

# Additional file 1

## Identification and transfer of Spatial Transcriptomics signatures for cancer diagnosis

### Tables

Dataset	%Trimmed	%ncRNA	%Mapped	%De-multiplexed	%Annotated	#Genes	#Reads
1	30.59%	18.58%	67.6%	97.9%	92%	23933	2337984
2	38.16%	10.3%	69.2%	97.64%	94%	23523	2224597
3	35.49%	19.44%	69.58%	97.89%	94%	24497	2637623
4	34.48%	10.79%	75.15%	97.37%	97%	23647	2659015

**Table S1** : Mapping statistics of four breast cancer datasets.

	Protein coding	Non-coding	Non-annotated	Total
ENSEMBL genes	11,251	1,902	-	13,153
ST tag clusters	17,137	2,457	5,585	25,179

**Table S2**: ST tag clusters and associated genes for four ST datasets together.

	1	2	3-5	6-10	>10
Number of ST tag cluster per gene	9,369	2,497	1,129	125	33

**Table S3**: Number of ST tag clusters per gene for four ST datasets.

	non-malignant	DCIS	IDC
ST-TCs	16,895	23,823	23,211
Genes associated to ST-TCs	10,262	12,830	12,708
Expert annotated ST spots	68	66	60
Correctly classified ST spots	67 (98%)	64 (97%)	55 (92%)

**Table S4:** The characteristics of the unsupervised ST breast cancer signatures. ST-TCs with at least one count were considered.