Color's Hereditary Genetic Testing

Actionable Insights to Inform Risk-Based Disease Management and Medication Response

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Executive Summary

Color offers a full suite of clinically actionable genetic tests designed to support informed care across oncology, pharmacogenomics, and adult preventive health. These tests empower healthcare providers and population health programs to identify individuals at increased risk for disease, optimize medication management, and enable earlier, more personalized interventions.

Built on a validated next-generation sequencing (NGS) platform, Color's assay deeply sequences the targeted genes and uses a full suite of highly refined bioinformatic tools for maximal sensitivity to detect complex DNA variants. Color's expert clinical interpretation teams bring rigor and transparency to variant classification and reporting, ensuring that results are accurate, clear and useful.

Color's testing is used by employers, health systems, research institutions, and public health programs to deliver affordable, scalable access to high-quality genetic insights, supporting both individual patient care and population-level impact. Within the Color Virtual Cancer Clinic, genetic testing is used in the context of criteria based testing programs, consistent with guidance from the National Comprehensive Cancer Network (NCCN), to identify and support individuals with an inherited risk for hereditary cancers.

Introduction

Advancements in genomic sequencing have transformed how we detect, manage, and prevent disease. Once prohibitively expensive and time-consuming, clinical-grade genetic testing is now accessible and increasingly embedded in routine care. Color's genetic testing platform brings this technology into cancer prevention and care, with a focus on identifying high-impact, actionable variants linked to well-established clinical protocols.[1-8]

Color's genetic tests evaluate risks for over 20 hereditary cancer types[1,3], and can include pharmacogenomics (PGx) to guide personalized care and avert adverse events associated with certain medications.[5-8] Each panel is designed with a focus on clinical validity and utility, incorporating guidance from organizations such as the American Cancer

Society (ACS)[8], the National Comprehensive Cancer Network (NCCN)[9,10], the American College of Medical Genetics and Genomics (ACMG)[11,12], and the Clinical Pharmacogenetics Implementation Consortium (CPIC)[13-15]. Genes are selected based on expert consensus and their relevance to care decisions, including enhanced screening, preventive strategies, or informing how genetic variation may affect response to certain medications.[9-11,13-15]

Test Overview

Color offers a menu of genetic tests. Each test panel is carefully curated to include genes with strong evidence for clinical validity and utility[2,5,12,18] guided by expert consensus, and established medical guidelines.[9,10-13] The tests are designed to detect a wide range of variant types, including single nucleotide variants (SNVs), small insertions and deletions (indels), copy number variants (CNVs)[2,19], and key pharmacogenetic alleles across diverse populations.[5,12,18]

The following table provides a high-level summary of some of Color's test offerings:

Test Area	Genes Covered	Clinical Focus
Hereditary Cancer	29 genes	Adult-onset cancer risk for breast, ovarian, uterine, colorectal, prostate, melanoma, stomach and pancreatic cancers.
BRCA1/2 and Lynch Syndrome	7 genes	Focused assessment of hereditary breast, ovarian, and colorectal cancer.
Pharmacogenomics (PGx)	20 genes	Identifies variants that may impact how individuals process or respond to medications.

Note: Detailed information on genes included in each test panel can be found in the Appendix. Additional test panels may be available for other programs.

Sequencing Technology & Methodology

Color's genetic testing platform is built on a robust, clinical-grade next-generation sequencing (NGS) infrastructure, optimized for accuracy, scalability, and affordability. All testing is performed in a CLIA-certified (05D2081492) and CAP-accredited (8975161) laboratory using validated protocols and automated quality control checks at each stage.[12,20,21]

Sample Collection and DNA Processing

DNA is extracted from validated sample types (saliva or blood) using automated extraction protocols. Quality and quantity are assessed using spectrophotometric and fluorometric methods to ensure sufficient input for library preparation. For most assays, high molecular weight genomic DNA is enzymatically fragmented and prepared for sequencing using the KAPA HyperPlus Library Prep Kit (Roche/Kapa Biosciences), automated on Hamilton STAR systems.[21]

Target Enrichment and Sequencing

Targeted enrichment is performed using Agilent's SureSelect capture probes, tailored to each test panel's design. Color's standard panels target the complete coding regions of selected genes, with inclusion of intron-exon boundaries (typically -15/+6bp) and additional non-coding regions known to harbor clinically relevant variants (e.g., deep intronic *MSH2* splice variants and regulatory *GREM1* regions).[22-24]

Sequencing is performed using Illumina's NovaSeq 6000 platform, with 150 bp paired-end reads and high-depth coverage across all target regions. Each run includes two fully characterized positive control samples (e.g., NA12878 and NA19240) and a no-template control to ensure run integrity.

Bioinformatics Pipeline

Color's custom bioinformatics pipeline uses industry-standard algorithms:

- Alignment: BWA-MEM against GRCh37 (hg19)[26]
- Variant Calling: GATK, DeepVariant, and proprietary algorithm for homopolymer regions (using BCFtools)[27-28]
- Structural Variant Detection: CNVkit (read depth), Dysgu (paired/split reads), and proprietary algorithms (including mobile element insertions)[24,29]
- Genotyping: challenging variants across all variant types using patented algorithm
- Pharmacogenomics: Aldy, and proprietary algorithm
- Specialized Regions:
    - *PMS2* exons 12–15 are resolved using long-range PCR and Sanger sequencing.[33,34]
    - *CYP2D6* copy number and hybrid rearrangements are resolved through combined read-depth and targeted analysis across exons 1, 6, and 9.[18,30-32]

The pipeline includes rigorous QC checkpoints and generates high-confidence variant calls across SNVs, indels, copy number variants (CNVs), and select structural rearrangements (e.g., inversions, mobile element insertions).

Coverage and Performance

At least 99.5% of regions in the reportable range meet or exceed 20x coverage. Median depth typically ranges from 200x to 300x, with high uniformity across targets. Regions that consistently fall below quality thresholds are excluded from analysis and documented in the test description.

Performance metrics such as accuracy, sensitivity, specificity, reproducibility, and repeatability have been validated across all test panels.[34-36]

Interpretation Framework

Color's interpretation framework is built to ensure that every reported variant meets high standards of analytical validity, clinical relevance, and transparency. Our approach combines automated data analysis with expert review to support high-confidence, clinically actionable results across all panels.

Variant Classification

All variants are classified using the American College of Medical Genetics and Genomics (ACMG) and Association for Molecular Pathology (AMP) guidelines for sequence variant interpretation.[12] Variants are assigned to one of five categories:

- Pathogenic
- Likely pathogenic
- Variant of uncertain significance (VUS)
- Likely benign
- Benign

Classification is based on multiple lines of evidence, including population frequency, computational predictions, functional data, segregation studies, and disease-specific case data.[37-40] Color incorporates allele frequency and variant annotation data from a range of public and internal sources, including gnomAD[37], ClinVar[38], BRCA Exchange[39], and others. Computational prediction tools, conservation metrics, and disease-specific variant evidence are used in line with ACMG/AMP guidelines.[12,40] Each classification is documented and tracked for consistency and transparency.

Expert Review and Curation

All clinically significant variants (pathogenic and likely pathogenic) undergo detailed review by Color's team of certified clinical geneticists and variant scientists. Where appropriate, variants are also reviewed by board-certified medical geneticists or pathologists. The curation team monitors emerging evidence and updates variant classifications as needed to reflect the most current understanding.[41]

Variant Confirmation

Variant calls with potential clinical impact may be confirmed using orthogonal methods, such as Sanger sequencing, MLPA, aCGH or variant-specific PCR, particularly for challenging regions and/or variant types. This step supports confidence in results before clinical reporting and aligns with best practices in molecular diagnostics.[20]

Pharmacogenomic-Specific Interpretation

Pharmacogenomic results are interpreted using standardized terminology and allele function assignments based on guidelines from the Clinical Pharmacogenetics Implementation Consortium (CPIC)[14], the Dutch Pharmacogenetics Working Group, PharmVar[43], and PharmGKB[44]. Phenotypes (e.g., "normal metabolizer," "poor metabolizer") are derived from diplotypes using consensus-based definitions.[13,43] Where applicable, annotations from the U.S. Food and Drug Administration's (FDA) Table of Pharmacogenomic Biomarkers in Drug Labeling are also considered.[45]

Star-allele resolution is based on detection of well-characterized variants and CNVs. Phenotypes are assigned per CPIC consensus definitions.[14] Reports present genotype and phenotype information alongside curated references. Instead, results are presented in a format that enables healthcare providers to consider how an individual's genetic variation may affect response to certain medications, in the context of clinical guidelines and patient-specific factors.

Limitations

While Color's genetic tests are highly sensitive and analytically validated, certain limitations are inherent to the technology, assay design, and current state of genomic knowledge. These limitations are important to consider in the clinical interpretation of results.

Technical Limitations

Incomplete detection of all variant types: Color's NGS assays are optimized for detecting single nucleotide variants (SNVs), small insertions and deletions (indels), and copy number variants (CNVs). However, the tests do not detect balanced translocations,deep intronic or regulatory variants outside of targeted regions, repeat expansions, low-level mosaicism, epigenetic changes (e.g., methylation).

Certain genomic regions are technically difficult to sequence due to high GC content, repetitive elements, or homology with pseudogenes (e.g., *PMS2, CYP2D6*). Color employs specialized methods to resolve known problematic regions, but rare or novel rearrangements may remain undetected or ambiguous.[31,33]

While the assay targets all coding exons and flanking intronic regions of selected genes, coverage may fall below reporting thresholds in limited regions. At least 99.5% of reportable regions meet or exceed 20x depth of coverage. Regions consistently underperforming are excluded from the reportable range and noted in the lab's test description.

Interpretive Limitations

Color uses targeted gene panels, not whole exome or whole genome sequencing. As a result, pathogenic variants in genes not included on the panel will not be detected.

Some genetic variants are classified as Variants of Uncertain Significance (VUS) due to limited or conflicting evidence. These findings are not used to guide clinical management. Variant classification reflects current knowledge and may be revised as new data emerge.[12,41]

Pharmacogenomic Testing Specifics

Diplotype inference and star-allele resolution: Star-allele assignments are inferred based on known combinations of observed variants. Rare alleles or novel haplotypes may be misclassified or unrecognized.[13,30]

CYP2D6 complexity: Despite robust CNV and rearrangement detection, full resolution of hybrid or complex *CYP2D6* configurations may be limited in some cases.[46,47]

Validation Data

Hereditary Cancer Genetic Test

Our validation strategy adhered to guidelines for NGS from the College of American Pathologists (CAP), the ACMG,[23] the Clinical and Laboratory Standards Institute,[48] the Nex-StoCT workgroup for Standardization of Clinical Testing by NGS[49] and FDA Standards for NGS.[50] The validation study included saliva samples, well-characterized cell lines and DNA specimens, previously extracted from blood from patients who had been diagnosed with hereditary cancer and whose genetic variants had been previously characterized elsewhere (Table 1). Together these groups constitute a good representation of the possible variant types across the genes in Color's Hereditary Genetic Tests.

Study 1: Reference materials with public data

Every sequencing run contains two positive controls (NA12878 and NA19240), which have been recommended as reference materials by the National Institute of Standards and Technology (NIST).[25] In addition, Color has sequenced the Ashkenazi Jewish father-mother-son trio NA24149, NA24143 and NA24385. Variant calls in these reference materials were compared against the union of reported variants by NIST [NCBI Get-RM] and Complete Genomics.[51,52] Several low-confidence variants in the NIST and Complete Genomics datasets were confirmed by Sanger sequencing at an independent laboratory.

Specimen	Number of non-pathogenic variants			Total
	SNVs	Indels	CNVs	
NA12878	60	4	0	64
NA19240	55	4	0	59
NA24143	46	2	0	48
NA24149	55	3	0	58
NA24385	54	2	0	56
Total	270	15	0	285

Table 1a. Study 1. Overview of variants, stratified by variant type. NIST reference materials.[50]

Study 2: Blinded specimens from patients with personal history of cancer

The hereditary genetics assay and tests were validated in part using two groups of patients who had previously been diagnosed with cancer. The first group consisted of 29 cell lines (Coriell Institute for Medical Research and American Type Culture Collection (ATCC)), many of which carry pathogenic variants in BRCA1 and BRCA2. The second group consisted of 507 anonymized DNA specimens provided by Mary-Claire King, Ph.D. and Tom Walsh, Ph.D. Of these 507 specimens, 183 specimens had pathogenic variants previously identified in at least one of 30 genes,[3,53–62] and the other 324 specimens had tested negative for germline variants in the same genes. Importantly, these clinical samples were provided to Color in a "blinded" manner; i.e. Color did not have information regarding the status or genetic makeup of the samples other than the past cancer history. After the Color test was performed, results were submitted to our collaborators to be compared against the previously identified variants. This allowed Color to test the accuracy of its assay in the absence of any a priori knowledge of genetic variants.

Specimen	**Number of pathogenic variants**			**Number of likely pathogenic variants**			**Total**
	SNVs	Indels	CNVs	SNVs	Indels	CNVs	
Cell lines (n=29)	14	18	NA	4	1	NA	37
Clinical samples, blinded group (n=507)	65	69	43	16	1	6	200
Total	79	87	43	20	2	6	237

Table 1b. Study 2. Overview of pathogenic and likely pathogenic variants, stratified by variant type: 29 cell lines [Coriell Institute and American Type Culture Collection] and 507 clinical samples.

Study 3: Independent confirmation of variants in consecutive Color cohort

As part of Color's quality control system, a set of 640 variants was submitted for confirmation by Sanger sequencing. This set contains 206 variants, detected in the initial consecutive cohort of Color's 19-gene breast and ovarian cancer genetic test, that had been classified as pathogenic or likely pathogenic.

Study 4: Technical precision: reproducibility and repeatability

Precision of the Color Genetic Tests is assessed with 3 replicate runs, which were performed by different operators. These runs used multiple lot numbers of critical reagents such as DNA polymerase and baits as well as multiple thermo-cyclers and sequencers. Intra-assay repeatability was computed by comparing results for 22 unique samples that had been replicated multiple times within the same run. Inter-assay reproducibility was assessed by comparing results for 61 unique samples that had been replicated multiple times across different runs. These precision measurements were calculated using all detected variants, independent of variant type (SNV/indel/CNV), classification and confirmation.

Study	Specimen	Number of variants	True Positives	False Positive*	False Negative*
1	NA12878 NA19240 NA24143 NA24149 NA24385	64 59 48 58 56	64 59 48 58 56	0 0 0 0 0	0 0 0 0 0
2	Coriell/ATCC cell lines (n=29)	37	37	0	0
2	Blinded samples (n=507)	200	200	0	0
Total	541	522	522	0	0

Table 2. Studies 1-2. Assessment of accuracy in detection of rare single nucleotide variants, insertions/deletions and copy number variants.

**Assessment of False Positives and False Negatives was based on all variants in the reportable range for the recommended NIST reference materials (Table 1a) and all (likely) pathogenic variants in the remaining validation specimens.*

Results

The Color Genetic Tests have proven analytical validity and 100% concordance with known, evaluated variants across 507 previously sequenced clinical samples and 34 cell lines. The 522 variants identified in previous clinical testing, including SNVs, small indels, and CNVs, were correctly detected in a blinded analysis. In this dataset, 237 variants had been classified as pathogenic or likely pathogenic, while no false positive pathogenic variants were called in any of these 541 samples (Table 2). In addition, all 640 germline variants submitted for Sanger sequencing were confirmed and no additional variants of relevance were detected (Table 3).

Gene	Total	True Positives	False Positives	False Negatives
ATM	94	94	0	0
BARD1	29	29	0	0
BRCA1	48	48	0	0
BRCA2	85	85	0	0
BRIP1	38	38	0	0
CDH1	23	23	0	0
CHEK2	77	77	0	0
MLH1	21	21	0	0
MSH2	52	52	0	0
MSH6	50	50	0	0
PALB2	32	32	0	0
PMS2	24	24	0	0

PTEN	2	2	0	0
RAD51C	13	13	0	0
RAD51D	11	11	0	0
STK11	8	8	0	0
TP53	9	9	0	0
Total	**616**	**616**	**0**	**0**
*NBN**	24	24	0	0

Table 3. Study 3. Overview of secondary confirmation results by Sanger sequencing for 640 variants, of which 206 variants had been classified as likely pathogenic or pathogenic in a consecutive cohort of patients taking the Color 19-gene genetic test for breast and ovarian cancer.

**NBN was removed from the panel in 2022*

Repeatability within-run amounted to 100% over 1212 variants (Jeffreys 95% Confidence Interval: 0.998-1), while reproducibility between-runs was 9613 of 9615 variants (99.98%, 95% CI: 0.999-1, see Table 4).

	Studies	**Results**	**Score [Jeffreys 95% CI]**
Accuracy Sensitivity Specificity PPV*	1-2 1-2 1-2 1-3	541/541 samples 522/522 variants 0 FPs** in 541 samples 0 FPs** in 522+640=1162 variants	100% [0.995-1] 100% [0.995-1] 100% [0.995-1] 100% [0.998-1]
Repeatability Reproducibility	4 4	1212/1212 variants 9613/9615 variants***	100% [0.998-1] 99.98% [0.999-1]

Table 4. Overview of Color Test performance across validation studies 1-4. *PPV = Positive Predictive Value. **FP = False Positive. ****Two likely benign variants, located in a homopolymer repeat and in a region of high GC content, were not reproduced in all replicates.*

Medication Response Genetic Test

Sample selection

To validate the sensitivity, specificity, and precision of the Color Medication Response Genetic Test, DNA derived from 426 cell line samples were compared to previously characterized results. The cell lines had consensus diplotypes reported by numerous studies.[18,31,35,63] The validation consisted of samples with a diplotype status falling into one of the following groups:

- Known “negative” or reference allele samples with a “normal” metabolizer status. e.g. (*1/*1)

- Known “positive” samples with reportable, non-normal diplotypes.

All samples were blinded to the operators and treated under identical experimental conditions

Data analysis

As described above, *1 indicates the absence of any tested allele, and is assay and analysis dependent; additionally, specific reporting of certain alleles depends on the inclusion or exclusion of other related refining alleles. It is therefore possible that analytically equivalent results can be reported as different diplotypes by different laboratories. Because published documentation for cell lines often only includes diplotypes without sufficient information about the set of tested alleles or the underlying genotypes, analysis of validation results followed a two-step process. Diplotype matches were counted as concordant. In cases of discordance at the diplotype level, a comparison of underlying contributing genotypes was made. Cases where all overlapping underlying genotypes were consistent were also counted as concordant.

Results

The Color Medication Response Genetic Test showed 100% concordance across all genes in all tested samples. In this dataset, 5,936 diplotype results were compared, with no false positives called in any of the 426 samples. In addition, the PGx variant calling pipeline, used to call and annotate key PGx variants for reporting, was able to accurately identify 99.98% (5111/5112) variants from these 426 samples.

The acceptance criteria for the study were met (Table 1). For diplotype calling, the true positive rate was 100% with 424 out of 424 cases correctly identified, and the false positive rate was 0% with no incorrect identifications. Similarly, PGx variant calling showed a true positive rate of 99.98% with 5111 out of 5112 cases correctly identified, and a false positive rate of 0.02% with only 1 incorrect identification.

Component	Metric	Expected	Observed
Diplotype calling	True positive	100%	100% (424/424)
	False positive	0%	0% (0/424)
PGx variant calling	True positive	>99.5%	99.98% (5111/5112)val
	False positive	<0.5%	0.02% (1/5112)

Table 5. Validation results. 464 samples were validated for diplotype calls (star-alleles) and key PGx variants.

CYP2D6 copy number

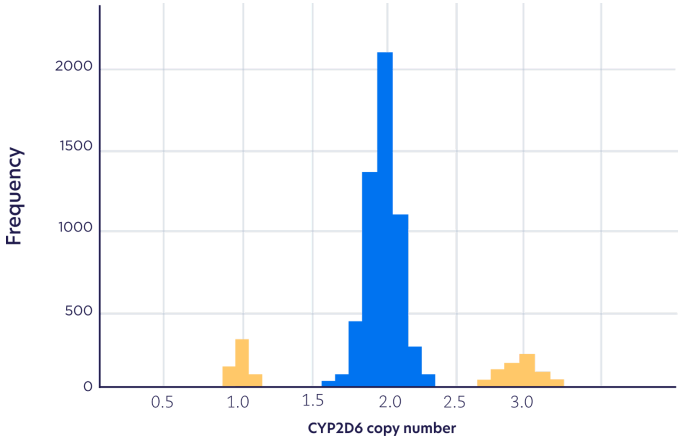

Figure 1. CYP2D6 mini-study. A set of 6266 samples were examined for copy number in representative sites within CYP2D6. Distinct separation of copy numbers was observed.

Correct analysis of the CYP2D6 gene requires extra complexity. In addition to being adjacent to two highly homologous pseudogenes, CYP2D7 and CYP2D8, it has over 100 reported alleles that vary in frequency by ethnicity.[30] These allelic variants are composed of single nucleotide polymorphisms (SNPs), insertions and deletions, copy number variants, larger rearrangements, and hybrid gene conversion events.[46] In particular, copy number changes are quite common. An estimated 12.6% of the US population has zero, one, or three or more copies.[32]

To derive a clear signal amidst these homology complications, CYP2D6 copy number is assessed by an analysis of exon 1, exon 6, and exon 9 (including flanking intronic regions). To confirm that homology does not confound copy number assessment, observed copy number across a set of 6266 samples was evaluated. A clear separation of integer copy numbers was observed. In addition, the validation set included 11 known copy number variants, and all were accurately detected.

Conclusion

Color's genetic testing platform delivers comprehensive, high-quality insights that support prevention, diagnosis, and personalized care across a wide spectrum of conditions. By combining analytical accuracy with clinical relevance, Color's hereditary and pharmacogenomic panels empower healthcare providers and research partners to make timely, evidence-based decisions.

Our testing methodology is rooted in a clinically validated next-generation sequencing platform that detects a broad range of variant types—including single nucleotide variants, indels, copy number variants, and select structural rearrangements. We employ rigorous bioinformatics pipelines, expert variant review, and continual updates based on evolving scientific guidelines to ensure that each result is as informative and actionable as possible.

Color's menu of genetic tests—including panels for hereditary cancer, hereditary heart health, and pharmacogenomics—reflects our commitment to:

- Supporting clinical care with meaningful, guideline-informed results
- Ensuring equitable access through population-aware panel design
- Maintaining scientific and technical excellence with every test

Color's integrated approach to genetic testing is designed to meet the needs of both today's clinical practice and tomorrow's research priorities—driving improved outcomes at both the individual and population levels.

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Supplement

Supplemental Table 1. Known associations between genes in Color's Hereditary Cancer Genetic Tests and cancer type.

Gene	Breast	Ovarian	Uterine	Colorectal	Melanoma	Pancreatic	Stomach	Prostate
BRCA1	●	●				●		●
BRCA2	●	●			●	●		●
MLH1		●	●	●		●	●	●
MSH2		●	●	●		●	●	●
MSH6		●	●	●			●	●
PMS2		●	●	●				●
EPCAM†		●	●	●		●	●	●
APC				●		●	●	
MUTYH†				●				
MITF†					●			
BAP1					●			
CDKN2A					●	●		
CDK4†					●			
TP53	●	●	●	●	●	●	●	●
PTEN	●		●	●	●			
STK11	●	●	●	●		●	●	
CDH1	●						●	
BMPR1A				●			●	
SMAD4†				●			●	
GREM1†				●				
POLD1†				●				
POLE†				●				
PALB2	●	●				●		
CHEK2	●			●				●
ATM	●					●		
BARD1	●							
BRIP1	●	●						
RAD51C	●	●						
RAD51D	●	●						

*† Analysis limited to positions known to impact cancer risk (genomic coordinates in GRCh37): in CDK4, only chr12:g.58145429-58145431 (codon 24); in EPCAM, only large deletions and duplications including 3′ end of the gene ; in GREM1, only duplications in the upstream regulatory region; in MITF, only chr3:g.70014091 (including c.952G>A); in MUTYH, only biallelic or at least two (likely) pathogenic variants in unknown phase; in *PMS2*: variants of uncertain significance are not reported for exons 12-15. Analysis excludes five variants commonly observed in the pseudogene *PMS2CL*: c.2182_2184delinsG, c.2243_2246del, c.2444_2445insTT, c.2523G>A, and deletion of exons 13-14 (chr7:g.6015768_6018727del). inPOLD1: analysis is limited to chr19:g.50909713 (including c.1433G>A); in POLE, only chr12:g.133250250 (including c.1270C>G), POLE: analysis is limited to chr12:g.133250250 (including c.1270C>G). SMAD4: Presence of the processed pseudogene may impact the ability to call structural variants in SMAD4.*

Supplemental Table 2. Medication Response Genetic testing, genes and alleles analyzed

Gene	Star alleles and variants analyzed
ABCG2	rs2231142
CACNA1S	ENST00000362061: reference, c.520C>T, c.3257G>A
CYP1A2	*1, *30 (*1F)
CYP2C cluster	rs12777823
CYP2C9	*1, *2, *3, *4, *5, *6, *8, *9, *11, *12, *13, *14, *15, *16, *23, *24, *26, *29, *31, *33, *35, *39, *42, *43, *44, *45, *46, *55, *61
*CYP2C19^*	*1, *2, *3, *4, *5, *6, *7, *8, *9, *10, *16, *17, *19, *22, *24, *25, *26, *35, *36 (whole gene deletion), *37 (partial gene deletion), *38
*CYP2D6^*	*1, *2, *3, *4, *4N (hybrid, a.k.a. *4.013), *5 (whole gene deletion), *6, *7, *8, *9, *10, *11, *12, *13 (hybrid), *14, *15, *17, *18, *19, *21, *29, *31, *32, *35, *36 (hybrid), *40, *41, *42, *45, *49, *54, *55, *56, *59, *68 (hybrid), *69, *114, *119, *xN
CYP3A4	*1, *20, *22
CYP3A5	*1, *3, *6, *7
CYP4F2	*1, *2, *3, *4, rs2108622
DPYD	ENST00000370192: reference (*1), c.299_302del (*7), c.557A>G, c.703C>T (*8), c.868A>G, c.1129-5923C>G (HapB3), c.1156G>T (*12), c.1314T>G, c.1475C>T, c.1679T>G (*13), c.1774C>T, c.1898del (*3), c.1905+1G>A (*2A), c.2279C>T, c.2639G>T, c.2846A>T, c.2983G>T (*10), rs3918290, rs55886062.1 A>C, rs75017182, rs56038477, rs67376798, rs115232898
F5	rs6025
*G6PD^*	"A- 202A_376G", "A- 968C_376G", "Asahi", "B (reference)", "Canton, Taiwan-Hakka, Gifu-like, Agrigento-like", "Chatham", "Chinese-5", "Gaohe", "Ilesha", "Kaiping, Anant, Dhon, Sapporo-like, Wosera", "Kalyan-Kerala, Jamnaga, Rohini", "Malaga", "Mediterranean, Dallas, Panama, Sassari, Cagliari, Birmingham", "Orissa", "Quing Yuan, Chinese-4", "Seattle, Lodi, Modena, Ferrara II, Athens-like", "Ube Konan", "Union, Maewo, Chinese-2, Kalo", "Viangchan, Jammu"
IFNL3	rs12979860
NUDT15	*1, *2, *3, *4, *6, *9, *14, rs116855232
RYR1	ENST00000359596: reference, c.38T>G, c.97A>G, c.103T>C, c.130C>T, c.131G>A, c.463C>A, c.487C>T, c.488G>T, c.529C>T, c.533A>G, c.742G>A, c.742G>C, c.982C>T, c.1021G>A, c.1021G>C, c.1201C>T, c.1202G>A, c.1202G>T, c.1565A>C, c.1565A>G, c.1589G>A, c.1597C>T, c.1615T>C, c.1615T>G, c.1630G>T, c.1654C>T, c.1655G>A, c.1840C>T, c.1841G>A, c.1841G>T, c.3166G>C, c.5183C>T, c.6349G>C, c.6387C>G, c.6487C>T, c.6488G>A, c.6488G>C, c.6488G>T, c.6502G>A, c.6612C>G, c.6617C>G, c.6617C>T, c.6628G>T, c.6757C>T, c.6838G>A, c.7007G>A, c.7035C>A, c.7036G>A, c.7042_7044del, c.7043A>G, c.7048G>A, c.7060G>A, c.7063C>T, c.7076G>A, c.7084G>A, c.7090T>G, c.7123G>A, c.7124G>C, c.7282G>A, c.7291G>A, c.7291G>T, c.7300G>A, c.7304G>A, c.7304G>T, c.7310C>T, c.7354C>T, c.7358T>C, c.7360C>T, c.7361G>A, c.7372C>T, c.7373G>A, c.7373G>T, c.7522C>T, c.7523G>A, c.7879G>C, c.8026C>T, c.9310G>A, c.11315G>A, c.11708G>A, c.11947C>T, c.11958C>G, c.11969G>T, c.12149C>A, c.12700G>C, c.12700G>T, c.14209C>T, c.14210G>A, c.14477C>T, c.14497C>T, c.14512C>G, c.14539G>C, c.14545G>A, c.14627A>G, c.14803G>A, c.14918C>T
SLCO1B1	*1, *5, *9, *14, *15, *20, *31, *46, *47, rs2306283, rs4149056
TPMT	*1, *2, *3A, *3B, *3C, *4, *8, *11, *14, *15, *23, *24, *29, *41, *42
UGT1A1	*1, *6, *27, *28, *36, *37
VKORC1	rs9923231, rs72547529, rs61742245

^ In CYP2D6, sensitivity to detect copy number variation >3 is limited and hybrid alleles other than those listed above will not be reported; in CYP2C19, if copy number cannot be determined for technical reasons, haplotypes will be called assuming 2 gene copies, not all partial deletions can be detected and duplications will not be reported; in G6PD, chromosome X aneuploidies will not be reported..