Evaluation of Rare Changes in Parkinson's Disease-Related Cutaneous Malignant Carcinoma Genes

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U ing a ema ic li e a e h n , e linked cep ibili gene fo CMM e e incl ded(1) ge mline high- h ea gene a ocia ed i h dome ic CMM(e.g., CDKN2A, CDK4);(2) ge mline common mode a e- h ea gene (e.g., MC1R);(3) gene gene all oma icall hi ed(e.g., BRAF); and(4) la el linked gene e , p o ha bo a e ph ical m a ion c edi ed o CMM(e.g., TRRAP, DCC). Gene e e named g o nded on de ned place in inhe i ed high- pene ance a o omal dominan complain (n = 2); an e ce of ph ical m a ion (n = 20); an e ce of common lo - pene ance h ea a ian (n = 3); o combina ion of he e (n = 4). All a e (MAF< 1) a ian ac o he e gene e e a e ed fo en ichmen in PD ca e compa ed i h innocen con ol .

We a e ed high- q ali a e a ian geno pe da a ded ced f om he Ne o chip on 6875 PD ca e and 6065 con ol (dbGaP S d Acce ionph 000918. 1.p1). Compac , he Ne o chip ha o gh , 000 p e elec ed a ian g o nded on anda d Ill mina e ome con en and o e , 000 c om con en ne ologic complain concen a ed a ian . Compac , ample lib a ie f om ca e and