### Supplementary Table 9. Primers and probes used for validation

#### A. Primers for making isoform specific probes.

| Probes   | Forward primer       | Reverse primer                     | Probe size |
|----------|----------------------|------------------------------------|------------|
| Cd44 Ect | GGCTGATATAGACAGAATC  | AGCACCAGTGCTCATGGAG                | ~700 nts   |
|          | AGCACCAGTGCTCATGGAG  | CGTTGGAGTCAGTAGCAAGA               |            |
|          |                      | GTCACCTCAGTTTCTCC                 |            |
| Cd44 TOT | GTACCGGTCCATCTTCCAT  | CTTGACCCGTTGTGC                   | ~730 nts   |
|          | CTTGACCCGTTGTGC      | GGAAGATCCAGGAGCAATG               |            |
|          |                      | GGACATCCTGGCAGATG                 |            |

#### B. Basescope probes were custom ordered from Advanced Cell Diagnostics for detecting skipping or inclusion of small exons. The catalog number (Cat No.) and the type of differential exon usage for the Basescope probes are as follows.

| Gene | Probe name                                      | Cat No. | Detecting isoforms |
|------|-------------------------------------------------|---------|--------------------|
| Flnb | BaseScope™ Probe- BA-Mm-Flnb-tvX1-E29E30        | 709401  | Skipping           |
|      | BaseScope™ Probe- BA-Mm-Flnb-tv2-E30E31         | 709391  | Inclusion          |
| Enah | BaseScope™ Probe- BA-Mm-Enah-tv1-E12E13         | 709371  | Skipping           |
|      | BaseScope™ Probe- BA-Mm-Enah-tvX2-E13E14        | 709361  | Inclusion          |
| Slk  | BaseScope™ Probe- BA-Mm-Slk-tv2-E12E13          | 709431  | Skipping           |
|      | BaseScope™ Probe- BA-Mm-Slk-tv1-E13E14          | 709421  | Inclusion          |

#### C. Primers for RT-PCR validation:

| Gene | Forward primer       | Reverse primer                     | PCR product sizes |
|------|----------------------|------------------------------------|-------------------|
| Lef1 | AGCTCCTGAAATCCC      | TGGATGAGGGATG                      | 126 bp, 217 bp    |
|      | CACCTTCTAC           | CCAGTTGTGTGG                       |                   |
| Evi5 | AATCCAGTCAGCTTA      | GGCTTCACCTCATG                     | 242 bp, 278bp, 426 |
|      | CCAAGTCC            | CTGGCTT                            |                   |
| Gene   | Stranded Targets | Forward Side | Reverse Side | Lengths |
|--------|------------------|--------------|--------------|---------|
| Lrrfip2 | ACAACGCCTCTAAGT  | CTGCACATGTGTTT | CTGCCT      | 290 bp, 362 bp |
|        |                  |              |              |         |
| Numa1  | CAAGTACGAAGGTGC  | CTTGTAATGCTCAG | CTGCCT    | 262 bp, 304 bp |
|        |                  |              |              |         |
| Ocr1   | TCGAGAAGGCTCTG   | TCTGCTGTAACCTT | TCCTGC | 177 bp, 221 bp |
|        |                  |              |              |         |
| Map2   | CTGCCGGACCTGAAG  | GGTACGTGGTGAG | CATTGTC | 262 bp, 344 bp |
|        |                  |              |              |         |
| Phactr4* | GCAGTGATAAGTTCA | GCTCCAGGTTGAG | CCAAGTC | 203 bp, 278bp*, 284 bp |
| Plod2  | TGGGTACTATGCTCG  | GCAGTTGATATCA | GCCGTCC | 252 bp, 315 bp |
|        |                  |              |              |         |
| Gpr137 | AAGCGTCGGGCAGA   | GCTGCCAGGTTGT | AACAGGC | 111 bp, 337 bp |
|        |                  |              |              |         |
| Myo1b  | GAAGCATCAGAAGGCG | ACAGCAACTGCAT | GCTTACG | 123 bp, 210 bp |
|        |                  |              |              |         |
| Slain2 | ATACCTCAGATGCAG  | GTGAGGAGGTGTA | TTGTGTGA | 169 bp, 247 bp |
|        |                  |              |              |         |
| Sorbs1 | CAGCTGATTACTGGAG | TGTAGATGTAACAA | ACGTCTCC | 157 bp, 315 bp |
|        |                  |              |              |         |
| Mta1   | GCAGCAATGGGGT    | GTCGATCCAGTTC | ATTCGCC | 163 bp, 199 bp |
|        | AGATG            |              |              |         |
|        |                  |              |              |         |
| Scarb1 | CTGATGCCAGGTTCTCA | GGCTTATAGGTGTCT | TCAGGAC | 118 bp, 247 bp |
|        |                  |              |              |         |
| Postn  | TTTGTGCTGGGCAGC  | CTCCGTGGATCAC | TTCTGTCA | 136 bp, 217 bp |
| exon 17| ACCTCC           |              |              |         |
|        |                  |              |              |         |
| Postn  | ACAGGAGGTGGAGA   | GTCAGTGGTGTTG | CTCTTACA | 215 bp, 299 bp |
| exon 21| AACAGGG          |              |              |         |
|        |                  |              |              |         |
| Syne2  | TCATGAAGACGACGA  | CTCAGTCTGGTCA | CTTCCA | 139 bp, 208 bp |
|        | GGAGG            |              |              |         |
|        |                  |              |              |         |
| Exoc1  | TGAAGATGACTGGCA  | TGGTTCCCCATGTC | CAGTACG | 156 bp, 201 bp |
|        | CCTCT            |              |              |         |
Phactr4 primers detect an extra PCR product, size of 278 bp, from A3SS beside the two predicted PCR products resulted from SE (203 bp and 284 bp).