

## Supplementary Materials:

### An Example of Personalized Treatment in HR+ HER2+ Long Survivor Breast Cancer Patient (Case Report)

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Table S1. Panel of SNPs investigated.

Gene	Rs Code	Polymorphism	Amino acid	Genotype	Functional effects
TRANSPORTERS					
ABCB1	rs1128503	C1236T		C/T	Decreased
	rs1045642	C3435T		C/T	
	rs4148738	G>A		T allele leads to lower activity G/A G allele increased Dabigatran	
ABCC1/MRP1	rs45511401	G761V-G>T		G/G normal activity	Normal activity
ABCC2/MRP2	rs8187710		Cys1515Tyr	G/G normal activity	Normal activity
ABCC2/MRP2	rs17222723	T > A	Val1188Glu	T/T normal activity	Normal activity
ABCC2-C-24T	rs717620			T/T T allele leads to lower expression	Lower Expression-
ABCG2	rs2231142	C421A	Q141K	C/C	
SLC15A2	rs2257212	C > T	L305F	C/C	
SLCO1B1	rs4363657	T521C	V174A	T/C	Decreased activity
	rs4149056	T>C		T/C C allele leads to lower activity of transporter	
5HTT-LPR				S/L S allele leads to lower gene trans- cription	Decreased activity
CYP					
CYP1A2*1C	rs2069514	G3860A		G/G normal activity	Normal activity
CYP1A2*1F	rs762551	C163A	Intron	A/A A allele leads to increased induci- bility	Increased
CYP2C19					
Normal activity					
CYP2C19*17	rs12248560	C806T	Upstream	C/C	Normal activity
CYP2C19*10	rs6413438	C1953T		C/C	
CYP2C19*2	rs4244285	G19154A		G/G	
CYP2C19*3	rs4986893	G17948A		G/G	
CYP2C19*4	rs28399504	A1G		A/A	
CYP2C19*5	rs56337013	C90033T		C/C	
CYP2C19*7	rs72558186	T19294A		T/T	
CYP2C9*2	rs1799853	C430T	Cys144Arg	C/C	Decreased
CYP2C9*3	rs1057910	A1075C	Ile359Leu	A/C C allele leads to lower activity	
CYP2D6					
Poor metabolizer					


CYP2D6*2	rs16947	C2850T	Arg296Cys	C/C	
CYP2D6*10	rs1065852	C100T	Pro34Ser	T/T	
CYP2D6*17	rs28371706	C1023T	Thr107Ile	C/C	
CYP2D6*6	rs5030655	1707delT	Trp152fs	IN3/IN3	
CYP2D6*20	rs72549354	insG	Leu213fs	DEL/DEL	
CYP2D6*5	-	Deletion	Stop codon	Absent	
CYP2D6*38	rs72549351	delGACT	Thr272fs	INS/INS	
CYP2D6*29	rs61736512	G1659A	Val136Met	G/G	
CYP2D6*2A	rs1080985	C1584G	Upstream	C/C	
CYP2D6*3	rs35742686	2549delA	Arg259fs	INS/INS	
CYP2D6*4	rs3892097	G1846A	Acceptor	A/A	
CYP2D6*41	rs28371725	G2988A	Intron	G/G	
CYP2D6*7	rs5030867	A2935C	His324Pro	A/A	
CYP2D6*9	rs5030656	2615_2617delAAG	Inframe del.	INS/INS	
CYP3A4*1B	rs2740574	A392G	Upstream	A/A	Normal activity
				C/C	
CYP3A4*22	rs35599367	C15389T	Intron	G alleles lead to increased activity	Normal activity
CYP3A5*3	rs776746	A6986G	Acceptor	G/G	Normal activity
				T/T	
CYP1A1	rs1048943	T>C	Ile462Val	C allele leads to increased activity	Normal activity
CYP2B6	rs2279343	A785G	Lys262Arg	A/G	Decreased (lower activity)
	rs3745274	G516T	Gln172His	G/T	
	rs3211371	C1459T	Arg487Cys	C/T	
	rs2279343	A785G	Lys262Arg	A/G	
CYP2B6	rs28399499	T983C	Ile328Thr	T/T	Normal activity
CYP2A6	rs28399433	A48C		A/A	Normal activity
	rs1801272	T>A		T/T	
CYP2C8*2	rs11572103	A805T	Ile269Phe	A/A	Normal activity
CYP2C8*4	rs1058930	C792G	Ile264Met	C/C	Normal activity
OTHER DRUG METABOLIZING ENZYMES					
TPMT*2	rs1800462	C>G	Ala80Pro	C/C	Normal activity
TPMT*3B	rs1800460	G460A	Ala154Thr	G/G	Normal activity
TPMT*3C	rs1142345	A719G	Tyr240Cys	A/A	
UGT1A1*28	rs8175347	(TA)(n) repeat sequence	(6/7TA) TATA box	6/6	Normal activity
UGT2B17		Deletion		Norma Genotype	Normal activity
DPYD	rs2297595	A166G		A/A	Normal activity
	rs67376798	A2846T	Asp949Val	A/A	
DPYD*6	rs1801160	G>A	Val732Ile	G/G	Normal activity
DPYD*2A	rs3918290	IVS 14+1G>A		G/G	-
COMT	rs4680	G>A	Val158Met	G/A	Decreased
	rs4633	C>T	His62His	C/T	
				C/G	
COMT	rs4818	C>G	Leu136Leu	G alleles lead to increased activity	Increased
MTHFR	rs1801133	C677T	Ala222Val	T/T	Normal activity
MTHFR	rs1801131	A1298C	Glu429Ala	A/A	Decreased
TSER-	rs45445694	28bpVNTR		3R/3R	Increased transcription
CBR3	rs1056892	G>A	Val244Met	G/G	Normal activity
CYBA	rs4673	C242T		C/T	
NCF4	rs1883112	A212G		G/G	
RAC2	rs13058338	T7508A		T/A	
NAT1*14B	rs4986782	G560A	Arg187Gln	G/G	Normal activity
NAT1*15B	rs5030839	C599T	Stop Codon	C/C	Normal activity
NAT1*17B	rs56379106	C190T	Arg64Trp	C/C	Normal activity

NAT1*22B	rs56172717	A752T	Asp251Val	A/A	Normal activity
NAT2*3	rs1801280	T341C	Ile114Thr	C/C C allele lead to lower activity	Decreased
NAT2*6	rs1799930	G590A	Arg197Gln	G/G	Normal activity
NAT2*7	rs1799931	G857A	Gly286Glu	G/G	
UMPS	rs1801019	G213A G>C	Gly213Asp Gly213Ala	G/C	-
CBS	rs234706	C699T		C/T Allele T associated with increased risk of ammonia and sulphite detoxification defects	
MTR	rs1805087	A2756G		A/G	Increased cardiovascular risk
MTRR	rs1801394	A66G		A/G	Increased cardiovascular risk
RECEPTORS					
DRD2/ANKK1-Q713K	rs1800497	C957T		C/C	Normal activity
DRD2-141-insC/delC	rs1799732	insC/delC	Upstream	InsC/InsC	Normal activity
DRD2-S311C	rs1801028	C932G	Ser311Cys	C/C	Normal activity
DRD3-S9G	rs6280	A25G	Gly9Ser	A/A	Normal activity
HTR2A	rs6314	C1354T	His452Tyr	C/T	
	rs7997012	A>G	Intron	A/G	
	rs6311	G1438A	Upstream	A/A	
HTR2C	rs6318	G68C	Cys23Ser	G/G	
OPRM1	rs1799971	A118G	Asn40Asp	A/G	More pain
VDR-BmsI	rs1544410	C>T		C/C	
VDR-TaqI	rs731236	A>G		A/A	
VDR-Apa	rs7975232	C>A		C/A	
VDR	rs4516035	1012T>C		T/T	
AGT	rs4762	C9369T	T174M	C/T T allele leads to high level of angiotensinogen and increased cardiovascular risk	Increased cardiovascular risk
AGT	rs699	T9543C	M235T	C/C C allele leads to increased cardiovascular risk and sodium related hypertension	Increased cardiovascular risk
AGTR1	rs5186	A1166C		A/C C allele leads to hypertension	Increased cardiovascular risk
ITGB3	rs5918	T1565C		T/T	Normal activity
OXIDATION REDUCTION ENZYMES					
GSTP1	rs1695 rs1138272	A313G C>T	Ile105Val V114A	A/G C/C G alleles lead to lower activity	Decreased
GSTM1		Deletion		Deleted	No activity
GSTT1		Deletion		Normal	Normal activity
DNA REPAIR ENZYMES					
ERCC1	rs3212986	C8092A	3 Prime UTR	C/A	-

	rs11615	T19007C	Asn118=	T/C	
XRCC1	rs25487	G28152A	Gln399Arg	G/A	
LIPID METABOLISM					
APOA1	rs1799837	G75A		G/G	
				Protective against cardiovascular event	
APOB1	rs5742904	G10580A	Arg3500Gln	G/G	
APOE	rs7412 rs429358			E3/E3	Normal activity
CETP	rs1532624	C>A	Intron	C/C	Normal activity
HMGCR	rs3761740	C911A	Upstream tra.	C/C	Normal activity
	rs5908	A>G	Ile585Val	A/A	Normal activity
PON1	rs662	A575G	Gln192Arg	A/A	Normal activity
	rs705379	C108T	Upstream	C/C	
COAGULATION ENZYMES					
VKORC	rs9923231	G1639A	Upstream	G/A C/T	
	rs9934438	C1173T	Intron	A/T alleles lead to less coagulating capacity	Decreased
CES1	rs2244613 rs8192935	A>C C>T	Intron	A/A C/C	Normal activity
F II	rs1799963	G20210A	3 Prime UTR	G/G	Normal activity
PAI	rs1799889	4G/5G	Upstream	4G/4	
F V	rs6025	G1691A	Arg506Gln	G/G	
β-fibrinogen	rs1800790	G455A	-	G/A A allele	Increased level of fibrin- ogenous
FattoreXIII	rs5985	G>T	Val135Leu	G/T	

**Abbreviation:** ABCB1, ATP binding cassette subfamily B member 1; ABCC1, ATP Binding Cassette Subfamily C Member 1; MRP1, Multidrug resistance-associated protein 1; ABCC2, ATP Binding Cassette Subfamily C Member 2; MRP2, Multidrug resistance-associated protein 2; ABCG2, ATP-binding cassette sub-family G membro 2; SLC15A2, Solute Carrier Family 15 Member 2; SLC01B1, solute carrier organic anion transporter family member 1B1; 5-HTTLPR, serotonin-transporter-linked polymorphic region; CYP1A2, Cytochrome P450 Family 1 Subfamily A Member 2; CYP2C19, cytochrome P450 family 2 subfamily C member 19; CYP2D6 Cytochrome P450 family 2 subfamily D member 6; CYP3A4, Cytochrome P450 family 3 subfamily A member 4; CYP3A5, Cytochrome P450 family 3 subfamily A member 5; CYP1A1 Cytochrome P450 family 1 subfamily A member 1; CYP2B6 Cytochrome P450 family 2 subfamily B member 6; CYP2C8, Cytochrome P450 family 2 subfamily C member 8; TPMT, Thiopurine methyltransferase; UGT1A1, uridine-diphosphoglucuronate glucuronosyltransferase; DPYD, dihydropyrimidinase; COMT, catechol O-methyltransferase; MTR, methionine synthase; TSER, synthase enhancer region; CBR3, carbonyl reductase 3; MTHFR, methylenetetrahydrofolate reductase; TYMS, thymidylate synthase; NAT1, Arylamine N-acetyltransferase 1; NAT2, Arylamine N-acetyltransferase 2; UMPS, Uridine Monophosphate Synthetase; DRD2, dopamine receptor D2; ANKK1, Ankyrin repeat and kinase domain containing 1; HTR2A, 5-Hydroxytryptamine Receptor 2A; HTR2C, 5-Hydroxytryptamine Receptor 2C; OPRM1, Opioid Receptor Mu 1; VDR, vitamin D receptor; AGT, angiotensinogen gene; ITGB3, integrin subunit beta 3; GSTP1, Glutathione S-Transferase P1; GSTM1, glutathione S-transferase Mu 1; GSTT1, Glutathione S-Transferase Theta 1; ERCC1, Excision Repair 1, Endonuclease Non-Catalytic Subunit; XRCC1, X-ray repair cross complementing protein 1; APOA1, Apolipoprotein A1; APOB1, Apolipoprotein B1; CETP, Cholesteryl ester transfer protein; HMGCR, 3-Hydroxy-3-Methylglutaryl-CoA Reductase; PON1, paraoxonase/arylesterase 1; VKORC, Vitamin K epoxide Reductase Complex; CES1 Carboxylic ester hydrolase; F II, coagulation factor II; PAI, Plasminogen Activator Inhibitor; F V, coagulation factor V; CBS, cystathionine beta-synthase; F XIII, coagulation factor XIII;

Colour legend

 Increased activity

 Decreased activity

 Absent activity