“Functional genomics in the pathogenesis of del(5q) myelodysplastic syndromes”

Interstitial deletion of 5q chromosome (del(5q)) constitutes the most common chromosomal abnormality in Myelodysplastic syndromes. Haploinsufficiency of genes located in the deleted region provide clonal advantage in the bone marrow and explain the severe anemia observed in patients. Although Lenalidomide treatment is very effective in del(5q) MDS patients, the majority eventually relapse. Here I show how integration of different genome-wide sequencing approaches from patient and disease models inform the dissection of the molecular mechanisms governing pathogenesis and therapy resistance in del(5q) MDS.