

Supporting Online Material for

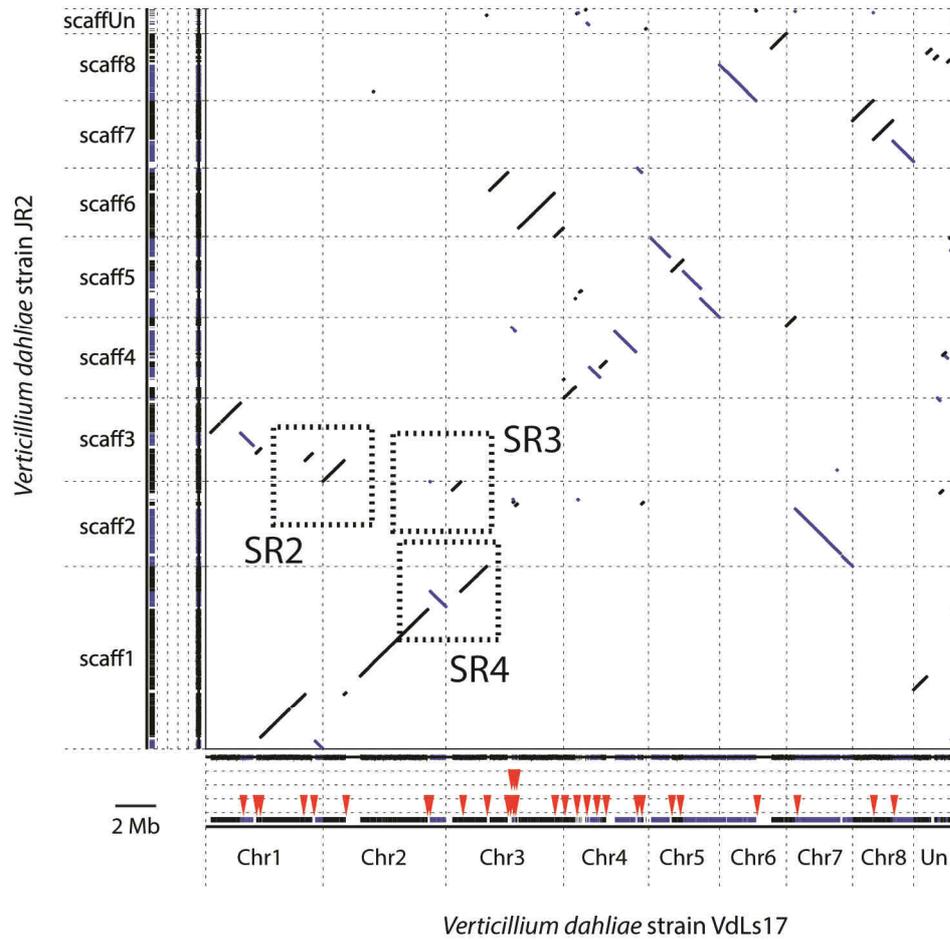
Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen

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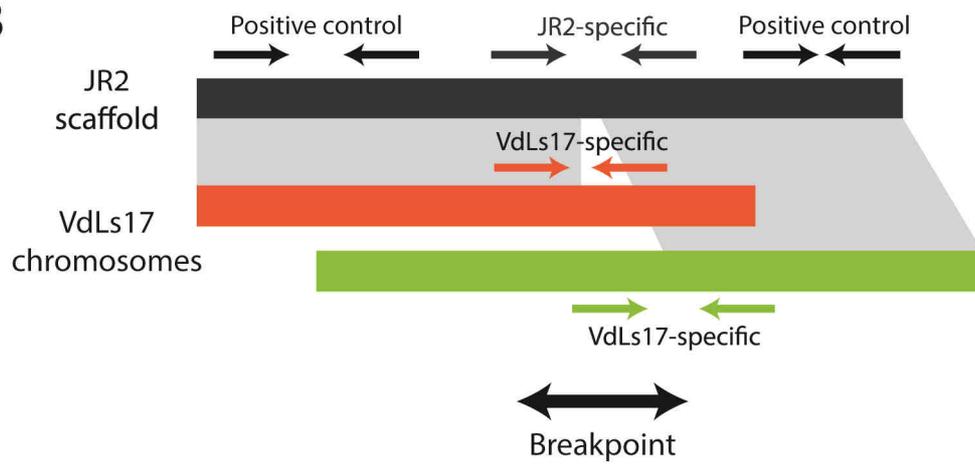
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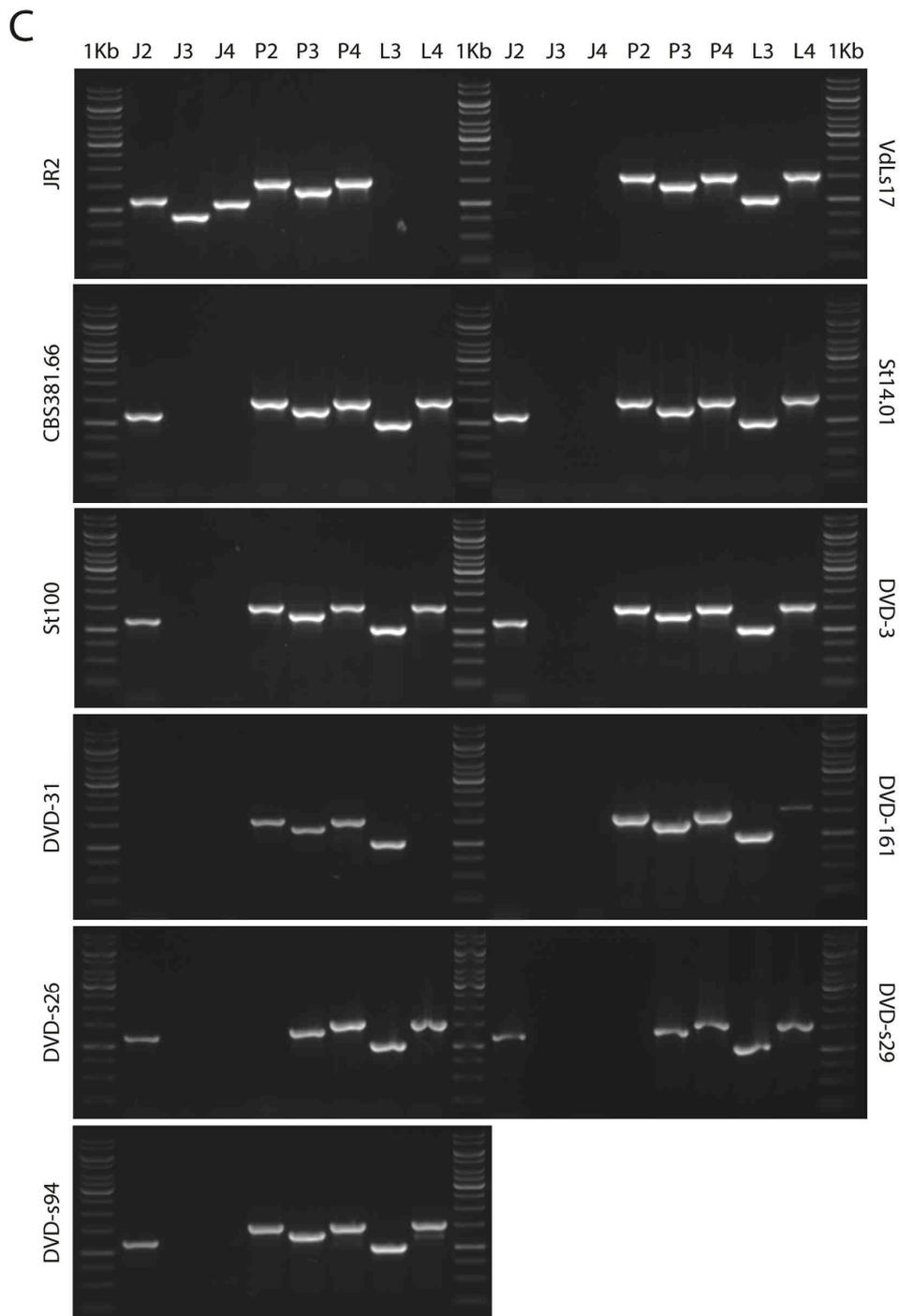
This PDF file includes: supplementary Figures and Legends 1-3; Supplementary Tables 1-12

A

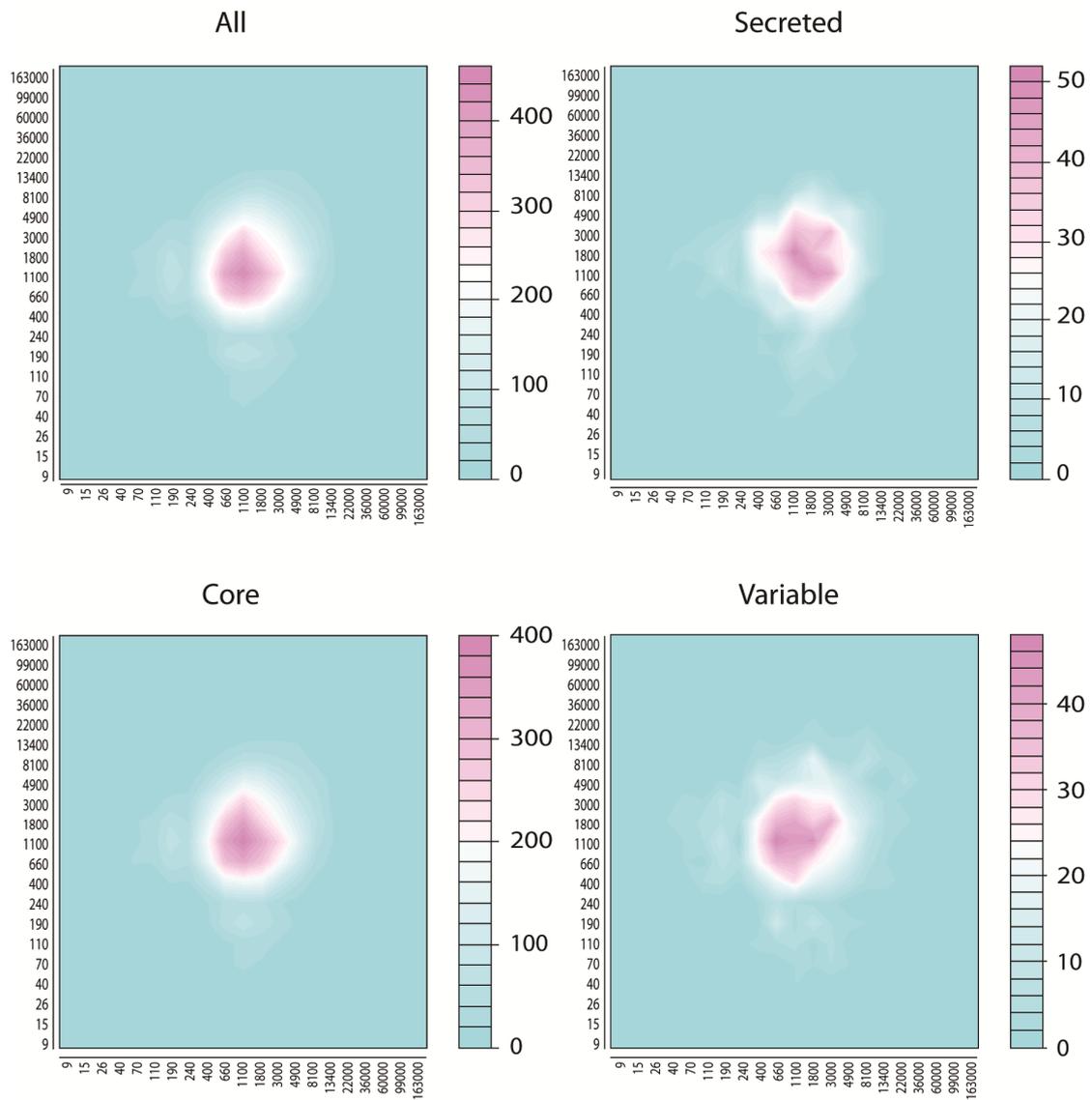


B



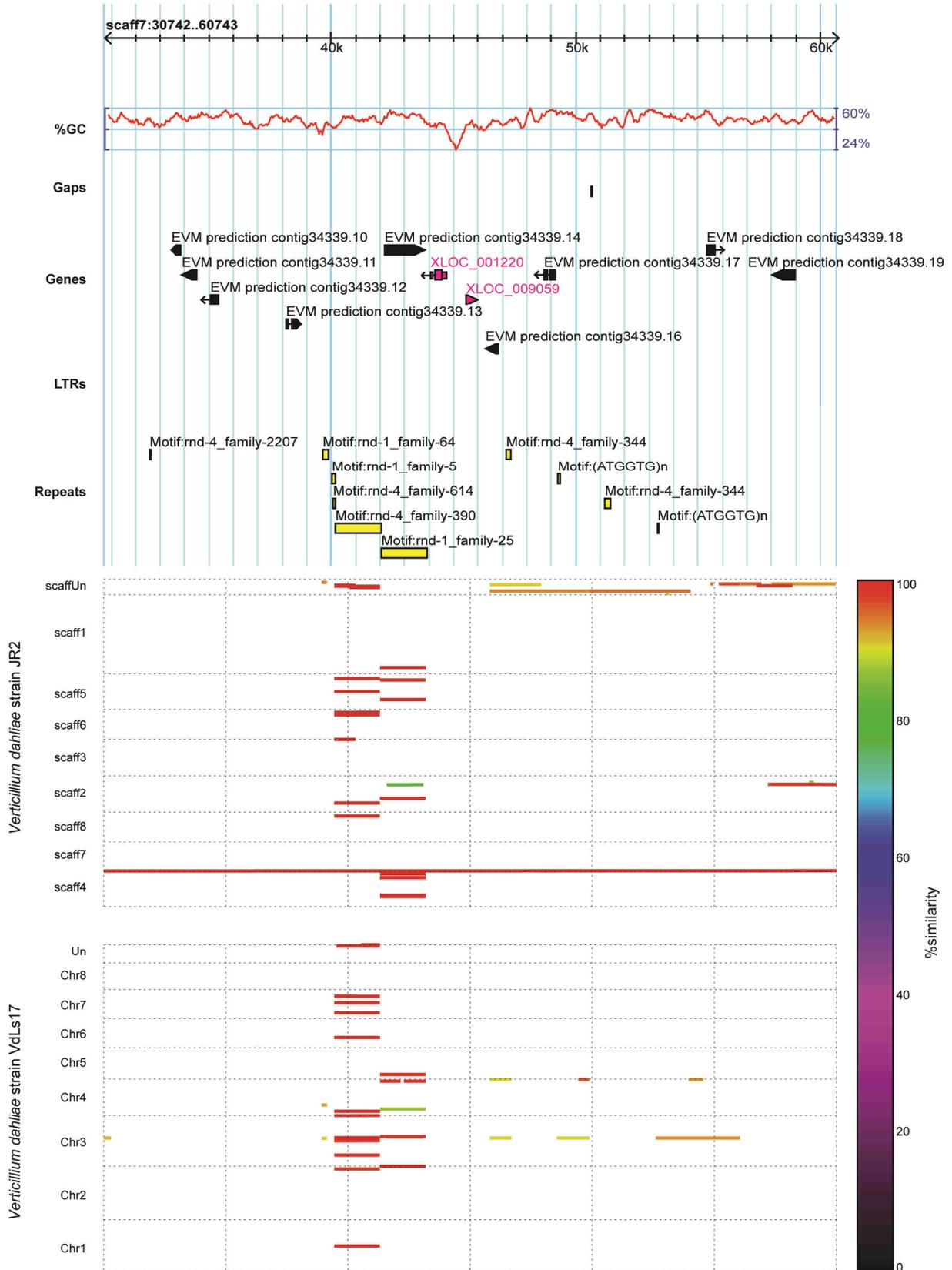


Supplemental Figure 1. Verification of chromosomal rearrangements by PCR. **A**, Whole-genome alignment of *Verticillium dahliae* strains VdLs17 and JR2 highlighting three PCR-verified rearrangements (boxed). **B**, Schematic representation of the PCR set-up, illustrating the positions of JR2- and VdLs17-specific primer sets and control primer sets. **C**, PCR amplification of structural rearrangements SR2, SR3 and SR4 in isolates JR2, VdLs17, St14.01, CBS381.66, St100, DVD-3, DVD-31, DVD-s26, DVD-s29, DVD-s94 and DVD-161 using JR2-specific primer sets J2, J3 and J4, respectively, and amplification of rearrangements SR3 and SR4 in JR2, VdLs17, St14.01, CBS381.66, St100, DVD-3, DVD-31, DVD-s26, DVD-s29, DVD-s94 and DVD-161 using VdLs17-specific primer sets L3 and L4, respectively. Control primer sets are shown by P2, P3 and P4.

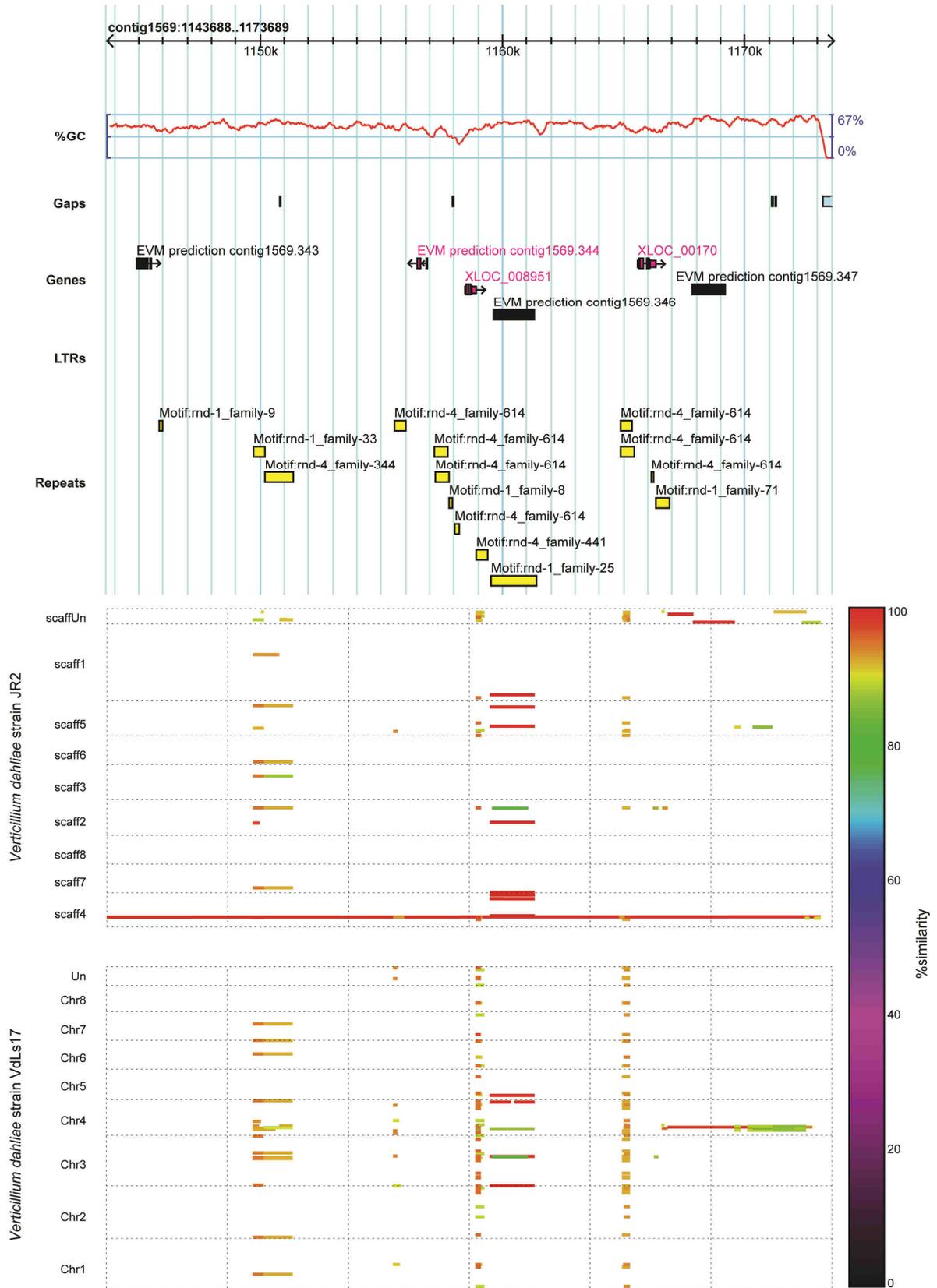


Supplemental Figure 2. Gene density plots for *Verticillium dahliae* strain JR2. 5'- and 3'-flanking intergenic regions were calculated and placed in two-dimensional bins. The figure was prepared using the *filled.contour* graph function in R.

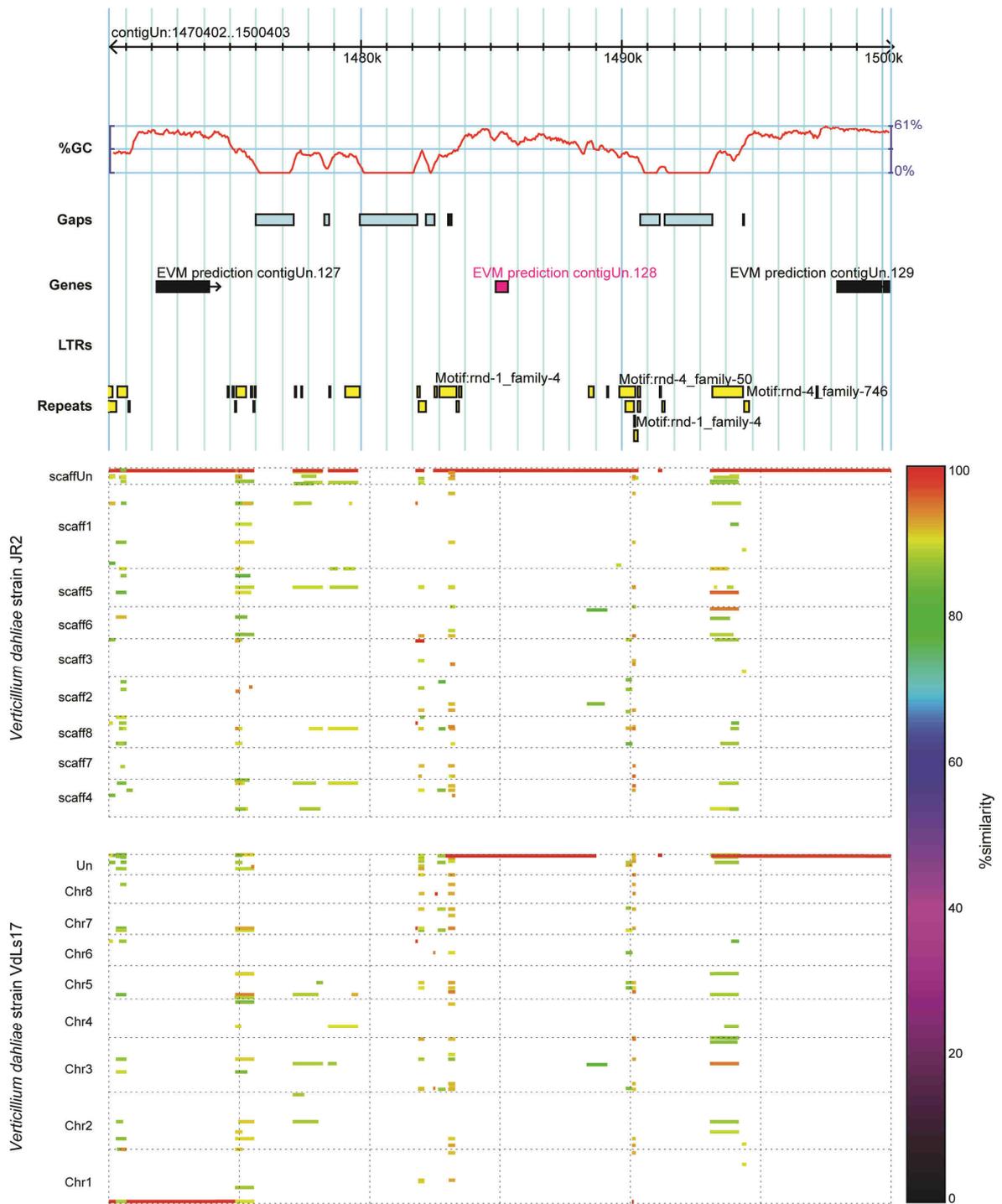
A) scaff7:30742..60743 | XLOC_009059 ; XLOC_001220



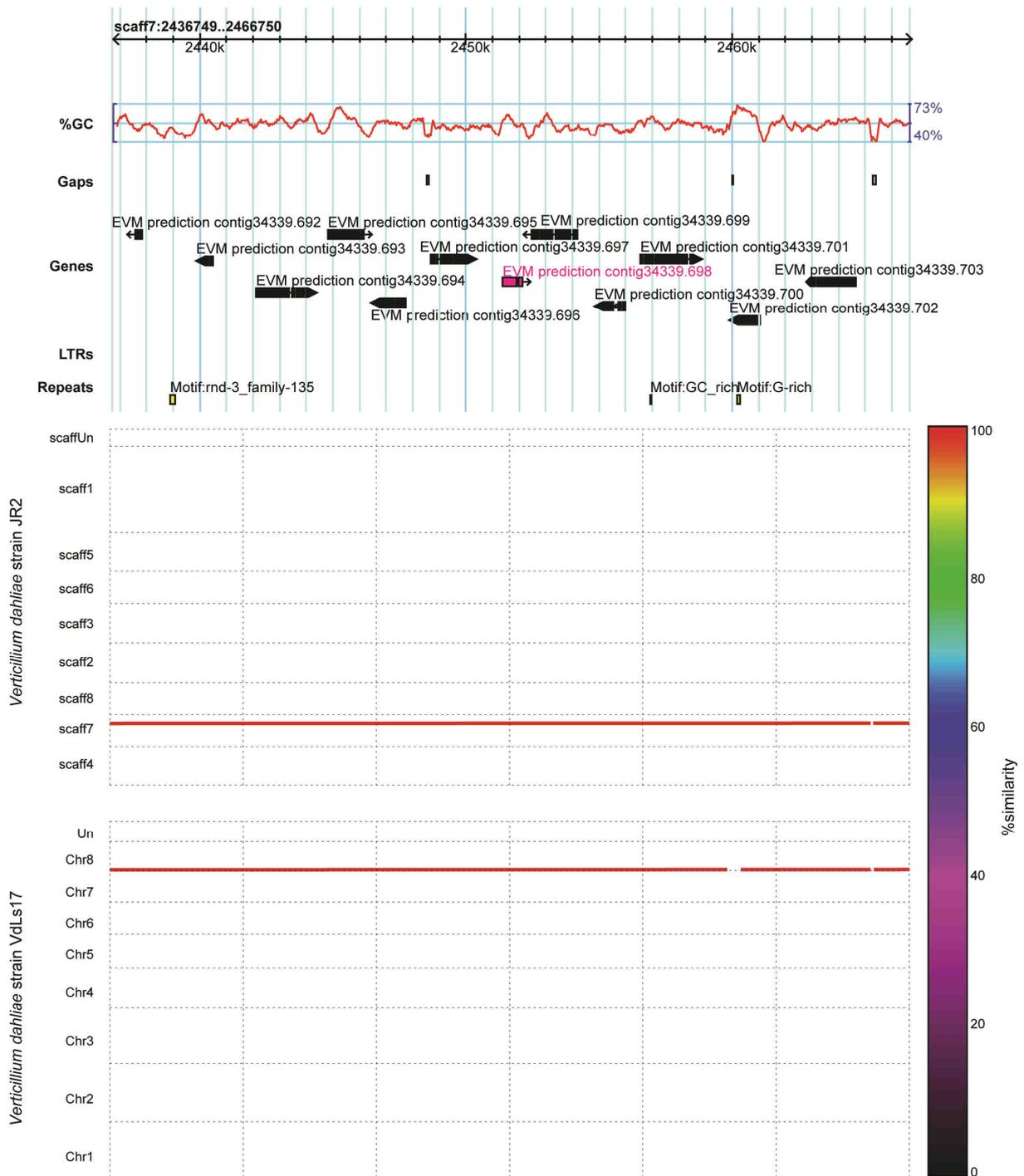
B) scaff4:1143688..1173689 | evm.model.contig1569.344 ; XLOC_008951 ; XLOC_00170



C) scaffUn:1470402..1500403 | evm.model.contigUn.128



D) scaff7:2436749..2466750 | *evm.model.contig34339.698*



Supplemental Figure 3. Genomic context of identified (candidate) effector genes found in variable genomic regions in *V. dahliae* strain JR2. A, Repetitiveness of the genomic context of *XLOC_009059* and *XLOC_01220*. B, Repetitiveness of the genomic context of *evm.model.contig1569.344*, *XLOC_008951* and *XLOC_00170*. C, Repetitiveness of the genomic context of *evm.model.contigUn.128*. D, Repetitiveness of the genomic context of *evm.model.contig34339.698*. The top section for panels A-D indicate the percentage GC, gaps, genes, LTRs (as predicted by the LTR_finder) and repeats (as predicted by the RepeatMasker using JR2-specific RepeatModeler repeat families). Notable repeat families identified include Ty1-Gypsy elements (rnd4_family614), LINE

elements (rnd4_family-344) and TcMar-Fol elements (rnd1_family-25; rnd4_family390). The bottom section for panels A-D highlight alignments between each scaffold section and the complete chromosome sequences of JR2 (top) and VdLs17 (bottom). The degree of conservation is indicated by a color scale, showing recent (red) and more ancient (orange to green) multiplications.

Supplementary Table 1. *Verticillium dahliae* strains used in this study.

Strain	Race	Originating host	Location	Year of collection	Tomato [#]	Tobacco*	Arabidopsis*
JR2	1	Tomato	ON, Canada	<1995	++	√	√
CBS381.66	1	Tomato	QC, Canada	1963	++	√	√
St14.01	1	Pistachio	CA, USA	?	++	√	√
St.100	n.a.	Soil	Belgium	?	-	√	√
DVD-3	2	Potato	Canada	1993	+	√	√
DVD-31	2	Tomato	Canada	1993	+	√	√
DVD-161	2	Potato	ON, Canada	1993	+/-	√	√
DVD-S26	2	Soil	Canada	1994	+	√	√
DVD-S29	2	Soil	Canada	1994	+/-	-	√
DVD-S94	2	Soil	Canada	1996	+/-	√	√
VdLs17	2	Lettuce	USA, CA	1995 ~ 2001	+/-	√	√

[#]Aggressiveness on susceptible tomato ranging from highly aggressive (++; severe stunting, wilting and chlorosis/necrosis), to aggressive (+; stunting and intermediate wilting), mildly aggressive (+/-; intermediate stunting, mild wilting) and non-pathogenic (-; no symptoms visible).

*Ability to infect this host (√) or not (-)

Supplementary Table 2. *Verticillium dahliae* strain VdLs17 genes under positive selection pressure.

#GeneId	Length (GENE)	Length (EXON)	dN ^(a)	dS ^(a)	Length (CDS)	NA ^(b)	NS ^(b)	Ka ^(c)	Ks ^(c)	Ka/Ks ^(d)	VarKa ^(e)	VarKs ^(e)	Z-test ^(f)	Secreted ^(g)	SignalP ^(h)	Annotated function
VDAG_000582	2999	2520	10	0	2517	1888,52	628,48	5,30E-03	0,00E+00	∞	2,79E-06	0,00E+00	3,17	-	0,11	dimethylguanosine trna methyltransferase
VDAG_00839	2322	2256	6	0	2253	1705,60	547,40	3,52E-03	0,00E+00	∞	2,06E-06	0,00E+00	2,45	-	0,10	transcription initiation factor TFIIID subunit 12
VDAG_01342	2656	2275	7	0	1731	1306,23	424,77	5,36E-03	0,00E+00	∞	4,08E-06	0,00E+00	2,65	-	0,12	nitrogen assimilation transcription factor nirA
VDAG_01486	537	537	8	0	534	391,65	142,36	2,04E-02	0,00E+00	∞	5,11E-05	0,00E+00	2,86	-	0,15	predicted protein
VDAG_02208	500	435	7	0	432	324,09	107,91	2,16E-02	0,00E+00	∞	6,52E-05	0,00E+00	2,67	-	0,12	predicted protein
VDAG_02267	1806	1806	9	0	1803	1343,07	459,93	6,70E-03	0,00E+00	∞	4,96E-06	0,00E+00	3,01	-	0,30	predicted protein
VDAG_02339	1803	1803	7	0	1800	1372,13	427,87	5,10E-03	0,00E+00	∞	3,70E-06	0,00E+00	2,65	-	0,10	HMG box-containing protein
VDAG_02840	318	318	6	0	315	237,54	77,46	2,53E-02	0,00E+00	∞	1,04E-04	0,00E+00	2,48	-	0,12	predicted protein
VDAG_03846	966	879	6	0	876	669,72	206,28	8,96E-03	0,00E+00	∞	1,33E-05	0,00E+00	2,46	-	0,11	D-arabinitol 2-dehydrogenase
VDAG_04361	1783	1704	14	1	1701	1251,81	448,88	1,12E-02	2,23E-03	5,01	8,82E-06	0,00E+00	2,41	-	0,13	dihydrolipoamide branched chain transacylase e2
VDAG_04808	509	399	14	0	396	303,03	92,97	4,62E-02	0,00E+00	∞	1,45E-04	0,00E+00	3,83	-	0,11	conserved hypothetical protein
VDAG_05878	1287	1287	10	0	1284	971,49	312,51	1,03E-02	0,00E+00	∞	1,05E-05	0,00E+00	3,18	-	0,12	DNA polymerase epsilon subunit C
VDAG_05906	429	429	6	0	426	319,25	106,76	1,88E-02	0,00E+00	∞	5,78E-05	0,00E+00	2,47	-	0,11	predicted protein
VDAG_06500	798	687	6	0	684	510,44	173,56	1,18E-02	0,00E+00	∞	2,28E-05	0,00E+00	2,46	-	0,34	predicted protein
VDAG_06885	4123	3619	81	12	3540	2672,07	867,93	3,03E-02	1,38E-02	2,19	1,10E-05	1,57E-05	3,19	-	0,11	conserved hypothetical protein
VDAG_07379	529	479	6	0	360	279,66	80,34	2,15E-02	0,00E+00	∞	7,51E-05	0,00E+00	2,48	-	0,45	hypothetical protein
VDAG_07402	1164	1164	6	0	1161	866,99	294,01	6,92E-03	0,00E+00	∞	7,93E-06	0,00E+00	2,46	-	0,12	conserved hypothetical protein
VDAG_08090	2863	2811	7	0	2808	2081,83	726,17	3,36E-03	0,00E+00	∞	1,61E-06	0,00E+00	2,65	-	0,13	conserved hypothetical protein
VDAG_09372	1635	1176	9	0	1173	887,88	285,12	1,01E-02	0,00E+00	∞	1,13E-05	0,00E+00	3,02	-	0,16	ZnF3
VDAG_09727	1547	1434	8	0	1305	989,01	315,99	8,09E-03	0,00E+00	∞	8,11E-06	0,00E+00	2,84	Y	0,60	cellulose-growth-specific protein
VDAG_10137	1784	1647	9	0	1644	1243,09	400,91	7,24E-03	0,00E+00	∞	5,78E-06	0,00E+00	3,01	Y	0,58	DUF1237 domain-containing protein

VDAG_10149	3662	3579	25	2	3576	2652,14	923,86	9,43E-03	2,16E-03	4,35	3,52E-06	2,34E-06	3,00	-	0,10	conserved hypothetical protein
VDAG_10153	1945	1458	7	0	1356	1031,18	324,82	6,79E-03	0,00E+00	∞	6,54E-06	0,00E+00	2,65	-	0,12	uridine kinase
VDAG_10193	1244	1194	9	0	1191	890,33	300,67	1,01E-02	0,00E+00	∞	1,12E-05	0,00E+00	3,02	Y	0,71	cellulose-binding family II
VDAG_10212	1262	1194	6	0	1191	889,74	301,26	6,74E-03	0,00E+00	∞	7,53E-06	0,00E+00	2,46	-	0,13	alpha/beta hydrolase fold protein
VDAG_10215	3223	3105	8	0	3102	2356,38	745,62	3,40E-03	0,00E+00	∞	1,44E-06	0,00E+00	2,83	-	0,13	extragenic suppressor of kinetochore protein
VDAG_10216	954	831	6	0	828	629,81	198,19	9,53E-03	0,00E+00	∞	1,50E-05	0,00E+00	2,46	-	0,11	conserved hypothetical protein
VDAG_10218	1546	1392	6	0	1389	1039,96	349,04	5,77E-03	0,00E+00	∞	5,52E-06	0,00E+00	2,46	-	0,16	nuclear distribution protein nudF
VDAG_10513	2077	1967	6	0	1605	1238,87	366,13	4,84E-03	0,00E+00	∞	3,89E-06	0,00E+00	2,46	-	0,12	sulfite oxidase

a) Number of non-synonymous (dN) and synonymous substitutions (dS).

b) Number of non-synonymous (NA) and synonymous sites (NS).

c) Non-synonymous substitutions per non-synonymous site (Ka) and synonymous substitutions per synonymous site (Ks)

d) Undefined (∞) means that zero synonymous substitutions were found; calculating a Ka/Ks ratio would require division by zero.

e) Variance of Ka (VarKa) and Ks (VarKs)

f) Z-test score for significance (Stukenbrock et al. 2012). Z-test ≥ 2.45 is considered significant with $p < 0.01$.

g) Secretome prediction by Klosterman et al., (2011).

h) Signal peptide prediction score according to SignalP4.0 (D-score; Petersen et al., 2011). Proteins with prediction score ≥ 0.5 are considered secreted.

Supplementary Table 3. Summary of the optical mapping results.

Statistic	Result
# of contigs	273
# of significant contigs (>30 kb)	75
# of contigs placed	81
% of contigs placed	29.7%
Total size of placed contigs	32.0 Mb
Total size of unplaced contigs	1.2 Mb
% of genome covered	93.62
Number of gaps over 2 kb	51
Average gap size	50.4 kb
Total size of gaps	3.2 Mb

Supplementary Table 4. Chromosome length statistics.

	VdLs17	JR2
Chr1 / scaff1	5,746,300	9,141,183
Chr2 / scaff2	6,048,892	4,240,912
Chr3 / scaff3	5,770,546	4,159,763
Chr4 / scaff4	4,180,501	4,033,922
Chr5 / scaff5	3,484,688	4,064,734
Chr6 / scaff6	3,28,934	3,411,043
Chr7 / scaff7	3,251,708	3,361,023
Chr8 / scaff8	2,995,396	3,353,035
Un / scaffUn	2,113,671	1,771,480

Supplementary Table 5. Primers used in this study.

Primer ID	Primer sequence	Target
J2-2-F	TTCATGTCTGTCTTTACCGATT	JR2 re-arrangement SR2
J2-2-R	TATGAGGTTTAGGGTTACCGTTT	JR2 re-arrangement SR2
J3-F	TTTTGGTCGTGGTTGCAATA	JR2 re-arrangement SR3
J3-R	CGGCAAATCAGAAGAACCTC	JR2 re-arrangement SR3
J4-F	CCACACAAAGCATCACAACC	JR2 re-arrangement SR4
J4-R	CCACACATACAGACCGCATC	JR2 re-arrangement SR4
P1-F	GGCAGAAGTCAGTACGAGGA	Positive control JR2 and Ls17 (around SR3)
P1-R	TGACATCAATCTCCAAAGCCT	Positive control JR2 and Ls17 (around SR3)
P2-F	GTCACGCACTATACGGACCT	Positive control JR2 and Ls17 (around SR4)
P2-R	CCTACTTCAAGTTTATGCGCGTC	Positive control JR2 and Ls17 (around SR4)
L3-F	AATTCTGTACCTCTGTCCGT	VdLs17 re-arrangement SR3
L3-R	CGCTACTTGATACTGTGAAAGG	VdLs17 re-arrangement SR3
L4-F	GGAGAAAGATACGGAGAAATGG	VdLs17 re-arrangement SR4
L4-R	GAGATTGAGATTGCGATGGGA	VdLs17 re-arrangement SR4
KO-VDAG_05180-F1	GGACTTAAUAGTTTTGCCTGACAGTAGGT	Knock-out construct VDAG_05180
KO-VDAG_05180-R1	GGGTTTAAUAATTGATAGTGAACGGCTTC	Knock-out construct VDAG_05180
KO-VDAG_05180-F2	GGTCTTAAUGGTTTTCTACGCCAGTATC	Knock-out construct VDAG_05180
KO-VDAG_05180-R2	GGCATTAAUTTGTCTGACATGTTTCTCGT	Knock-out construct VDAG_05180
KO-XLOC_009059-F1	GGTCTTAAUCTCTCCGCTCAGCCTCTCTA	Knock-out construct XLOC_009059
KO-XLOC_009059-R1	GGCATTAAUTTGAAGCTAAACCGGGTCTG	Knock-out construct XLOC_009059
KO-XLOC_009059-F2	GGACTTAAUTACGCGGAGGATCCAGTTAC	Knock-out construct XLOC_009059
KO-XLOC_009059-R2	GGGTTTAAUGTTGGGATGCCTCACTGTTT	Knock-out construct XLOC_009059
KO-XLOC_008951-F1	GGTCTTAAUAGGCGATATAAGTCTTGTCTC	Knock-out construct XLOC_008951
KO-XLOC_008951-R1	GGCATTAAUCGGTTAGGTTAGTGATGGGA	Knock-out construct XLOC_008951
KO-XLOC_008951-F2	GGACTTAAUTTCCAACATATACGTGTTACGACC	Knock-out construct XLOC_008951
KO-XLOC_008951-R2	GGGTTTAAUATCTGGTTCGCTTTAGAAAGATCC	Knock-out construct XLOC_008951
SIRub-F1	GAACAGTTTCTCACTGTTGAC	Tomato <i>RuBisCo</i>
SIRub-R1	CGTGAGAACCATAAGTCACC	Tomato <i>RuBisCo</i>
VdGAPDH-F	CGAGTCCACTGGTGTCTTCA	<i>V. dahliae</i> GAPDH
VdGAPDH-R	CCCTCAACGATGGTGAACCT	<i>V. dahliae</i> GAPDH
qVDAG_05180-F1	CCGAAGGACATGCAGTCATACCGG	<i>V. dahliae</i> VDAG_05180 (qRT-PCR)
qVDAG_05180-R1	TGCTGATATGGTTCCATTCCGTGAGG	<i>V. dahliae</i> VDAG_05180 (qRT-PCR)

Supplementary Table 6. Location of breakpoints in VdLs17 and JR2 compared to each other.

VdLs17				JR2			
Chromosome	Start	Stop	Note ^(a)	Chromosome	Start	Stop	Note ^(a)
Chr1	1704928	1706838	IA	scaff1	464643	594004	IA
Chr1	2328810	2463411	IA	scaff1	2753856	2758331	IE
Chr1	2697567	2699850	IE	scaff1	6995538	7139184	IA
Chr1	4872136	4878089	IE	scaff1	7897589	7897588	IE
Chr1	5228212	5376603	IE	scaff2	2866260	3034775	IE
Chr2	1044841	1050896	IE ^(d)	scaff2	3115342	3116872	IE
Chr2	5151980	5262461	IE	scaff2	3192107	3197557	IE
Chr2	5280848	5280848	IE ^(e, f)	scaff2	3219697	3319456	IE
Chr3	723015	723015	IE ^(e, f)	scaff2	3663360	3663360	IE
Chr3	2001273	2150654	IE ^(c)	scaff2	4207425	4219600	IE
Chr3	3028284	3224254	IE	scaff3	1040257	1063663	IE
Chr3	3288396	3291734	IE	scaff3	1389038	1412796	IA
Chr3	3299414	3299973	IA	scaff3	1618226	1793692	IA
Chr3	3333364	3353845	IA	scaff3	2399925	2455297	IA
Chr3	3362443	3364549	IE	scaff4	931820	1275376	IE ^(b)
Chr3	3401115	3401126	IE	scaff4	1310827	1447892	IE ^(b)
Chr3	3500684	3566578	IE	scaff4	2288393	2307859	IA
Chr3	5314358	5337999	IA	scaff4	2853122	3027752	IA
Chr4	581875	582875	IE ^(b)	scaff5	527587	527588	IA ^(b)
Chr4	1149458	1159458	IE ^(b)	scaff5	935464	1028503	IA
Chr4	1797634	1806462	IA	scaff5	1485866	1533273	IA
Chr4	2088923	2098923	IA ^(b)	scaff5	3292265	3340655	IE
Chr4	2515463	2516463	IA ^(b)	scaff5	3527359	3647028	IE
Chr4	3611686	3624632	IE	scaff6	404908	434785	IA
Chr4	3841997	3844002	IE	scaff6	2153111	2308961	IA
Chr5	1030032	1138681	IA	scaff6	3184558	3191977	IE
Chr5	1685298	1706203	IA	scaff7	1345514	1430174	IA
Chr6	1789976	1803976	IA ^(c)	scaff7	2367775	2368961	IA
Chr7	423482	441582	IE	scaff8	1783883	1926229	IA
Chr8	1020271	1020372	IA ^(c)				
Chr8	1966542	1979754	IA				

a) Inter-chromosomal (IE) and intra-chromosomal (IA) re-arrangements

b) Variable region-associated breakpoint, large region delimited

c) Gap-associated translocation where breakpoint location is assessed and determined by manual inspection of the flanking sequence and the sequence in the unpositioned scaffolds.

d) Inter-chromosomal re-arrangement SR2 verified by PCR (Figure S1)

e) Inter-chromosomal re-arrangement SR3 verified by PCR (Figure S1)

f) Inter-chromosomal re-arrangement SR4 verified by PCR (Figure S1)

Supplementary Table 7. Classes of repetitive elements in *V. dahliae* genomes VdLs17 and JR2.

	VdLs17	JR2
Sequence summary:		
Number of chromosomes	9	9
total length	36,874,636	37,006,893
total length excluding Ns	32,903,115	33,040,648
GC level (%)	55.85	55.52
bases masked	1,331,148 (4.05%)	1,429,941 (4.33%)
Repetitive Elements (number of elements, length occupied, percentage of total genome sequence):		
SINEs	0; 0 bp; 0%	0; 0 bp; 0%
LINES	71; 116,971 bp; 0.36%	63; 61,416 bp; 0.19%
LTR elements	395; 586,279 bp; 1.78%	600; 671,062 bp; 2.03 %
DNA elements	93; 88,379 bp; 0.27%	70; 61,486 bp; 0.19%
Unclassified	1,030; 311,043 bp; 0.95%	1,311; 408,003 bp; 1.23%
Total interspersed repeats	1,589; 1,102,672 bp; 3.35%	2,044; 1,201,967 bp; 3.64%
Small RNA	0; 0 bp; 0%	0; 0 bp; 0%
Satellites	0; 0 bp; 0%	0; 0 bp; 0%
Simple repeats	3,240; 154,570 bp; 0.47%	3,206; 151,249 bp; 0.46%
Low complexity	1,483; 76,153 bp; 0.23%	1,598; 79,866 bp; 0.24%

Supplementary Table 8. Location of LTR-retrotransposons in VdLs17 and JR2.

VdLs17						
Chromosome	Start	Stop	LTR Length (left)	LTR Length (right)	Length	Strand
Chr1	232748	239575	433	433	6828	-
Chr1	1467297	1473831	131	126	6535	?
Chr1	1936363	1944039	757	757	7677	+
Chr1	2466498	2473257	330	330	6760	-
Chr1	3774395	3775661	117	117	1267	-
Chr1	4604465	4610321	1918	1919	5857	-
Chr1	4872216	4878088	213	213	5873	-
Chr2	423992	430925	476	476	6934	+
Chr2	1044842	1050896	213	213	6055	-
Chr2	5224340	5231285	476	476	6946	-
Chr2	5787305	5794256	476	476	6952	-
Chr3	32535	45163	202	193	12629	-
Chr3	216935	233759	666	666	16825	-
Chr3	904118	910797	478	476	6680	+
Chr3	1014092	1021006	476	476	6915	-
Chr3	1434408	1441536	476	476	7129	-
Chr3	1729772	1735644	213	213	5873	-
Chr3	2477096	2482971	213	213	5876	-
Chr3	2888264	2903870	408	408	15607	-
Chr3	2889822	2896756	476	476	6935	-
Chr3	3063640	3068319	260	257	4680	+
Chr3	3136289	3146055	788	784	9767	+
Chr3	3183995	3189870	213	213	5876	+
Chr3	3338562	3343726	213	213	5165	-
Chr3	3350704	3360308	188	189	9605	+
Chr3	3404359	3411293	476	476	6935	+
Chr3	3684414	3691342	433	433	6929	+
Chr3	3684414	3693831	433	433	9418	+
Chr3	3716751	3722620	210	210	5870	+
Chr3	5254911	5260785	213	213	5875	-
Chr3	5657284	5663156	213	213	5873	-
Chr3	5757090	5764127	433	433	7038	+
Chr4	47636	51776	151	151	4141	+
Chr4	526461	532335	215	215	5875	-
Chr4	530661	548131	1673	1673	17471	-
Chr4	661354	666909	159	159	5556	-
Chr4	755113	760803	153	153	5691	+
Chr4	755113	775006	153	153	19894	+
Chr4	758842	775006	1962	1952	16165	+
Chr4	787818	793653	176	176	5836	-
Chr4	823182	832667	116	116	9486	+
Chr4	931901	937455	159	159	5555	+
Chr4	1533154	1538888	180	178	5735	-
Chr4	1681039	1687507	213	213	6469	-

Chr4	2582207	2601042	107	106	18836	-
Chr4	3543202	3550025	476	476	6824	-
Chr4	3611686	3618554	454	454	6869	-
Chr4	3929068	3935061	213	213	5994	+
Chr4	4108115	4113988	213	213	5874	+
Chr4	4150365	4156237	213	213	5873	-
Chr5	570367	577243	454	454	6877	-
Chr5	735486	741358	213	213	5873	+
Chr5	2323580	2333066	213	213	9487	+
Chr5	2327019	2333066	186	186	6048	+
Chr5	2890687	2896569	213	213	5883	+
Chr6	346942	353878	476	476	6937	+
Chr6	1145586	1154887	794	792	9302	+
Chr6	1299406	1305288	213	213	5883	-
Chr6	1374692	1380564	213	213	5873	-
Chr6	3159078	3165946	454	454	6869	-
Chr6	3170253	3177187	476	476	6935	+
Chr7	2487966	2493838	213	213	5873	+
Chr7	2889807	2896634	433	433	6828	-
Chr8	960404	967270	454	454	6867	+
Chr8	960404	970578	454	454	10175	+
Chr8	970323	987674	256	256	17352	+
Chr8	987199	994133	476	476	6935	+
Un	753543	760477	476	476	6935	+
Un	785854	791726	213	213	5873	-
Un	1401660	1407089	438	438	5430	+
Un	1820737	1826609	213	213	5873	-
JR2						
Chromosome	Start	Stop	LTR Length (left)	LTR Length (right)	Length	Strand
scaff1	1663038	1664304	117	117	1267	-
scaff1	4778033	4784999	286	286	6967	+
scaff1	7608022	7613596	144	143	5575	+
scaff1	8716844	8722716	213	213	5873	+
scaff2	1393525	1399051	225	225	5527	+
scaff2	2876087	2882107	1807	1737	6021	-
scaff2	2876127	2882107	1767	1804	5981	-
scaff2	3232559	3240942	464	463	8384	+
scaff2	3232559	3244351	464	462	11793	+
scaff2	3251515	3260848	2243	2244	9334	+
scaff2	3313902	3319428	225	225	5527	+
scaff2	3513677	3527658	213	213	13982	-
scaff2	3513691	3533318	199	199	19628	-
scaff2	3527446	3533315	210	210	5870	-
scaff2	3547587	3553169	202	196	5583	-
scaff3	559660	565532	213	213	5873	-
scaff3	3672376	3678945	131	126	6570	?
scaff4	3337472	3343344	213	213	5873	+
scaff5	672124	678040	229	229	5917	+

scaff5	1101352	1107224	213	213	5873	-
scaff5	1488597	1507688	161	161	19092	-
scaff5	3247215	3266109	106	107	18895	+
scaff6	541037	557402	168	164	16366	-
scaff6	2634537	2640409	213	213	5873	-
scaff6	2787014	2793944	153	152	6931	+
scaff7	581	6107	225	225	5527	-
scaff7	1279841	1282993	333	328	3153	-
scaff8	574703	580575	213	213	5873	-
scaff8	658408	663797	181	180	5390	+
scaff8	2482666	2488538	213	213	5873	+
scaff8	3095533	3101405	213	213	5873	-
scaffUn	120005	139675	2349	2307	19671	?
scaffUn	554749	564666	162	163	9918	+

Supplementary Table 9. Location of non-LTR retrotransposons (LINEs) in VdLs17 and JR2.

VdLs17			JR2		
Chromosome	Start	Stop	Chromosome	Start	Stop
Chr1	1621205	1626726	scaff1	3638144	3638651
Chr2	139284	141786	scaff1	5422731	5424039
Chr2	3819771	3819927	scaff2	1480369	1480695
Chr3	45862	46207	scaff2	3261344	3263212
Chr3	46378	48105	scaff2	3500575	3500631
Chr3	48858	49414	scaff2	3500635	3500972
Chr3	61992	62753	scaff2	3501969	3503008
Chr3	84793	85428	scaff2	3510820	3511187
Chr3	173733	174238	scaff2	3511234	3511478
Chr3	225140	225569	scaff2	3514358	3514853
Chr3	234161	234328	scaff2	3554882	3555213
Chr3	234493	235697	scaff2	3559099	3559128
Chr3	236088	236255	scaff3	2857422	2859699
Chr3	247709	247921	scaff4	1047065	1047239
Chr3	269428	269491	scaff4	1114090	1114682
Chr3	269561	269963	scaff4	1129438	1129671
Chr3	270740	274033	scaff4	1130117	1130447
Chr3	2886969	2888243	scaff4	1130447	1131001
Chr3	2903876	2905338	scaff4	1133153	1133339
Chr3	2987264	2988735	scaff4	1141450	1141550
Chr3	2990694	2990928	scaff4	1149729	1150189
Chr3	3082377	3082749	scaff4	1150189	1151392
Chr3	3131518	3137058	scaff4	1322172	1322785
Chr3	3145272	3146041	scaff4	1322955	1323018
Chr3	3147189	3150293	scaff4	1323028	1323706
Chr3	3169247	3169799	scaff4	1323724	1327045
Chr3	3170025	3170294	scaff5	689537	689644
Chr3	3170534	3172299	scaff5	842033	842154
Chr3	3172300	3172382	scaff5	878215	879028
Chr3	3199582	3199795	scaff5	3375098	3375358
Chr3	3232217	3232763	scaff5	3376625	3376681
Chr3	3233540	3236174	scaff5	3376685	3377022
Chr3	3237846	3243419	scaff5	3376996	3377036
Chr3	3260759	3260836	scaff5	3492058	3493146
Chr3	3260867	3261869	scaff5	3493148	3497235
Chr3	3279557	3283421	scaff5	3514656	3515658
Chr3	3283423	3284533	scaff5	3515689	3515766
Chr3	3361440	3362492	scaff5	3533142	3535478
Chr3	3363486	3363526	scaff5	3538246	3538416
Chr3	3363500	3363837	scaff5	3540088	3542722
Chr3	3363841	3363897	scaff5	3543499	3544045
Chr3	3364944	3365101	scaff6	345252	350747
Chr3	3366191	3366451	scaff6	625506	625534
Chr3	3767735	3773303	scaff6	986135	986215

Chr3	4135228	4135308	scaff6	3045454	3046728
Chr3	5685844	5687448	scaff6	3061012	3062508
Chr3	5690678	5691403	scaff6	3144381	3145852
Chr4	651570	652035	scaff6	3147811	3148045
Chr4	652069	652145	scaff7	47143	47354
Chr4	678522	678874	scaff7	51201	51412
Chr4	695634	696781	scaff7	564420	569993
Chr4	776915	781799	scaff8	584045	584312
Chr4	833095	833218	scaffUn	29865	30536
Chr4	879182	879395	scaffUn	113287	113585
Chr4	883243	884812	scaffUn	185363	185748
Chr4	885740	885796	scaffUn	409445	409627
Chr4	910754	916216	scaffUn	438336	438645
Chr4	965573	970758	scaffUn	438805	439996
Chr4	970781	971074	scaffUn	440183	440354
Chr4	1164510	1166593	scaffUn	460296	460361
Chr4	1166593	1166659	scaffUn	462168	467010
Chr4	1166662	1167776	scaffUn	470474	471870
Chr4	1198216	1198375	scaffUn	471872	472031
Chr4	1198377	1199773	scaffUn	502376	503495
Chr4	1203510	1208362	scaffUn	503498	503564
Chr4	1210174	1210239	scaffUn	503564	505647
Chr4	1230294	1230465	scaffUn	994069	994534
Chr4	1230652	1231858	scaffUn	994564	994644
Chr4	1232003	1232325	scaffUn	1129408	1129598
Chr4	1699464	1699836			
Chr4	3569897	3570006			
Chr4	3570003	3571236			
Chr4	3977966	3978421			
Chr4	4059635	4065145			
Chr4	4105461	4105674			
Chr6	1219454	1219721			
Chr6	1717016	1722537			
Chr6	3268577	3274097			
Chr7	1853341	1858861			
Un	640195	640702			

Supplementary Table 10. Location of repetitive DNA elements in VdLs17 and JR2.

VdLs17			JR2		
Chromosome	Start	Stop	Chromosome	Start	Stop
Chr1	2772515	2774379	scaff1	726445	728310
Chr1	3147051	3148252	scaff1	1036050	1037226
Chr1	5513182	5513197	scaff1	5483630	5484248
Chr1	5513198	5515063	scaff1	5494219	5494492
Chr2	196479	196860	scaff1	5499151	5499424
Chr2	2925820	2925859	scaff1	5506319	5506616
Chr2	3640796	3641414	scaff1	7015584	7015621
Chr2	3645326	3647191	scaff2	1052394	1054258
Chr2	3650426	3650699	scaff2	1313351	1313456
Chr2	3655546	3655843	scaff2	1314176	1315149
Chr2	5231747	5232043	scaff2	1328820	1330021
Chr2	5742694	5744558	scaff2	1330299	1330658
Chr3	768	2633	scaff2	1558652	1560517
Chr3	2634	3944	scaff2	2285749	2285988
Chr3	5630	5904	scaff2	3170092	3171108
Chr3	17474	17981	scaff2	3174616	3176225
Chr3	23167	25031	scaff2	3219697	3221481
Chr3	25273	26962	scaff2	3224831	3225151
Chr3	35631	36103	scaff2	3481215	3483077
Chr3	36120	36161	scaff2	3494560	3494717
Chr3	45206	45437	scaff2	3546078	3547813
Chr3	151818	153652	scaff2	3548016	3548377
Chr3	157117	157437	scaff2	3552978	3553186
Chr3	163232	163380	scaff3	194516	194897
Chr3	179988	180412	scaff3	4156012	4156023
Chr3	213191	213817	scaff3	4156024	4156887
Chr3	232780	232820	scaff4	1094113	1094140
Chr3	240035	240183	scaff4	1159530	1161395
Chr3	240889	242271	scaff4	1310827	1312692
Chr3	247130	247551	scaff4	2288393	2289269
Chr3	267580	269343	scaff4	2307672	2307811
Chr3	274712	274770	scaff4	2308417	2308463
Chr3	1266460	1268326	scaff4	3309885	3311750
Chr3	1921718	1921729	scaff4	3736291	3738156
Chr3	1921730	1923592	scaff5	865962	866922
Chr3	1925327	1927192	scaff5	935700	935727
Chr3	2896920	2898784	scaff5	1125129	1126994
Chr3	2958514	2960379	scaff5	1637483	1637563
Chr3	3002379	3002504	scaff5	1697506	1698706
Chr3	3049460	3050249	scaff5	1699312	1699358
Chr3	3068332	3070197	scaff5	2078295	2080159
Chr3	3070134	3070209	scaff5	2660088	2661288
Chr3	3173277	3175142	scaff5	2661894	2661940
Chr3	3245496	3247360	scaff5	3364939	3366804

Chr3	3322160	3323943	scaff5	3366740	3366816
Chr3	3327371	3327635	scaff5	3529201	3531065
Chr3	3346831	3347096	scaff5	3552174	3552857
Chr3	3347270	3347957	scaff6	2069097	2069829
Chr3	3347996	3348156	scaff6	2787336	2789200
Chr3	3374732	3374743	scaff6	2789138	2789211
Chr3	3374744	3376609	scaff6	3088090	3088104
Chr3	3673708	3675573	scaff6	3088105	3089969
Chr3	5221788	5222520	scaff6	3159726	3159851
Chr3	5764832	5766696	scaff7	40185	42049
Chr3	5769686	5770505	scaff7	42058	43923
Chr4	54838	56702	scaff7	3321777	3321824
Chr4	532785	532942	scaff7	3322572	3323276
Chr4	538269	538453	scaff7	3329847	3330058
Chr4	541324	543188	scaff8	2461889	2461935
Chr4	785218	787083	scaff8	2462541	2462784
Chr4	1227482	1227651	scaff8	2462785	2463955
Chr4	1909423	1909503	scaff8	2923609	2925473
Chr4	1969352	1970552	scaff8	3239500	3239546
Chr4	1971158	1971204	scaff8	3240152	3240556
Chr4	3186859	3186905	scaff8	3252337	3253153
Chr4	3187511	3188491	scaffUn	86122	86458
Chr4	3188955	3189192	scaffUn	442997	443166
Chr4	3897166	3898199	scaffUn	629132	629494
Chr4	3901739	3903434	scaffUn	805030	806276
Chr4	3919726	3921591	scaffUn	958219	960083
Chr4	3970501	3971296	scaffUn	978837	979038
Chr4	4021153	4021469	scaffUn	1074463	1075326
Chr4	4037338	4038198	scaffUn	1099975	1100852
Chr4	4101897	4102919			
Chr5	494110	495975			
Chr5	1138484	1138820			
Chr5	1139426	1139472			
Chr5	1706326	1707202			
Chr6	1155714	1157578			
Chr6	3158294	3158340			
Chr6	3158946	3159077			
Chr6	3165946	3166224			
Chr6	3179976	3180792			
Chr7	641143	643007			
Chr7	1023991	1024223			
Chr7	1773804	1775668			
Chr7	1978200	1979203			
Chr7	1979923	1980128			
Chr7	2503603	2505467			
Chr8	955854	955901			
Chr8	956512	957504			
Chr8	974516	974727			
Un	752134	752180			

Un	752786	753545
Un	760479	760899
Un	1322279	1324144
Un	1975111	1976890
Un	2104667	2105435

Supplementary Table 11. Location of unclassified repetitive elements in VdLs17 and JR2.

VdLs17			JR2		
Chromosome	Start	Stop	Chromosome	Start	Stop
Chr1	223078	223473	scaff1	12834	13314
Chr1	223452	223684	scaff1	13299	13452
Chr1	223536	223844	scaff1	13870	14482
Chr1	223887	224267	scaff1	14472	15301
Chr1	228435	228652	scaff1	16210	16701
Chr1	230323	230576	scaff1	17207	17476
Chr1	231025	231627	scaff1	244123	244331
Chr1	231663	232738	scaff1	247835	247959
Chr1	232745	233958	scaff1	318608	318713
Chr1	239080	239575	scaff1	385617	385962
Chr1	278484	278710	scaff1	390503	390566
Chr1	281766	281779	scaff1	403445	404397
Chr1	452023	452137	scaff1	405500	405705
Chr1	499347	499518	scaff1	464676	464976
Chr1	500327	500511	scaff1	465132	465415
Chr1	689878	689994	scaff1	465612	465843
Chr1	848370	848621	scaff1	586922	587154
Chr1	856760	857038	scaff1	590529	591045
Chr1	1001458	1001608	scaff1	590896	591199
Chr1	1073245	1073504	scaff1	591530	591574
Chr1	1103695	1103826	scaff1	592433	592642
Chr1	1317463	1317591	scaff1	612286	612481
Chr1	1324252	1324449	scaff1	615474	615656
Chr1	1347314	1347548	scaff1	660699	664164
Chr1	1347511	1347564	scaff1	664233	664889
Chr1	1363376	1363535	scaff1	864996	865125
Chr1	1501162	1501364	scaff1	902169	902292
Chr1	1510587	1510850	scaff1	906635	906742
Chr1	1543808	1543953	scaff1	1080998	1081282
Chr1	1617674	1617853	scaff1	1633324	1633584
Chr1	1620978	1621076	scaff1	1663039	1663154
Chr1	1626724	1626863	scaff1	1663680	1663893
Chr1	1636535	1636797	scaff1	1664190	1664304
Chr1	1675369	1675497	scaff1	1678323	1678584
Chr1	1704473	1705020	scaff1	1678737	1678844
Chr1	1718459	1718708	scaff1	1680294	1680472
Chr1	1751658	1751760	scaff1	1827642	1827775
Chr1	1767340	1767508	scaff1	1841296	1841554
Chr1	1775557	1775802	scaff1	1846504	1846782
Chr1	1775764	1775806	scaff1	2020386	2020553
Chr1	1844218	1844479	scaff1	2039767	2040048
Chr1	1884157	1884418	scaff1	2040095	2040169
Chr1	1884414	1884723	scaff1	2089297	2089423
Chr1	1884707	1885456	scaff1	2178144	2178275
Chr1	1885457	1885767	scaff1	2341323	2341450
Chr1	1885753	1886257	scaff1	2522849	2522977
Chr1	2014655	2015089	scaff1	2557048	2557275
Chr1	2015103	2015485	scaff1	2579238	2579561
Chr1	2125672	2125870	scaff1	2814248	2814496

Chr1	2150342	2150517	scaff1	2835146	2835342
Chr1	2325190	2325494	scaff1	2835167	2835547
Chr1	2325497	2325799	scaff1	2835525	2835990
Chr1	2328663	2329101	scaff1	2835985	2836354
Chr1	2329094	2330786	scaff1	2837472	2837581
Chr1	2465881	2466349	scaff1	3000286	3000756
Chr1	2473244	2473603	scaff1	3000747	3001194
Chr1	2475765	2476893	scaff1	3001337	3001646
Chr1	2683258	2683469	scaff1	3001617	3001755
Chr1	2683611	2683819	scaff1	3001893	3001968
Chr1	2694287	2694511	scaff1	3002286	3002671
Chr1	2696957	2697308	scaff1	3002736	3002843
Chr1	2697114	2699206	scaff1	3043811	3044053
Chr1	2718109	2718304	scaff1	3223530	3223649
Chr1	2721297	2721479	scaff1	3223793	3224109
Chr1	2748607	2749274	scaff1	3272033	3272284
Chr1	2770865	2772514	scaff1	3607105	3607233
Chr1	2774380	2776193	scaff1	3625287	3625495
Chr1	2776262	2776918	scaff1	3680512	3680719
Chr1	2976420	2976549	scaff1	4053477	4053596
Chr1	3013475	3013598	scaff1	4084205	4084440
Chr1	3017917	3018024	scaff1	4145138	4145575
Chr1	3192389	3192672	scaff1	4165227	4166083
Chr1	3744305	3744565	scaff1	4166129	4166321
Chr1	3774396	3774511	scaff1	4173764	4173860
Chr1	3775037	3775250	scaff1	4173895	4173952
Chr1	3775547	3775661	scaff1	4341724	4342934
Chr1	3789742	3790003	scaff1	4348758	4348856
Chr1	3790156	3790263	scaff1	4348989	4349087
Chr1	3791713	3791891	scaff1	4358132	4359582
Chr1	3939148	3939281	scaff1	4359640	4360289
Chr1	3952802	3953060	scaff1	4633587	4633906
Chr1	3958010	3958288	scaff1	4709863	4710018
Chr1	4130629	4130798	scaff1	4710063	4710540
Chr1	4150013	4150294	scaff1	4778020	4778370
Chr1	4150341	4150415	scaff1	4779649	4780011
Chr1	4199517	4199643	scaff1	4780161	4780404
Chr1	4287867	4287998	scaff1	4783488	4783611
Chr1	4451233	4451360	scaff1	4784620	4785014
Chr1	4634877	4635005	scaff1	4907013	4907291
Chr1	4671116	4671343	scaff1	5077702	5077940
Chr1	4693259	4693582	scaff1	5077944	5077979
Chr1	4918557	4918812	scaff1	5449686	5449815
Chr1	4940968	4941705	scaff1	5449810	5449882
Chr1	4971356	4971419	scaff1	5454013	5454077
Chr1	5034346	5034473	scaff1	5484196	5485408
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scaff8	3250806	3251315
scaff8	3251529	3252094
scaff8	3320853	3321052

scaff8	3321232	3321473
scaff8	3325856	3326064
scaff8	3351771	3351856
scaff8	3352018	3352332
scaff8	3352570	3353036
scaffUn	8989	9315
scaffUn	9794	9848
scaffUn	16073	16782
scaffUn	21569	22117
scaffUn	22093	22203
scaffUn	23936	24053
scaffUn	24049	24697
scaffUn	29633	29760
scaffUn	45023	45961
scaffUn	45964	46046
scaffUn	46147	46579
scaffUn	66884	67604
scaffUn	67612	67646
scaffUn	67647	67753
scaffUn	67750	67890
scaffUn	69405	69531
scaffUn	69754	69973
scaffUn	70515	70570
scaffUn	71558	71723
scaffUn	74666	74916
scaffUn	78146	78192
scaffUn	173882	174667
scaffUn	178191	178787
scaffUn	179084	179398
scaffUn	180192	182151
scaffUn	182113	182241
scaffUn	184182	184491
scaffUn	192436	192639
scaffUn	194628	194667
scaffUn	197457	198268
scaffUn	198063	199064
scaffUn	199265	200557
scaffUn	211697	211777
scaffUn	221633	222348
scaffUn	223052	223081
scaffUn	223182	225327
scaffUn	248577	249831
scaffUn	252838	253385
scaffUn	254247	254867
scaffUn	262060	262427
scaffUn	267749	268558
scaffUn	268755	268944
scaffUn	271908	273163
scaffUn	274699	274766
scaffUn	275348	275520
scaffUn	275747	277625
scaffUn	277778	278626
scaffUn	279436	279585
scaffUn	279587	279753

scaffUn	279942	279973
scaffUn	284855	285188
scaffUn	303146	303228
scaffUn	303266	303439
scaffUn	308546	308908
scaffUn	314262	314598
scaffUn	314627	315449
scaffUn	318084	318518
scaffUn	318147	318610
scaffUn	318855	318941
scaffUn	322315	323590
scaffUn	324252	324946
scaffUn	329966	330251
scaffUn	333545	333861
scaffUn	334204	334411
scaffUn	334393	334779
scaffUn	335927	336180
scaffUn	337266	337624
scaffUn	337690	337862
scaffUn	349824	349986
scaffUn	386597	386732
scaffUn	392032	392215
scaffUn	399490	399818
scaffUn	399821	400408
scaffUn	403903	404040
scaffUn	404956	405312
scaffUn	418918	419234
scaffUn	421400	421428
scaffUn	421529	422117
scaffUn	434916	435503
scaffUn	510801	511100
scaffUn	516247	516989
scaffUn	521811	522746
scaffUn	535340	535438
scaffUn	541161	541337
scaffUn	546527	546777
scaffUn	547468	547691
scaffUn	552708	553206
scaffUn	554397	554543
scaffUn	573699	573979
scaffUn	573913	575185
scaffUn	591796	592483
scaffUn	592483	593283
scaffUn	597528	598472
scaffUn	614634	616761
scaffUn	618033	618136
scaffUn	618118	618532
scaffUn	622009	622431
scaffUn	625628	626175
scaffUn	628801	629124
scaffUn	636244	636468
scaffUn	637080	637208
scaffUn	637387	637459
scaffUn	660919	661691

scaffUn	667463	668713
scaffUn	676006	677230
scaffUn	677581	677645
scaffUn	678485	678720
scaffUn	679069	679519
scaffUn	691715	692965
scaffUn	703088	704049
scaffUn	703974	704153
scaffUn	709618	709907
scaffUn	714886	715069
scaffUn	722419	722489
scaffUn	722496	723322
scaffUn	735155	735500
scaffUn	735499	735622
scaffUn	736714	737964
scaffUn	747888	748353
scaffUn	748204	748520
scaffUn	748504	748627
scaffUn	750571	750649
scaffUn	755110	756116
scaffUn	756335	756789
scaffUn	762855	763101
scaffUn	770555	771075
scaffUn	771419	771494
scaffUn	781975	782882
scaffUn	784185	785805
scaffUn	788770	789071
scaffUn	789073	789290
scaffUn	794076	795082
scaffUn	797195	798059
scaffUn	803686	804247
scaffUn	804283	804751
scaffUn	813516	814143
scaffUn	814815	815390
scaffUn	820177	820491
scaffUn	820832	821146
scaffUn	821108	821579
scaffUn	821893	822013
scaffUn	821998	822060
scaffUn	822035	822274
scaffUn	825411	825618
scaffUn	825596	826326
scaffUn	826330	826402
scaffUn	826469	826636
scaffUn	826652	826724
scaffUn	826862	827170
scaffUn	827354	827545
scaffUn	832103	832576
scaffUn	832573	832946
scaffUn	833193	833423
scaffUn	833427	833731
scaffUn	833592	833808
scaffUn	833798	834202
scaffUn	834180	834694

scaffUn	857703	858506
scaffUn	859064	859222
scaffUn	863878	864004
scaffUn	868697	870652
scaffUn	877689	878276
scaffUn	878278	878625
scaffUn	879480	879519
scaffUn	879730	880281
scaffUn	880530	880635
scaffUn	887100	887459
scaffUn	888699	889350
scaffUn	889146	889396
scaffUn	889704	890037
scaffUn	890127	890430
scaffUn	890432	890811
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scaffUn	899485	901054
scaffUn	914495	914538
scaffUn	914639	915688
scaffUn	928439	929660
scaffUn	942632	942773
scaffUn	942853	942945
scaffUn	950376	951082
scaffUn	951090	951165
scaffUn	951170	951472
scaffUn	951323	952050
scaffUn	953084	954635
scaffUn	954694	954880
scaffUn	962996	963715
scaffUn	963575	963868
scaffUn	969634	969753
scaffUn	970395	970614
scaffUn	971519	971598
scaffUn	976477	976563
scaffUn	976488	976918
scaffUn	985818	986205
scaffUn	1002639	1002906
scaffUn	1003430	1003475
scaffUn	1007548	1007733
scaffUn	1007728	1007797
scaffUn	1007737	1007803
scaffUn	1013636	1013694
scaffUn	1039224	1039365
scaffUn	1057331	1057759
scaffUn	1057738	1058143
scaffUn	1058101	1058153
scaffUn	1058147	1058471
scaffUn	1058467	1059507
scaffUn	1060394	1061060
scaffUn	1067525	1069076
scaffUn	1069135	1069505
scaffUn	1077390	1077527

scaffUn	1087468	1087640
scaffUn	1088367	1088585
scaffUn	1088915	1089241
scaffUn	1092292	1092410
scaffUn	1112728	1112846
scaffUn	1118684	1118743
scaffUn	1120848	1120906
scaffUn	1126746	1126925
scaffUn	1144502	1144550
scaffUn	1144651	1146244
scaffUn	1149910	1150374
scaffUn	1151632	1152590
scaffUn	1161404	1162461
scaffUn	1165368	1165401
scaffUn	1165401	1165595
scaffUn	1165596	1166286
scaffUn	1208068	1208881
scaffUn	1221703	1222776
scaffUn	1223745	1224252
scaffUn	1224353	1225610
scaffUn	1230715	1231458
scaffUn	1235571	1235761
scaffUn	1236943	1237300
scaffUn	1237299	1237585

Supplementary Table 12. Location of lineage-specific sequences in VdLs17 and JR2.

VdLs17				JR2			
Chromosome	Start	Stop	Length	Chromosome	Start	Stop	Length
Chr1	223000	229000	6000	scaff4	0	3000	3000
Chr1	230000	233000	3000	scaff4	131000	132000	1000
Chr1	234000	240000	6000	scaff4	229000	231000	2000
Chr1	253000	254000	1000	scaff4	239000	241000	2000
Chr1	275000	277000	2000	scaff4	319000	320000	1000
Chr1	282000	284000	2000	scaff4	332000	333000	1000
Chr1	334000	337000	3000	scaff4	386000	387000	1000
Chr1	340000	341000	1000	scaff4	392000	394000	2000
Chr1	410000	411000	1000	scaff4	433000	434000	1000
Chr1	488000	489000	1000	scaff4	493000	494000	1000
Chr1	495000	496000	1000	scaff4	497000	498000	1000
Chr1	503000	504000	1000	scaff4	576000	577000	1000
Chr1	517000	519000	2000	scaff4	604000	606000	2000
Chr1	536000	537000	1000	scaff4	661000	662000	1000
Chr1	549000	550000	1000	scaff4	691000	692000	1000
Chr1	639000	640000	1000	scaff4	872000	873000	1000
Chr1	799000	800000	1000	scaff4	877000	880000	3000
Chr1	900000	901000	1000	scaff4	892000	893000	1000
Chr1	904000	906000	2000	scaff4	932000	934000	2000
Chr1	940000	941000	1000	scaff4	1029000	1094000	65000
Chr1	971000	972000	1000	scaff4	1105000	1167000	62000
Chr1	1019000	1021000	2000	scaff4	1171000	1173000	2000
Chr1	1108000	1109000	1000	scaff4	1270000	1328000	58000
Chr1	1110000	1111000	1000	scaff4	1445000	1448000	3000
Chr1	1137000	1139000	2000	scaff4	1462000	1463000	1000
Chr1	1141000	1142000	1000	scaff4	1627000	1628000	1000
Chr1	1184000	1185000	1000	scaff4	1704000	1705000	1000
Chr1	1186000	1187000	1000	scaff4	1727000	1728000	1000
Chr1	1189000	1190000	1000	scaff4	1750000	1751000	1000
Chr1	1211000	1212000	1000	scaff4	1779000	1780000	1000
Chr1	1317000	1318000	1000	scaff4	1796000	1797000	1000
Chr1	1355000	1357000	2000	scaff4	1817000	1818000	1000
Chr1	1378000	1379000	1000	scaff4	1874000	1875000	1000
Chr1	1382000	1383000	1000	scaff4	1882000	1883000	1000
Chr1	1452000	1453000	1000	scaff4	1897000	1898000	1000
Chr1	1462000	1463000	1000	scaff4	1908000	1909000	1000
Chr1	1499000	1500000	1000	scaff4	1936000	1937000	1000
Chr1	1507000	1510000	3000	scaff4	1966000	1968000	2000
Chr1	1515000	1516000	1000	scaff4	2030000	2031000	1000
Chr1	1526000	1527000	1000	scaff4	2079000	2083000	4000
Chr1	1532000	1534000	2000	scaff4	2122000	2124000	2000

Chr1	1541000	1542000	1000	scaff4	2256000	2257000	1000
Chr1	1617000	1618000	1000	scaff4	2302000	2304000	2000
Chr1	1621000	1624000	3000	scaff4	2337000	2338000	1000
Chr1	1647000	1648000	1000	scaff4	2396000	2398000	2000
Chr1	1707000	1708000	1000	scaff4	2411000	2412000	1000
Chr1	1712000	1716000	4000	scaff4	2414000	2415000	1000
Chr1	1738000	1739000	1000	scaff4	2500000	2502000	2000
Chr1	1754000	1756000	2000	scaff4	2504000	2506000	2000
Chr1	1806000	1807000	1000	scaff4	2566000	2568000	2000
Chr1	1833000	1834000	1000	scaff4	2571000	2572000	1000
Chr1	1853000	1854000	1000	scaff4	2579000	2582000	3000
Chr1	1871000	1873000	2000	scaff4	2588000	2589000	1000
Chr1	1884000	1887000	3000	scaff4	2855000	2858000	3000
Chr1	1892000	1893000	1000	scaff4	3026000	3027000	1000
Chr1	1916000	1917000	1000	scaff4	3067000	3068000	1000
Chr1	1940000	1941000	1000	scaff4	3154000	3155000	1000
Chr1	1966000	1967000	1000	scaff4	3158000	3160000	2000
Chr1	1983000	1984000	1000	scaff4	3161000	3162000	1000
Chr1	2005000	2006000	1000	scaff4	3302000	3303000	1000
Chr1	2007000	2008000	1000	scaff4	3306000	3307000	1000
Chr1	2057000	2058000	1000	scaff4	3310000	3318000	8000
Chr1	2074000	2075000	1000	scaff4	3324000	3325000	1000
Chr1	2100000	2101000	1000	scaff4	3329000	3344000	15000
Chr1	2171000	2172000	1000	scaff4	3443000	3444000	1000
Chr1	2188000	2189000	1000	scaff4	3462000	3463000	1000
Chr1	2191000	2192000	1000	scaff4	3470000	3472000	2000
Chr1	2328000	2330000	2000	scaff4	3480000	3481000	1000
Chr1	2464000	2465000	1000	scaff4	3525000	3526000	1000
Chr1	2466000	2471000	5000	scaff4	3611000	3612000	1000
Chr1	2473000	2478000	5000	scaff4	3614000	3615000	1000
Chr1	2486000	2487000	1000	scaff4	3637000	3638000	1000
Chr1	2512000	2513000	1000	scaff4	3647000	3648000	1000
Chr1	2532000	2533000	1000	scaff4	3736000	3738000	2000
Chr1	2537000	2538000	1000	scaff4	3788000	3789000	1000
Chr1	2578000	2579000	1000	scaff4	3810000	3811000	1000
Chr1	2581000	2582000	1000	scaff4	3815000	3816000	1000
Chr1	2585000	2586000	1000	scaff4	3936000	3937000	1000
Chr1	2638000	2640000	2000	scaff4	4025000	4031000	6000
Chr1	2697000	2700000	3000	scaff7	0	64000	64000
Chr1	2757000	2759000	2000	scaff7	68000	69000	1000
Chr1	2767000	2771000	4000	scaff7	288000	290000	2000
Chr1	2772000	2775000	3000	scaff7	295000	296000	1000
Chr1	2776000	2777000	1000	scaff7	298000	300000	2000
Chr1	2788000	2789000	1000	scaff7	303000	308000	5000
Chr1	2795000	2796000	1000	scaff7	327000	328000	1000
Chr1	2804000	2807000	3000	scaff7	338000	339000	1000

Chr1	2813000	2814000	1000	scaff7	357000	360000	3000
Chr1	2830000	2831000	1000	scaff7	361000	362000	1000
Chr1	2894000	2898000	4000	scaff7	369000	370000	1000
Chr1	2904000	2905000	1000	scaff7	371000	374000	3000
Chr1	2925000	2926000	1000	scaff7	412000	413000	1000
Chr1	2942000	2944000	2000	scaff7	418000	419000	1000
Chr1	3048000	3050000	2000	scaff7	470000	471000	1000
Chr1	3053000	3054000	1000	scaff7	487000	488000	1000
Chr1	3073000	3074000	1000	scaff7	526000	528000	2000
Chr1	3086000	3087000	1000	scaff7	537000	538000	1000
Chr1	3100000	3101000	1000	scaff7	567000	571000	4000
Chr1	3102000	3103000	1000	scaff7	577000	578000	1000
Chr1	3107000	3108000	1000	scaff7	594000	595000	1000
Chr1	3123000	3125000	2000	scaff7	704000	706000	2000
Chr1	3129000	3130000	1000	scaff7	808000	809000	1000
Chr1	3147000	3149000	2000	scaff7	815000	817000	2000
Chr1	3159000	3161000	2000	scaff7	922000	924000	2000
Chr1	3169000	3170000	1000	scaff7	952000	953000	1000
Chr1	3183000	3184000	1000	scaff7	965000	966000	1000
Chr1	3191000	3192000	1000	scaff7	1017000	1018000	1000
Chr1	3215000	3216000	1000	scaff7	1170000	1171000	1000
Chr1	3329000	3330000	1000	scaff7	1174000	1175000	1000
Chr1	3342000	3344000	2000	scaff7	1176000	1177000	1000
Chr1	3576000	3577000	1000	scaff7	1178000	1181000	3000
Chr1	3652000	3653000	1000	scaff7	1223000	1224000	1000
Chr1	3655000	3656000	1000	scaff7	1231000	1232000	1000
Chr1	3762000	3763000	1000	scaff7	1280000	1281000	1000
Chr1	3770000	3771000	1000	scaff7	1310000	1311000	1000
Chr1	3881000	3883000	2000	scaff7	1345000	1346000	1000
Chr1	3924000	3925000	1000	scaff7	1417000	1425000	8000
Chr1	3971000	3972000	1000	scaff7	1428000	1429000	1000
Chr1	3985000	3986000	1000	scaff7	1523000	1524000	1000
Chr1	3997000	3998000	1000	scaff7	1589000	1591000	2000
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Chr1	4033000	4036000	3000	scaff7	1773000	1774000	1000
Chr1	4068000	4070000	2000	scaff7	1780000	1782000	2000
Chr1	4101000	4102000	1000	scaff7	1800000	1801000	1000
Chr1	4303000	4306000	3000	scaff7	1802000	1804000	2000
Chr1	4307000	4308000	1000	scaff7	1824000	1825000	1000
Chr1	4325000	4326000	1000	scaff7	1841000	1842000	1000
Chr1	4380000	4381000	1000	scaff7	1861000	1862000	1000
Chr1	4385000	4386000	1000	scaff7	1891000	1893000	2000
Chr1	4523000	4524000	1000	scaff7	1993000	1994000	1000
Chr1	4598000	4600000	2000	scaff7	2013000	2014000	1000
Chr1	4610000	4611000	1000	scaff7	2023000	2024000	1000
Chr1	4684000	4685000	1000	scaff7	2047000	2048000	1000

Chr1	4703000	4704000	1000	scaff7	2053000	2054000	1000
Chr1	4712000	4713000	1000	scaff7	2061000	2062000	1000
Chr1	4736000	4737000	1000	scaff7	2087000	2088000	1000
Chr1	4867000	4868000	1000	scaff7	2108000	2109000	1000
Chr1	4872000	4878000	6000	scaff7	2112000	2113000	1000
Chr1	4892000	4893000	1000	scaff7	2132000	2133000	1000
Chr1	4925000	4926000	1000	scaff7	2135000	2136000	1000
Chr1	4937000	4938000	1000	scaff7	2171000	2172000	1000
Chr1	4956000	4957000	1000	scaff7	2261000	2263000	2000
Chr1	4977000	4978000	1000	scaff7	2266000	2267000	1000
Chr1	4988000	4990000	2000	scaff7	2294000	2295000	1000
Chr1	5047000	5048000	1000	scaff7	2298000	2299000	1000
Chr1	5050000	5051000	1000	scaff7	2302000	2303000	1000
Chr1	5112000	5113000	1000	scaff7	2316000	2317000	1000
Chr1	5124000	5125000	1000	scaff7	2335000	2336000	1000
Chr1	5131000	5132000	1000	scaff7	2344000	2345000	1000
Chr1	5136000	5137000	1000	scaff7	2480000	2481000	1000
Chr1	5155000	5156000	1000	scaff7	2490000	2491000	1000
Chr1	5169000	5170000	1000	scaff7	2516000	2517000	1000
Chr1	5177000	5178000	1000	scaff7	2523000	2524000	1000
Chr1	5180000	5181000	1000	scaff7	2608000	2609000	1000
Chr1	5211000	5212000	1000	scaff7	2613000	2614000	1000
Chr1	5375000	5376000	1000	scaff7	2648000	2649000	1000
Chr1	5385000	5386000	1000	scaff7	2661000	2662000	1000
Chr1	5403000	5404000	1000	scaff7	2713000	2714000	1000
Chr1	5433000	5434000	1000	scaff7	2744000	2745000	1000
Chr1	5448000	5449000	1000	scaff7	2753000	2754000	1000
Chr1	5513000	5515000	2000	scaff7	2768000	2769000	1000
Chr1	5534000	5535000	1000	scaff7	2775000	2776000	1000
Chr1	5683000	5684000	1000	scaff7	2781000	2783000	2000
Chr1	5745000	5746000	1000	scaff7	2792000	2794000	2000
Chr2	92000	93000	1000	scaff7	2827000	2828000	1000
Chr2	138000	140000	2000	scaff7	2882000	2883000	1000
Chr2	189000	190000	1000	scaff7	2899000	2900000	1000
Chr2	216000	217000	1000	scaff7	2919000	2920000	1000
Chr2	271000	272000	1000	scaff7	2936000	2940000	4000
Chr2	274000	275000	1000	scaff7	2942000	2943000	1000
Chr2	295000	296000	1000	scaff7	2959000	2961000	2000
Chr2	318000	319000	1000	scaff7	2980000	2981000	1000
Chr2	366000	367000	1000	scaff7	3048000	3049000	1000
Chr2	388000	390000	2000	scaff7	3050000	3051000	1000
Chr2	421000	431000	10000	scaff7	3085000	3086000	1000
Chr2	470000	471000	1000	scaff7	3094000	3095000	1000
Chr2	558000	562000	4000	scaff7	3098000	3099000	1000
Chr2	565000	566000	1000	scaff7	3121000	3122000	1000
Chr2	587000	588000	1000	scaff7	3323000	3324000	1000

Chr2	598000	599000	1000	scaff7	3325000	3328000	3000
Chr2	604000	605000	1000	scaff7	3361000	3361023	23
Chr2	638000	639000	1000	scaff8	296000	297000	1000
Chr2	651000	652000	1000	scaff8	360000	361000	1000
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