Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

Product Description:	Seraseq® Pharmacogenomics DNA Mix		
Material Number:	0750-9503	Batch Number:	10771343
Material Description:	A genomic DNA mutation mix containing deletions, insertions, duplications, and single nucleotide variants blended with GM24385 DNA as reference wild-type background		
Date of Manufacture:	01 AUG 2025	Expiration Date:	01 AUG 2029
Fill Volume:	20 µL		
Nominal Concentration:	30 ng/µL		
Concentration (Qubit dsDNA BR Assay):	34.3 ng/µL		
dPCR Test Method:	Bio-Rad QX200 Droplet Digital™ System		
NGS Assay Test Method:	Next Generation Sequencing testing using HealthInCode Pharmacogenetics Global Panel.		

Gene	Nucleotide Change	Protein Change	Star Allele	dbSNP NIH	VAF (%) (dPCR)	VAF (%) (NGS)
CYP2B6	c.983T>C	p.I328T	*18	rs28399499	43.1	54.9

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	c.785A>G	p.K262R	*4 (*6, 87, *13)	rs2279343	56.0	14.3
	c.516G>T	p.Q172H, Splice defect	*9 (*6)	rs3745274	49.2	53.4
CYP2C cluster	g.96405502G>A	N/A	N/A	rs12777823	44.3	53.0
CYP2C19	c.1A>G	p.M1V	*4B	rs28399504	45.0	54.9
	c.332-23A>G	Splice defect	*35	rs12769205	44.0	49.5
	c.358T>C	p.W120R	*8	rs41291556	44.0	49.4
	c.395G>A	p.R132Q	*6	rs72552267	44.0	50.4
	c.431G>A	p.R144H	*9	rs17884712	44.0	51.9
	c.636G>A	p.W212X	*3	rs4986893	45.4	51.1
	c.680C>T	p.P227L	*10	rs6413438	46.9	43.7
	c.681G>A	Splice defect	*2	rs4244285	47.4	43.7
	c.-806C>T	Expression	*17	rs12248560	43.5	49.5
	c.819+2T>A	Splice defect	*7	rs72558186	46.9	45.8
	c.1297C>T	p.R433W	*5	rs56337013	43.5	53.8
CYP2C9	c.269T>C	p.L90P	*13	rs72558187	44.5	53.2
	c.430C>T	p.R144C	*2	rs1799853	44.5	57.2
	c.449G>A	p.R150H	*8	rs7900194	44.5	56.8
	c.485C>A	p.S162X	*15	rs72558190	45.1	52.1
	c.818delA	p.K273fs	*6	rs9332131	44.0	48.9
	c.1003C>T	p.R335W	*11	rs28371685	44.9	55.2
	c.1075A>C	p.I359L	*3	rs1057910	44.9	52.3
	c.1080C>G	p.D360E	*5	rs28371686	44.9	53.1
	c.1465C>T	p.P489S	*12	rs9332239	46.2	49.5
CYP2D6	c.100C>T	p.P34S	*10	rs1065852	73.8	78.1
	c.124G>A	p.G42R	*12	rs5030862	45.9	50.3
	c.137dup	p.L47fs	*15	rs774671100	45.9	49.0
	c.320C>T	p.T107I	*17	rs28371706	45.1	57.9
	c.358T>A	p.F120I	*49	rs1135822	41.1	42.1
	c.406G>A	p.V136M	*29 (*107,*149)	rs61736512	41.1	41.2
	c.454del	p.W152fs	*6	rs5030655	41.1	40.8
	c.505G>T	p.G169X	*8	rs5030865	41.1	89.9
	c.505G>A	p.G169*	*14	rs5030865	45.3	89.9
	c.506-1G>A	Splice defect	*4	rs3892097	45.3	46.8
	c.514_522dup	p.174_175insFRP	*40	rs72549356	45.3	45.7
	c.775del	p.R259fs	*3	rs35742686	47.2	47.2
Gene	**Nucleotide Change**	**Protein Change**	**Star Allele**	**dbSNP NIH**	**VAF (%) (dPCR)**	**VAF (%) (NGS)**
CYP2D6	c.805dup	p.R269fs	*21	rs72549352	47.2	52.1
	c.841_843del	p.K281del	*9	rs5030656	47.2	46.7

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	c.886C>T	p.R296C	*2, *8,*11, *12,*14, *17	rs16947	74.1	79.2
	c.971A>C	p.H324P	*7	rs5030867	47.2	52.6
	c.975G>A	Splice defect	*59	rs79292917	47.2	53.5
	c.985+39G>A	Splice defect	*41	:rs28371725	47.2	54.5
	c.1012G>A	p.V338M	*29	rs59421388	47.2	48.9
	c.1030C>T	p.R344X	*56	rs72549347	47.2	48.0
	c.1088_1089dup	p.Q364fs	*42	rs72549346	47.2	44.0
	c.1319G>A	p.R440H	*31	rs267608319	46.9	41.6
	c.1457G>C	p.S486T	*2	rs1135840	100.0	ND
CYP3A4	c.522-191C>T	Splice defect	*22	rs35599367	44.1	48.6
	c.1461dup	p.P487fs	*20	rs67666821	44.4	55.8
CYP3A5	c.219-237A>G	Splice defect	*3	rs776746	100.0	ND
	c.624G>A	Splice defect	*6	rs10264272	44.8	51.9
	c.1035_1036insT	p.T346fs	*7	rs41303343	47.3	53.8
CYP4F2	c.1297G>A	p.V433M	*3	rs2108622	72.0	76.0
DPYD	c.1156G>T	p.E386*	*12	rs78060119	43.0	53.4
	c.1236G>A	p.E412E	HapB3	rs56038477	43.0	52.3
	c.1314T>G	p.F438L	N/A	rs186169810	43.0	51.8
	c.1601G>A	p.S534N	*4	rs1801158	45.7	59.1
	c.1627A>G	p.I543V	*5	rs1801159	45.7	60.2
	c.1679T>G	p.I560S	*13	rs55886062	45.7	55.4
	c.1775G>A	p.R592Q	N/A	rs138616379	44.9	56.3
	c.1898delC	p.P633fs	3*	rs72549303	44.9	49.2
	c.1905+1G>A	p.IVS14	*2A	rs3918290	44.9	50.0
	c.2846A>T	p.D949V	N/A	rs67376798	44.2	58.2
	c.2872A>G	p.K958E	N/A	rs141044036	44.2	58.3
NUDT15	c.415C>T	p.R139C	*3	rs116855232	46.0	45.4
	c.416G>A	p.R139H	*4	rs147390019	40.5	44.8
	c.50delGAGTCG	p.del17_18GV	*9	rs746071566	47.5	27.9
	c.80_81insCGGG	p.C28fs	*14	rs777311140	47.5	54.7
TPMT	c.2T>G	p.M1W	*29	rs267607275	42.2	54.7
	c.95dup	p.W33fs	*42	rs759836180	42.2	54.1
	c.238G>C	p.A80P	*2	rs1800462	44.5	54.3
	c.395G>A	p.C132T	*11	rs72552738	44.4	53.9
	c.460G>A	p.A154T	*3A	rs1800460	42.8	50.7
Gene	**Nucleotide Change**	**Protein Change**	**Star Allele**	**dbSNP NIH**	**VAF (%) (dPCR)**	**VAF (%) (NGS)**
TPMT	c.719A>G	p.Y240S	*3C	rs1142345	41.4	51.9
UGT1A1	c.862-6800AT[8]	Splice defect	*28	rs3064744	42.2	35.1
	c.862-6536G>A	p.G71R	*6	rs4148323	42.2	48.3

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VKORC1	c.-1639G>A	N/A	N/A	rs9923231	99.9	100.0
	c.106G>T	p.D36Y	N/A	rs61742245	42.1	50.7
	c.196G>A	p.V66M	N/A	rs72547529	42.4	48.9

VAF = variant allele frequency
NA = not applicable
ND = not detected

Approval:

Prepared By

08 AUG 2025

Date