



Supplementary information

Protocol for a pilot trial to implement diagnostics for clonal hematopoiesis of indeterminate potential into routine clinical care of older patients with breast cancer

Nina Rosa Neuendorff, Ann-Kathrin Bittner, Sarah Flossdorf, Tessy Mauer, Florian Schmitz, Nils von Neuhoff, Johannes Köster, Felix Mölder, Markus Schneider, Amin T. Turki, Rainer Kimmig, Hans Christian Reinhardt, Oliver Hoffmann, Bastian von Tresckow

Table S1. Questionnaire on patient satisfaction and potential fears.

		<i>I totally agree</i>	<i>I agree</i>	<i>I neither agree nor disagree</i>	<i>I don't agree</i>	<i>I strongly disagree</i>
Questions on satisfaction with the study						
1)	I was happy to take part in the study.					
2)	It gives me a very good feeling personally, that I was able to contribute to the research about my illness.					
3)	I think that the participation in this study has an additional value on my health.					
4)	Dealing with my illness was an emotionally draining task.					
Questions on study organization, comprehension and quality of informed consent						
5)	The process and the explanation of the study was clear and comprehensible.					
6)	I basically understood why individual study parts were realized.					
7)	I was satisfied with the information about the CHIP-diagnostic.					
Questions on patient education						
8)*	The CHIP-Positivity was intelligibly explained to me.					
9)*	The information letter concerning CHIP helped me to have the most important information at hand again after the medical consultation.					
10)*	I think it's reasonable that my primary care physician received information about my CHIP-Positivity.					
Questions on potential fears						
11)*	The presence of CHIP worries me a lot.					
12)*	Knowing I'm CHIP-positive stresses me out.					
13)*	I wish I didn't know that I'm CHIP-positive.					

*Questions 8-13 are only provided to patients who are tested as CHIP positive.

Table S2. Genes included in targeted sequencing (myeloid panel).

ABL1	CSNK1A1	IDH2	PAX5	SF3B1
ANKRD26	CTCF	IKZF1	PDGFRA	SH2B3
ARID1A	CUX1	JAK1	PHF6	SMC1A
ASXL1	CXCR4	JAK2	PIGA	SMC3
ASXL2	DDX41	KAK3	PML	SOS1
ATM	DHX15	KDM6A	PPM1D	SRP72
ATRX	DNMT3A	KIT	PRPF40B	SRSF2
BCOR	EED	KMT2A	PTEN	STAG1
BCORL1	ELANE	KMT2D	RAD21	STAG2
BRAF	ETNK1	KRAS	RAF1	STAT3
BRCC3	ETV6	LUC7L2	RB1	STAT5B
CALR	EZH2	MECOM	RBBP6	SUZ12
CBL	FANCA	MET	RPS19	TERC
CBLB	FANCL	MPL	RTEL1	TERT
CBLC	FLT	MYC	RUNX1	TET2
CCND2	GATA1	NF1	SAMD9	THPO
CDKN2A	GATA2	NOTCH1	SAMD9L	TP53
CEBPA	GNAS	NOTCH2	SBDS	U2AF1
CHEK2	GNB1	NPM1	SETBP1	U2AF2
CREBBP	HNRNPK	NRAS	SETD2	WT1
CSF3R	HRAS	NSD1	SF1	ZBTBP7A
CSMD1	IDH1	NUP214	SF3A1	ZRSR2

Genes in bold are included as required in WHO classification of myeloid malignancies.

Table S3. Size of confidence intervals in relation to number of approached versus participating patients.

N \ P						
	50	100	150	200	250	300
0.5	0.289	0.203	0.165	0.143	0.127	0.116
0.6	0.284	0.199	0.162	0.14	0.125	0.114
0.7	0.267	0.187	0.152	0.131	0.117	0.107
0.8	0.237	0.165	0.134	0.115	0.103	0.094
0.9	0.185	0.127	0.103	0.088	0.078	0.071

N: number of approached patients; p: real participation rate.