

SUPPLEMENTAL MATERIAL

Simultaneous Detection of Common Founder Mutations using a Cost-Effective Deep Sequencing Panel

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Keywords: NGS, panel sequencing, Inherited retinal diseases, primers

Supp Figure S1

2. ABCA4- c.5882G>A, chr1:94486960C>G
TGTTCCCTGCTATTTCATCTCGGGCACTGACACAGGGCCTCAGTGAGAATCACTCCAGCTG
AGCATCATTCCCTTTTCTGTGTTCTGTTTCTGCAGAGCATGGGTCAGCCTCGAGATGTCT
CAGTACTCACCACACCTCTGTGCCTGCCCATGTCAATATGTAACCTCCTAGTGCTGGTAG
TTTTCTCCTAAACCATCCTTTGCTCTTTGTTCCCTCTTCCCTCCCTTGCTCTCACCTGT
CTCAGTTCTCAGTCCGGTTTCTTCGTATCTTGCAGATTTATCCAGGCACCTCCAGCCCAG
CAGTGGACAGGCTGTGTGTCGGAGTTCGCCCTGGAGAGGTGGGTACTCTGCAGACCACGT
GTGAAAGGCTTCCGAACATCAGCTCTTGTGCCTGCCTCTCCTCCCCATAAGGCAGAGCTA
TTCAATAGGAACATAATGCCATAATGCAAGTCACATATGTAATTTTAAATCTTCCACTAG
CCACATGAGAAAAGTAAAAAGAAAATAGGTAAAATTAATTTTATTAGTATTTTTTATTTT

An example of a sequence that was used as an input in FastPCR. In this figure one of the founder mutations from the panel is presented (marked in yellow). The brackets (marked in red) are used to define the preferred primer location. The software designs the primers in the areas bounded by the brackets. The selected primers are marked in green.