These are the phosphosites that cluster 75% of the time or more in parental cells, but less than 25% of the time in 24H cells

First Gene_Site	Second Gene_Site	Parental (fraction times clustering	24H (fraction times clustering)
PIK3R2_Y464	DSC3_Y818	1.00	0.22
YES1_Y426	EPHB2_Y602	1.00	0.23
YES1_Y426	KIAA1217_Y393	1.00	0.24
CDK1_Y15	PTPN11_Y62	0.99	0.17
AFAP1L2_Y413	PIK3R2_Y464	0.99	0.22
ANXA2_Y238	ENO1_Y44	0.98	0.08
KIAA1217_Y393	ERBB2IP_Y1104	0.98	0.14
INSR_Y1189	PTK2_Y576	0.98	0.17
ERBB2IP_Y1104	EPHB2_Y602	0.98	0.22
YES1_Y426	ERBB2IP_Y1104	0.97	0.19
SLC38A2_Y20	PTK2_Y576	0.95	0.19
BCAR1_Y234	ERBB2IP_Y1104	0.95	0.12
DYRK1A_Y321	SHB_Y268	0.95	0.20
EGFR_Y1197	SHC1_Y427	0.95	0.23
ANXA2_Y238	PIK3R2_Y464	0.95	0.08
ANXA2_Y238	DSC3_Y818	0.95	0.11
AFAP1L2_Y413	ANXA2_Y238	0.95	0.11
PKP3_Y176	PTK2_Y397	0.93	0.16
BCAR3_Y266	ERBB2IP_Y1104	0.93	0.10
INSR_Y1189	CTNND1_Y228	0.92	0.20
PTK2_Y576	MPZL1_Y263	0.92	0.25
EPHA2_Y588	DYRK1A_Y321	0.91	0.16
SLC38A2_Y20	CTNND1_Y228	0.90	0.23
DSC3_Y818	PXN_Y118	0.88	0.19
CAV1_Y14	GPRC5A_Y347	0.88	0.19
CAV1_Y14	CRKL_Y132	0.88	0.24
ANXA2_Y238	PXN_Y118	0.86	0.08
YES1_Y426	TFRC_Y20	0.86	0.25
PIK3R2_Y464	ERBB2_Y1248	0.86	0.20
FAM59A_Y453	PTK2_Y576	0.86	0.22
PTPRA_Y798	ERBB2_Y1248	0.84	0.14
ERBB2IP_Y1104	PXN_S84_Y88	0.83	0.12
ANXA2_Y238	ERBB2_Y1248	0.80	0.19
INSR_Y1189	PTK2_Y397	0.80	0.16
SLC38A2_Y20	PTK2_Y397	0.80	0.16
EPHA2_Y588	INSR_Y1185	0.80	0.14
PTK2_Y397	PTK2_Y576	0.79	0.16
PTPRA_Y798	ENO1_Y44	0.79	0.19
EPHA2_Y588	GPRC5A_Y347	0.79	0.14
BCAR1_Y234	PXN_S84_Y88	0.79	0.21
BCAR3_Y266	TFRC_Y20	0.79	0.21
MAPK1_T185_Y187	PTK2_Y576	0.79	0.22
BCAR3_Y266	PXN_S84_Y88	0.78	0.14
INSR_Y1185	SHB_Y268	0.78	0.22
EPHA2_Y588	CRKL_Y132	0.78	0.14
PTPRA_Y798	ANXA2_Y238	0.78	0.20
PKP3_Y176	PTK2_Y576	0.77	0.19
PTPRA_Y798	DSC3_Y818	0.77	0.19
SH2D3A_S218_Y231	PTK2_Y397	0.76	0.16
ALB_Y164	EPHA2_Y772	0.76	0.16
EPHA2_Y772	ERBB2IP_Y1104	0.75	0.12
PXN_Y118	ERBB2_Y1248	0.75	0.14

These are the number of times that site appears in a quartile swap (moving from 75% or more in Parental to <25% in 24H)
Highlights: Blue (focal adhesions), Orange (cell junctions), purple (ERBB2)

Item	Number of times it appears
ANXA2_Y238	7
ERBB2IP_Y1104	7
PTK2_Y576	7
PTK2_Y397	5
DSC3_Y818	4
EPHA2_Y588	4
ERBB2_Y1248	4
PIK3R2_Y464	4
PTPRA_Y798	4
YES1_Y426	4
BCAR3_Y266	3
INSR_Y1189	3
PXN_S84_Y88	3
PXN_Y118	3
SLC38A2_Y20	3
AFAP1L2_Y413	2
BCAR1_Y234	2
CAV1_Y14	2
CRKL_Y132	2
CTNND1_Y228	2
DYRK1A_Y321	2
ENO1_Y44	2
EPHA2_Y772	2
EPHB2_Y602	2
GPRC5A_Y347	2
INSR_Y1185	2
KIAA1217_Y393	2
PKP3_Y176	2
SHB_Y268	2
TFRC_Y20	2
ALB_Y164	1
CDK1_Y15	1
EGFR_Y1197	1
FAM59A_Y453	1
MAPK1_T185_Y187	1
MPZL1_Y263	1
PTPN11_Y62	1
SH2D3A_S218_Y231	1
SHC1_Y427	1

These are the phosphosites that cluster 75% of the time or more in 24H cells, but less than 25% of the time in P cells

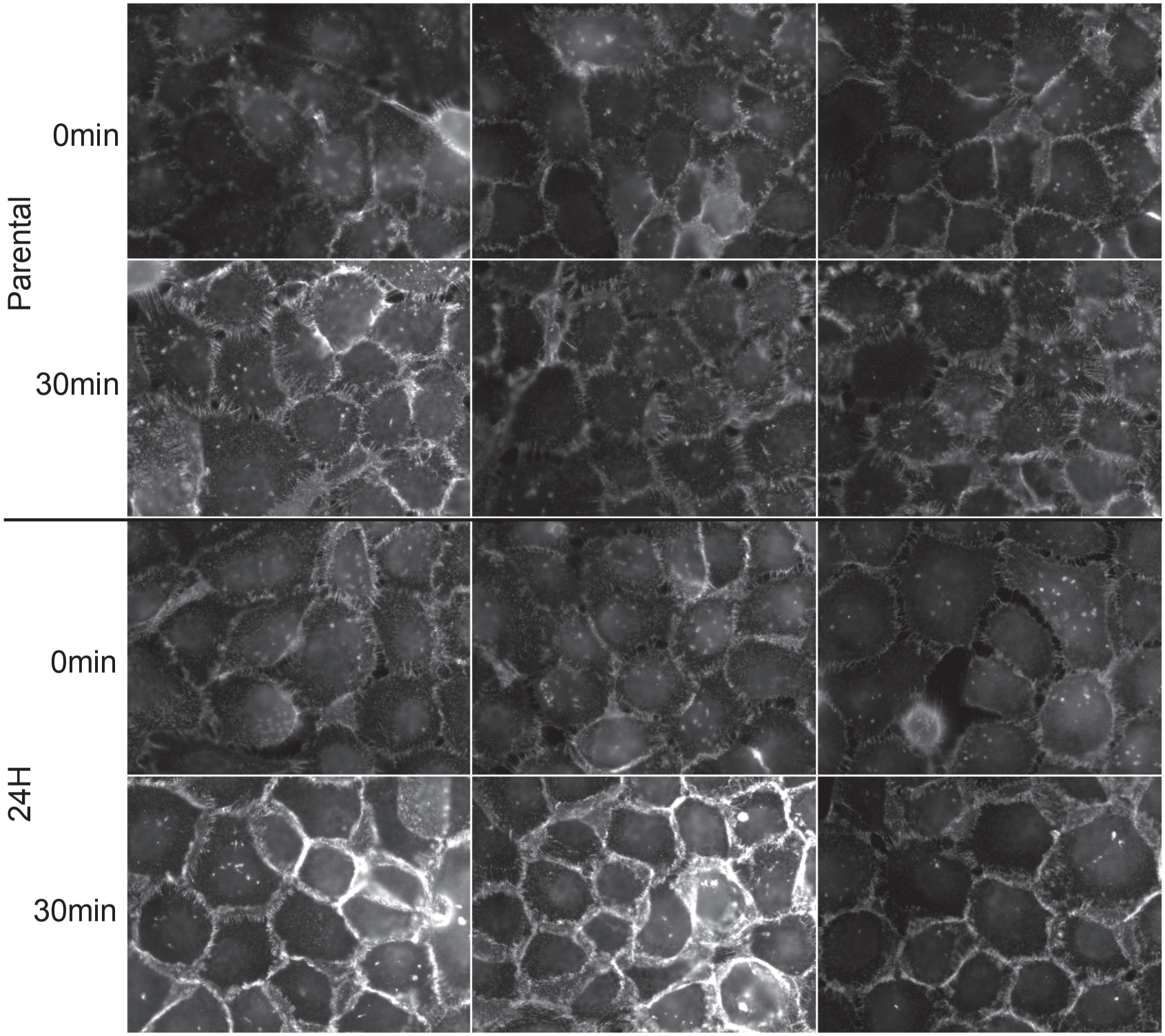
First Gene_Site	Second Gene_Site	Parental (fraction times clustering	24H (fraction times clustering)
ITGB4_Y1207	PXN_Y118	0.25	1.00
SHC1_Y349	CTNND1_Y228	0.22	0.97
KIAA1217_Y393	PTK2_Y397	0.16	0.97
MAPK3_Y204	CTNND1_Y228	0.24	0.95
CRKL_Y132	PRPF4B_Y849	0.18	0.93
ANXA2_Y238	TFRC_Y20	0.16	0.92
MAPK1_Y187	CTNND1_Y228	0.23	0.91
PTK2_Y397	EPHB2_Y602	0.16	0.90
EFNB2_Y304	PTK2_Y397	0.22	0.88
TNK2_Y859	CAV1_Y14	0.25	0.88
EPHA2_Y588_Y594	PTPN11_Y62	0.16	0.87
BCAR3_Y266	BCAR1_Y327	0.09	0.86
EFNB2_Y304	EPHA2_Y588	0.22	0.86
GIT1_Y545	PXN_S84_Y88	0.19	0.83
TFRC_Y20	PTPN11_Y62	0.16	0.81
MAPK14_Y182	PTK2_Y576	0.20	0.81
MAPK1_T185_Y187	PIK3R2_Y464	0.20	0.80
EGFR_Y1092	CAV1_Y14	0.23	0.80
CAV1_Y14	INPPL1_Y986	0.23	0.80
SHC1_Y427	GPRC5A_Y347	0.24	0.80
FAM59A_Y453	PIK3R2_Y464	0.25	0.80
ANXA2_Y238	EPHA2_Y588_Y594	0.16	0.77
PRPF4B_Y849	PXN_Y118	0.17	0.77
SHC1_Y349_Y350	PIK3R2_Y464	0.23	0.75

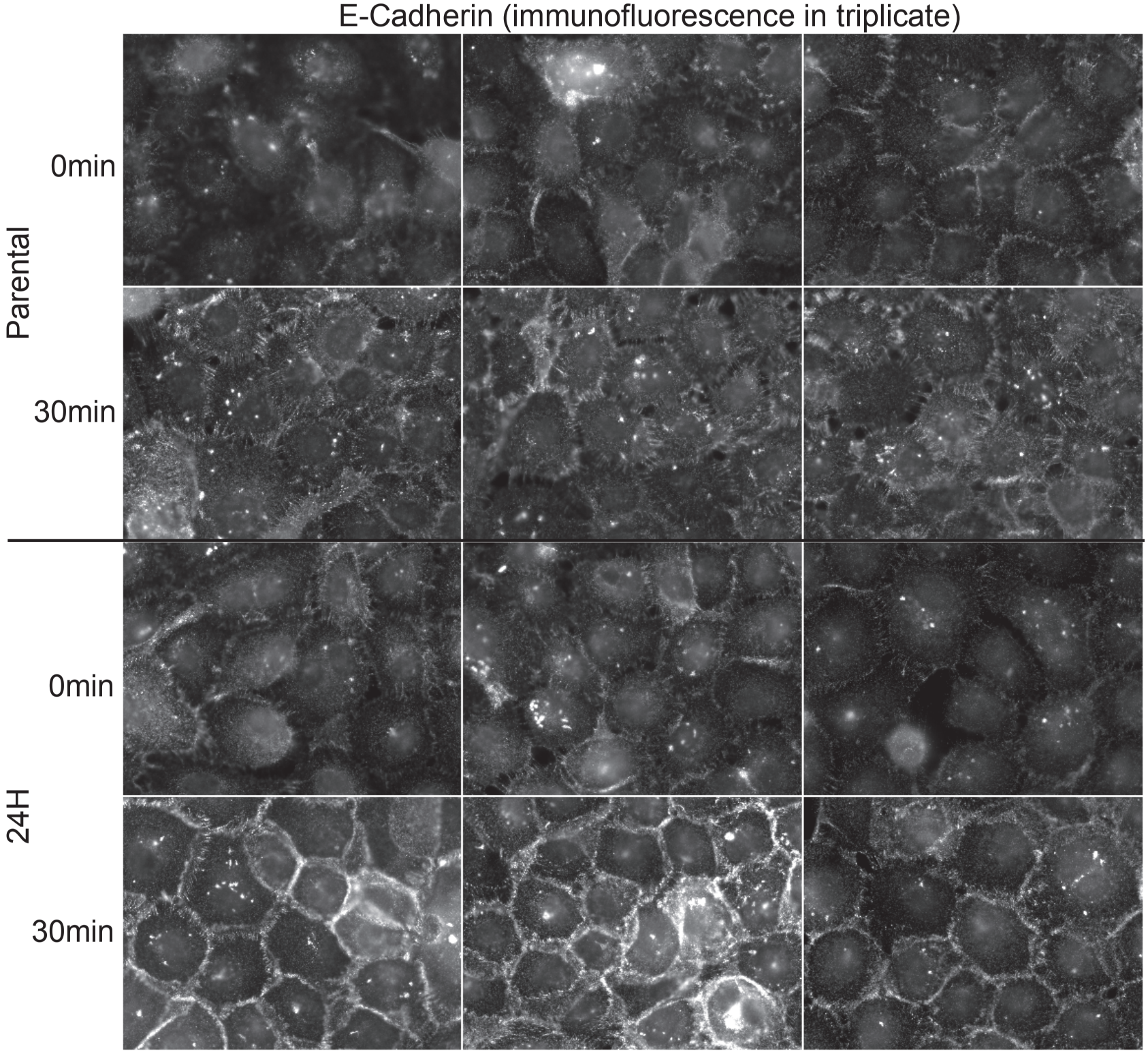
These are the number of times that site appears in a quartile swap (>75% of the time in 24H, <25% in P)
Highlights: Blue (focal adhesions), Orange (cell junctions), purple (ERBB2)

Item	Number of times
CTNND1_Y228	3
CAV1_Y14	3
PIK3R2_Y464	3
PTK2_Y397	3
ANXA2_Y238	2
EFNB2_Y304	2
EPHA2_Y588_Y594	2
PRPF4B_Y849	2
PTPN11_Y62	2
PXN_Y118	2
TFRC_Y20	2
BCAR1_Y327	1
BCAR3_Y266	1
CRKL_Y132	1
EGFR_Y1092	1
EPHA2_Y588	1
EPHB2_Y602	1
FAM59A_Y453	1
GIT1_Y545	1
GPRC5A_Y347	1
INPPL1_Y986	1
ITGB4_Y1207	1
KIAA1217_Y393	1
MAPK14_Y182	1
MAPK1_T185_Y187	1
MAPK1_Y187	1
MAPK3_Y204	1
PTK2_Y576	1
PXN_S84_Y88	1
SHC1_Y349	1
SHC1_Y349_Y350	1
SHC1_Y427	1
TNK2_Y859	1

Comparison of direct correlation between vectors in P and 24H (Pearson Correlation) and average clustering differences (Average Co-Occ Difference)
Average Co-Occ Difference: The avereage of the absolute value of P-24H co-occurrence matrix (vectorized for the peptide).
Highlighted is the cutoff used in the paper for significant difference in co-occurrence

Gene_site	Average Co-Occ Difference	Pearson Correlation
ANXA2_Y238	0.317	0.597
PTK2_Y397	0.309	0.734
EPHA2_Y588	0.282	0.833
PTPRA_Y798	0.248	0.918
CAV1_Y14	0.239	0.824
PTPN11_Y62	0.221	0.327
PXN_Y118	0.218	0.779
PIK3R2_Y464	0.214	0.940
SHC1_Y427	0.213	0.990
PXN_S84_Y88	0.210	0.953
CTNND1_Y228	0.210	0.995
DSC3_Y818	0.210	0.857
ERBB2IP_Y1104	0.208	0.887
PTK2_Y576	0.208	0.320
DYRK1A_Y321	0.203	0.631
ARHGAP35_Y1105	0.202	0.471
SHB_Y268	0.201	0.841
GPRC5A_Y347	0.201	0.973
PRPF4B_Y849	0.199	-0.829
CRKL_Y132	0.198	0.778
ANXA2_Y24	0.196	0.867
ENO1_Y44	0.192	0.946
INSR_Y1185	0.187	0.626
AFAP1L2_Y413	0.186	0.905
PTRF_Y308	0.185	0.849
ALB_Y164	0.184	-0.749
LDLR_Y845	0.183	0.891
ERBB2_Y1248	0.182	0.901
ITGB4_Y1207	0.182	0.951
ACP1_Y132	0.175	0.981
SGK223_Y413	0.169	-0.243
FAM59A_Y453	0.166	0.996
SH2D3A_S218_Y231	0.164	0.984
YES1_Y426	0.162	-0.479
INSR_Y1189	0.162	0.649
BCAR1_Y327	0.159	0.625
SLC38A2_Y20	0.159	0.940
TFRC_Y20	0.157	0.953
MPZL1_Y263	0.153	0.765
BCAR1_Y387	0.153	0.642
MAPK1_T185_Y187	0.152	0.995
GSK3A_Y279	0.152	0.515
ANXA2_Y30	0.150	0.982
SHC1_Y349_Y350	0.149	0.990
BCAR1_Y234	0.149	0.805
CDK1_Y15	0.147	0.808
EPHB2_Y602	0.146	0.992
KIAA1217_Y393	0.146	0.931
GIT1_Y545	0.143	0.960
PKP3_Y176	0.141	0.899
SHC1_Y349	0.140	0.907
EFNB2_Y304	0.137	0.950
EPHA2_Y772	0.135	0.867
BCAR3_Y266	0.134	0.462
EGFR_Y1092	0.132	0.998
INPPL1_Y986	0.132	0.994
EPHA2_Y588_Y594	0.132	0.885
STAT3_Y704	0.127	0.898
MAPK3_Y204	0.127	0.967
BCAR1_Y249	0.126	0.875
EGFR_Y1172	0.126	0.972
EGFR_Y1197	0.126	0.989
MAPK14_Y182	0.123	0.963
STAT3_Y705	0.122	0.939
MAPK1_Y187	0.121	0.998
RIN1_Y36	0.114	0.903
TNK2_Y859	0.109	0.967
EPHA2_Y575	0.104	0.808


CTNND1 (immunofluorescence in triplicate)
Parental
0min
30min
24H
0min
30min


E-Cadherin (immunofluorescence in triplicate)
Parental
0min
30min
24H
0min
30min