ERRATUM

Erratum to: DNA damage response and hematological malignancy

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In the original publication of the article, Figs. 4, 5 and 6 were swapped. The figures should appear as in this erratum.

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Fig. 4 Non-homologous end joining. MRN complex is recruited to DSBs early and is thought to promote bridging of the DNA ends. The initial step in NHEJ is the recognition and binding of the KU70/80 heterodimer to the DSB. Then, KU70/80 heterodimer recruits PRKDC (DNA-PK), XRCC4, NHEJ1 (XLF/CERENUN-NOS), and LIG4. PRKDC can phosphorylate several own stream targets. NHEJ requires two DNA blunt ends to join them together. Single-strand overhangs are processed by DCLRE1C (ARTEMIS). After creation of blunt ends, XRCC4/LIG4 complex mediates ligation of the DSB

Fig. 5 Homologous recombination repair. Homologous recombination is initiated by the binding of the MRN complex and ATM. The nuclease-bearing subunit MRE11A and RBB8 (CTIP) initiates the nucleolytic processing of the 5' ends at the DNA break site (which is known as 5'–3' resection). Created single-strand DNA is rapidly bound by the RPA. The RPA is replaced with RAD51, which is mediated by BRCA1, PALB2 and BRCA2. Then, homology search and DNA strand invasion are mediated by the RAD51. DNA strand exchange between the target DNA and the Rad51 filament leads to a structure known as the displacement loop (D-loop). After strand invasion, a DNA polymerase extends the end of the invading 3' strand. This changes the D-loop to a cross-shaped structure known as a Holliday junction. Three different pathways, synthesis dependent strand annealing (SDSA), break-induced replication (BIR) and double-strand break repair (DSBR), resolving overhang are proposed

Fig. 6 Fanconi pathway.

Following exposure to DNA damaging agents the FANCM anchor complex, comprising FANCM, FAAP24, CENPS and CENPX, recognizes the damage, remodels the fork, and promotes the recruitment of the FA core complex. The FA core complex, which is comprised of three sub-complexes—FANCB/FANCL/FAAP100, FANCC/FANCE/FANCF, and FANCA/FANCG/FAAP20—together with the E2 ubiquitin-conjugating enzyme UBE2T/FANCT, constitutes an active multi-subunit E2/E3 ubiquitination enzyme complex. This E2/E3 enzyme complex catalyzes the site-specific monoubiquitination of FANCD2 K561 and FANCI K523. Schematic of downstream steps of the FA pathway. During the later stages of ICL repair, SLX4 and ERCC4 catalyze the unhooking of the ICL. The unhooked ICL is then bypassed by REV7 and REV3L. Downstream of FANCD2 and FANCI monoubiquitination, HRR facilitates DNA repair [30]