

A

ChrX:136173873

PROX	CHRX	136173831	TTTGGAGTCACAGGTGGTGGCTTGCCTTAACATAACATAGTATCATTCAGCCTTCCACCCCAACCCCTATTCTTACTCCACCCCCACCCAGGCAGGCTCCA	136173930
S1		1	TTTGGAGTCACAGGTGGTGGCTTGCCTTAACATAACATAGTATCATTCAGCCTTCCAAAGTGTGGTATTACAGGTGTGAACCCACACCCAGCTAGTATT	100
DIST	CHRX	135619931	CCCAGGCAGGTCTTAGATTCTGACCTCGAGCGATCCTCCACTTCAGCCTTCCAAAGTGTGGTATTACAGGTGTGAACCCACACCCAGCTAGTATT	135620030

ChrX:135619986

ChrX:136259908

PROX	CHRX	136259860	CAAAGGACAGATGCCAGAGAGAACATGGAGGGGTAACGTAGAGACCAGCAACTGATCGGACATCAGAAGGGGTGCAGAAATGGGAGGGTTTGAAAAT	136259959
S11		1	CAAAGGACAGATGCCAGAGAGAACATGGAGGGGTAACGTAGAGACCAGCAAGAGGAGTGTCTCAGTGTGCAGGAGAAAAACATGAGAAGGTGAGTTTCT	100
DIST	CHRX	135601977	TTGAGCATTGGAGGTGAGACACAGGAGAAGGGGCCAGAAAAAGAGATCGAAGAGGAGTGTCTCAGTGTGCAGGAGAAAAACATGAGAAGGTGAGTTTCT	135602076

ChrX:135602028

ChrX:136254970

PROX	CHRX	136254921	AACCACCTCTTTGCTCTGCTCTTTCATCTAGCTTACAGAGAGTATCTTGTTCATTGCTGTATCTTCATAATTGCCCTCCAGTTGCTTTTCAGATTCTTTC	136255020
S15		1	AACCACCTCTTTGCTCTGCTCTTTCATCTAGCTTACAGAGAGTATCTTGTCCAAGTCCAGTTCATTGGAAAGCCACTACCTCTTCCCTTTCAGAGTATAA	100
DIST	CHRX	135596395	TTCTTCTCAAGTAGTAATAGCTCTGGGCTCTTTGTGAAGCCCTGAGGACCCAAGTCCAGTTCATTGGAAAGCCACTACCTCTTCCCTTTCAGAGTATAA	135596494

ChrX:135596446

B

chrX:136126345

PROX	CHRX	136126322	ATTCATGATACAACCACACCTCAAATCCCATAGTGATTTGGCACATATGTTTTCATGGTCCCTTTTTTATTATGTGTGTTTACCATTAAAACTTTTTG	136126421
S13		1	ATTCATGATACAACCACACCTCAAAGTTTGCAAAACCTGTGCTTGTCTCCGGCTCTACCTGGTCCCAGTGTATTATTCATTCAACAAGTAATTACTGA	100
DIST	CHRX	135549198	TAAACTAGAATATGTCCTGGCAGCTAAGCTCAGTCCATTGATCTGTGTGGAGAGCTATATTCATTTTATTTCATTTCATTCACAAGTAATTACTGA	135549297

chrX:135549274

135554730 CTTGTGCTTGTCTCCGGCTCTACCTGGTCCCAGTGTTT 135554767

*mutation C>T also exist in the normal CN segment

GTTTGCAAA can be matched to 3 positions at ~20 kb surrounding the breakpoint

- >1 TCCTAGAAGCTGTGTTTGCAAAACCTGAAACAAAATCA 136119567-136119576 (+)
- >2 GTTTGATGGACCTCAGGAAAGGGTGTGTTGCAAAACCTGAATGGGCTTGACCATCCAAAG 135533870-135533861 (-)
- >3 TGTGCGGCATCAAAATACTATTGTTTGCAAAATGTTTGTGAATCTTCCAAGTTAAGCA 135485271-135485262 (-)

chrX:136191776

PROX	CHRX	136191725	AAGAAGGAACCATTTTTGAATTTAGTTTTTATAATTTTCATATATTTGATACATAGGTGTGTATCCTCAAACAATGCATGGTATTGTTGTATAAATGG	136191824
S14		1	AAGAAGGAACCATTTTTGAATTTAGTTTTTATA-----*---TATTTGATACAGTCTATTTCTAGGAGGGCAGTCAGAATGGTAGCATTTAAAATGAAAG	100
DIST	CHRX	135622242	TTGCTGCAGTCACCTCCTAATTTGGTCTCATTGCTTCTTCCCTTCCCTCCTTCAGTCTATTTCTAGGAGGGCAGTCAGAATGGTAGCATTTAAAATGAAAG	135622341

*de novo mutation

chrX:135622296

chrX:136192229

PROX	CHRX	136192187	TTCTTTGAGTAAAAATTTGATCACATATGATGAAGGAAATGGGGGCCCATCCCTTATCCAAAGTCCCTAAGTGTCCACTGGTACAAGGTGCTGGGATAGA	136192286
S10		1	TTCTTTGAGTAAAAATTTGATCACATATGATGAAGGAAATGGGGGCCGCAAGGGGTGCTGCAGTAGTCCAGTTGAGAGGTGATGGTTAATAGATGGTTA	100
DIST	CHRX	135601383	CGCTGAGAGGAGGACAAACAGTGAAGGGCTGGTGGGAAAAGGTGGCCGCAAGGGGTGCTGCAGTAGTCCAGTTGAGAGGTGATGGTTAATAGATGGTTA	135601482

chrX:135601430

chrX:136123779

PROX	CHRX	136123733	TTGCTTGAACGTGGTATTGTTTGGTGGCTGTAGAGATCTTGCCAAAATGCCTCAAATGAGGACTACGAAAAATAGGATTATGTTTCCACATTTAGGC	136123832
S16		1	TTGCTTGAACGTGGTATTGTTTGGTGGCTGTAGAGATCTTGCCAA (ins) ATACATATATGCACATATATACATATACGAGTATACATGTGTTAACAT	100
DIST	CHRX	135533278	ATACATATATACATATATGCATATATATACATATATACATATATACATATATACATATATACATATATACATATATACATATATACATATATACATAT	135533377

chrX:135533330

ins: chrX: 136117823-136118113
 CTGATCATTTCCTAGAGACAGTTCCCGTATAATCACTCACAGTATTATTAATTCCTAGCTTCGTGCTGGCCATGGT
 ACAGAATCCTGGGTGGCATGCAGCTCAAGCGGTAGTTTGTTCAGACTCAATGATTTTACAATCACCTGGGAGGCAGTGA
 AGCTGCTAGAAGTGGCCAGAGACAAAGGCCAGTCTTCTTGACCTTCCATTTTATTGTTGGTTGTGACCATGCCGAG
 ACTGCTAGGTCCAGCAGGGGACCTCTAGACACATGTTAAAGATTGGTGC