2	CCGCGTGTACAAGTCACTGAA	CACGTACAACACGCAGGTCAA
SUMO1	CAGTTACCTAATCATGTTGAA	CTGAAGTGCCTTCTGAATCAA
HNRNPM	AAGACTTGGAAGCACAGTATT	AAGCTGTGCAAGCTATATCTA
UPF1	TGGCGTCATCATTGTGGGCAA	ATCAAGGTCCCTGATAATTAT
ESPL1	CAGCAGCTGACTGCTAAGCTA	CAACTAGTGGACAGTTGTAAA
RRM2	GCGGGATTAAACAGTCCTTTA	AGCAAGCGATGGCATAGTAAA
POT1	TGCCGCTATTACAACTTACAA	GAGGGCGATTTGGATATAATT
PCNA	ATGGATTTAGATGTTGAACAA	AAGGATCTTAGGCATTCTTAA
C7orf11	TAGAGATTTACCGTTTCCATA	CCCAGGGTTCTCCAAGGACAT
LMNA	CCAGGAGCTTCTGGACATCAA	AACTGGACTTCCAGAAGAACA
RNF8	CCTCATCGTATCTAAGGATAA	CAAATGGTAAACTGTACGCTA
DHFR	AACCTCCACAAGGAGCTCATT	AAGAATTAATTGAGCCCACGA
PARP3	CCAGAGCGAGTACCTCATCTA	CAAGGCCATACCCGCAGAGAA
CACNA1G	CCTGGTGTACATCCTTCGTAA	CCGGAGCTTCATGCGGCTCAA
RAD51L3	TCAGAGCAGAGTGCCACATTA	CCAAATCTTCCCGACAGCCAA
FEN1	TAAGTCCATTGTTACATGAAA	CACCATTCGCATGATGGAGAA
NTHL1	ACCGTCTGTGAAGTGGCTTTA	CAGGCTGAGGTGGACCAAGAA
ERCC5	AAGAAGATGCTAAACGTATTA	CGCCATGGGAACTCAATAGAA
DCLRE1B	CCAGATCTCTATAGCAAAGAA	CACCTACAGGTATCTAAGCAA
BRCA1	ACCATACAGCTTCATAAATAA	CAGGAAATGGCTGAACTAGAA
EEF1E1	TTGAAGATAAAGTCTACCTTA	ACCTTACAGGGTATAACTTTA
RPS19BP1	CAAGTCGGCACTGGACGAGTA	CAGAGTAAACCTGAAGTTTCT
MSH5	CAGGATGAGAATATGACTCGA	TTGCCAGACATTAGTGGATAA
TINF2	ACCAACCCAGGTCATATCTAA	AACGCCTTTGTATGGGCCTAA
FANCA	CCGCAGGTCACGGTTGATGTA	CAGGGCCATGCTTTCTGATTT
RPA1	CAGGAATTATGTCGTAAGTCA	TCCCTAGAACTGGTTGACGAA
PTTG1	CAGAATGGCTACTCTGATCTA	AAGACCTGCAATAATCCAGAA
MAD2L2	CACCCGGAGCTGAATCAGTAT	AAGATGCAGCTTTACGTGGAA
SRSF1	TTGGCAGGATTTAAAGGATCA	CTGGACTGCCTCCAAGTGGAA
FANCF	CTGCGCTTCAATGGCTATAGA	AAGATTAGGAATCTACGCATA
GTF2H1	CCCAGAGCTGATGCTATTGTA	CGGATCCAACCCAGTTAGTTA
GTF2H3	ATGGCATTAATCAACATAGAA	ATCAAGGATATTGGTGATTAA
RFC4	CAGAAGTCTATTATCACAGAA	CCGATTCTGTCTTATCTGTAA
FAM175A	ATCGACTGGAACATTCCTTAT	CAGTACAAGCCTGGTAATCCA
SLX4	CAGCGAAAGCTTCTCCAGGAA	CAGGCCCAATTTGAACAAAGA
XRCC6	ACCGAGGGCGATGAAGAAGCA	AAGCTCTATCGGGAAACAAAT
LIG3	CTGGGAAGAGCTGGAAGATAA	CTGGAAGATAATGAGAAGGAA
NBN	AAGGAAGACTGCCCTACTATA	ATGGATATGCTCCAAAGGCAA
REV1	CTCCGGGAACAAGTAGAGCAA	ATCGGTGGAATCGGTTTGGAA
DMC1	GAGGATCAAGTTGTGGCGGAA	AACGTACTTTATGCACGTGCA
NEIL2	CACCATCGTGAAAGATGGGAA	AGCTGCTTGTTTACTCCTTAA

SBDS	TTGGAAGTACTCAATCTGAAA	TTCCGAGAAATTGATGAGCTA
RBM14	AACAGTTCGCCTTCGTGCACA	CTCTCTGATTACCGCCGTTTA
RAD54L	AAGCATTTATTCGAAGCATTT	AGGGACTGCCCATGAATTCAA
LIG1	CCGGACGTTTGAGAAGATCGA	CAGCGAGGTCCTGAAACGCTT
UHRF1	CCGCTACGATGGCATCTACAA	CCACGTGAAATACGACGACTA
XRCC1	TCGCATGTTTGGGCCTGACAA	CCGCTCCGAGCTGCGAGATAA
TK1	TCGGCTCTGCTACTTCAAGAA	CGGGCCGATGTTCTCAGGAAA
ABL1	AAAGACAAAAAGACCAACTTG	AACTTGGTGAAGGTAGCTGAT
MAD1L1	CACGCTCAGGTTGAAGGTCGA	CACGAGCAGCAGATTAAGGAT
XPA	TGGGAGCTGAGTGCTAGAGTA	AGGGAGACGATTGTTCATCAA
CBX5	TTCCTACAGGATGGGATCTAA	TGCCGATGACATCAAATCTAA
CRY2	CCCGGGTGGCAGAGTTGCCAA	AAGGACGACGGTGGCCAACTA
NUP98	CTCACTAAGGTTGGTTACTAT	AACCCTATTGCCAAACCTATT
C19orf40	AAAGGAATTGTAGTCGTTGAA	TTCGGGTTAGAAATTCCAATA
FANCB	CTGCCATAGCTAAACATGAAA	TACGGCAGCATCTGTTGCTTA
DCK	TTGGTATAAATTAATTTGTTA	AAGTTGCAAAGTGGAATTAAA
RPIA	TCGCTTCATCGTGATCGCTGA	AACCACGTGAGGAATAACCAA
FANCC	CGCGAGGACCACCCGATTTAA	TAGACTCTCCCTGATAGTTTA
RNF168	CAGTGCGGGATCTGCATGGAA	ACGTGGAACTGTGGACGATAA
GEN1	TTCGAATTGTTAAGACTCGAA	CACCTAAGGATCATGAACGTA
ERCC3	CCGGTTCACCTCCGATGCCAA	CTCGTCCGCGAAGATGACAAA
MBD4	AAGCTTCTCATCGCTACTATA	CAGGACCCGAAGCAAGTGCAA
ALKBH3	ATCGCTATCATCTTTAGGCAA	CAGAGAGGATATAACTTATCA
HMGB2	CTGCAAAGAAATTGGGTGAAA	AAAGGAGAAGTCGAAGTTTGA
POLL	CCGGGCAGAACTCTTTGAGAA	CAGCCCATCTCTGATGATGAA
SFPQ	AATATGGAGAACCAGGAGAAG	GAGAGGAAAGTTACAGCCGAA
TREX1	CTGGCAGCGCATGGGCGTCAA	CAGCATCTACACTCGCCTGTA
MLH3	CAGAAGGTTGCTATATAGTAT	ACGAATATAAGTTATGGGCTA
RAD23B	CTGGGATGACTTGGGCTCATA	TAGGTGTCTAATTACTGTTTA
GADD45G	TGCGAGAACGACATCGACATA	TCCGAGCTGAGGACTCTGCAA
RAD1	CAGCACCAATGTTATTAATAA	CAGTATATGATTAGAAATGAA
FAN1	CTGCAGGATGACAGTTGCTTA	CTGGTGGACGCCTTTCTCAAA
FANCL	CACTCTCAAGTTGAAGGCAAA	TAGGATAGTGTTGCCTGAAGA
RPA2	AACAGTGGATTCGAAAGCTAT	AGGGTGGGATTTCTTGAGGAA
XRCC5	AAGCGAGTAACCAGCTCATAA	AAGCATAACTATGAGTGTTTA
TDP2	CGGAACGAATGAATCAGTTAA	CCCAAGACCTATGTTGACCTA
RPL5	CAGCGTAACTCCAGACATGAT	TACATGCGCTACTTAATGGAA
ATR	CAGGCACTAATTGTTCTTCAA	AAGGACATGTGCATTACCTTA
RPA3	CACCACGTATCATTCCGCAAA	TCCGCGCATTTAATTGGCGAA
HERC2	CAAGTCGGTGGCCACCTATAA	CAGCGACGATTCAGATAACGA
TDG	AGGACGTATTCTAGTACAGAA	TAGGTATTGCTTTGGTATATA
CHAF1B	CACCAATGTCAGGATCTGGAA	ACGGAAAGTCTGGACCCTTGA
ATRX	CTCCAGTGCATTTCTATCGTA	CCCAGCAATCACAGAAGCCGA
CHEK2	CTCCGTGGTTTGAACACGAAA	CAGGATGGATTTGCCAATCTT
RALY	AACGTACCTGTCAAGCTCTTT	TCAGGCAAGCAATGTAACCAA
POLE	ACAGATCGGAATATTCCGGAA	AACCGTATTTCTACATTGCGA
PNKP	CGGGAAGTCCACCTTTCTCAA	CAAGCTGGTGATCTTCACCAA
POLM	CCCAGACCACTCATCACATTA	CTGCTGGACATAAGCTGGTTA
BCL2L1	TAGGGTGGCCCTTGCAGTTCA	CAGCTGCCTCACTTCCTACAA
FANCG	CTCATTGAGGTAGAATTACTA	CCGGCTCGTTCGACAGGCCAA
HMGB1	TCCTTTCATATAGTTAGCTAA	AACCTTTACATGAGGACTCTA
SIRT1	AGCCATCGGAATGTTAAATTA	TTGGGTCTTCCCTCAAAGTAA
TOP3A	AACAGCGACTGTACGAGTTTA	TTCTCGAAAGTTGAGAATAAA
INTS3	CTCGAAGTCGAAAGAATGCCA	AAGACACGAAACCGAAGCCTA
FANCM	AAAGAGGTACTAGCTAATGTA	TTCGACGATGTGAGTCTTTCA

WRNIP1	ATGAATTAATGTTATAAGGAA	CAAGCGGTTGCTGCCTACCAA
MLLT1	CCGCAAAGACTCCGAGAGCAA	CAAGCCTGAGAAGATCCTCAA
UBE2B	GAGGCTCATGCGGGATTTCAA	CAGAATCGATGGAGTCCAACA
VRK3	AAGTATCCAAGCGGCATTCAA	CAGACCTTTGTCAATCCACAT
RAD51C	CTGCAAATTATCAGAAGAGAA	AAGAGAATGTCTCACAAATAA
RFC1	TTGGAGTAATACCAAGTGGAA	TCGGACTATGCCAGGCAAGAA
POLG2	AAGGAACAGCTAGTAGCATTT	CTCCGGATTCTGTTAACGGTA
CTPS2	CTGCTACGCCTCTGTGTTCAA	CACGGTGAAGTCTTCGTCTTA
SLX1A	CTGGGAGATGGTGCTCGTCGT	CGAGAGCTTGTTCCGAAGCAA
RAD50	CAGGAACAGATTCAACATCTA	CAGAAAGTGTATAATAAGAAA
PARP4	CAGGATGAGAGCCTGACATTA	CAGAAGGCGAGCAGTTCTGAA
TOPBP1	CTAGGTGGATTGGTGATAGAA	ATGAACCGCTTTCAGAGTAAA
SMARCAL1	TTGATTGGGTACAATGCGGAA	CAGAACAGCATCAGAGGACTA
RPA4	TCAGGACGTTGTACCGTGTAA	AACGATGAGAGTCACCGCAAT
PRKDC	GACCCTGTTGACAGTACTTTA	TTCGGCTAACTCGCCAGTTTA
TDP1	CTGGAGTTAAGCCAAAGTATA	GTGGATAGATGTCATTCACAA
TERF1	CACAGTATACTCAGCTAACAA	AACATGGATGAGTACCATATA
KPNA1	CCTCACGGTCATGGACTCTAA	CTGGTATGAGGATTTCGAATA
OGG1	TCCGTGGACTCCCACTTCCAA	CGGATCAAGTATGGACACTGA
PMS2P4	CTCATTGAAGTTTCAGACAAT	TGCGGTGAAGGAGTTAGTAGA
TOP2A	CACGTAGGCTGTTTAAAGAAA	ACGAATAACCATAGAAATGAA
HNRNPU	CTGGCCGTGGTAGTTACTCAA	AGGATATTATTGAATACCCAA
GADD45A	AACATCCTGCGCGTCAGCAAC	TCAATGGGTTCCAGTGATTAA
PMS2P3	TCTGCATGTTTCCAAGAGCAA	CAGCACCTAGGCGGACGCGGA
EP300	CCCGGTGAACTCTCCTATAAT	ACCAAGGGTTGCAAACGGAAA
MLH1	GTGGCTCATGTTACTATTACA	AACCATCGTCTGGTAGAATCA
RAD51L1	TAGGAAATACCTGGAGTCACA	AAAGTTCATCTTTATCGGGAA
RPL11	AAGGTGCGGGAGTATGAGTTA	CTGGTTCCAGCAGAAGTATGA
C11orf30	TTGGCTCTTCCCTAACGACAA	AAGGCCGTTGTTCCAGTCTCA
DDX17	CCGGGAGCTACCAATATGATA	CAGATCTGATATGGGACTATT
KPNA3	CTGTTCGGACACTATAGTCTA	CCAGATGGCTACCAAATGATA
BUB3	ATGCATGATTTGAACACTGAT	AAGTTGGGATCAGACAGTTAA
PML	CACCCGCAAGACCAACAACAT	CAGGAGCAGGATAGTGCCTTT
SIRT6	TGGAAGAATGTGCCAAGTGTA	CCGGCTCTGCACCGTGGCTAA
OBFC2B	CAGTGTCCTTATCCACCCTAA	AGGCCGAGTGACCAAGACAAA
PER1	CCCAGCGGTTGTCCAGCCCTA	CCCGGACTCTCCACTGTTCAA
SPO11	TTGCATCATGATTACGGGAAA	TACCTTCTACGATACAACTAA
FANCE	GAGGAAGTGCATCTCCTATTA	CCCGAACATAAGTCACTGGAA
XRCC2	CAGGGTACTACGCAAGCCTTA	GTGCATGGTGATATTCTTGAA
ERCC4	CTGCTCGACACTGACGGGCTA	CTCCTTGATGCACCACGTTAA
CHEK1	TTGGAATAACTCACAGGGATA	CCCGCACAGGTCTTTCCTTAT
MCM2	CTCATTGGAGATGGCATGGAA	GAGGCCCTATGCCATCCATAA
UIMC1	CCCTGATGGAGTAGACCCTAA	CAGATTGCTTAGTGGACTTTA
POLD1	CCGAGAGAGCATGTTTGGGTA	CTGGTCCACCTTCATCCGTAT
XRCC3	CCGCTGTGAATTTGACAGCCA	AAGCCAAACTGAAATCGGTAA
TOP1	GCCCGAGGATATAATCATCAA	TCCGGCATGATAACAAGGTTA
RMI1	CTGGTGTTCGGTGGTGAGTCA	CAGGTAGTTCCTCAAATACCA
BUB1	TGGCACTTACATGAAAGTGAA	CAGCTTGTGATAAAGAGTCAA
EME1	GAGGAGTGCAGCAGATAACAA	CACAGCCAGTCAGGTTGCTAA
RPS9	CGGAGCTGGGTTTGTCGCAAA	CCCGGGCCGCGTGAAGAGGAA
EME2	TACCAAGGCTCTCGCCCAGTA	GTGCGTGATGCCAAGGCTGAA
SUPV3L1	CTGGCACATGAGATCTTCGAA	ATGGCCTTTACTTCCACCTAA
CSNK1E	GTGGTTGTTAATTTGAAGTAA	GAGCTTTATCGTGGTTGTTAA
POLD2	CCGGGTGCCAGTGGCAACCTA	CAGTGGAGTGGGAGTGAAGAA
RAD17	CTCAGTGGAGATAATAATCAA	TATCGGGATTCTCATACTTTA

BRIP1	TAGATAGTATGGTCAACAATA	ACAGTCAAGAGTCATCGAATA
SMC1A	CACCATCACACTTTAATTCCA	AAGGGTCGACAGATTATCGGA
REV3L	ATGAGTATGGATCATATACAA	CGGGATGTAGTCAAACTGCAA
POLR1C	TACGTGAACCACAAAGTGTAT	CCCGGTAACTATTCCGGTTAT
APTX	AAGCATTGGGCTGGTTATACA	AACATTGGAATTCTTTCAATA
ERCC6	CAGGATGACATTAGCAGGTAT	CAGGACTCGTGGTTCAAATTA
YY1	AACAATAGCTTGCCCTCATAA	CAGAAGTGTGATTGGGAATAA
SUCLA2	ATGCGCTGTGATGTTATTGCA	AAAGAACCTATTGATATTGAA
IGHMBP2	CACGACTGTGGTTGAGATCAT	CCAGTTGAGCTTGGACCGAGA
RAD23A	CAGGCCTATTTCGCGTGTGAA	AAGGTGCTAAAGGAGAAGATA
RECQL4	CTCGGCCGCTACTTTGAGGAA	TTCCATTATCATTTACTGCAA
SETMAR	ATGTTTATAATGGGCAGGTAA	CCAAGTGTTCAAGACGCATAA
RAD9A	GCCCGCCATCTTCACCATCAA	CAGGGTCATCCTGCGCAGCTA
C10orf92	TGCGTATTACTTGGAAGCGTA	CAAGTTCGTCGTGGACCCATA
SMUG1	CAAGAGCATCCTAAACGACCA	CAGATTATGAGCTTACAGAAA
APEX1	CTGCATTCTATTTCTCATGTA	CCAGATATACTGTGCCTTCAA
ATRIP	CCAGACGGAGTCAGGATACAA	CAGGTTCTTATGATGGGTCAT
SUPT16H	CAGCATATGCATGACCGAGAT	TCCCTAGTAATCAATAGCAAA
RAD54B	CTGGATCAAATTAAGAATATA	ACCCAAGAAATTATAAATAAA
POLG	CAGATGCGGGTCACACCTAAA	CAGCCCTTTGCTGAGCGCTTA
UBE2I	ACCACCATTATTTCACCCGAA	CAAGAAGTTTGCGCCCTCATA
LIG4	ATCTGGTAAGCTCGCATCTAA	TGGTGAGATGATGGCCTATAA
DDB2	CTGGATTCTTACCGGATATTA	AGGGATCAAGCAGTTATTTGA
ERCC8	CAGAGTCAACACGGAGAGTTT	CTCCAGCAGACAATCTTATTA
CENPE	CACGATACTGTTAACATGAAT	CAGGTTAATCCTACCACACAA
SSBP1	AGCCTAAAGATTAGACTGTAA	TCGGGTTAGATCGTCAGGAAA
MSH3	CGCCGCTAGAATTACAATACA	CAGCAAGGAGTTATGGATTAA
TNKS2	CCCAGTGTAAATGGCCTAGCA	TTGCTGCAAGCTGCACGAGAA
IP6K3	CTGAGATACGTTACCCAATTA	AAGACTGGTGGACAAGTGTAA
ERCC2	AAGAACTGTGCCAGAGATTGA	AAGACGGTGCTCAGGATCAAA
SSRP1	CTGGAGTTCAACGACGTCTAT	TACGATGAATATGCTGACTCT
NEIL1	GGCCGTGATGATGTTTGTTTA	ATGATGTTTGTTTATGAGTTA
DNA2	TACCGCTTAAATCTAAGTCAA	CGACGTCTTAATGTTGCTATA
MAD2L1	CTGAAAGTAACTCATAATCTA	ATGGATATTTGTACTGTTTAA
MSH6	ATCGCCATTGTTCGAGATTTA	TGGCTGTAGGACCATAGTCTA
SHFM1	AACTAGAGAAACATGGTTATA	GACAGTCGAGATGTCAGAGAA
DDX1	AAGGCACCGGATGGTTACATT	TCCCGGGAGTTAGCTGAACAA
ERCC6L	ATCCTCGATGAAGCACATAAA	AAGGATTGTTTCAGATGGCGA
CETN2	AACTGGGAAGATTTCGTTCAA	AAGCACATGTAACTAGATTTA
RECQL5	CCCTGTAATTGTTGCAACCAT	CACTTGCTAACCCTAAAGGTA
TERF2IP	TTGGGATAGATTCCAAATAAA	CCGGATGTCTTTCTTTACCTA
MMS19	ATGGCTGTACAAAGAACATAA	CAGCTTGTTGGCATCCGTACA
DDX3X	CTCGTAGTGATTCAAGAGGGA	AACGAGAGAGTTGGCAGTACA
MSH4	ATAGCCCTACCTAGTGATCAA	TTCGACCAGAATTTACTGATA
PELP1	CGGGCTTGTGGTTCTCTCAAA	TTGGTGAGTCTCAGTAATGCA
TMPO	AACCAGGAAGCTATATGAGAA	AAAGATGATCTAGATGTAACA
TREX2	CCGCTGATTAAAGGCCGCCTA	CCAGGCCTCATTGTTGGCCAA
APC	ACGCGGAATTGGTCTAGGCAA	AAGACCTGTATTAGTACGCCA
TYMS	CCGTGACCTATCAGTTATTAA	CAGAGATATGGAATCAGATTA
RDM1	AAGGGTATCTCTCGGATTTCA	TCCCAAGGCGAGGTCATGTAA
PIF1	AGGGAAGTCATATCTGCTAAA	GAGCCTAACCAAAGAACATAA
POLI	AAGCCTCATACAGTGAGATTA	TTCGGATTAGCGGTTTATTAA
UBE2V2	CAGAAGCTCCTCCGTCAGTTA	AGGAGTTAAAGTTCCTCGTAA
MNAT1	AAGAGCAACTTCAGGGTACAA	AAGGAGGTTGAGATCAGGAAA
HIST1H2BK	CTCGAAGAAAGCCGTGACTAA	AGCGCTAAGTAAACTTGCCAA

HDAC1	CCCGTTCTTAACTTTGAACCA	CGGGATTGATGACGAGTCCTA
MSH2	CCCATGGGCTATCAACTTAAT	AAGAAGATGCAGTCAACATTA
RRM1	CAGCTACATTGCTGGGACTAA	ATCGCCTGAATTCTGCTATTA
POLA1	CTGCATGAAAGCTACACTTCA	CAGGATCTTAACACTGAGACA
NEIL3	CCTGGATATTCTAACAGTGAA	CAGATGGCCCTCGTACCTTAA
BLM	AAGCGACATCAGGAGCCAATA	GACGCTAGACAGATAAGTTTA
WRN	CGGATTGTATACGTAACTCCA	TCCGCTGTAGCAATTGGAGTA
USP1	AACCCTATGTATGAAGGATAT	ACAGGCATTAATATTAGTGGA
XPC	TAGATGAGTGTTAAACTAGAT	ATCGTCTGCGAGGAATTCAAA
HDAC2	GACCCATAACTTGCTGTTAAA	TCCCAATGAGTTGCCATATAA
RAX2	CAGCTGTCAGCCCATTCTATA	CACCGTGTGCTCGCCATGTGA
MUS81	CCGGGTATACCTGGTGGAAGA	ACCATTAAGTGTGGGCGTCTA
ERCC1	CAGCAAGGAAGAAATTTGTGA	TGGGCGGTACCTGGAGACCTA
DDX21	AAGCGGAGTTTCAGTAAAGCA	ATCCGAGTATATAGTGGTCAT
ENOSF1	CTGCATGAGCATTTCAAGTAT	CGAGACATGATTGGACCGGAA
POLN	CCCGGAACGTGCTATTTCAAA	CAGGAGGCACATCAACAATTT
CHAF1A	AAGCGCTTTCGCGTCCTGCAA	TTCCGAGAACTCAGTGTATGA
RPS3A	CTCCATGATGTCTTCGTTAGA	CTCACGTTGATGTCAAGACTA
MUTYH	CCAGGTTGCCACTGTGATCAA	AACCGGTGTGGTGGATGGCAA
RAE1	TTCCTGCGTAATGCAGCCGAA	CTGCCTCATCTCTGTACGAAT
MRE11A	CACATCTTTATTGAACTTGAA	AAGGGTTATTTGAGCAAGTAA
H2AFX	AAGCACCTAGATACCAGCACA	TGCCTCCTAGGAGGACATTTA
APEX2	CTGGCTATCGTTGAGGGTTAT	ACGCTGCAGCACAACAATCAA
NHEJ1	TCGATTGAAGACAGAACCATT	AGGCAACAGGTTAAACTACCA
RAD52	ACGGTCCATGCCTTTAATGTT	AAGGATGGTTCATATCATGAA
TERT	CCAGAACGTTCCGCAGAGAAA	CTGGAGCAAGTTGCAAAGCAT
POLD4	CCGGAAGCGGCTCATCACTGA	CTGGAGGTGTCAGAGGCTCAA
XRCC4	CAGCATGCCTATAATTACATA	TTGGAAGATACCGGAAGTAGA
POLH	CTGGTTGTGAGCATTCGTGTA	CCCGCTATGATGCTCACAAGA
CLK2	CAGCTACAGACGCAACGATTA	CCGAAAGACAAGAAAGCAGAA
HIST1H4A	CCGCAAGGTGTTGCGTGACAA	ATCCGTGACGCTGTCACCTAT
NCOA6	CAGCGTGCGTGTGACATTCAA	CCAGTGTACGCTCGATAGTAA
TFAP2A	TAGGTCAATCTCCCTACACGA	CTGCCTGCAGGGAGACGTAAA
BRCA2	CAGGACACAATTACAACTAAA	AAGTTGCGTATTGTAAGCTAT
POLQ	AACCAGAATGTTTATATGAAA	ATCAGTGTCTATAGCATCAAA
SPAG11B	TTCTGCCATTCTGGTGAGAAA	CAGGGATGTTGAAGTATCCCA
ATM	CACCTGTTTGTTAGTTTATTA	TTGGCTTATACGCGCAGTGTA
HIST1H2AB	AGCCATCATAAGGCCAAGGGA	CGCGGCAAACAAGGCGGTAAA
UBR2	CTGGGAAGTATTATTGGATAT	AAGAAACTATTTGCTGTTCGA
RRM2B	GAGCAGTTCAGTGGTACATAA	AACCAGGAGGTTATCATGGTA
RAD51	AAGGGAATTAGTGAAGCCAAA	CACGGTTAGAGCAGTGTGGCA
RAD51AP1	TGCCGTCAAATCAGAATCTCA	CTCTGTCTTCAGATACCACTA
GTF2H5	CTCAATATCTTAGGTGACTGA	AACATGGTCAACGTCTTGAAA
NONO	CCAAGTGGACCGCAACATCAA	CTGTGTTTGATTTGTCTCATA
POLK	AGCTGTGAGTAAAGAGGTTAA	AAGATTATGAAGCCCATCCAA
HSPA5	TGGGATAAGGAAACACTTCTA	TAGGGTGTGTGTTCACCTTCA
CDK7	GAGGCTTTAAGGTAGCTTTAA	CCGGATGGCTCTGGACGTGAA
BUB1B	CAGATTTAGCACATTTACTAT	ACGAGAATACCTAATATGTGA
RUVBL2	CCAGGACGCCTTCCTCTTCAA	AACCGTTACAGCCACAACCAA
UVRAG	GCCCGGAACATTGTTAATAGA	TTGGATTAAGAGGCTAGACGA
KCTD13	CTGCCGGAGAGTACGAGAGAA	CAGCGTTATCAGTCTGTTTCA
PARP1	CCGAGAAATCTCTTACCTCAA	CAGGGAGACCCAATAGGCTTA
NUDT1	CCGGGTTTCATCTGGAATTAA	CTCCTGCTTCAGAAGAAGAAA
PALB2	TACGGTTGCGCCTGATGATAA	CCAGGAGGATTACCTATACAA
TF	CACCGAAGACTGCATCGCCAA	CCGGAAGCCGGTAGATGAATA

KIF4A	CTGGTCAAGTTGTTTCTTATT	AACTGTGGAACCATCAGAGAA
TNKS	CACCGCCACAAATTAATCAAA	CAGATACAATGTCATTCGAAT
DDX5	TCGGGTTATTCGAGTGACCGA	CCCGCCAACCGCAACCATTGA
QPCT	CTCTATGGGTCTCGACACTTA	CAGGTTCATTCATTCAACGAT
DCLRE1C	CTGGCAACTGGTGAGAGTATA	CTCCTCCTACAGTGAGATTAA
NME4	CAGCACATGGGTGGTACACTA	CTGCCTGTCCCAAACCACTTA
FANCI	TTCGGTTGTAAAGAGCTTTAA	TACGAAGACCTAGATGATATA
GTF2H2	TGGGATTTCCTCAGCACACCA	CTGAACTTTCAGGAAACCCAA
FANCD2	CTCCGTATTTCCGGTTACTGA	AAGCAGCTCTCTAGCACCGTA
TPP1	CCAGCTCTCCTCAATACGGAA	TTCAAGGATTACTGGATAGAA
HUS1	AGCAATCACCTTGTTATTGAA	TCCCACAAAGGCCTTATGCAA
THOC1	CAGATTGAGTGTGACAGTGAA	CTGAAGGTATTTGTACCGCAT
CDKN2A	TACCGTAAATGTCCATTTATA	CAGAACCAAAGCTCAAATAAA
HELQ	CTGGTCGTGCTGGAATAGATA	AAGAACGTTGTCAACAGGCTA
TP53	TTGGTGAACCTTAGTACCTAA	TTGCAGTTAAGGGTTAGTTTA
PARP2	AAGTACTATCTGATTCAGCTA	GGGCGAGAGCATTAAATGAAA
GTF2H4	CTGAACCGAGTACACCTACAA	CCAGGTTTCATTGTCGTGGAA
POLD3	TCGAGTCAGCATTGACGATAT	TGGCATTATGTCTAGGACTAA
UBE2N	TCCCAATTTGACAATCGTATT	CTGGCCCTGAGCATGCATAAA
TFAM	GGCGGAGTGGCAGGTATATAA	AGGGTGATTCACCGCAGGAAA
TP53BP1	CAGGACAGTCTTTCCACGAAT	TTGTTTGACCAGAGCAATAAA
DPYD	TTCGGCCAAGAAATTAGACAA	TCCAACTAATCTTGATATTAA
MGMT	CCGGCTCTTCACCATCCCGTT	AAGGTTGTGAAATTCGGAGAA
PMS1	TAGCAATCGAGTAATCAAGAA	ACAGTCGACCAGTACATCAAA
MTHFR	GACGTGATTGAGCCAATCAAA	TGCCCTGTAACTTATCTAGAA
DHX9	CCAGAGCCTTTCATCAATGAA	CTGGGCTATATCCATCGAAAT
RBBP8	AAAGACGACTTGATACCTCTA	GACGTCAGCCTTACAACGCAA
CSNK1D	CCGGTCTAGGATCGAAATGTT	CGCATCGAATACATTCATTCA
RECQL	TACTACGGCTTTGGAGATATA	GCAGGTCGAGATGACATGAAA
CCNH	CTGAGCTTGCACTTAACGTAA	AGGAAGCATATCAAACGTTTA
PMS2	TCCGATGCTCTGCATAATCTT	TAGTGATGTCAACAAGCTAAA
KPNA2	CCGGGCTGGTTTGATTCCGAA	ACGAATTGGCATGGTGGTGAA
KIF18A	CTCGAAGTGTAAATTACCCGA	CAGGAGGACTTGGACTCTACA
DCLRE1A	TAGCTTCATAACAATGTTACA	GACACTCATGATATCGATGAA
C6orf167	CTGGACCCTTCTTTCCATATA	TTCCGGATCATAGATTGTTTA
DUT	AAGCCTTGGATGACACCGAAA	TCCCTTCTCTTCACTAGTCTA
NDC80	CCGAGACCACTTAATGACAAA	CAGCGGGAATACCAACTAGTT
KPNA4	TAGGCTGCCCATATAAGTCAA	CAGATCGTCAGTGCCTGAGAA
TOP3B	CAGCATCCCTGTGCATATCAA	CACGAGTACACTGGGACCTTT
UBE2A	AAGCGTGTTTCTGCAATAGTA	TACCAGGAGAACAAACGGGAA
UNG	ATGGGATTTGTTGCAGAAGAA	CTGGCTAAATCAGAACTCGAA
RAD18	ATGGTTGTTGCCCGAGGTTAA	TCCGGGCCTGGCAGTCATGAA
DDB1	CCACTAGATCGCGATAATAAA	AAGCTCAACGTTGACAGTAAT
MDC1	ACCGTTCGTAAGACCAGGCAA	TCCGAGACTGTGGGAGCCTTA

NCBI gene symbol	Target seq 3	Target seq 4
POLE2	CCCAGTGTATTGGGCATATGA	CCCGATCTACTTGTCATTGCA
MPG	ACCGCAGCATCTATTTCTCAA	CAACCGAGGCATGTTCATGAA
NFKBIL2	TCCAATCACCTGGGTCCCGAA	CCCATCCGGGTTCGAGTTCAA
CA14	AAGCAGGATCCTCGTATACCA	TTGCATGAAGTCAGGCATAAA
TGFB2	TCCCAAGATTTAGAACCTCTA	CAGCGCTACATCGACAGCAAA
PRPF19	CAGATCTACATCTGCAAACAA	CACGCCAAGTTCATCGCTTCA
TERF2	TACCCATTTGTTAACCGAACA	CAGGAGCATGGTTCCTAATAA
HIST1H1E	CCGCATCAAGCTGGGTCTCAA	ACCCAAGGCGGCTAAACCAAA
DNAJC5	CAGGTTCTAAGCTTGGACCTA	CGGGTTCAACTAAATCCAGGA
EXO1	GAACGAGTGATTAGTACTAAA	AGGGTTAAATCTCCCAAGGAA
BTG2	TAGTAGTATGTTTGTAAGCTA	AAGGTTACTAATTGTATGATA
POLB	CAGGTTGATACCCAAAGATCA	CAAGATATTGTACTAAATGAA
ALKBH2	CCACGGGAGCTTACTAATGAT	CCCGACCAACACGCACTGGTA
XAB2	CACCCGCGGCATCTACCAGAA	CCGGCATGCCATGGCCGTGTA
SUMO1	CAGGTTGAAGTCAAGATGACA	CTGAATCAAGGATTTAATTAA
HNRNPM	TGGCATCTTGTTGACATCGAA	CAGCTGCTATTTGATAGACCA
UPF1	ACGGAGCGCTGCACACCGAAA	CACCATGAGCGTGGAGGCGTA
ESPL1	CTCCAGGAAGATCGTTTCCTA	CAAGCTTCCCTGAATCATAAA
RRM2	CGGGATTAAACAGTCCTTTAA	CACACCATGAATTGTCCGTAA
POT1	CACCGTCTTGGACATTACTAA	CAGGGTCTTGCCAGAAAGTAA
PCNA	CTCAGTATGTCTGCAGATGTA	TCTGGTCTAGTTAACCTAGAA
C7orf11	TTGGATAATTAGTAAGGTCTT	ACAGCAATACTCAAACATTCA
LMNA	CCCACCAAAGTTCACCCTGAA	CAGGCAGTCTGCTGAGAGGAA
RNF8	CTGCCCATGATTACTGATCAA	CAGCCTGTGATAGGCATTCAA
DHFR	AAGGTAACTAACGGAAGGAAA	TTGAGGTACGGAGAAACTGAA
PARP3	CCAGACCAACATCGAGAACAA	CACGCAGAAGCTCATCACTAA
CACNA1G	CACCCACAAGATGTTCGACCA	CCGGCACAAGTACAACTTTGA
RAD51L3	CTCACTCTCTGTAAGCATATA	CTGGGTGGAAATAAGCTTATA
FEN1	ACCCAAGGGATCCACTAAGAA	CAAGAGCTACTTTGGCCGTAA
NTHL1	GAGCAAGGTGAAATACATCAA	GTGGACCAAGAAGGCAACCAA
ERCC5	CCCGGACTCTTTCAGCCATTA	CGGCATGTCTATAGAAACTTT
DCLRE1B	CACCTCTTGCATCGTCACCTA	CAGGGTATTCTTCCAGGAGAT
BRCA1	TGGGATCGATTATGTGACTTA	GAGGGATACCATGCAACATAA
EEF1E1	CACACTGTTGAAGGATCTTAA	CAAGTCTAACAGGATTGACTA
RPS19BP1	CCGGCCTGTGGCCAAGACCAA	CCGGAAGACGAAGGCAATTCA
MSH5	CCCGGGACTATGGCTACTCAA	CAGACTTGATCCGCAGTGGAA
TINF2	TCCTGTGGATTTGGCCTCGAA	CAGGCTTGGATTGCCTAACTA
FANCA	AGGCCTATGCTAATCATTCTA	AAGAAGCTGTCTTCCCTGTTA
RPA1	CAAGGTGTATTATTTCTCGAA	CCGTGTGACGATCCCATGTTA
PTTG1	ATGGGAGATCTCAAGTTTCAA	CAGATGATGCCTATCCAGAAA
MAD2L2	CCCGTGGGCATCTTCCAGAAA	GTGGAAGAGCGCGCTCATAAA
SRSF1	ATGCGTGAAGCAGGTGATGTA	CATCATAGTGCTTGCGTTTAA
FANCF	TACTAGGGAGATAGACCTTTA	AACCAGCATTAGAGCTTTATA
GTF2H1	TCGGCTGAATACAGGGTCAAA	AAGGCAAAGATAGATTTACAA
GTF2H3	TGGAGTAATGGCATTAATCAA	TAGCAGATTCTTTGTTGGGAA
RFC4	ATGCATCTGATGAACGTGGAA	CTGATGAACATTTGCAACTCA
FAM175A	ATGGCTAGAGTTGCCAGATAA	TCAGGCGAAGTAAATGAGCAA
SLX4	CAGCAGGAGTTTGCACGGGTA	AAGCGGAGACTTTGTTGAAAT
XRCC6	TTTGTACTATATACTGTTAAA	GAGGATCATGCTGTTCACCAA
LIG3	ATGCGCCATGGTGGCCGATAA	CAGCTGGTTGAAGGTCAACAA
NBN	AAGACTCACTATGGTCAGCTA	CTACATGTTATTCTAGTACTA
REV1	CTGCCAGGTCCAAGCAATATA	CAGCGCATCTGTGCCAAAGAA
DMC1	TCCCTGATTTATGATAACTAT	TAGGTGGTGAATTGATGCAAA
NEIL2	AACCTAGAGCGGTGACATGAA	CAGGGCTAGGGAACATCATTA

SBDS	GAGGGTCATTATGGTATCGTA	TTGGATGATGTTCCTGATTAT
RBM14	ATCGCGCAGCTCAACGGCAAA	TAGGGTTACAGATCCAGGTTA
RAD54L	TCCCTCCTGGTTACAGCTCTA	CAAAGTAGTGCTGGTGTCGAA
LIG1	CACCTGCGAATACAAATATGA	CCCGTCATTTCTTTCAATAAA
UHRF1	TCGGATCATCTTCGTGGACGA	CAGGACGGCGCGGGAACTCTA
XRCC1	AAGCCTGAAGTATGTGCTATA	CCGATGGATCTACAGTTGCAA
TK1	GAGGCGCAATGAGCTGCATTA	CGGGCCGGACAACAAAGAGAA
ABL1	AACCAAGCCTTTGAAACAATG	AACGGCTGATGTGGACTGTCT
MAD1L1	CAGCGATTGTGAAGAACATGA	CAGGACCAAAGTGCTGCACAT
XPA	TTGAGTTGTACGAGTCTGAAA	CTGATGATAAACACAAGCTTA
CBX5	AACGGTGTGCGACATGGGAAA	AGGCGCGTGGTTAAGGGACAA
CRY2	GAGGCCATAGACAGATCTAAA	CCGGCTTAACATTGAACGAAT
NUP98	CAGTGTATTACTGCTATGAAA	CTGGAGTTAGCACTAACATAA
C19orf40	CCGGATGAGTGAACAATACTT	ATCCAGTTGGTTCAAGAGCAA
FANCB	TAGCTTAGTACTGATAGATGA	CCGGCTATGCCCTGAATTCAA
DCK	AGGCAGCCTGCTATAAAGTTA	CTCCAGAGACATGCTTACATA
RPIA	CAGTGATCTCCTGATGCCTTA	CGAGGTCATCCCAATGGCCTA
FANCC	AAGGCAGGATTAATTCAGTTA	CTGGCCCGAGAGCTCCTTAAA
RNF168	AAGGGAGTGCTTTGTGATCTA	CAGGAAAGACTCCGTATCTAA
GEN1	CTGGTTGGATTAGCAATACTT	ATGGAGAATTTGCTTTATTAA
ERCC3	CCGAGCGGACCGCGACAAGAA	ACCCATGTGCATGAGTACAAA
MBD4	CACGACGTAAAGCCTTTAAGA	AAGAGAATCTGTGTGTAATAA
ALKBH3	AAGAATCACTATGGAACCAAA	ATCAGAGAGGATATAACTTAT
HMGB2	TTGCTAAGAATGTGAATTCAA	AGGAATTAGTATCAATAGTAA
POLL	CAGGGCTTCCGAAGTCTGGAA	CACCGGCTCTGCACACTTCAA
SFPQ	TGGCACGTTTGAGTACGAATA	TGGCATAGGTTATGAAGCTAA
TREX1	CTGGTGCCTGGTGGCACACAA	CAGCAGCAGGTACGTACCCAA
MLH3	GAGGAATTTATCCGAGAACAA	CTCCAAACCAATCGTCCGTAA
RAD23B	AACTGTGGCTCAGGCTCCAAC	ATAGGTCGAGAGAATCCTCAA
GADD45G	CGGCGTCTACGAGTCAGCCAA	CTAAAGGATGCTGCTGTTGAA
RAD1	AGGTATCTATTCGGACAGATA	TCGAATGTGTTACCAAGGTTA
FAN1	AAGAAATTGTCGAGACGAATA	TTGGGAAGCCTAGCATCTAAA
FANCL	ATGCGGATACCTGCTTCAGTA	TCAGAGCTCCTTAATAAGCAT
RPA2	AAGGCTTGTCCAAGACCTGAA	CCAGGTGTTGAATTTGATTAA
XRCC5	TTCCGCTATGGAAGTGATATA	ACCCTCATAAGTCGTCACTAA
TDP2	CAGATGTGGTGGTTTACCCAA	AAGAAGGATATTTCACAGCTA
RPL5	AAAGCTCATGCTGCTATACGA	AACGCTTGGTGATACAAGATA
ATR	GACCGGATACTTACAGATGTA	GCCGCTAATCTTCTAACATTA
RPA3	TCGCTGATTGGTGCCGAGAAA	AAGGGAGTAAATCGACCCTCA
HERC2	GAGGAACATGTTCGTTATCCA	TGGAATCAGCAGCTACGATAA
TDG	ATGGTGGTGCTTACGGAGAAA	TCCAGTAAAGAATTTCGTGAA
CHAF1B	CTCCACCAAGTTCTGTACCAA	AAGAATTAGGAAGATGAGAAA
ATRX	AGCAGCTACAGTGACGACTAA	ACCGCTGAGCCCATGAGTGAA
CHEK2	ACGCCGTCCTTTGAATAACAA	AAAGAACAGATAAATACCGAA
RALY	ATGCCTTTGTTCAGTACTCCA	CTGGCTAAGCTCATCATTGTT
POLE	CTGGATGGATCCATCTAACTA	CCGCATCATCCTCTGTACAAA
PNKP	CACGTGAACAGGGACACGCTA	CACGTGTGAGACAGCCCTGAA
POLM	CAGAGAGGTACCAGACCATGA	CGGGAAGGACTGCGAACCTTA
BCL2L1	TTGGCTTTGGATCTTAGAAGA	CTGCTTGGGATAAAGATGCAA
FANCG	CCCAGGTAATCGAGACACTTA	CCGCGGGAACTAACTCTTCAA
HMGB1	AAGAGTAATCAATCTACTCAA	AAGGATATTGCTGCATATCGA
SIRT1	CAGGATTATTGTATTTACGTT	CAAGCGATGTTTGATATTGAA
TOP3A	TGGACTGACTGTGATAGAGAA	CACGGCTTGCCTAGTTCTCTA
INTS3	CGGGATCTCGTAAGACTACTT	AAGGATAGCATTATGAACATA
FANCM	ATGGGTAGAACTGGCCGTAAA	CTCGACGTGCAGTAATGCTAA

WRNIP1	TGCAGCGGTTATGCTTATGAA	GAGGCGCAGTTCTTTCGAATA
MLLT1	CAGCTCAGACTCAGACTTCGA	CACCTTCGACTTCGACCTCTT
UBE2B	ACCTCTCATTAGAAAGGCTAA	CCCAGTATTAGCAATGAATTA
VRK3	CTCACTCAAACTGGATGCCAA	CCGAGTGACCACCTCACTTGA
RAD51C	CCCTCCGAGCTTAGCAAAGAA	AAGAAGTGTACAGCACTGGAA
RFC1	AAGGCGATTGTTGCTGAGTCA	GAGGCCAAGTCTCTAATTGAA
POLG2	CACGGTGCCTTGGAACACTAT	CAAGGGCTATTTAATGAGTTA
CTPS2	TCGGTTCGAGGTAAACCCTAA	ATCGACGTGAAATTCACGTAA
SLX1A	CAGACCTGCTGGAGACCTGAT	ACCCTAGGTCACGGCAATCAA
RAD50	CTGGCTACATAGTAAATCAAA	CTGCGACTTGCTCCAGATAAA
PARP4	TAAGTTGGACAGAGTCATGTA	CCGATATCTTAGCTTATTGTA
TOPBP1	CGGCTCTGTAATAGTCGACTA	ACGAGTATACAGAGACCTTAA
SMARCAL1	TTGAGTTATGAGTTAGGTCAA	CAGCTTTGACCTTCTTAGCAA
RPA4	AAGGATTATGCGATCAGGTGA	CAAAGTGTTTGGTATCCTCAA
PRKDC	CTCGTGTATTACAGAAGGAAA	TAAAGCTATAATTATGGCTTA
TDP1	CACAAGCGCAAATCTGTCCAA	CCAGAACTGTATGGAAGTAAA
TERF1	TTGCCAGTTGAGAACGATATA	ATCATCTTGATGTCTATGATA
KPNA1	AGGAAGCATGTTGGACGATAT	TAAGGCGTTGCTCATTACAAA
OGG1	CACCGTGTGGGCGAGGCCTTA	CGGGACCTACACCTCAGGAAA
PMS2P4	CAGAACTGTGAGTCAATTAAA	TGCCACCAATATTGATCTAAA
TOP2A	AACCAGCGTGTTGAGCCTGAA	CCGCGTGGTCAAAGAGTCATT
HNRNPU	TTGGCTGGTCACTAACTACAA	CTGGGAATCGTGGCGGATATA
GADD45A	AAGGATCCTGCCTTAAGTCAA	CTGGAGAGCAGAAGACCGAAA
PMS2P3	CTAGACTAGGCCGTCGCTGTA	TATGATTATCACCAAGCCAAA
EP300	TTGGACTACCCTATCAAGTAA	CACCGATAACTCAGACTTGAA
MLH1	CAGTGGATTGATTATAAATAA	CACCAGATGGTTCGTACAGAT
RAD51L1	CCCAGTTATCTTGACGAATCA	CCCGGCATGGGTAGCAAGAAA
RPL11	CGGGAACTTCGCATCCGCAAA	ATGGCGCAGGATCAAGGTGAA
C11orf30	TTCATGCGTATTCAGAATGTA	ATGGTGCAATTATGACAACTA
DDX17	CGGGATCGTAGTGAAACCGAT	CTGGAGTGCATTTGATAGTTA
KPNA3	CTGATAATGGCCGGTGATGAA	AAGCGTATGTTTAAACTGCAA
BUB3	AACGAGATGCAGAACCCTTGA	GAGGACTAGATCATCAATTGA
PML	CTCCAAGATCTAAACCGAGAA	CAGGGACCCTATTGACGTTGA
SIRT6	GTCGAGGATGTCGGTGAATTA	CTCCCTGGTCTCCAGCTTAAA
OBFC2B	CAGAACGACAGCAACCCTTCA	AACCCTGTTAGTAACGGCAAA
PER1	CAGCAATGGTTCAAGTGGCAA	CCAGCGCGTCATGATGACCTA
SPO11	ACAACTAATGTTAACGCATAA	CAGAGTGTACTTACCTAACAA
FANCE	TCGAATCTGGATGATGCTAAA	AACGCCGAGGAGAGCTTGTAA
XRCC2	CTCCGGCTAGTTACAATTCTT	CACGATGTATACTTCCCAAAT
ERCC4	CTCGCCGTGTAACAAATGAAA	CAGCACCTCGATGTTTATAAA
CHEK1	AACTGAAGAAGCAGTCGCAGT	AAGAAAGAGATCTGTATCAAT
MCM2	CACGGTCATTGCTGCCGCCAA	CAGCGACATGTGCAAAGAGAA
UIMC1	CACGTCGTGACTTAAATGAAT	CAGTATTGACTCGGAGACAAA
POLD1	CCGGTTCATGGTGGACACGGA	CAGTTGGAGATTGACCATTAT
XRCC3	GAGACACTTAAGGGAAATTAA	CAGAATTATTGCTGCAATTAA
TOP1	CACAACGATTCCCAGATCGAA	CGGGAAGGACTCCATCAGATA
RMI1	AAGGTAATCTAGTTAACTAGA	GAGGTTTCAAGTAATCCACTA
BUB1	AACCAGTGAGTTCCTATCCAA	AGGGCCCTACGTAATAGGCTA
EME1	AAGGACCTGATCTTAGATCCA	CAGAATTTGCTCGCAGACATA
RPS9	CCCGCGGAGACCCTTCGAGAA	ACGGCGTCTGTTCGAAGGCAA
EME2	TGGGCAAACCTGGACGTGCTA	CTGGGAGATCTCAGACTCCGA
SUPV3L1	TGGGACTTAATTTGAGCATAA	CACGATTGTCAGGAACCTTAA
CSNK1E	CGGGTCCTTCGGAGATATCTA	CCCGTTCTCCTGTGTCTACTA
POLD2	GAGCAGGGATTCTATCAATAA	CCGGGTTATCCTCGCTGGCAA
RAD17	CCCTGTGGCACCAACAATTAT	CAGTGGTTTCTAATAAATAAA

BRIP1	AAGATAAACAGTCCACTTCAA	TAGCATGGCAACAATCTCTTA
SMC1A	TCGGAAGTGAATGACAAGAAT	CGGCGTATTGATGAAATCAAT
REV3L	CACCGTCACCCTAACGAGAAT	TGGCGATAGTATTGTTCACAA
POLR1C	CCCGGGTTCGAGATCATTATA	ACGCGCGAGATAGAACCTCTA
APTX	CACCTTGAACTCCTTAAGCAT	CACCAGCGAATCAGACTTCCA
ERCC6	CAGAGCGTTTAGAAAGTGAAA	ATGGATGGTACCACTACAATA
YY1	ATGCCTCTCCTTTGTATATTA	GACGACGACTACATTGAACAA
SUCLA2	CAGAATGGACTGTTTGTACGA	AAGGTCCTGTATTAATAGGAA
IGHMBP2	CCCAGCCTCCTCACTCATAGA	AAACGTGGTCCTTGCAACAAA
RAD23A	CAGAACCGTGTCTCTGATAAA	CCCAGAGAGCCTGGTCATCCA
RECQL4	ACGGCTCAACATGAAGCAGAA	CCTCGATTCCATTATCATTTA
SETMAR	TTGACCCTACTTATATAGGAA	TACCTTGGAATTTATACCGAA
RAD9A	CAGGCTCACCTTCCTAAGGAA	TGGCGCTGACTTGGAATTCTA
C10orf92	CAGGAGAGGCGAGGACCTGAA	CACGCTCAACTTGGTCCTGTA
SMUG1	CAGGATACCTACCCATCCTTA	CTCGAAGTCATTCTTGGCCAA
APEX1	CTCAAAGTTTCTTACGGCATA	CTGGGATGAAGCCTTTCGCAA
ATRIP	CAGGGTCATCCCTAAGCCTTT	CACGGTGATGTTGCACAGACA
SUPT16H	ACGCTTATTATCGGCGAGTGA	ACCGGAGTAATCCGAAACTGA
RAD54B	AAGCTACTGGCACATAGTGAA	AACCCTCTCCTGTTTACTGAA
POLG	CTCACTGACAATAGTGCCATA	CACGAGCAAATCTTCGGGCAA
UBE2I	AAGGGATTGGTTTGGCAAGAA	AAGGGTCCGAGCACAAGCCAA
LIG4	AACCTTACTAACGTTAACAAA	CACCGTTTATTTGGACTCGTA
DDB2	TCCCTCCATGATCTTCGCATA	GACGTGTTCGATGGAAACTCA
ERCC8	ATGGGATACAAATACATTACA	TTGGTAGCAGTTGGTACTAGA
CENPE	TGGGACCAGTTCAGCCTGATA	TAAGATGGTCCTTGAGGAGAA
SSBP1	TCCCTGAATCGTGTGCACTTA	CGAATTTATTTGGAAGGGAAA
MSH3	AGCCCGAGAGCTCAATATTTA	TCGAGTCGAAAGGATGGATAA
TNKS2	CACAACCATGCCAATGAACGA	GAAGGTATGGTCGATGGATAA
IP6K3	ATGGTGGGCACTGAGAGACAA	CTCCGAGTACCCAGAGAACAA
ERCC2	CCCATACTTCCTTGCTCGATA	CCCGCTCACCCTCCTTGCTAA
SSRP1	CCGGGATGAGAAGAAGCGGAA	TTCGTTGACTCTGAACATGAA
NEIL1	CAGAGACTCTCCGCAACAGAA	CGACTGTTCGTTGGTGCTTAA
DNA2	CAGCGCCAGAACAAGTTGAAA	CAGGTTGTTCTGTACACTCTA
MAD2L1	ACGGACTCACCTTGCTTGTAA	CAGAAAGCTATCCAGGATGAA
MSH6	CACGCCATCCTTGCATTACGA	AAGCCTATTGTGTGCTTGTTA
SHFM1	AAGAAGTGTTGAAGTAACCTA	CCGGTAGACTTAGGTCTGTTA
DDX1	ATGAAAGTCTGTAGTCTTAAA	CACGGTGTTCCTTATGTTATA
ERCC6L	AAGCCTAGTGCTCTAGCTCAA	CACGGGCTTGTTGTTTGCTAA
CETN2	AAGCTCTTTGATGATGATGAA	CAGAACGACTTTAGACAAGCA
RECQL5	TGCGACCATGGCTGTAGTAAA	CAGGAGGCTGATAAAGGGTTA
TERF2IP	CTCGGAGGATTGAATTTCGAA	ATGGTAGGTGAGGTGGTTAAA
MMS19	CAGCGGCGGACAATCCTTGAA	CTAGACTGTTCTGACAATCTA
DDX3X	CAGATTCGTAGAATAGTCGAA	CACAGGTGTGATACAACTTAA
MSH4	ATGCAGTGAGGTCTAACATAA	ATCAATTGTCTTGGATGCCAA
PELP1	CACGGTTCGGACCAAGGTGTA	CAAGGTGTATGCGATATTAGA
TMPO	GACAGATACAGTGACAATGAA	CCGGACTTCTCCAGTGACGAA
TREX2	CACGACGAGTCTGGTGCCCTA	CACAATGGCTTTGATTATGAT
APC	CAGACTAAGCATTGAGCATAA	CCGGTGATTGACAGTGTTTCA
TYMS	AAGGATGTTGCCACTGGCAAA	AAGAGTGATTGACACCATCAA
RDM1	ATGCCAAGAACTGGCGAATTA	AAGGTTCGTCTTGGCACCAGA
PIF1	CTGGGCGATGTCCATCCACAA	TCCGGACACTACGCTGGTGAA
POLI	GCGGTTTATTAAGCTCTTCTA	ACCGGGAACATCAGGCTTTAA
UBE2V2	AAGACGTCTAATGATGTCCAA	GTCAGTTAGATTTGTAACAAA
MNAT1	TCGGTGTAAGACCACCAAATA	GTGGATTTGGACAACACCAAA
HIST1H2BK	AAGCACAATTGCCTTCGGTTA	AGGCTCGTAGTTCGCCTTCAA

HDAC1	CCACAGCGATGACTACATTAA	CACCCGGAGGAAAGTCTGTTA
MSH2	TTGGATATTACTTTCGTGTAA	TCCAGGCATGCTTGTGTTGAA
RRM1	AACGGATATATTGAGAATCAA	CAGGGCCCATACGAAACCTAT
POLA1	CAGGTCGAGAGTACAGAAGAA	CTGGAGAAACTTACTACCGAT
NEIL3	TCGGATATACAGCATATTCCA	ACGGATTCATTTCGGAATGAA
BLM	CTGACCATCTGTGACTATAAA	CCGAATCTCAATGTACATAGA
WRN	CTACGTGACTTTGATATCAAA	CCACGGAGGGTTTCTATCTTA
USP1	CTGGGACCCATGAATCTGATA	ATGTGGCAGAATTACCTACTA
XPC	TCGGAGGGCGATGAAACGTTT	TAGCAAATGGCTTCTATCGAA
HDAC2	CTGGGTTGTTTCAATCTAACA	ACGGTCAATAAGACCAGATAA
RAX2	CAGGTGTCCCGTGGAAATCGA	ACCGCTGACTCTGTAAGATGA
MUS81	CGGGAGCACCTGAATCCTAAT	CACGCGCTTCGTATTTCAGAA
ERCC1	TACGCCGAATATGCCATCTCA	CCCTGGGAATTTGGCGACGTA
DDX21	GCGCTCCTTGATCAACTCAAA	CTGGGTTGTAATACAGTTTAT
ENOSF1	CTGGTGCAGCACCTGATTATA	ATCCCGGCTACTCAACAGAAA
POLN	CTGCGAGACCTTCATCCATTA	ACGGTTTCTTATAACGAGCAA
CHAF1A	CACGCACGTTTCCACCCGGAA	ACCTAACGAGGCAGTGTATAA
RPS3A	ACGCAACAATCAGATACGGAA	ATGGATCTTACCCGTGACAAA
MUTYH	CACATCAAGCTGACATATCAA	CAGGAGGAATTTCACACCGCA
RAE1	TTGGGATACTCGATCGTCAAA	CAGCAGTAACCAAGCGATACA
MRE11A	TGCGATTCAGTTCACCGCTAA	ATGCGACAGCTTTACTTTAAA
H2AFX	CACGACTAGAACCTTAGGCAT	CCGGGACGAAGCACTTGGTAA
APEX2	AACATGGATGAGTTTACCCAA	CCCGGGTACAGACATGCCAAA
NHEJ1	TAGCAACGTTACTTCATATGA	CTGCAAGGAATCGATAGCCAA
RAD52	TGGGCCCAGAATACATAAGTA	CAGGAGTGACTCAAGAATTAA
TERT	CTGGGAATTTGGAGTGACCAA	CCCGGTGTACGCCGAGACCAA
POLD4	GACCCATGATCTGGCAAGTTA	TTCACTAATGCTTATCAATAA
XRCC4	CAGCGAATGCAAAGAAATCTT	CAGCTGATGTATACACGTTTA
POLH	GAGGCAGTGTCATAAAGTAAA	CAGCCAAATGCCCATTCGCAA
CLK2	AAGAGCGATATGAAATCGTTA	TCGCCTGGATTGGGATGAGAA
HIST1H4A	GCGGATCTCTGGTCTGATCTA	CAGCTTGCATTTCTGAACCAA
NCOA6	AGGCGGGATTTCCTATGGCAA	AAGGAGCTAATGCCATTATAA
TFAP2A	CCGGGTATTAACATCCCAGAT	CAGCTCCACCTCGAAGTACAA
BRCA2	AAAGTGCTTCTGGTTATTTAA	TTGGAGGAATATCGTAGGTAA
POLQ	AAGACTGTAGGTACTATGAAA	CACATTTATATCCCAAACTAA
SPAG11B	CTGCTACGCCACGCAGTGAAA	CACATTGTCCTTTGAGAATGA
ATM	AACCATGAGTCTAGTACTTAA	AAGGCTATTCAGTGTGCGAGA
HIST1H2AB	AAGTGAAGAGTTAACGCTTCA	CCGCAATGACGAGGAGCTTAA
UBR2	AAAGCTGTTAACTGTACACAA	ATCATCGATATAGGATGACAA
RRM2B	CTCATCGAGAATGTTCACTCA	AAGGGCTTATGGACTGAGAAA
RAD51	CACTTCTAAATTAATGGTAAA	CAGGATAAAGCTTCCGGGAAA
RAD51AP1	CAGCTTTACAAGGGTGTTTAT	ATGGCATATGTCTCCGATTTA
GTF2H5	CAGGAGCGAGTGGGTGAATTA	ATGGACCATTTAGGAATTATA
NONO	AAGGCATTGTTGAGTTCTCAG	TCTGTGTGGTATATTGTTTAA
POLK	AACCTCTAGAAATGTCTCATA	TGGAATTAGAACAAAGCCGAA
HSPA5	CTCCTGCGTCGGCGTGTTCAA	CTGACTCGGGCCAAATTTGAA
CDK7	GACGACTTACTAGATCTCATA	TTGGACATAGATCAGAAGCTA
BUB1B	AAGCTCGAGTGTCTCGGCAAA	CTGGATGTTTGGGATAGGTAT
RUVBL2	CACGCAGTACATGAAGGAGTA	CCGGAGATCCGTGATGTAACA
UVRAG	AAGGATCTATGCACTGAATGA	CAGCGGGCAAATGTTATCAAA
KCTD13	GACGAGCGTCCTCATGGCCAA	CCCGAACAGCAAATACGTGAA
PARP1	ACCCAAGGGCTAATAGTAATA	ACGGTGATCGGTAGCAACAAA
NUDT1	TCAGGACACCATCCTGGACTA	CGAGTTCTCCTGGGCATGAAA
PALB2	AAGGTAGCAGTGAACTTACTA	CTGCATAAACATTCCGTCGAA
TF	TGCACTTTCCGTAGACCTTAA	CAGGGCCATTGCGGCAAACGA

KIF4A	CTGAATTATGTTTCAATAGTA	CAGGTCCAGACTACTACTCTA
TNKS	ATGCAAAGTACTATTCGAGAA	AAGGATGTTGTAGAACACTTA
DDX5	AAGAGCGTGACTGGGTTCTAA	GTGCTTCGTGAAGCTAATCAA
QPCT	TTCGAAAGACTTCAAGCAATT	CAGGTGGTTCGAAAGACTTCA
DCLRE1C	CAGGTTCATGTGAATAAGCTA	AAGTACGGAGCCAAAGTATAA
NME4	GACGCCTTTATGCAAGTTGTA	ACCAACTACCTCCGTCAGCAA
FANCI	CACGGGCATCTGGGAGATATA	CTGGCTAATCACCAAGCTTAA
GTF2H2	ATGGCGCATTTGGATGGCAAT	CAGTAGTACTTCATTCAATTA
FANCD2	CGGCTTCTCGGAAGTAATTTA	CAGAGTTTGCTTCACTCTCTA
TPP1	CCAGGAGGAAGCTGTAACGAA	AAGATGCGTGATACTCAACAT
HUS1	CTCCGTGGAGCTGTTATCTAT	ACCAGTCTTGAAGACTATGAA
THOC1	AACACCTGAGAATCTGATTAA	GTGCTCTATTCCAATTGATTA
CDKN2A	CACGCCCTAAGCGCACATTCA	GCCCGCATAGATGCCGCGGAA
HELQ	ATGCCTCGAGGATATATACAA	TTGGGTGATCATTCTATGAAA
TP53	CAGCATCTTATCCGAGTGGAA	AAGGAAATTTGCGTGTGGAGT
PARP2	AGGCAGGTTACCAGTCTCTTA	GACCAACACTATAGAAACCTA
GTF2H4	CAGCAGATAATCCATTTCCTA	AGCCCACCCAGTGATGCTCAA
POLD3	AAACCCGTACAATGAGATAAA	CTGAATTGTTAGTAGGTCTAA
UBE2N	AAGATAGTACTGAATGGAGTA	ACCTTGTCTCTTGCAGTTTAA
TFAM	AAGGAATTATATATTCAGCAT	AGGACGAAACTCGTTATCATA
TP53BP1	CTCCAGAACTACCGTAATTAT	TTGATGCTTTCTACAAGTGAA
DPYD	CATCACAAGTATTGCAAACAA	TCGAGAGTATCCTGGCTTTAA
MGMT	AAGCTGCTGAAGGTTGTGAAA	GACAAGGATTGTGAAATGAAA
PMS1	CAGCGAATGGTTTCAAGATAA	ACGACTTGTTATGGACCATTA
MTHFR	AAGCGCCGAGAGGAAGATGTA	CTCGGGAGAACCAAACCGGAA
DHX9	AGCGTTCGATTTGAGTCTATA	TTGGTTGTTGAAGTAACCAAA
RBBP8	CATGTCCGATACATAGAACAA	CTGGCGTTAACCGGCTACGAA
CSNK1D	CCCTTCCGAATTTGCCACATA	CTCCCTGACGATTCCACTGTA
RECQL	CCCATTGATCTCTCTTATGGA	AAGCAAGGAGATTTACTCGAA
CCNH	CAGATGCAAAGCCGTGGCCAA	AAGATGATGATTACGTCTCAA
PMS2	AAAGACCTCTTTGATAGGAAT	TGGATGTTGAAGGTAACTTAA
KPNA2	TTCGTTAAGCTTAATTGAGAA	CCGAGACTTGGTTATTAAGTA
KIF18A	CAGGTGGAACTAATCTGGTTA	ATCCGTCTACAGTAACCTTAA
DCLRE1A	CGAGGATTCAGTAGTAGTTAA	ATGTAGCTTGTTAGTAGTTAA
C6orf167	CAGCCACTATTCCACCAATAT	CTGGTTGAATAAACTACTTAA
DUT	ACCCGCCATTTCACCCAGTAA	AAGCCTGTATTTAACTCATAT
NDC80	CACAATTAGCAGAGTATCACA	TCCCTGGGTCGTGTCAGGAAA
KPNA4	AAAGATCTTTGCATGAGGTAA	ATGGGATCTGCTGCTGCATTA
TOP3B	GCGGTTGTTAGCAGAAGGTAT	CACGGCTACTATAAGATTGAT
UBE2A	CCCTTCTACCCTCTCCTTAAA	AACACCCTCTATGAAATCAAA
UNG	TACGCGAGGTTTGTTAATAAA	CTACGCGAGGTTTGTTAATAA
RAD18	CAAGACAGAATCGCCGCACAA	AAGACTAGGATGCGTCTTGAA
DDB1	ACCTATCACAATGGTGACAAA	ATGCAGAATCGACTCAATAAA
MDC1	TAGGGCGGCTACATATCTTTA	CAGGGTCAGCCATTATACATA