

**Supporting Information Table S2 Information of the selected 81 SSR markers from published studies**

	Marker <sup>a</sup>	Name <sup>b</sup>	Chr.	Forward Primers (5'-3')	Reverse Primers (5'-3')	Physical Position(V3)	Physical Position(V4) <sup>c</sup>	P
The first selected 19 SSR markers between P1 and P2	901		7	CGTAGTAGGGCTTGGGCAAG	TTTCTCGGAGACAGGCCATG	10854180-10854465	11248040-11248323	
	927		7	TGCCACCCACATTGACTCTC	TTGCGGCAGAGATAGCAACA	11519940-11520131	12007969-12008160	
	972		7	GCCAGTGAATTGGTTTCCGC	CGCTAGCGCCTGTAGAGAAT	12873508-12873714	13462219-13462425	
	<b>992</b>	<b>P3</b>	7	<b>CGGGACCTGATTGCTCGTAG</b>	<b>TCGCTCCTCTAGGCTCTCTC</b>	<b>13231795-13232004</b>	<b>13824683-13824892</b>	<b>P</b>
	<b>1029</b>	<b>P4</b>	7	<b>CAATCAAACGCCGTGATCCC</b>	<b>AGCATTTTGACCTCTTGCGA</b>	<b>14197331-14197483</b>	<b>14732666-14732818</b>	<b>P</b>
	1067		7	TCGCTACTTGCCTGTTTCAAG	CGCAGCGGTTGTAGTCTGTA	14785512-14785605	15399596-15399688	
	1125		7	ATGGGTCGCTTAGGGAGACT	TCGCTTTGCCTTGTGGTGTG	15652264-15652654	16284340-16284730	
	<b>1153</b>	<b>P5</b>	7	<b>CCTGGCTTGTACTCAAATCTGC</b>	<b>CTGGCATAACTTGTCCGGGT</b>	<b>16163525-16163719</b>	<b>16823929-16824123</b>	<b>P</b>
	1194		7	TAGTTGGGCGAGCAACACAT	TGTGTTGGCACCTTCCAAGT	17349333-17349540	18105102-18105308	
	1661		7	CGCACACCCAAACCTGAAAG	GCACGGGTACTIONCACCTAGTG	29305425-29305588	28216112-28216275	
	<b>1677</b>	<b>P6</b>	7	<b>ACAGGCGACTAAACCTTCGG</b>	<b>TGTGAAGTCACCTTGGGCTG</b>	<b>29715364-29715554</b>	<b>28606159-28606349</b>	<b>P</b>
	1690		7	CCTCGTCGTGTTGGCCTAAA	GGTGCTCTGATGAATTGGTGC	29849982-29850209	28757849-28758076	
	<b>1717</b>	<b>P7</b>	7	<b>GAGCACACACCTGCCAAAAT</b>	<b>CCACCAGTAGTCCTGCTGTG</b>	<b>30540782-30540994</b>	<b>29510995-29511207</b>	<b>P</b>
	<b>1746</b>	<b>P8</b>	7	<b>TTCACCCGGACGGTTAGTTG</b>	<b>ACCACGCAGTTCTCCTAGTT</b>	<b>31349971-31350103</b>	<b>30362128-30362260</b>	<b>P</b>
	1790		7	CGGCCGAGAGTCTGATTTGA	TCGAAACCCACTCCGACAAC	32426181-32426332	31223578-31223728	
	1835		7	TGCCAGCTGATGAACGTCTT	GAACGTCATGCATGCACACA	33515488-33515584	32451032-32451128	
	1870		7	TCTTTCTAGGGTTGGCCGAAG	CACCGTGCCATCTCTGTGAT	34510104-34510296	33530631-33530823	
1906		7	ATCAAGACCATGGCCCAAGG	CCAAGAGATCGAGCGGTACC	35546196-35546533	34595429-34595766		
<b>1933</b>	<b>P9</b>	7	<b>CGTTAGATATGATGCCAGCAAG T</b>	<b>ACCCATGAGTGTTCGACGT</b>	<b>36203853-36204062</b>	<b>35260523-35260732</b>	<b>P</b>	
<b>The</b>	<b>1232</b>	<b>P10</b>	7	<b>GCTTGGCTGGAGCACTTTTT</b>	<b>ACCTTTTCATGTCCATGTTGC</b>	<b>17709018-17709233</b>	<b>18422707-18422923</b>	<b>P</b>

second selected 62 SSR markers between P5 and P6	1253		7	CCGCATACACAGGGCTCTAG	CCTCGTGGAGTTGCTTCACT	18179486-18179991	18966656-18967161	
	1294		7	GTGGAGACGCAACTCACAGA	TCGTCTTCCTTCCACCTTGC	19141214-19141282	19975949-19976013	
	1337		7	TTGTCTTGGCCCTGACGAAA	CAGATGACTCTGCACCTCAAGA	19978823-19979006	20841981-20842164	
	1370		7	CGCCCAAGATGAGATGTGCT	GTCAATGCCTCTGGACCTTGA	20744322-20744548	21788805-21789031	
	1408		7	GGCTAACATGTAGTGCGGGT	AAGGAACTGTCTGGAGTCGC	21264205-21264333	22317688-22317816	
	<b>1426</b>	<b>P11</b>	<b>7</b>	<b>CATGCTGCTGCTCAGGGAC</b>	<b>CCATGGCAGTCCTTACCCTG</b>	<b>21623669-21623884</b>	<b>22698588-22698803</b>	<b>P</b>
	1444		7	GCGTGTTCGAGAAAATTGGT	CACCACTCCTGTTCACAGCA	22002576-22002706	23065521-23065653	
	1461		7	TTTGTGAAGCCGAAGCCTCA	AGCCAGAGGTGCAACTTCAA	22496228-22496401	23581295-23581468	
	1472		7	GGAGGCTTCGAAGGACATGT	TCCCTTGGACGTACCCTCTC	22637728-22637931	23725554-23725757	
	<b>1525</b>	<b>P12</b>	<b>7</b>	<b>TGAAGCCTCAACGCAGACAT</b>	<b>CGCAGCCCTATCTTCGTCAT</b>	<b>25925543-25925708</b>	<b>24741196-24741361</b>	<b>P</b>
	<b>1538</b>	<b>P13</b>	<b>7</b>	<b>GTGCTCGATCGCCTCTGTAA</b>	<b>AAAGCTTGGTGGAGAGACCG</b>	<b>26382426-26382656</b>	<b>25228666-25228891</b>	<b>P</b>
	<b>1540</b>	<b>P14</b>	<b>7</b>	<b>CGCGTACGAAAATGCACACT</b>	<b>TGCCCATATACTCCACGGGA</b>	<b>26457074-26457237</b>	<b>25302228-25302391</b>	<b>P</b>
	1549		7	AGTGAATTGGCATCAGCAGA	AAATTCATTCCCTCGCGGCT	26659345-26659548	25457660-25457863	
	1551		7	CACATGGGGTCAAATAGGCCT	CACCGGTTGGAGTCGATCAA	26874068-26874402	25715930-25716264	
	1554		7	CTCTCGGACTCGTTAACCGG	TTCCCGCCGTCCCAAAAATA	26929730-26930101	25853323-25853694	
	1556		7	TGGGACATAATAGGTGAGAGCAC	AAGTGTTACTTGGCCGAACC	27041104-27041305	25921229-25921431	
	<b>1557</b>	<b>P15</b>	<b>7</b>	<b>AATGACCCACGATCGTACCG</b>	<b>AGAGTCCATTAGCATCCCTAC CT</b>	<b>27056876-27057049</b>	<b>25936995-25937168</b>	<b>P</b>
	1559		7	CGTCTTTGGCTCCTTCAGGA	AGGGGTCGCTTTGAGCTTTT	27059056-27059188	25939175-25939306	
	1560		7	TGCTTCCACCCTTGTTACACA	TCATCAAGCAAGTGAAAGGGC	27106072-27106355	25976667-25976947	
	1562		7	CCCTCCTGCGGATTTACACA	CTCCTCGTCTCGATCTGTG	27327034-27327295	26217320-26217580	
1563		7	GTAGAAGACGAGGGACTGCG	ACGTGTTCTCGACAAGTCC	27327296-27327393	26218312-26218409		
1567		7	TGGCAATTACTGTGCTAACGC	TCCTTCCCCCAGGATCTGAC	27539733-27539937	26379099-26379309		
1570		7	GCATGTGAAAAACAAAAGGA CA	TGTTGTCATCAATCATCTCGAAA A	27685798-27685912	26594019-26594130		

1571		7	TACCCATCAGGCCTTTGCAG	GTGCCGAGTGCCACATAGTA	27742581-27742769	26652092-26652278	
1572		7	GCTACCAGTTGCTCTTGGA	ATGCGGTGCAGGTTTGAATC	27751596-27751749	26660337-26660490	
1573		7	CGCGAGCACGGCTAGTATAT	ATCCGCGTGTACACTCTTT	27907597-27907804	26818732-26818937	
1574		7	TCACTGTGTCTCGTGTCTCT	AGAAGGGGAGCAATCTTGACA	27991395-27991603	26900975-26901183	
<b>1575</b>	<b>P16</b>	<b>7</b>	<b>CTAGGTTTGTTCGCGGCAAG</b>	<b>CATGCATGTCCCCCTTGT</b>	<b>27993961-27994144</b>	<b>26903541-26903724</b>	<b>P</b>
1576		7	GGGTCCAATCCTCCTCCCTT	GAAGTTGGAAGAACGATGCGA	27999281-27999410	26908861-26908988	
1577		7	GGATAACCACGCGTCATCT	GTGCTTGCTCTAGGTTGTTCC	28009768-28009975	26919346-26919553	
1578		7	GCACAGGGAGAGACGAGAGA	TGTAGAGGATGTTTGTAGGTGCT	28017589-28017789	26927167-26927367	
1579		7	TGCTTGATCTTTCGGTCGT	GCAAGAACACCATAGCCCCT	28023201-28023356	26932778-26932933	
1580		7	TGGAGAAGGAGACGTCGACA	CCACTACTAAAATATCGAACCC AGA	28024056-28024272	26933633-26933849	
1582		7	AGGGTTGTTGGAAGGATGCC	GCGATTTTCGTGGCTTTCGA	28025086-28025305	26934663-26934882	
1583		7	CTCCTTCCACCTTTGCCGAT	GAGGTGCGAACAGAGCAGTA	28025396-28025554	26934973-26935131	
1584		7	CAGGCCTTTCAGCGGTCTAA	ACGGAGTAGGAGACAAAAAGC A	28025874-28025966	26935451-26935543	
1585		7	CACCTATCGGAAGCCCAAGG	GCTTCTGCAACAGTAGCTGC	28099805-28100026	26969389-26969608	
1586		7	TGGGGATCAGCACCTGTACT	CCACATGCACTTACTCTCCCA	28101860-28102065	26971442-26971644	
1587		7	ACAAGGAGATCACGGGAGGA	GTGGCGGGCCTAGAGTTTAG	28102946-28103179	26973333-26973560	
1588		7	GATGGCAGTGTCTAAGGGGG	ACCCATCCCGTTTTTCATCCC	28113443-28113593	26983025-26983175	
1589		7	ATGCATCAGACTAGCCGCAG	GTGGATCCACAGCACAGTGT	28114508-28114692	26984090-26984274	
1590		7	GGATAGCAATGCCCGGTGT	TGGCAGCGTCATGGTAACTT	28114905-28114988	26984487-26984569	
1591		7	ACCCTTGCAAGTCCGTATAC	CGAACGGGAGTACAACGACA	28117135-28117315	26986766-26986946	
1592		7	AAGAGAAGGGCTGAAGGGGA	CGACAAGTCACCAAGATGGGT	28121369-28121489	26991000-26991120	
1594		7	CTGCTCAGTTCGGTGTGCTA	GCATCGCTGTACCTTCTCT	28208498-28208641	27084585-27084728	
1595		7	CTGCCGTCACCTACACCG	TGACGACTCAGACGACTCCA	28252402-28252597	27129166-27129359	

1596		7	GTCAACCAGTAAAGCGTGCG	TGGCTGTGACTTCCCCTACT	28330785-28330932	27213602-27213747	
1599		7	TCGCGTGTAAGCCGAGATAC	CGGCTTGGGTGCATTCTCTA	28364133-28364382	27240611-27240860	
1600		7	CCAGGTGCATTTTAGTGCCG	ACAACACTGTGTCCAACCGA	28365190-28365304	27241668-27241784	
1601		7	GGCCGAGCGCTGCATATATA	CGGACCGAGAAAGGCAAGAT	28366046-28366250	27242526-27242730	
1604		7	TGGTTGGATTGCTCGACCTG	CTAGTGAAGGACCGCCTGTC	28393839-28394068	27269934-27270160	
1606		7	TGTGGTGGTGTGTAGTGGTG	GGGGTGATCGAACTGAGCTT	28395318-28395530	27270585-27270797	
<b>1607</b>	<b>P17</b>	7	<b>GCACAACCTGATTCTCCCA</b>	<b>ATAGGACGAGCCGACCAAAC</b>	<b>28397396-28397615</b>	<b>27273852-27274065</b>	<b>P</b>
1611		7	AGTCGAGACGAAGAGGACGA	CAACATTCCGCCCCGAATTC	28447279-28447408	27322535-27322664	
1615		7	GGTACAGGAGGAGACAAAGTCA	CGCAAGAAGGACAGTGGCTA	28604517-28604723	27478940-27479146	
1617		7	TGTTGTCTGGTCCGTACGTG	CCGTGGAACCAAATACTCCCA	28661333-28661528	27535749-27535944	
1630		7	GATGAGGAACACGAGGGCAA	AATACTTCTACTGCCCTGAACTA A	28708217-28708478	27574208-27574469	
1632		7	CTGCATACACGGCATCATGC	AGACGGAAGCACACACTGTT	28778981-28779234	27707552-27707805	
1645		7	CTCTTAGGCGTCACCCGTTT	ATGCTCGGACGCCATAAGAG	29008092-29008294	27897440-27897642	
<b>1648</b>	<b>P18</b>	7	<b>TATGTTGTACGGGTGCTGCT</b>	<b>CGGTCCGGACTCTTCTCTTT</b>	<b>29054891-29055079</b>	<b>27946097-27946285</b>	<b>P</b>
1658		7	GCGTCGAATGAGTAGGGGAG	GAACCGAACTAGCACCACCA	29220573-29220775	28120526-28120728	

<sup>a</sup>The information cited from previous study (Xu et al., 2013), <sup>b</sup> Marker name used in map-based clong of *mn2-ml* in this study, <sup>c</sup> The physical position (V4) by Blast search *Zea mays*

(Ensembl Genomes 56) by us. Chr., Chromosome; P, Polymorphic both between the two parents and the two DNA pools.