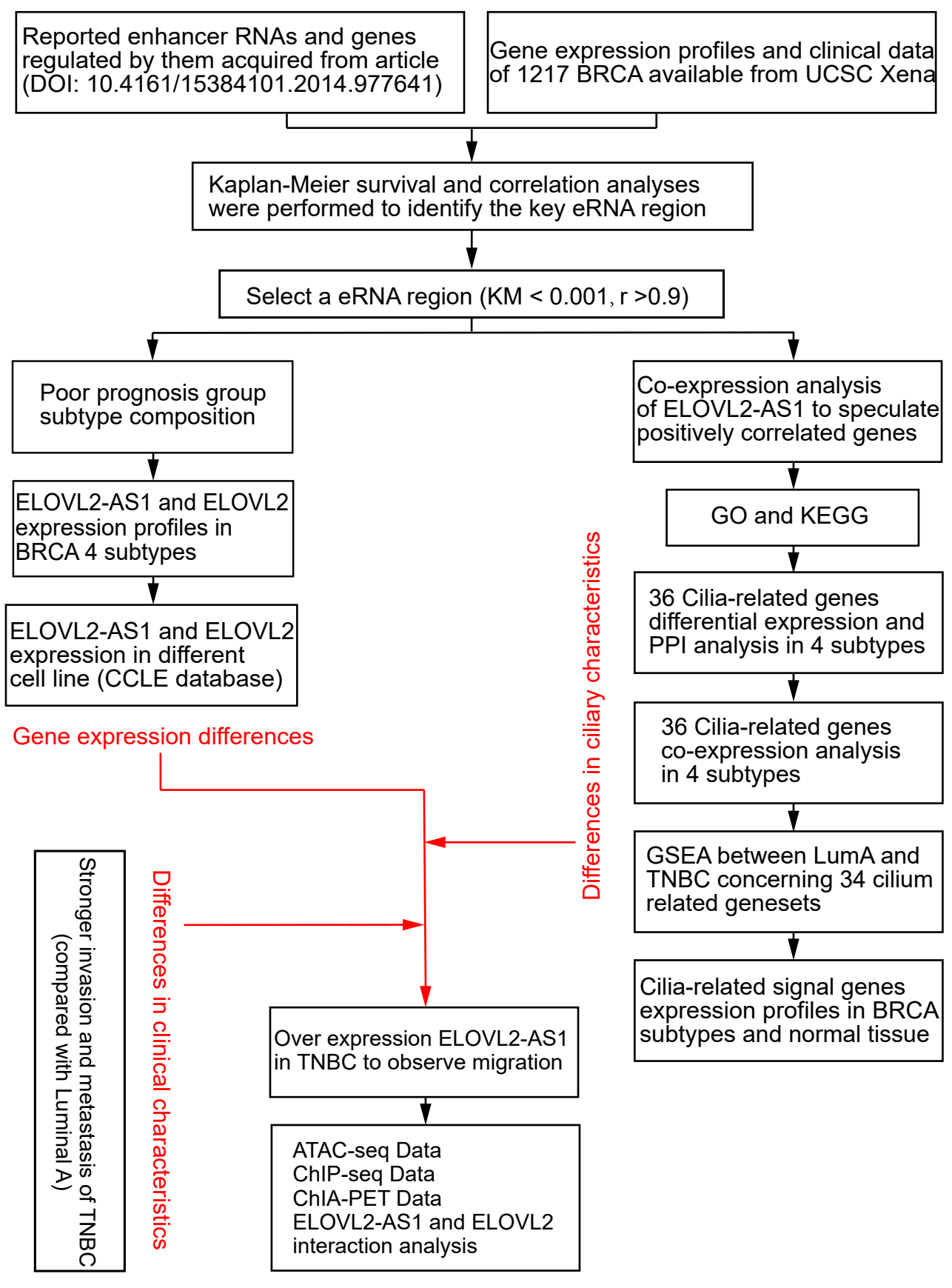
Reported enhancer RNAs and genes regulated by them acquired from article (DOI: 10.4161/15384101.2014.977641)
Gene expression profiles and clinical data of 1217 BRCA available from UCSC Xena
Kaplan-Meier survival and correlation analyses were performed to identify the key eRNA region
Select a eRNA region (KM < 0.001, r >0.9)
Poor prognosis group subtype composition
ELOVL2-AS1 and ELOVL2 expression profiles in BRCA 4 subtypes
ELOVL2-AS1 and ELOVL2 expression in different cell line (CCLE database)
Co-expression analysis of ELOVL2-AS1 to speculate positively correlated genes
GO and KEGG
36 Cilia-related genes differential expression and PPI analysis in 4 subtypes
36 Cilia-related genes co-expression analysis in 4 subtypes
GSEA between LumA and TNBC concerning 34 cilium related genesets
Cilia-related signal genes expression profiles in BRCA subtypes and normal tissue
Gene expression differences
Differences in ciliary characteristics
Differences in clinical characteristics
Stronger invasion and metastasis of TNBC (compared with Luminal A)
Over expression ELOVL2-AS1 in TNBC to observe migration
ATAC-seq Data
ChIP-seq Data
ChIA-PET Data
ELOVL2-AS1 and ELOVL2 interaction analysis