

Mutation spectra of the MRN (MRE11, RAD50, NBS1/NBN) break sensor in cancer cells

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Supplementary Table S1. Summary of MRE11, NBS1 and RAD50 mutations catalogued on COSMIC. For some mutations COSMIC provides references which are listed in the right column. For more details, please visit the COSMIC database.

Tissue	MRE11 ORF Mutations	References
Biliary Tract	c.163A>G, c.952C>T	[1]
Breast	p.A440T, p.E451Q, p.Q679K, p.R503C, p.N115D, p.Q218K p.R402K, p.H302Y, p.V429=, p.S632F	[2]
Central Nervous System	p.G683V, p.Q459E, p.V462E, p.D650Y, p.R483Q	[3-5]
Cervix	p.E374Q, p.S641*, p.P318A, p.L274V, p.E466=, p.R503C	N/A
Endometrium	p.G415=, p.S547I, p.V150A, p.K255E, p.M200L, p.R502C, p.T36=, p.D394Y, p.R366Q, p.G172*, p.S681=, p.E494K, p.G285C, p.R708I, p.E518*, p.G58D, p.I497=, p.E460*, p.A440T, p.R188Kfs*9, p.R69M, p.A528T, p.D131N, p.R604C, p.I15L	[6]
Esophagus	p.G172E, p.G371E, p.N699=, p.Q591E, p.R351H, p.S563L, p.V31=	[7, 8] [9, 10]
Hematopoietic and Lymphoid	p.T408K, p.Q477E, p.T627A	[11]
Kidney	p.V304M, p.I125T, p.A595S, p.T658=, p.R628*, p.T627A, p.L44V, p.L94=, p.A4S	[12, 13]
Large Intestine	p.R488H, p.E51K, p.N322*, p.F321S, p.N511Ifs*13, p.E494K, p.A542=, p.N511Ifs*13, p.V458A, p.A440T, p.S586L, p.D53G, p.T481Hfs*43, p.M157V, p.G180C, p.K66=, p.R576*, p.T507=, p.K298N, p.E494K, p.R488H, p.A528=, p.L286=, p.K281N, p.N316=, p.A542=, p.L76=, p.R349W, p.R288H, p.N195=, p.D394Y, p.A539=, p.R380H, p.S649L, p.N617H, p.G114D, p.R380C, p.R366*, p.A390=, p.E77K, p.E460*, p.A528T, p.R572Q, p.F399Sfs*29, p.R380H, p.D517=, p.D236=, p.A47S	[14-19]
Liver	p.D29E, p.E406K, p.E500D, p.G114D, p.G24=, p.G291E, p.I118V, p.I263V, p.I674N, p.K609=, p.L40I, p.L79F, p.N699K, p.Q232*, p.R502S, p.R604S, p.R87=, p.Y82C	[20, 21]
Lung	p.A177G, p.A551T, p.D206Y, p.D368Y, p.D53Y, p.D695Y, p.D86N, p.E10Q, p.E248K, p.E310*, p.E348V, p.E350*, p.G114A, p.G182*, p.G24*, p.G24V, p.G285C, p.G453W, p.G593E/K/R, p.K405E, p.K609N, p.L181F, p.N354I, p.P132H, p.P166L, p.P657T, p.Q48L, p.Q582=, p.R520P, p.R525S, p.R572*, p.S209F, p.S563L, p.T19A, p.T303A, p.V122=, p.V159L, p.Y111S	[22-28]
Ovary	p.A526Gfs*16, p.T199=	[29]
Pancreas	p.D694G, p.N65I	[30]
Pleura	p.K442N	[31]
Prostate	p.A526V, p.D131V, p.I418=, p.I418T, p.N511Ifs*13 p.R572G	[32, 33]
Skin	p.E506*, p.E652K, p.F237= p.G134V/W, p.G182*, p.H397Y, p.H73N, p.I497=, p.K196N, p.K66R, p.L485F, p.L57=, p.P121S, p.P696S, p.Q330K, p.Q357K, p.Q48*, p.R520C, p.R606K, p.S273F, p.S563L, p.S676=, p.T603I, p.V519=, p.V643=	[34-37]
Stomach	p.A6T, p.D543=, p.E10G, p.F321Ifs*8, p.F399Sfs*29, p.G134R, p.G154E, p.I395T, p.L473S, p.N511Ifs*13, p.N634S, p.Q477=, p.R364*, p.R604S, p.S156P, p.S586=	[38-40]
Thyroid	p.D130G, p.E27V, p.E403K, p.E406K, p.E652*, p.E690*, p.M84V, p.Q404K, p.R505I, p.R592*, p.R705I	N/A
Upper Aerodigestive Tract	p.A623V, p.E494K, p.G154*, p.S608*, p.V31I, p.Y190H	[41-43]
Urinary Tract	p.F399=, p.H152N, p.H297=, p.N413S, p.Q438E, p.R349L, p.R502G, p.S119L, p.S558F, p.V109=, p.V31G	[44]
Not Specified	p.D695del, p.H22Y, p.R388W	[45, 46]
Tissue	MRE11 Intronic, 5' and 3' UTR Mutations	References
Biliary Tract	c.315-4del, c.*1743del, c.*1743dup, c.1500+1225dup, c.20+643del, c.1017+175del, c.1995-1978dup, c.1500+1225dup, c.1501-178dup, c.1018-730A>G, c.1563+2202dup	N/A
Breast	c.545-641C>A, c.1327-467C>A, c.20+28G>A, c.2071-853dup, c.1564-887G>T, c.660-155A>T, c.1501-467G>T, c.1500+1299A>G, c.1226-1435C>G, c.403-6G>A, c.315-1487C>T, c.544+32A>G, c.1225+916G>A, c.1868-4177C>T, c.2070+3509A>G, c.1784-66A>G, c.315-1422G>T, c.153+2260G>C, c.1500+654A>C, c.1994+1176G>A, c.1225+197T>G, c.1564-3285C>G, c.1994+2772G>T, c.21-112del, c.660-2033A>T, c.153+722C>G, c.2071-2087G>A, c.1501-949A>T, c.545-1101A>G, c.1564-1469_1564-1468del, c.1564-44A>G, c.660-1431G>C, c.315-2931G>A, c.1017+290_1017+308del, c.1500+1225A>C, c.154-614C>G, c.*725_*743del, c.1563+2106G>C, c.2070+2028C>G, c.2070+3170C>A, c.1327-673G>A, c.545-971C>G, c.2071-2932C>T, c.1867+4147T>C, c.2071-91C>T, c.1226-713C>T, c.20+141G>A, c.1994+674C>G	N/A
Central Nervous System	c.*656_*659dup, c.*1743dup, c.2070+1820G>T, c.403-1G>A, c.1868-2284C>T, c.20+50C>A	[5]
Endometrium	c.20+139G>T, c.*119A>C, c.-80C>T, c.20+73G>T, c.1098+1287A>G	N/A
Esophagus	c.1018-217G>A, c.1995-2021G>T, c.845+241G>C, c.2070+716A>T, c.1995-1167A>T, c.1327-115A>G, c.1500+1148A>C, c.659+1066C>T, c.1868-3390G>A, c.1226-627C>G, c.315-264T>G, c.1867+681C>T, c.660-	N/A

	2135C>T, c.1994+1531A>C, c.403-6G>A, c.1995-1061C>G, c.315-1527C>T, c.2070+2905G>T, c.1868-2055T>G, c.545-671A>T, c.315-2918T>G, c.1226-221C>T, c.2071-2821G>A, c.315-2593C>T, c.153+1322C>T	
Hematopoietic and Lymphoid	c.1017+74T>C, c.659+127T>G, c.*726G>A, c.21-798T>A, c.1563+130G>A, c.1867+1890_1867+1891insC, c.1784-66A>G, c.2070+3011del, c.1500+1276T>G, c.1500+1517T>A, c.1563+2208T>G, c.1225+19T>C, c.1500+1519T>A, c.403-84T>G, c.2070+4650C>T, c.2071-945A>C, c.*682C>G, c.-120T>C, c.2071-2209C>T, c.1501-596A>G, c.315-96A>G, c.314+1516C>T, c.*2667A>G, c.659+1084T>G, c.1564-4304G>A, c.20+28G>A, c.403-6G>A, c.1926+27T>G, c.1017+2T>C, c.1867+2757A>C, c.21-279T>A, c.1868-771A>G	[47-50]
Kidney	c.1995-1781A>T, c.1867+1889A>C, c.2070+1724C>T, c.*3832T>G, c.1994+2601C>G, c.1994+2600G>A, c.1783+450del, c.660-2190T>G, c.153+2133C>T, c.1994+993G>T, c.660-531A>T, c.154-1966A>T, c.1500+1519T>A, c.2071-1173A>T, c.1867+230A>T, c.-106+70G>A, c.1995-1867A>G	[51]
Large Intestine	c.1564-134A>T, c.1225+19T>C, c.1225+24T>C, c.2071-167G>T, c.20+73G>T, c.2070+2592C>A, c.314+126A>T, c.*82dup, c.659+96C>A, c.1994+195T>C, c.660-31C>T, c.1563+188C>T, c.1867+1410G>A, c.1099-218C>T, c.1564-22T>G, c.845+25A>G, c.545-163del, c.1868-90A>G, c.1017+2T>C, c.1868-3211A>T, c.1564-1939T>A, c.660-158T>C, c.1098+1378T>G, c.154-76del, c.1225+31del, c.*12G>A, c.1099-27C>T, c.1017+174_1017+175del, c.403-64C>T, c.154-71C>T, c.1867+84T>C, c.659+50A>T, c.1098+2T>A, c.402+107C>T, c.1098+1211G>A, c.1326+148T>C, c.846-28A>G, c.1226-568A>T, c.1099-94G>A, c.1225+39A>G, c.1994+48A>C, c.2071-4386T>G, c.845+35A>C, c.153+863C>T, c.845+92G>A, c.1926+170del, c.1868-85_1868-84del	[14, 15, 52, 53]
Liver	c.1226-1298C>T, c.21-601A>G, c.1564-2517A>G, c.1327-120A>T, c.545-797_545-791del, c.1327-114G>T, c.153+1078C>T, c.1564-1058G>A, c.2070+4011G>A, c.659+33G>A, c.1995-1068C>T, c.2071-865C>T, c.1099-1659T>A, c.1564-1748T>C, c.1564-1689A>G, c.1994+1772A>G, c.315-4del, c.2071-709C>A, c.1563+60A>G, c.1563+2029A>G, c.*2419A>G, c.1564-308C>T, c.2071-2732T>C, c.1563+4202G>A, c.1868-1320A>G, c.845+38C>A, c.1995-2003A>G, c.1867+801A>G, c.2070+4072G>C, c.659+19A>G, c.1500+249del, c.545-958A>G, c.1868-2681A>C, c.154-267A>C, c.1927-271A>G, c.1995-111G>T, c.1501-1059T>C, c.1017+30C>G, c.1098+10A>G, c.1867+2850A>G, c.1098+10A>G, c.1500+1467A>G, c.1501-153G>A, c.1017+55C>A, c.544+1038A>G, c.1564-2A>T, c.*660C>T, c.846-448A>G, c.1994+113A>C, c.1868-4162T>C, c.153+23C>G, c.1995-1142T>A, c.1326+353A>G, c.2071-347G>T, c.659+19A>G, c.20+273T>C, c.1563+684C>A, c.1995-1238G>A, c.2070+4662A>G, c.1994+113A>C, c.1098+829A>G, c.154-355G>T, c.1563+3177dup, c.1225+850A>G, c.314+6T>C, c.1867+668A>C, c.1867+1888A>C, c.1868-2966G>T, c.659+21A>G, c.1868-4229A>T, c.*2837del, c.846-448A>G, c.1017+391A>G, c.660-356A>G, c.1868-3485G>A, c.153+1071C>T, c.315-145del, c.402+370T>C, c.544+1038A>G, c.545-1057A>G, c.1098+777G>T, c.154-945G>A, c.153+735A>G, c.1564-2594T>C, c.1867+597T>G, c.1564-1238T>G, c.2070+1308G>C, c.402+184A>G, c.545-624C>A, c.1225+167A>G, c.314+6T>C, c.153+288C>G, c.1927-136del, c.1563+3003G>C, c.1098+1683C>G, c.1563+587A>G	[54]
Lung	c.-65G>T, c.545-18A>C, c.1099-1G>T, c.544+34G>T, c.20+37G>T, c.1326+146T>C, c.545-116A>C, c.846-60T>A	[55]
Meninges	c.1868-419G>T	[56]
Ovary	c.314+2799A>G, c.314+13A>G, c.1994+25A>G, c.*656T>C, c.1868-1527A>T, c.315-4del, c.1564-2307A>T, c.1783+505C>T, c.659+981C>G, c.314+13A>G, c.2070+2110T>C, c.1327-2A>G, c.659+709C>A, c.1564-893G>A, c.154-11C>T, c.659+344G>C, c.403-322T>C	[57]
Pancreas	c.402+174T>G, c.1017+1185T>G, c.154-870C>G, c.314+268C>T, c.1995-1799G>C, c.154-1790T>A, c.1867+1885A>C, c.1326+220G>A, c.1017+1185T>G, c.1995-1756C>T, c.1018-31G>A, c.1868-1565T>A, c.660-337T>G, c.1017+1185T>G, c.1099-357G>T, c.1225+419G>T, c.660-1178A>T, c.1500+1344C>T, c.1564-931C>G, c.1868-1565T>A, c.1018-736G>A, c.659+1095A>T, c.1868-1565T>A, c.154-17C>T, c.2071-826G>A, c.1017+1185T>G, c.1563+288C>T, c.659+977T>C, c.545-75T>A	N/A
Prostate	c.1564-4417C>T, c.2071-4640dup, c.1018-958C>A, c.*4355C>G, c.2071-4640dup, c.1867+2223C>G, c.1564-4417C>T, c.1867+3908G>A, c.20+826C>T, c.1225+231G>A, c.2071-4640dup, c.1500+1491G>T, c.154-76del, c.1563+2934A>T, c.1225+231G>A, c.1563+2327T>C, c.1564-4417C>T, c.154-1959C>A, c.1564-4417C>T, c.314+1619A>G, c.1225+390A>G, c.2071-4640dup, c.1500+1517T>A, c.1500+1491G>T, c.2071-1830T>C, c.2070+103C>G, c.154-2367A>T, c.2071-4640dup, c.1926+219A>G, c.21-592G>T, c.314+805T>C, c.1017+1012G>A, c.1994+1886G>T, c.1994+1730G>T, c.1927-326C>T, c.1017+1012G>A, c.2070+4696T>A, c.2070+4510T>G, c.154-2302C>G, c.1501-1517_1501-1510delinsGAAAGA, c.314+574G>T, c.2071-4640dup, c.1926+351T>C, c.1500+1491G>T, c.2070+3038G>C	[32]
Skin	c.154-3C>G, c.20+23C>T, c.20+50C>A, c.20+78C>G, c.315-3050T>C, c.2070+3962C>T, c.*94C>T, c.-53C>A	[36]
Soft Tissue	c.1868-904_1868-895del	[58]
Stomach	c.153+51A>G, c.1098+481C>G, c.845+82T>G, c.-47T>A, c.315-5_315-4del, c.1994+46_1994+52del, c.154-76del, c.2071-3745C>T, c.1099-202T>C, c.1326+55T>A, c.153+105C>A, c.315-75A>G, c.1501-337T>G, c.154-76del, c.1226-1408C>A, c.1500+1519T>A, c.1994+99C>A, c.1098+1088A>G, c.154-76del, c.659+617G>T	[59]
Upper Aerodigestive Tract	c.153+1del, c.403-44A>T	[60]
Urinary Tract	c.*44G>C, c.1326+1G>C, c.1326+1G>C	N/A
NS	c.545-1G>A	[45]

Tissue	RAD50 ORF Mutations	References
Autonomic Ganglia	p.N934Kfs*10, p.L622F, p.L475P	[61, 62]
Biliary Tract	p.G382V, p.I505V, p.E75V, p.L84V	[62, 63]
Bone	p.V842A, p.R1260C	[64]
Breast	p.E362Q, p.S373A, p.N395K, p.E444K, p.E463K, p.V497A, p.S560R, p.D675=, p.L719=, p.K722Rfs*14, p.Q74E, p.E75del, p.R759I, p.Q811R, p.L848=, p.R850C, p.R87C, p.E962D, p.E1037Q, p.E1056=, p.R1069I, p.R1077Q, p.M1107I, p.D1120N, p.D1122E, p.T1127S, p.R1198Q, p.T121I, p.D1231E, p.L1237V, p.L151=, p.L251F, p.T26S, p.E291D, p.E328K	[62, 65-71]
Central Nervous System	p.E468G, p.K545E, p.S635N, p.I649=, p.E676*, p.E834K, p.D855G, p.R1077*, p.C1222S, p.E1232D, p.M140I, p.E257*	[5, 62, 72, 73]
Cervix	p.I1227=, p.E283D, p.G41=	[62]
Endometrium	p.I443L, p.I45T, p.E526D, p.S557P, p.S557Y, p.R558M, p.D561E, p.R686K, p.E693D, p.R706*, p.E770*, p.A785V, p.D804Y, p.R807=, p.K838N, p.R884C, p.N953D, p.E962D, p.V101A, p.E1033*, p.E1062D, p.R1069I, p.A1074T, p.R1077Q, p.K1079T, p.R1093*, p.R1098W, p.Y1124D, p.E1171K, p.L1223P, p.D1294N, p.S143Y, p.V150A, p.E205*, p.D21Y, p.E222K	[62, 74]
Esophagus	p.I45V, p.R593T, p.R850H, p.K973M, p.M1140I, p.R1166W	[7, 62, 75]
Hematopoietic and Lymphoid Tissue	p.D358H, p.F396V, p.M415I, p.Y462N, p.Y462F, p.Y462*, p.D549E, p.L615R, p.R656*, p.D69Y, p.M735K, p.V78L, p.P780S, p.T793R, p.A908T, p.L929Sfs*10, p.N934Kfs*10, p.I954V, p.K959=, p.E1061*, p.N1072S, p.F111Y, p.I1165V, p.A1218V, p.P1233S, p.L1276F, p.A188G	[48, 62, 72, 76-82]
Kidney	p.T44=, p.C48=, p.L567M, p.S624G, p.D675Tfs*45, p.R726C, p.N758=, p.T879=, p.M1004L, p.A1074=, p.N1172K, p.T1193A, p.L1208=, p.I1253L, p.R254H, p.K279Efs*7	[13, 51, 62, 83]
Large Intestine	p.S336Y, p.Q350*, p.R352H, p.E362*, p.R385H, p.S389G, p.E390=, p.R391=, p.F396L, p.T410Lfs*5, p.T437A, p.K501R, p.I505V, p.R519H, p.E526D, p.S582=, p.N598=, p.E626K, p.S653*, p.R656Q, p.A657S, p.F66S, p.D69N, p.Q689Rfs*31, p.K721Q, p.K722Gfs*5, p.K722Rfs*14, p.E723Gfs*5, p.R725W, p.R726C, p.R726H, p.R736=, p.K745N, p.L774=, p.V78M, p.S784R, p.A813E, p.I860T, p.R87C, p.E897K, p.E92K, p.N934Kfs*10, p.E949*, p.H955N, p.Y957H, p.M958I, p.E977*, p.R98I, p.E995Rfs*2, p.E1029D, p.E1033*, p.R1038K, p.L1042V, p.K1043N, p.E1062D, p.R1069I, p.A1074S, p.R1077*, p.E1084*, p.H1087N, p.K1089N, p.R1093*, p.R1093Q, p.R1098W, p.E110D, p.I1109T, p.M1111I, p.K1134E, p.H1136R, p.I1146S, p.R1148C, p.R1152Q, p.R1156C, p.R1166Q, p.R1185Q, p.R1198Q, p.R1200Q, p.R120I, p.K1206R, p.L1211F, p.R1214C, p.R1214H, p.T1220=, p.A1246V, p.R1256C, p.F1286L, p.N1292S, p.V1304A, p.R193W, p.Q197=, p.R254C, p.R254H, p.E259*, p.R278Q, p.E291D, p.E302D	[14-17, 52, 62, 84, 85]
Liver	p.Q392H, p.K446E, p.C48F, p.N494K, p.L541P, p.A660S, p.E75K, p.V757=, p.R763H, p.M800V, p.R823L, p.L839F, p.Q856*, p.V101=, p.C102Y, p.H1041Y, p.Q1052K, p.R1077Q, p.L114V, p.V117F, p.S1174L, p.Y1182Lfs*2, p.C1222Y, p.N1236D, p.E1243*, p.E1251*, p.A134S, p.G16E, p.T228A	[20, 86]
Lung	p.L339=, p.L347P, p.R352H, p.Y51C, p.L541Afs*7, p.L566P, p.T61P, p.E620K, p.E639*, p.K651I, p.Q672E, p.D69Y, p.M7T, p.K722R, p.R725W, p.E744K, p.I747K, p.G776S, p.K838T, p.V89G, p.K973=, p.L1042Ffs*15, p.H1071Y, p.N1072S, p.K1126N, p.S1137I, p.R1166Q, p.A1169S, p.K1190=, p.K1190N, p.C1201F, p.A1216=, p.E1232K, p.G124C, p.L1245F, p.G1278R, p.E1281V, p.Q1295*, p.E1298Q, p.I141F, p.V154=, p.T191I, p.R196L, p.D21E, p.T228S, p.S287G, p.V315L, p.R320W	[22, 23, 25-27, 62, 87, 88]
NS	p.R352C, p.N934Ifs*6, p.H158Y, p.R385H, p.A1246S, p.S895F	[45, 46, 62]
Ovary	p.E431D, p.L742S, p.A1248G, p.R1288S, p.R327H	[29, 62]
Pancreas	p.L439Kfs*4, p.I587=, p.T773I, p.K845M, p.R87C, p.N1144S, p.E160K, p.H326Y	[62, 89, 90]
Penis	p.R365Q	[62]
Pleura	p.R278Q, p.A182E	[31]
Prostate	p.A357P, p.Y462C, p.I505V, p.K722Rfs*14, p.L875V, p.N934Ifs*6, p.E1044A, p.A1169T, p.A1169V, p.Y1182C, p.P58S, p.S1137G, p.R1180Q, p.R1185Q, p.E1240=, p.I155S, p.M282I	[34, 38, 62, 91-93]
Salivary Gland	p.K722Rfs*14	[94]
Skin	p.R352C, p.R359C, p.I364=, p.K394E, p.K452=, p.Q523*, p.T536I, p.Q523*, p.T536I, p.P58S, p.A662=, p.Q689*, p.P70L, p.E796=, p.R823Q, p.T867S, p.R87C, p.R87H, p.S895F, p.E897K, p.E920K, p.A940E, p.H955Y, p.L1024S, p.V1050I, p.R1077Q, p.E110K, p.R1098L, p.D1170N, p.R1180=, p.R1200*, p.R1214C, p.L1223F, p.G1226S, p.R1239Q, p.V127=, p.F1286L, p.P250L, p.Q298*	[34-37, 62, 95-100]
Small Intestine	p.R1279H	[62]
Soft Tissue	p.L629Q, p.E239K, p.I272S	[62, 101]
Stomach	p.D417G, p.M502T, p.L594H, p.R617Efs*26, p.K628M, p.C681=, p.V683I, p.K722Rfs*14, p.E723Gfs*5, p.R726C, p.V78M, p.P780=, p.R1077*, p.E1084K, p.D1120E	[38, 62, 102],[75]
Testis	p.M282I	[62]
Thyroid	p.Q465L, p.H559Q, p.E562Q, p.Q589H, p.N598S, p.R850S, p.W1017R, p.K1103=, p.Y1104C, p.Y1104*, p.Q1158H, p.L1237H, p.A171S, p.V203L, p.S237*, p.N310S	[62, 103]
Upper Aerodigestive System	p.R365Q, p.R519H, p.F86V, p.R87H, p.I94L, p.V96L, p.E1015V, p.E1106Q, p.Q207E, p.K238M	[41-43, 62, 104, 105]
Urinary Tract	p.E431Q, p.Q454=, p.L457=, p.E468K, p.E492K, p.L518Q, p.S604F, p.Q685H, p.D69N, p.R79T, p.A810P, p.R823*, p.E869Q, p.K906N, p.Q924K, p.N934Ifs*6, p.V951F, p.E977*, p.M1133I, p.E1161Q, p.S1174L, p.D1177H, p.L1189=, p.R1256C, p.R138*, p.G145R, p.A149Gfs*10, p.E259Q	[44, 62, 71, 106]

Tissue	RAD50 Intronic, 5' and 3' UTR Mutations	References
Autonomic Ganglia	c.*317C>A	N/A
Biliary Tract	c.129+567del, c.213+7825del	N/A
Breast	c.1051+234G>C, c.1452+121A>T, c.1452+547C>T, c.1453-531G>C, c.1794-1269G>A, c.213+166C>A, c.213+242A>T, c.213+3398G>A, c.213+4182T>A, c.213+4441G>A, c.213+5551C>A, c.213+7826A>T, c.213+8000G>C, c.214-4567C>A, c.2207+1283G>C, c.2207+1482G>A, c.2207+889_2207+890insTAATGGTCT, c.2208-1985A>T, c.2208-340G>C, c.2718+1238C>A, c.2718+1382A>C, c.2719-940G>A, c.3036+313G>C, c.3036+997C>G, c.3037-2061A>G, c.3037-2958A>G, c.3037-3170_3037-3169insAT, c.3165-391G>A, c.3165-4A>T, c.3165-692A>T, c.3165-83A>G, c.3389+1671C>T, c.3389+2132T>A, c.3389+2579A>T, c.3389+5475_3389+5476del, c.3389+5496C>T, c.3389+8768G>C, c.3389+8776G>C, c.3390-1106T>C, c.3390-3095C>G, c.3390-3901C>G, c.3390-7535A>T, c.3390-801G>T, c.3390-8448G>T, c.3390-8963A>C, c.3390-9282G>C, c.-355G>C, c.757-2819C>T, c.757-2886C>A, c.757-665G>A, c.757-81C>T, c.757-896A>G	[65]
Central Nervous System	c.*2078G>A, c.*2163T>A, c.2923-1G>A, c.3165-1G>A, c.3619-1G>A	[62, 107]
Endometrium	c.*2826C>G, c.214-6058C>T, c.3390-6351G>A, c.366-875G>C, c.756+479T>C	N/A
Esophagus	c.*286C>T, c.1052-125G>A, c.1052-126dup, c.1052-175C>T, c.213+120G>A, c.213+1357T>G, c.213+4843A>T, c.2207+1514A>C, c.2207+1563A>T, c.2208-3565T>G, c.2718+697C>T, c.3037-2537C>G, c.3389+1132del, c.3389+1593G>T, c.3389+2424T>C, c.3389+6090T>G, c.3389+6656G>T, c.3476-110T>C, c.366-96del, c.757-139_757-138insCTG, c.757-298C>G	[75]
Hematopoietic and Lymphoid Tissue	c.*2898T>C, c.1051+58A>T, c.1245+19A>T, c.1246-198A>G, c.129+141G>A, c.1452+402G>A, c.1636-196T>G, c.214-7850C>T, c.2207+1467T>G, c.2208-3557T>A, c.2524+166T>G, c.2718+644T>A, c.2719-1699A>G, c.3037-1301A>T, c.3037-1343A>T, c.3037-3156_3037-3155del, c.3037-665G>A, c.3164+515A>G, c.3165-528G>A, c.3389+1542C>A, c.3389+1587T>G, c.3389+1589T>G, c.3389+6143C>T, c.3475+62A>G, c.3618+1149G>A, c.3618+857G>T, c.551+123T>C	[48]
Kidney	c.*1249A>G, c.1636-32_1636-31dup, c.214-2566T>A, c.214-992G>A, c.2208-74C>G, c.3036+25C>A, c.3619-687G>T, c.365+460A>G, c.365+997C>G, c.756+1488C>A	[51]
Large Intestine	c.*1596A>T, c.*623_*625del, c.1052-6del, c.1246-136T>C, c.1246-149A>C, c.1636-9del, c.2207+2256G>T, c.2524+192A>C, c.3165-2A>G, c.-32G>A, c.3390-1471T>G, c.3475+322del, c.3475+331T>C, c.3475+38G>T, c.3476-1G>A, c.3619-73A>G, c.366-96del, c.3753-86T>C	[14, 52, 62]
Liver	c.*1078A>G, c.*1132A>G, c.*40C>T, c.*559G>T, c.*996C>T, c.1052-237A>G, c.129+252C>A, c.130-616G>A, c.1452+207A>G, c.1635+12C>A, c.1793+1351A>G, c.1793+771A>G, c.1794-190T>G, c.1794-571T>A, c.213+1794A>G, c.213+2057C>T, c.213+233C>G, c.213+2848A>G, c.213+3061A>G, c.213+3805G>T, c.213+5224T>A, c.213+6024G>A, c.213+6877T>G, c.213+7121A>G, c.213+714T>C, c.213+7599A>G, c.214-125C>T, c.214-285A>T, c.214-3682A>G, c.214-3900C>G, c.214-452A>G, c.214-5308G>T, c.214-5309G>T, c.214-6150A>G, c.2207+3176G>A, c.2207+3409A>C, c.2207+3423T>G, c.2208-1301G>C, c.2208-1526C>T, c.2208-1985A>G, c.2208-2814_2208-2812dup, c.2718+1459G>A, c.2718+960C>G, c.2719-202A>G, c.3036+3101A>G, c.3036+3161G>A, c.3036+3177G>T, c.3037-1197del, c.3037-3102A>G, c.3165-171G>T, c.3165-203A>G, c.3165-210G>A, c.3165-234G>T, c.3165-252A>G, c.3165-33del, c.3165-476G>A, c.3165-511T>G, c.3389+1542C>A, c.3389+3778A>T, c.3389+39A>G, c.3389+609C>T, c.3389+67C>G, c.3389+7035G>T, c.3389+733A>C, c.3389+8796A>G, c.3389+8963A>G, c.3390-2303A>G, c.3390-2A>T, c.3390-3488G>T, c.3390-3542G>T, c.3390-395T>C, c.3390-6651G>T, c.3390-6938G>A, c.3390-7711A>T, c.3475+107A>G, c.3475+128A>G, c.3475+245T>C, c.3475+329C>T, c.3618+762A>T, c.3619-1070A>G, c.3619-1091A>G, c.3619-1123A>G, c.365+1408A>G, c.366-911A>C, c.3752+151C>A, c.3752+294C>T, c.3752+640C>G, c.3753-638T>C, c.551+11C>G, c.551+28G>T, c.756+1218A>T, c.756+1692G>C, c.756+1738G>A, c.756+1854A>G, c.756+2044A>G, c.756+3120A>C, c.756+3268T>A, c.756+3587A>G, c.756+777A>G, c.757-2456A>G, c.757-790G>A	N/A
Lung	c.1052-16A>T, c.1635+21C>G, c.1636-1G>T, c.214-151A>G, c.2525-152A>C, c.2719-154A>C, c.2922+1G>A, c.3476-110T>C, c.3618+95G>C, c.551+78A>G, c.552-1G>T, c.885+11G>A	[23, 45, 62]
Ovary	c.*1029C>T, c.213+2875T>G, c.213+3829A>G, c.2208-3629C>T, c.2718+322G>T, c.2719-1568T>C, c.3389+5851A>G, c.3389+6657G>C, c.3390-8621T>C, c.3618+1G>A, c.365+1582T>G, c.757-1665A>T	[62]
Pancreas	c.*1269C>T, c.*2842C>A, c.1051+292C>G, c.1453-528A>T, c.1794-1261A>C, c.213+2301T>C, c.213+4334G>A, c.213+6024G>A, c.214-2611G>A, c.214-7675A>G, c.2208-2840A>G, c.2208-389A>C, c.2718+590G>C, c.3165-145T>C, c.3389+1542C>A, c.3389+1546A>C, c.3389+1591T>G, c.3389+2639C>T, c.3389+9348G>T, c.3390-2082A>G, c.3390-3857C>T, c.3390-8020C>T, c.3475+323C>T, c.3618+918G>T, c.366-1410C>T, c.3752+481G>A, c.3753-145G>A, c.756+1280C>T, c.756+3006G>A, c.757-332A>T, c.757-3646C>T	N/A
Prostate	c.*1027C>T, c.1246-4_1248del, c.1636-14T>G, c.1794-852T>G, c.213+3944C>A, c.213+5936A>G, c.213+5T>G, c.214-231A>G, c.2207+3143G>T, c.2719-1619G>A, c.2719-582C>G, c.3036+112G>A, c.3036+2454C>T, c.3036+2530A>G, c.3037-1086C>T, c.3165-476G>A, c.3389+1077A>G, c.3389+1589T>G, c.3389+1593G>T, c.3389+4511del, c.3389+6097del, c.3389+7466G>A, c.3389+9123A>C, c.3389+9395A>T, c.3390-4270G>A, c.3390-4882A>G, c.3390-6843G>C, c.3390-7019C>A, c.3390-8256dup, c.366-1663del, c.366-96del, c.366-96dup, c.756+1553G>T, c.756+3030G>C, c.756+448_756+450del, c.756+978G>A, c.757-103C>T, c.757-994T>A	[62, 108]
Skin	c.*2958A>C, c.130-520T>G, c.1453-560C>T, c.1636-1G>A, c.1453-560C>T, c.1636-1G>A, c.3036+1994_3036+1998del, c.3389+5426C>T, c.3619-82G>T, c.552-2A>G, c.757-1971C>T, c.757-2597A>G	[36, 109]
Soft Tissue	c.214-7703T>A	[58]

Stomach	c.1636-9del, c.2207+2256G>T, c.2525-26T>C, c.-32G>T, c.3390-5944A>G, c.3390-7436C>A, c.885+11G>A	[59, 110]
Thyroid	c.1793+879G>T	N/A
Upper Aerodigestive System	c.3390-3042del, c.3752+29G>C	N/A

Tissue	NBN ORF Mutations	References
Autonomic Ganglia	p.S195R	[111]
Biliary Tract	p.T178I, p.M83Cfs*9	[62]
Bone	p.V314M	[64]
Breast	p.C119S, p.L302V, p.E36D, p.D586Y, p.I290F, p.E610K, p.K236*, p.K29R, p.H540N, p.S213L, p.H540Y, p.S123P, p.K236N	[62, 112, 113]
Central Nervous System	p.L723P, p.L302F, p.E610K, p.V243I, p.E726K, p.V314M, p.G246D, p.S486F	[62, 114]
Cervix	p.E185K	N/A
Endometrium	p.P354S, p.S355I, p.S418*, p.R43Q, p.S447Y, p.R466Gfs*18, p.T526I, p.E543K, p.P6S, p.R624C, p.E636*, p.L654Afs*5, p.F685V, p.R714*, p.A740V, p.V155M, p.I166T, p.Q216*, p.R218I, p.T268M, p.D284G	[62]
Esophagus	p.V346M, p.R43Q, p.I455V, p.S499=, p.R551Gfs*8, p.K635N, p.V691L, p.*755Qext*13, p.M83Cfs*9, p.G100A, p.N142S, p.P191A, p.D211Y	[9, 10, 62, 75, 115-117]
Hematopoietic and Lymphoid Tissue	p.L34=, p.D399=, p.I41S, p.P672=, p.K105E, p.E185Q, p.E185*, p.K219Nfs*16, p.K219N, p.Q220E	[80, 118]
Kidney	p.M389V, p.I439V, p.E619K, p.Y679H, p.L68=, p.A713Gfs*29, p.N731Ifs*20, p.K125Rfs*34, p.G206Lfs*26, p.L230F, p.S240Cfs*8	[62, 119, 120]
Large Intestine	p.L34=, p.V346=, p.I35T, p.L352R, p.S355=, p.N359S, p.Y363=, p.E383*, p.D399=, p.S411C, p.Y429H, p.R43Q, p.R466Gfs*18, p.L490*, p.P498L, p.E505*, p.E512Q, p.D519G, p.N520S, p.T526I, p.S530Y, p.R551Gfs*8, p.R551K, p.M553Wfs*6, p.V556=, p.V608I, p.S647G, p.L654Afs*5, p.K653N, p.S661*, p.S667P, p.P672=, p.A696=, p.D70Y, p.A710S, p.L723=, p.Q732=, p.L739P, p.E81K, p.M83Cfs*9, p.R89Q, p.A131=, p.L135P, p.R169C, p.E185Q, p.R215W, p.R218I, p.V25I, p.P266=, p.N307fs*5, p.L302I, p.A313V, p.F316L, p.Y322C, p.G327C,	[14, 16, 17, 62, 72, 84, 85, 121]
Liver	p.R43*, p.S488=, p.F52L, p.T570R, p.Q616K, p.D677G, p.E728=, p.V153=, p.P15=, p.E23K, p.Q234H, p.H235Q, p.V242L, p.P325T	[62]
Lung	p.P338L, p.L34=, p.K351R, p.A356T, p.A365P, p.D373H, p.W375C, p.E390*, p.D399=, p.S418*, p.I455=, p.S486=, p.E512G, p.V54=, p.K549E, p.K550I, p.E561K, p.L574I, p.D646Y, p.V65A, p.L656M, p.R660=, p.I664M, p.P672=, p.N684K, p.F685I, p.N716D, p.T717A, p.E721*, p.E726*, p.V729L, p.E737K, p.A8T, p.S88T, p.G103Efs*6, p.G103V, p.S118C, p.V122=, p.G124R, p.E185Q, p.D201V, p.P203L, p.G206*, p.R215W, p.R215L, p.F222=, p.F222=, p.G224V, p.G224A, p.G245A, p.R250M, p.F262L, p.P266L, p.G267A, p.D284H, p.K287=, p.G301S, p.K320E, p.Q326E, p.I33F	[22-25, 62, 72, 87, 88, 122, 123]
NS	p.R466Gfs*18, p.P191L, p.R551Gfs*8, p.N503Y, p.P572S	[45, 62]
Ovary	p.I41=, p.D272N	N/A
Pancreas	p.Y363H, p.A372V, p.R394I, p.R466Gfs*18, p.R592S, p.S667C, p.E185Q,	[62, 90, 124, 125]
Penis	p.T337N, p.V157F, p.K715N	[62]
Placenta	p.E658K	[62]
Pleura	p.T657A	[31]
Prostate	p.T361K, p.Y363=, p.R551Gfs*8, p.K642R, p.R714L, p.Q732K, p.K82E	[32, 62, 92, 126, 127]
Salivary Gland	p.P694T	[128]
Skin	p.L342H, p.A356V, p.S387F, p.R394I, p.S418*, p.R466K, 25759019, p.D469N, p.E491*, p.H540Y, p.R551=, p.L574S, p.Q644*, p.Q644=, p.V65I, p.S669F, p.D121N, p.L165H, p.P170L, p.S186F, p.S207N, p.L297=, p.V314M	[34-37, 62, 129, 130]
Small Intestine	p.V346M	[62]
Soft Tissue	p.P338S, p.P354L, p.R466Gfs*18, p.N517K, p.V153Kfs*17, p.W2C	[62, 131-133]
Stomach	p.T337I, p.S432P, p.K464E, p.R466Gfs*18, p.R551Gfs*8, p.L563F, p.D596N, p.I675M, p.Q84H, p.K125E, p.A131D, p.V172=, p.L181M, p.R215=, p.S240=, p.Y322H	[38, 59, 62]
Testis	p.N640S	[62]
Thyroid	p.P381S, p.I426M, p.L656=, p.R660I, p.E728D, p.E81K, p.E109*, p.E185Q, p.R215W	[62, 103, 134]
Upper Aerodigestive System	p.L377F, p.S418*, p.P461L, p.T485M, p.T717S, p.R17T	[43, 60, 135]
Urinary Tract	p.E36A, p.N37T, p.E379K, p.R394G, p.S40=, p.R43Q, p.A46V, p.S499L, p.E510Q, p.R551Kfs*5, p.S615F, p.R670T, p.D677N, p.H712Y, p.E737Q, p.R89Q, p.I162V, p.E254K, p.F263L	[44, 62]

Tissue	NBN Intronic, 5' and 3' UTR Mutations	References
Adrenal Gland	c.481-1G>C	[136]
Biliary Tract	c.896+1769del, c.1397+747del, c.2070+109_2070+111del, c.1914+41C>T, c.897-983dup, c.*502A>G, c.480+1026T>A, c.1397+747dup, c.1397+747del, c.584+2906A>T	N/A
Bone	c.2071-2A>G	[62]
Breast	c.1397+314C>G, c.320+212C>T, c.2070+335C>T, c.2070+607C>T, c.2070+986C>G, c.994+637G>T, c.2184+2131_2184+2139del, c.2185-1483C>T, c.896+220C>T, c.*2065C>T, c.1846-1391T>C, c.584+1627G>A, c.1846-1559C>T, c.1397+266G>A, c.897-732C>T, c.2185-1483C>T, c.2184+2T>A, c.2184+245T>C, c.897-1646C>G, c.*2065C>T, c.1124+54G>C, c.1397+266G>A, c.585-399G>T, c.2185-1209G>A, c.995-2016C>G, c.1845+418T>G, c.2185-1031C>G, c.584+26A>G, c.321-47C>T, c.1124+663T>A, c.1397+656C>G, c.896+1709C>T, c.2184+2709T>A, c.1846-542G>A, c.2071-84C>A, c.*1017C>T, c.480+95A>G, c.2235-1G>A, c.994+595G>C, c.584+3379G>C, c.480+398G>T, c.1124+444C>T, c.480+589C>T, c.897-711C>T, c.1846-529C>G,	[62, 70]
Central Nervous System	c.1124+292G>A,	N/A
Endometrium	c.2184+882C>T	N/A
Esophagus	c.1398-10del, c.171+55A>G, c.2185-2670G>C, c.585-930A>C, c.994+843T>G, c.995-1G>A, c.995-780C>G	[75]
Eye	c.*724_*725insTG	[137]
Hematopoietic and Lymphoid Tissue	c.*486T>A, c.1124+18C>T, c.1125-79C>A, c.1397+259del, c.1397+72A>T, c.1846-23T>A, c.1846-2424T>G, c.1846-2574_1846-2569del, c.1846-402T>C, c.1846-644G>A, c.1915-7A>G, c.2071-2A>G, c.2184+1494A>T, c.2184+1686T>C, c.2185-122T>C, c.2185-1393C>T, c.2185-655C>T, c.2185-919A>G, c.2234+687A>T, c.584+2682T>A, c.703-18G>A, c.896+728_896+730del	[138]
Kidney	c.1915-1G>A, c.2185-121C>T, c.2185-1733G>A, c.585-1779G>T, c.585-2196G>A, c.585-492G>A, c.994+2722T>A, c.995-511G>A	N/A
Large Intestine	c.*1977T>C, c.1124+125G>A, c.1397+10dup, c.1397+41del, c.1398-10del, c.1914+74del, c.1915-162A>G, c.2184+123G>A, c.2185-1385G>T, c.2185-1387G>T, c.2185-577T>G, c.2235-433G>A, c.2235-4G>C, c.38-18A>T, c.38-1G>T, c.38-27C>A, c.585-117del, c.703-174G>A, c.896+1065G>A, c.896+517C>T, c.896+63del, c.897-84del	[14, 62, 139, 140]
Liver	c.*1167A>G, c.*143A>G, c.1124+66A>G, c.1125-164A>G, c.1398-154A>G, c.1398-457A>G, c.1398-483A>T, c.172-229G>A, c.1845+1571G>A, c.1845+2595C>G, c.1846-2248T>A, c.1846-75C>G, c.1914+318C>T, c.1915-122A>G, c.2071-22T>C, c.2184+1518G>T, c.2184+2174C>A, c.2184+689A>G, c.2185-93del, c.2234+495_2234+498del, c.37+79C>T, c.38-241T>G, c.38-249A>G, c.480+1080dup, c.481-110C>T, c.481-191A>G, c.584+1367G>T, c.584+160A>G, c.584+217T>C, c.584+409A>G, c.585-2796G>T, c.585-3347T>C, c.702+12A>T, c.703-232C>A, c.-79G>C, c.896+117G>T, c.896+33C>A, c.896+75C>G, c.897-1242G>C, c.994+1221A>T, c.994+2676dup, c.995-3C>A, c.995-766C>A	N/A
Lung	c.*1524G>T, c.1124+18C>T, c.1124+37C>T, c.1124+91C>A, c.1398-152A>C, c.172-578G>T, c.1845+2085T>C, c.1915-7A>G, c.2070+1G>T, c.2071-30A>T, c.-22C>G, c.320+1G>T, c.37+20C>A, c.38-1G>T, c.481-1G>C, c.896+120G>C	[23, 62, 141]
NS	c.1845+2T>C	[62]
Ovary	c.1125-960T>C, c.2184+1545A>C, c.2185-1665A>G, c.481-1051G>T, c.584+2922T>A, c.584+789A>G, c.897-1363A>G, c.897-425C>G, c.995-1212C>G, c.995-1263T>G, c.995-808C>A	N/A
Pancreas	c.*1320A>G, c.*2163C>T, c.1124+1056A>C, c.1124+41C>G, c.1124+81C>G, c.1397+230G>A, c.1398-10T>A, c.1398-728G>A, c.2070+1110C>T, c.2184+1740C>A, c.2185-1393C>T, c.2185-1646T>G, c.2185-641C>T, c.2234+176G>A, c.37+163C>T, c.38-19A>T, c.481-1205C>A, c.584+2743G>T, c.585-2656G>A, c.896+1170G>T, c.896+2403G>T, c.896+2404G>T, c.897-170G>A, c.994+1436G>T, c.994+2231T>A, c.994+273G>T, c.994+513A>G, c.994+842A>T, c.995-1794C>T, c.995-258C>G, c.995-264A>T, c.995-336C>T	N/A
Prostate	c.1124+761G>A, c.1398-10T>A, c.1846-24G>T, c.2070+832A>G, c.2184+840G>C, c.2185-1374_2185-1373del, c.2185-2449G>A, c.2234+180C>T, c.2234+395A>G, c.480+575G>A, c.480+80_480+81insT, c.584+1255A>G, c.584+147_584+150del, c.584+1725C>G, c.584+2599C>T, c.584+894dup, c.585-117del, c.994+266_994+267insCCA, c.995-1074T>G, c.995-1798_995-1796del, c.995-403A>G	[32, 33]
Skin	c.1125-643_1125-642insTC, c.1398-1G>A, c.1915-7A>G, c.481-741T>C, c.896_896+1delinsAA, c.994+513A>T	[34, 36]
Soft Tissue	c.1397+46del, c.2071-61A>T, c.-26G>A, c.703-18G>A, c.896+10dup	[132, 133]
Stomach	c.2071-752G>A, c.2071-839G>A, c.2184+1455T>C, c.38-20T>A, c.584+292A>G, c.703-149G>A, c.896+100G>T	N/A
Thyroid	c.897-2A>T	[103]
Upper Aerodigestive System	c.1914+2T>A, c.2235-563G>T, c.481-766A>G	[62]
Urinary Tract	c.2071-13_2077del, c.2184+6T>C,	[142]

References

1. Wardell, C.P., et al., *Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations*. J Hepatol, 2018. **68**(5): p. 959-969.
2. Malhotra, A., et al., *Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations*. Genome Med, 2015. **7**(1): p. 6.
3. Nomura, M., et al., *Distinct molecular profile of diffuse cerebellar gliomas*. Acta Neuropathol, 2017. **134**(6): p. 941-956.
4. Killela, P.J., et al., *The genetic landscape of anaplastic astrocytoma*. Oncotarget, 2014. **5**(6): p. 1452-7.
5. Patil, V., J. Pal, and K. Somasundaram, *Elucidating the cancer-specific genetic alteration spectrum of glioblastoma derived cell lines from whole exome and RNA sequencing*. Oncotarget, 2015. **6**(41): p. 43452-71.
6. Le Gallo, M., et al., *Exome sequencing of serous endometrial tumors identifies recurrent somatic mutations in chromatin-remodeling and ubiquitin ligase complex genes*. Nat Genet, 2012. **44**(12): p. 1310-5.
7. Gao, Y.B., et al., *Genetic landscape of esophageal squamous cell carcinoma*. Nat Genet, 2014. **46**(10): p. 1097-102.
8. Sawada, G., et al., *Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population*. Gastroenterology, 2016. **150**(5): p. 1171-1182.
9. Cheng, C., et al., *Genomic analyses reveal FAM84B and the NOTCH pathway are associated with the progression of esophageal squamous cell carcinoma*. Gigascience, 2016. **5**: p. 1.
10. Zhang, L., et al., *Genomic analyses reveal mutational signatures and frequently altered genes in esophageal squamous cell carcinoma*. Am J Hum Genet, 2015. **96**(4): p. 597-611.
11. Ljungstrom, V., et al., *Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations*. Blood, 2016. **127**(8): p. 1007-16.
12. Dietz, S., et al., *Patient-specific molecular alterations are associated with metastatic clear cell renal cell cancer progressing under tyrosine kinase inhibitor therapy*. Oncotarget, 2017. **8**(43): p. 74049-74057.
13. Durinck, S., et al., *Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes*. Nat Genet, 2015. **47**(1): p. 13-21.
14. Giannakis, M., et al., *Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma*. Cell Rep, 2016. **15**(4): p. 857-865.
15. Cancer Genome Atlas, N., *Comprehensive molecular characterization of human colon and rectal cancer*. Nature, 2012. **487**(7407): p. 330-7.
16. Giannakis, M., et al., *RNF43 is frequently mutated in colorectal and endometrial cancers*. Nat Genet, 2014. **46**(12): p. 1264-6.
17. Mouradov, D., et al., *Colorectal cancer cell lines are representative models of the main molecular subtypes of primary cancer*. Cancer Res, 2014. **74**(12): p. 3238-47.
18. Kim, T.M., et al., *Clonal origins and parallel evolution of regionally synchronous colorectal adenoma and carcinoma*. Oncotarget, 2015. **6**(29): p. 27725-35.
19. Liu, Z., et al., *The landscape of somatic mutation in sporadic Chinese colorectal cancer*. Oncotarget, 2018. **9**(44): p. 27412-27422.
20. Jhunjunwala, S., et al., *Diverse modes of genomic alteration in hepatocellular carcinoma*. Genome Biol, 2014. **15**(8): p. 436.
21. Kan, Z., et al., *Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma*. Genome Res, 2013. **23**(9): p. 1422-33.

22. Imielinski, M., et al., *Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing*. Cell, 2012. **150**(6): p. 1107-20.
23. McMillan, E.A., et al., *Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer*. Cell, 2018. **173**(4): p. 864-878 e29.
24. Liu, J., et al., *Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events*. Genome Res, 2012. **22**(12): p. 2315-27.
25. George, J., et al., *Comprehensive genomic profiles of small cell lung cancer*. Nature, 2015. **524**(7563): p. 47-53.
26. Seo, J.S., et al., *The transcriptional landscape and mutational profile of lung adenocarcinoma*. Genome Res, 2012. **22**(11): p. 2109-19.
27. Li, C., et al., *Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma*. Sci Rep, 2015. **5**: p. 14237.
28. Wagner, A.H., et al., *Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer*. Nat Commun, 2018. **9**(1): p. 3787.
29. Cancer Genome Atlas Research, N., *Integrated genomic analyses of ovarian carcinoma*. Nature, 2011. **474**(7353): p. 609-15.
30. Murphy, S.J., et al., *Genetic alterations associated with progression from pancreatic intraepithelial neoplasia to invasive pancreatic tumor*. Gastroenterology, 2013. **145**(5): p. 1098-1109 e1.
31. Bueno, R., et al., *Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations*. Nat Genet, 2016. **48**(4): p. 407-16.
32. Robinson, D., et al., *Integrative clinical genomics of advanced prostate cancer*. Cell, 2015. **161**(5): p. 1215-1228.
33. Kumar, A., et al., *Substantial interindividual and limited intraindividual genomic diversity among tumors from men with metastatic prostate cancer*. Nat Med, 2016. **22**(4): p. 369-78.
34. Sharpe, H.J., et al., *Genomic analysis of smoothed inhibitor resistance in basal cell carcinoma*. Cancer Cell, 2015. **27**(3): p. 327-41.
35. Krauthammer, M., et al., *Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma*. Nat Genet, 2012. **44**(9): p. 1006-14.
36. Pickering, C.R., et al., *Mutational landscape of aggressive cutaneous squamous cell carcinoma*. Clin Cancer Res, 2014. **20**(24): p. 6582-92.
37. South, A.P., et al., *NOTCH1 mutations occur early during cutaneous squamous cell carcinogenesis*. J Invest Dermatol, 2014. **134**(10): p. 2630-2638.
38. Wang, K., et al., *Whole-genome sequencing and comprehensive molecular profiling identify new driver mutations in gastric cancer*. Nat Genet, 2014. **46**(6): p. 573-82.
39. Liu, J., et al., *Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer*. Nat Commun, 2014. **5**: p. 3830.
40. Wang, K., et al., *Exome sequencing identifies frequent mutation of ARID1A in molecular subtypes of gastric cancer*. Nat Genet, 2011. **43**(12): p. 1219-23.
41. Martin, D., et al., *The head and neck cancer cell oncogenome: a platform for the development of precision molecular therapies*. Oncotarget, 2014. **5**(19): p. 8906-23.
42. Fadlullah, M.Z., et al., *Genetically-defined novel oral squamous cell carcinoma cell lines for the development of molecular therapies*. Oncotarget, 2016. **7**(19): p. 27802-18.
43. Stransky, N., et al., *The mutational landscape of head and neck squamous cell carcinoma*. Science, 2011. **333**(6046): p. 1157-60.

44. Guo, G., et al., *Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation*. *Nat Genet*, 2013. **45**(12): p. 1459-63.
45. Van Allen, E.M., et al., *The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma*. *Cancer discovery*, 2014. **4**(1): p. 94-109.
46. Dutton-Regester, K., et al., *Melanomas of unknown primary have a mutation profile consistent with cutaneous sun-exposed melanoma*. *Pigment Cell Melanoma Res*, 2013. **26**(6): p. 852-60.
47. Puente, X.S., et al., *Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia*. *Nature*, 2011. **475**(7354): p. 101-5.
48. McGirt, L.Y., et al., *Whole-genome sequencing reveals oncogenic mutations in mycosis fungoides*. *Blood*, 2015. **126**(4): p. 508-19.
49. Jiang, L., et al., *Exome sequencing identifies somatic mutations of DDX3X in natural killer/T-cell lymphoma*. *Nat Genet*, 2015. **47**(9): p. 1061-6.
50. Welch, J.S., et al., *The origin and evolution of mutations in acute myeloid leukemia*. *Cell*, 2012. **150**(2): p. 264-78.
51. Sato, Y., et al., *Integrated molecular analysis of clear-cell renal cell carcinoma*. *Nat Genet*, 2013. **45**(8): p. 860-7.
52. van de Wetering, M., et al., *Prospective derivation of a living organoid biobank of colorectal cancer patients*. *Cell*, 2015. **161**(4): p. 933-45.
53. Yang, J., et al., *Genome landscapes of rectal cancer before and after preoperative chemoradiotherapy*. *Theranostics*, 2019. **9**(23): p. 6856-6866.
54. Totoki, Y., et al., *High-resolution characterization of a hepatocellular carcinoma genome*. *Nat Genet*, 2011. **43**(5): p. 464-9.
55. Yin, S., et al., *Exome sequencing identifies frequent mutation of MLL2 in non-small cell lung carcinoma from Chinese patients*. *Sci Rep*, 2014. **4**: p. 6036.
56. Bi, W.L., et al., *Genomic landscape of high-grade meningiomas*. *NPJ Genom Med*, 2017. **2**.
57. Jones, S., et al., *Low-grade serous carcinomas of the ovary contain very few point mutations*. *J Pathol*, 2012. **226**(3): p. 413-20.
58. Behjati, S., et al., *Recurrent PTPRB and PLCG1 mutations in angiosarcoma*. *Nat Genet*, 2014. **46**(4): p. 376-379.
59. Chong, I.Y., et al., *The genomic landscape of oesophagogastric junctional adenocarcinoma*. *J Pathol*, 2013. **231**(3): p. 301-10.
60. Al-Hebshi, N.N., et al., *Exome sequencing of oral squamous cell carcinoma in users of Arabian snuff reveals novel candidates for driver genes*. *Int J Cancer*, 2016. **139**(2): p. 363-72.
61. Pugh, T.J., et al., *The genetic landscape of high-risk neuroblastoma*. *Nat Genet*, 2013. **45**(3): p. 279-84.
62. Zehir, A., et al., *Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients*. *Nat Med*, 2017. **23**(6): p. 703-713.
63. Li, M., et al., *Whole-exome and targeted gene sequencing of gallbladder carcinoma identifies recurrent mutations in the ErbB pathway*. *Nat Genet*, 2014. **46**(8): p. 872-6.
64. Crompton, B.D., et al., *The genomic landscape of pediatric Ewing sarcoma*. *Cancer Discov*, 2014. **4**(11): p. 1326-41.
65. Maresca, L., et al., *Functional Interaction Between BRCA1 and DNA Repair in Yeast May Uncover a Role of RAD50, RAD51, MRE11A, and MSH6 Somatic Variants in Cancer Development*. *Front Genet*, 2018. **9**: p. 397.
66. Guerini-Rocco, E., et al., *The repertoire of somatic genetic alterations of acinic cell carcinomas of the breast: an exploratory, hypothesis-generating study*. *J Pathol*, 2015. **237**(2): p. 166-78.

67. Stephens, P.J., et al., *The landscape of cancer genes and mutational processes in breast cancer*. Nature, 2012. **486**(7403): p. 400-4.
68. Ferrari, A., et al., *A whole-genome sequence and transcriptome perspective on HER2-positive breast cancers*. Nat Commun, 2016. **7**: p. 12222.
69. Serra, V., et al., *Clinical response to a lapatinib-based therapy for a Li-Fraumeni syndrome patient with a novel HER2V659E mutation*. Cancer Discov, 2013. **3**(11): p. 1238-44.
70. Lefebvre, C., et al., *Mutational Profile of Metastatic Breast Cancers: A Retrospective Analysis*. PLoS Med, 2016. **13**(12): p. e1002201.
71. Hyman, D.M., et al., *HER kinase inhibition in patients with HER2- and HER3-mutant cancers*. Nature, 2018. **554**(7691): p. 189-194.
72. Abaan, O.D., et al., *The exomes of the NCI-60 panel: a genomic resource for cancer biology and systems pharmacology*. Cancer Res, 2013. **73**(14): p. 4372-82.
73. Wu, G., et al., *The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma*. Nat Genet, 2014. **46**(5): p. 444-450.
74. Le Gallo, M., et al., *Somatic mutation profiles of clear cell endometrial tumors revealed by whole exome and targeted gene sequencing*. Cancer, 2017. **123**(17): p. 3261-3268.
75. Dulak, A.M., et al., *Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity*. Nat Genet, 2013. **45**(5): p. 478-86.
76. Papaemmanuil, E., et al., *Clinical and biological implications of driver mutations in myelodysplastic syndromes*. Blood, 2013. **122**(22): p. 3616-27; quiz 3699.
77. Mareschal, S., et al., *Whole exome sequencing of relapsed/refractory patients expands the repertoire of somatic mutations in diffuse large B-cell lymphoma*. Genes Chromosomes Cancer, 2016. **55**(3): p. 251-67.
78. Gunawardana, J., et al., *Recurrent somatic mutations of PTPN1 in primary mediastinal B cell lymphoma and Hodgkin lymphoma*. Nat Genet, 2014. **46**(4): p. 329-35.
79. Leich, E., et al., *Multiple myeloma is affected by multiple and heterogeneous somatic mutations in adhesion- and receptor tyrosine kinase signaling molecules*. Blood Cancer J, 2013. **3**: p. e102.
80. Bea, S., et al., *Landscape of somatic mutations and clonal evolution in mantle cell lymphoma*. Proc Natl Acad Sci U S A, 2013. **110**(45): p. 18250-5.
81. Landau, D.A., et al., *Evolution and impact of subclonal mutations in chronic lymphocytic leukemia*. Cell, 2013. **152**(4): p. 714-26.
82. Zhang, J., et al., *Deregulation of DUX4 and ERG in acute lymphoblastic leukemia*. Nat Genet, 2016. **48**(12): p. 1481-1489.
83. Gadd, S., et al., *A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor*. Nat Genet, 2017. **49**(10): p. 1487-1494.
84. Lim, B., et al., *Genome-wide mutation profiles of colorectal tumors and associated liver metastases at the exome and transcriptome levels*. Oncotarget, 2015. **6**(26): p. 22179-90.
85. Seshagiri, S., et al., *Recurrent R-spondin fusions in colon cancer*. Nature, 2012. **488**(7413): p. 660-4.
86. Huang, J., et al., *Exome sequencing of hepatitis B virus-associated hepatocellular carcinoma*. Nat Genet, 2012. **44**(10): p. 1117-21.
87. Shi, J., et al., *Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study*. PLoS Med, 2016. **13**(12): p. e1002162.
88. Liu, P., et al., *Identification of somatic mutations in non-small cell lung carcinomas using whole-exome sequencing*. Carcinogenesis, 2012. **33**(7): p. 1270-6.
89. Biankin, A.V., et al., *Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes*. Nature, 2012. **491**(7424): p. 399-405.

90. Yachida, S., et al., *Genomic Sequencing Identifies ELF3 as a Driver of Ampullary Carcinoma*. *Cancer Cell*, 2016. **29**(2): p. 229-40.
91. Grasso, C.S., et al., *The mutational landscape of lethal castration-resistant prostate cancer*. *Nature*, 2012. **487**(7406): p. 239-43.
92. Lindberg, J., et al., *The mitochondrial and autosomal mutation landscapes of prostate cancer*. *Eur Urol*, 2013. **63**(4): p. 702-8.
93. Lim, B., et al., *Genetic alterations and their clinical implications in gastric cancer peritoneal carcinomatosis revealed by whole-exome sequencing of malignant ascites*. *Oncotarget*, 2016. **7**(7): p. 8055-66.
94. Kang, H., et al., *Whole-Exome Sequencing of Salivary Gland Mucoepidermoid Carcinoma*. *Clin Cancer Res*, 2017. **23**(1): p. 283-288.
95. Wagle, N., et al., *MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition*. *Cancer Discov*, 2014. **4**(1): p. 61-8.
96. Krauthammer, M., et al., *Exome sequencing identifies recurrent mutations in NF1 and RASopathy genes in sun-exposed melanomas*. *Nat Genet*, 2015. **47**(9): p. 996-1002.
97. Sanborn, J.Z., et al., *Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination*. *Proc Natl Acad Sci U S A*, 2015. **112**(35): p. 10995-1000.
98. Hoogstraat, M., et al., *Detailed imaging and genetic analysis reveal a secondary BRAF(L505H) resistance mutation and extensive inpatient heterogeneity in metastatic BRAF mutant melanoma patients treated with vemurafenib*. *Pigment Cell Melanoma Res*, 2015. **28**(3): p. 318-23.
99. Durinck, S., et al., *Temporal dissection of tumorigenesis in primary cancers*. *Cancer Discov*, 2011. **1**(2): p. 137-43.
100. Harms, P.W., et al., *The Distinctive Mutational Spectra of Polyomavirus-Negative Merkel Cell Carcinoma*. *Cancer Res*, 2015. **75**(18): p. 3720-3727.
101. Shern, J.F., et al., *Comprehensive genomic analysis of rhabdomyosarcoma reveals a landscape of alterations affecting a common genetic axis in fusion-positive and fusion-negative tumors*. *Cancer Discov*, 2014. **4**(2): p. 216-31.
102. Kim, T.M., et al., *The mutational burdens and evolutionary ages of early gastric cancers are comparable to those of advanced gastric cancers*. *J Pathol*, 2014. **234**(3): p. 365-74.
103. Pozdeyev, N., et al., *Genetic Analysis of 779 Advanced Differentiated and Anaplastic Thyroid Cancers*. *Clin Cancer Res*, 2018. **24**(13): p. 3059-3068.
104. Hedberg, M.L., et al., *Genetic landscape of metastatic and recurrent head and neck squamous cell carcinoma*. *J Clin Invest*, 2016. **126**(1): p. 169-80.
105. Hayes, T.F., et al., *Integrative genomic and functional analysis of human oral squamous cell carcinoma cell lines reveals synergistic effects of FAT1 and CASP8 inactivation*. *Cancer Lett*, 2016. **383**(1): p. 106-114.
106. Hurst, C.D., et al., *Genomic Subtypes of Non-invasive Bladder Cancer with Distinct Metabolic Profile and Female Gender Bias in KDM6A Mutation Frequency*. *Cancer Cell*, 2017. **32**(5): p. 701-715 e7.
107. Parker, M., et al., *C11orf95-RELA fusions drive oncogenic NF-kappaB signalling in ependymoma*. *Nature*, 2014. **506**(7489): p. 451-5.
108. Berger, M.F., et al., *The genomic complexity of primary human prostate cancer*. *Nature*, 2011. **470**(7333): p. 214-20.
109. Gonzalez-Vela, M.D.C., et al., *Shared Oncogenic Pathways Implicated in Both Virus-Positive and UV-Induced Merkel Cell Carcinomas*. *J Invest Dermatol*, 2017. **137**(1): p. 197-206.
110. Kakiuchi, M., et al., *Recurrent gain-of-function mutations of RHOA in diffuse-type gastric carcinoma*. *Nat Genet*, 2014. **46**(6): p. 583-7.

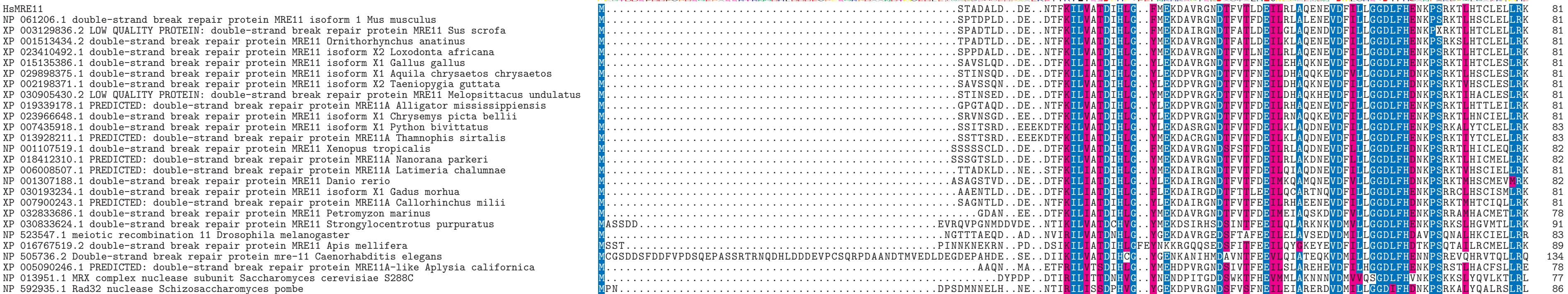
111. Molenaar, J.J., et al., *Sequencing of neuroblastoma identifies chromothripsis and defects in neuritogenesis genes*. Nature, 2012. **483**(7391): p. 589-93.
112. Ellis, M.J., et al., *Whole-genome analysis informs breast cancer response to aromatase inhibition*. Nature, 2012. **486**(7403): p. 353-60.
113. Nik-Zainal, S., et al., *Mutational processes molding the genomes of 21 breast cancers*. Cell, 2012. **149**(5): p. 979-93.
114. Shankar, G.M., et al., *BRAF alteration status and the histone H3F3A gene K27M mutation segregate spinal cord astrocytoma histology*. Acta Neuropathol, 2016. **131**(1): p. 147-50.
115. Agrawal, N., et al., *Comparative genomic analysis of esophageal adenocarcinoma and squamous cell carcinoma*. Cancer Discov, 2012. **2**(10): p. 899-905.
116. Chang, J., et al., *Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations*. Nat Commun, 2017. **8**: p. 15290.
117. Lin, D.C., et al., *Genomic and molecular characterization of esophageal squamous cell carcinoma*. Nat Genet, 2014. **46**(5): p. 467-73.
118. Li, B., et al., *Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL*. Nat Med, 2015. **21**(6): p. 563-71.
119. Varela, I., et al., *Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma*. Nature, 2011. **469**(7331): p. 539-42.
120. Dalglish, G.L., et al., *Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes*. Nature, 2010. **463**(7279): p. 360-3.
121. Yu, J., et al., *Novel recurrently mutated genes and a prognostic mutation signature in colorectal cancer*. Gut, 2015. **64**(4): p. 636-45.
122. Kan, Z., et al., *Diverse somatic mutation patterns and pathway alterations in human cancers*. Nature, 2010. **466**(7308): p. 869-73.
123. Peifer, M., et al., *Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer*. Nat Genet, 2012. **44**(10): p. 1104-10.
124. Wang, L., et al., *Whole-exome sequencing of human pancreatic cancers and characterization of genomic instability caused by MLH1 haploinsufficiency and complete deficiency*. Genome Res, 2012. **22**(2): p. 208-19.
125. Witkiewicz, A.K., et al., *Whole-exome sequencing of pancreatic cancer defines genetic diversity and therapeutic targets*. Nat Commun, 2015. **6**: p. 6744.
126. Barbieri, C.E., et al., *Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer*. Nat Genet, 2012. **44**(6): p. 685-9.
127. Bova, G.S., et al., *Integrated clinical, whole-genome, and transcriptome analysis of multisampled lethal metastatic prostate cancer*. Cold Spring Harb Mol Case Stud, 2016. **2**(3): p. a000752.
128. Dalin, M.G., et al., *Comprehensive Molecular Characterization of Salivary Duct Carcinoma Reveals Actionable Targets and Similarity to Apocrine Breast Cancer*. Clin Cancer Res, 2016. **22**(18): p. 4623-33.
129. Li, Y.Y., et al., *Genomic analysis of metastatic cutaneous squamous cell carcinoma*. Clin Cancer Res, 2015. **21**(6): p. 1447-56.
130. Berger, M.F., et al., *Melanoma genome sequencing reveals frequent PREX2 mutations*. Nature, 2012. **485**(7399): p. 502-6.
131. Zhang, L., et al., *Whole-exome sequencing identifies a somatic missense mutation of NBN in clear cell sarcoma of the salivary gland*. Oncol Rep, 2016. **35**(6): p. 3349-56.
132. Shankar, G.M., et al., *Sporadic hemangioblastomas are characterized by cryptic VHL inactivation*. Acta Neuropathol Commun, 2014. **2**: p. 167.

133. Kohsaka, S., et al., *A recurrent neomorphic mutation in MYOD1 defines a clinically aggressive subset of embryonal rhabdomyosarcoma associated with PI3K-AKT pathway mutations*. Nat Genet, 2014. **46**(6): p. 595-600.
134. Ibrahimipasic, T., et al., *Genomic Alterations in Fatal Forms of Non-Anaplastic Thyroid Cancer: Identification of MED12 and RBM10 as Novel Thyroid Cancer Genes Associated with Tumor Virulence*. Clin Cancer Res, 2017. **23**(19): p. 5970-5980.
135. Pickering, C.R., et al., *Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers*. Cancer Discov, 2013. **3**(7): p. 770-81.
136. Pinto, E.M., et al., *Genomic landscape of paediatric adrenocortical tumours*. Nat Commun, 2015. **6**: p. 6302.
137. Martin, M., et al., *Exome sequencing identifies recurrent somatic mutations in EIF1AX and SF3B1 in uveal melanoma with disomy 3*. Nat Genet, 2013. **45**(8): p. 933-6.
138. Walter, M.J., et al., *Clonal architecture of secondary acute myeloid leukemia*. N Engl J Med, 2012. **366**(12): p. 1090-8.
139. Sanz-Pamplona, R., et al., *Exome Sequencing Reveals AMER1 as a Frequently Mutated Gene in Colorectal Cancer*. Clin Cancer Res, 2015. **21**(20): p. 4709-18.
140. Cho, J., et al., *Colon cancer-derived oncogenic EGFR G724S mutant identified by whole genome sequence analysis is dependent on asymmetric dimerization and sensitive to cetuximab*. Mol Cancer, 2014. **13**: p. 141.
141. Pleasance, E.D., et al., *A small-cell lung cancer genome with complex signatures of tobacco exposure*. Nature, 2010. **463**(7278): p. 184-90.
142. Balbas-Martinez, C., et al., *Recurrent inactivation of STAG2 in bladder cancer is not associated with aneuploidy*. Nat Genet, 2013. **45**(12): p. 1464-9.

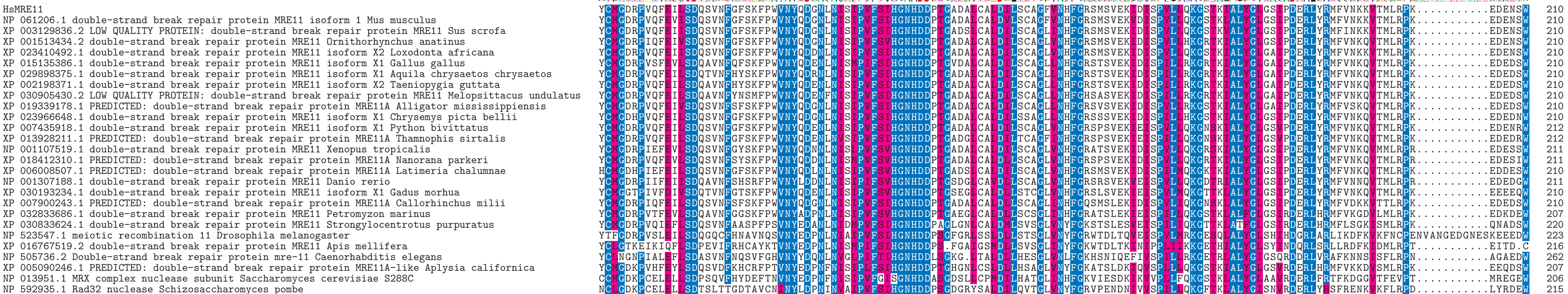
Supplementary Figure S1. Sequence alignment of MRE11, RAD50 and NBN.

A. MRE11

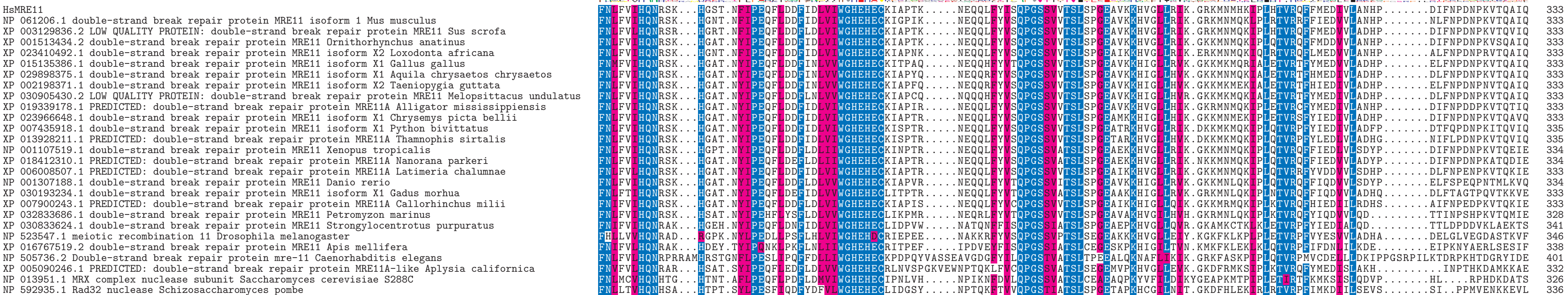
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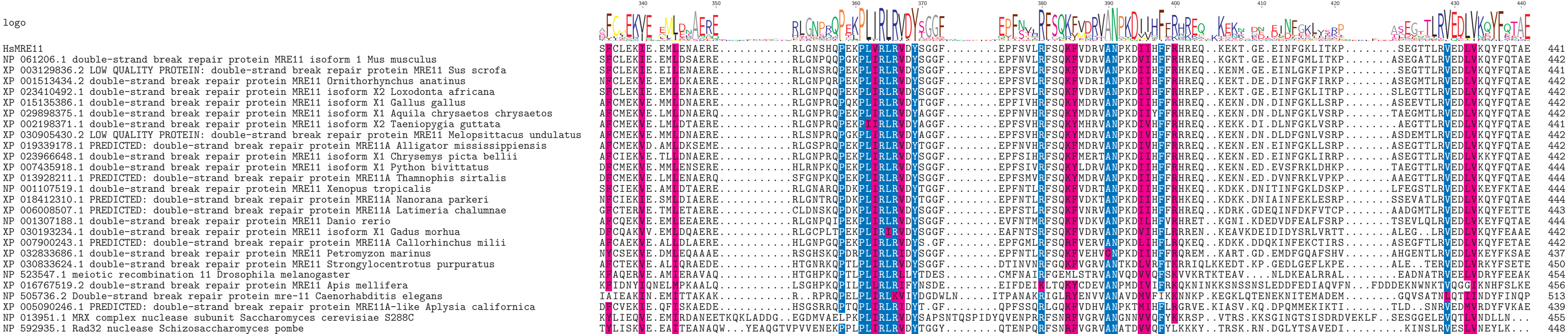


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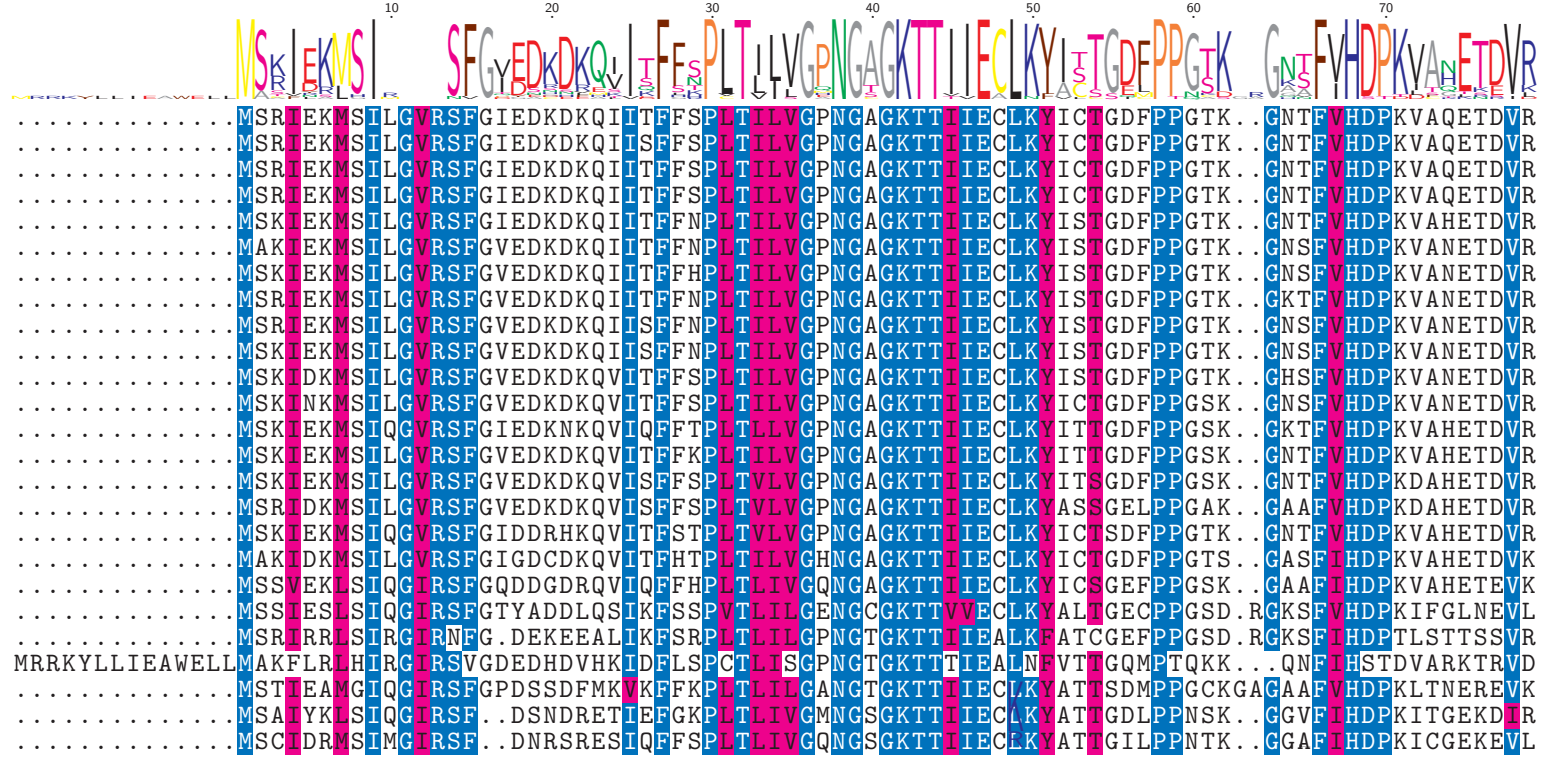
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B. RAD50

LGPR

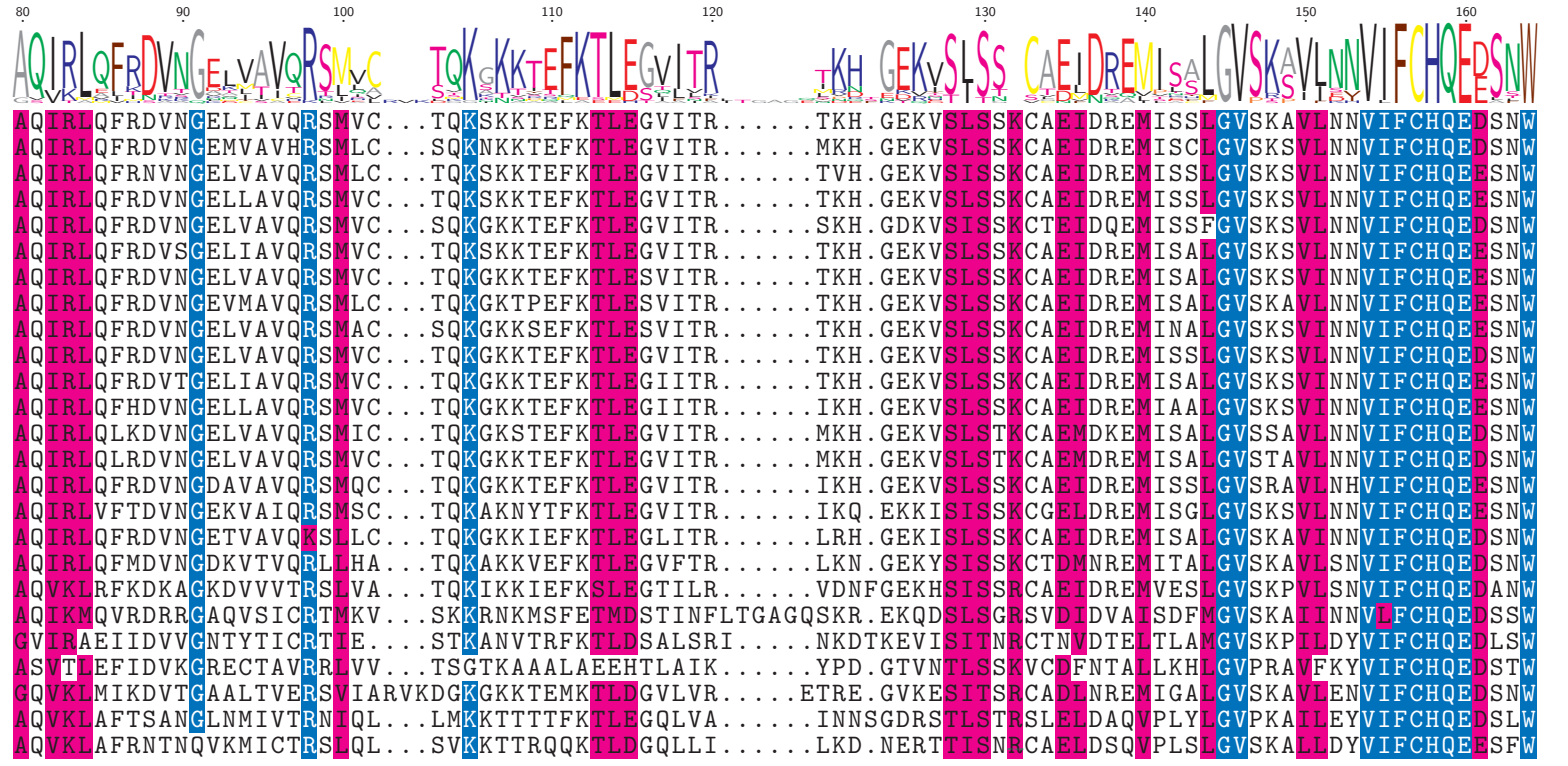
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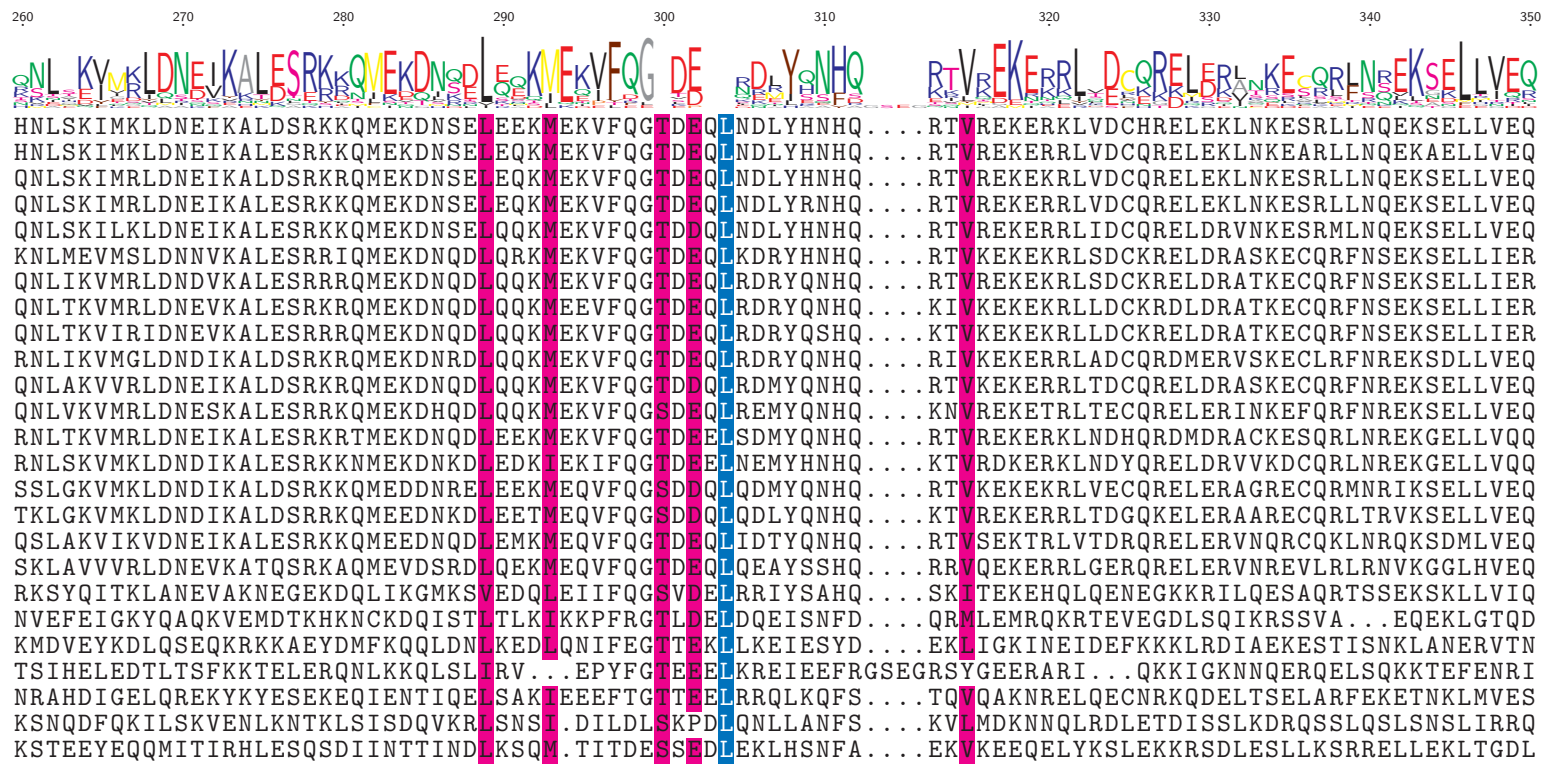
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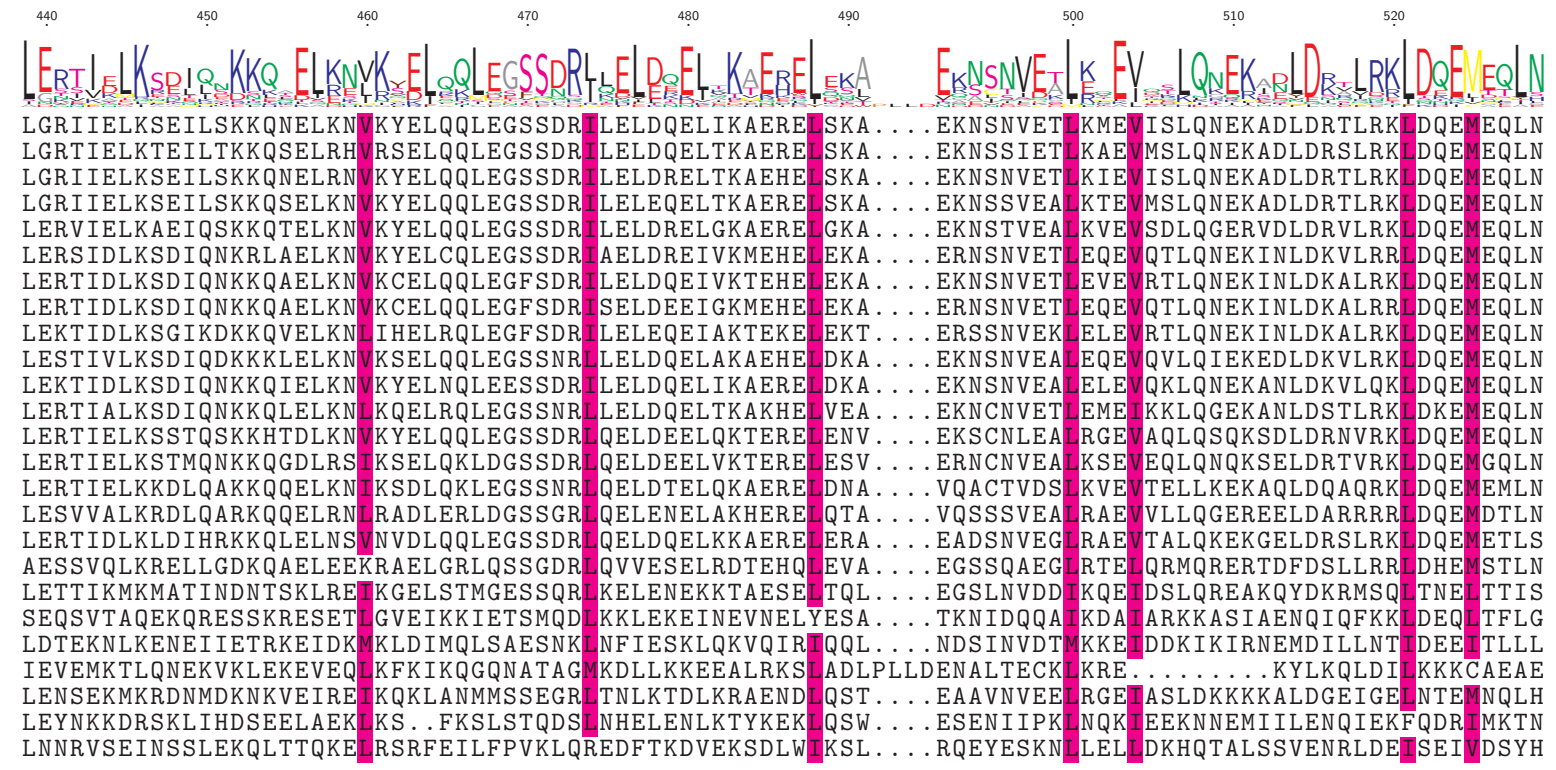
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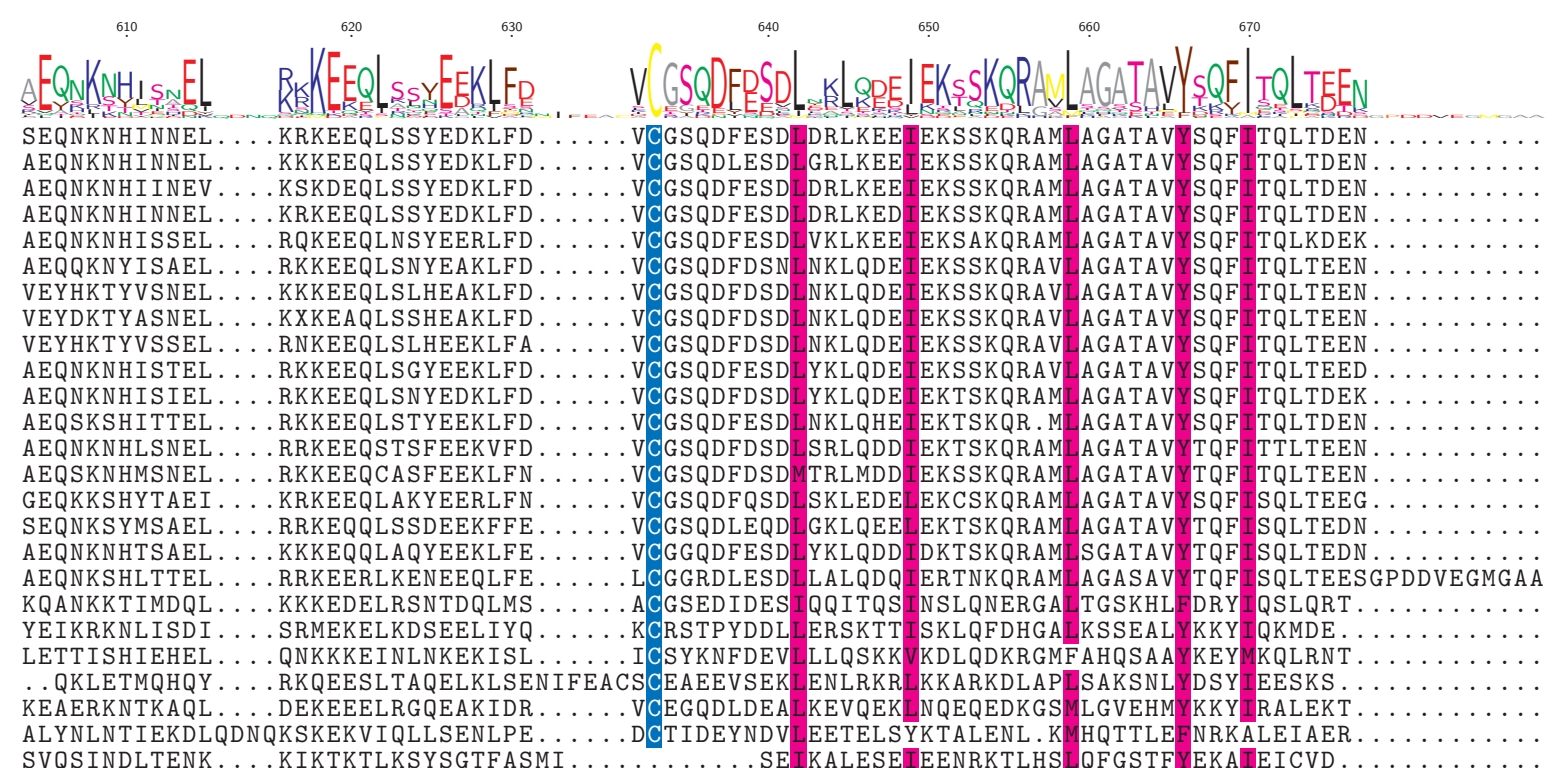
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XP 018418728.1 PREDICTED: DNA repair protein RAD50 Nanorana parkeri
XP 005167995.1 DNA repair protein RAD50 Danio rerio
XP 030217475.1 DNA repair protein RAD50 Gadus morhua
XP 007900169.1 PREDICTED: DNA repair protein RAD50 Callorhinchus milii
XP 032811404.1 DNA repair protein RAD50 Petromyzon marinus
XP 030837044.1 DNA repair protein RAD50 Strongylocentrotus purpuratus
NP 001246461.1 rad50, isoform E Drosophila melanogaster
XP 026298578.1 DNA repair protein RAD50 Apis mellifera
NP 001122999.1 Zinc-hook domain-containing protein Caenorhabditis elegans
XP 005102891.1 PREDICTED: DNA repair protein RAD50-like Aplysia californica
NP 014149.1 MRX complex DNA-binding subunit Saccharomyces cerevisiae S288C
NP 001342968.1 DNA repair protein Rad50 Schizosaccharomyces pombe

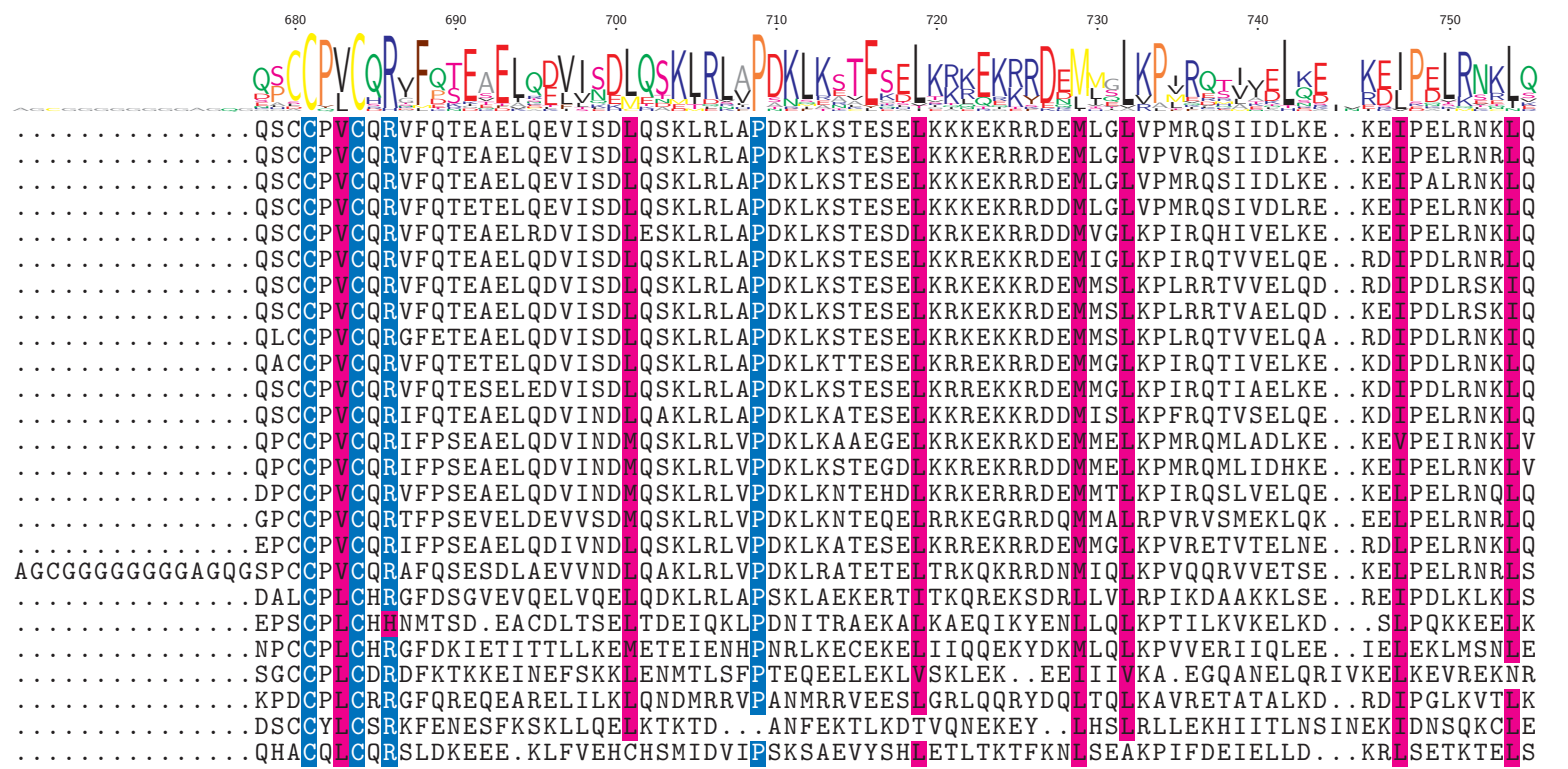


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XP 003405070.1 DNA repair protein RAD50 Loxodonta africana
XP 028906603.1 DNA repair protein RAD50 Ornithorhynchus anatinus
XP 414645.3 DNA repair protein RAD50 isoform X2 Gallus gallus
XP 029854070.1 DNA repair protein RAD50 Aquila chrysaetos chrysaetos
XP 032606694.1 LOW QUALITY PROTEIN: DNA repair protein RAD50 Taeniopygia guttata
XP 005147338.2 DNA repair protein RAD50 Melopsittacus undulatus
XP 014453124.1 PREDICTED: DNA repair protein RAD50 Alligator mississippiensis
XP 008169432.1 DNA repair protein RAD50 Chrysemys picta bellii
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XP 012815225.1 DNA repair protein RAD50 Xenopus tropicalis
XP 018418728.1 PREDICTED: DNA repair protein RAD50 Nanorana parkeri
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NP 001246461.1 rad50, isoform E Drosophila melanogaster
XP 026298578.1 DNA repair protein RAD50 Apis mellifera
NP 001122999.1 Zinc-hook domain-containing protein Caenorhabditis elegans
XP 005102891.1 PREDICTED: DNA repair protein RAD50-like Aplysia californica
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NP 001342968.1 DNA repair protein Rad50 Schizosaccharomyces pombe



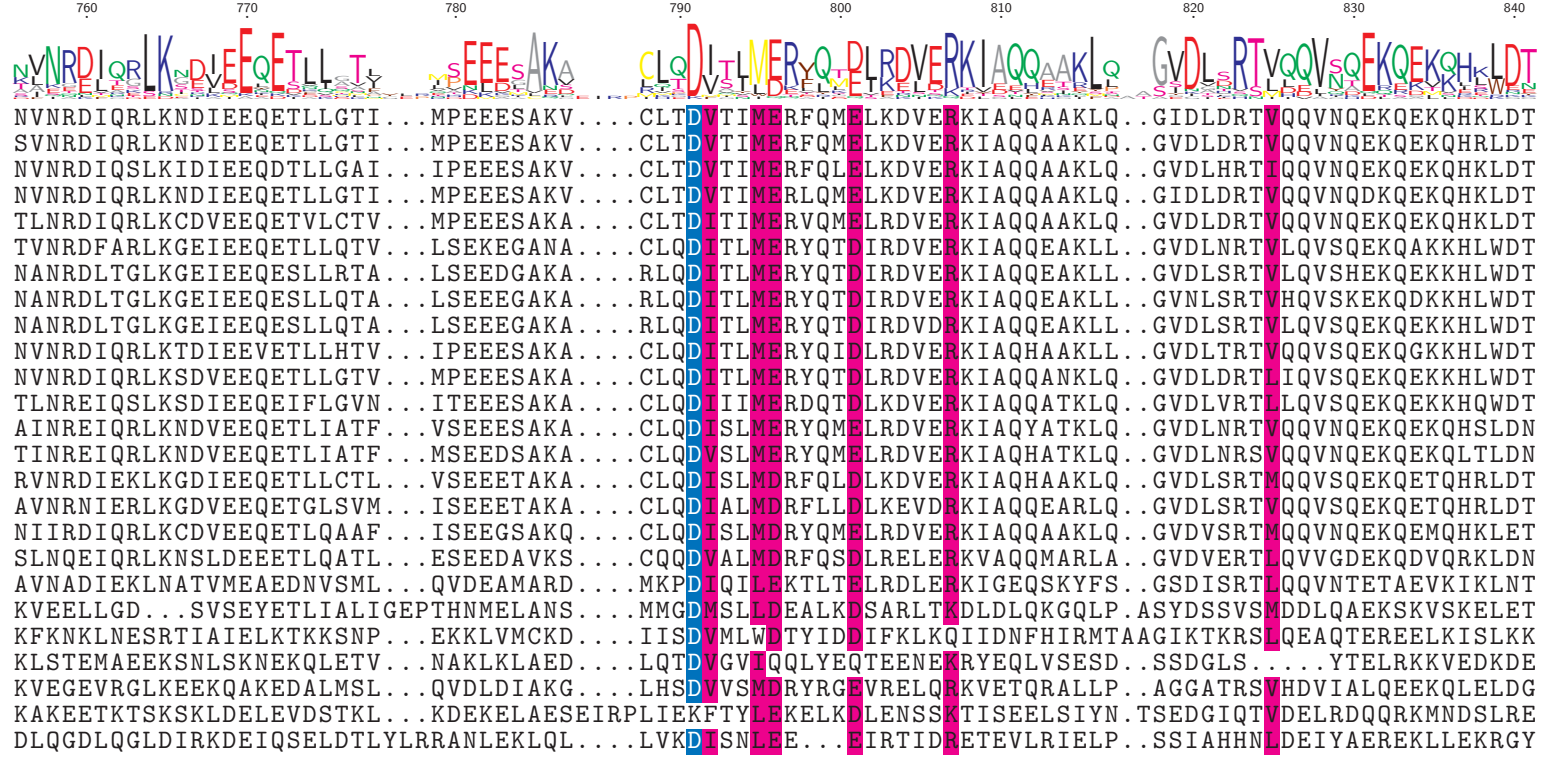
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HsRAD50
 NP 033038.2 DNA repair protein RAD50 *Mus musculus*
 XP 003354322.2 DNA repair protein RAD50 *Sus scrofa*
 XP 003405070.1 DNA repair protein RAD50 *Loxodonta africana*
 XP 028906603.1 DNA repair protein RAD50 *Ornithorhynchus anatinus*
 XP 414645.3 DNA repair protein RAD50 isoform X2 *Gallus gallus*
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 XP 032606694.1 LOW QUALITY PROTEIN: DNA repair protein RAD50 *Taeniopygia guttata*
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 XP 008169432.1 DNA repair protein RAD50 *Chrysemys picta bellii*
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 XP 018418728.1 PREDICTED: DNA repair protein RAD50 *Nanorana parkeri*
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 XP 032811404.1 DNA repair protein RAD50 *Petromyzon marinus*
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 NP 001246461.1 rad50, isoform E *Drosophila melanogaster*
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 NP 014149.1 MRX complex DNA-binding subunit *Saccharomyces cerevisiae* S288C
 NP 001342968.1 DNA repair protein Rad50 *Schizosaccharomyces pombe*



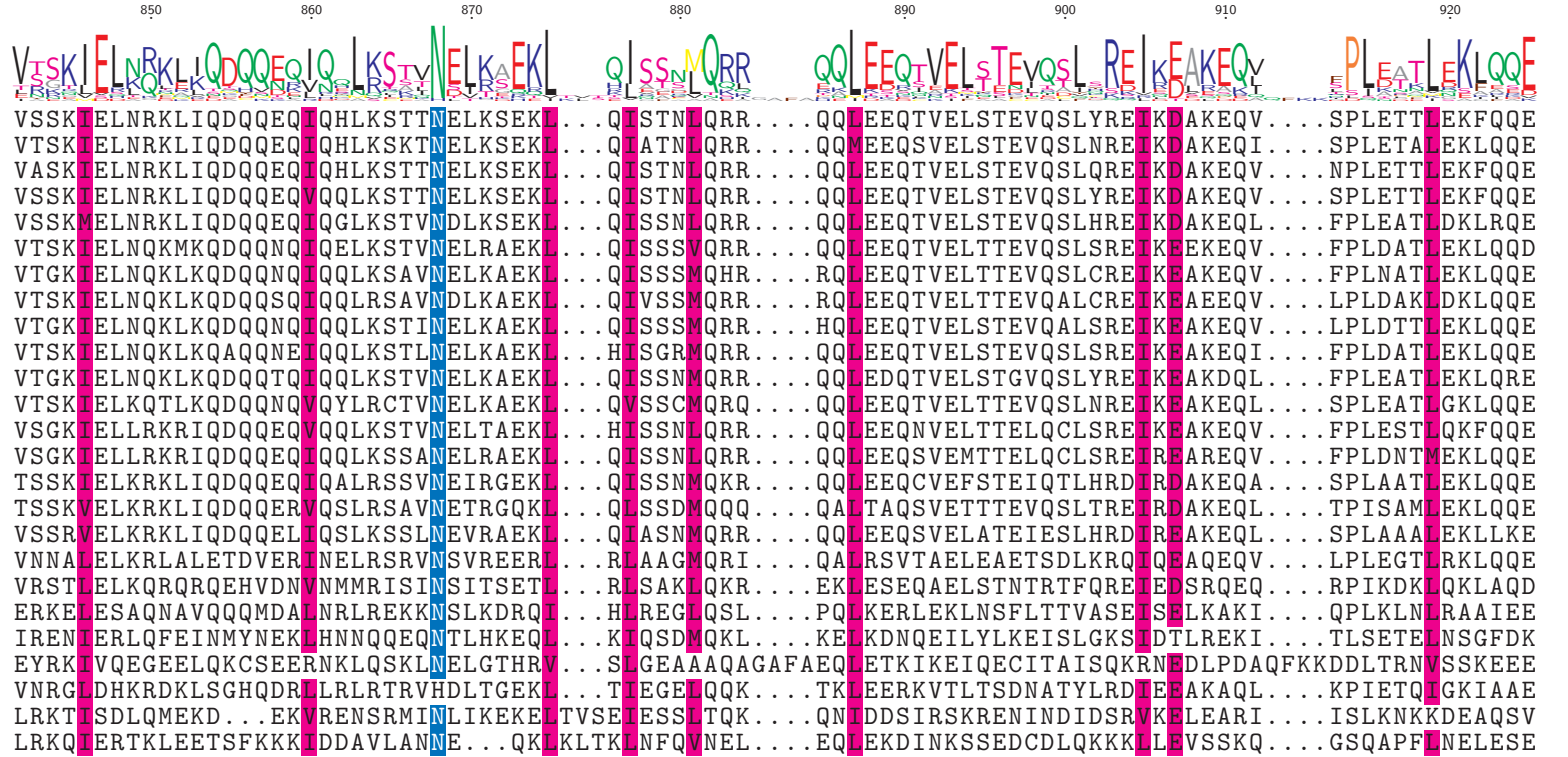
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HsRAD50
 NP 033038.2 DNA repair protein RAD50 *Mus musculus*
 XP 003354322.2 DNA repair protein RAD50 *Sus scrofa*
 XP 003405070.1 DNA repair protein RAD50 *Loxodonta africana*
 XP 028906603.1 DNA repair protein RAD50 *Ornithorhynchus anatinus*
 XP 414645.3 DNA repair protein RAD50 isoform X2 *Gallus gallus*
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 XP 005147338.2 DNA repair protein RAD50 *Melopsittacus undulatus*
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 XP 008169432.1 DNA repair protein RAD50 *Chrysemys picta bellii*
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 XP 032811404.1 DNA repair protein RAD50 *Petromyzon marinus*
 XP 030837044.1 DNA repair protein RAD50 *Strongylocentrotus purpuratus*
 NP 001246461.1 rad50, isoform E *Drosophila melanogaster*
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 NP 001122999.1 Zinc-hook domain-containing protein *Caenorhabditis elegans*
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 NP 014149.1 MRX complex DNA-binding subunit *Saccharomyces cerevisiae* S288C
 NP 001342968.1 DNA repair protein Rad50 *Schizosaccharomyces pombe*



logo

HsRAD50
 NP 033038.2 DNA repair protein RAD50 *Mus musculus*
 XP 003354322.2 DNA repair protein RAD50 *Sus scrofa*
 XP 003405070.1 DNA repair protein RAD50 *Loxodonta africana*
 XP 028906603.1 DNA repair protein RAD50 *Ornithorhynchus anatinus*
 XP 414645.3 DNA repair protein RAD50 isoform X2 *Gallus gallus*
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logo

HsRAD50
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logo

HsRAD50

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XP 414645.3	DNA repair protein RAD50 isoform X2	Gallus gallus	115
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logo

HsRAD50

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NP 001342968.1	DNA repair protein Rad50	Schizosaccharomyces pombe	1186

logo

HsRAD50

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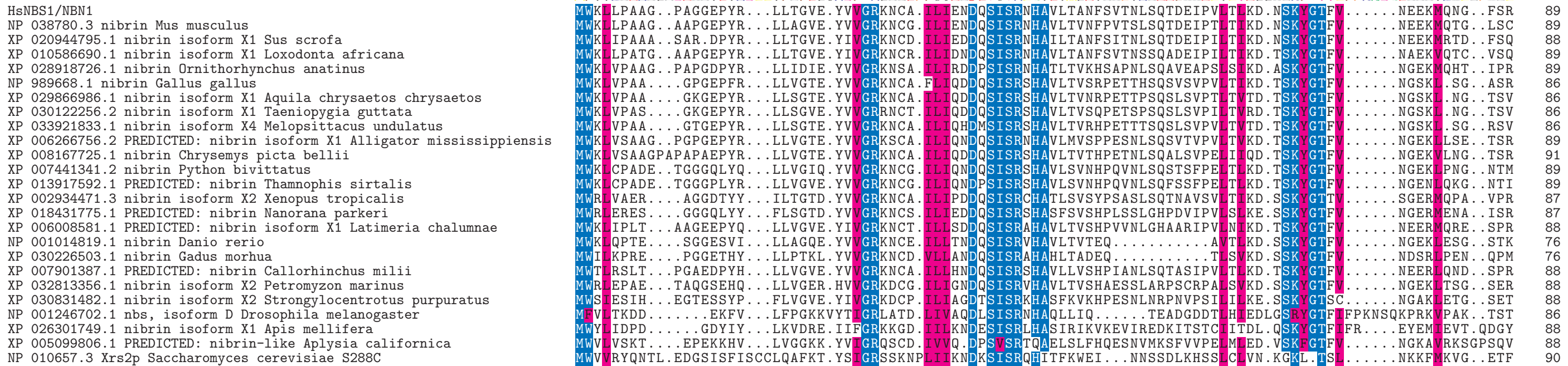
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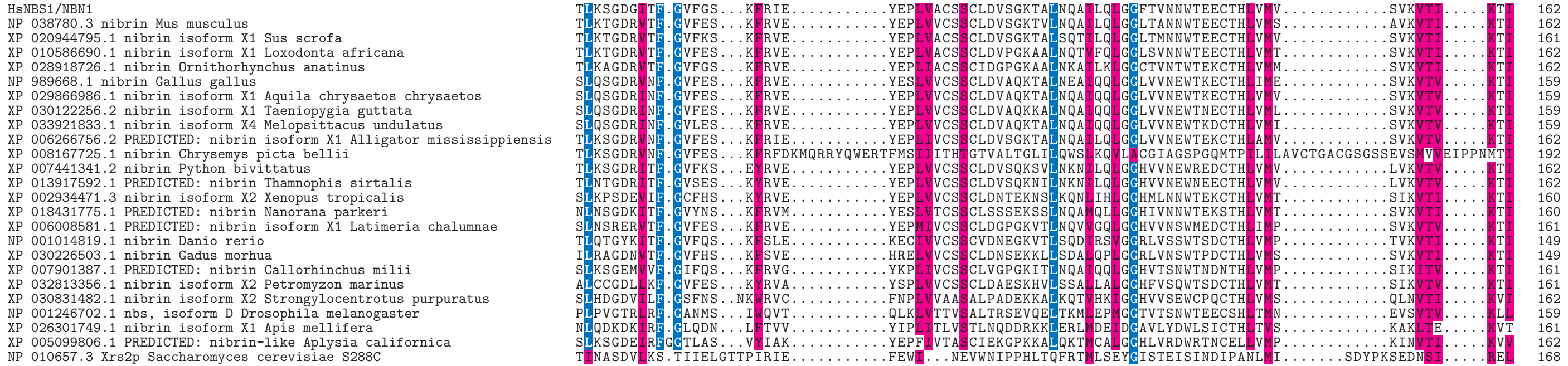
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C. NBN

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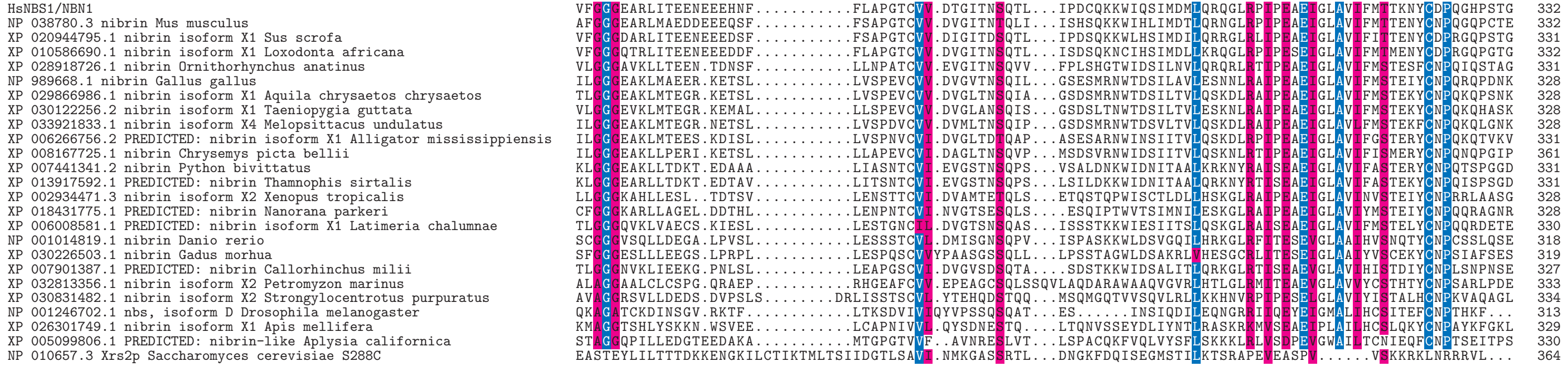
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HsNBS1/NBN1
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 XP 028918726.1 nibrin Ornithorhynchus anatinus
 NP 989668.1 nibrin Gallus gallus
 XP 029866986.1 nibrin isoform X1 Aquila chrysaetos chrysaetos
 XP 030122256.2 nibrin isoform X1 Taeniopygia guttata
 XP 033921833.1 nibrin isoform X4 Melopsittacus undulatus
 XP 006266756.2 PREDICTED: nibrin isoform X1 Alligator mississippiensis
 XP 008167725.1 nibrin Chrysemys picta bellii
 XP 007441341.2 nibrin Python bivittatus
 XP 013917592.1 PREDICTED: nibrin Thamnophis sirtalis
 XP 002934471.3 nibrin isoform X2 Xenopus tropicalis
 XP 018431775.1 PREDICTED: nibrin Nanorana parkeri
 XP 006008581.1 PREDICTED: nibrin isoform X1 Latimeria chalumnae
 NP 001014819.1 nibrin Danio rerio
 XP 030226503.1 nibrin Gadus morhua
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 XP 032813356.1 nibrin isoform X2 Petromyzon marinus
 XP 030831482.1 nibrin isoform X2 Strongylocentrotus purpuratus
 NP 001246702.1 nbs, isoform D Drosophila melanogaster
 XP 026301749.1 nibrin isoform X1 Apis mellifera
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 NP 010657.3 Xrs2p Saccharomyces cerevisiae S288C

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HsNBS1/NBN1
 NP 038780.3 nibrin Mus musculus
 XP 020944795.1 nibrin isoform X1 Sus scrofa
 XP 010586690.1 nibrin isoform X1 Loxodonta africana
 XP 028918726.1 nibrin Ornithorhynchus anatinus
 NP 989668.1 nibrin Gallus gallus
 XP 029866986.1 nibrin isoform X1 Aquila chrysaetos chrysaetos
 XP 030122256.2 nibrin isoform X1 Taeniopygia guttata
 XP 033921833.1 nibrin isoform X4 Melopsittacus undulatus
 XP 006266756.2 PREDICTED: nibrin isoform X1 Alligator mississippiensis
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 XP 030226503.1 nibrin Gadus morhua
 XP 007901387.1 PREDICTED: nibrin Callorhynchus milii
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 XP 030831482.1 nibrin isoform X2 Strongylocentrotus purpuratus
 NP 001246702.1 nbs, isoform D Drosophila melanogaster
 XP 026301749.1 nibrin isoform X1 Apis mellifera
 XP 005099806.1 PREDICTED: nibrin-like Aplysia californica
 NP 010657.3 Xrs2p Saccharomyces cerevisiae S288C

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 XP 008167725.1 nibrin Chrysemys picta bellii
 XP 007441341.2 nibrin Python bivittatus
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 XP 026301749.1 nibrin isoform X1 Apis mellifera
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 NP 010657.3 Xrs2p Saccharomyces cerevisiae S288C

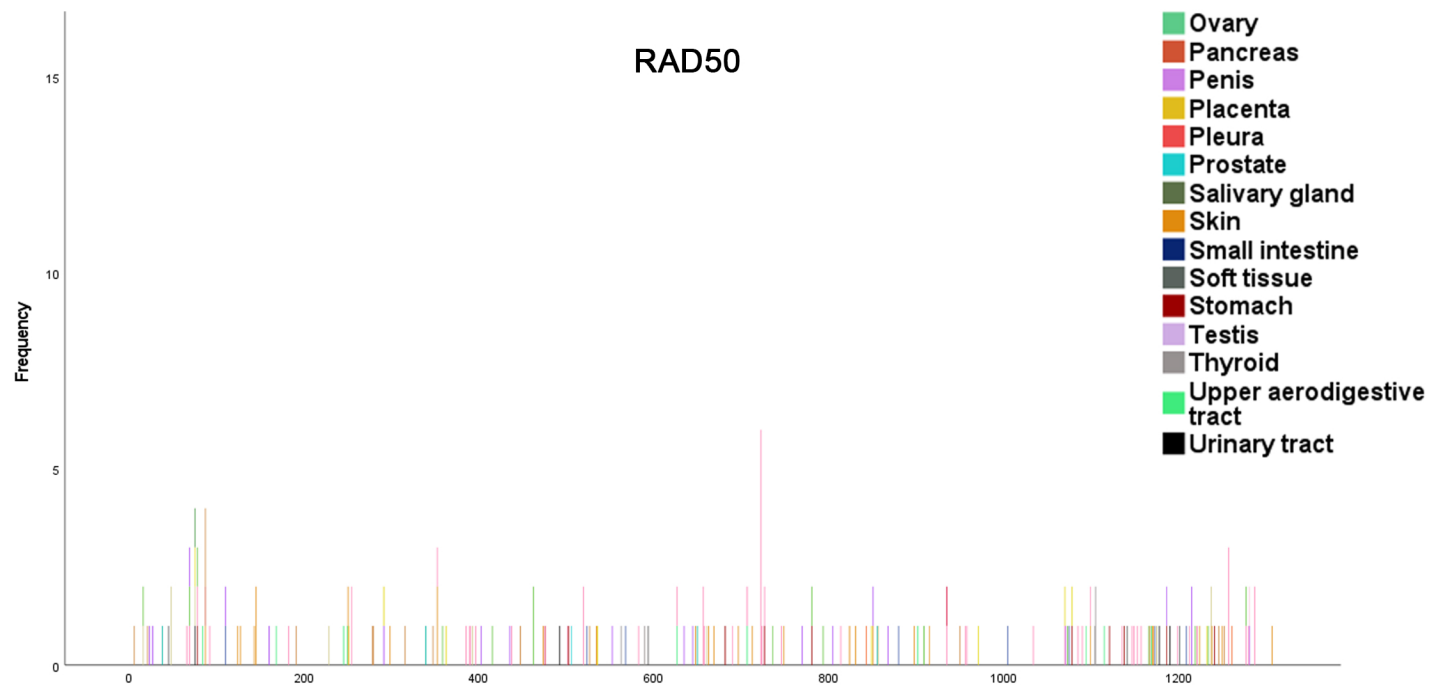
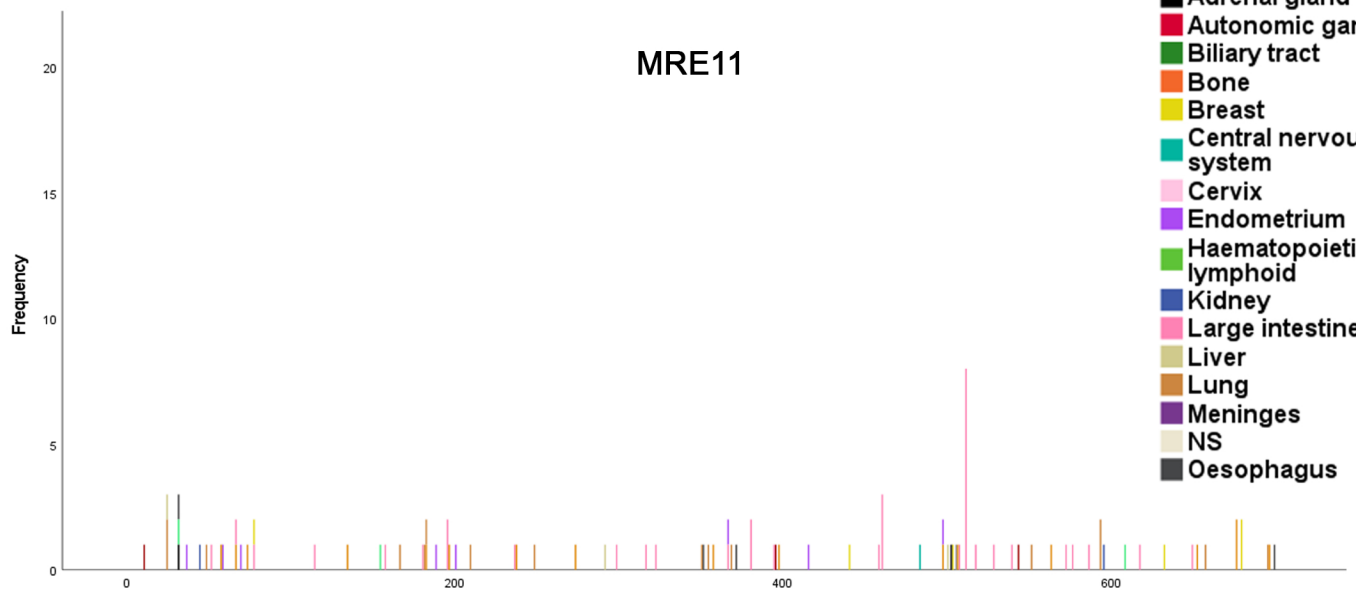
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HsNBS1/NBN1
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 XP 020944795.1 nibrin isoform X1 Sus scrofa
 XP 010586690.1 nibrin isoform X1 Loxodonta africana
 XP 028918726.1 nibrin Ornithorhynchus anatinus
 NP 989668.1 nibrin Gallus gallus
 XP 029866986.1 nibrin isoform X1 Aquila chrysaetos chrysaetos
 XP 030122256.2 nibrin isoform X1 Taeniopygia guttata
 XP 033921833.1 nibrin isoform X4 Melopsittacus undulatus
 XP 006266756.2 PREDICTED: nibrin isoform X1 Alligator mississippiensis
 XP 008167725.1 nibrin Chrysemys picta bellii
 XP 007441341.2 nibrin Python bivittatus
 XP 013917592.1 PREDICTED: nibrin Thamnophis sirtalis
 XP 002934471.3 nibrin isoform X2 Xenopus tropicalis
 XP 018431775.1 PREDICTED: nibrin Nanorana parkeri
 XP 006008581.1 PREDICTED: nibrin isoform X1 Latimeria chalumnae
 NP 001014819.1 nibrin Danio rerio
 XP 030226503.1 nibrin Gadus morhua
 XP 007901387.1 PREDICTED: nibrin Callorhynchus milii
 XP 032813356.1 nibrin isoform X2 Petromyzon marinus
 XP 030831482.1 nibrin isoform X2 Strongylocentrotus purpuratus
 NP 001246702.1 nbs, isoform D Drosophila melanogaster
 XP 026301749.1 nibrin isoform X1 Apis mellifera
 XP 005099806.1 PREDICTED: nibrin-like Aplysia californica
 NP 010657.3 Xrs2p Saccharomyces cerevisiae S288C

Supplementary Figure S2. Tissue distribution of MRN mutations of unknown origin.

Legend

- Adrenal gland
- Autonomic ganglia
- Biliary tract
- Bone
- Breast
- Central nervous system
- Cervix
- Endometrium
- Haematopoietic and lymphoid
- Kidney
- Large intestine
- Liver
- Lung
- Meninges
- NS
- Oesophagus



- Ovary
- Pancreas
- Penis
- Placenta
- Pleura
- Prostate
- Salivary gland
- Skin
- Small intestine
- Soft tissue
- Stomach
- Testis
- Thyroid
- Upper aerodigestive tract
- Urinary tract

