

Supplementary Table 3. Significant STAC regions identified in neuroblastoma dataset. STAC results were first filtered to exclude those locations with stack size ≤ 3 . Regions reported have p -value ≤ 0.05 at all locations for at least one of the statistics. **a)** **Gains.** STAC analysis identifies 94 distinct regions of gain covering 332 Mb of genomic sequence and 86 known cancer related genes^b. Average region size: 3.53 Mb. **b) Losses.** STAC analysis identifies 79 distinct regions of loss covering 305 Mb of genomic sequence. Average region size: 3.86 Mb. ^a genomic coordinates based on UCSC build 16 of human genome.

Supplementary Table 3a
Statistically significant regions of gain identified by STAC: Neuroblastoma data

Genomic Change	Start^a	Stop^a	Footprint <i>p</i>-value	Frequency <i>p</i>-value
chr1p+	39000001	41000000	0.0033	0.0633
chr1p+	50000001	54000000	0.0005	0.5483
chr1p+	56000001	59000000	0.0005	0.0008
chr1p+	77000001	80000000	0.0005	0.0001
chr1p+	82000001	85000000	0.0005	0.0170
chr1p+	114000001	118000000	0.0005	0.0037
chr1q+	141000001	145000000	0.0184	1.0000
chr1q+	147000001	154000000	0.0046	0.9919
chr1q+	157000001	160000000	0.0008	0.0245
chr1q+	173000001	179000000	0.0086	1.0000
chr1q+	194000001	195000000	0.0027	1.0000
chr1q+	205000001	207000000	0.0150	0.0019
chr1q+	238000001	246000000	0.0008	0.9919
chr2p+	10000001	18000000	0.0003	0.0001
chr2p+	19000001	21000000	0.0126	0.0148
chr2p+	28000001	29000000	0.0307	0.9930
chr2p+	39000001	45000000	0.0003	0.3459
chr2q+	96000001	98000000	0.0189	1.0000
chr2q+	206000001	209000000	0.0007	0.7465
chr2q+	217000001	218000000	0.0007	0.0827
chr2q+	218000001	226000000	0.0007	0.0827
chr2q+	231000001	235000000	0.0007	0.0827
chr2q+	238000001	244000000	0.0007	0.0827
chr3q+	140000001	143000000	0.0134	0.2047
chr3q+	185000001	189000000	0.0002	0.0442
chr3q+	199000001	200000000	0.0002	0.2047
chr4p+	1	2000000	0.0007	0.0398
chr4p+	5000001	7000000	0.0014	0.0078
chr4q+	191000001	192000000	0.0004	0.0002
chr5p+	1	3000000	0.0003	0.0001
chr5q+	176000001	179000000	0.0021	0.8987
chr5q+	180000001	181000000	0.0005	0.0001
chr6p+	36000001	42000000	0.0137	0.0654
chr6p+	50000001	53000000	0.0232	1.0000
chr6q+	66000001	72000000	0.0005	0.3868
chr6q+	81000001	90000000	0.0389	0.9942
chr6q+	100000001	102000000	0.0027	0.7991
chr6q+	170000001	171000000	0.0005	0.0001
chr7p+	1	7000000	0.0007	0.2190
chr7p+	54000001	56000000	0.0087	1.0000
chr7q+	71000001	75000000	0.0489	1.0000
chr7q+	92000001	95000000	0.0168	1.0000

chr7q+	129000001	133000000	0.0042	0.6567
chr8p+	6000001	9000000	0.0008	0.4954
chr8p+	20000001	23000000	0.0320	1.0000
chr8p+	41000001	43000000	0.0008	1.0000
chr8q+	82000001	86000000	0.0005	0.0004
chr8q+	139000001	146000000	0.0005	0.0013
chr9q+	92000001	96000000	0.0002	0.0001
chr9q+	128000001	129000000	0.0025	0.0009
chr9q+	131000001	132000000	0.0025	0.0009
chr9q+	134000001	135000000	0.0002	0.0049
chr10q+	42000001	45000000	0.0002	0.7363
chr10q+	52000001	56000000	0.0339	0.9962
chr10q+	118000001	120000000	0.0007	0.2425
chr10q+	129000001	136000000	0.0002	0.0073
chr11p+	53000001	54000000	0.0001	0.1076
chr11q+	58000001	59000000	0.0002	0.0421
chr11q+	85000001	90000000	0.0060	0.1875
chr11q+	133000001	135000000	0.0002	1.0000
chr12p+	1	4000000	0.0016	0.2878
chr12q+	65000001	67000000	0.0006	1.0000
chr12q+	108000001	113000000	0.0014	0.5718
chr12q+	126000001	127000000	0.0025	0.0165
chr12q+	130000001	133000000	0.0006	0.0007
chr13q+	28000001	31000000	0.0004	0.2483
chr13q+	97000001	101000000	0.0004	0.0013
chr13q+	110000001	114000000	0.0011	0.2483
chr14q+	56000001	60000000	0.0004	0.0001
chr14q+	100000001	106000000	0.0004	0.3269
chr15q+	80000001	83000000	0.0085	0.0069
chr15q+	89000001	92000000	0.0042	0.8422
chr15q+	97000001	101000000	0.0145	1.0000
chr16p+	1	4000000	0.0002	0.0001
chr16q+	49000001	53000000	0.0003	1.0000
chr16q+	54000001	62000000	0.0003	0.0205
chr17p+	16000001	20000000	0.0005	0.1204
chr17q+	27000001	30000000	0.0013	1.0000
chr17q+	63000001	64000000	0.0102	0.1433
chr17q+	65000001	66000000	0.0075	0.1433
chr17q+	75000001	78000000	0.0348	0.9392
chr18p+	1	8000000	0.0014	0.9997
chr18q+	56000001	60000000	0.0004	0.0017
chr18q+	71000001	74000000	0.0078	0.0613
chr19q+	41000001	42000000	0.0112	0.0751
chr19q+	45000001	49000000	0.0005	0.0006
chr20p+	23000001	26000000	0.0014	0.0021
chr20q+	29000001	33000000	0.0088	1.0000
chr20q+	40000001	46000000	0.0012	0.0020

chr21q+	29000001	33000000	0.0010	0.0088
chr21q+	44000001	47000000	0.0003	0.0006
chr22q+	16000001	18000000	0.0018	0.1113
chr22q+	26000001	32000000	0.0028	0.9952
chr22q+	49000001	50000000	0.0005	0.0001

Supplementary Table 3b.
Statistically significant regions of loss identified by STAC: Neuroblastoma data

Genomic Change	Start^a	Stop^a	Footprint <i>p</i>-value	Frequency <i>p</i>-value
chr1p-	3000001	8000000	0.0014	0.0028
chr1p-	19000001	22000000	0.0274	0.0573
chr1p-	30000001	31000000	0.0211	0.0141
chr1p-	36000001	37000000	0.0231	0.0141
chr1p-	40000001	44000000	0.0327	0.9994
chr1p-	56000001	57000000	0.0014	0.9994
chr1p-	57000001	58000000	0.0014	1.0000
chr1q-	196000001	199000000	0.0004	0.0001
chr2p-	1	5000000	0.0007	0.0481
chr2q-	106000001	115000000	0.0002	0.0077
chr2q-	235000001	242000000	0.0002	0.0011
chr3p-	4000001	8000000	0.0043	1.0000
chr3p-	11000001	12000000	0.0331	1.0000
chr3p-	14000001	16000000	0.0011	0.5906
chr3p-	70000001	74000000	0.0011	0.9079
chr3q-	99000001	102000000	0.0003	0.0001
chr3q-	112000001	115000000	0.0011	0.4400
chr3q-	124000001	126000000	0.0003	0.0001
chr3q-	130000001	136000000	0.0003	0.0001
chr3q-	137000001	138000000	0.0019	1.0000
chr3q-	199000001	200000000	0.0003	0.9995
chr4p-	4000001	7000000	0.0009	0.0022
chr4q-	141000001	145000000	0.0153	0.9508
chr4q-	191000001	192000000	0.0003	0.5130
chr5p-	2000001	3000000	0.0036	0.0536
chr5p-	16000001	20000000	0.0051	0.2535
chr5q-	111000001	116000000	0.0002	0.1246
chr5q-	162000001	171000000	0.0013	0.4386
chr5q-	172000001	181000000	0.0002	0.0001
chr6p-	41000001	42000000	0.0311	0.0180
chr6p-	43000001	47000000	0.0004	0.0001
chr6q-	100000001	102000000	0.0003	1.0000
chr6q-	151000001	171000000	0.0003	0.0001
chr7p-	47000001	48000000	0.0478	0.2433
chr7p-	49000001	50000000	0.0341	0.2433
chr7q-	107000001	108000000	0.0004	0.3633
chr7q-	121000001	124000000	0.0004	0.0001
chr7q-	138000001	145000000	0.0004	0.0031
chr8q-	48000001	53000000	0.0002	0.1131
chr8q-	67000001	71000000	0.0002	0.1131
chr8q-	145000001	146000000	0.0002	0.9306
chr9p-	8000001	11000000	0.0011	0.0024

chr9p-	28000001	31000000	0.0374	1.0000
chr9q-	85000001	88000000	0.00160	0.0050
chr9q-	117000001	123000000	0.0003	0.0001
chr9q-	134000001	135000000	0.0003	0.1450
chr10p-	1	5000000	0.0074	0.9486
chr10p-	34000001	39000000	0.0014	1.0000
chr10q-	44000001	46000000	0.0008	1.0000
chr10q-	118000001	122000000	0.0008	0.0001
chr11p-	2000001	7000000	0.0057	0.9892
chr11q-	90000001	94000000	0.0005	0.9146
chr11q-	121000001	122000000	0.0193	0.0181
chr12q-	51000001	54000000	0.0017	0.9923
chr12q-	104000001	105000000	0.0004	0.2335
chr12q-	108000001	113000000	0.0004	0.7037
chr12q-	126000001	133000000	0.0004	0.7037
chr13q-	35000001	46000000	0.0005	0.0001
chr14q-	74000001	79000000	0.0045	0.0163
chr14q-	102000001	106000000	0.0006	0.9997
chr15q-	21000001	24000000	0.0007	0.0074
chr15q-	27000001	29000000	0.0064	0.0707
chr16p-	2000001	9000000	0.0006	0.0029
chr16q-	77000001	90000000	0.0191	0.4924
chr16q-	78000001	79000000	0.0037	0.1938
chr17p-	1	4000000	0.0084	1.0000
chr17p-	8000001	16000000	0.0499	0.9094
chr17q-	33000001	34000000	0.0099	0.0036
chr17q-	47000001	50000000	0.0004	0.0214
chr18q-	39000001	43000000	0.0308	0.9999
chr18q-	54000001	57000000	0.0011	0.5256
chr18q-	73000001	75000000	0.0183	0.9311
chr19p-	6000001	8000000	0.0005	0.0037
chr19q-	42000001	46000000	0.0335	0.0599
chr20p-	18000001	24000000	0.0008	0.0066
chr20q-	44000001	47000000	0.0003	0.2161
chr20q-	48000001	49000000	0.0003	0.9807
chr20q-	49000001	50000000	0.0003	0.6392
chr21q-	40000001	46000000	0.0007	0.3028
chr22q-	49000001	50000000	0.0006	0.0001