

## Comparison chart **exaota** / **exaota Basic**

No.	Features	<b>exaota</b> Tissue and blood based	<b>exaota</b> Blood based	<b>exaota Basic</b> Tissue and blood based	<b>exaota Basic</b> Blood based
1)	Analysed genes	511 genes	411 genes	511 genes	411 genes
2)	Gene rearrangements / InDels	51 genes	12 genes	51 genes	12 genes
3)	Gene amplifications	354 genes	409 genes	354 genes	409 genes
4)	Chemoresistance profile of cytotoxic drugs	up to 70 substances	up to 70 substances	up to 70 substances	up to 70 substances
5)	mTOR, EGFR, VEGFR1, VEGFA, VEGFR2 expression analysis through ICC	✓	✓	✓	✓
6)	Gene expression: ca 20.800 genes	✓(tissue)	✓(exosomal)	✗	✗
7)	Tumour mutation burden (TMB)	✓(TMB)	✓(blood TMB)	✓(TMB)	✓(blood TMB)
8)	Microsatellite instability/ MMR gene analysis	✓(MSI/MMR)	Germline sequencing of MMR genes	✗	✗
9)	IHC analysis	✓	✗	✗	✗
	AR, PD-L1 28-8 and 22C3 IHC analysis (for all solid tumours)	✓	✗	✗	✗
	HER2 IHC analysis (breast, endometrium, esophagus, stomach, colon, gall bladder)	✓	✗	✗	✗
	ER, PR IHC analysis (breast, ovaries, endometrium)	✓	✗	✗	✗
10)	Number of circulating tumour cells	✓	✓	✓	✓
11)	Blood-based HMAF	✓	✓	✗	✓
12)	Pharmacogenetics	✓	✓	✗	✗
13)	Simultaneous analysis of tissue DNA and cellfree DNA	✓	✗	✗	✗
14)	Sectoral BRCA1/2 gene sequencing	✓	✗	✓	✗
15)	BRCA1/2 MLPA analysis (breast, ovaries, pancreas, prostate)	✓	✓	✗	✗
16)	Complementary substances	Based on RNA, optional chemosensitivity	Based on RNA, optional chemosensitivity	Optional	Optional

HMAF: Highest mutant allele frequency

MLPA: Multiplex ligation-dependent probe amplification