Hemo ID™
DONOR QUICK SCREEN (DQS) PANEL

Cost-effective extended antigen typing for rare donor identification

FACILITATING ACCESS TO RARE DONORS

Every year, international blood donor programs lose rare donors due to sickness, age, or other factors. The Hemo ID™ DQS Panel, developed for use on the MassARRAY® System, simplifies the identification process for new donors by quickly and easily testing thousands of samples.

AN IDEAL LABORATORY WORKFLOW

With a rapid and robust protocol that takes only five and a half hours from DNA to report, you can obtain predicted phenotypes from as few as 12 to as many as 2,000 samples per day.

BLOOD GROUP ANTIGENS INCLUDED IN THE HEMO ID™ DQS PANEL
Rh: ce, Ce, cE, CE, C^w, C^x, V, VS, hrB, hrS, Crawford
Kell: k/ K, Kp^a/ Kp^b, Js^a/ Js^b
Duffy: Fy^a/ Fy^b, Fy^x, GATA
Kidd: Jk^a/ Jk^b
MNS: M/ N, S/ s, U, U^{var} P2, U^{var} NY, U^{neg}
Lutheran: Lu^a/ Lu^b
Dombrock: Do^a/ Do^b, Hy +/-, Jo^a +/-
Landsteiner Wiener: LW^a/ LW^b
Diego: Di^a, Di^b
Colton: Co^a/ Co^b
Scianna: Sc1/ Sc2
Cartwright: Yt^a/ Yt^b

BETA GLOBIN VARIANTS
Hemoglobin C: HbC
Hemoglobin E: HbE
Hemoglobin S: HbS

See details on reverse side

For Research Use Only. Not for use in diagnostic procedures.

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HOW IT WORKS

Genomic DNA samples are amplified using the provided PCR primers, PCR enzyme, and dNTPs. Residual dNTPs are dephosphorylated with SAP. Following single nucleotide primer extension and termination reactions, the extension products are transferred to a support surface (SpectroCHIP® Array) and loaded into the MassARRAY mass spectrometer for data acquisition. Data analysis software then makes genotype assignments and generates predicted phenotypes.

PERFORMANCE

Genotype and predicted phenotype call rates of > 99% were observed at two independent test sites (n= 768). There was a greater than 99% concordance between the predicted phenotype calls generated by the Hemo ID DQS Panel and those derived from using the Immucor PreciseType™ HEA Test or serology (n=88).

ORDERING INFORMATION

CAT NO	FORMAT	SAMPLES/KIT
17934	10x96	192

REFERENCES

1. Gassner C, Meyer S, Frey BM, Vollmert C. Matrix-assisted laser desorption/ionisation, time-of-flight mass spectrometry-based blood group genotyping--the alternative approach. *Transfus Med Rev*. 2013;27(1):2-9.
2. Meyer S, Vollmert C, Trost N, Brönnimann C, Gottschalk J, Andreas B, Frey BM, and Gassner C. High-throughput Kell, Kidd, and Duffy matrix-assisted laser desorption/ionization, time-of-flight mass spectrometry–based blood group genotyping of 4000 donors shows close to full concordance with serotyping and detects new alleles. *Transfusion*. 2014;54(12):3198-207.

HEMO ID™ DQS PANEL GENES AND NUCLEOTIDES

BLOOD GROUP	ANTIGENS	GENE	NUCLEOTIDE
Rh	ce, Ce, cE, CE	*RHCE*	307C>T, i2(109bp ins), 676G>C
	C^w	*RHCE*	122A>G
	C^x	*RHCE*	106G>A
	V / VS / hrB	*RHCE*	48G>C, 733C>G,1006G>T
	hrS	*RHCE*	48G>C, 712A>G, 733 C>G
	Crawford	*RHCE*	48G>C, 697C>G, 733C>G
Kell	k / K	*KEL*	578C>T
	Kp^a / Kp^b	*KEL*	841C>T
	Js^a / Js^b	*KEL*	1790T>C
Duffy	Fy^a / Fy^b	*DARC*	125A>G
	Fy^x	*DARC*	125A>G, 265 C>T
	GATA	*DARC*	−67T>C, 125A>G
Kidd	Jk^a / Jk^b	*SLC14A1*	838A>G
MNS	M / N	*GYPA*	59C>T; 72T>G
	S / s	*GYPB*	143C>T
	U	*GYPB*	Intron 5 +5G>T
	U^{var} P2	*GYPB*	143C>T; Intron5+5G>T
	U^{var} NY	*GYPB*	143C>T; 208G>T; 230C>T; 251C>G
	U^{neg}	*GYPB*	Deleted GYPB
Lutheran	Lu^a / Lu^b	*BCAM*	230G>A
Dombrock	Do^a / Do^b	*ART4*	793A>G
	Hy+/-	*ART4*	323G>T
	Jo^a+/-	*ART4*	350C>T
Landsteiner Wiener	LW^a / LW^b	*ICAM4*	299A>G
Diego	Di^a / Di^b	*SLC4A1*	2561C>T
Colton	Co^a / Co^b	*AQP1*	134C>T
Scianna	Sc1 / Sc2	*ERMAP*	169G>A
Cartwright	Yt^a / Yt^b	*ACHE*	1057C>A

HEMOGLOBIN TYPE	GENE	NUCLEOTIDE
Hemoglobin C (HbC)	*HBB*	19G>A
Hemoglobin E (HbE)	*HBB*	79G>A
Hemoglobin S (HbS)	*HBB*	20A>T

vB

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