deletions, and insertions. Here we report about two single-exon deletions found in patients with MS.

Materials and Methods: Genomic DNA samples from 62 patients with suspected MS or MS-like phenotypes were screened using multiplex ligation-dependent probe amplification (MLPA). MLPA analysis was carried out using SALSA kits P065 (MRC-Holland, lot 0506, 0305, 0205) and P066-2 lot (MRC-Holland, lot 0508). Amplification products were run on ABI Prism 310 Genetic Analyzer.

Results: Two gross heterozygous deletions were identified in FBN1. Exon 3 deletion which was previously reported was found in 17-year old male patient with tall stature, dolichostenomelia, arachnodactyly and mitral valve prolapse. Novel exon 49 deletion was detected in 25-year old female patient with classic MS manifested aortic root dilatation, lens dislocation, high myopia, abnormalities of the skeletal system including tall stature, arachnodactyly and pectus carinatum.

Conclusions: We identified two single-exon deletions in patients with MS. To our knowledge, 49 exon deletion has not been reported before in patients with MS.

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Searching for osteoporosis genes: The use of WGS in an extended Maltese family with osteoporosis

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Introduction: Osteoporosis is a complex metabolic and skeletal disease having a strong genetic background. Indeed, heritability of bone mineral density (BMD) in twin and family studies ranges from 50 to 85%. The aim of the study was to identify known and/or novel genes and gene variants that play a role in the susceptibility of primary osteoporosis in an extended Maltese family.

Materials and Methods: A 2-generation family having multiple relatives with osteoporosis (T-score: <-2.5 or Z-score: <-2.0) at the spine or hip were recruited. Biochemical analysis was performed to exclude other bone diseases. Whole genome sequencing was performed on 12 members and comprehensive filtering strategies were carried out on the single nucleotide variant and indel files. *In silico* modelling and prediction tools were used to determine potential causality of the variants.

Results: Eleven shortlisted variants segregating in a dominant inheritance pattern were identified in the affected relatives having a minor allele frequency of ≤2%. Variants included missense variants within *ADAMTS20* (rs138035327), ARSD (rs78034736), *BMP1* (rs368615556), *CLDN18* (rs114998965), *SELP* (rs754086574), TGFβ2 (rs773943154), TRIM45 (rs146244405), PCDHGA11 (rs138408376), PLEC (rs138924815) and SPARC (rs41290587), and one stop gain variant within WDR89 (rs944955056).

Conclusions: Future studies will evaluate the shortlisted variants by replicating in the Malta Osteoporotic Fracture Study - a case-control collection of more than 1000 Maltese postmenopausal women and other extended Maltese pedigrees so as to determine association with osteoporosis and low-trauma fracture risk at different anatomical sites. Top candidates will in turn be assessed using functional studies.

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Identification of a new FGRF2 mutation using NGS coupled gene panel testing in Pfeiffer syndrome

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Introduction: The skeletal dysplasias are an extremely heterogeneous group of conditions that affect bone development. They encompass over 400 disorders and most are the result of genetic defects. Pfeiffer syndrome is inherited in an autosomal dominant pattern. It is characterized by the premature fusion of certain skull bones. This early fusion prevents the skull from growing normally and concerns the shape of the head and face. Here we are presenting a case of a 5 months old girl, with healthy parents and with a skeletal phenotype.

Materials and Methods: Total genomic DNA was extracted from her salive sample and analyzed with a comprehensive skeletal dysplasias and disorders gene panel test, that contains the most relevant genes for a skeletal phenotype. We have targeted all of the coding excons with exon-intron boundaries of 186 genes using PCR-based library preparation method. Sequencing reads were mapped to the reference genome (hg19) and after variant calling the variants were classified based on ESP, ExAc, ClinVar and HGMD information.

Results: Gene panel test identified a likely pathogenic heterozygous mutation in the FGFR2 gene (c.940-4_945delCTAGGCCGCC) which encompass the splice site and two codons of exon 8. Currently, this mutation is not