# SUPPLEMENTARY MATERIAL

## Characterization of Chromosomal Translocation Breakpoint Sequences in Solid Tumours: "An *In Silico* Analysis"

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**Table S1. Nucleotide sequence of fusion partners retrieved from TICdb of major translocations.**

| Sr. No | Translocations | TICdb reference ID | Fusion sequences(FS) | Length of FS in bps | Partner Chr. Having 100% identity | Partner Genes [5' / 3'] | BLAT result of FS | UCSC location of FS | UCSC location for 500US /DS From Breakpoint |
|---|---|---|---|---|---|---|---|---|---|
| **(1)** | t(2;2) | 17625570 | atataatgtctaactcgggagactatgaaatattgtacTTGTACCGCCGGAAGCACCAGGAGCTGCAAGCCATGCAGATGGAGCTGC | 87 | Chr2 | 5' EML4 (I) | 1-39 | 42552656- 42552694 | 42552194-42553194 |
| | | | | | Chr2 | 3' ALK (I) | 40-87 | 29446347- 29446394 | 29445847-29446847 |
| **(2)** | t(10;10) | 10931090 | cccgagtagctggtattacaggcacacggcaccacacctggctgctttttgtaTTATCTCCTCAGCTGAGATGACCTTCCGGAGGCCCGCCCAGGCCTTCCCGGTCAGCTACTCCTCTTCCGGTG | 125 | Chr10 | 5' CCDC6 (I) | 1-55 | 61553383- 61553437 | 61552937-61553937 |
| | | | | | Chr10 | 3' RET (I) | 56-125 | 43610053- 43610122 | 43609553-43610553 |
| **(3)** | t(12;15) | 9949179 | atactgcatcagaaccatgaagaagATGTGCAGCACATTAAGAGGAGAGAC | 51 | Chr12 | 5'ETV6(I) | 1-25 | 12006471 12006495 | 12005995-12006995 |
| | | | | | Chr15 | 3'NTRK3(I) | 24-51 | 88483959 88483986 | 88483486-88484486 |
| **(4)** | t(5;6) | 18083107 | aagcccactgacgctccaccgaaagATGATTTTTGGATACCAGAAACAAGTTTCATACTT | 60 | Chr5 | 5'CD74(I) | 1-25 | 149784243 149784267 | 149783743-149784743 |
| | | | | | Chr6 | 3'ROS1(I) | 24-60 | 117645544 117645580 | 117645080-117646080 |
| **(5a)** | t(21;21) | 16575875 | cgctggcctactctggaagttcagAACTCTCCTGATGAATGCAGTGT | 47 | Chr21 | 5'TMPRSS2(I) | 1-24 | 42861433 42861456 | 42860933-42861933 |

| Sr. No | Translocations | TICdb reference ID | Fusion sequences(FS) | Length of FS in bps | Partner Chr. Having 100% identity | Partner Genes [5' / 3'] | BLAT result of FS | UCSC location of FS | UCSC location for 500US /DS From Breakpoint |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | Chr21 | 3'ERG(I) | 24-47 | 39795460 39795483 | 39794983-39795983 |
| **(5b)** | t(21;21) | 16575875 | gcaagatggctttgaactcagAAGCCTTATCAGTTGTGAGTG | 42 | Chr21 | 5'TMPRSS2(I) | 1-21 | 42870045 42870065 | 42869545-42870545 |
| | | | | | Chr21 | 3'ERG(I) | 21-42 | 39817523 39817544 | 39817044-39818044 |
| **(6)** | t(15;7) | 17671502 | caactaacactgcggcttcctgagTGCCTATGATCAGAAGCCACAAGTG | 49 | Chr15 | 5'HMGN2P46 (I) | 1-24 | 45806138 45806161 | 45805661-45806661 |
| | | | | | Chr7 | 3'ETV1(I) | 23-49 | 13975497 13975523 | 13975023-13976023 |
| **(7)** | t(1;X) | 9393982 | gtggttccatgatgggaagtgacatgCTGCCTGTGTCAGGGAATCTGCTT | 50 | Chr1 | 5'SFPQ(I) | 1-26 | 35652602 35652627 | 35652102-35653102 |
| | | | | | ChrX | 3'TFE3(I) | 26-50 | 48891743 48891767 | 48891267-48892267 |
| **(8)** | t(5;8) | 9525740 | tctgcgactcattcatcgccctccagATTGGCCAAAATGGGAAGGATTGGA | 51 | Chr5 | 5'LIFR(I) | 1-26 | 38595363 38595388 | 38594863-38595863 |
| | | | | | Chr8 | 3'PLAG1(I) | 25-51 | 57083724 57083750 | 57083250-57084250 |
| **(9)** | t(12;3) | 8988031 | tttcacaggaatgacagcatctatgaggagCCACAACAAGTTGTTCAGAAGAAGCCTGCT | 60 | Chr12 | 3'HMGA2(I) | 29-60 | 66345161 66345192 | 66344661-66345661 |
| | | | | | Chr3 | 5'FHIT(I) | 1-30 | 59908072 59908101 | 59907572-59908572 |
| **(10a)** | t(12;9) | 9484777 | agttgttcagaagaagcctgctcagTCCTGGTACCTGGGCTAGCTTGGTTCCTTTCCAAG | 60 | Chr12 | 5'HMGA2(I) | 1-25 | 66345171 66345195 | 66344695-66345695 |
| | | | | | Chr9 | 3'NFIB(I) | 23-60 | 14088291 14088328 | 14087828-14088828 |
| **(10b)** | t(12;9) | 9484777 | CcaagaggcagacctaggaaatggTCCTGGTACCTGGGCTAGCTTGGTTCCTTTCCAAGTG | 61 | Chr12 | 5'HMGA2(I) | 1-24 | 66232326 66232349 | 66231849-66232849 |
| | | | | | Chr9 | 3'NFIB(I) | 24-61 | 14088289 14088326 | 14087826-14088826 |
| **(11)** | t(9;15) | 17934517 | tatgtcaagtcttgtttacagaaaaagcaaaggaaaccgttctCATCTGCATTGCCGGGACCGGATATGAGCATGAAACCTAGT | 84 | Chr9 | 5'BRD3(I) | 1-43 | 136901154 136901196 | 136900654-136901654 |
| | | | | | Chr15 | 3'NUTM1(I) | 43-84 | 34640170 34640210 | 34639670-34640670 |
| **(12)** | t(22;21) | S82335 | ctattcctctacacagccgactagttatgatcatCAGATTCTTGGACCAACAAGTAGCCGCCTTGCAAATCCAG | 74 | Chr22 | 5'EWSR1(I) | 1-33 | 29682912 29682944 | 29682444-29683444 |

| Sr. No | Translocations | TICdb reference ID | Fusion sequences(FS) | Length of FS in bps | Partner Chr. Having 100% identity | Partner Genes [5' / 3'] | BLAT result of FS | UCSC location of FS | UCSC location for 500US /DS From Breakpoint |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | Chr21 | 3'ERG(I) | 33-74 | 39762917 39762958 | 39762458-39763458 |
| **(13a)** | t(22;11) | 18602673 | agcagcagctacgggcagcagaACCCTTCTTATGACTCAGTC | 42 | Chr22 | 5'EWSR1(I) | 1-22 | 29683102 29683123 | 29682623-29683623 |
| | | | | | Chr11 | 3'FLI1(I) | 23-42 | 128675261 128675280 | 128674761-128675761 |
| **(13b)** | t(22;11) | S62665 | AGCCAACAGAGCAGCAGCTACGGGCAGCAGAGTCCTCCC CTTGGAGGGGCACAAACGATC | 66 | Chr22 | 5'EWSR1(I) | 1-33 | 29683093 29683125 | 29682625-29683625 |
| | | | | | Chr11 | 3'FLI1(I) | 32-60 | 128677075 128677103 | 128676575-128677575 |

***Note:*** Sequence in lower case represents 5' partner gene and upper case represents 3' partner gene. US: upstream, DS: downstream.

**Table S2. Analysis and characterization of various parameters for 1000bps (500 bp Upstream & 500 bp Downstream) sequence around breakpoint.**

| Sr no. | Translocations | Chr. partners | Location of RSS | Location of Repeats | Partner Gene [5' / 3' ends] & Intronic(I)/ Exonic (E) Break | # of SIDD sites [Threshold cut off of G(x) <4] |
|---|---|---|---|---|---|---|
| **(1)** | t(2;2) | Chr2 | U(435 – 462, 225 – 263, 250 – 288) | D (518-585)€ | 5' EML4 (I) | 1 |
| | | Chr2 | D(534 - 561,795 – 833) | D(802-1215)€ | 3' ALK (I) | 5 |
| **(2)** | t(10;10) | Chr10 | U (75 - 113) | W(323-610)€/D(694-714) T | 5' CCDC6 (I) | 7 |
| | | Chr10 | U(127 – 165)<br>D(851 – 889) | U(112-282)¥ | 3' RET (I) | 1 |
| **(3)** | t(12;15) | Chr12 | U(244 - 282 ,288 - 326 ),<br>D(839 - 866 ,959 - 986 ) | U(1-128)€ ,D(592-639)¥ , D(815-1000) D | 5'ETV6(I) | 3 |
| | | Chr15 | D(551 - 578 ) | D(702-790 , 983-1000)€ , D(841-968)D | 3'NTRK3(I) | 2 |
| **(4)** | t(5;6) | Chr5 | U(28 - 55 , 291 - 329 ) | U(2-37)€ | 5'CD74(I) | 1 |
| | | Chr6 | D(686 - 724 , 709 - 747) | D(639-718 , 952-1000) D | 3'ROS1(I) | 11 |
| **(5a)** | t(21;21) | Chr21 | U(105 - 132,105 - 143,<br>267 - 305), D(676 - 703 ) | D(873-1000)€ | 5'TMPRSS2(I) | 3 |

| Sr no. | Translocations | Chr. partners | Location of RSS | Location of Repeats | Partner Gene [5' / 3' ends] & Intronic(I)/ Exonic (E) Break | # of SIDD sites [Threshold cut off of G(x) <4] |
|---|---|---|---|---|---|---|
| | | Chr21 | U(26 - 53, 32 - 59 ) ,<br>D(573 - 611,822 - 860 ) | U(22-60)$^{S}$ ,U(118-146)$^{\pounds}$, D(643-918)$^{\text{€}}$ , D(922-945)$^{S}$ | 3'ERG(I) | 4 |
| **(5b)** | t(21;21) | Chr21 | D(956 - 994) | ___ | 5'TMPRSS2(I) | 2 |
| | | Chr21 | U(134 - 172 ) , D(936 - 974) | U(8-191)$^{\text{€}}$ | 3'ERG(I) | 4 |
| **(6)** | t(15;7) | Chr15 | U(271 - 309) | U(12-502)$^{\yen}$,D(511-598,924-1000)$^{\yen}$ , D(600-923)$^{\text{€}}$ | 5'HMGN2P46(I) | 3 |
| | | Chr7 | U(413 - 451 ) | D(994-1000)$^{\pounds}$ | 3'ETV1(I) | 8 |
| **(7)** | t(1;X) | Chr1 | D(951 - 989 ) | U(409-435)$^{S}$ ,<br>D(948-1000)$^{\text{€}}$ | 5'SFPQ(I) | 7 |
| | | ChrX | ___ | ___ | 3'TFE3(I) | 1 |
| **(8)** | t(5;8) | Chr5 | U(132 - 170) | U(64-208)$^{D}$ ,<br>D(785-877, 972-1000)$^{\text{€}}$ | 5'LIFR(I) | 4 |
| | | Chr8 | U(466 - 493 ) , D(837 - 864 ) | D(832-857)$^{\pounds}$ | 3'PLAG1(I) | 10 |
| **(9)** | t(12;3) | Chr12 | U(50 - 77) | U(52-357)$^{\text{€}}$ ,<br>D(763-791)$^{\pounds}$ | 3'HMGA2(I) | 9 |
| | | Chr3 | ___ | ___ | 5'FHIT(I) | 6 |
| **(10a)** | t(12;9) | Chr12 | U(16 - 43) | U(20-325)$^{\text{€}}$ , D(733-761)$^{\pounds}$ | 5'HMGA2(I) | 10 |
| | | Chr9 | ___ | U(348-375)$^{\pounds}$ | 3'NFIB(I) | 10 |
| **(10b)** | t(12;9) | Chr12 | U(108 - 146 ) | D(904-947)$^{S}$ | 5'HMGA2(I) | 8 |
| | | Chr9 | ___ | U(348-375)$^{\pounds}$ | 3'NFIB(I) | 12 |
| **(11)** | t(9;15) | Chr9 | U(364 - 402 ) | ___ | 5'BRD3(I) | 1 |
| | | Chr15 | U(49 - 87) ,<br>D(624 - 662 ,844 - 882 ) | U(1-112 , 128-407)$^{\text{€}}$ | 3'NUTM1(I) | 3 |
| **(12b)** | t(22;21) | Chr22 | U(222 - 249,305 - 332, 356 - 383) | U(1-264)$^{\text{€}}$ ,<br>D(754-1000)$^{\text{€}}$ | 5'EWSR1(I) | 6 |
| | | Chr21 | U(5 - 43 , 313 - 340 ) ,<br>D(874 - 912 ) | U(1-255)$^{\pounds}$ | 3'ERG(I) | 6 |
| **(13a)** | t(22;11) | Chr22 | U(43 - 70,126 - 153 , | U(1-77)$^{\text{€}}$ , | 5'EWSR1(I) | 4 |

| Sr no. | Translocations | Chr. partners | Location of RSS | Location of Repeats | Partner Gene [5' / 3' ends] & Intronic(I)/ Exonic (E) Break | # of SIDD sites [Threshold cut off of G(x) <4] |
|---|---|---|---|---|---|---|
| | | | 177 - 204), D(883 - 910 ) | D(565-1000)$^{€}$ | | |
| | | Chr11 | ___ | U(68-287)$^{€}$ | 3'FLI1(I) | 8 |
| **(13b)** | t(22;11) | Chr22 | U(41 - 68 , 124 - 151,175 - 202) ,D(881 - 908) | U(1-73)$^{€}$ ,<br>D(562-1000)$^{€}$ | 5'EWSR1(I) | 4 |
| | | Chr11 | ___ | U(75-378)$^{¥}$ ,<br>D(733-929)$^{€}$ | 3'FLI1(I) | 7 |

***Note:*** W: within, U: upstream, D: downstream of the breakpoint. €=Sine, ¥ = Line, £= Low complexity repeat, T=Tandem repeats, D = DNA Repeat, S= simple repeat

**Table S3. Analysis of physico-chemical parameters/AT% within destabilized region (SIDD) & 1000 bps sequence around breakpoint.**

| Serial No. | Translocation | Chromosome Partner | Partner Gene [5' / 3' ends] | Base pair Location | Flexibility (kJ /mol A$^2$) | Melting Temperature ($^{o}$C) | Stacking Energy (kcal/mol) | AT (%) |
|---|---|---|---|---|---|---|---|---|
| | | | | | **Expected Values** | | | |
| | | | | | **7.931** | **73.622** | **-8.080** | |
| **(1)** | t(2;2) | Chr2 | EML4 | 1..1001 | 8.602 | 66.943 | -7.297 | 64.1 |
| | | | | 495..600 | 9.001 | 55.519 | -6.136 | 69.5 |
| | | Chr2 | ALK | 1..1001 | 7.766 | 73.333 | -7.958 | 48.5 |
| | | | | 663..803 | 9.458 | 62.461 | -6.760 | 57.9 |
| **(2)** | t(10;10) | Chr10 | CCDC6 | 1..1001 | 8.544 | 69.180 | -7.502 | 59.3 |
| | | | | 654..813 | 9.433 | 62.831 | -6.794 | 65.3 |
| | | Chr10 | RET | 1..1001 | 7.042 | 77.745 | -8.459 | 38.7 |
| | | | | 418..454 | 8.459 | 74.581 | -8.344 | 74.1 |
| **(3)** | t(12;15) | Chr12 | 5'ETV6 | 1..1001 | 8.189 | 71.104 | -7.756 | 55.8 |
| | | | | 488..623 | 9.121 | 67.538 | -7.341 | 65.7 |
| | | Chr15 | 3'NTRK3 | 1..1001 | 7.925 | 72.920 | -7.916 | 53.7 |
| | | | | 425..599 | 7.924 | 74.195 | -8.133 | 62.5 |
| **(4)** | t(5;6) | Chr5 | 5'CD74 | 1..1001 | 7.542 | 75.690 | -8.179 | 45.8 |
| | | | | 523..622 | 7.888 | 72.598 | -7.945 | 53.9 |
| | | Chr6 | 3'ROS1 | 1..1001 | 9.023 | 65.170 | -7.046 | 71.4 |
| | | | | 443..549 | 9.920 | 60.957 | -6.593 | 82.5 |

| Serial No. | Translocation | Chromosome Partner | Partner Gene [5' / 3' ends] | Base pair Location | Flexibility (kJ /mol A$^2$) | Melting Temperature ($^o$C) | Stacking Energy (kcal/mol) | AT (%) |
|---|---|---|---|---|---|---|---|---|
| | | | | | Expected Values | | | |
| | | | | | **7.931** | **73.622** | **-8.080** | |
| **(5a)** | t(21;21) | Chr21 | 5'TMPRSS2 | 1..1001 | 7.813 | 72.936 | -7.929 | 35.2 |
| | | | | 539..670 | 8.391 | 70.153 | -7.687 | 48.4 |
| | | Chr21 | 3'ERG | 1..1001 | 7.834 | 73.090 | -7.981 | 54.3 |
| | | | | 486..620 | 8.584 | 70.674 | -7.745 | 65.3 |
| **(5b)** | t(21;21) | Chr21 | 5'TMPRSS2 | 1..1001 | 7.829 | 73.131 | -7.928 | 53.1 |
| | | | | 440..672 | 9.037 | 66.783 | -7.250 | 67.8 |
| | | Chr21 | 3'ERG | 1..1001 | 8.327 | 71.554 | -7.786 | 56.3 |
| | | | | 490..710 | 9.129 | 67.834 | -7.352 | 65.2 |
| **(6)** | t(15;7) | Chr15 | 5'HMGN2P46 | 1..1001 | 8.345 | 70.454 | -7.640 | 60.5 |
| | | | | 451..597 | 8.505 | 69.878 | -7.615 | 63.6 |
| | | Chr7 | 3'ETV1 | 1..1001 | 9.026 | 66.615 | -7.199 | 65.8 |
| | | | | 459..598 | 9.274 | 67.475 | -7.248 | 76.3 |
| **(7)** | t(1;X) | Chr1 | 5'SFPQ | 1..1001 | 8.653 | 68.140 | -7.388 | 63.6 |
| | | | | 324..471 | 9.373 | 65.499 | -7.033 | 69.3 |
| | | ChrX | 3'TFE3 | 1..1001 | 7.863 | 73.596 | -7.958 | 49.2 |
| | | | | 519..596 | 8.008 | 73.803 | -7.934 | 61.6 |
| **(8)** | t(5;8) | Chr5 | 5'LIFR | 1..1001 | 8.208 | 71.100 | -7.734 | 55.6 |
| | | | | 338..486 | 8.543 | 71.271 | -7.652 | 66.1 |
| | | Chr8 | 3'PLAG1 | 1..1001 | 8.886 | 66.034 | -7.165 | 66.2 |
| | | | | 413..580 | 9.117 | 67.847 | -7.343 | 73.4 |
| **(9)** | t(12;3) | Chr12 | 3'HMGA2 | 1..1001 | 8.805 | 67.061 | -7.265 | 64.1 |
| | | | | 385..579 | 9.667 | 63.274 | -6.804 | 74.3 |
| | | Chr3 | 5'FHIT | 1..1001 | 8.518 | 68.835 | -7.523 | 60.2 |
| | | | | 472..626 | 8.655 | 69.445 | -7.599 | 71.4 |
| **(10a)** | t(12;9) | Chr12 | 5'HMGA2 | 1..1001 | 8.776 | 67.293 | -7.293 | 64.4 |
| | | | | 408..606 | 9.722 | 63.428 | -6.807 | 73.7 |
| | | Chr9 | 3'NFIB | 1..1001 | 9.166 | 65.848 | -7.123 | 67.3 |
| | | | | 300..546 | 9.319 | 68.225 | -7.302 | 74.7 |

| **Serial No.** | **Translocation** | **Chromosome Partner** | **Partner Gene [5' / 3' ends]** | **Base pair Location** | **Flexibility (kJ /mol $A^2$)** | **Melting Temperature ($^o$C)** | **Stacking Energy (kcal/mol)** | **AT (%)** |
|---|---|---|---|---|---|---|---|---|
| | | | | | **Expected Values** | | | |
| | | | | | **7.931** | **73.622** | **-8.080** | |
| **(10b)** | t(12;9) | Chr12 | 5'HMGA2 | 1..1001 | 9.379 | 65.759 | -7.116 | 68.3 |
| | | | | 414..548 | 9.606 | 66.236 | -7.106 | 79.1 |
| | | Chr9 | 3'NFIB | 1..1001 | 9.153 | 65.944 | -7.135 | 67.1 |
| | | | | 490..716 | 9.264 | 64.234 | -6.959 | 70.3 |
| **(11)** | t(9;15) | Chr9 | 5'BRD3 | 1..1001 | 7.420 | 76.818 | -8.321 | 43.2 |
| | | | | 493..600 | 8.882 | 69.527 | -7.585 | 61.4 |
| | | Chr15 | 3'NUTM1 | 1..1001 | 7.908 | 73.850 | -7.999 | 49.5 |
| | | | | 385..578 | 9.219 | 68.324 | -7.348 | 63.4 |
| **(12)** | t(22;21) | Chr22 | 5'EWSR1 | 1..1001 | 8.200 | 71.633 | -7.787 | 55.1 |
| | | | | 389..514 | 9.382 | 67.398 | -7.336 | 65.3 |
| | | Chr21 | 3'ERG | 1..1001 | 8.331 | 70.033 | -7.629 | 57.4 |
| | | | | 419..541 | 8.950 | 68.334 | -7.434 | 64.6 |
| **(13a)** | t(22;11) | Chr22 | 5'EWSR1 | 1..1001 | 8.245 | 71.199 | -7.736 | 55.2 |
| | | | | 489..611 | 9.265 | 67.670 | -7.308 | 66.7 |
| | | Chr11 | 3'FLI1 | 1..1001 | 8.765 | 68.196 | -7.410 | 61.3 |
| | | | | 472..601 | 8.863 | 67.694 | -7.311 | 63.8 |
| **(13b)** | t(22;11) | Chr22 | 5'EWSR1 | 1..1001 | 8.261 | 71.150 | -7.729 | 55.1 |
| | | | | 486..611 | 9.173 | 67.639 | -7.305 | 64.5 |
| | | Chr11 | 3'FLI1 | 1..1001 | 8.560 | 69.460 | -7.545 | 58.3 |
| | | | | 659..817 | 9.312 | 65.801 | -7.163 | 68.2 |

**Table S4. Analysis & characterization of various parameters of housekeeping gene GAPDH taken as control.**

| Sr No. | Genomic location of GAPDH Gene(12p13.31) (feb 2009/hg19) | Length of exonic sequences (Bps) | Genomic location of RSS (feb 2009/hg19) | Genomic Location of Repeats (feb 2009/hg19) | # of SIDD sites [Threshold cut off of G(x) <4] | Flexibility (kJ /mol $A^2$) | Melting Temperature ($^o$C) | Stacking Energy (kcl/mol) | AT (%) |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | **Cutoff Values (ROC)** | | | |
| | | | | | | **7.9**<br>**Sp=100**<br>**Sn=96.7** | **73.6**<br>**Sp =100**<br>**Sn =100** | **-8.1**<br>**Sp=100**<br>**Sn=100** | **47.5**<br>**Sp=100**<br>**Sn=96.7** |
| **(1)** | 6643977 – 6644026 (E) | 51 | 0 | 0 | 0 | 7.4 | 77.3 | -8.5 | 40.0 |
| **(2)** | 6646087 – 6646176 (E) | 90 | 0 | 0 | 0 | 7.3 | 77.2 | -8.5 | 40.1 |
| **(3)** | 6646268 – 6646382 (E) | 115 | 0 | 0 | 0 | 7.5 | 73.6 | -8.0 | 47.3 |
| **(4)** | 6646476 – 6646556 (E) | 81 | 0 | 0 | 0 | 7.3 | 74.2 | -8.1 | 47.5 |
| **(5)** | 6646749 – 6647162 (E) | 413 | 0 | 0 | 0 | 7.2 | 77.2 | -8.4 | 40.7 |
| **(6)** | 6643927 – 6644026 (I/E) | 100 | 0 | 0 | 0 | 7.1 | 80.4 | -8.85 | 34.3 |
| **(7)** | 6646037 – 6646136 (I/E) | 100 | 0 | 0 | 0 | 7.5 | 75.4 | -8.15 | 41.9 |
| **(8)** | 6646218 – 6646317 (I/E) | 100 | 0 | 0 | 0 | 7.3 | 75.9 | -8.25 | 42.4 |
| **(9)** | 6646426 – 6646525 (I/E) | 100 | 0 | 0 | 0 | 7.1 | 77.5 | -8.4 | 39.8 |
| **(10)** | 6646701 – 6646800 (I/E) | 100 | 0 | 0 | 0 | 7.3 | 76.7 | -8.3 | 41.1 |

***Note:*** E: Core Exonic sequence; I/E: Intron exon flanking sequence; Sp: Specificity; Sn: Sensitivity.

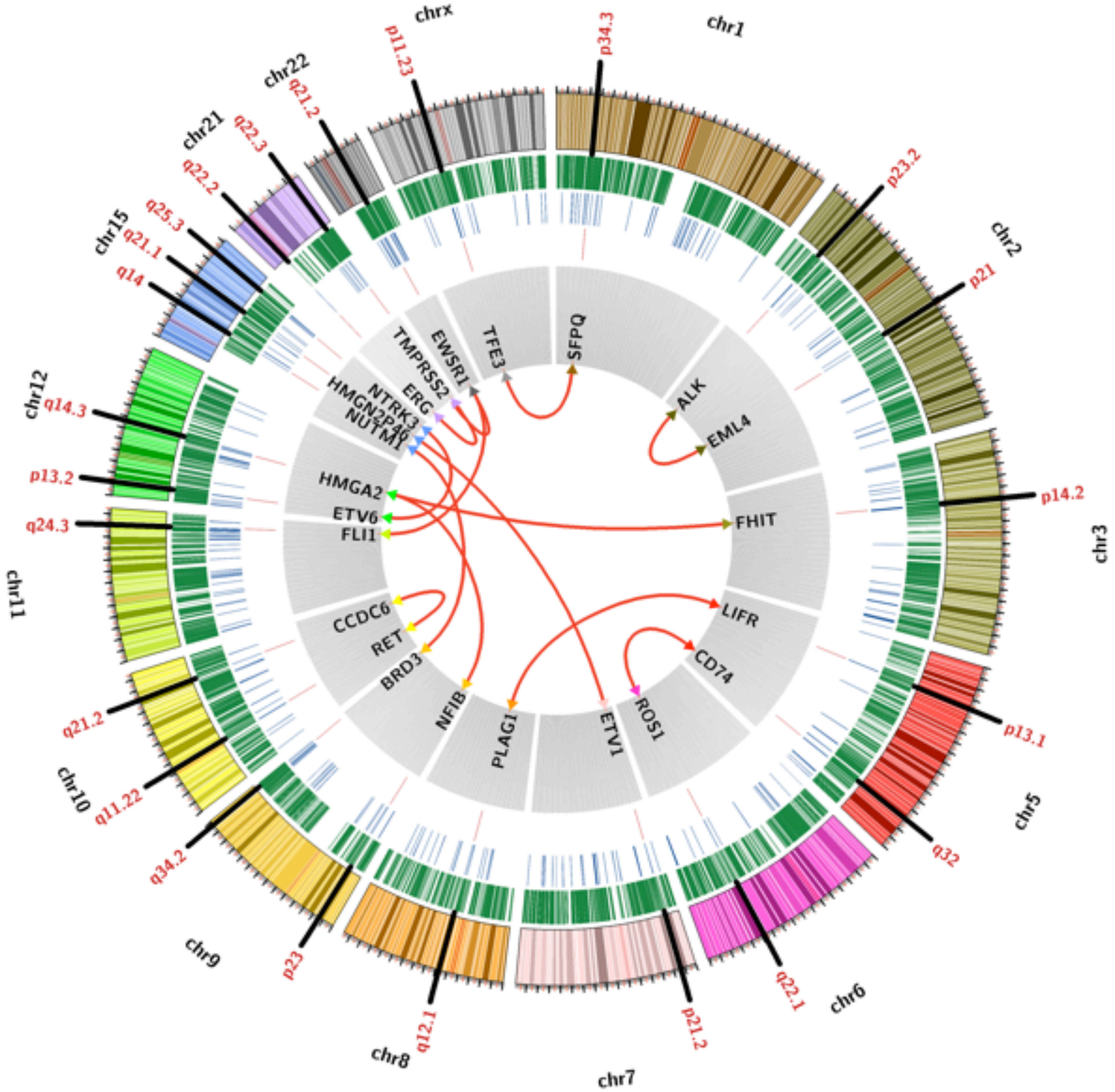

**Fig. (S1). Circos plot of chromosomal translocations (Oncogenic Fusion genes) in solid tumors.** Outer most track indicates the total length of the chromosomal coordinates in the clockwise direction (scale 1 = 1000000bps). The second track is denoting the complete set of genes of respective chromosomes. The next (blue bands) shows the total numbers of cancerous genes present within each of these chromosomes and the innermost track (red bands) depicts oncogenic fusion genes involved in the rearrangements which are shown by connecting lines and their cytobands (red) are shown on the outermost circle.

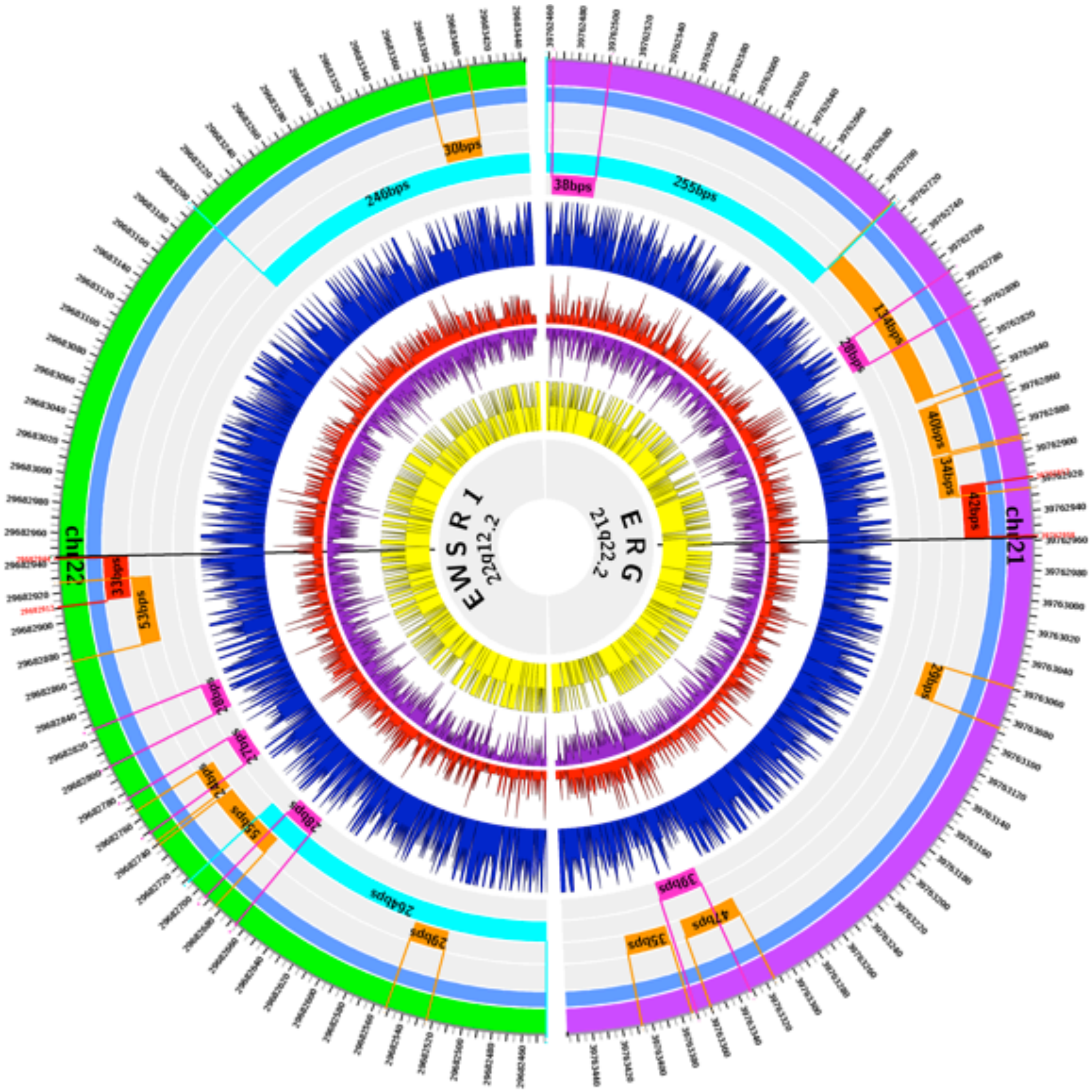

**Fig. (S2). Circos plot of various physico-chemical parameters at BpI for translocation t(21;22)**. Sequential/ systematic depiction of all the parameters at or near the breakpoint region that are scrutinized in our study. The outermost trail demarcates the *BpI* sequence of 1000 bps of chr 21 (magenta) and 22 (fluorescent Green) in clockwise direction. While the inner trails demarcate various parameters as mentioned: Intronic region(blue); TICdb fusion sequence (red); SIDD regions(orange); Repeats (turquoise blue); Recombination signal sequence region (RSS-pink); graphical representation of Flexibility (dark blue); Stability(red); Stacking Energy (purple); Percentage of AT content(yellow); name of genes and their locations are mentioned in innermost circle. Horizontal black line indicates the exact breakpoint location and the respective features present at that particular point of break.