

Corneal Dystrophy Analysis Kit

– all you need in one box –

Reliable and up to date

- List of relevant publications is available on Genorama website
- Intensively used throughout years and hundreds of screened samples
- Based on established and validated APEX technology
- Genorama is keeping a close eye on new discoveries in the field

Genorama Corneal Dystrophy Analysis KIT includes all consumables for successful analysis process and provides all necessary reagents, PCR primers and barcoded arrays for 25 tests

- PCR primers and purification Kit
- APEX Template Preparation Kit
- APEX Reaction Mixture Kit
- Corneal Dystrophy microarrays

APEX technology

Arrayed Primer EXTension (APEX) genotyping is based upon an array of oligonucleotides, immobilized on glass surface via their 5' end. Patient's DNA is amplified by PCR, digested enzymatically and annealed to the immobilized primers, which promote sites for template-dependent DNA polymerase extension reactions using four unique fluorescently labelled dideoxy nucleotides. The mutation is detected by the change in primer sites colour code using the previously installed Genorama genotyping platform.

Ordering information

Cat #	Product name
G60108	Corneal Dystrophy Analysis KIT for 25 reactions

For further information please contact Genorama representatives

Genetic variations in test

HST6 c.1A>T; c.6G>A; c.7C>A; c.15_16delCG; c.15_16insATGCTGTGCG; c.16_40del25; c.44T>C; c.51delG; c.52C>T; c.65T>G; c.91C>T; c.94_100del7; c.124C>T; c.137T>C; c.148C>T; c.149G>T; c.152C>T; c.155G>A; c.161C>T; c.166G>A; c.167T>G; c.172C>T; c.180delC; c.182A>C; c.189C>G; c.196G>C; c.197T>A; c.198delC; c.199T>A/G; c.202T>C; c.208A>T; c.213G>T; c.214C>T; c.217G>A/C; c.226G>A; c.231G>C/A; c.244C>T; c.271_273delGCTinsA; c.274G>C; c.277C>A; c.278G>A; c.290G>C; c.293C>T/G; c.294C>G; c.304T>G; c.305G>A; c.320T>C; c.329A>G; c.340C>T; c.363C>G; c.365A>C; c.369G>A; c.375_376insGGCCGTG; c.379C>T; c.383C>T; c.391T>C; c.392C>T; c.414_415insTT; c.418C>T; c.459C>A; c.484C>G; c.494G>A; c.494G>C; c.495C>T; c.495C>G; c.497G>C; c.500C>T; c.518T>C; c.521A>G; c.529C>T; c.530G>A; c.533T>G; c.545delA; c.573_574insC; c.578T>C; c.581_586delACCTACinsGGT; c.587_588insACG; c.593T>A; c.599T>G; c.604C>A; c.606_607delCG; c.607G>A; c.609C>A; c.611C>A/G; c.612_614delGCCinsAT; c.614G>T/A; c.616G>A; c.617C>T; c.629C>T; c.631C>T; c.632G>A; c.649G>A; c.661G>T; c.663C>G; c.668G>A; c.682A>G; c.683C>A; c.696G>A; c.738C>G; c.740delG; c.744C>G; c.746A>C; c.803A>G; c.814C>A; c.815G>A; c.820G>A; c.827T>C; c.925G>T; c.985G>C; c.991C>T; c.993G>T; c.1000C>T; c.1002_1012delinsTTG; c.1039G>T; c.1046G>A; c.1047C>G; c.1052_1059dupGTGCGCTG; c.1072T>G

COL8A2 c.1069G>C/A; c.1349T>G; c.1363C>A; c.1724C>T

CYP4V2 c.130T>A; c.181G>A; c.237G>T; c.253C>T; c.283G>A; c.332T>C; c.335T>G; c.367A>G; c.400G>T; c.518T>G; c.655T>C; c.732G>A; c.802-8_810del17/insGC; c.971A>T; c.974C>T; c.992A>C; c.1021T>C; c.1091-2A>G; c.1157A>C; c.1187C>T; c.1198C>T; c.1199G>A; c.1226-6_1235del16; c.1348C>T; c.1445C>A; c.1523G>A; c.1526C>T

GSN c.640G>A/T

KRT12 c.386T>C; c.389A>C; c.395T>A/C; c.399T>G; c.403A>G; c.404G>C/T; c.405A>C; c.409G>C; c.419T>G; c.427G>C; c.905G>T; c.1197_1198ins27; c.1276A>G; c.1277T>G; c.1285T>G; c.1286A>G; c.1289G>C

KRT3 c.1493A>T; c.1508G>C; c.1525G>A

TACSTD2 c.2T>G; c.84_85insG; c.198C>A; c.250A>T; c.322T>C; c.341T>G; c.352C>T/G; c.355T>A; c.480delC; c.493_494insCCACCGCC; c.509C>A; c.551A>G; c.557T>C; c.561_564delC; c.581T>A; c.619C>T; c.632delA; c.653delA; c.672C>A/G; c.679G>A; c.772_783del12/insT; c.811_812delA

TGFBI c.337G>A; c.367G>C; c.370C>T/A; c.371G>T/A; c.373_378delACGGAG; c.805C>T; c.1501C>A; c.1514T>A; c.1526T>G; c.1553T>G/C; c.1580T>G; c.1612A>C; c.1613C>G; c.1616T>A; c.1618_1620delT; c.1619T>C; c.1631A>G; c.1636G>A; c.1637C>A; c.1640T>C; c.1652C>A; c.1663C>T; c.1664G>A; c.1706T>G; c.1714_1716delCAC; c.1715A>G; c.1781G>T; c.1856T>A; c.1864A>C; c.1866T>G/A; c.1868G>A; c.1874T>A; c.1870_1875delGTGGTC; c.1877A>G/C; c.1879delG; c.1887_1888insCCAATGTTC; c.1892T>A; c.1998G>C

VSX1 c.50T>C; c.432C>G; c.475T>A; c.479G>A; c.496C>T; c.731A>G; c.740C>G

SOD c.169+50_56del7

SLC4A11 c.99_100delTC; c.140delA; c.246_247delTTinsA; c.306delC; c.334C>T; c.427G>A; c.618_619delAG; c.625C>T; c.637T>C; c.638C>T; c.695G>A; c.697C>T; c.720G>A; c.812C>T; c.859_862delGAGinsCCT; c.878_889del12; c.985A>T; c.1091-1G>C; c.1156T>C; c.1195G>A; c.1202C>A; c.1253G>A; c.1317_1322del6insAGTGGGTG; c.1378_1381delTACinsA; c.1391G>A; c.1463G>A; c.1466C>T; c.1744_1745delCT; c.1751C>A; c.1813C>T; c.1894G>T; c.2014_2016delTTTC (c.2017_2019delITTC); c.2067-6_-16delinsGGCCGGCCGG; c.2126G>A; c.2233_2240dupTATGACAC; c.2240+1G>A; c.2261C>T; c.2263C>T; c.2264G>A; c.2318C>T; c.2389_2391delGAT; c.2398C>T; c.2407C>T; c.2411G>A; c.2420delTTinsGG; c.2423_2454del32; c.2437-1G>A; c.2470G>A; c.2498C>T; c.2528T>C; c.2566A>G; c.2605C>T; c.2606G>A; c.2623C>T

TCF8/ ZEB1 c.2T>G; c.640C>T; c.929_930insA; c.973C>T; c.1124delT; c.1332_1335delCAAT; c.1348C>T; c.1387_1390delCCTT; c.1482dupA; c.1568delA; c.1576_1577insG; c.2087A>G; c.2157C>G; c.2182G>T; c.2324_2325dupA; c.2916_2917delITG; 2988_2989delAG

UBIAD1 c.305A>G; c.335A>G; c.353A>G; c.355A>G; c.361C>T/G; c.511T>C; c.524C>T; c.530G>C; c.556G>A; c.695A>G; c.708C>G