6. The method of claim 3, wherein determining (1) the proportion of alternatively spliced mRNA isoforms of the human genes relative to the total mRNA isoforms of the human genes in the sample or (2) the proportion of alternatively spliced gene expression products of the human genes relative to the total gene expression products in the sample comprises

determining the value of ψ_{sample} for each of the human genes, wherein ψ_{sample} = (i) total number of alternative exon inclusion mRNA isoform reads in the sample /((total number of alternative exon inclusion mRNA isoform reads in the sample) + (total number of alternative exon exclusion mRNA isoform reads in the sample)), or (ii) total number of alternative exon inclusion gene expression product reads in the sample/((total number of alternative exon inclusion gene expression product reads in the sample) + (total number of alternative exon exclusion gene expression product reads in the sample)), respectively,

wherein a level of $\Delta\psi$ = -0.1 or less for each of ENAH, SLC37A2, MBNL1 and FLNB, indicates that the tumor is not likely to metastasize or is not likely to have metastasized already,

and wherein a level of $\Delta\psi$ = +0.1 or more for each of MLPH and ARHGEF11 indicates that the tumor is likely to metastasize or is likely to have metastasized already,

wherein $\Delta\psi = \psi_{sample} - \psi_{control}$, and wherein $\psi_{control}$ = (i) total number of alternative exon inclusion mRNA isoform reads in a control /((total number of alternative exon inclusion mRNA isoform reads in the control) + (total number of alternative exon exclusion mRNA isoform reads in a control)), or (ii) total number of alternative exon inclusion gene expression product reads in a control /((total number of alternative exon inclusion gene expression product reads in the control) + (total number of alternative exon exclusion gene expression product reads in the control)), respectively.

7. The method of any of claims 1-6, wherein the sample is a breast cancer sample.

8. The method of ~~any of~~ claim~~s~~ 1~~-7~~, wherein the tumor is an invasive duct carcinoma.

9. The method of ~~any of~~ claim~~s~~ 1~~-8~~, wherein the sample is obtained by fine needle aspiration.

10. The method of ~~any of~~ claim~~s~~ 1~~-8~~, wherein the alternatively spliced mRNA isoforms or alternatively spliced gene expression products result from a skipped exon, a mutually exclusive exon, a retained intron, an alternative 5' splice site, an alternative 3' splice site, an alternative 3' UTR, an alternative first exon, and/ or an alternative last exon.

11. The method of ~~any of~~ claim~~s~~ 1~~-10~~, wherein quantitating the alternatively spliced mRNA isoforms is effected indirectly by isolating mRNA from the sample and subjecting it to a reverse transcriptase polymerase chain reaction so as to produce cDNAs corresponding to the alternatively spliced mRNA isoforms and then quantitating the cDNA corresponding to the alternatively spliced mRNA isoforms.

12. The method of ~~any of~~ claim~~s~~ 1~~-10~~, wherein quantitating the alternatively spliced gene expression products is effected indirectly by isolating alternatively spliced gene expression products corresponding to the alternatively spliced mRNA isoforms and then quantitating the alternatively spliced gene expression products corresponding to the alternatively spliced mRNA isoforms.

13. The method of claim 4, 5 or 6 wherein a level of $\Delta\psi$ = -0.2 or less for each of CD44, NUMB, FAM62B, SLK, ENAH, H2AFY and OSBPL8 (claim 4); CD44, NUMB, FAM62B, SLK, ENAH, H2AFY, OSBPL8, C17orf61 / PLSCR3, STARD10/ CENTD2, MAP3K7, BMP1, and BTG3 (claim 5); or ENAH, SLC37A2, MBNL1 and FLNB (claim 6), indicates that the tumor is not likely to metastasize or is not likely to have metastasized already,

and wherein a level of $\Delta\psi$ = +0.2 or more for each of SCRIB, CLSTN1, MLPH, TXNDC14 and CTNND1 (claim 4); YWHAB, ILF3, PAM, SCRIB, CLSTN1, MLPH, and TXNDC14 and/or CTNND1 (claim 5); or MLPH and ARHGEF11 (claim 6), indicates that the tumor is likely to metastasize or is likely to have metastasized already.

14. The method of claim 4, 5 or 6 wherein a level of $\Delta\psi$ = -0.3 or less for each of CD44, NUMB, FAM62B, SLK, ENAH, H2AFY and OSBPL8 (claim 4); CD44, NUMB, FAM62B, SLK, ENAH, H2AFY, OSBPL8, C17orf61 / PLSCR3, STARD10/ CENTD2, MAP3K7, BMP1, and BTG3 (claim 5); or ENAH, SLC37A2, MBNL1 and FLNB (claim 6), indicates that the tumor is not likely to metastasize or is not likely to have metastasized already,

and wherein a level of $\Delta\psi$ = +0.3 or more for each of SCRIB, CLSTN1, MLPH, TXNDC14 and CTNND1 (claim 4); YWHAB, ILF3, PAM, SCRIB, CLSTN1, MLPH, and TXNDC14 and/or CTNND1 (claim 5); or MLPH and ARHGEF11 (claim 6), indicates that the tumor is likely to metastasize or is likely to have metastasized already.

15. The method of ~~any one of~~ claim~~s~~ 1~~-14~~, wherein the control proportion corresponds to the alternatively spliced mRNA isoforms proportion in a non-malignant, non-tumor epithelial cell of the tissue type that the tumor is present in.

16. The method of ~~any one of~~ claim~~s~~ 1~~-14~~, wherein the control proportion corresponds to the alternatively spliced mRNA isoforms proportion in a benign fibroadenoma cell.

17. The method of ~~any one of~~ claim~~s~~ 1~~-16~~, wherein the tumor is in a subject.

18. The method of ~~any one of~~ claim~~s~~ 1~~-17~~, wherein the tumor is a primary tumor which has been excised from a subject and the method is for identifying if the tumor has likely metastasized.

19. The method of ~~any one of~~ claim~~s~~ 1~~-17~~, wherein the method is for identifying if the tumor will likely metastasize.

20. The method of claim 1~~-6 or 10-19~~, wherein the tumor is a pancreas, prostate, colon, brain, liver, lung, head or neck tumor, or a secretory epithelial tumor.

21. The method of ~~any of~~ claim~~s~~ 1~~-20~~ wherein the determining the levels of alternatively spliced mRNA isoforms is effected using an exon microarray.

22. A method for identifying a tumor as likely to metastasize via lymph nodes in a subject, or likely to have metastasized via lymph nodes in a subject, comprising ~~obtaining~~ providing a sample of the tumor and determining if an alternatively spliced skipped exon mRNA isoform for SLC37A2 gene is present in the sample, wherein the absence of an alternatively spliced skipped exon mRNA isoform for SLC37A2 gene present in the sample, or a reduced level of an alternatively spliced skipped exon mRNA isoform for SLC37A2 gene present in the sample as compared to a non-metastatic control sample, indicates that the tumor is likely to metastasize via lymph nodes in the subject, or has likely metastasized via lymph nodes in the subject.

23. The method of claim 22, wherein the presence of the alternatively spliced skipped exon mRNA isoform for SLC37A2 gene is determined by performing a quantitative reverse transcriptase polymerase chain reaction ("qRT-PCR") on the sample with a primer pair targeting the skipped exon and a primer pair targeting an independent constitutive exon of SLC37A2, wherein a ratio of the quantity of the cDNAs comprising sequences corresponding to the primer pair targeting the skipped exon to the quantity of the cDNAs comprising sequences corresponding to the primer pair targeting the independent constitutive exon of SLC37A2 of 0.5 or less indicates that the tumor is likely to metastasize via lymph nodes in the subject, or has likely metastasized via lymph nodes in the subject.

24. A method for identifying an agent for inhibiting metastasis of a cancer comprising: a) ~~obtaining~~ providing a sample of the cancer; b) quantitating alternatively spliced mRNA isoforms of a cell motility gene, a cell adhesion gene and /or an actin cytoskeletal remodeling gene in the cancer or of any of the genes exhibiting positive M-E.deltaPsi values in inc/excBound column of Table 5; c) contacting the sample with the agent; and d) quantitating the alternatively spliced mRNA isoforms of the cell motility gene, cell adhesion gene and /or actin cytoskeletal remodeling gene in the sample, or of any of the genes exhibiting positive M-E.deltaPsi values in inc/excBound column of Table 5,

wherein a reduction in the amount of alternatively spliced mRNA isoforms of the cell motility gene, cell adhesion gene and /or the actin cytoskeletal remodeling gene or of any of the genes exhibiting positive M-E.deltaPsi values in inc/excBound column of Table 5 in the presence of the agent indicates that the agent inhibits metastasis of a cancer.

25. The method of claim 24, wherein the genes are chosen from ENAH, SLC37A2, MBNL1, FLNB, MLPH, and ARHGEF11.

26. The method of claim 24 or 25, wherein at least one of the alternatively spliced mRNA isoforms encodes a hinge region (HI) located between stretches of filamin repeats.

27. The method of claim 24~~, 25 or 26~~, wherein at least one of the alternatively spliced mRNA isoforms encodes an extracellular domain of a transmembrane protein.

28. The method of ~~any of~~ claim~~s~~ 24~~-27~~, wherein quantitating the alternatively spliced mRNA isoforms is effected indirectly by isolating mRNA from the sample and subjecting it to a reverse transcriptase polymerase chain reaction so as to produce cDNAs corresponding to the alternatively spliced mRNA isoforms and then quantitating the cDNA corresponding to the alternatively spliced mRNA isoforms.

29. The method of ~~any of~~ claim~~s~~ 24~~-27~~, wherein quantitating the alternatively spliced mRNA isoforms is effected indirectly by isolating protein isoforms corresponding to the alternatively spliced mRNA isoforms and then quantitating the protein isoforms corresponding to the alternatively spliced mRNA isoforms.

30. A method for identifying an agent for inhibiting metastasis of a cancer comprising: a) ~~obtaining~~ providing a sample of the cancer; b) quantitating, in the absence of the agent, the level of one or more of the RNA binding proteins listed in the specification; c) contacting the sample with the agent; and d) quantitating RNA binding proteins levels for one or more RNA binding proteins listed in the specification in the sample in the presence of the agent,

wherein a fold change of at least 1.5x either up or down in the sample in the presence of the agent as compared to a predetermined control RNA binding protein level indicates that the agent inhibits metastasis of a cancer.

31. The method of claim 30, wherein the predetermined control RNA binding proteins levels are determined from non-malignant epithelial cells.

32. The method of claim 30 or 31, wherein the RNA binding proteins are chosen from the group consisting of MBNL1, RBM9, PTBP1, PTBP2, HNRNPF, HNRNPH, ESRP1, ESRP2, RBM47.

33. The method of ~~any of~~ claim~~s~~ 24~~-32~~, wherein the method is carried out in vitro.

~~34. A method of inhibiting metastasis of a tumor in a subject comprising administering to the subject an amount of an agent which (i) inactivates or reduces expression of one or more genes having a negative M-E.deltaPsi value in M-E.deltaPsi Column of Table 5 or (ii) inactivates or reduces activity of an alternatively spliced exon gene expression product of one or more genes having a negative M-E.deltaPsi Column of Table 5.~~

~~35. A method of inhibiting metastasis of a tumor in a subject comprising administering to the subject an amount of an agent which (i) activates or increases expression of one or more genes having a positive M-E.deltaPsi Column of Table 5 or (ii) activates or increases activity of an alternatively spliced exon gene expression product of one or more genes having a positive M-E.deltaPsi Column of Table 5.~~

~~36. The method of any of claims 24-35 wherein the agent is a monoclonal antibody.~~

~~37. The method of any of claims 24-35 wherein the agent is small organic molecule having a mass of 1200 daltons or less.~~

~~38. The method of any of claims 24-35 wherein the agent is an siRNA.~~

~~39. The method of any of claims 24-35 wherein the agent is an shRNA.~~

~~40~~34. A method of determining a treatment type for a patient having a tumor comprising determining in a sample of the tumor the proportion of (1) alternatively spliced mRNA isoforms of one or more genes having a positive M-E.deltaPsi Column of Table 5 relative to the total mRNA isoforms of the one or more genes having a positive M-E.deltaPsi value in M-E.deltaPsi Column of Table 5 in the sample or (2) the proportion of alternatively spliced gene expression products of one or more genes having a positive M-E.deltaPsi Column of Table 5 relative to the total gene expression products of the one or more genes having a positive M-E.deltaPsi Column of Table 5 in the sample,

wherein determination of a proportion of (1) alternatively spliced mRNA isoforms, or (2) alternatively spliced gene expression products, respectively, for the one or more genes which is equal to, or greater than, that of a control proportion indicates that the patient should be treated with one or more chemotherapeutic anti-tumor agents,

and wherein determination of a proportion of alternatively spliced mRNA isoforms, or alternatively spliced gene expression products, respectively, for the one or more genes less than that of a control proportion indicates that the patient should be treated with one or more non-chemotherapeutic anti-tumor agents.

~~41~~35. The method of claim ~~40~~ 34, wherein the control proportion is 0.1.

~~42~~36. The method of claim ~~40~~ 34, wherein the control proportion is 0.2.

~~43~~37. The method of claim ~~40~~ 34, wherein the control proportion is 0.3.

~~44~~38. The method of claim ~~40~~ 34, wherein the control proportion is determined from a tumor sample from one or more subjects susceptible to chemotherapy.

~~45~~39. A product comprising an exon microarray which comprises a plurality of oligonucleotides having sequences corresponding to the sequences of the exons of the genes recited in claims 1, 2 or 3.

~~46~~40. A product comprising an exon microarray which comprises a plurality of oligonucleotides having sequences corresponding to the sequences of exon:exon junctions found in the wildtype of the of the genes recited in claims 1, 2 or 3.

~~47~~41. The product of claim ~~45 or 46~~ 39, further comprising one or more cDNA probes derived from a tumor being tested for likelihood of metastases.

~~48~~42. The product of claim ~~46 or 47~~ 40, wherein the plurality of oligonucleotides having sequences corresponding to the sequences of exon:exon junctions found in the wildtype of the of the genes recited in claims 1 , 2 or 3 comprises oligonucleotides having sequences corresponding to the sequences of every exon:exon junction found in the wildtype of the of the genes recited in claims 1, 2 and/or 3.

~~49~~43. The product of claim ~~45, 46 or 47~~ 39, wherein the plurality of oligonucleotides further comprises probes corresponding to skipped exon splice variant(s), mutually exclusive exon splice variant(s), alternative first exon splice variant(s), alternative last exon splice variant(s), retained intron splice variant(s), alternative to 5' splice site splice variant(s), alternative to 3' splice site splice variant(s) and/or tandem 3' UTR splice variants of the genes recited in claims 1, 2 and/or 3-.