Appendix for "Haploinsufficient phenotypes promote selection of PTEN and ARID1A-deficient clones in human colon"

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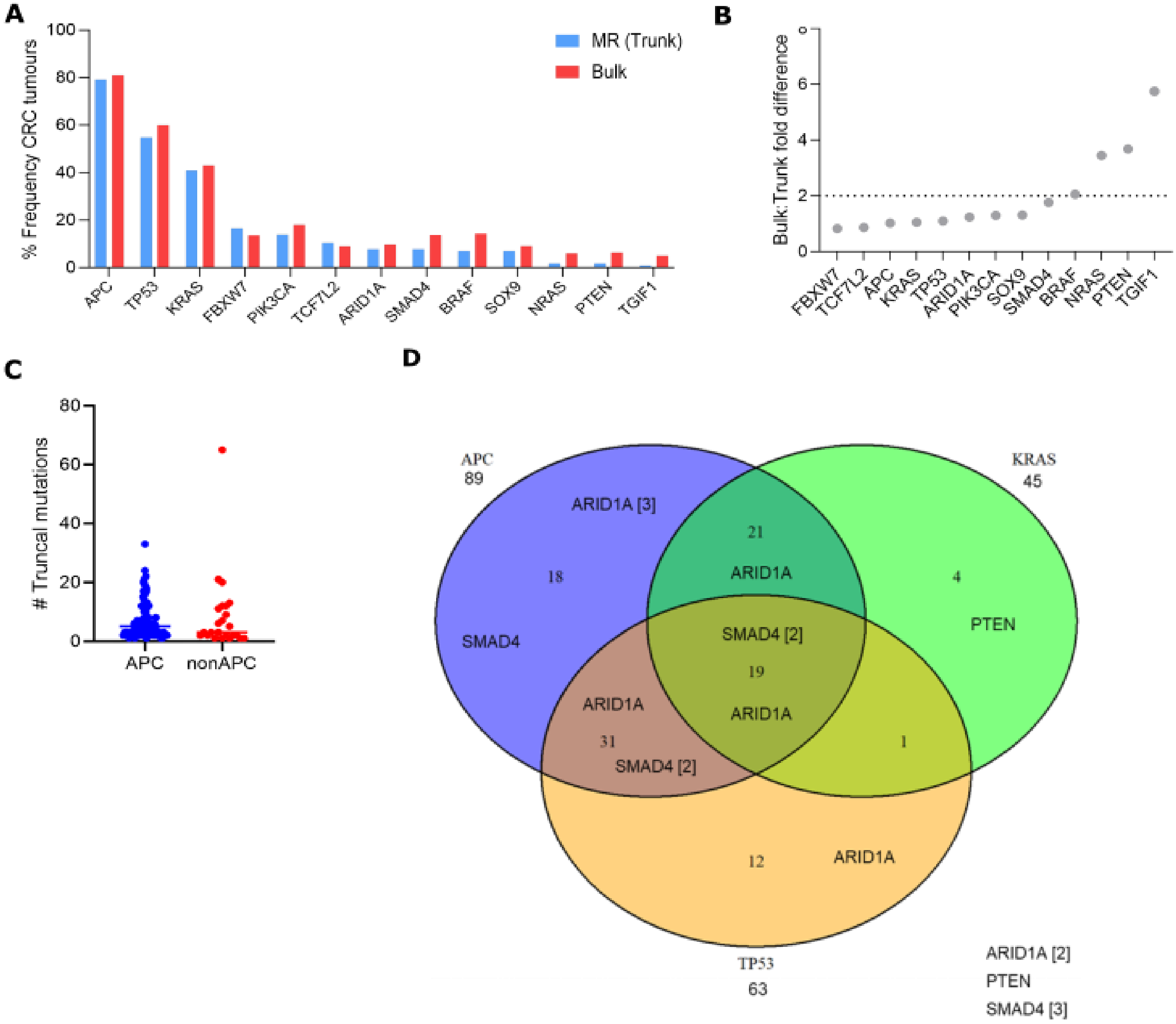
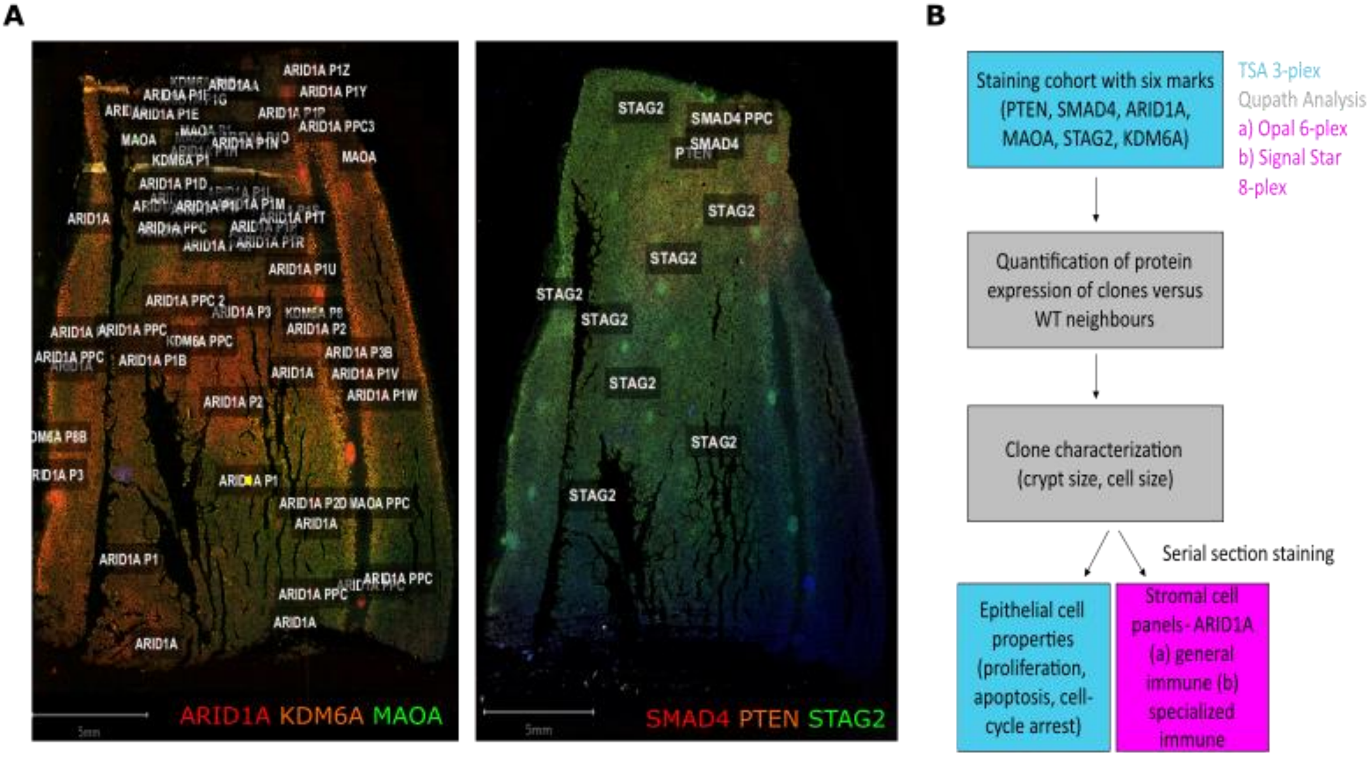
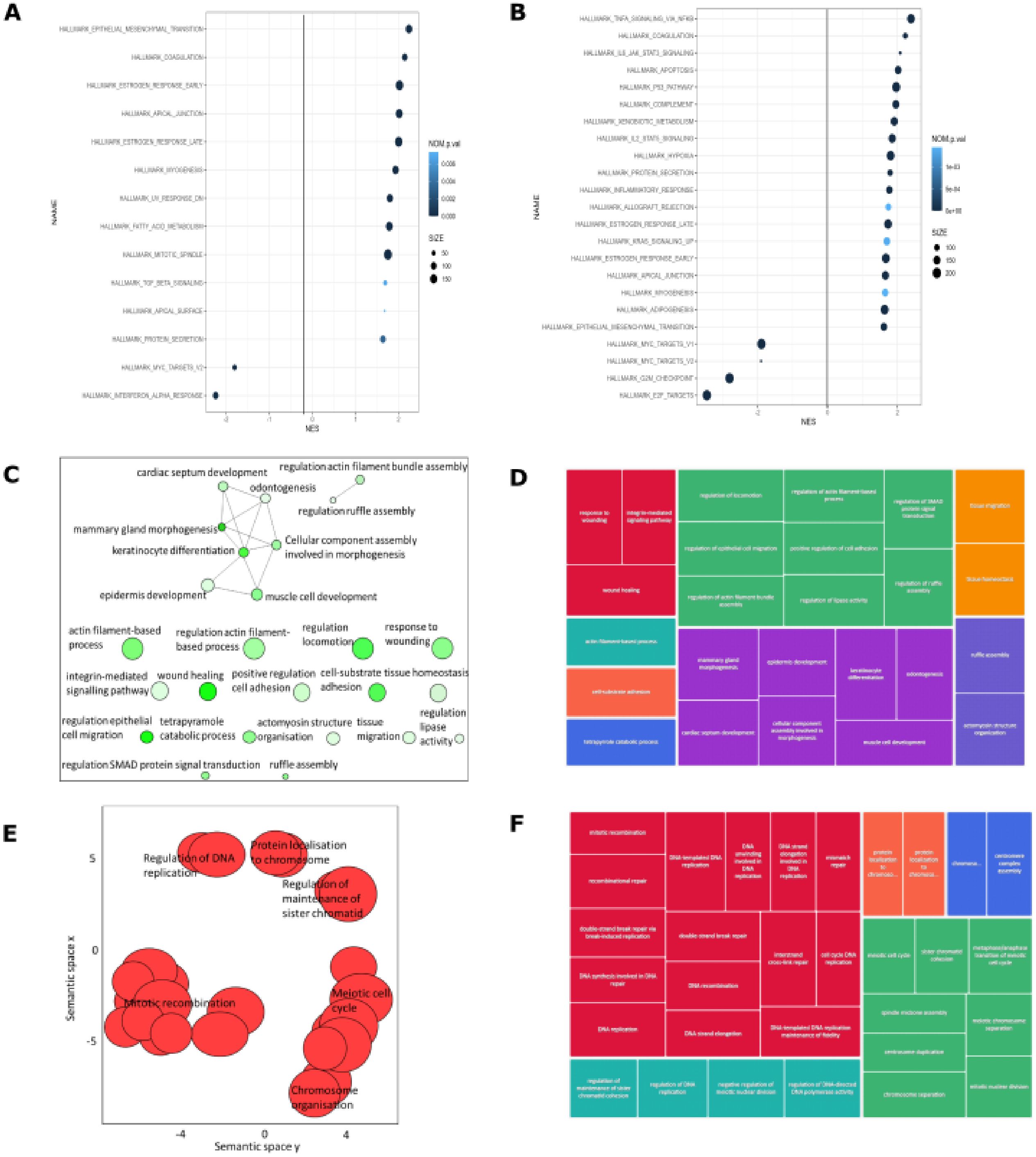


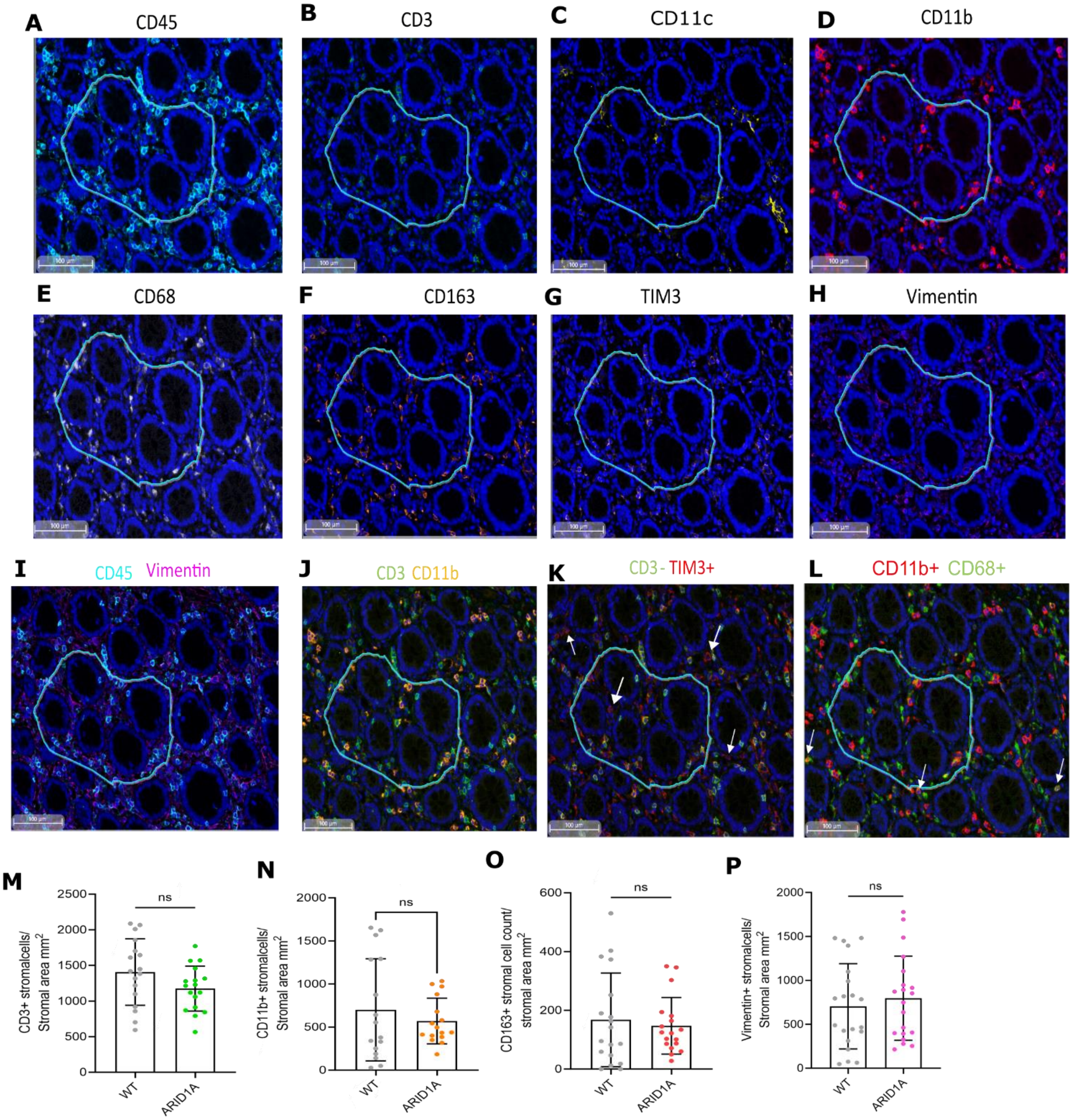
Appendix Figure S1: Metanalysis of truncal mutations identified using multi-regional sampling approaches. (A) Comparison of mutation frequency from the trunk of phylogenetic trees created from multi-regional studies or bulk sequencing (TCGA data). Includes genes with dN/dS >1 (q <0.001 Martincorena et al., 2017 CRC). (B) Fold difference in bulk versus trunk mutation frequency. 1:1 ratio would suggest early events and larger deviance from that would suggest higher frequency as a subclonal event. (C) Number of truncal mutations in APC or non-APC driven tumours. Considers mutations in all detected genes. (D) Venn diagram of relationship between APC, TP53 and KRAS driven tumours. PTEN, SMAD4 and ARID1A mutations annotated. Multiregional studies, N=115 tumours.



Appendix Figure S2: Use of sections for multiplexing immunofluorescence. (A) Whole slide imaging and annotation of clones. Stained as two 3-plex panels over two serial sections. (B) Layout of use of sections for selected patient cohort and application of multiplexing panels.



Appendix Figure S3: Gene set enrichment analysis (GSEA) for PTEN het and ARID1A het human colonic organoids vs WT. Considering gene sets FDR q-value < 1%. (A, C, D) PTEN het vs WT. (B, E, F) ARID1A het vs WT. (A-B) GSEA for hallmark pathways. (C) Interaction graph of positively enriched Gene Ontology Biological Processes (GOBP) generated in Revigo. Size of dot indicates logsizeof dataset and darker colour indicates higher enrichment score. (D, F) Tree map generated in Revigo. Cluster representatives (remaining terms after redudancy removal) are joined in high level groups. (E) Scatterplot showing cluster representatives in a two dimensional space derived by applying multidimensional scaling to a matrix of the GOBP term semantic similarities. Negatively enriched GOBP gene sets.



Appendix Figure S4: Signal star specialised stromal cell panel to profile cell populations within and around ARID1A patches. (A-H) Individual markers around an ARID1A patch shown in blue. Arranged in order of staining. (I) Separation of immune cells (CD45+) and mesenchymal cells (Vimentin+). (J) Separation of lymphocytic T-cells (CD3+) and myeloid cells (CD11b+). (K) TIM3+ is a marker of both T-cells and macrophages. TIM3+ cells that are CD3- are indicated by the arrows. (L) CD68+ cells are a sub cluster of CD11b+ cells (indicated by the arrows). (M-P) Quantification of stromal cells in WT ad ARID1A deficient patches. Showing non-significantly different stromal populations. (M) CD3+ cells. N= 17 ARID1A and WT clones. (N) CD11b+ cells. N= 16 ARID1A and WT clones. (O) CD163+ cells. N= 18 ARID1A and WT clones. (P) Vimentin+ cells. N= 20 ARUD1A and WT clones. Data information: Data presented as mean ± SD. Scale bars indicate 100 µm. Paired Wilcoxon test was performed to assess statistical significance. (M) p =0.0638, (N) p = 0.495, (O) p = 0.766, (P) p = 0.648.

Appendix Table S1: Patient ages and gender.

Tissue Bank ID	*Age*	*Sex*
TB18.2900	*77*	*M*
TB18.3648	*72*	*M*
TB18.2315	*61*	*F*
TB18.3985	*81*	*M*
TB18.3753	*56*	*M*
TB18.3919	*70*	*M*
TB18.4180	*75*	*F*
TB18.3127	*71*	*F*
TB18.2870	*57*	*M*
TB18.3062	*71*	*M*
TB18.2959	*65*	*M*
TB18.2766	*84*	*M*
TB18.1979	*83*	*M*
TB18.1314	*59*	*F*
TB18.1270	*89*	*M*
TB18.2984	*79*	*M*
TB18.3071	*74*	*F*
TB18.4183	*76*	*F*
TB18.4560	*87*	*M*
TB15.4012	*78*	*F*
TB16.0049	*85*	*M*
TB16.0126	*72*	*F*
TB18.0210	*80*	*M*
TB18.1020	*79*	*F*
TB18.0068	*85*	*M*
TB17.2797	*70*	*F*
TB16.2117	*72*	*F*
TB17.1198	*30*	*M*
TB17.1215	*36*	*M*
TB16.0622	*37*	*M*
TB16.1540	*82*	*M*
TB16.0121	*72*	*F*
TB18.2520	*71*	*M*
TB18.2156	*79*	*F*
TB18.1962	*38*	*F*
TB18.0219	*48*	*F*
TB18.0459	*48*	*F*
TB18.1997	*52*	*M*
TB16.0623	*70*	*M*
TB18.3910	*67*	*F*
TB18.4571	*60*	*F*
TB13.0420	*78*	*M*
TB12.2355	*77*	*F*
TB12.1904	*79*	*F*
TB12.1256	*81*	*M*
TB12.0017	*64*	*M*

TB11.1545	*79*	*M*
TB18.4245	*84*	*M*
TB19.1770	*57*	*M*
TB19.02072	*62*	*M*
TB19.02084	*62*	*F*
TB19.02261	*69*	*M*
TB19.02388	*79*	*F*
TB19.1496	*41*	*F*
TB19.1497	*62*	*F*
TB19.1589	*80*	*F*
TB19.1166	*68*	*F*
TB19.1674	*61*	*F*
TB19.1682	*57*	*F*
TB18.4761	*70*	*M*
TB18.5023	*62*	*F*
TB18.3673	*75*	*F*
TB18.4562	*59*	*F*
TB18.5947	*79*	*M*
TB18.5484	*78*	*M*
TB18.4864	*74*	*M*
TB18.5487	*42*	*M*
TB18.5262	*33*	*M*
TB18.4167	*76*	*F*
TB18.4844	*86*	*F*
TB18.4797	*87*	*M*
TB18.5068	*65*	*F*
TB19.0995	*39*	*F*
TB19.0996	*78*	*M*
TB18.3920	*58*	*F*
TB19.0997	*38*	*M*
TB19.0994	*62*	*M*
TB18.4121	*47*	*F*
TB19.1748	*62*	*M*
TB19.1721	*50*	*F*
DW20.1126	*74*	*F*
DW20.1122	*43*	*M*
DW20.1121	*83*	*F*
DW20.1130	*78*	*M*
DW21.1238	*49*	*F*
DW20.0901	*62*	*M*
DW20.1234	*67*	*F*
DW20.1235	*72*	*F*
DW20.1231	*54*	*F*
DW20.1125	*56*	*F*
TB20.01933	*40*	*F*
TB20.01912	*71*	*F*
DW20.0905	*87*	*F*
DW20.0904	*61*	*F*
TB17.1858	*83*	*M*
DW20.0907	*71*	*F*
TB17.2518	*40*	*M*

DW20.1129	*81*	*F*
TB20.01932	*72*	*F*
TB21.00044	*89*	*M*
TB20.01965	*59*	*F*
TB18.2700	*39*	*F*
TB17.1172	*46*	*F*
TB17.1274	*64*	*M*
TB17.1446	*80*	*F*
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TB17.2171	*48*	*F*
TB18.0493	*34*	*M*
TB18.1667	*63*	*M*
318_85	*56*	*F*
1130_85	*58*	*F*
TB16.0229	*48*	*M*
TB16.1164	*77*	*F*
TB17.1469	*75*	*F*
TB17.1465	*72*	*M*
TB17.1476	*84*	*F*
TB17.1512	*65*	*M*
TB17.2235	*82*	*F*
TB18.0650	*80*	*M*
TB15.1120	*55*	*F*
983_85	*66*	*F*
TB17.1522	*69*	*M*
TB18.0626	*72*	*M*
TB15.3375	*85*	*F*
TB18.0630	*35*	*M*
TB16.0052	*69*	*M*
TB17.2294	*80*	*M*
TB15.0995	*70*	*F*
TB16.0273	*56*	*F*
TB16.1125	*74*	*F*
TB17.2190	*78*	*F*
TB18.0342	*72*	*M*
TB15.1196	*64*	*F*
472_85	*84*	*F*
1092_85	*82*	*M*
5900_85	*65*	*F/M*
TB15.4025	*89*	*M*
TB17.1490	*76*	*F*
TB18.5138	*72*	*F*
TB18.5543	*65*	*F*
TB18.5801	*79*	*M*
19B_R_032	*64*	*M*
TB18.5961	*64*	*M*
TB18.5880	*81*	*M*
TB18.5823	*66*	*M*
TB19.0223	*81*	*M*
TB18.5704	*57*	*F*
TB19.1108	*75*	*M*

TB19.1064	*75*	*M*
TB21.00351	*76*	*M*
TB21.00227	*68*	*M*
TB21.00228	*71*	*M*
TB21.00340	*72*	*F*
TB21.00343	*71*	*M*
TB21.00342	*83*	*M*
TB21.00201	*66*	*F*
TB21.00180	*75*	*F*
TB21.00398	*74*	*M*
TB18.2657	*75*	*M*
TB16.0059	*49*	*F*
10464_85	*68*	*F*
TB16.0624	*68*	*F*
TB16.0382	*83*	*F*
TB16.0431	*83*	*F*
TB16.1083	*74*	*M*
TB16.2167	*68*	*F*
TB16.0136	*77*	*F*
TB17.1245	*77*	*M*
TB17.1508	*71*	*M*
TB17.1538	*82*	*M*
TB17.1879	*57*	*M*
TB17.2722	*61*	*M*
TB17.1862	*61*	*F*
TB11.1767	*91*	*F*
TB17.2426	*80*	*M*
TB18.1283	*79*	*F*
TB17.1524	*64*	*M*
TB17.1292	*67*	*F*
13S 09820 AB	*60*	*M*
13S 08692 B	*42*	*M*
TB15.4011	*80*	*F*

Appendix Table S2: Multiplex IF panels.

Panel name	**Targets order**	**Fluorophore order**	**Multiplexing method**
Clonal Marks-1	SMAD4 PTEN STAG2	Cy5, Cy3, 488	Standard TSA
Clonal Marls-2	ARID1A KDM6A MAOA	Cy5, Cy3, 488	Standard TSA
Epithelial clonal properties lineage	MUC2 MCM2 ChgA	Cy5, Cy3, 488	Standard TSA
Epithelial clonal properties cell cycle	ANLN CA2+pH3	Cy5, Cy3 + 488	Standard TSA
General Immune cells	CD8 NE CD4 CD20 CD68 Ecadherin	480, 520, 570, 620, 690, 780	Opal TSA
Specialized Immune cells	Round 1: CD45 CD3 CD11c CD11b Round 2: CD68 CD168 TIM3 Vimentin	488, 594, 647, 750	Signal Star

Appendix Table S3: Fluidigm Primers for PTEN exon coverage used for Juno chip and pooling strategy. Lower case letters indicate intron binding.

Amplicon	Sequence F' primer	Sequence R' primer	Product Size	Multiplex Group
TXA0022214	TTTTCTTTCTCTAGGTGAAGCTGT	TTCATGGTGTTTTATCCCTCTTGA	235	MP1
TXA0429431	CCACAGTTGCACAATATCCTTTT	AAAAATTTGCCCCGATGTAATAA	190	MP1
TXA0343717	TCTGTCTTTTGGTTTTTCTTGAT	GTTGTTTTAGAAGATATTTGCAAGC	190	MP1
TXA0394520	TATTGCCCCTTAAGACCTTCCAG	ACAAAAACATATTACACAGCTACACA	219	MP1
TXA0001811	AACATAGGTGACAGATTTTCTTTT	GCTCTATACTGCAAATGCTATCG	217	MP1
TXA0052316	GACCCGGGCCGGTTTTA	GCCGCTTGGCTCTGGAC	229	MP1
TXA0342048	GTCAGAGGCGCTATGTGTATTATT	TCCTGCATAAATTTCAAATGTGGTAA	240	MP1
TXA0018633	TCACTGTAAAGCTGGAAAGGGAC	TCAGATCCAGGAAGAGGAAAGGA	172	MP2
TXA0429393	GCTGCAACCATCCAGCAG	CTGTGGCTGAAGAAAAAGGAG	177	MP2
TXA0001785	AGCTCATTTTTGTTAATGGTGGCTT	ACTCTACCTCACTCTAACAAGCAGA	184	MP2
TXA0429400	GCTACCTGTTAAAGAATCATCTGG	ACTTCTAGATATGGTTAAGAAAACTG	163	MP2
TXA0342046	TCCAAACATTATTGCTATGGGATTTC	TCACAAAGTATCTTTTTCTGTGGCTT	180	MP2
TXA0429383	CCAATTCAGGACCCACACGA	AAACACCTGCAGATCTAATAGAAAAC	240	MP2
TXA0429384	TCAAGATTGCAGATACAGAATCCA	ATGAACTTGTCTTCCCGTCGT	211	MP3
TXA0005243	GTGTCACATTATAAAGATTCAGGCAA	ACAGTAAGATACAGTCTATCGGGTT	210	MP3
TXA0116015	CAAATCCAGAGGCTAGCAGT	AAAGGTCCATTTTCAGTTTATTCA	216	MP3
TXA0032268	GGACCAGAGGAAACCTCAGAAAA	ACACACATCACATACATACAAGTCA	240	MP3
TXA0346890	GAACGCCGGAGAGTTGG	CGGAATGGGGAGAAGACG	189	MP3
TXA0342045	AGGAGAAGCAGGCCCAGTC	CGATCTCTTTGATGATGGCTGTC	231	MP4
TXA0018629	TCTGTCCACCAGGGAGTAACTAT	TGGAAGGATGAGAATTTCAAGCACT	182	MP4
TXA0429386	AGTAGAGTTCTTCCACAAACAGAAC	TCACCAATGCCAGAGTAAGCAAA	179	MP4
TXA0149228	GATATTCTGACACCACTGACTCT	CAAGATTGGTCAGGAAAAGAGAA	222	MP4
TXA0061549	AGCGTGCAGATAATGACAAGGAA	GCTGTACTCCTAGAATTAAACACACA	183	MP4
TXA0343718	TCTTCCTAAGTGCAAAAGATAAC	TCGATAATCTGGATGACTCATTATT	189	MP4
TXA0429390	AGGGAGGGGGTCTGAGT	GAGAAGACGAATAATCCTCCGAA	222	MP5
TXA0030487	TGACCACCTTTTATTACTCCAGCTA	AGCATTCTTACCTTACTACATCATCA	228	MP5
TXA0115976	TGAGGTTATCTTTTTACCACAGTTGC	TGCACATATCATTACACCAGTTCGT	180	MP5
TXA0429387	AAAGATCATGTTTGTTACAGTGCTT	TGAACTGCTAGCCTCTGGATTTG	202	MP5
TXA0001787	ATGGCTACGACCCAGTTACCATA	TTCCGCCACTGAACATTGGAATA	230	MP5
TXA0429391	CAGCCGTTCGGAGGATTATT	ACTTGGCGGTAGCTGATG	182	MP6
TXA0429399	TGTTCTTAAATGGCTACGACCCAG	TCCAGATGATTCTTTAACAGGTAGC	171	MP6
TXA0429432	TGCAACATTTCTAAAGTTACCTACT	CGTCCCTTTCCAGCTTTACA	220	MP6
TXA0001779	TCTTTTAGTTTGATTGCTGCATATTT	TTTCTAAATGAAAACACAACATGAAT	211	MP6
TXA0343730	GATAGTTTATTTTGTTGACTTTTTGC	TCACATAGACTTCCATTTTCTACT	219	MP6
TXA0031783	TCGTTTTTGACAGTTTGACAGTT	AGCATCTTGTTCTGTTTGTGGAA	230	MP6
TXA0429389	ACAAAATGTTTCACTTTTGGGTAA	TGCTTTGTCAAGATCATTTTTTGT	182	MP7
TXA0429392	GAAGAAGCCCCGCCACC	GTGACAGAAAGGTAAAGAGGAGCA	190	MP7
TXA0031393	TTTTAGCATGTGCTTCTGCTTATT	ACATACTTTAGCCTTGGCCTCTAC	219	MP7
TXA0429394	CCTCCTCTTCGTCTTTTCTAACC	CCCAGCCCTGGAAATGG	220	MP7
TXA0429385	GTCTGCCAGCTAAAGGTGAAGAT	TCCCAATGAAAGTAAAGTACAAACCT	177	MP8
TXA0342047	CAATCATGTTGCAGCAATTCAC	AGAAACCCAAAATCTGTTTTCCA	221	MP8
TXA0129573	CGTCTTTTCTAACCGTGCAG	AGAAGGGGAGAGACCAACTC	240	MP8
TXA0377194	aTTTCCATCCTGCAGAAGAAGCC	CCCACGTTCTAAGAGAGTGACAG	220	MP8
TXA0429388	AGATGAGTCATATTTGTGGGTTTTCA	TCTTCATCAAAAGGTTCATTCTCTGG	205	MP8
TXA0429398	TGTTACTAGTTTACGTGTTTACAG	CACTGTCTTCCACCTATACATCT	207	MP8

Appendix Table S4: Fluidigm Primers for ARID1A exon coverage used for Juno chip and pooling strategy. Lower case letters indicate intron binding.

Amplicon	Sequence F’ primer	Sequence R’ primer	Product Size	Multiplex Group
TXA0429468	GGGCGTAATGACATGACCTATAA	GGGGCAGAGGGACCATA	182	MP1
TXA0429470	AGAGTAGCTTCACTGATGGG	GCAGGATGTTGATGGTATCTAATG	176	MP1
TXA0068511	AGTAAGCCTGCCTGGTTTATCAAT	ATTGGTTTCCTCTCTGCCCCTAT	229	MP1
TXA0068558	ATGGATCAGATGGGCAAGATGAG	ACAGCAACAAGGGTCAAGGTAAT	240	MP1
TXA0429480	GAGAGCATTTGCCTGCCTGTC	GGGGTGTGGCCAGAATCA	187	MP1
TXA0429438	AACCAGCAAAGTCCTCACCC	CCGGGGACTGCTGATGTG	181	MP1
TXA0429481	CAGGGCTGCTGCTCATCC	CGAGTGTAACCAAGGTGTTTTCC	180	MP1
TXA0429487	CCTCAGTGACCGAAAGAACCC	ACTAGTTGGCTCAAAGGGTGG	220	MP1
TXA0013937	CAACAACATGGCGGACAACAAAG	GGAGCTCAGCGCGTAGG	189	MP1
TXA0429479	AGATCTTTGGCATTTTAAAGGAGT	CTGAAGCTGGCTTGTCCTTG	219	MP1
TXA0429489	CCGAGGATGGAGCTAAGAGTT	GCACAAATGACAGGCTTCG	216	MP1
TXA0429450	ACAGCTAAACTTACTGGACTTGA	TCCTTCCTATCACTGAAAAAGAT	217	MP1
TXA0001721	AGGAAAATGCTAAGCAAGTAGTAGG	CAGGTGAGGGGAGGTATGA	236	MP1
TXA0429448	GGCATGGCTGGAGGCATAAA	GACAGCAGTTTCTTGGGTTTTCC	219	MP1
TXA0068523	TGCTGCCAGCTCCTTGAAAA	CATATCCTGAATAAGAGGCCAGGG	216	MP1
TXA0378755	GGTCTCGGTGCTGCTATGGAT	TAGTTTTCAAGGCGAACCTGCAT	220	MP1
TXA0068560	AAAGTCCCAGGATAAGGATGGAG	ATAGCTCCCCATGGAGTTCTGC	216	MP1
TXA0001746	GTGAGCACATCAGGGATTTCCA	AGTCACCTTTCCCTCTCCCTAAA	223	MP2
TXA0386811	GGGCCGAGAGCAATGGG	GTAGGGTTGCCCGAAGCC	236	MP2
TXA0001728	GCAATGCCTATCCTGCCACT	TAGGTCATGTCATTACGCCCCTG	223	MP2
TXA0068507	GGGCCAGACTCCATATTACAACC	CGACTGCTGGGAGGGGTAT	223	MP2
TXA0068559	CAACCTGGGCTTGGTGGATAG	AAGATCCCAAACCCTCTCAATCT	218	MP2
TXA0429441	TATCAATACCAGGCCATCACAGC	ACCTTTCAGAAGGTGCAGAAATA	188	MP2
TXA0068565	CATGGCGTGAACCGAACAGATG	GAGAGGTGCGGTTCTCCATT	232	MP2
TXA0429440	GAACTCCCCAGCCCACC	CTTTGTTGGGCCCCTCCC	214	MP2
TXA0429453	TGTGGGCACATCAAGCAGT	GGCCGCTGACCCCATC	185	MP2
TXA0429458	TGGGTCAAAGGGTAGATTACCAG	GTCCCATCGCCACATTTCCTA	178	MP2
TXA0068517	AGGGATTTCTTCAAGAGTCACATCA	AGGACACAAAGTTGAAAGGAGTCA	218	MP2
TXA0429483	AGGTCCTAAACTAGAAGAGGAAG	CAAGCTTATCTGAGCAGTCCA	188	MP2
TXA0429485	CCACACAGTTCCAGCAGAG	GTGATACCGAGATGTCCAACAG	180	MP2
TXA0429477	GAACCCCACAGTAAGGATGAG	CTTGTGGTGCAGCAGGAT	189	MP2
TXA0001760	TATATGCAGAGGAACCCCCAGAT	ACTGTTTTCTCCTCTCACCCGTA	217	MP2
TXA0429486	GTTCTTAGGCCACTTTTCTCCCT	GACACCTTGCTGAACCTCCCA	190	MP3
TXA0429434	GCAGCAAGGACATGGGT	CTCACAGATCAGATTTTGGACAG	176	MP3
TXA0378744	AGGCTACCCCAATATGAATCAAGG	GCTGCCATCCCTGTAAAAGAGAAA	240	MP3
TXA0211687	CAACGGCGGGATGGGTG	GCAGATTGAGCCCACTATAGCTT	176	MP3
TXA0429471	AATGATGTCCCTCAAGTCTGGT	TGGCTAAAGATGAGACATTCCC	190	MP3
TXA0068544	CATCCCACCTTATGGCACACTC	CTTGCACTGACACCCTCTCT	231	MP3
TXA0068557	GGCCTCTTCATGAGCCATTTCTA	CTCAAATGTCTGCCCTAGCTCC	239	MP3
TXA0068561	GTCCTCTCAGCCTCCATACTCC	GCAGTTTGCTGGGACTGCT	237	MP3
TXA0068514	CAGCAGAACTCTCACGACCAC	CCCCATGGCCCCGAAG	231	MP3
TXA0429463	CACCCCCTGGCACCAAT	CTCTGATCTGTGTGCAGCATTTC	217	MP3
TXA0068531	GACTTCTGAGACCCTTAGCACAG	TAGAGGTCCAGAGGTTTCCTACC	237	MP3

TXA0429488	TGACAACAGCAGAGGGTACA	GGGCTAATGCCAAATGGAAAC	190	MP3
TXA0068546	GAAGTGACTCCACATTCCAGAAG	CTGAGCCATTCTCAAGATTTCC	217	MP3
TXA0068564	GGAAAACCAGGCGGGAGATATAC	CTGGGACTTCTTGGAATCAGCA	233	MP3
TXA0429482	TCTTGGAAACCCTCAGCAAACTC	GCTGTCCCCCTGAGCC	185	MP3
TXA0386804	ATGGCCTCGCAGTGTT	ACTGAGGGGAGCCCAA	240	MP4
TXA0378770	GATGACATGTTGTCTACTCGGT	CTTCGAATGGTATTGGACACAC	236	MP4
TXA0386808	TGAAGCCCAGGACCCCTTTT	CAGCAGTACCACAGCCATCTC	223	MP4
TXA0429473	TTTTAAAGGAGTATGAGGTGGGT	GATCAGCTTCTCCTCACTATTCT	230	MP4
TXA0001737	GGAGATGTACAGCGTGCCATA	GCCAAACTGGAATGGAAATTGGT	223	MP4
TXA0001752	CAAGGCCCCCTCCATCTAACTA	GTGATATCCCGCCGAATCATGG	226	MP4
TXA0001765	GTGAGCCTGAGAGGAAGATGTG	AGCCAGTGAGTACCTAGAAAGGG	221	MP4
TXA0429444	TCCTAGTTAGAATTCCCAGGCTT	CCCCTCCCCAACACCCA	177	MP4
TXA0429447	ATGGGCAACCGGCCTTATG	GCATCTCAATAATCTGAGTGGGTCT	219	MP4
TXA0013935	TGATGGGAACTGGACCTCCTTAT	TTTAGCTGTGATGTGACTCTTGA	166	MP4
TXA0429454	GATGGGGCTTGGGGCTTATG	TCTCCCCGTTCAATCTTGCATTC	208	MP4
TXA0429456	GACTCCTGCGTGTCCTTTGTTAT	CAGAGGTATTCATACTGGGCTGA	190	MP4
TXA0429459	CTGCCCACCCTAATCCTG	AGACTTCAACACGTTAGATTAGTT	218	MP4
TXA0068556	TCATCAGTGCATAGCTTCTCACA	GATACGAAGGTTGGGCATGAGG	237	MP4
TXA0429451	AGAGGAAGATGTGGGTGGAC	GAAACCACAGGGGCAGTCAAG	182	MP5
TXA0001747	GGCTTGTCAACTTACCAGTTTGTTC	GGACAGGAGCTGGGGTCAT	224	MP5
TXA0429455	TGTGAGAGTTAAACACTGTCATGC	CATCTGCCCCTGCTCTTGG	217	MP5
TXA0429472	AGAAGAATGATCCATTTGTGGTG	TTGTCCCTGGTGTACCCT	222	MP5
TXA0386815	GGCTTCGGGCAACCCT	TAGGCGCTGCGGTTGG	221	MP5
TXA0001734	TGTTTGGTGTTCTAGAGTTGAGAG	GAGTGTGCCATAAGGTGGGATG	220	MP5
TXA0429443	CTCATACCTCCCCTCACCT	TGGAAGACTAGGGCTCCTT	190	MP5
TXA0429433	GGGTTATATATTCAGTGGCCAGAGG	GCTGCGGGGTCTGGGA	214	MP5
TXA0429437	CCACAGCTCCAGTCCTCTCA	GTGCTGGCTGCTGAGGT	184	MP5
TXA0378765	CTTCCTAGAGGACAGCCTTG	ACAAATGACTTGTGAAACCAATGA	238	MP5
TXA0378771	GACTTTGAGATGTCCAAACACC	GGTATGGAGATAGGTCCAACTG	238	MP5
TXA0429465	AAATGCAGAAGGCAGGTCCC	TTAGGCAACCGAATGAGGAAGAT	190	MP5
TXA0429469	CCTTCCCCTCAGCAAGATGTAT	CAGCTGATGCCTGTATGGG	208	MP5
TXA0013973	GATGGAGAGCATTTGTTCGCATT	CCCATGCCTGTGTGTATCTGTC	169	MP6
TXA0386806	ccctcaaccAACTGCTCA	CTCCCGGGGCTCATGG	217	MP6
TXA0068535	CAAACTATAATGCCTTGCCCAAT	GACACATCCCTGACCCAAC	216	MP6
TXA0429478	AAGGTGGACGAGAACCAC	GTTTCTAAGTTCTCCACACACG	190	MP6
TXA0068566	CACTGTCATGCCAAGCAAACTAC	CCCATGCACTTATCTTCAGCCAT	236	MP6
TXA0429452	CCCTTAGCACAGGCTTTGAATCT	GTCATGCCCATGGCCTTCT	187	MP6
TXA0429484	TGAGCTGCAACAAAGTGGAGT	GGGAAAGGACGGCATTGGG	219	MP6
TXA0001733	CAGAGGCCATCAAAGCTCAGG	CCCTGCATGGTCATCGGGTA	217	MP6
TXA0429466	CCACCAAGCATGCAGAATCACA	TTCAACAGAGCCAGGTGGGAA	219	MP6
TXA0001708	GCAAAACATGCCACCACAAATGA	CCATGGGAAGGCCACGAG	228	MP6
TXA0429460	ACAGAGTGAGGTAAGCATGAC	AGGAGAATACATCCCCGAGT	190	MP6
TXA0429436	CACAGCCACAGGCTCAGT	TAGTCACACACAGGGAAGGG	190	MP6
TXA0429475	GGGACACCACTGAGCAT	ATAGTGGCTGTGATCCGTTTTTC	187	MP6
TXA0068506	TTTATGTCCCTGAGTGCAGAGTA	GTATACATCTTGCTGAGGGGAAGG	237	MP6
TXA0378761	CATCAAGATCCTAGAGGACGAAC	TAAGTTAGTGGTGCCTGCTTC	240	MP7
TXA0429462	GGCACGAAGGGGAGATGTA	CGGCGCTCAGTAGCAG	190	MP7
TXA0386814	GCAGCAGCGGGAGGAG	GTTCCCGTTCGAGTTCTTCAGG	232	MP7
TXA0429442	GCTCTTGGTTGTTTAAGGAAAATGC	GCTGGATTACTCTGCTCTCCTTG	214	MP7

TXA0429446	AGTTGAGAGATATTAGTGAGTTGCT	CTGTCCATGCATTTGACCTC	178	MP7
TXA0429457	TCCAGGATGCCTTTAATGATGGA	AGCACAAGTTCAAATAGCAATCAG	189	MP7
TXA0378769	GCCGCCTGGAGAAGTTGTAT	GGTTCTGCATGTGGAGGAGG	237	MP7
TXA0386817	ACCCTGAAGCTATAGTGGGCTC	ATCCATAGCAGCACCGAGA	219	MP7
TXA0378772	GACAGAGCTGCTGCCTT	GAAACTTGCTGCTCTCCTTGAT	233	MP7
TXA0001730	TTCCTGCACTCTGGGATGAAAAT	AAGATGGAAAGGGGCAGATTAGG	227	MP7
TXA0386807	TGGGGAGGTCTCTCAAGTCAATA	CCCTCCATGGGAGCTGGAC	239	MP7
TXA0429435	TCATGCAGGAGAGTCAGTGCTAA	GGTCTGGGACGGTGGTTG	175	MP7
TXA0429449	ACTAGATGATCACACAGCACTATTT	GGTTGATCATGCCAGCCATAC	189	MP7
TXA0429474	tgatgaggaGATAGCCTTTTCAG	GTCTGGATATGCTCAGTGGTG	219	MP7
TXA0068534	ACAGCACTATTTGGCTCCAGTTC	GCACTTACCTGCAGAATTGTTGG	235	MP8
TXA0429439	CCGCCGGGCAGGAAAG	GGCTCCGTGAGGTTATTGTTCA	202	MP8
TXA0429476	AGTTTGACAAGCTTCCAGTAAAG	TTCCGAGGGGCTGGTG	217	MP8
TXA0378766	CTTGGAGATGCTCCGGGAAA	ATTGTTGTCCTGGATGCTGAGTT	238	MP8
TXA0386810	GCGCTGCTTGCCTTGG	GCATAAATAAAGGGCAACAGTCA	231	MP8
TXA0001711	CCCCCTACTCACAGCCACAG	GTTCTCATGACACTAACCCCCAA	230	MP8
TXA0429467	ATCTTGGCATCTGTGGGCTTTAT	AACTGCTGCTGCTGAGG	185	MP8
TXA0429464	CACAGATCAGAGGGCCAACC	CAGGAATGGAGACTTGCTAGGAG	220	MP8
TXA0013972	TTCAATAGATGACCTCCCCAT	CAACACTGGCGGGAGAG	188	MP8
TXA0429445	GATGCCCCAGTACAGTTCCC	CCCGTATCTACTCCTAACTGGGT	180	MP8
TXA0068503	TGGAGGAATTGGTTTATTTGTGGTT	ATCAGTCACCTTTCCTCATGCTG	234	MP8
TXA0429461	AGGGAAACATGAGCACTGG	CAAAGAAACACAGGATTAGGGTG	189	MP8