

Supplementary Information for the manuscript: High diversity, inbreeding and a dynamic Pleistocene demographic history revealed by African buffalo genomes

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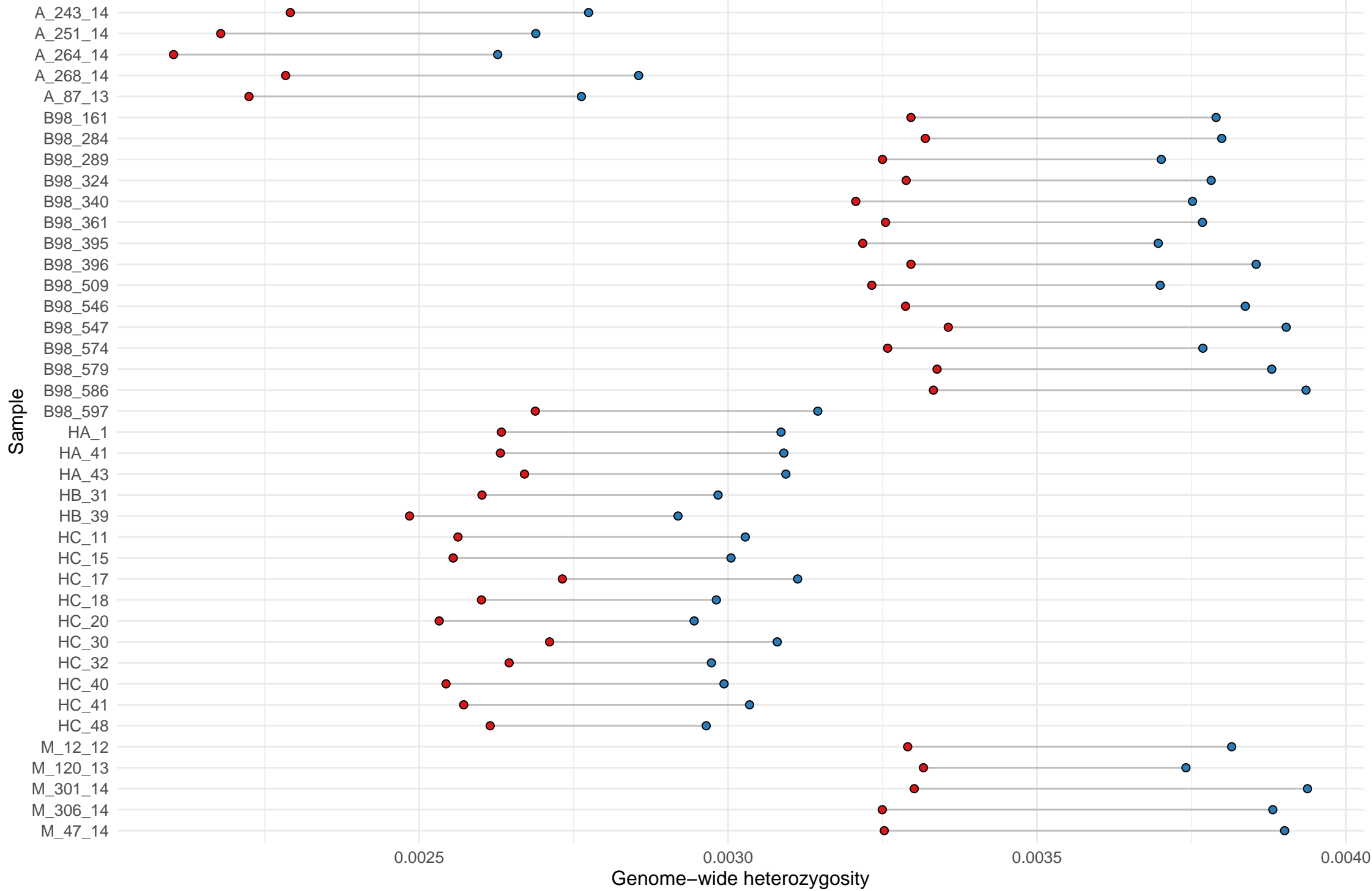
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³Veterinary Genetics Laboratory, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa

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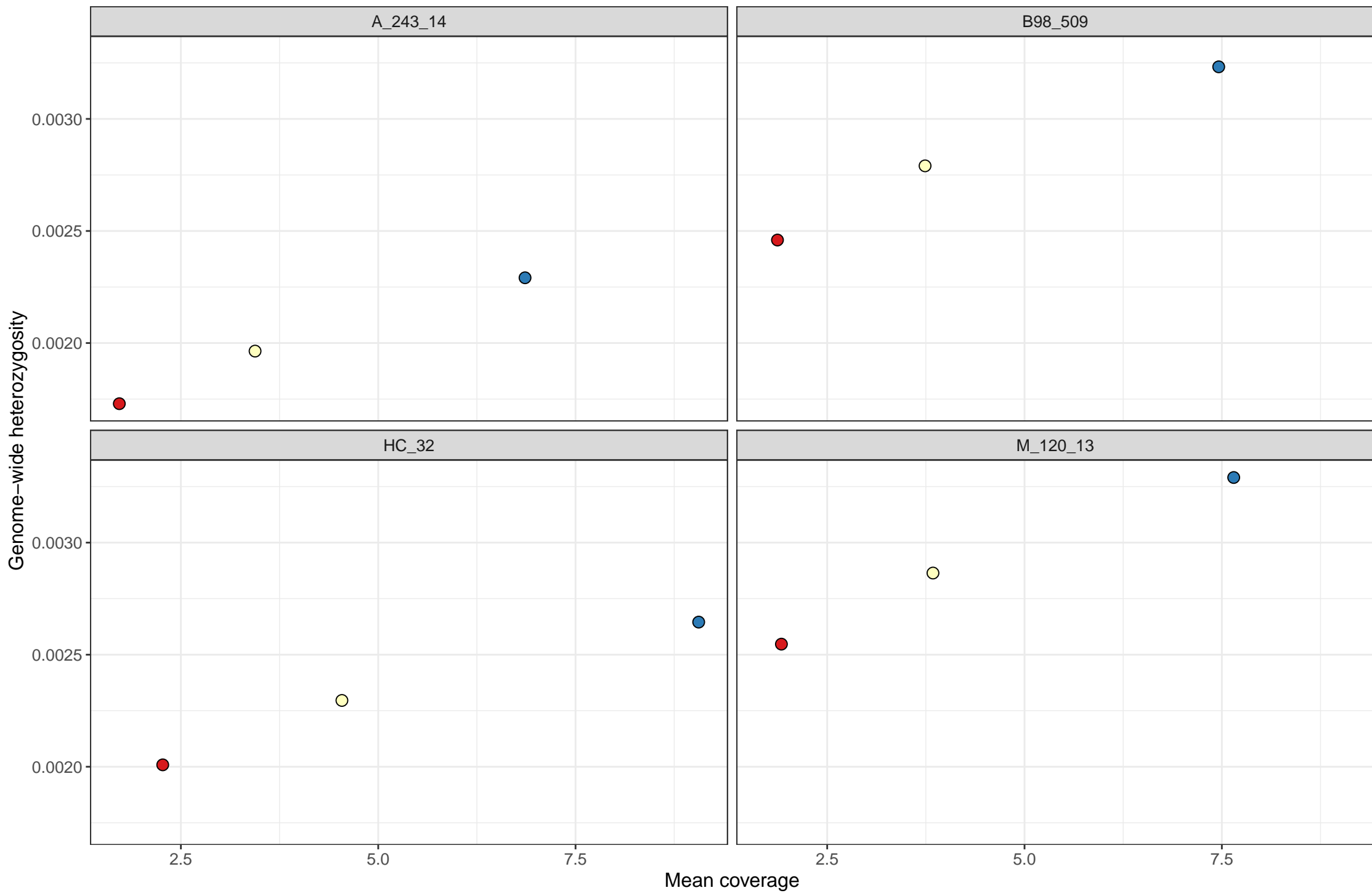
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Genotype likelihood model: ● -GL 1 (Samtools) ● -GL 2 (GATK)



Supplementary Fig. 1. Comparison of genome-wide heterozygosity estimates using different genotype likelihood models in ANGSD.

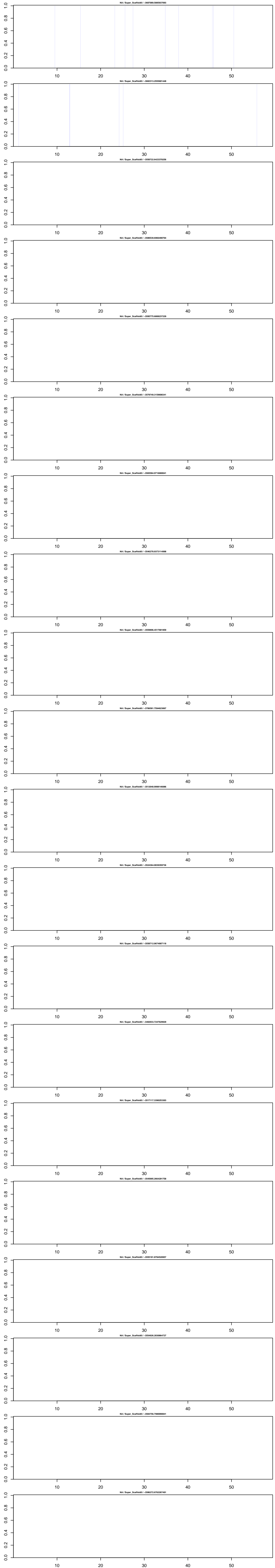
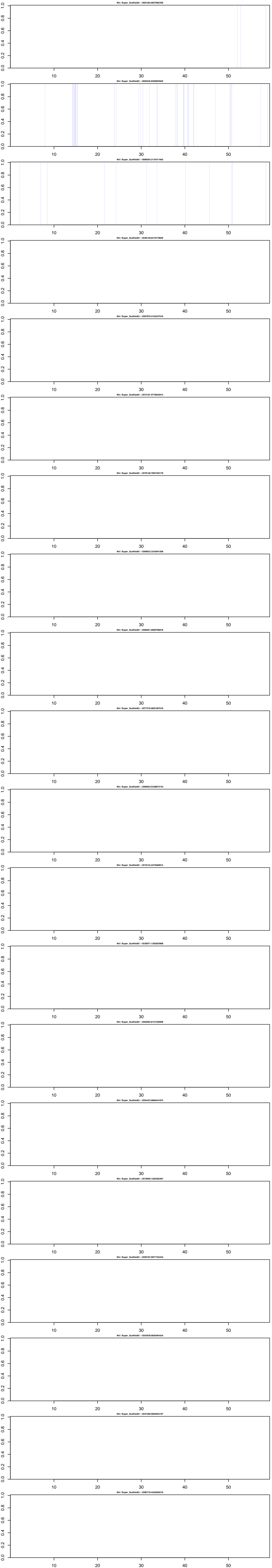
Coverage category (proportion reads subsampled): ● Low (25% reads) ● Medium (50% reads) ● High (no subsampling)

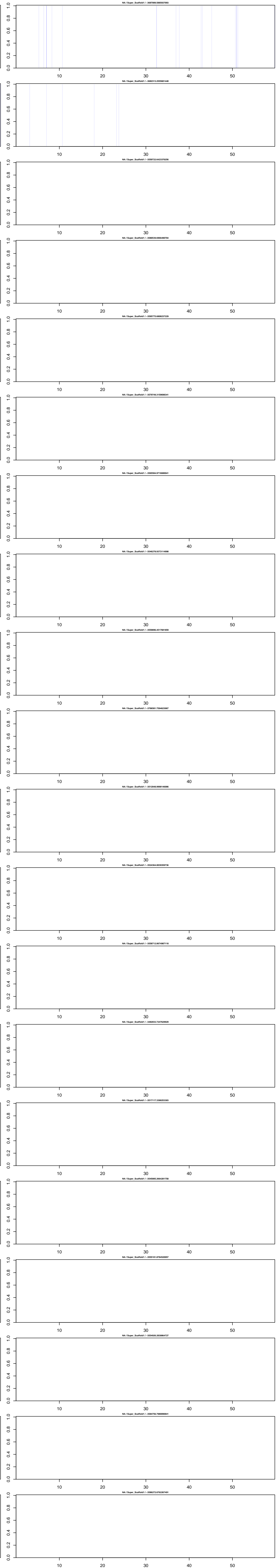
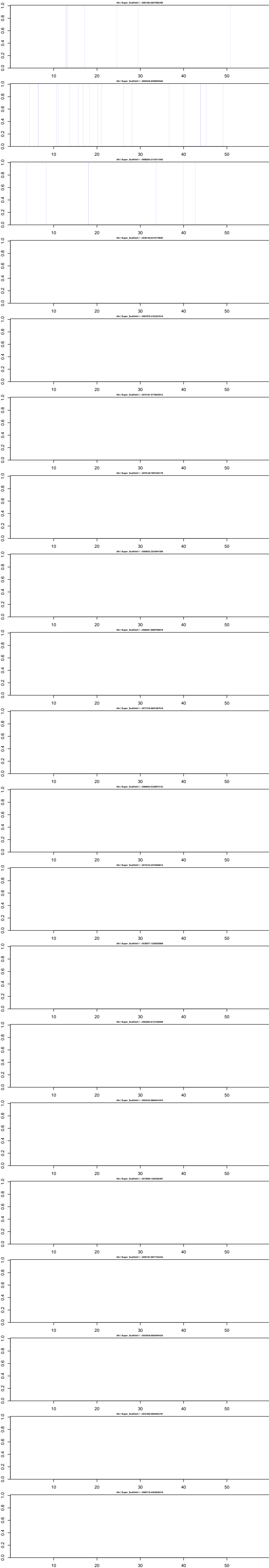


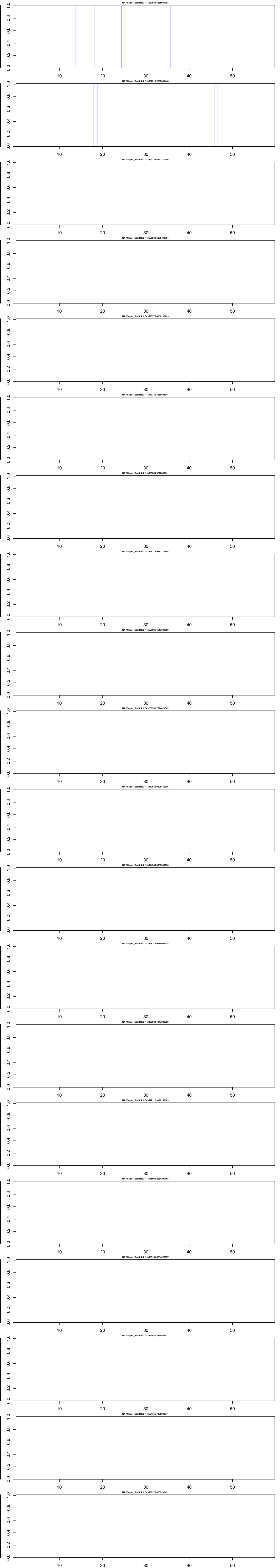
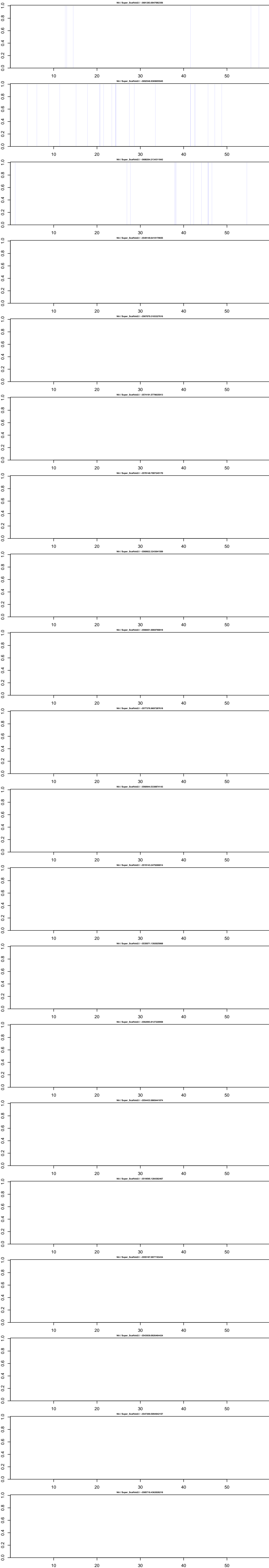
Supplementary Fig. 2. Comparison of genome-wide heterozygosity estimates across different depth of coverage categories.

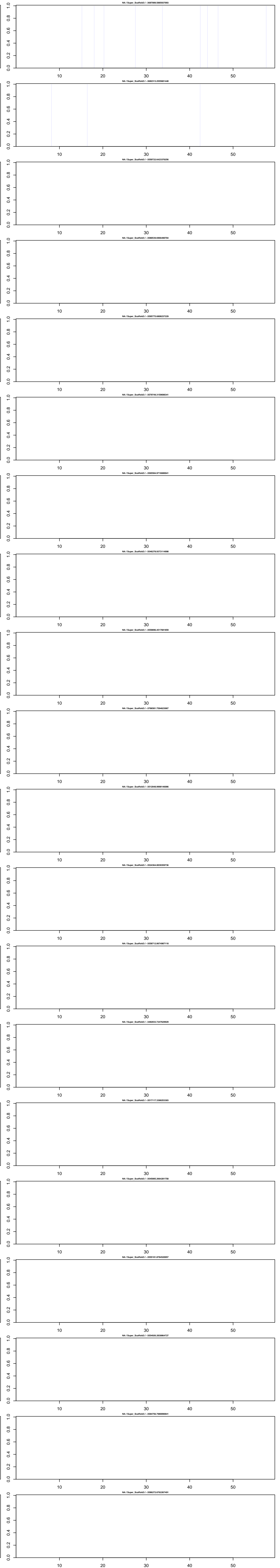
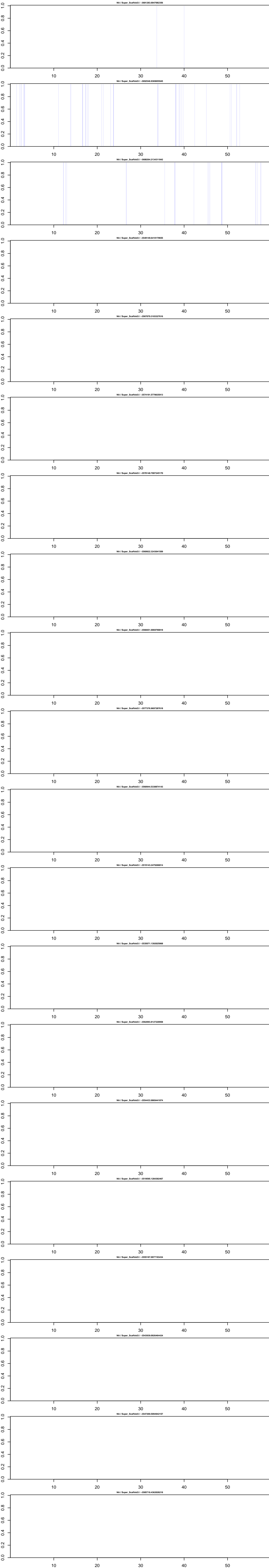
Key for Supplementary Fig. 3. The plots in this figure are arranged by sample (following the pattern below) and then by super-scaffold, starting from Super-Scaffold0 through to Super-Scaffold50. Each page thus contains the inbreeding tracts plot for each sample for a particular super-scaffold. Sampling locality is shown in parenthesis. AENP: Addo Elephant National Park, KNP: Kruger National Park, HiP: Hluhluwe-iMfolozi Park, MNP: Mokala National Park

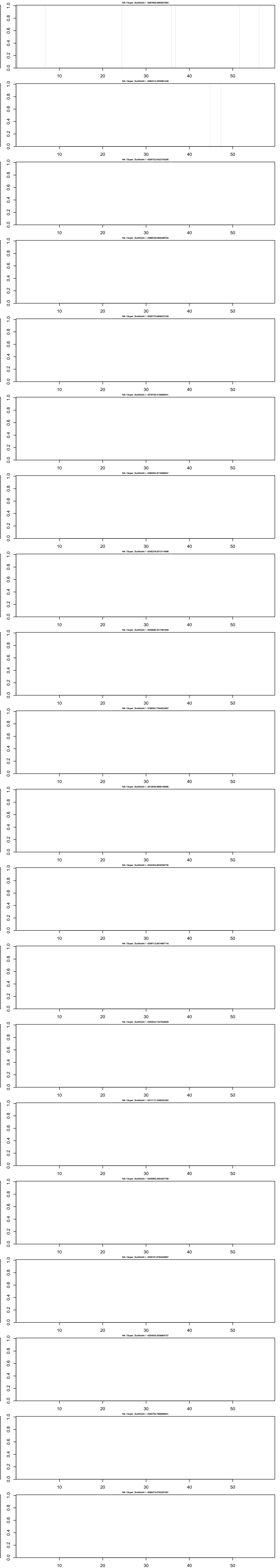
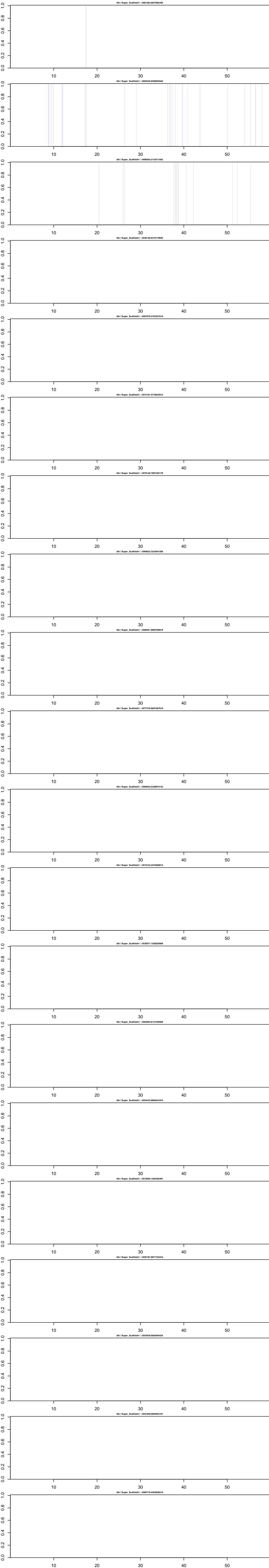
A_243_14 (AENP)	A_251_14 (AENP)
A_264_14 (AENP)	A_268_14 (AENP)
A_87_13 (AENP)	B98_161 (KNP)
B98_284 (KNP)	B98_289 (KNP)
B98_324 (KNP)	B98_340 (KNP)
B98_361 (KNP)	B98_395 (KNP)
B98_396 (KNP)	B98_509 (KNP)
B98_546 (KNP)	B98_547 (KNP)
B98_574 (KNP)	B98_579 (KNP)
B98_586 (KNP)	B98_597 (KNP)
HA_1 (HiP)	HA_41 (HiP)
HA_43 (HiP)	HB_31 (HiP)
HB_39 (HiP)	HC_11 (HiP)
HC_15 (HiP)	HC_17 (HiP)
HC_18 (HiP)	HC_20 (HiP)
HC_30 (HiP)	HC_32 (HiP)
HC_40 (HiP)	HC_41 (HiP)
HC_48 (HiP)	M_120_13 (MNP)
M_12_12 (MNP)	M_301_14 (MNP)
M_306_14 (MNP)	M_47_14 (MNP)

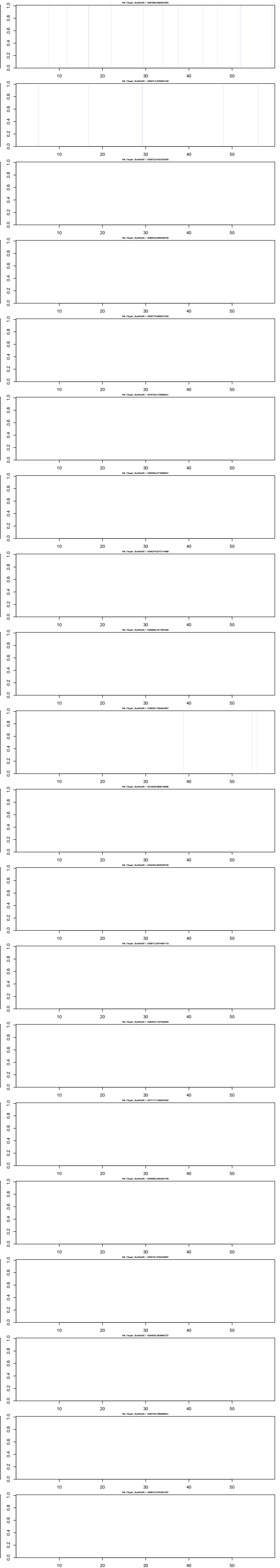
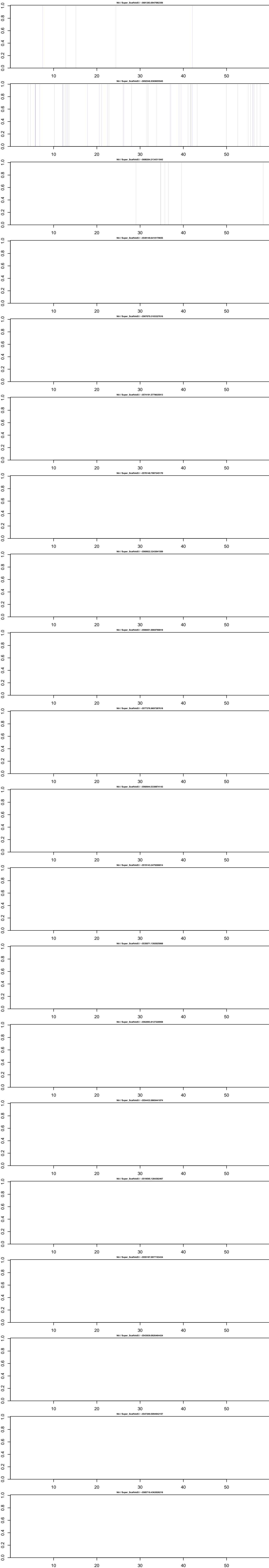


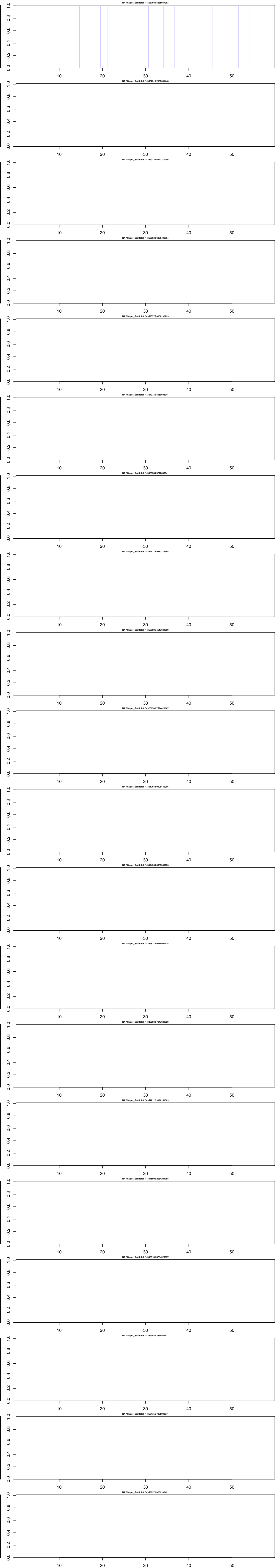
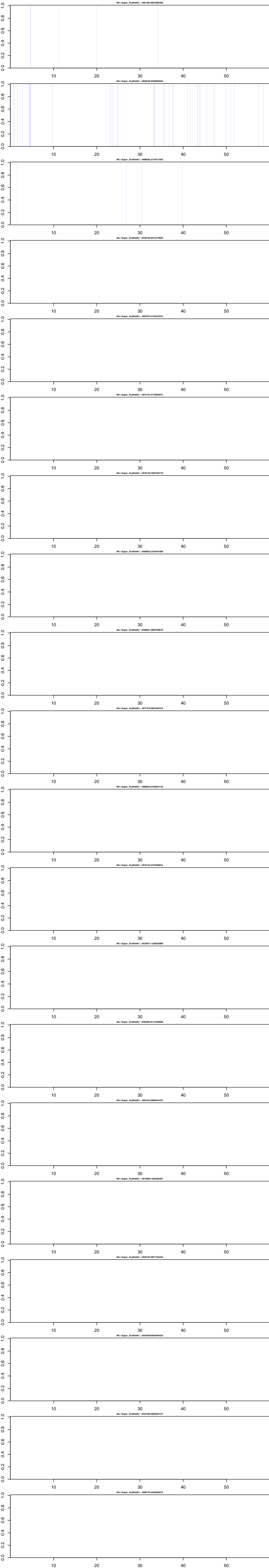


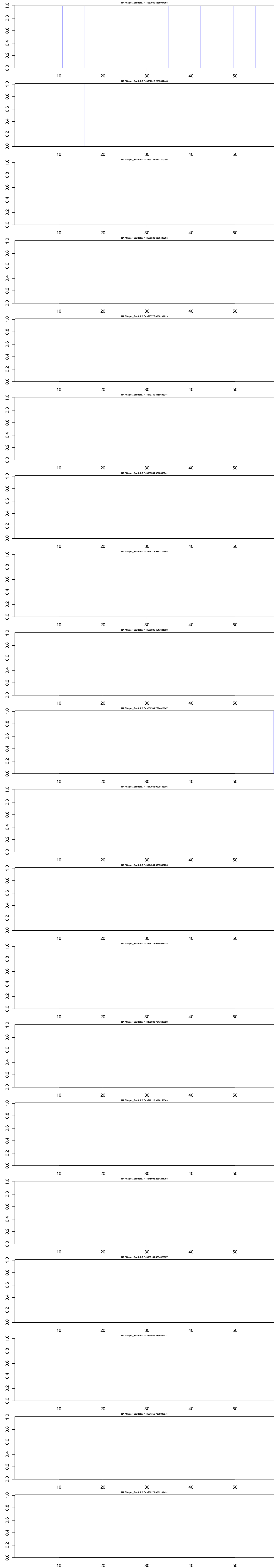
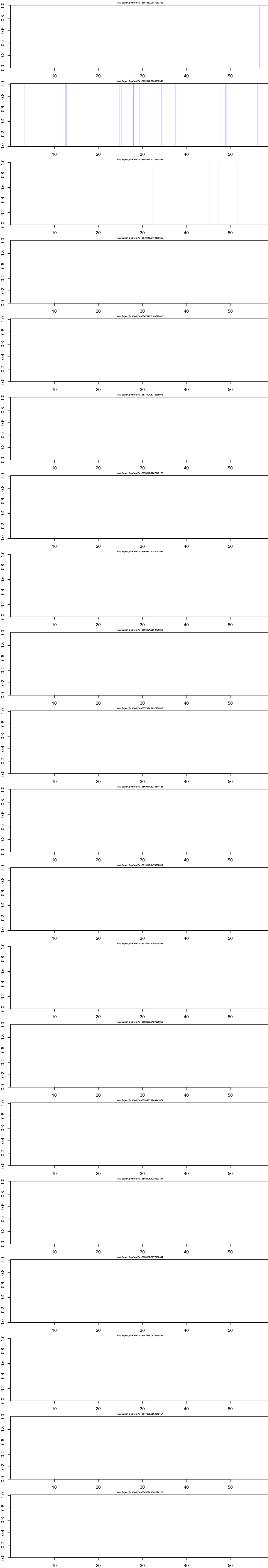


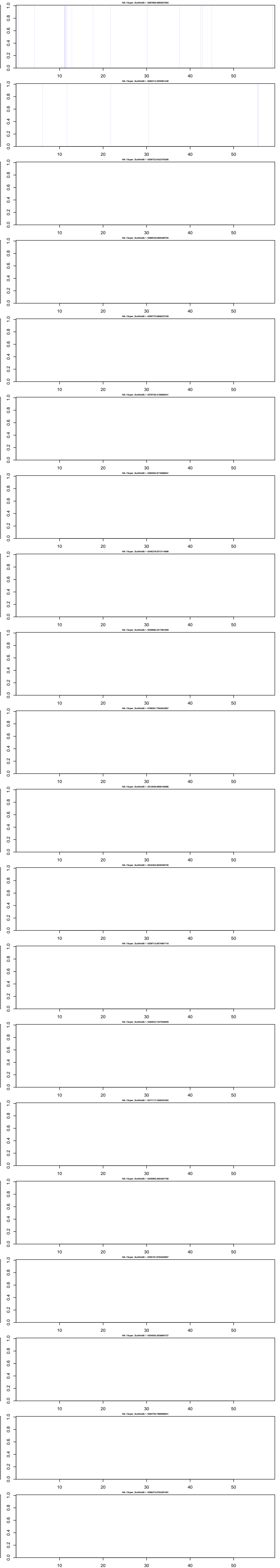
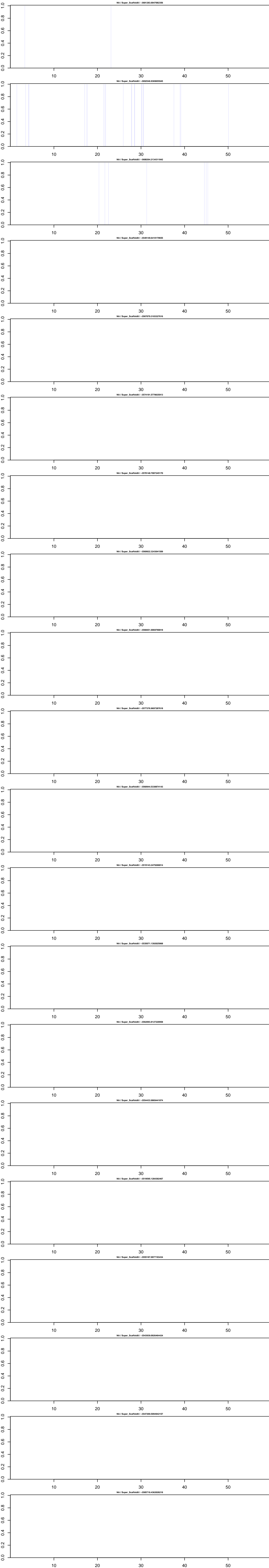


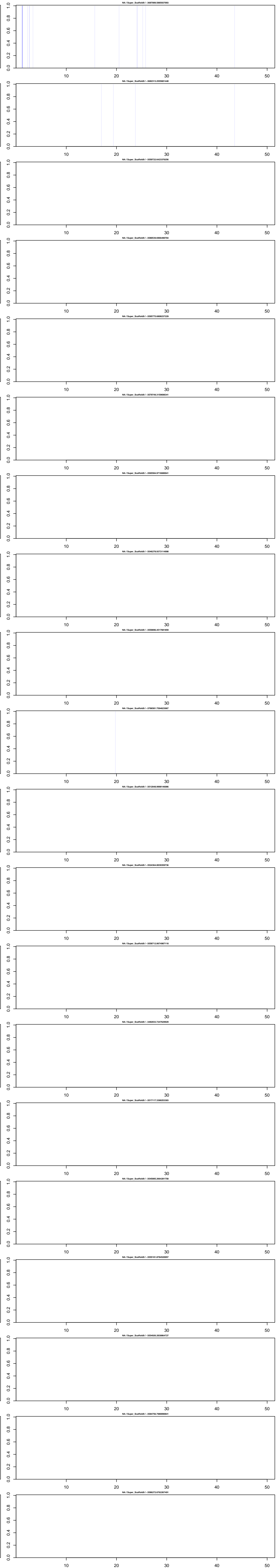
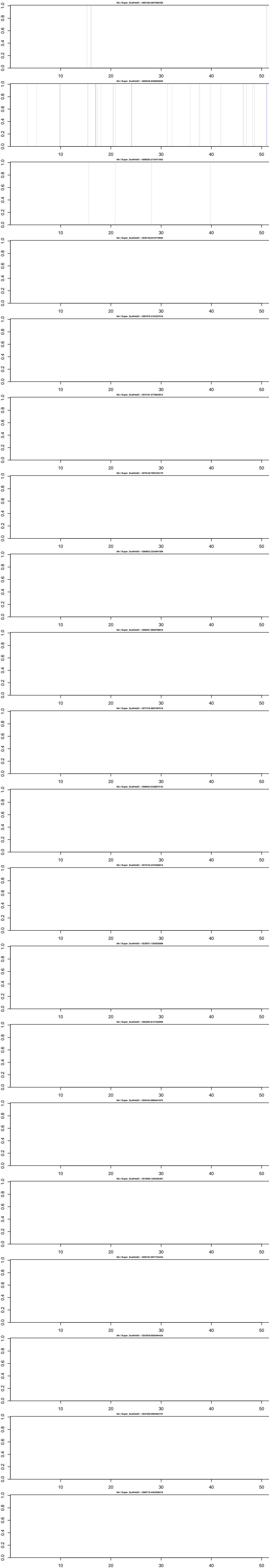


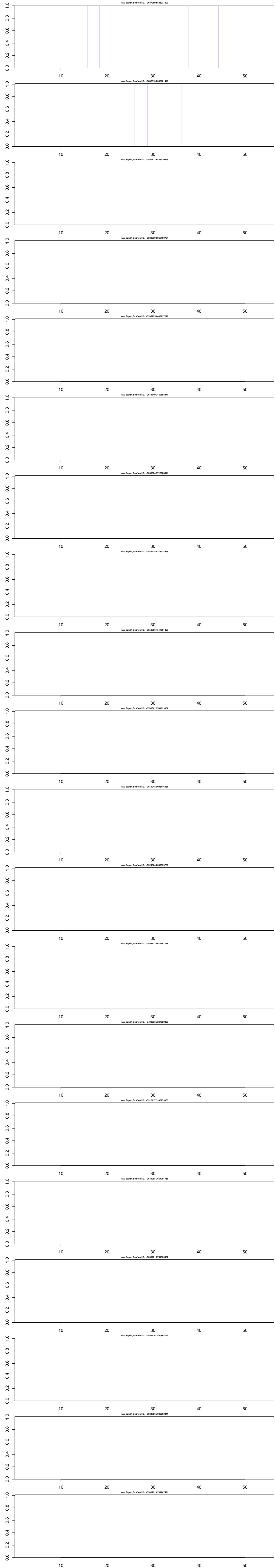
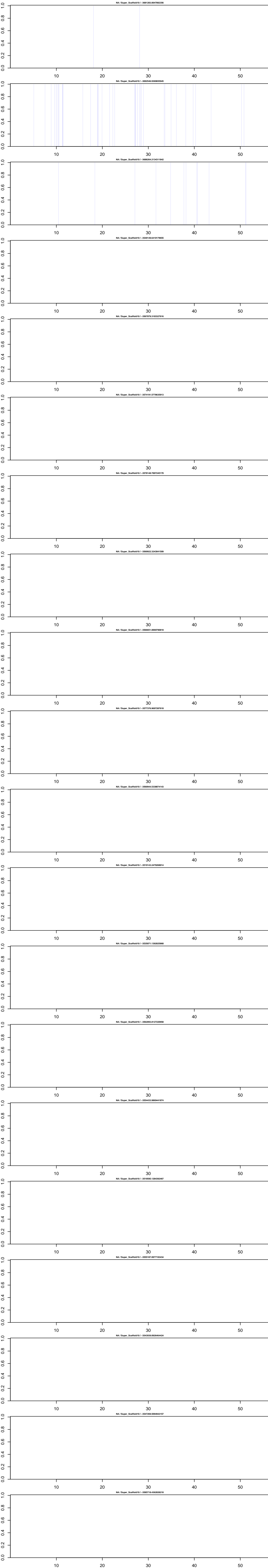


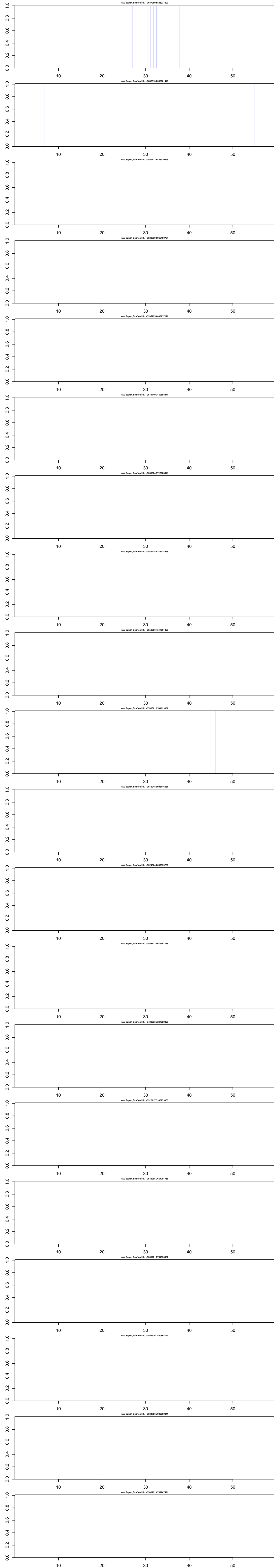
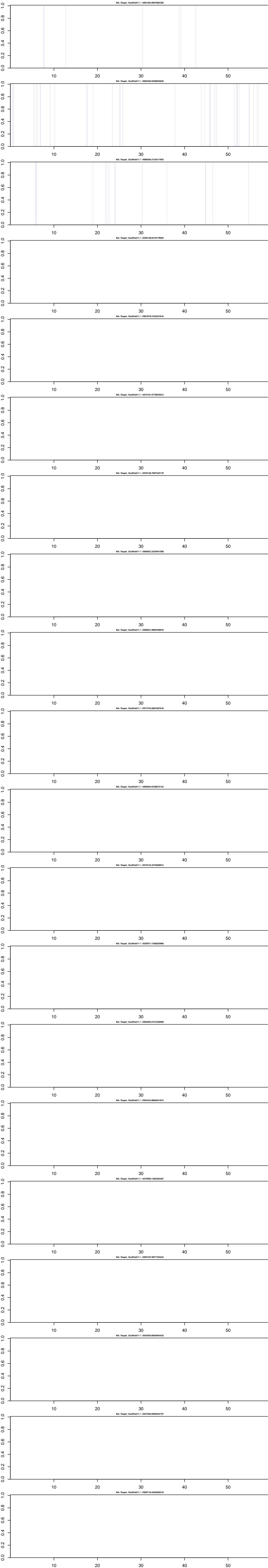


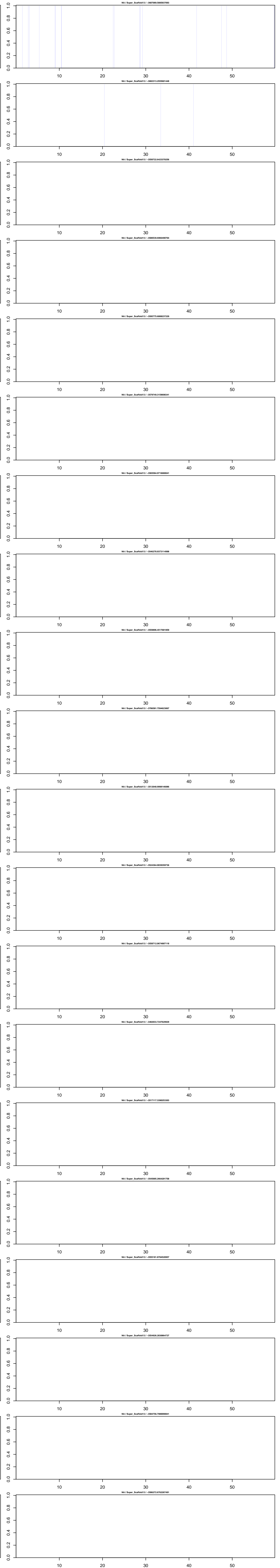
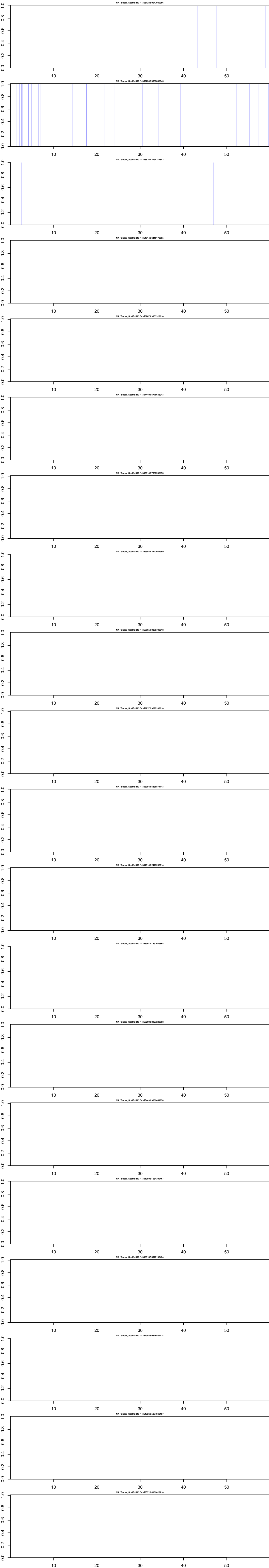


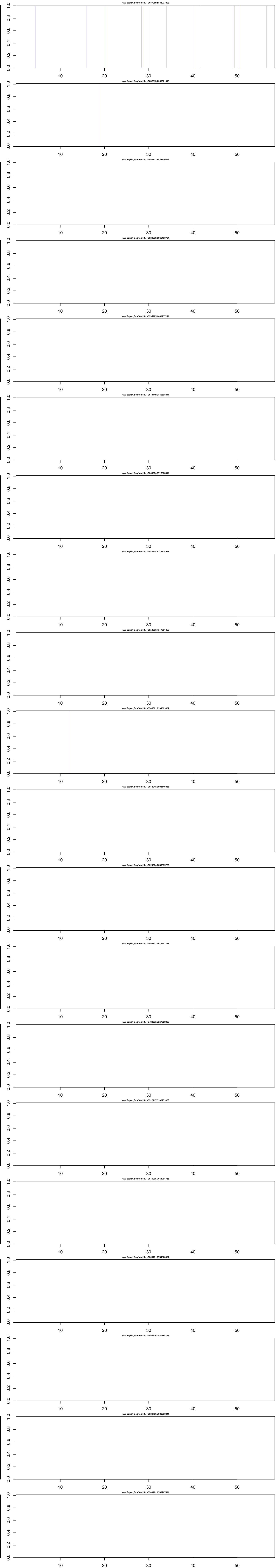
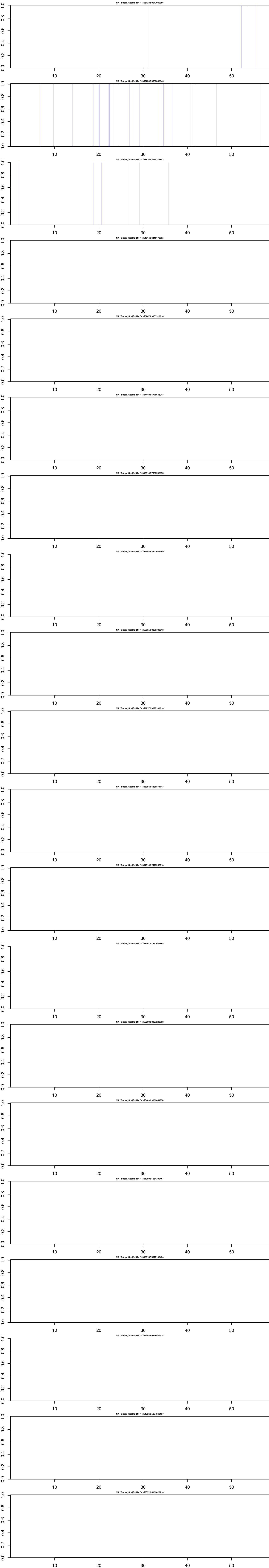


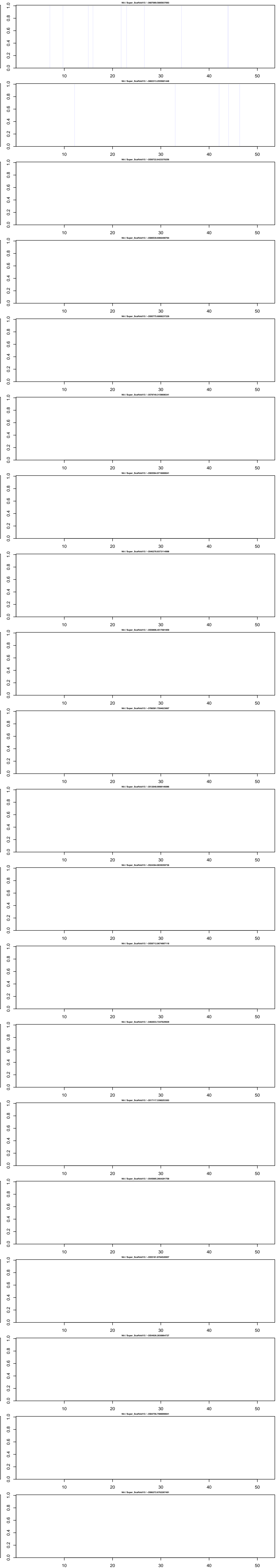
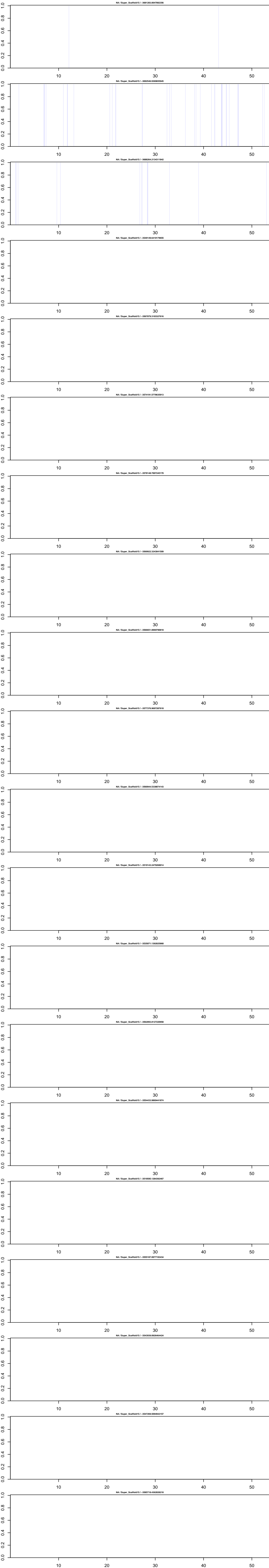


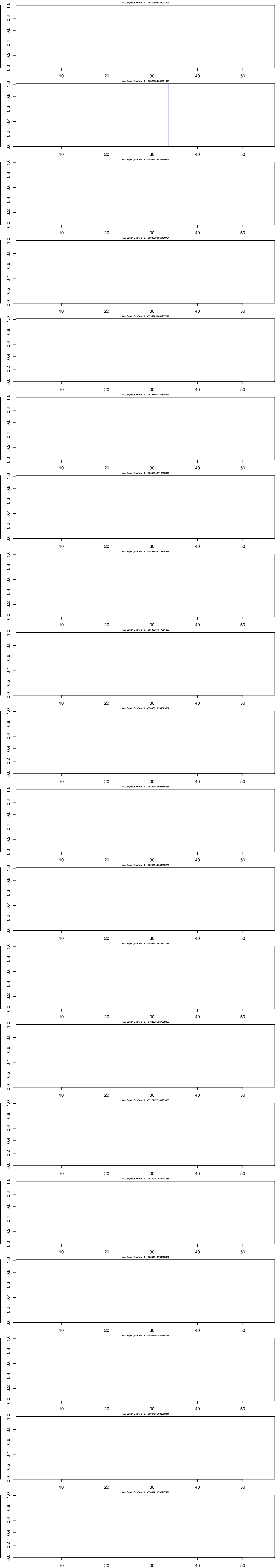
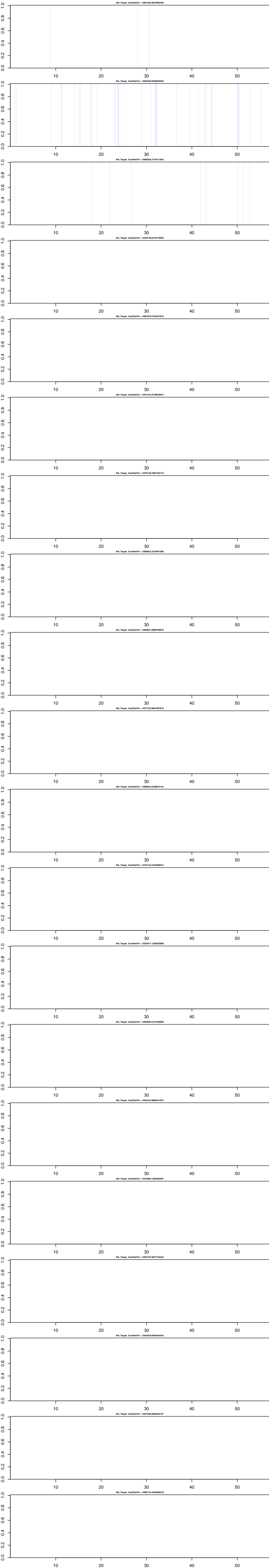


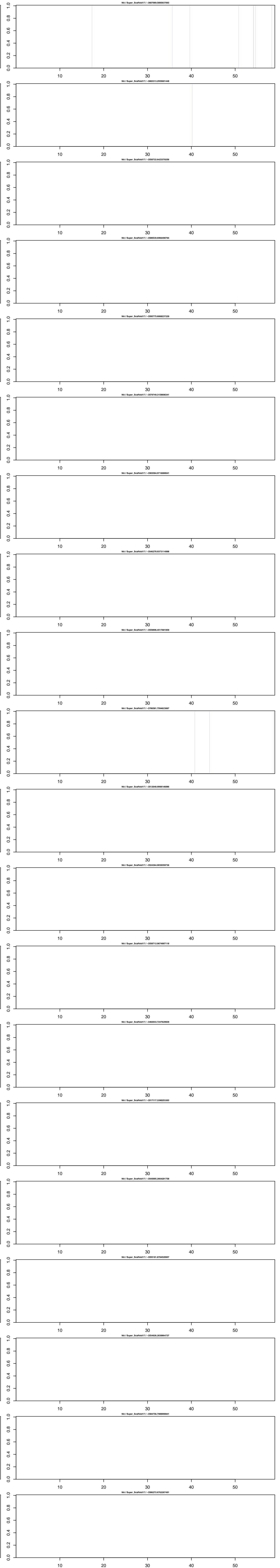
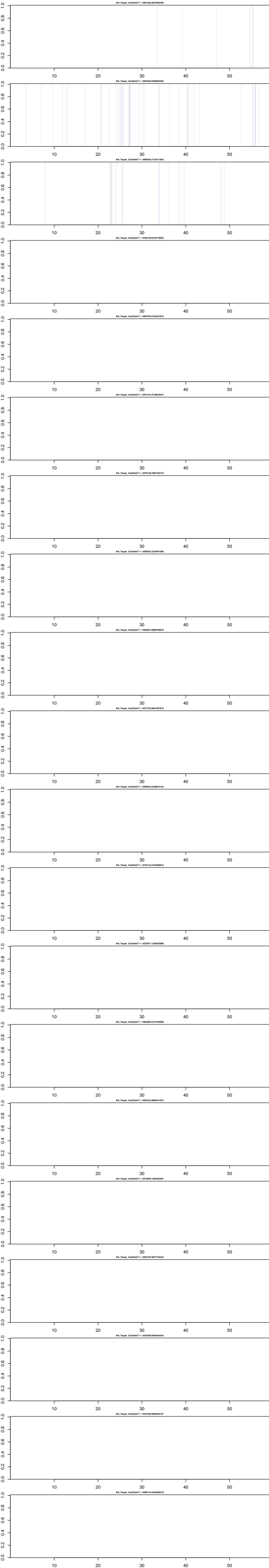


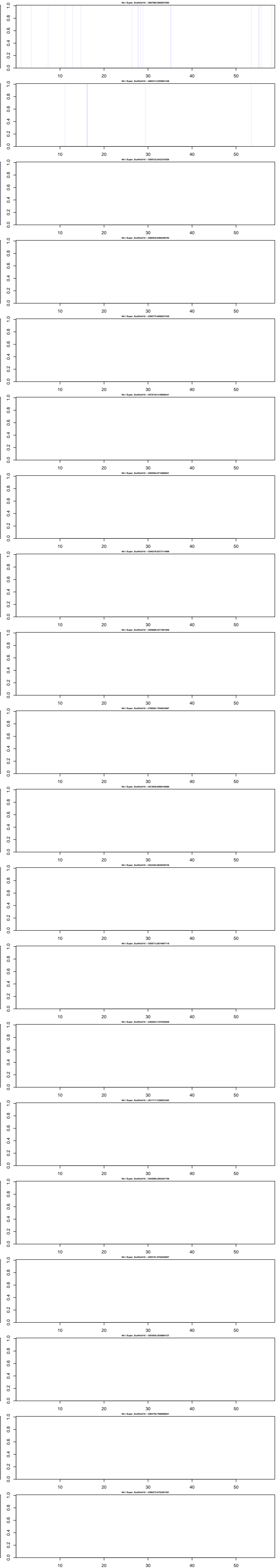
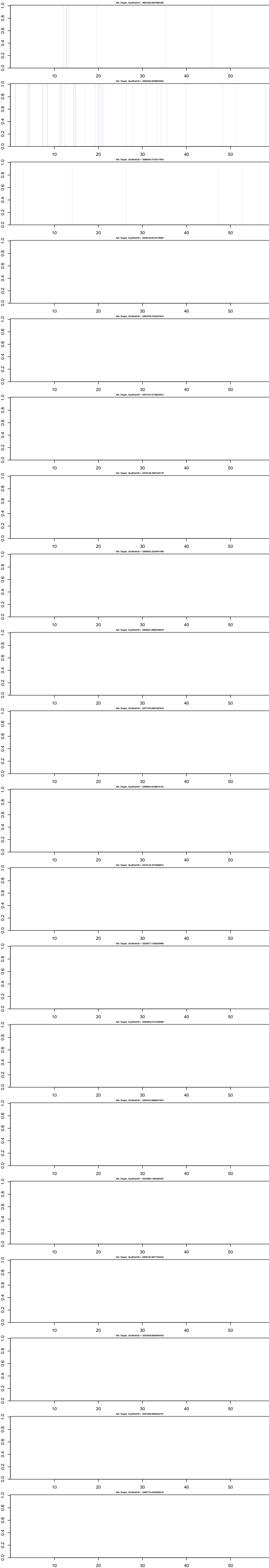


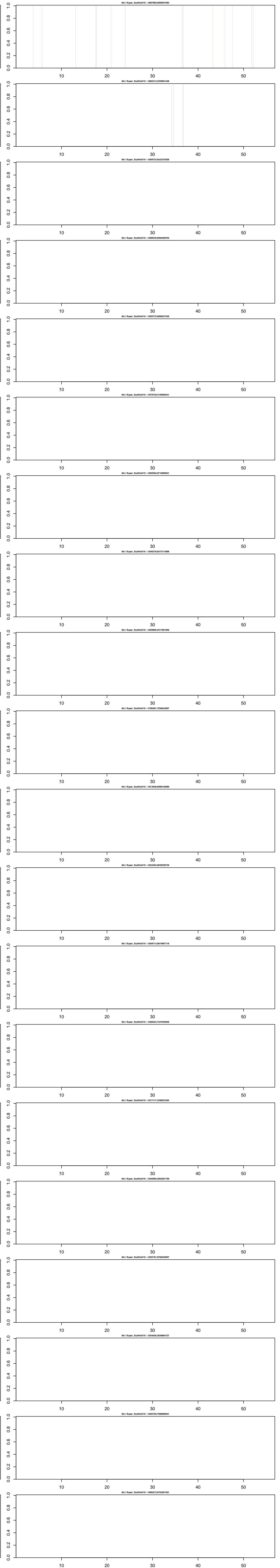
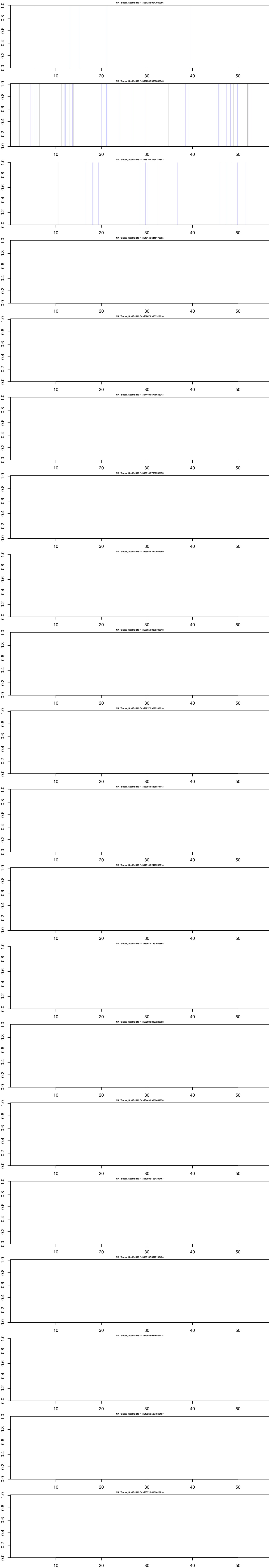


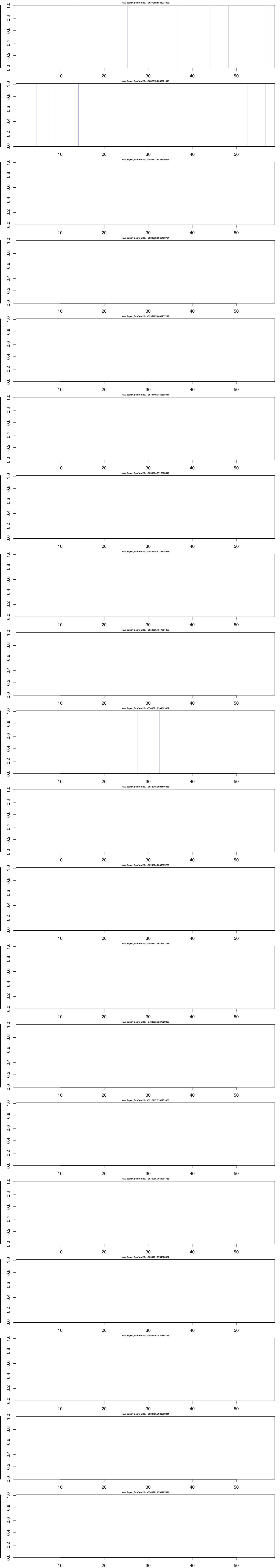
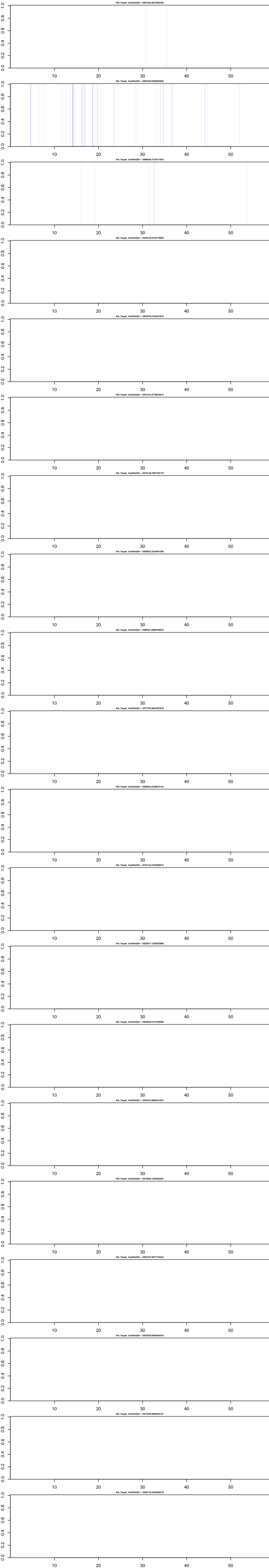


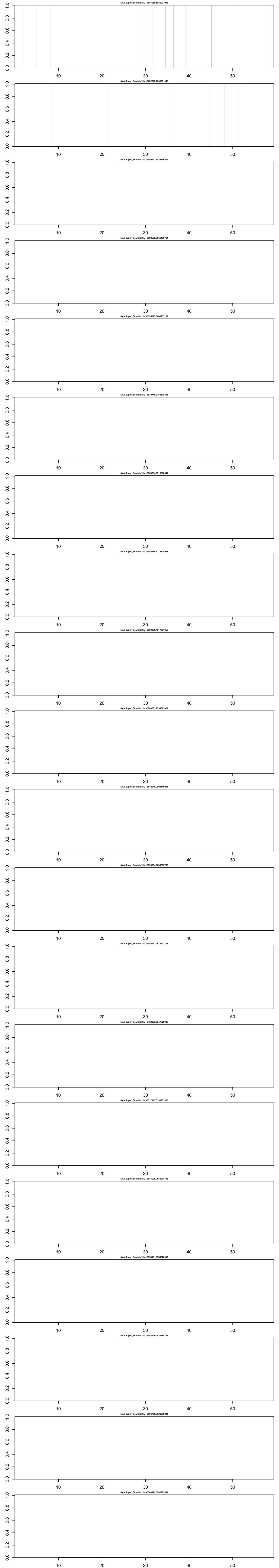
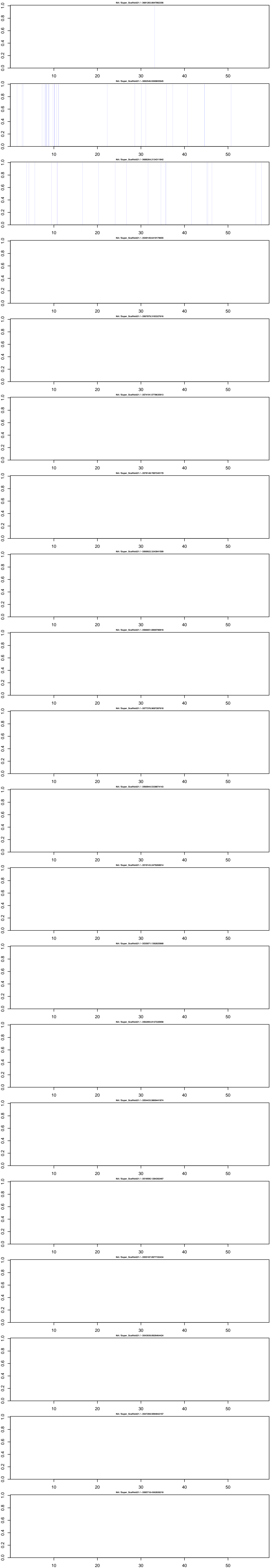


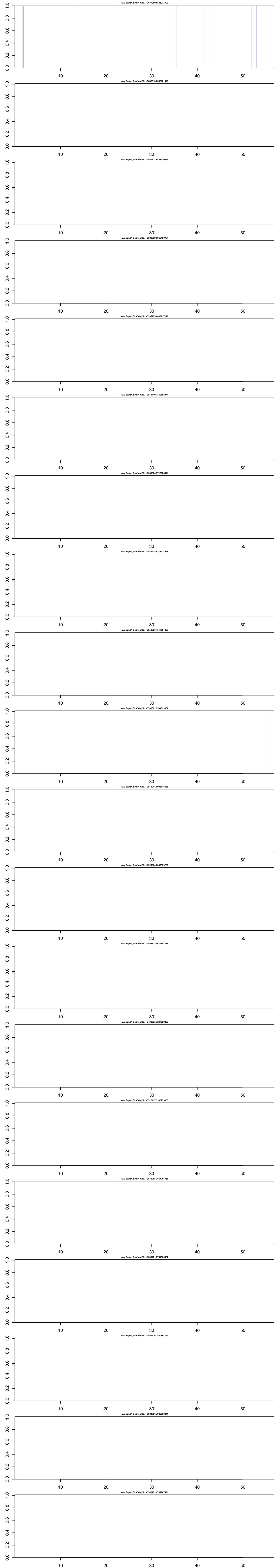
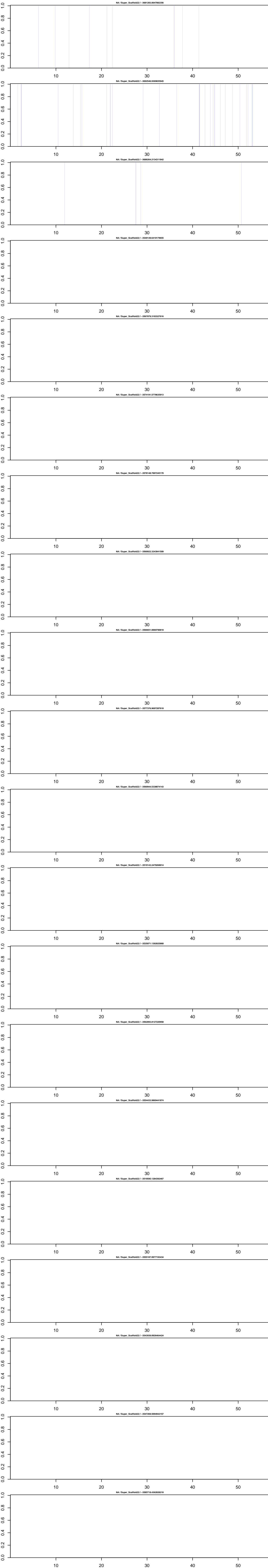


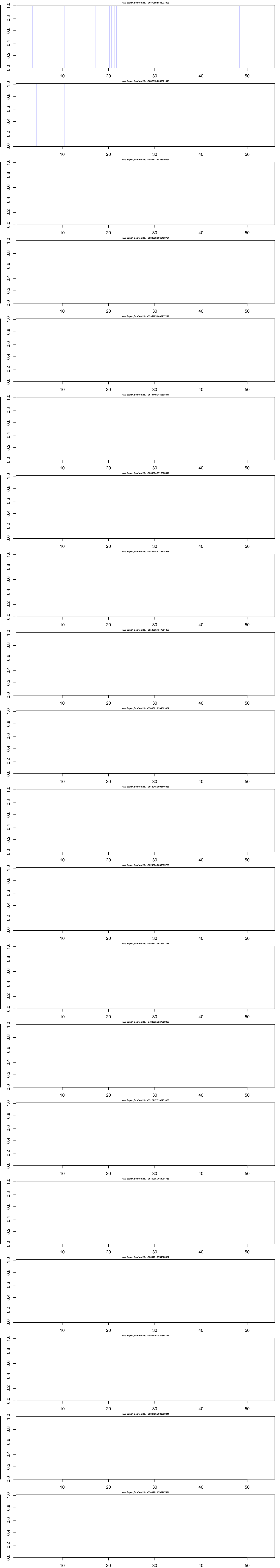
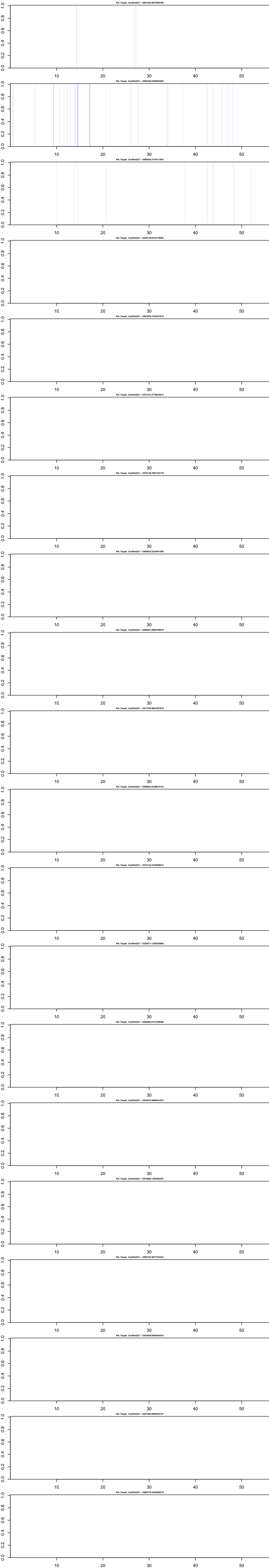


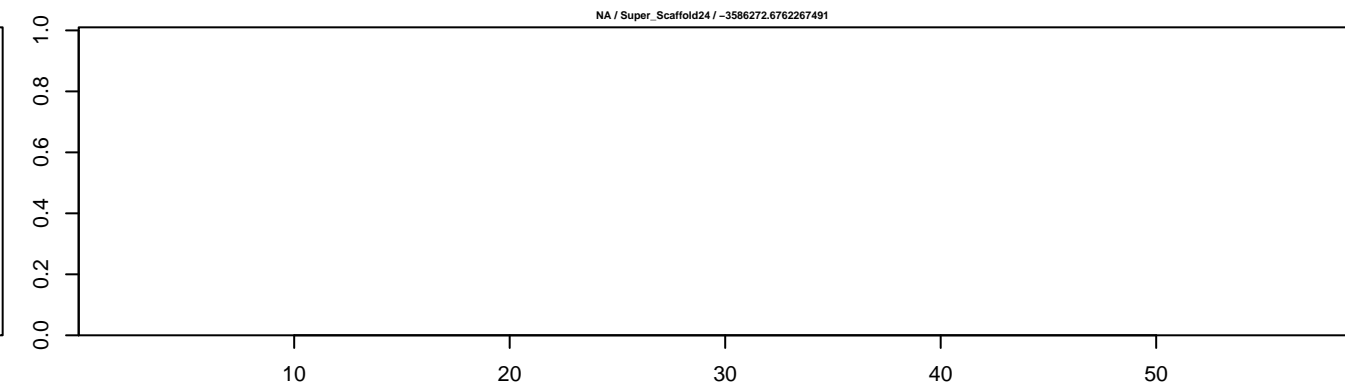
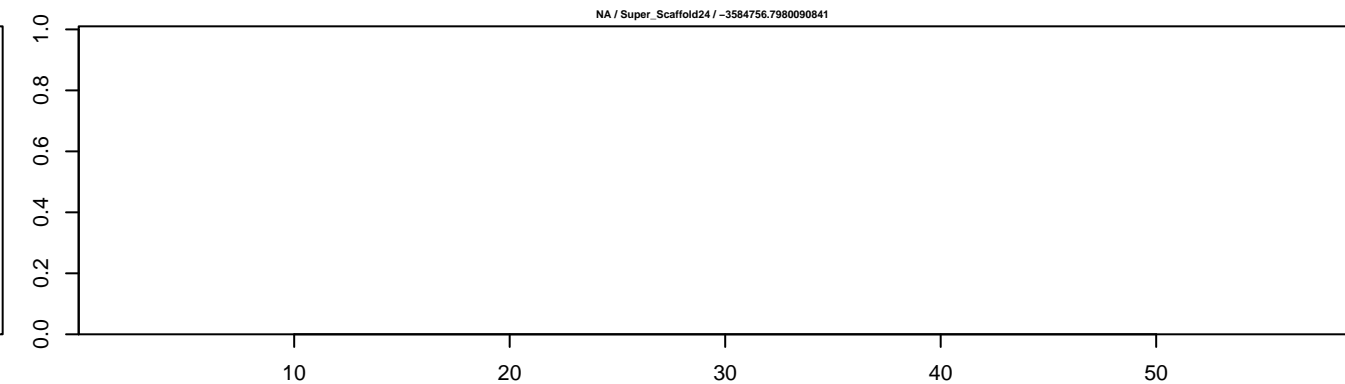
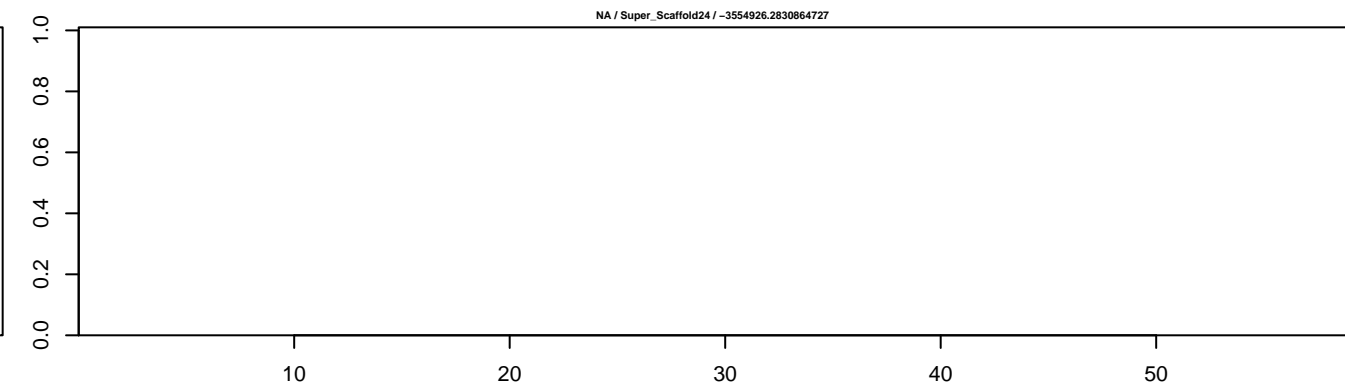
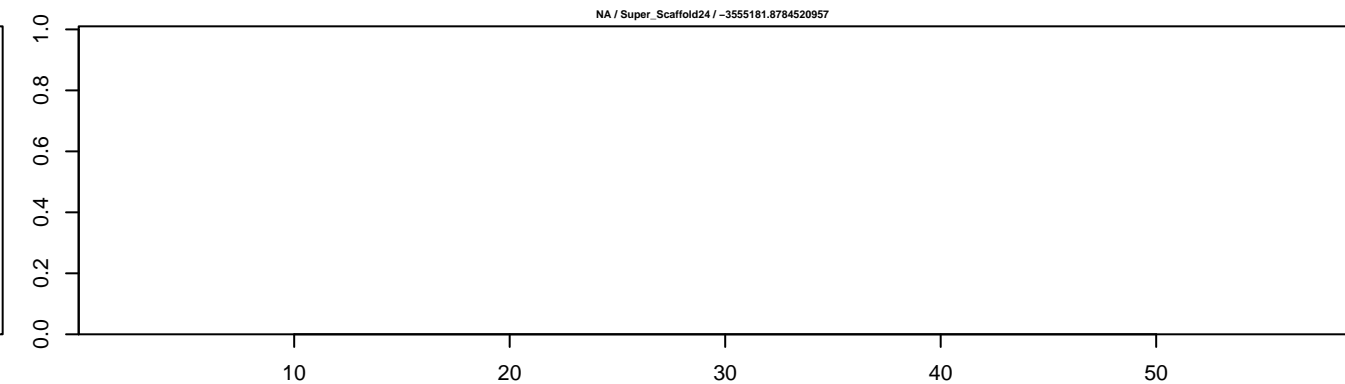
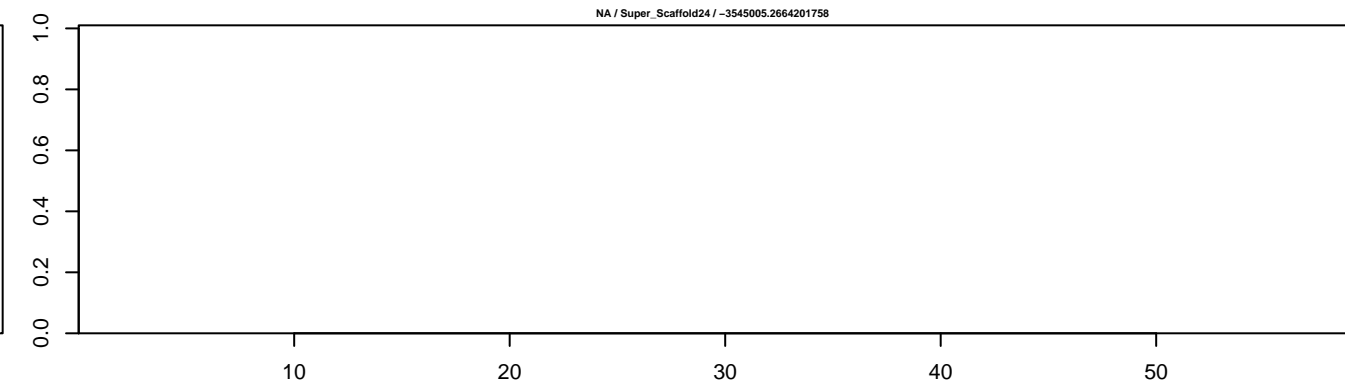
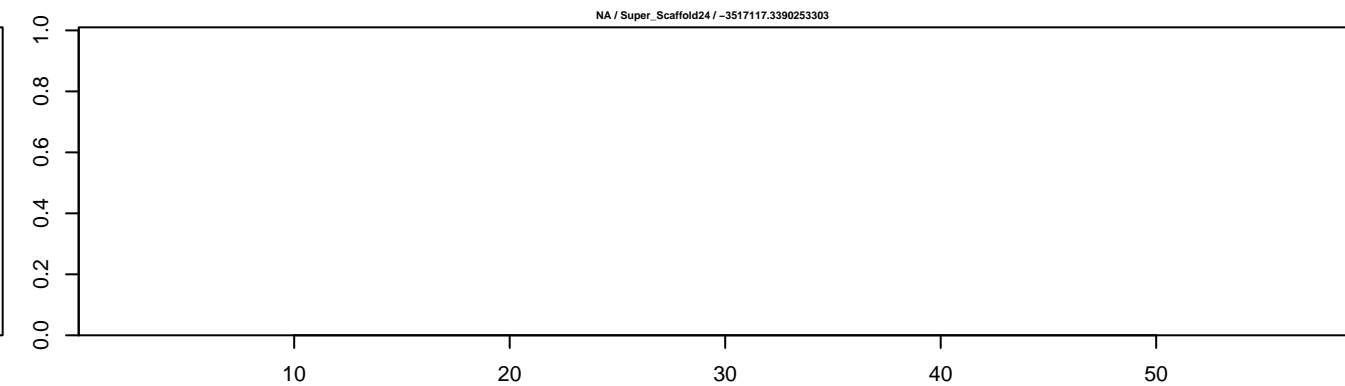
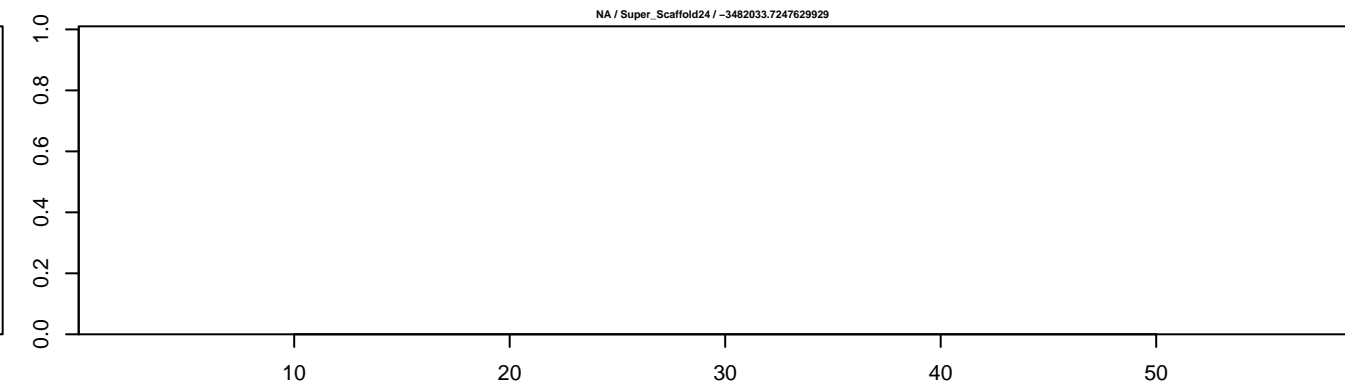
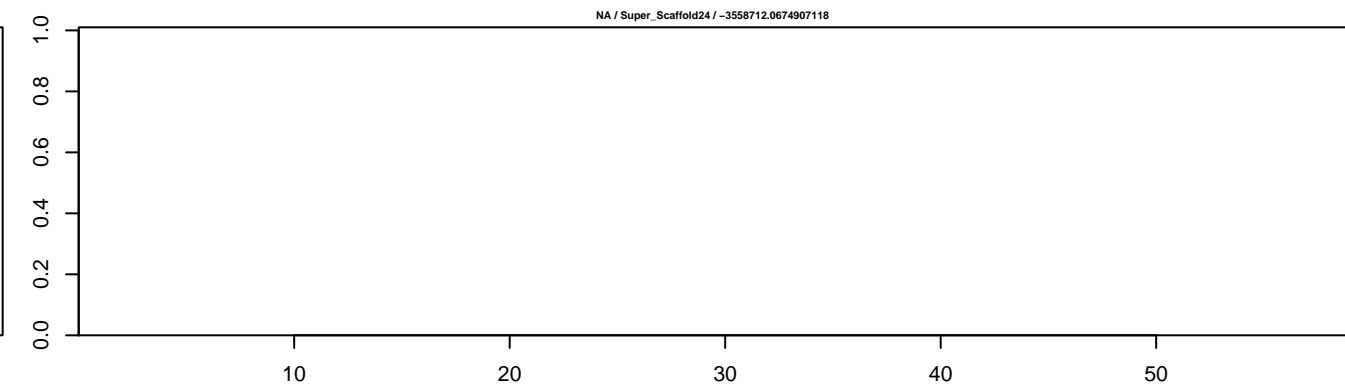
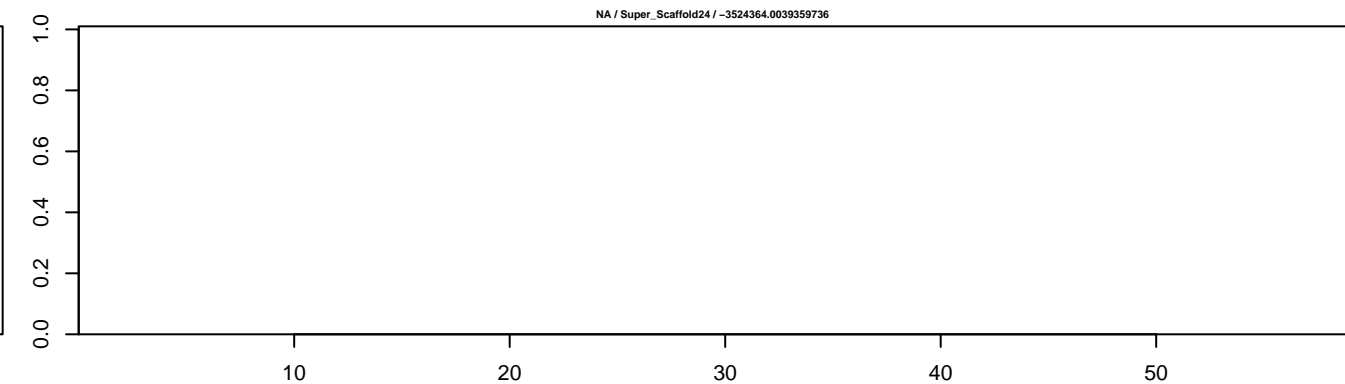
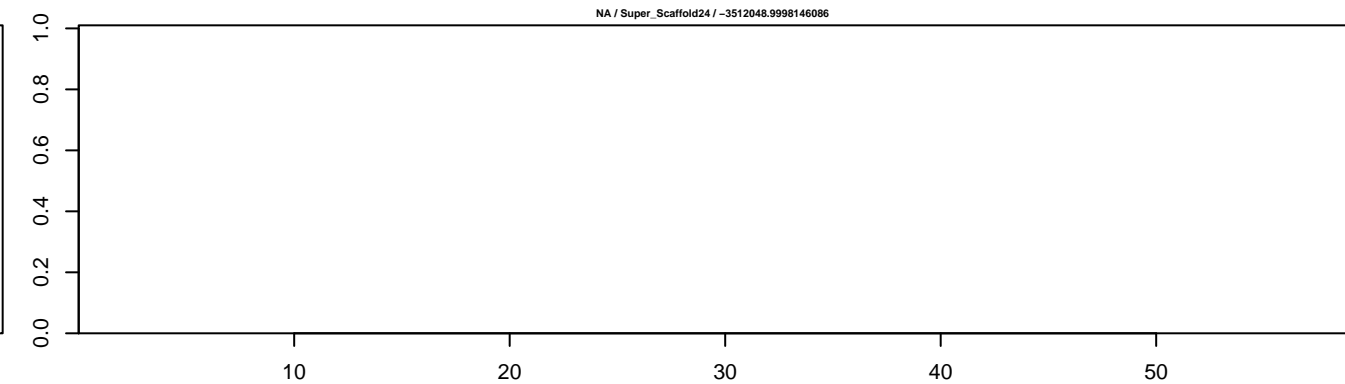
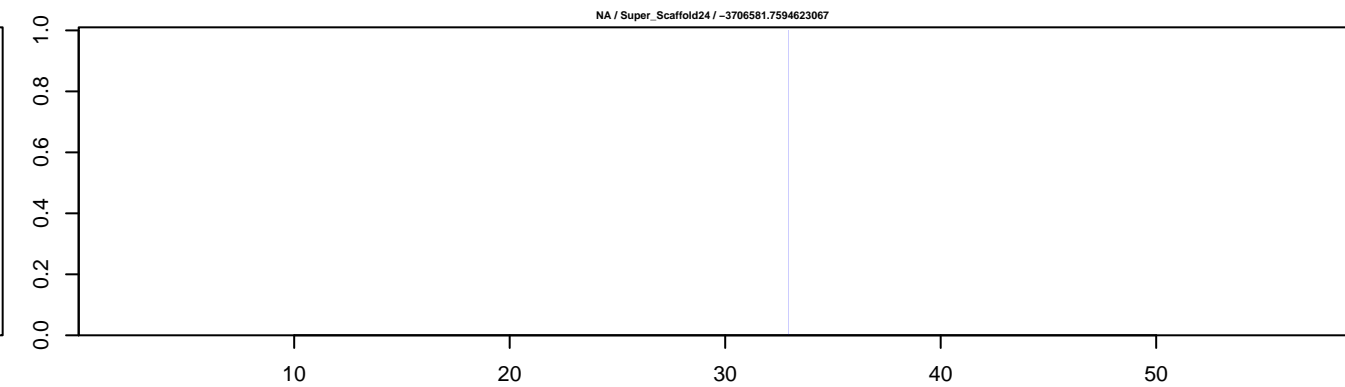
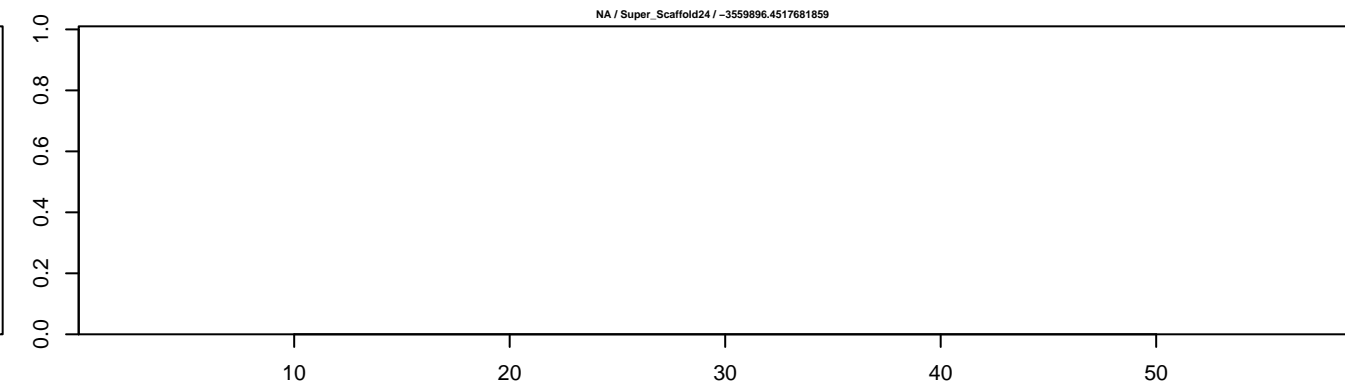
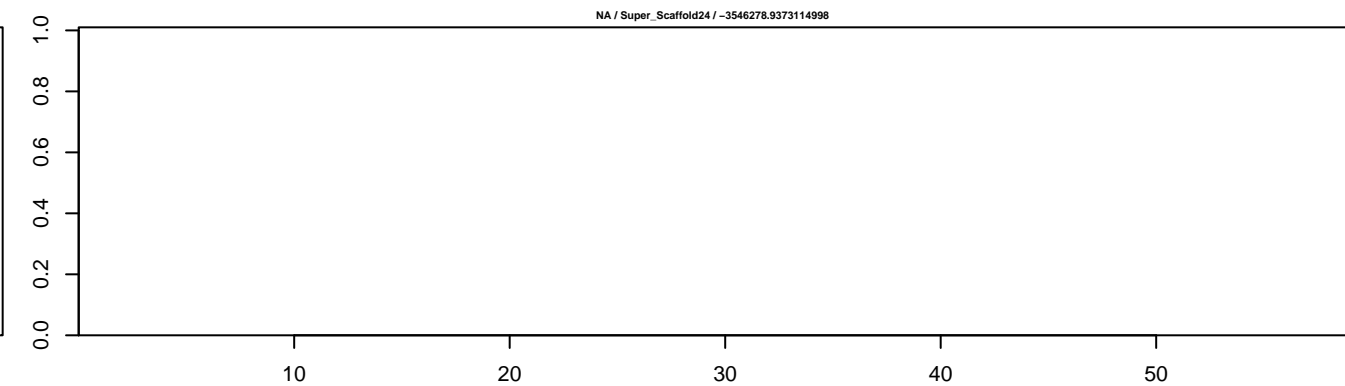
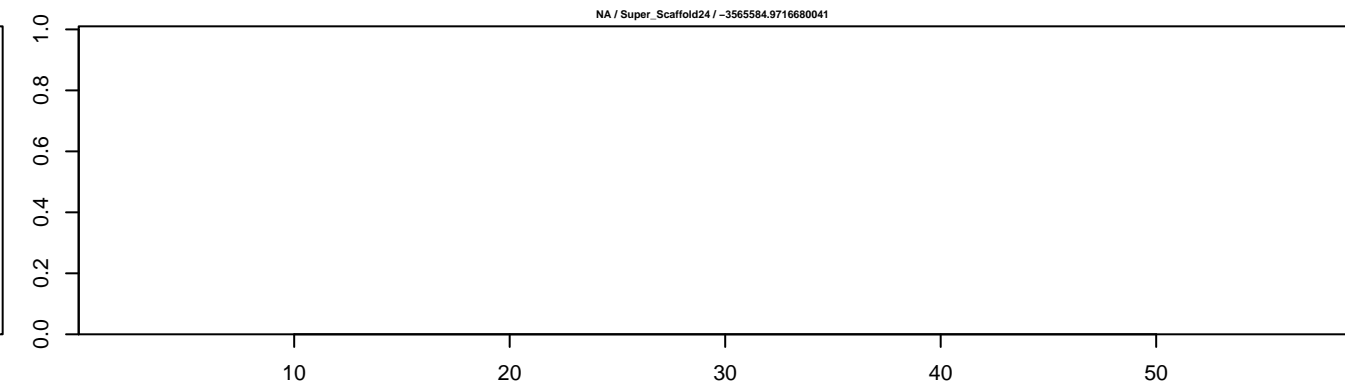
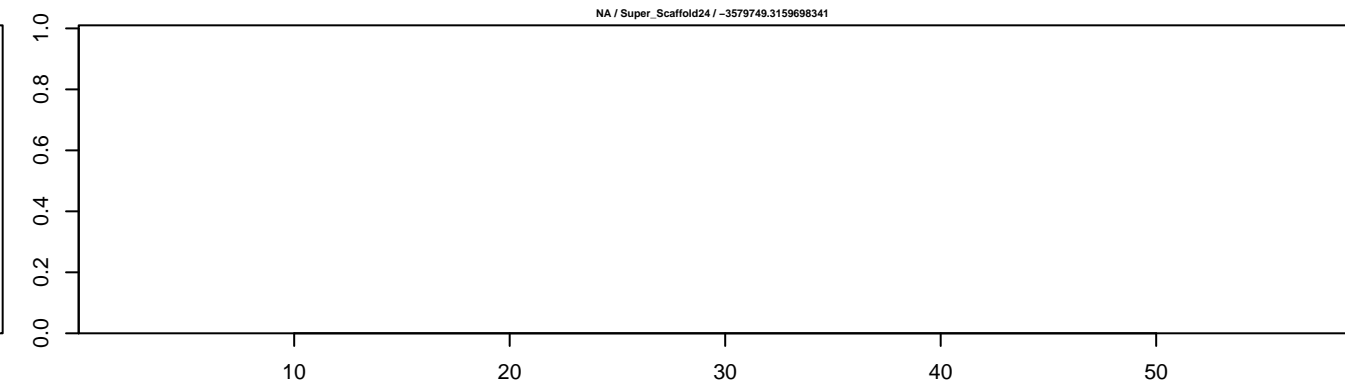
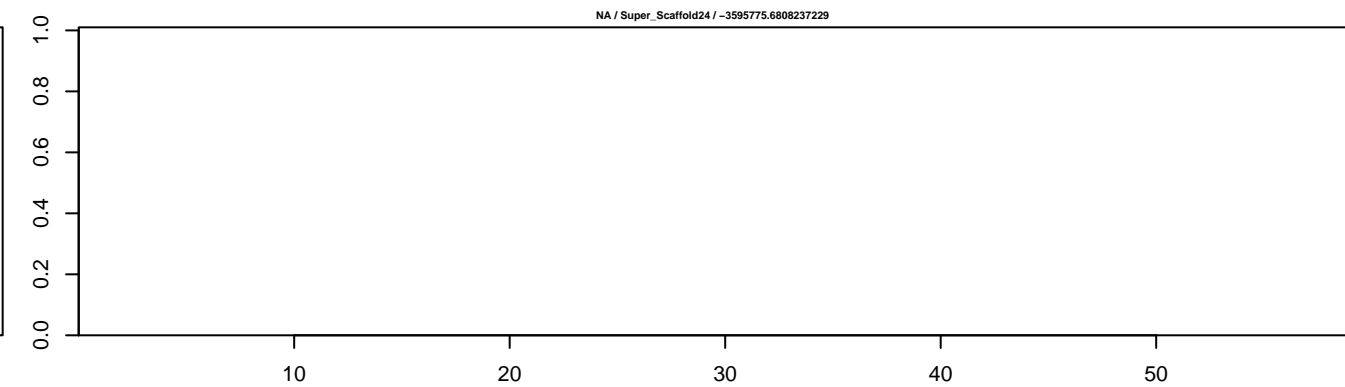
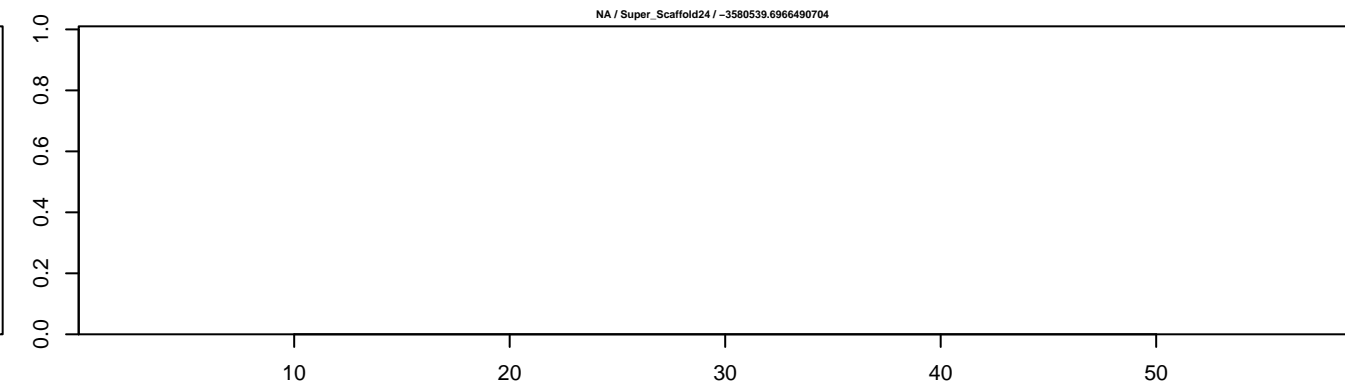
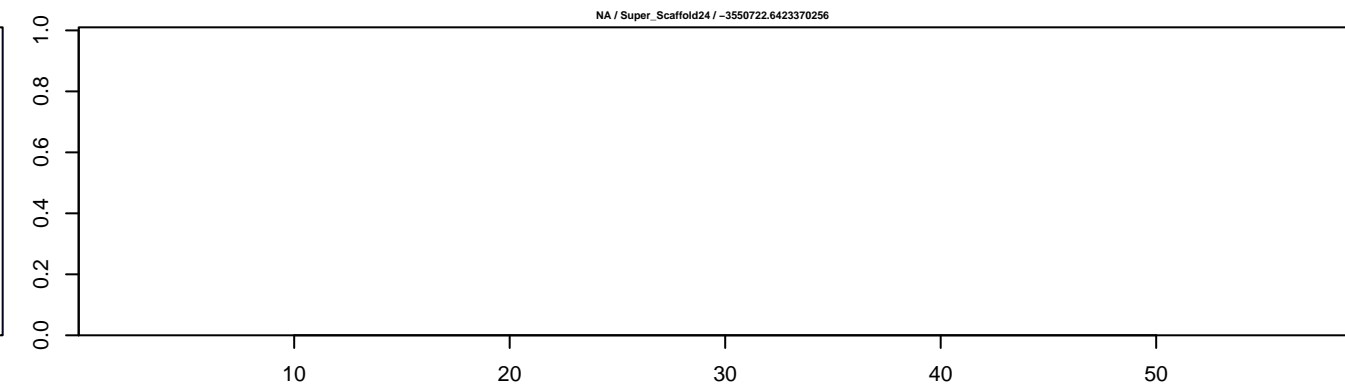
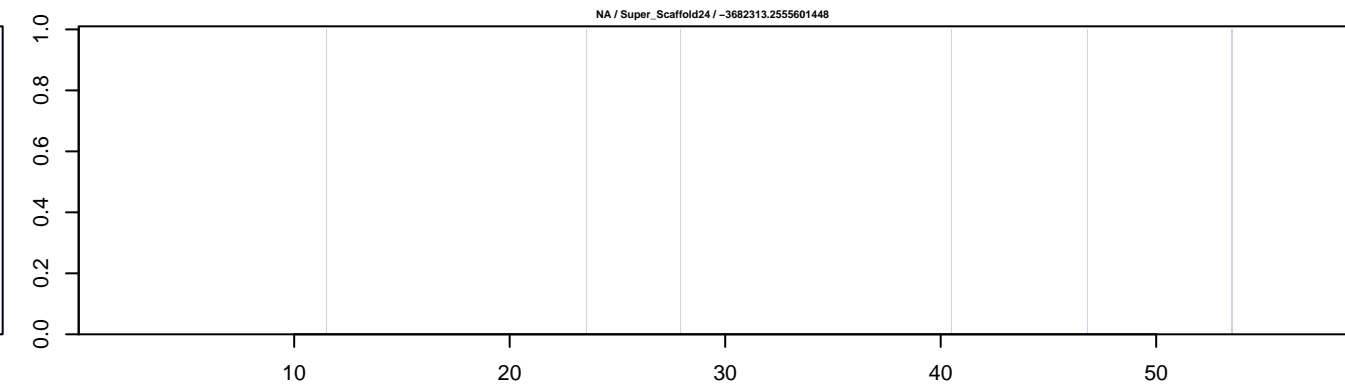
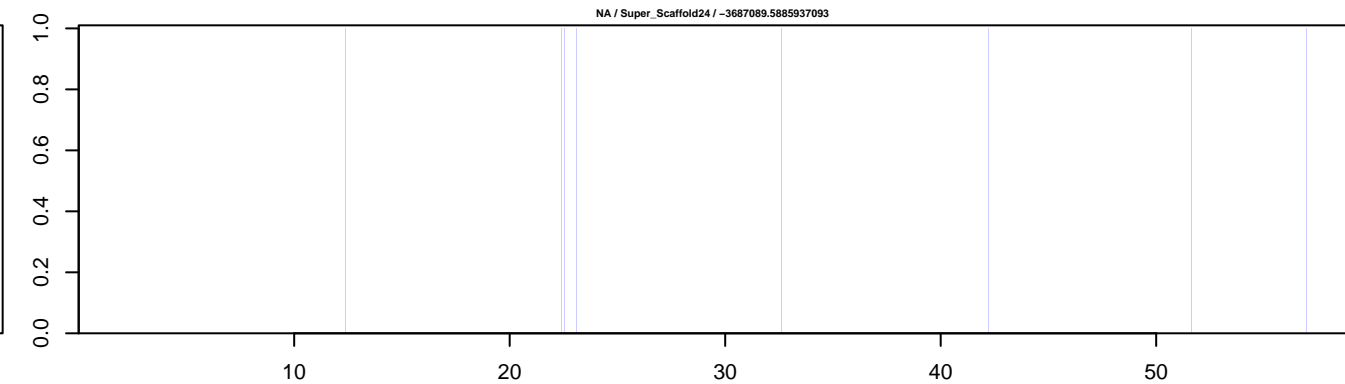
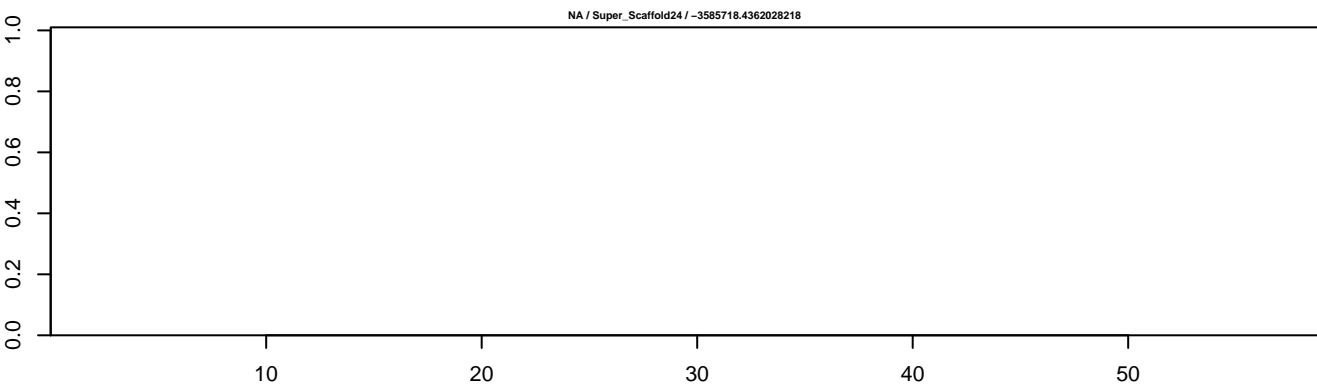
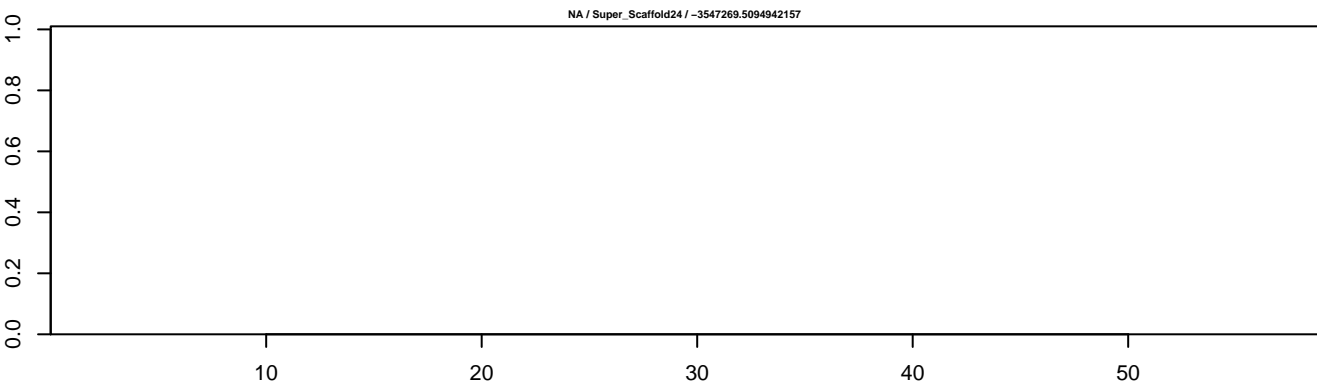
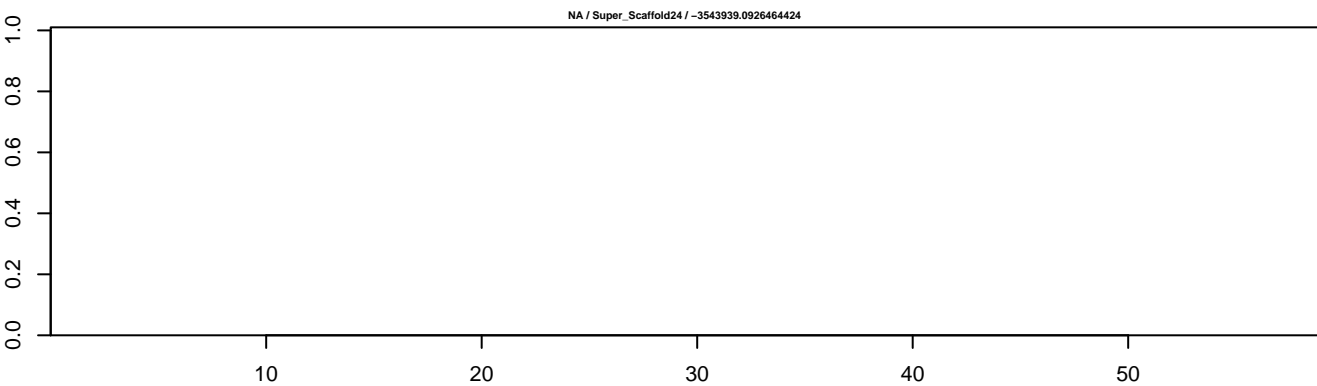
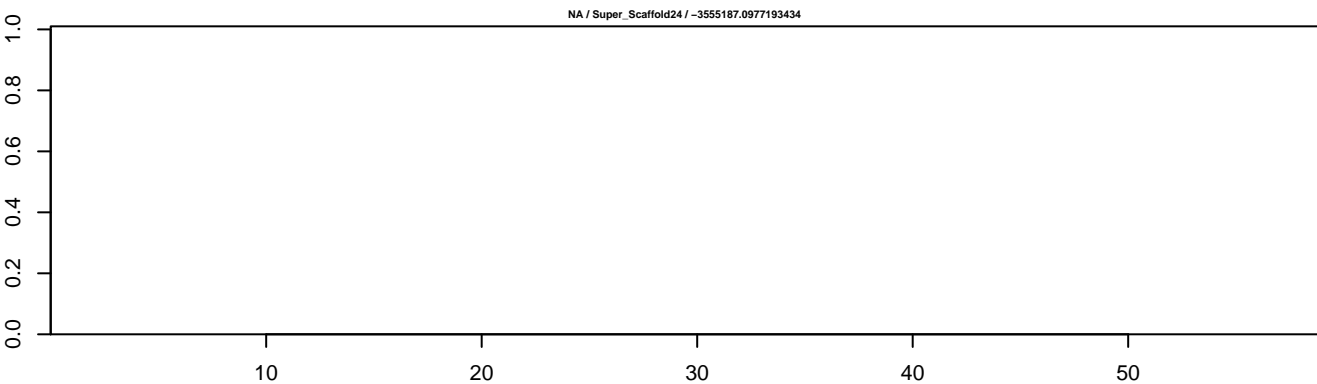
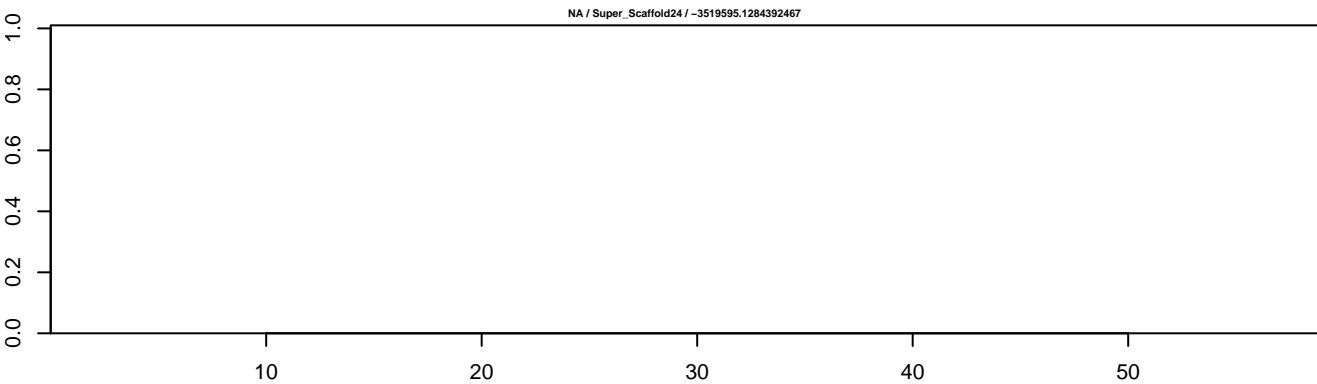
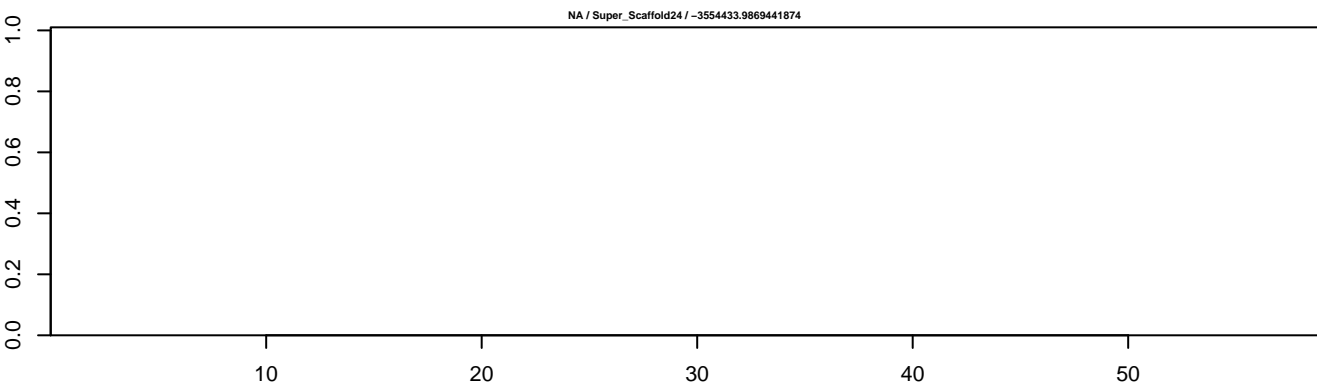
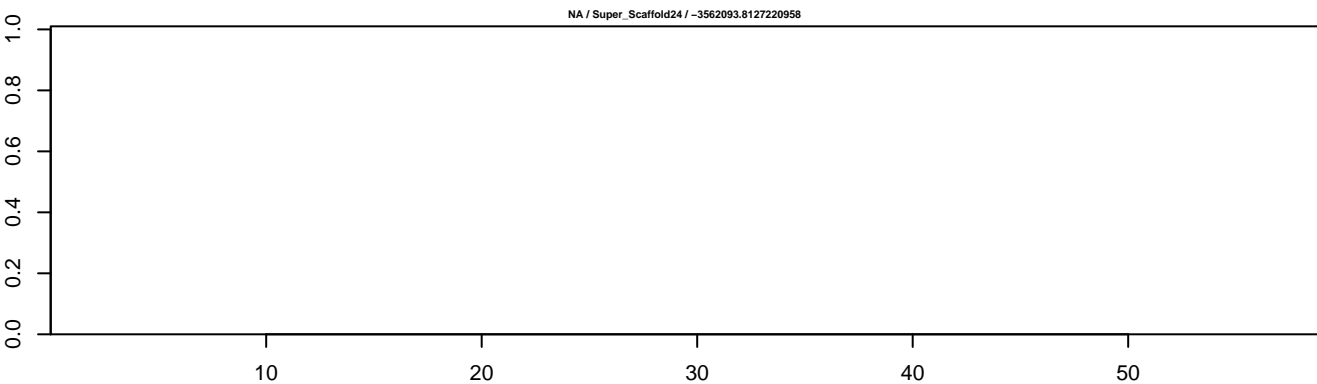
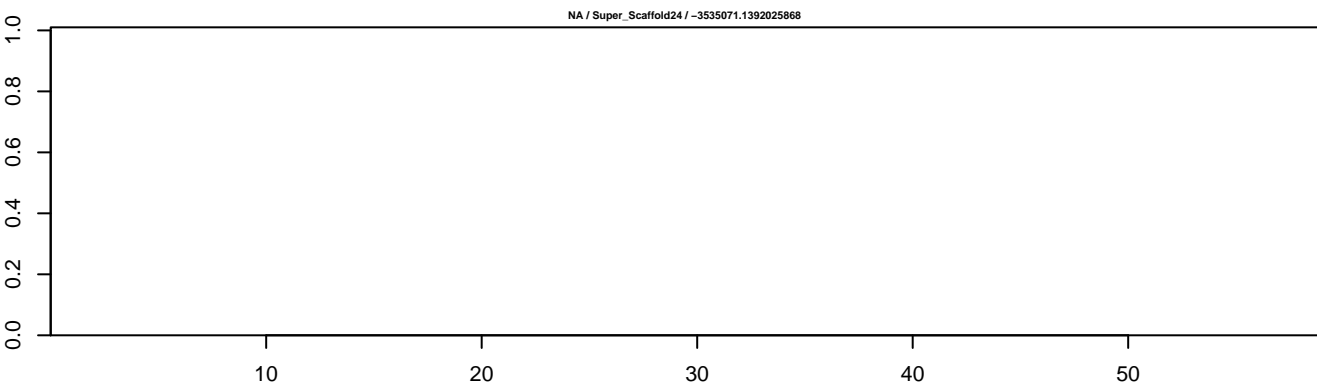
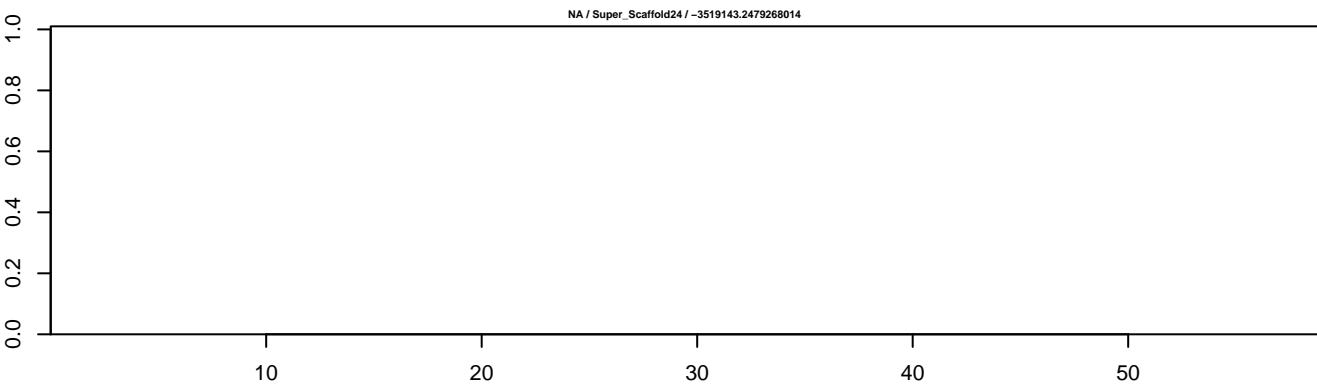
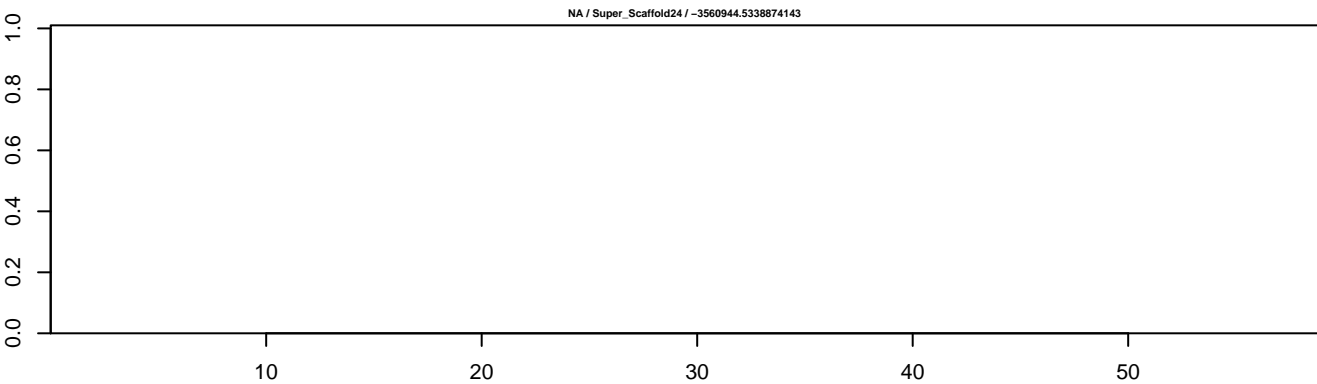
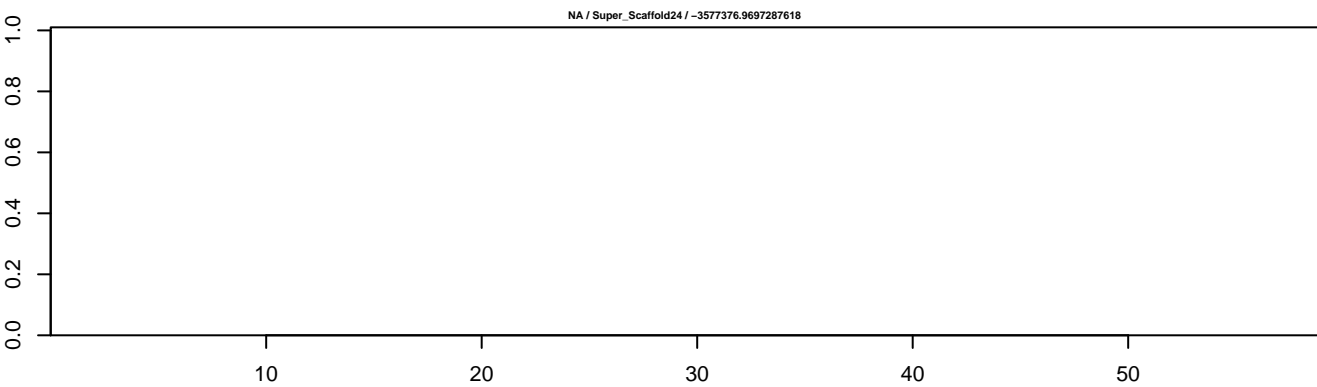
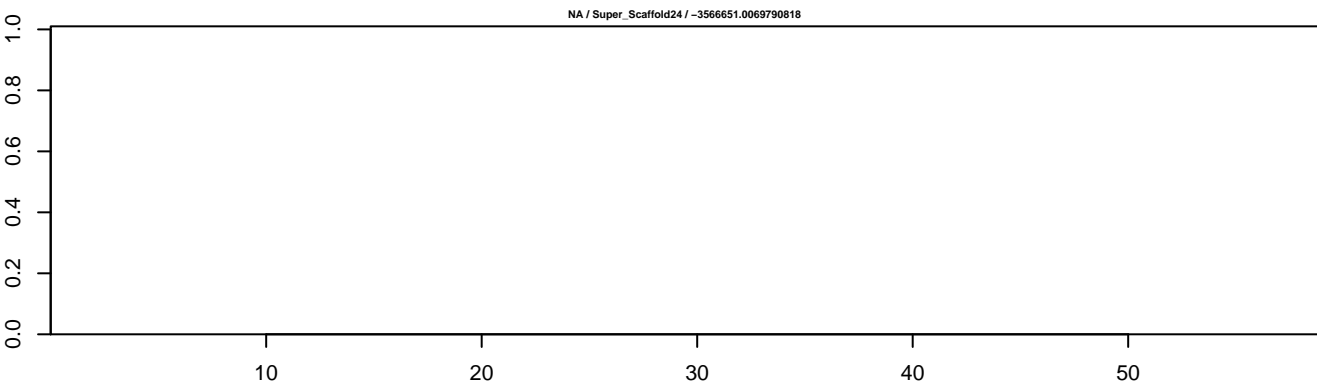
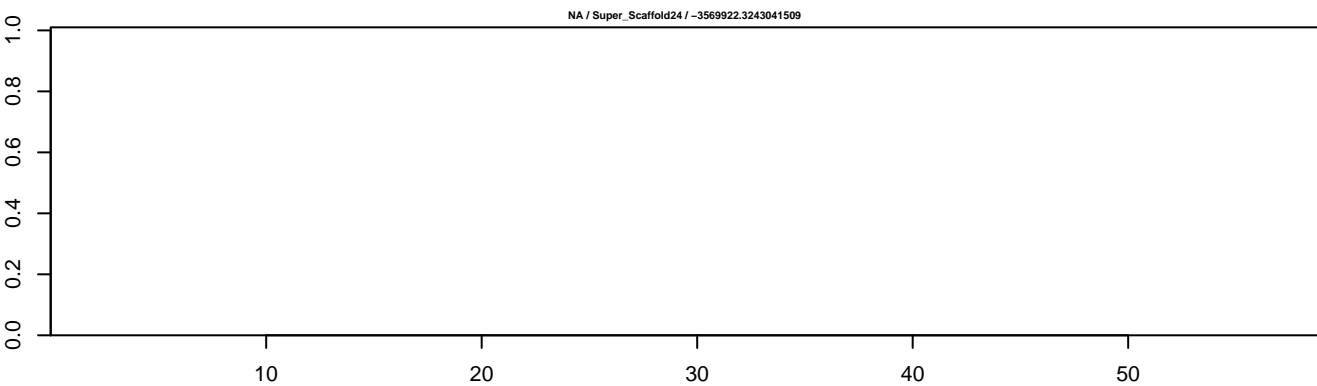
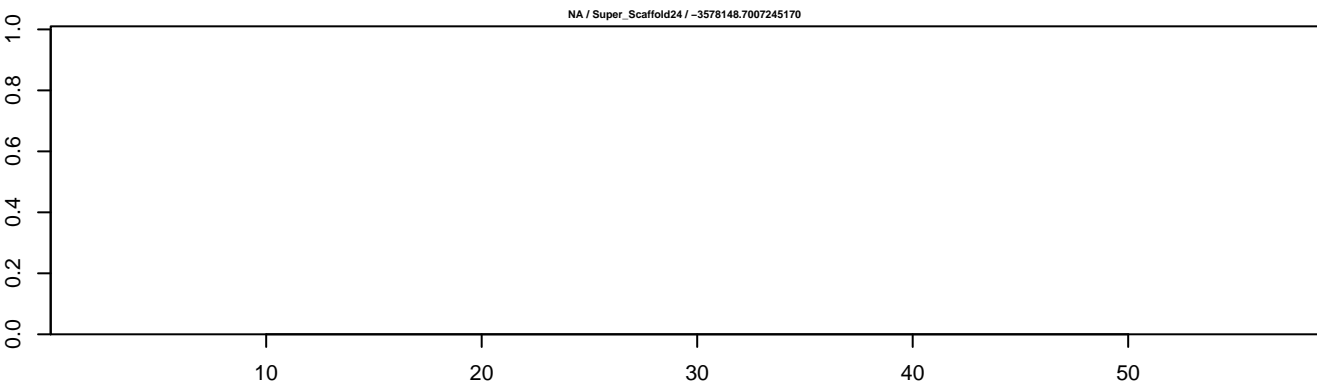
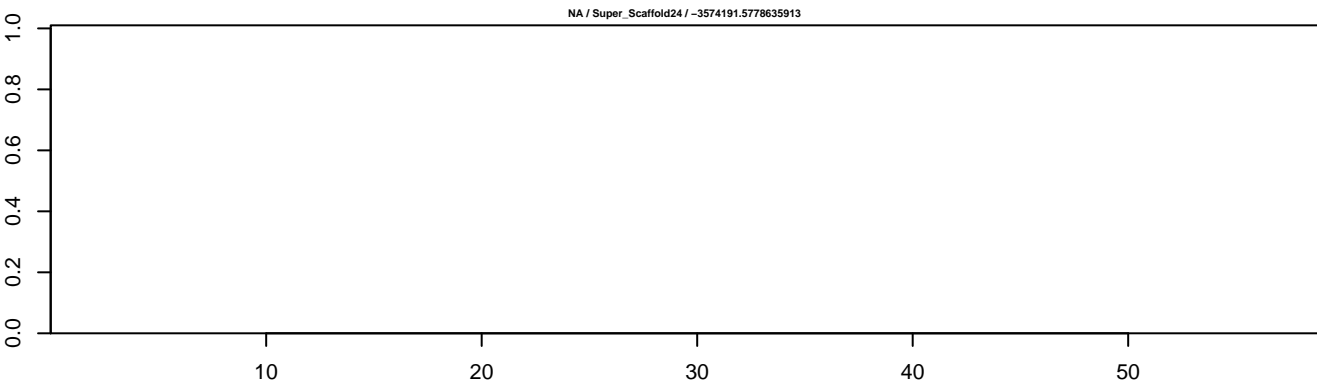
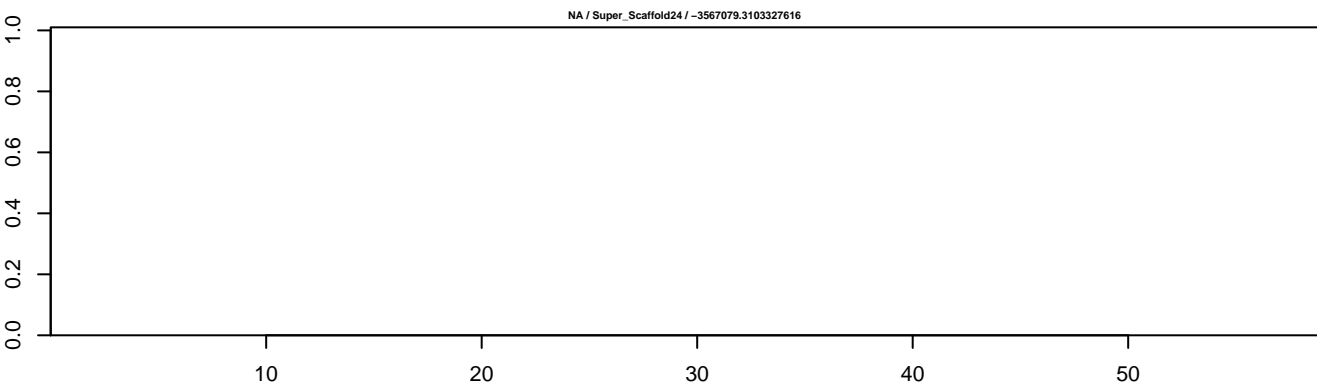
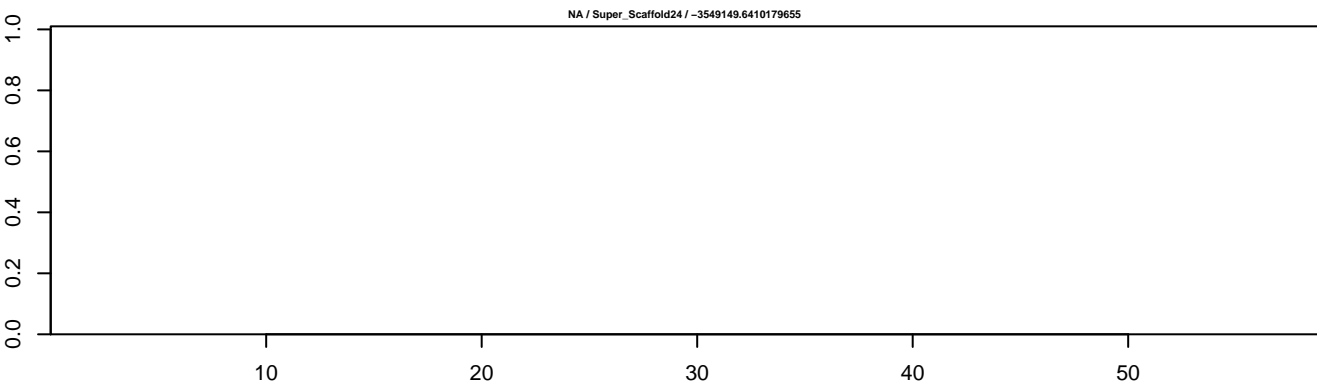
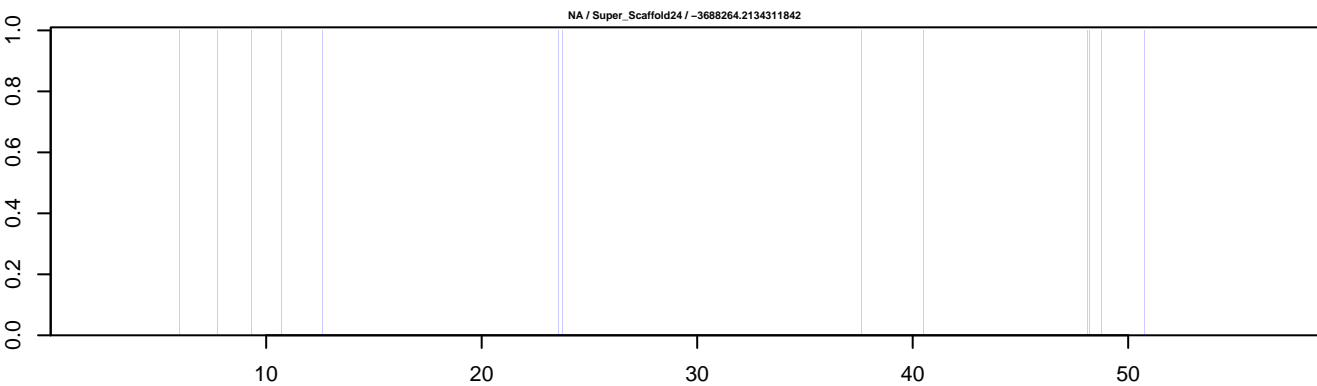
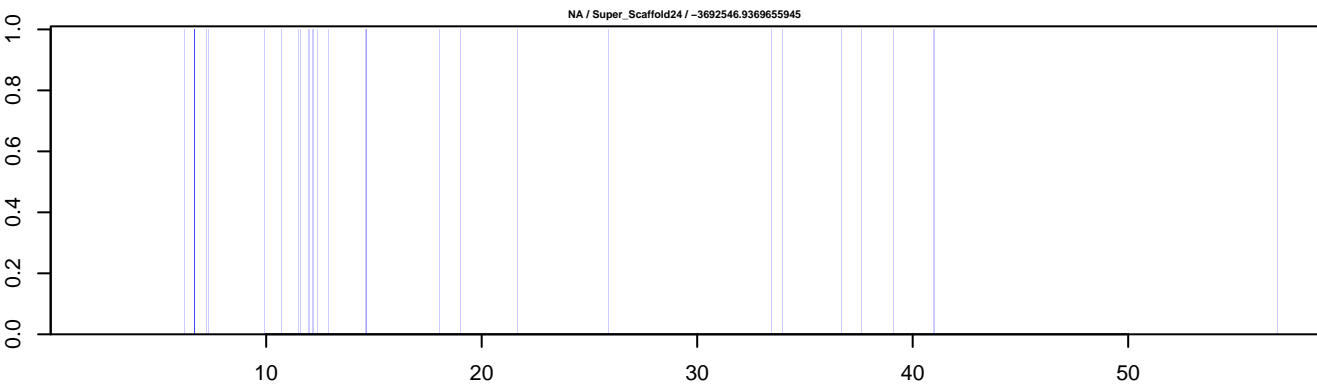
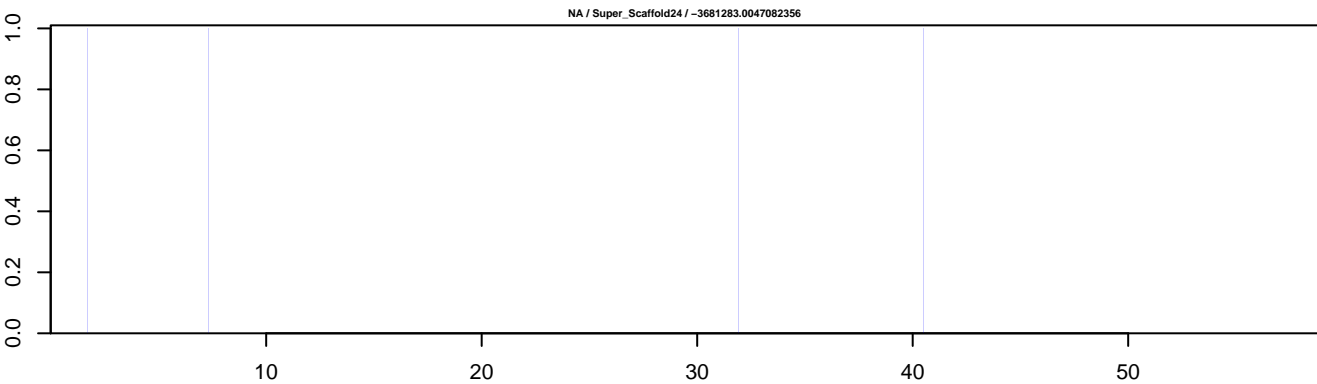


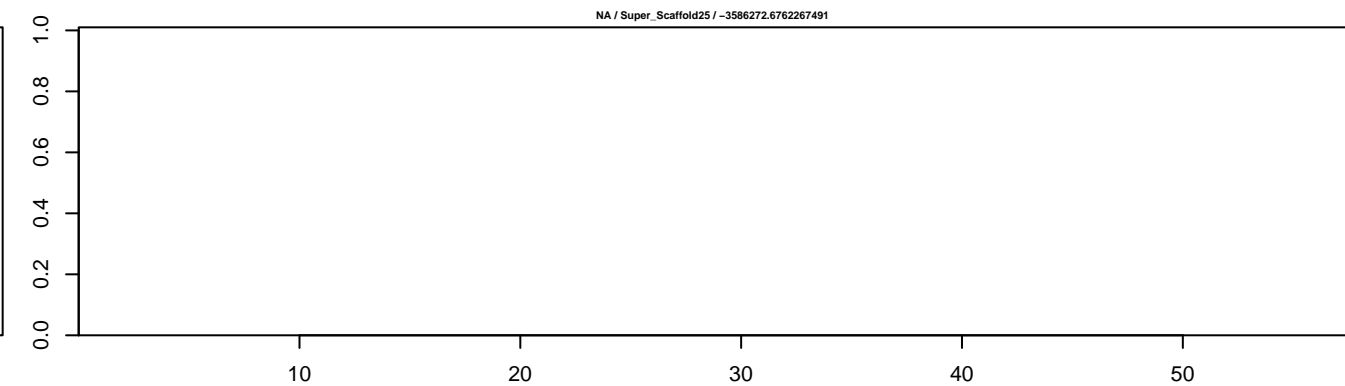
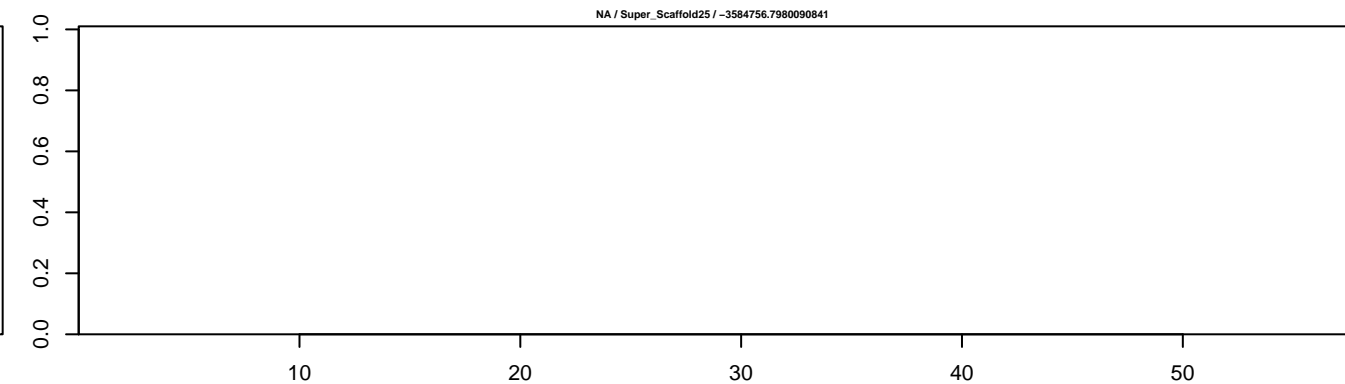
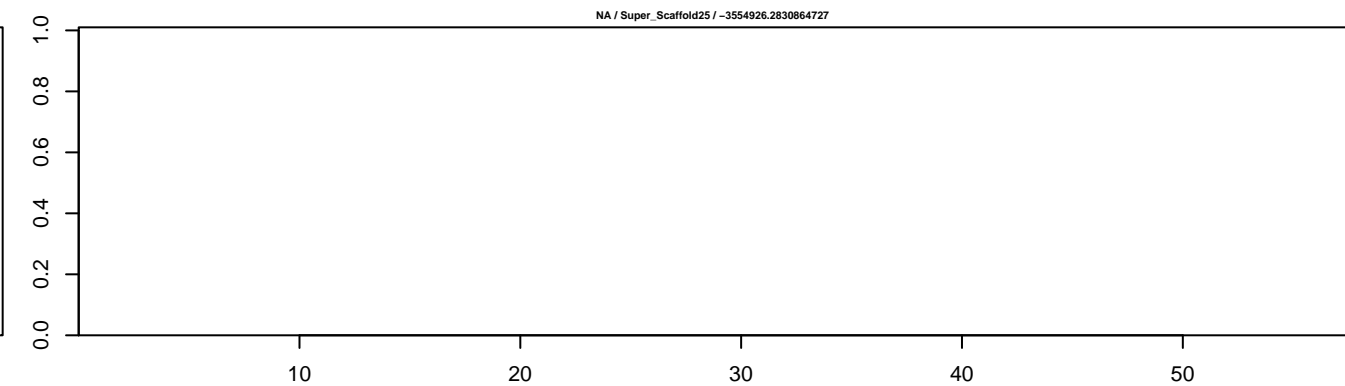
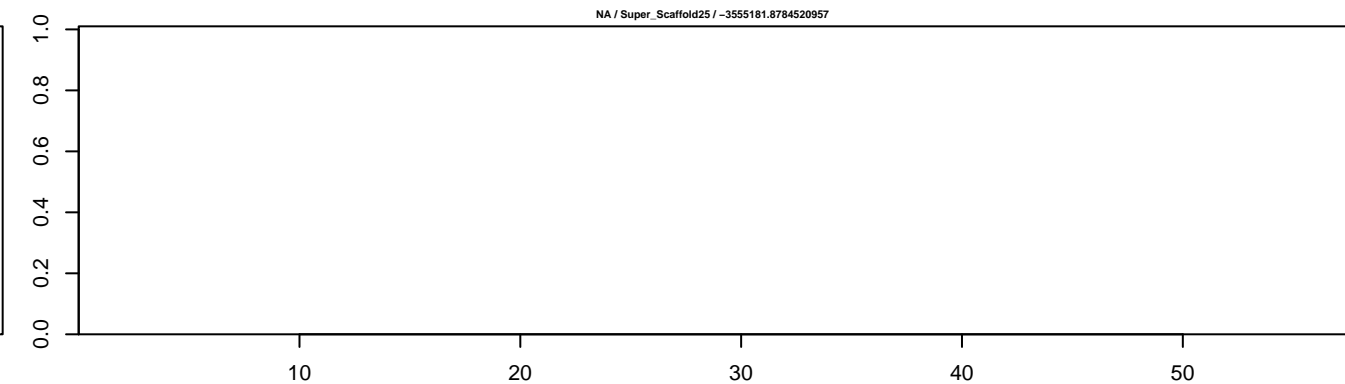
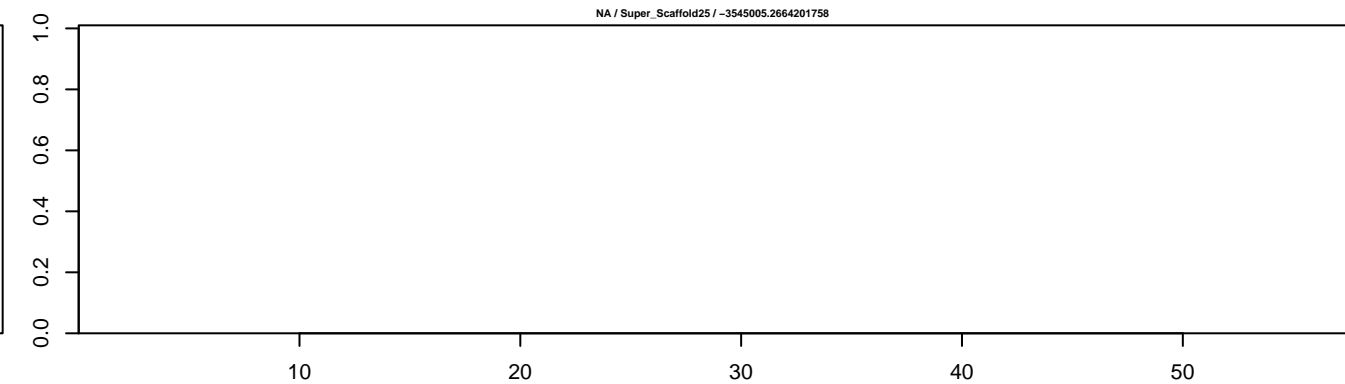
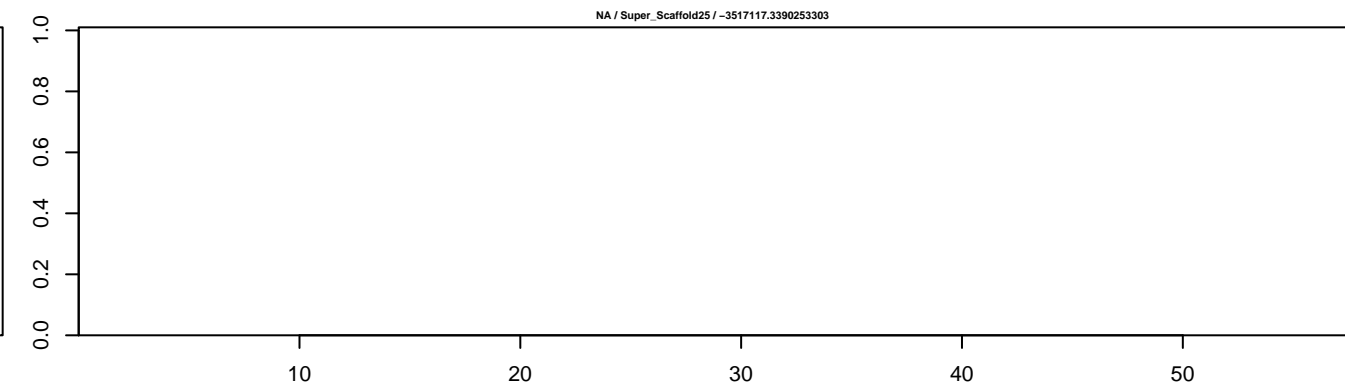
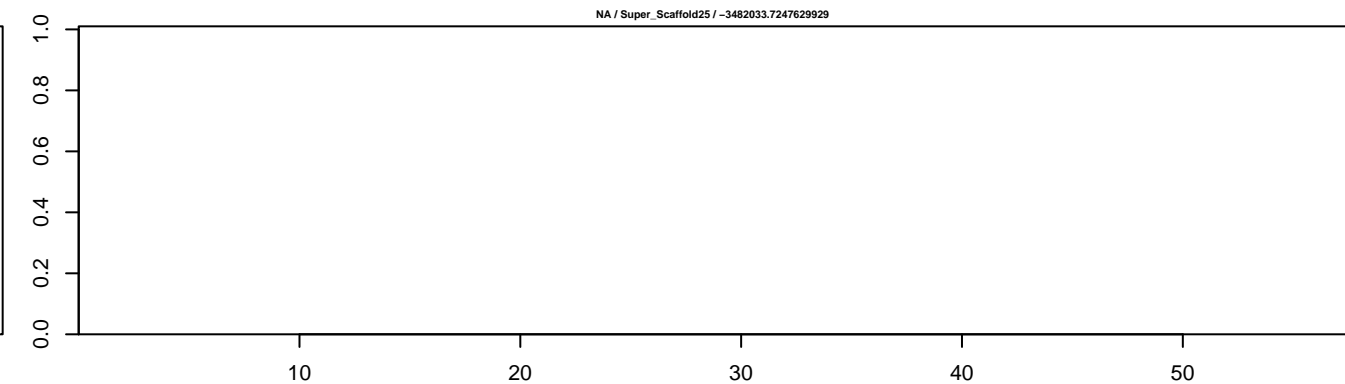
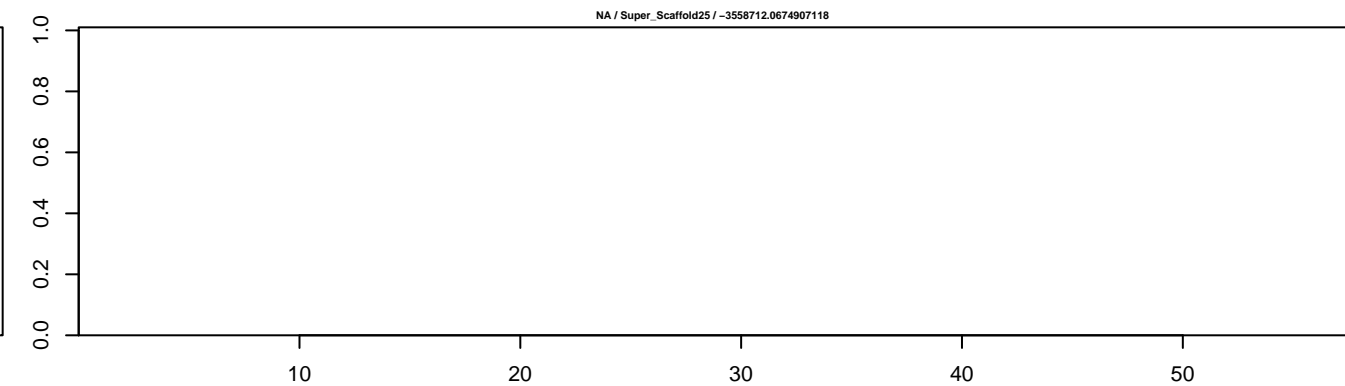
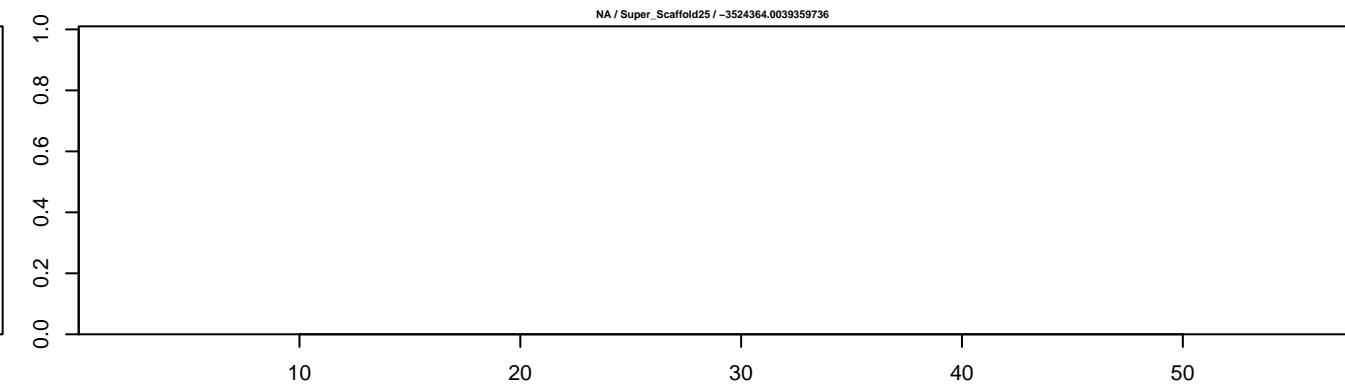
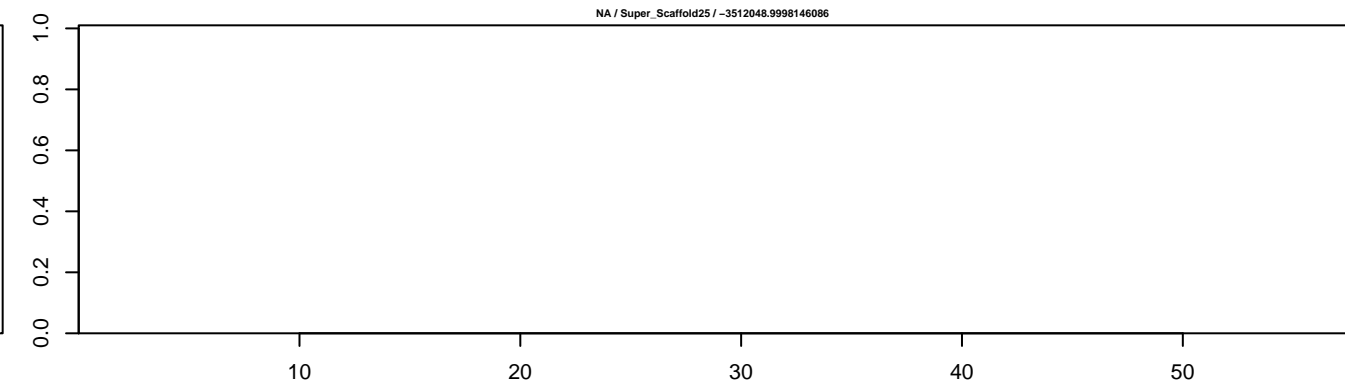
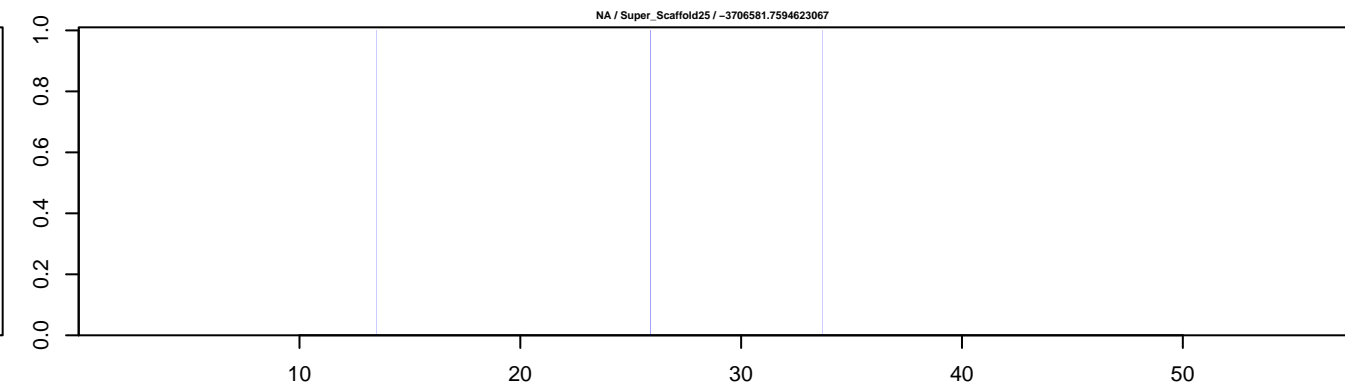
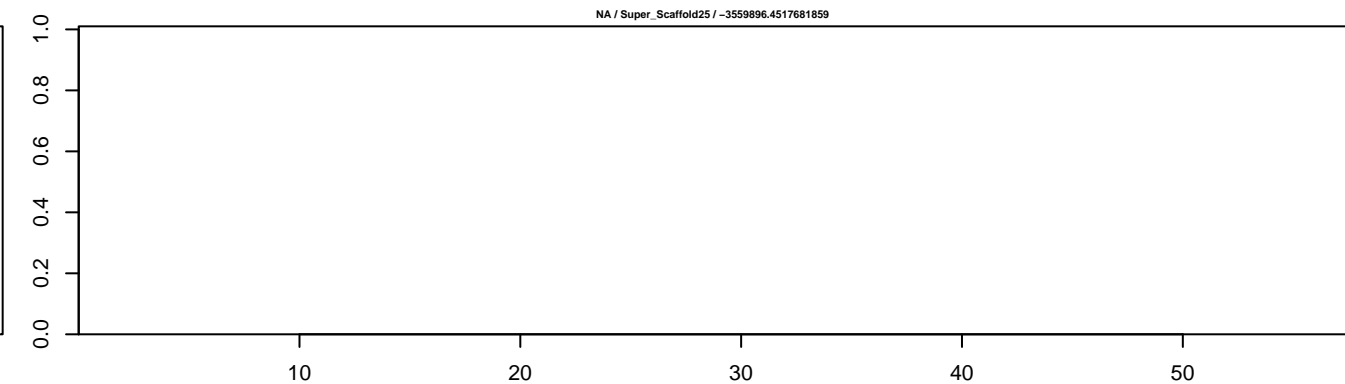
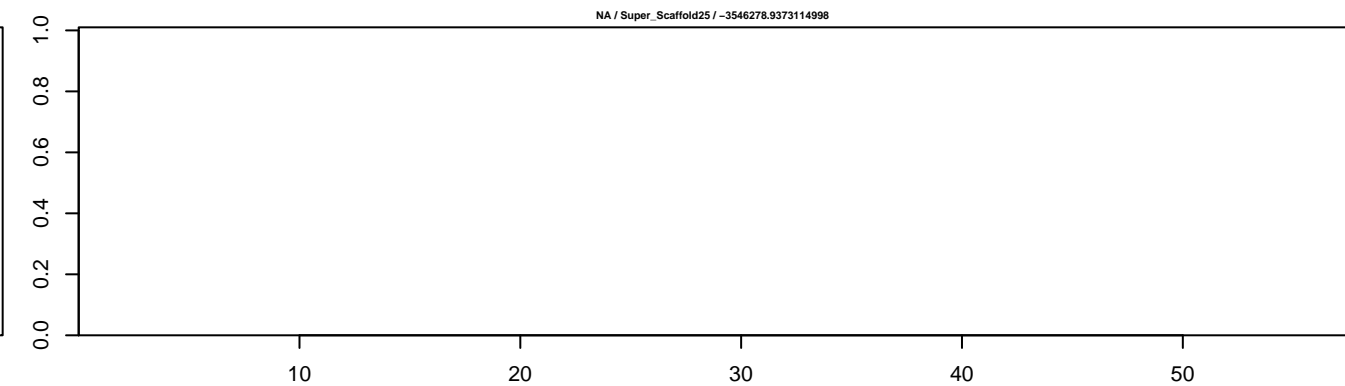
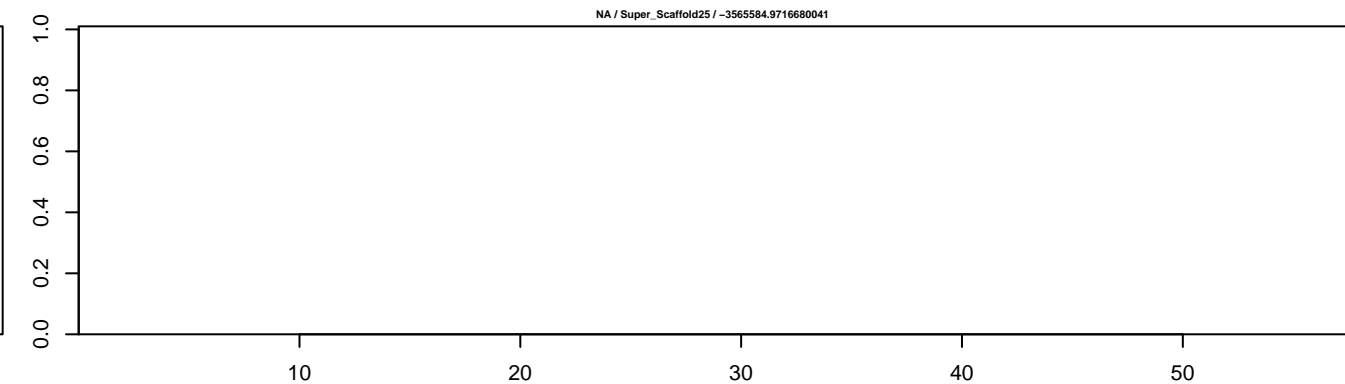
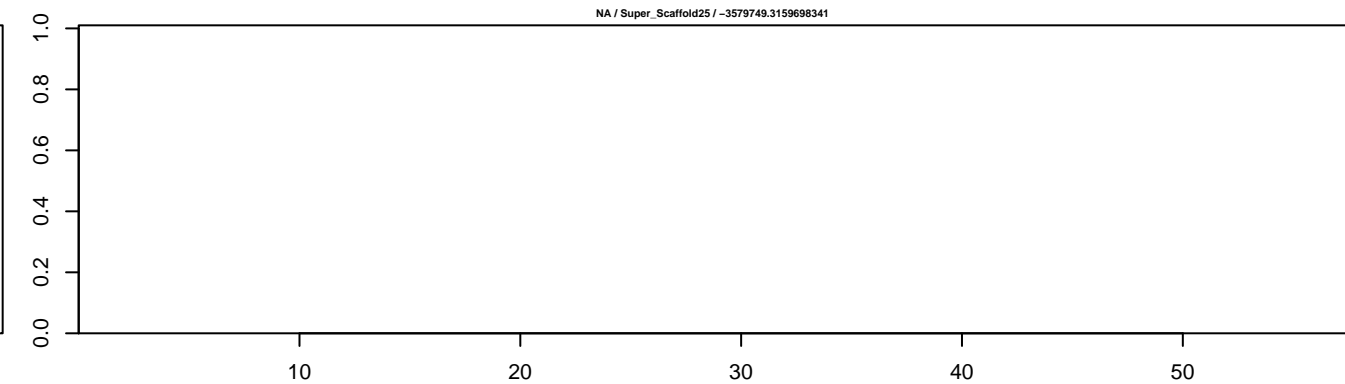
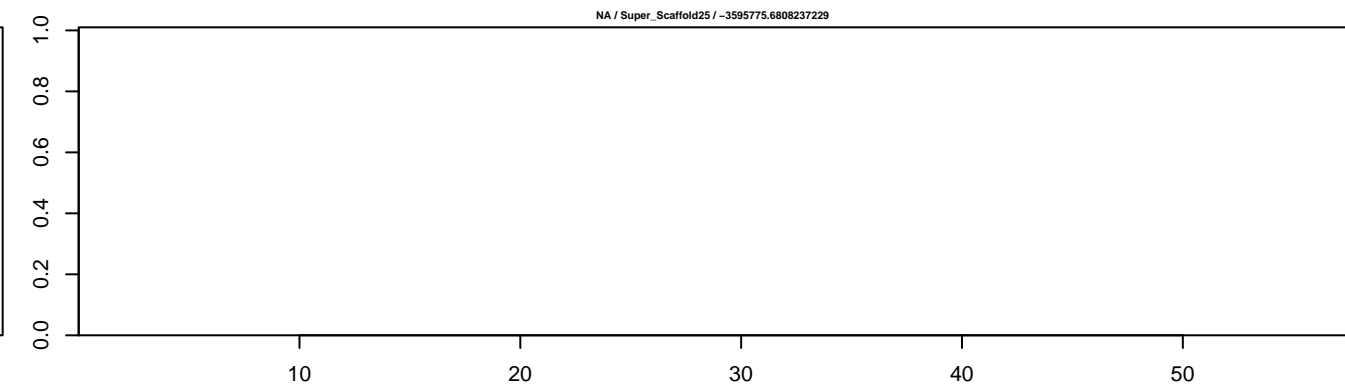
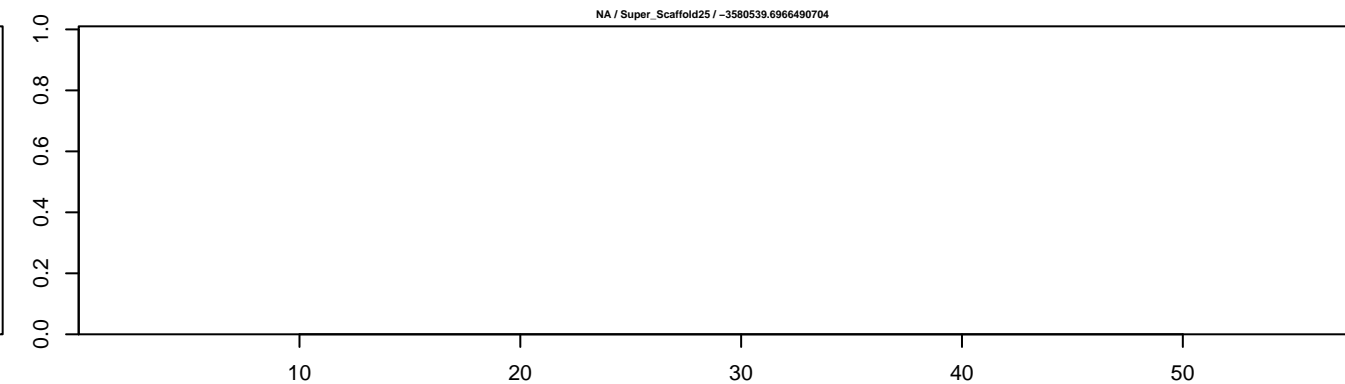
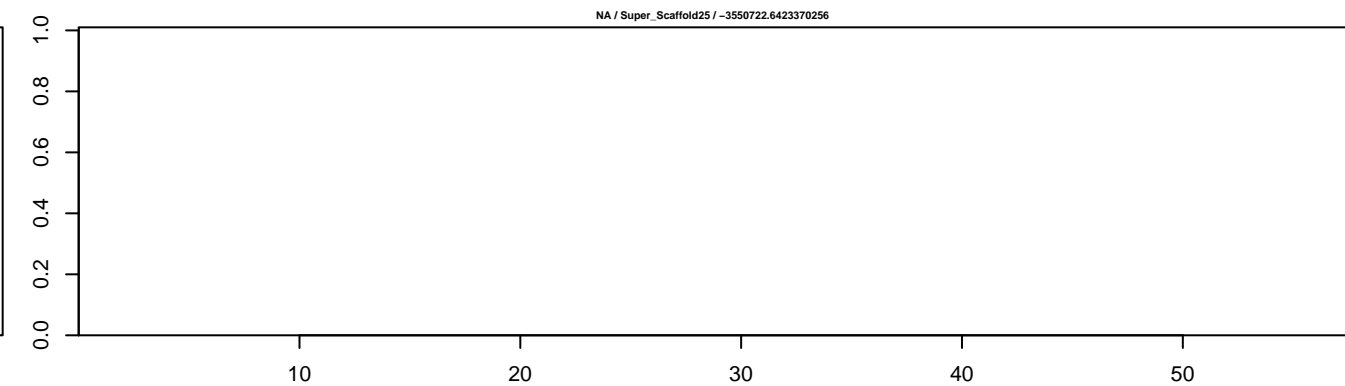
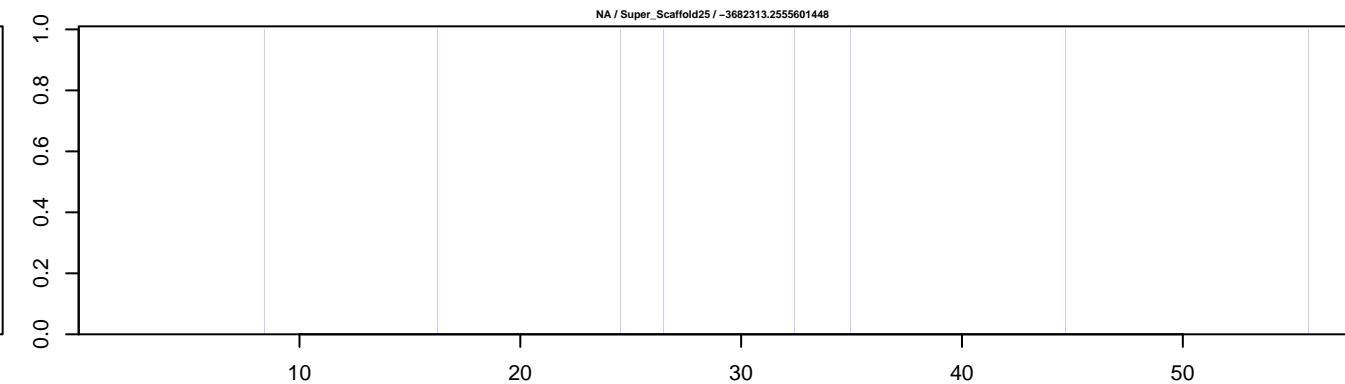
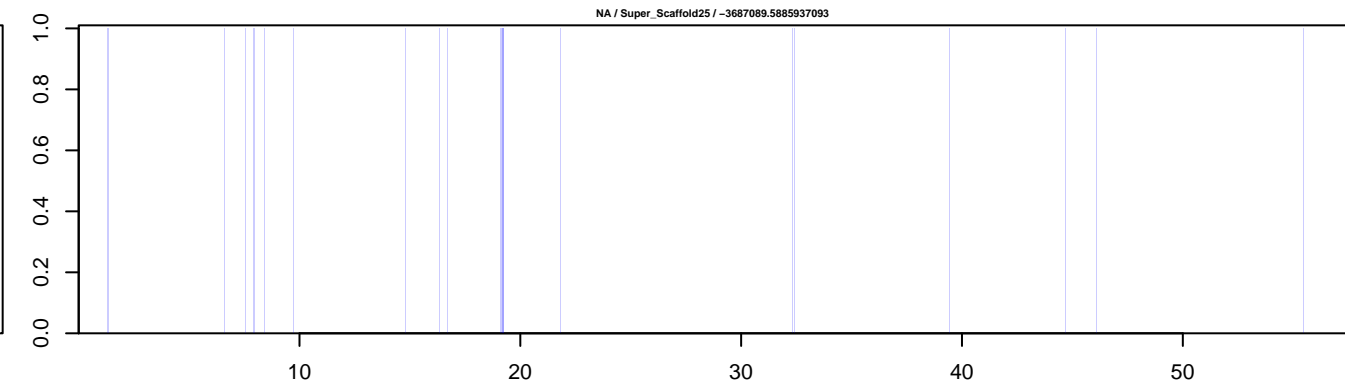
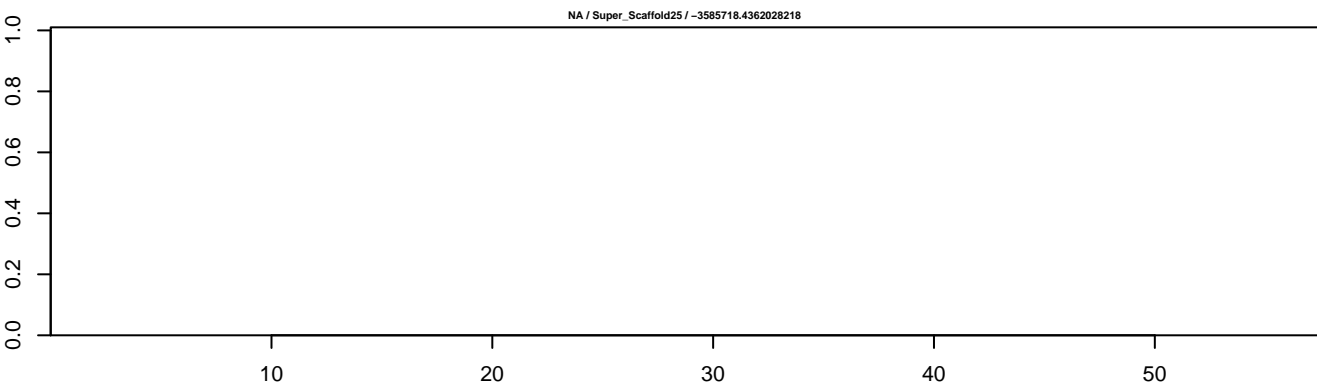
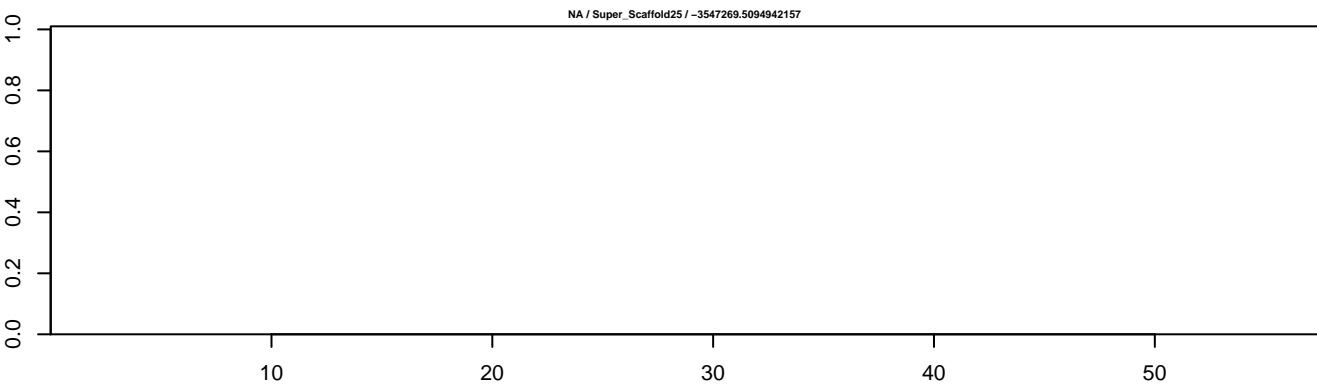
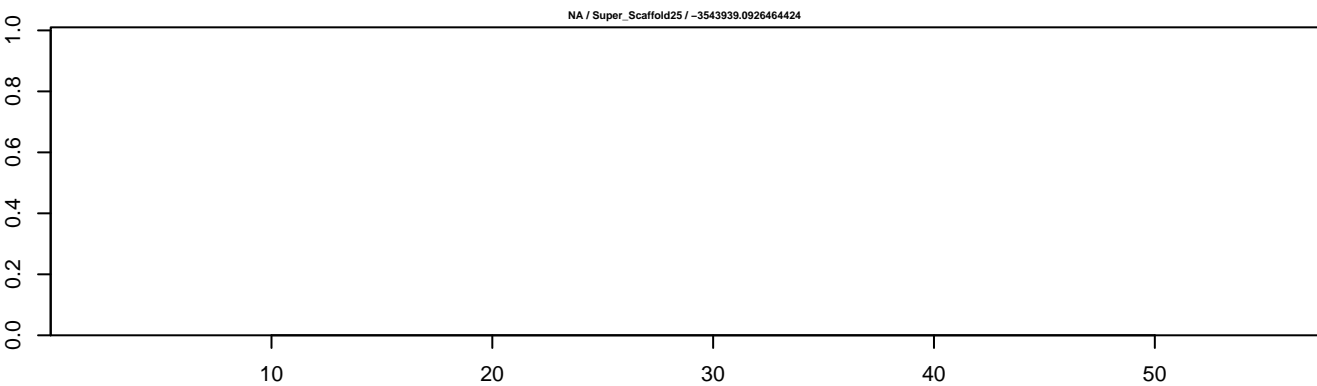
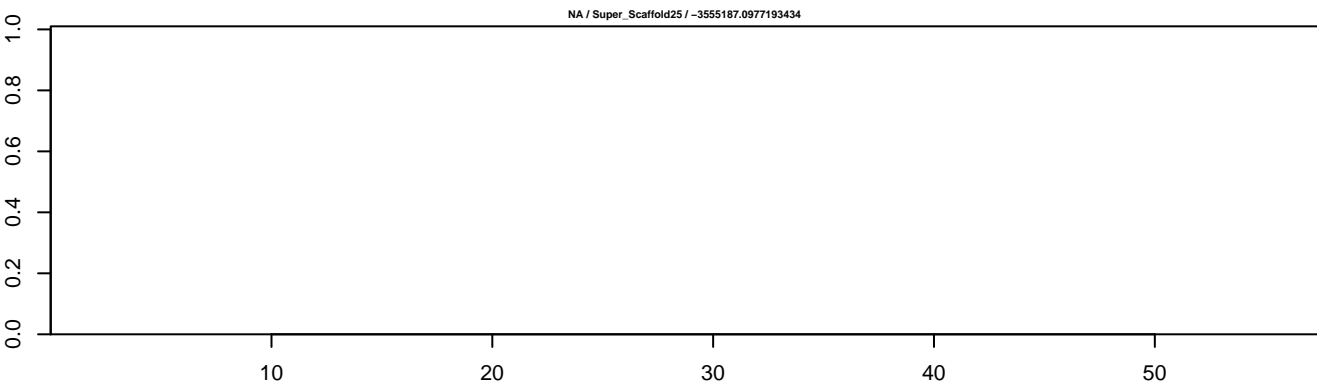
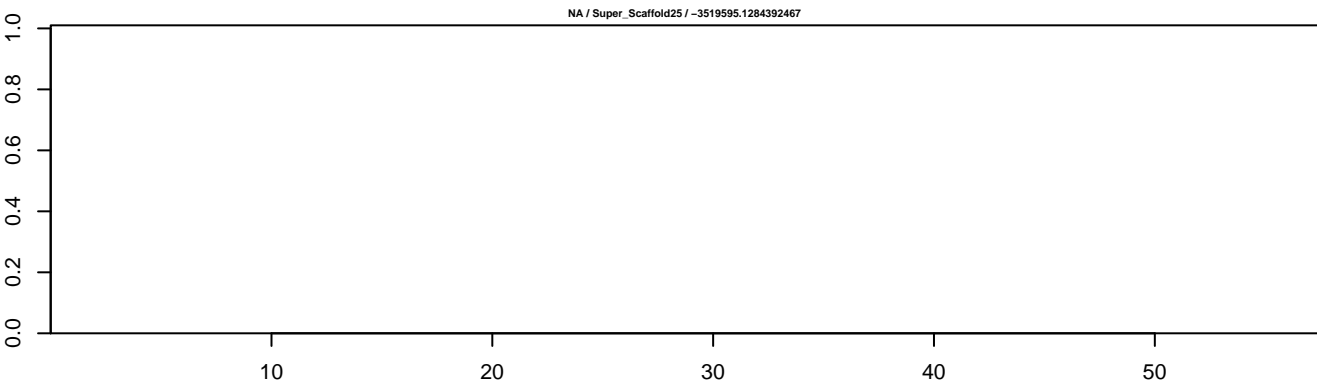
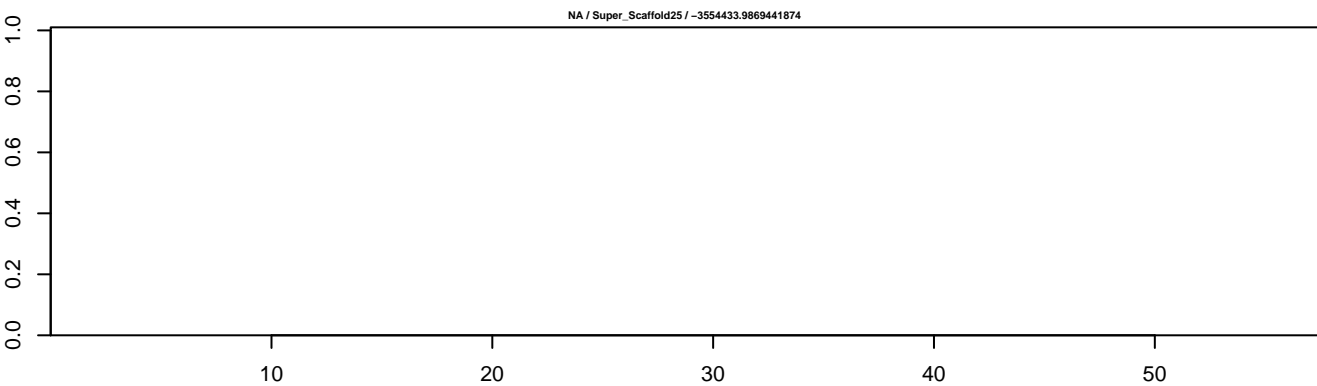
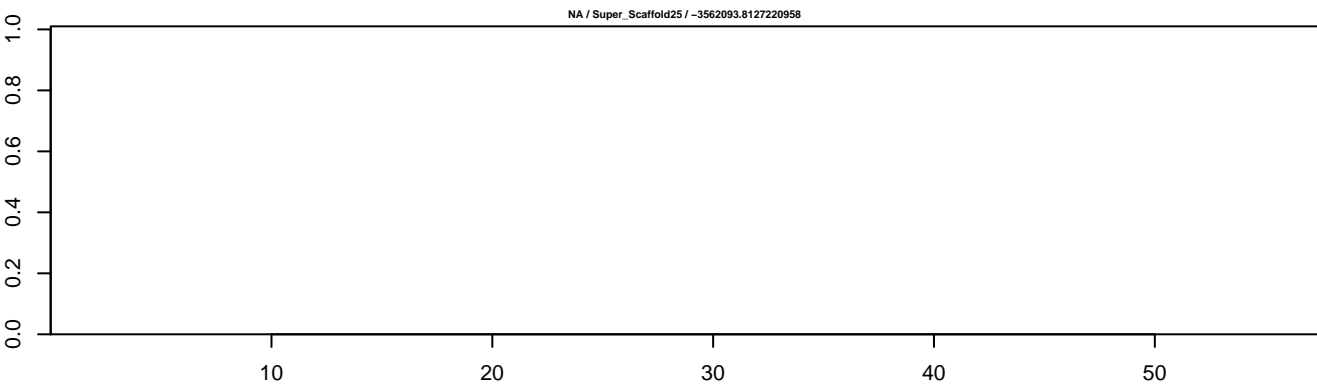
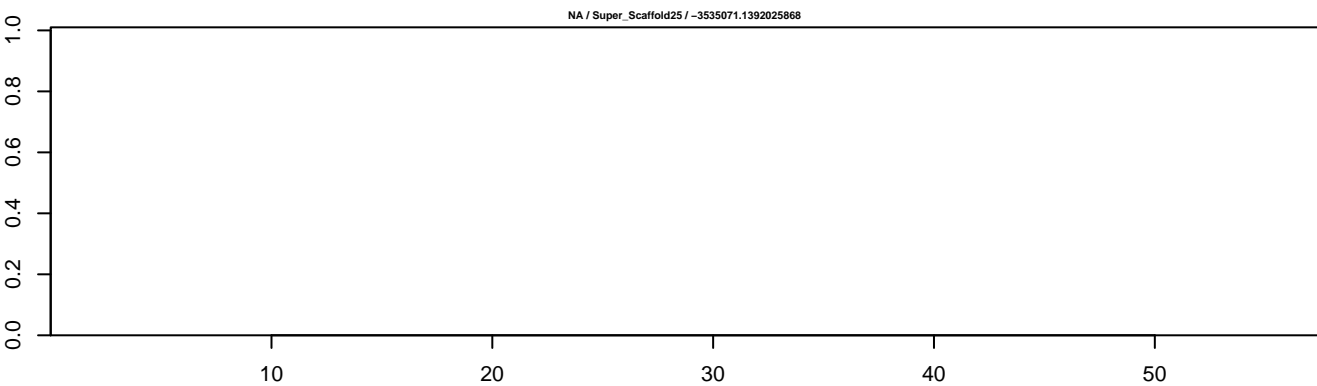
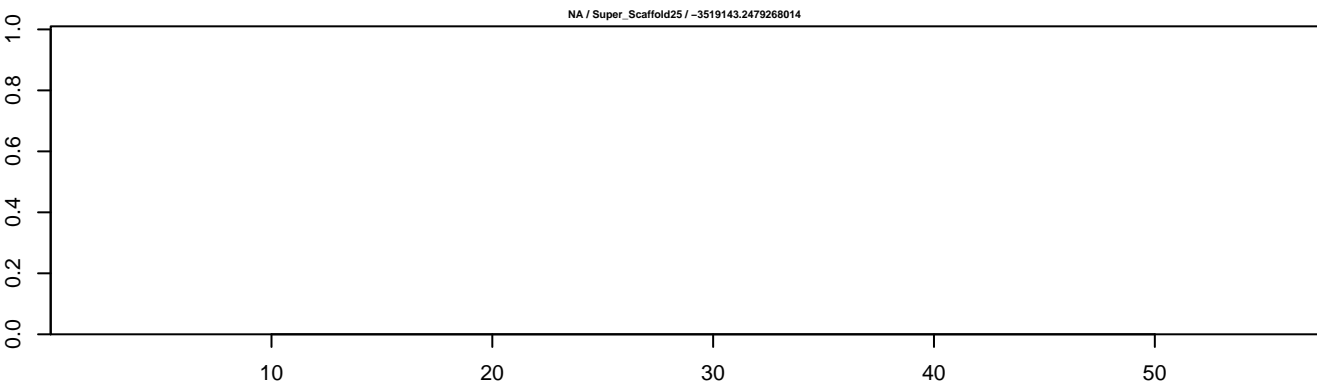
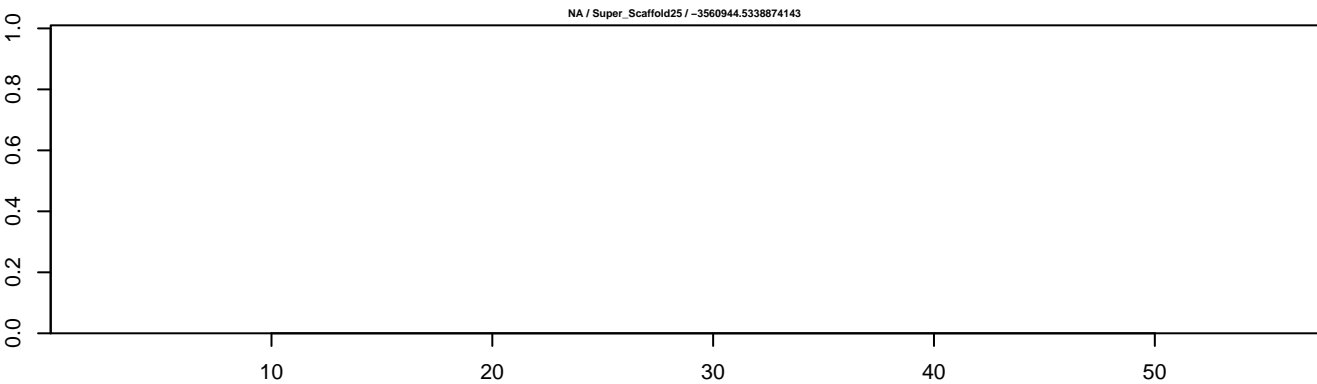
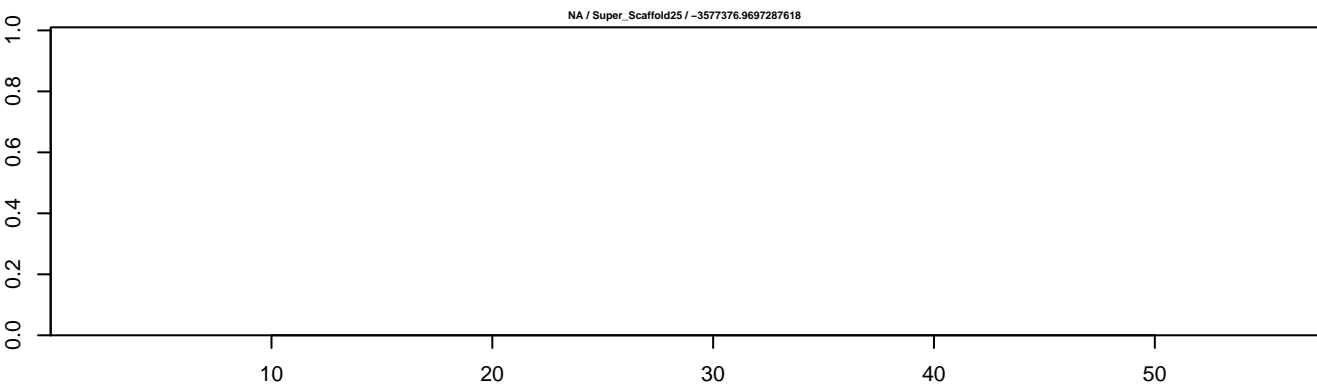
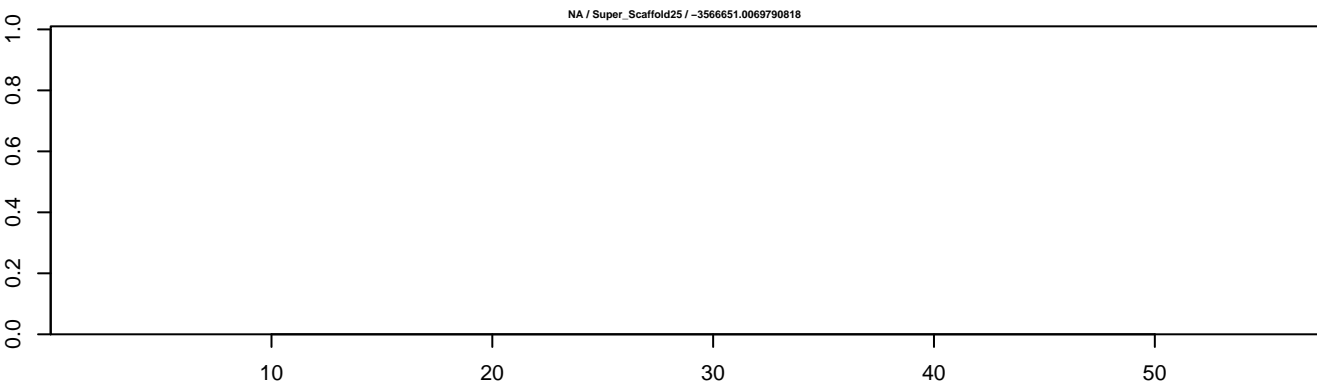
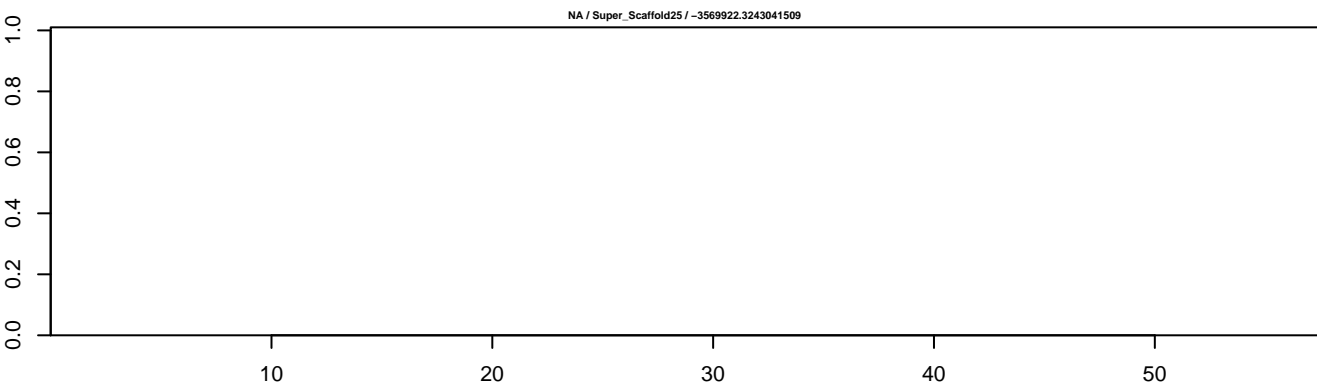
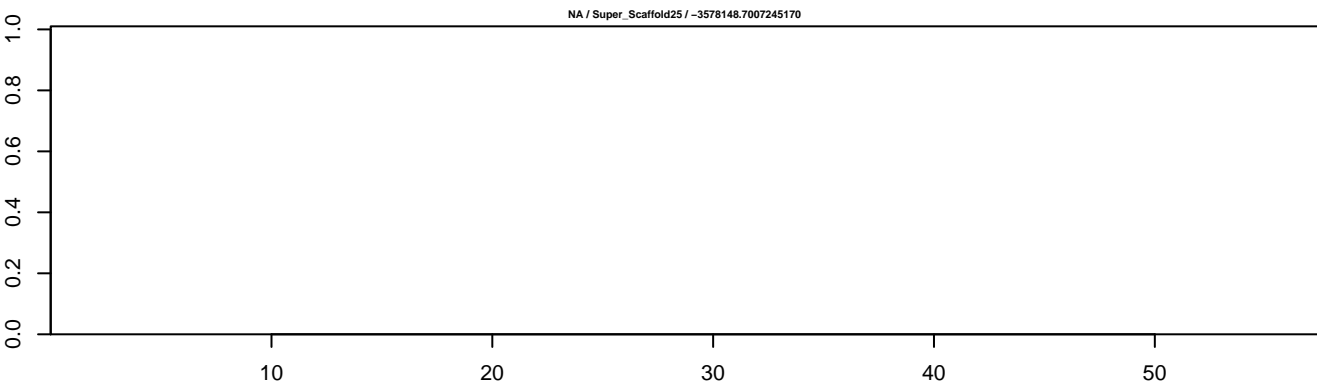
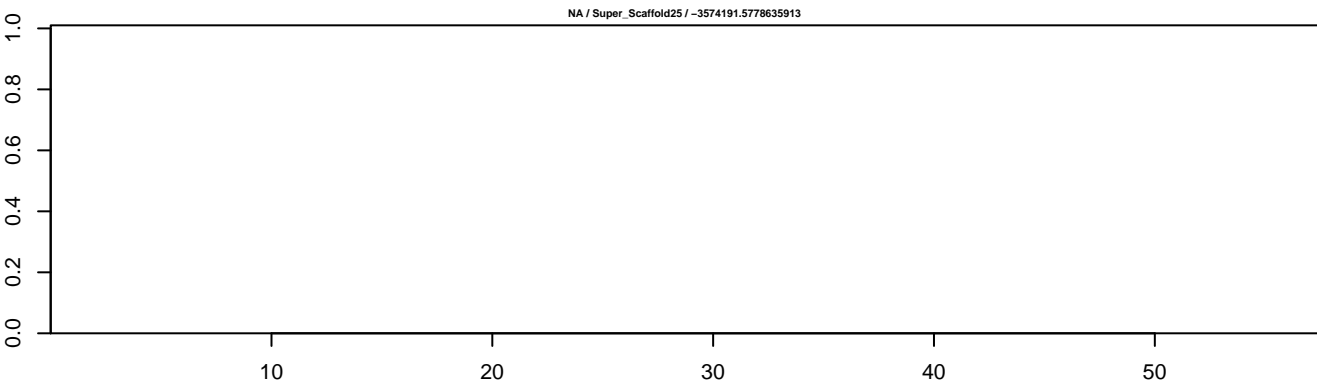
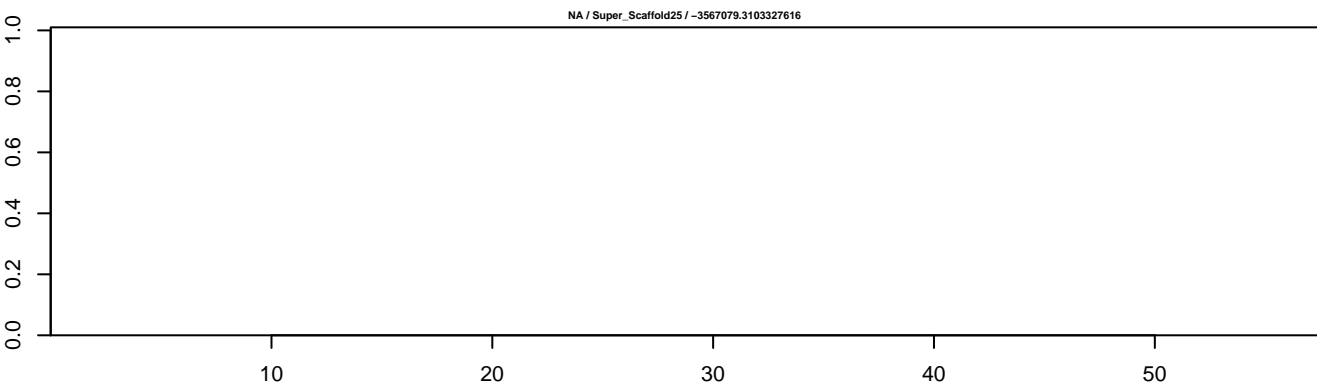
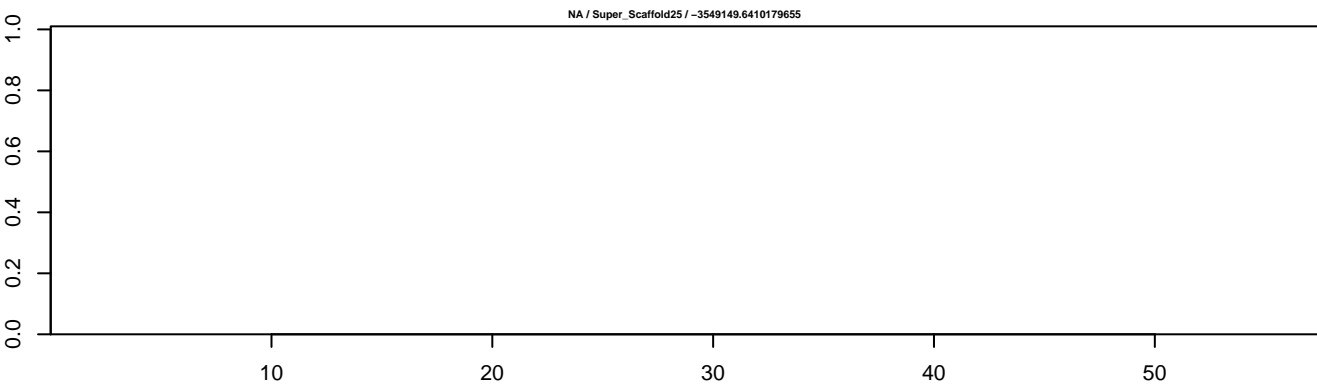
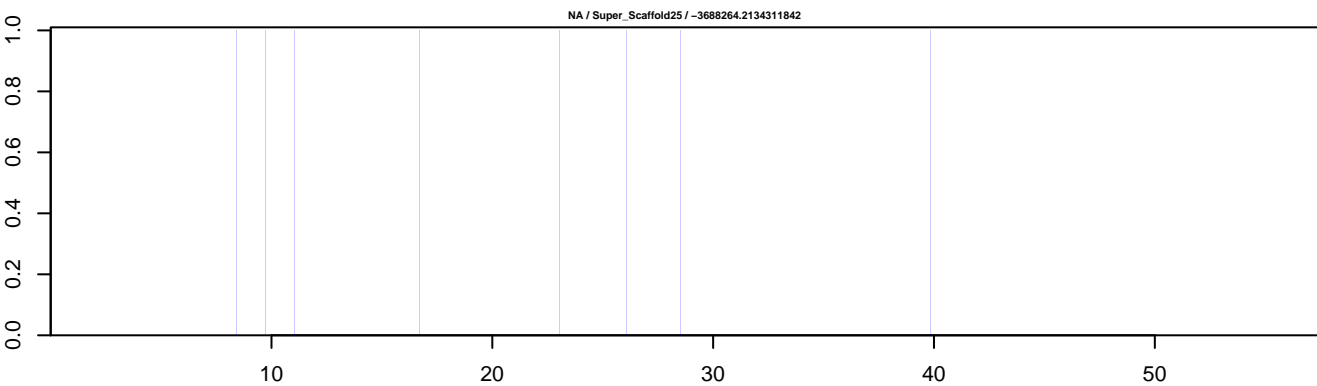
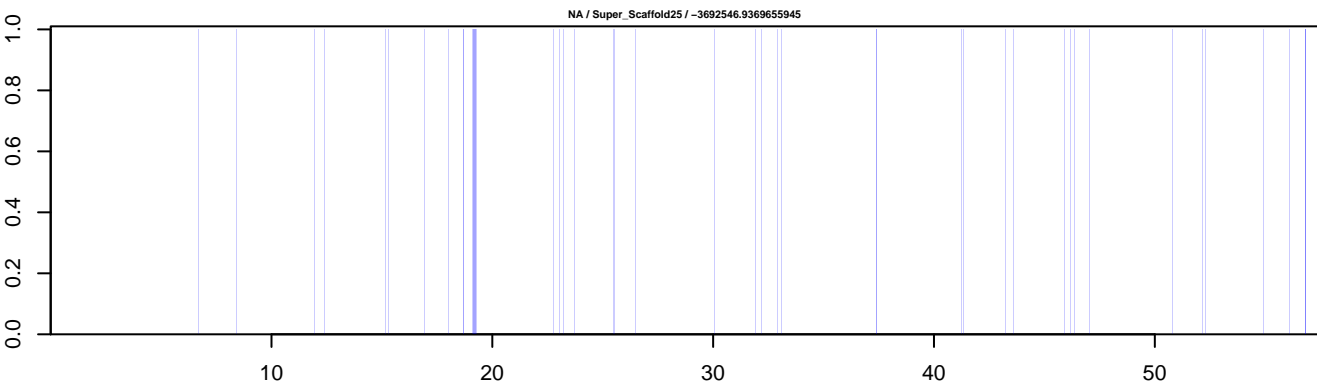
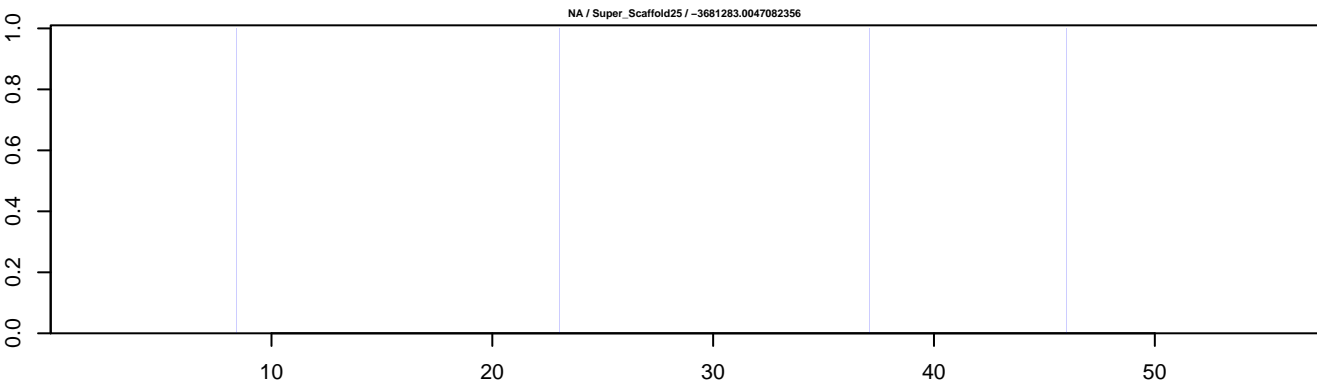


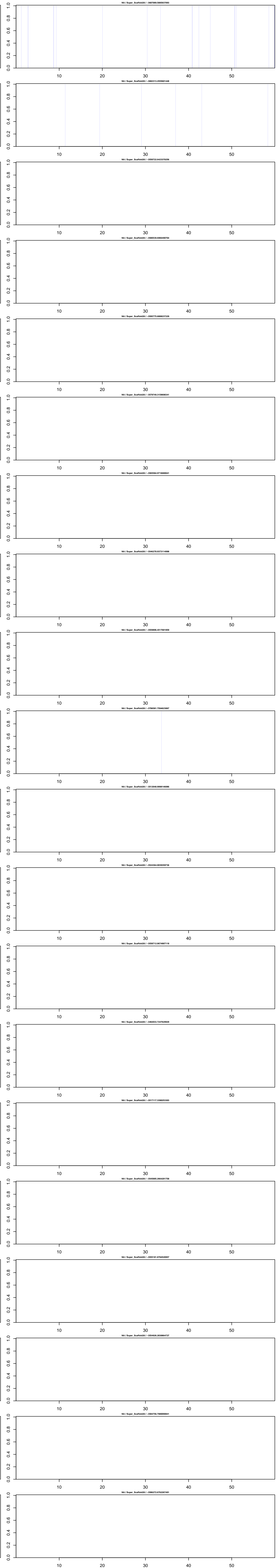
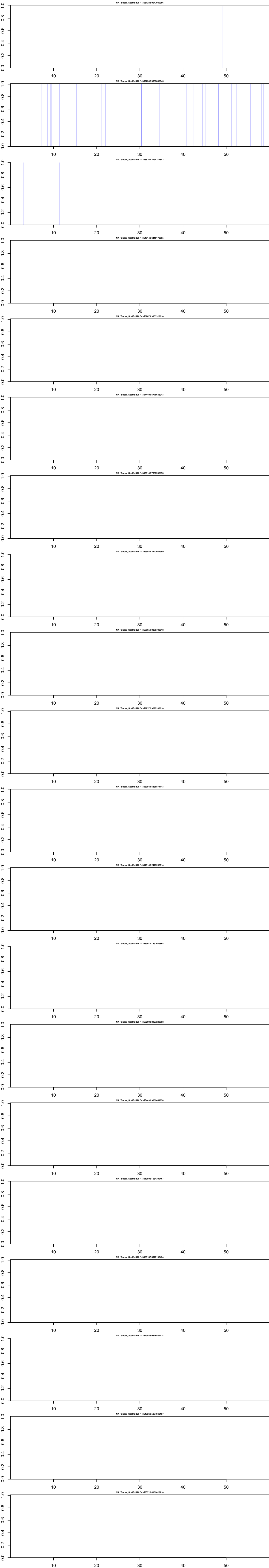


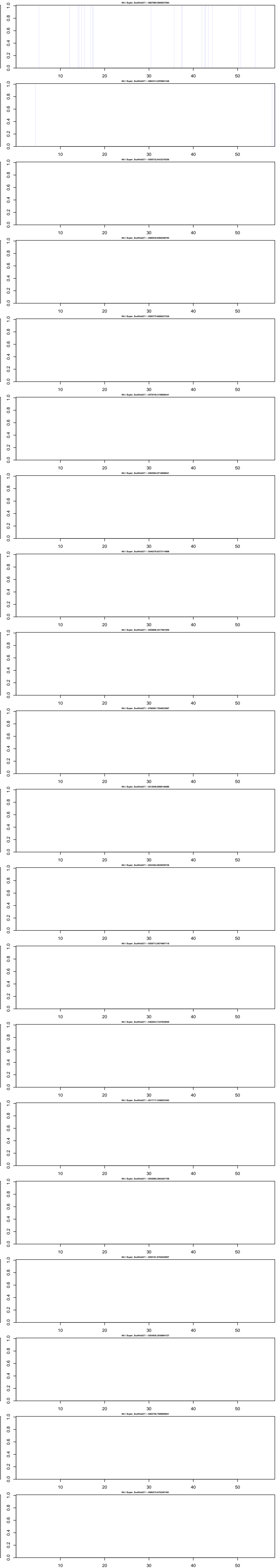
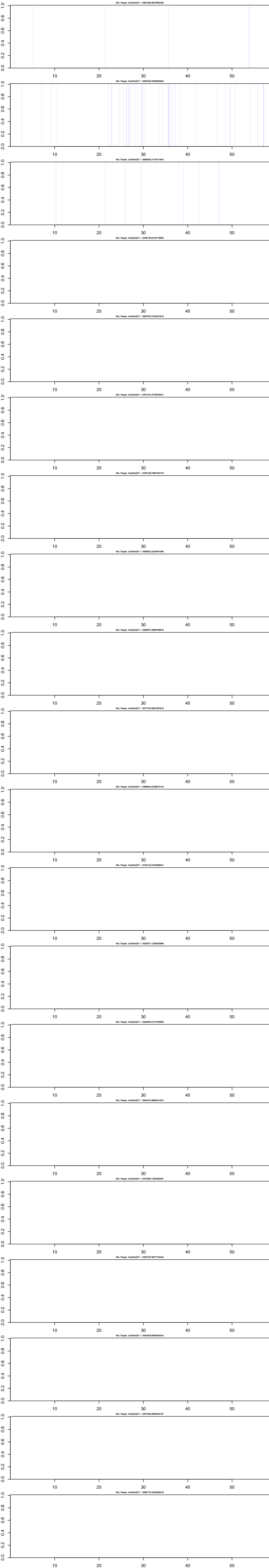


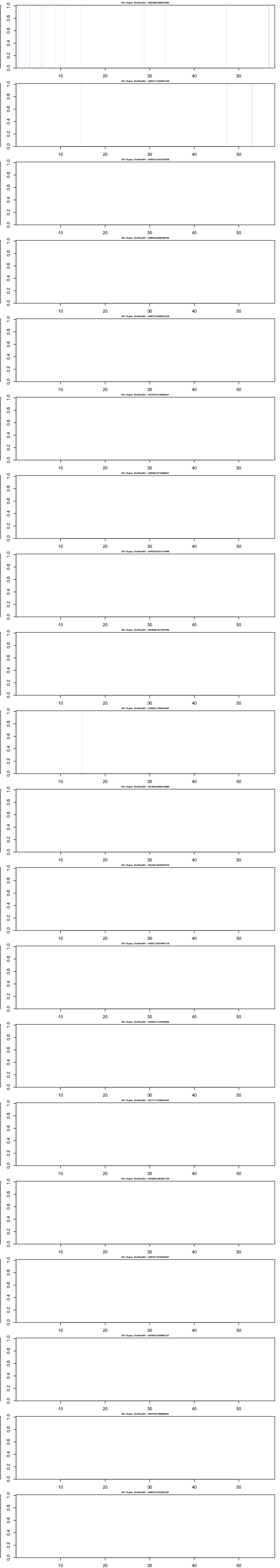
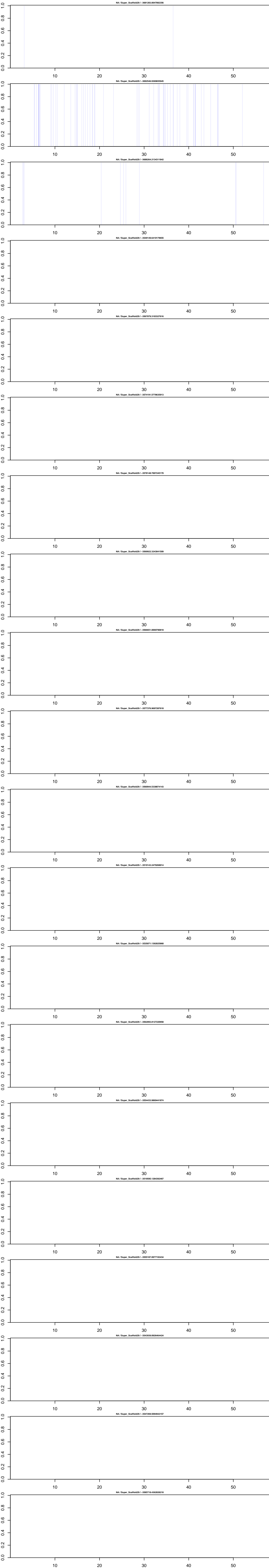


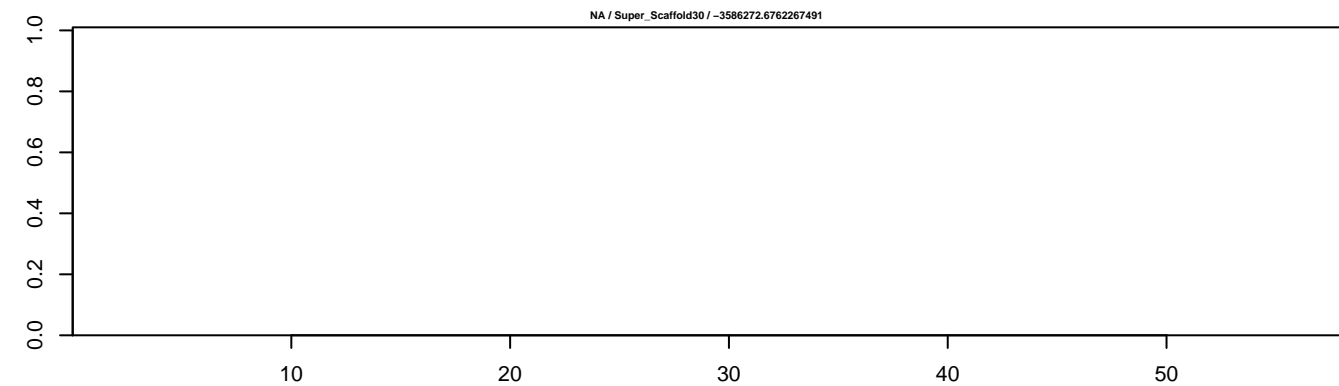
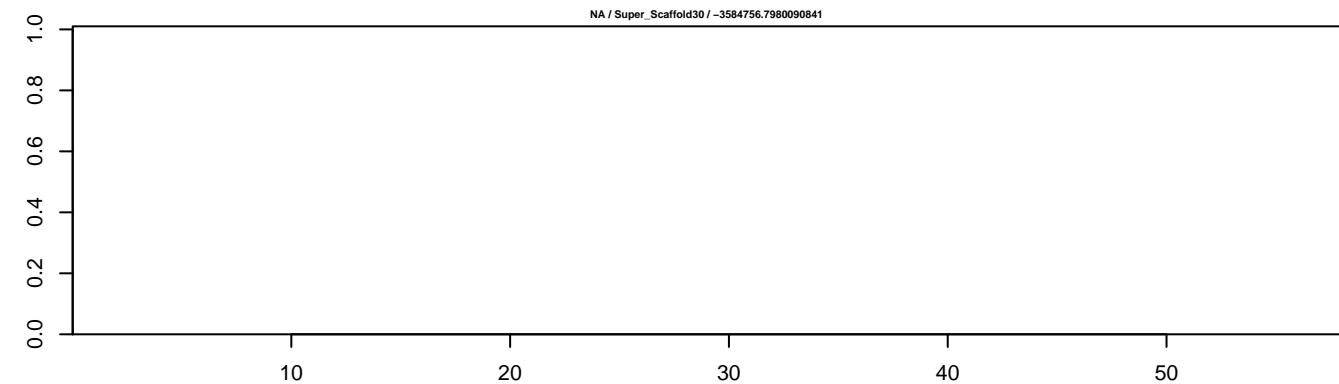
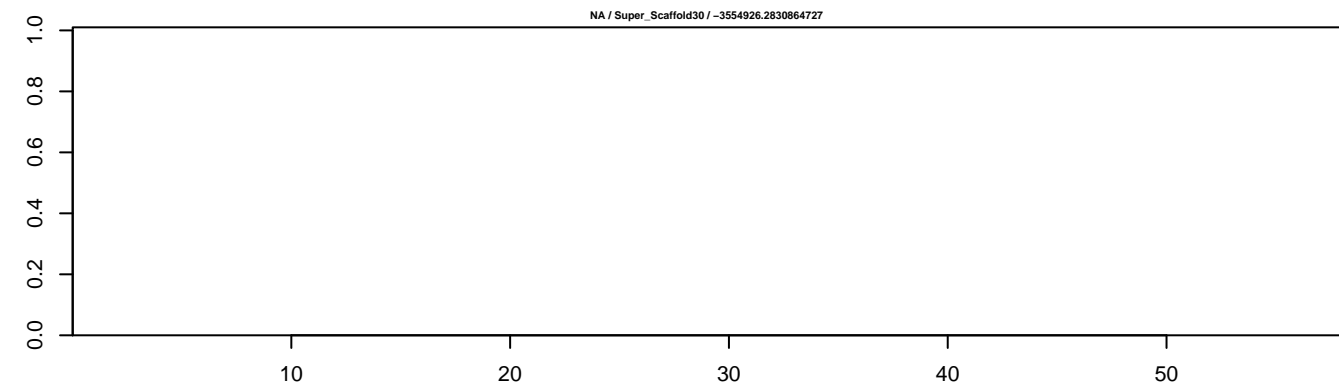
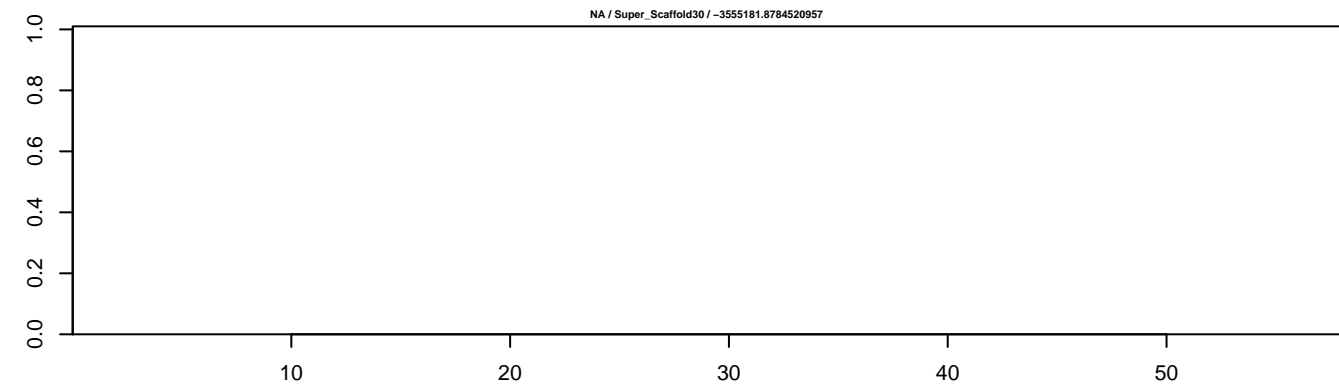
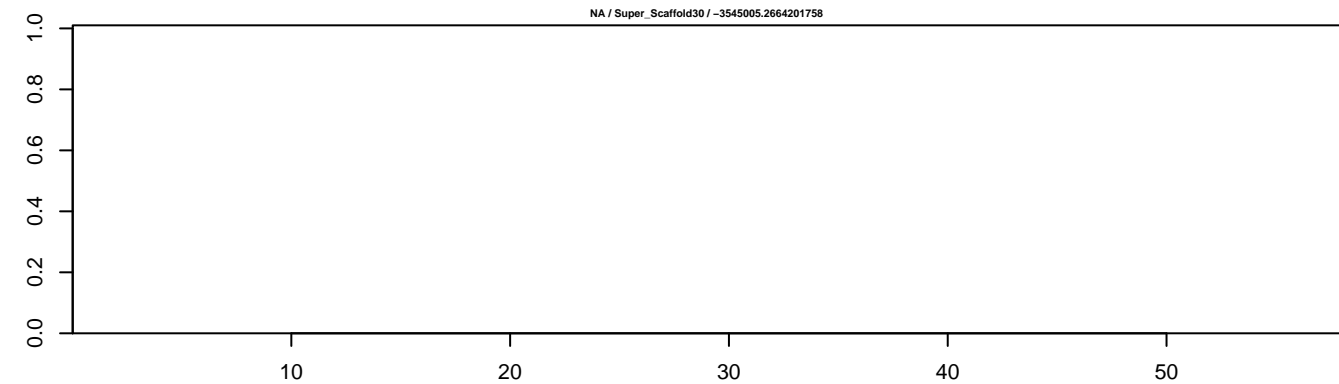
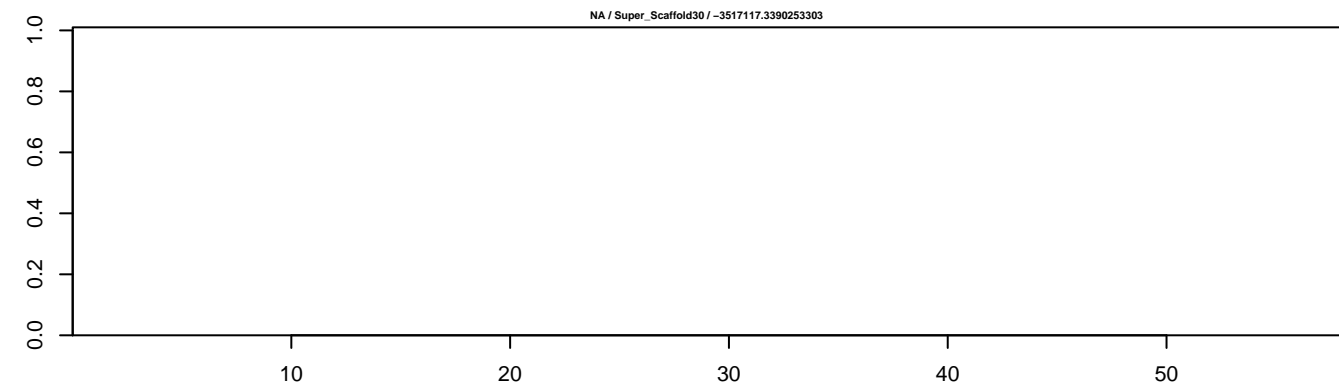
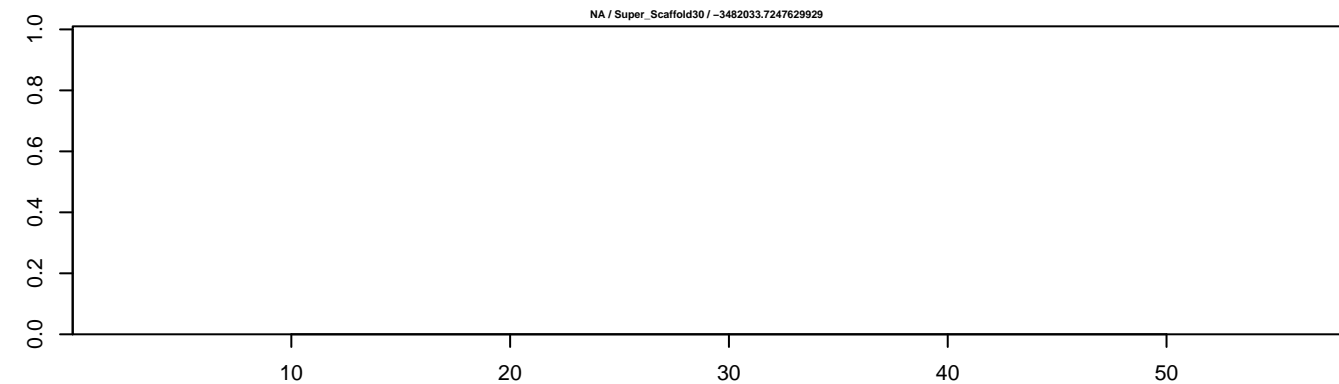
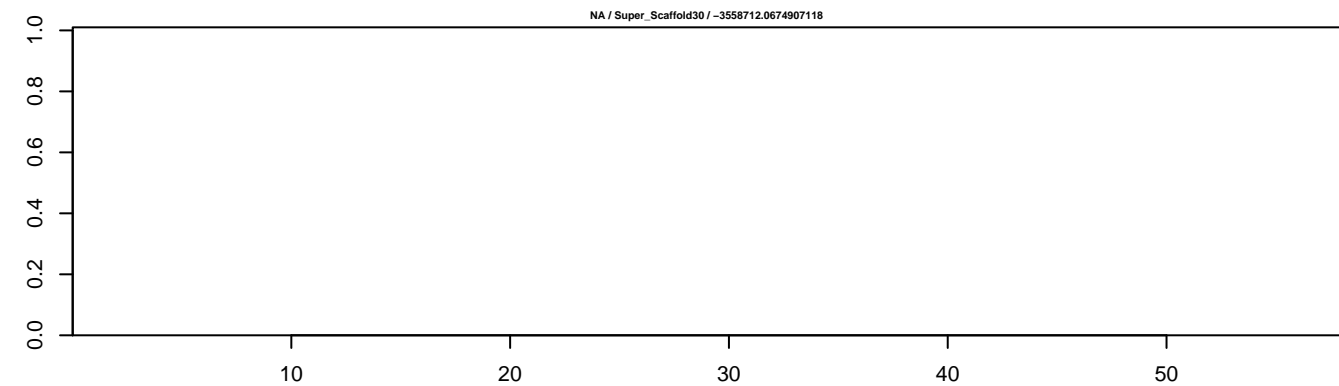
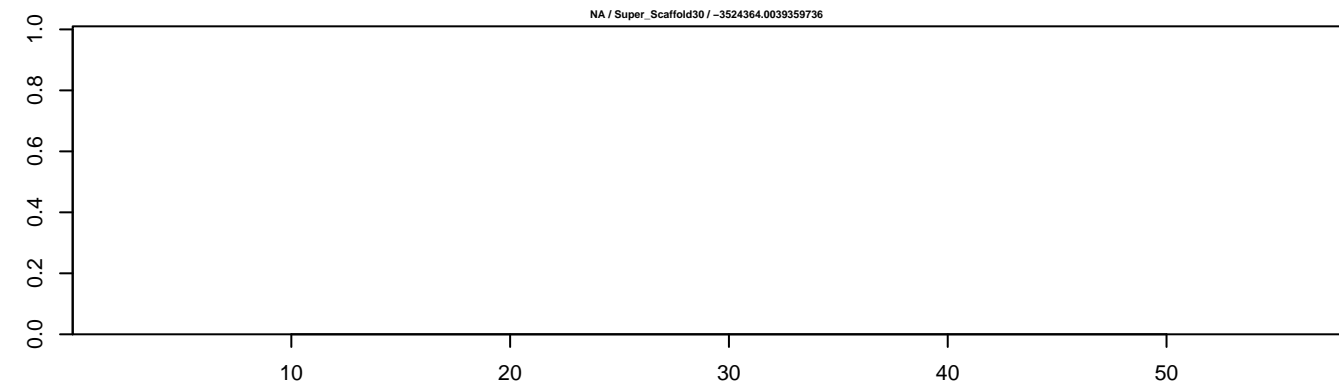
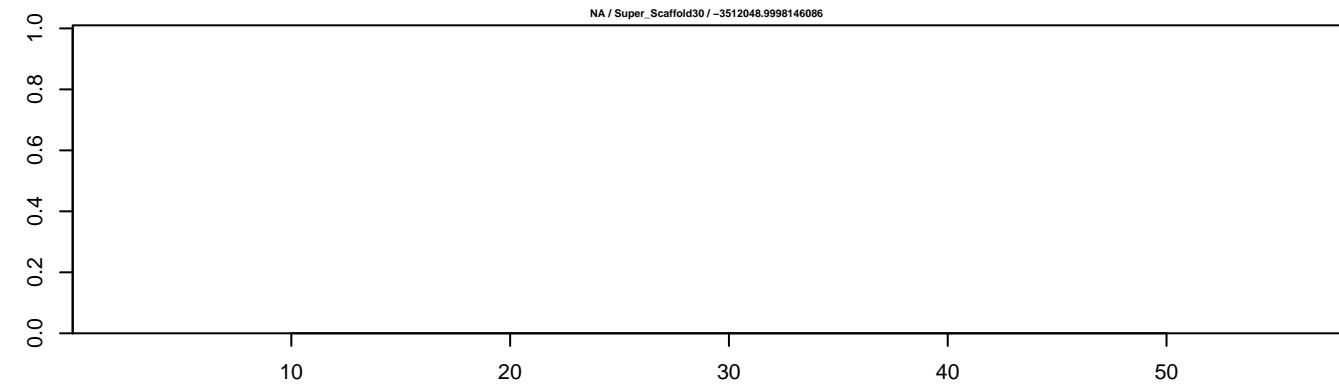
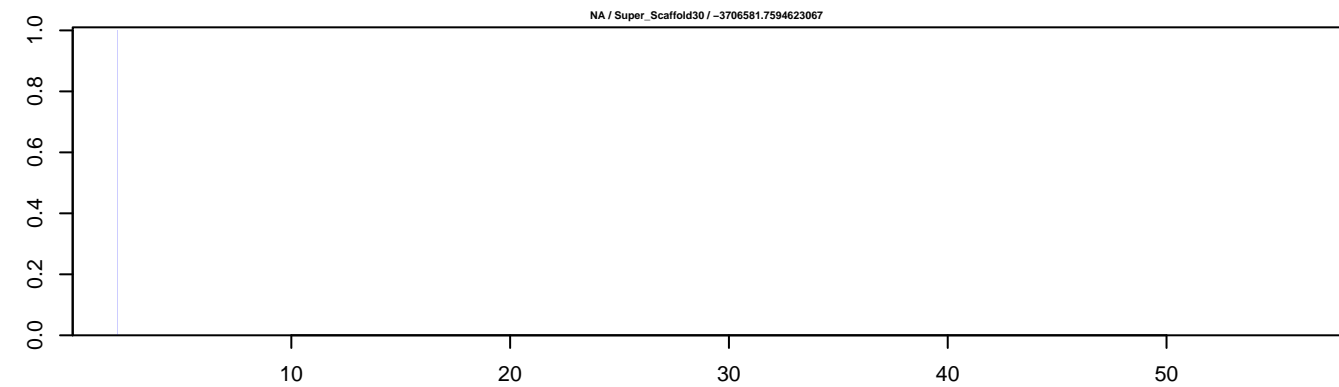
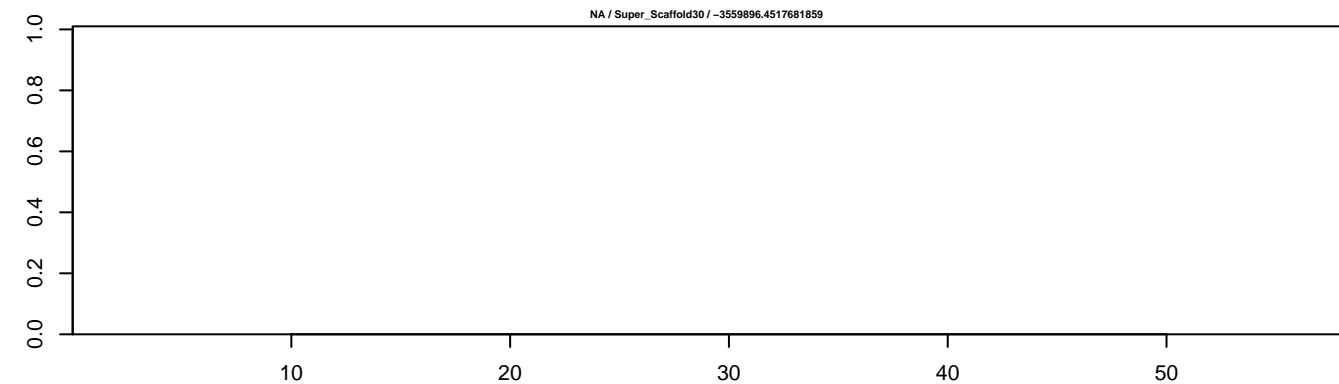
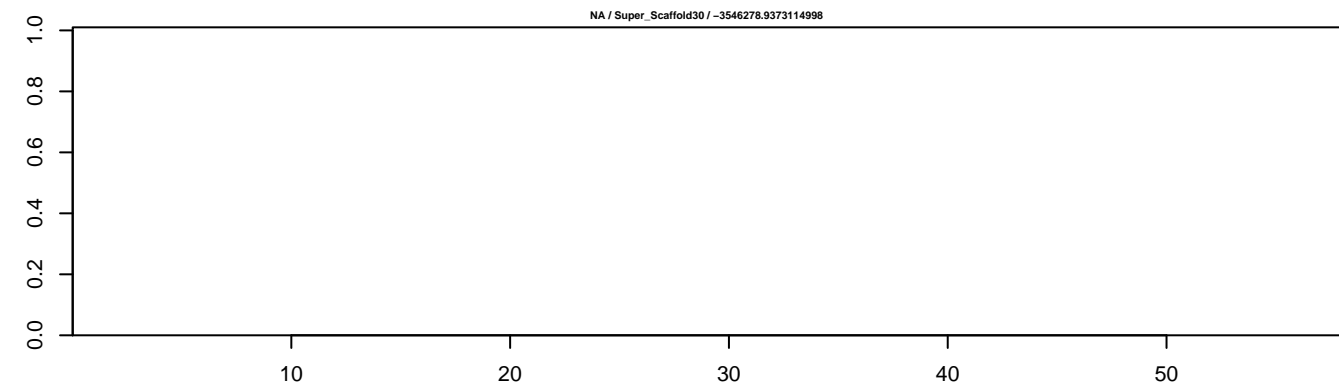
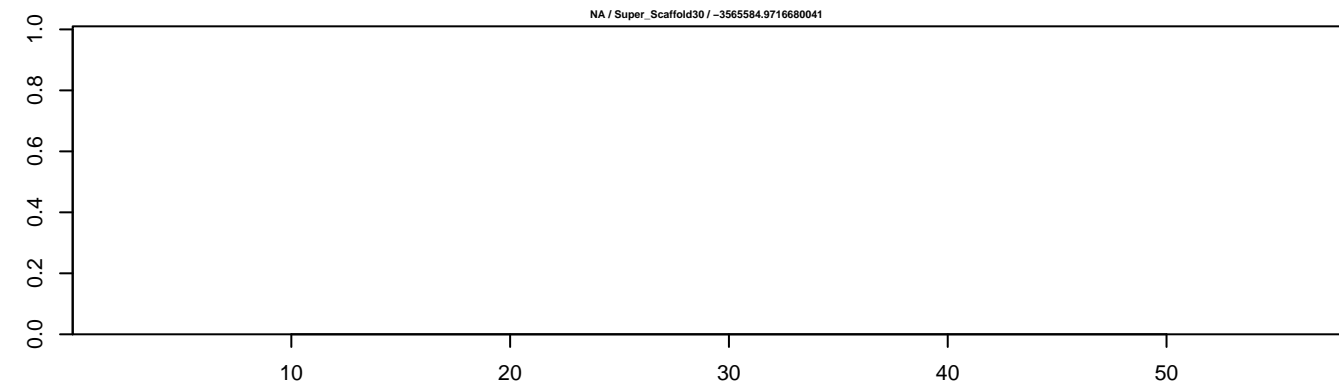
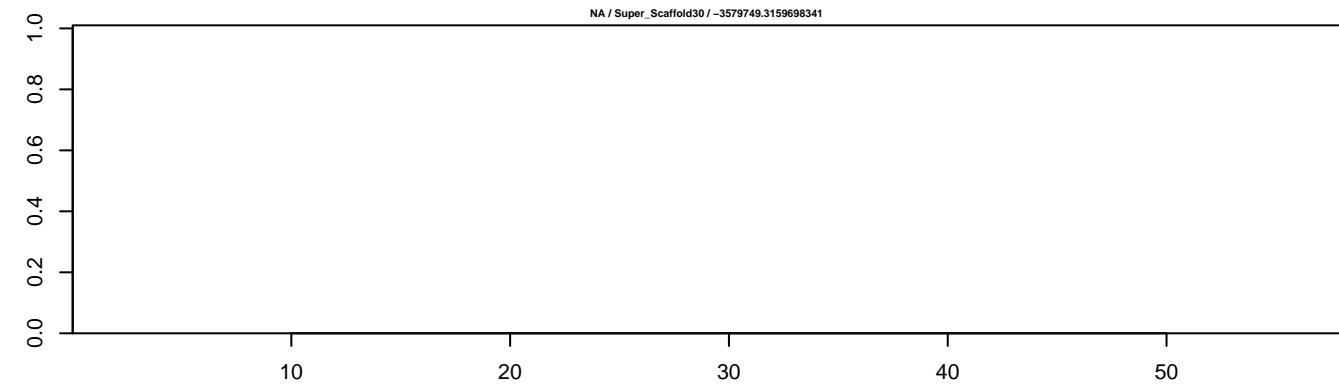
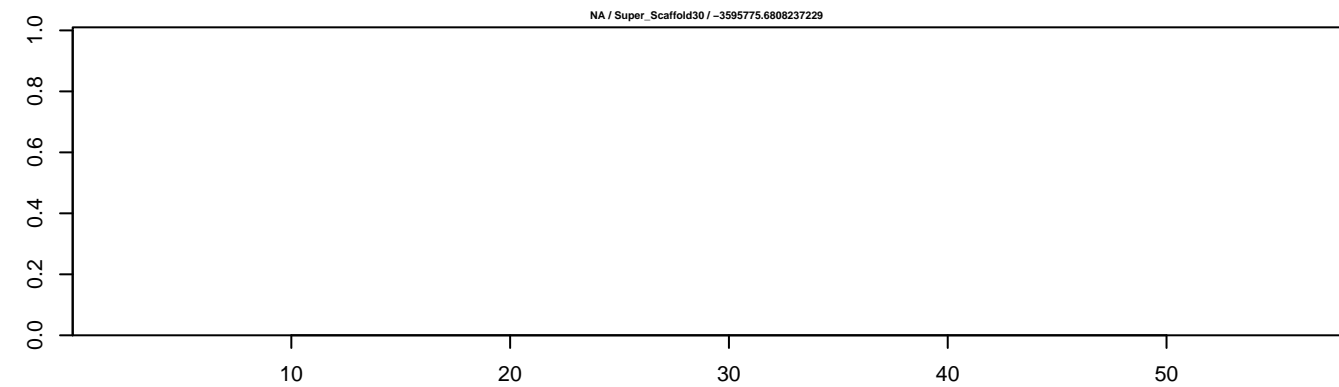
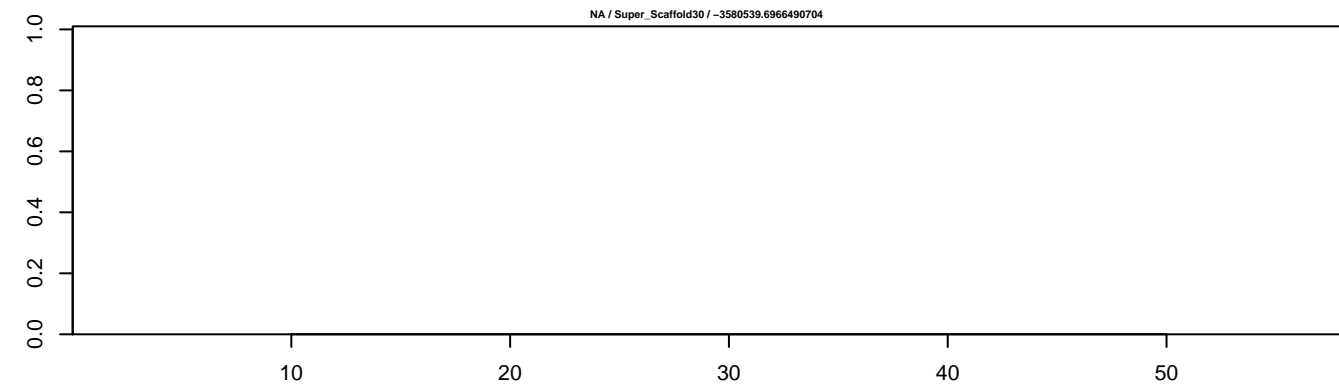
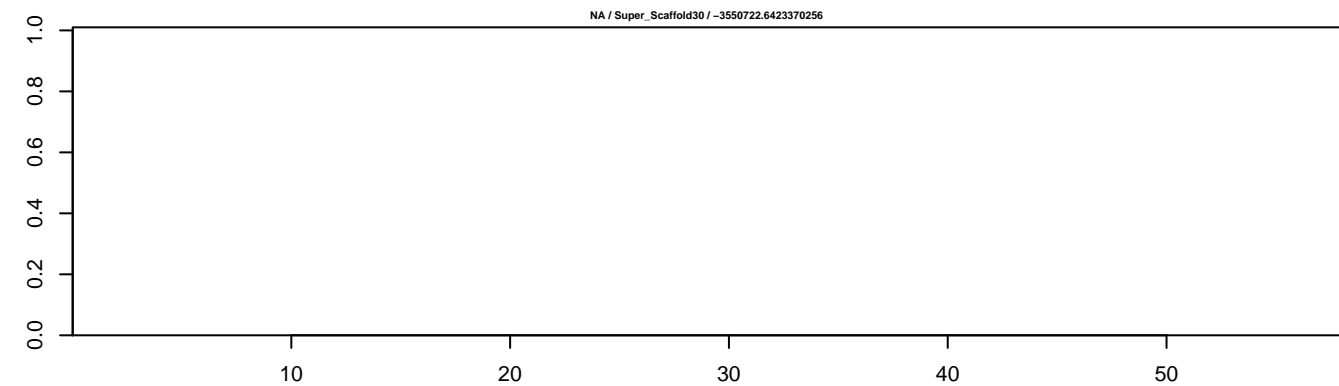
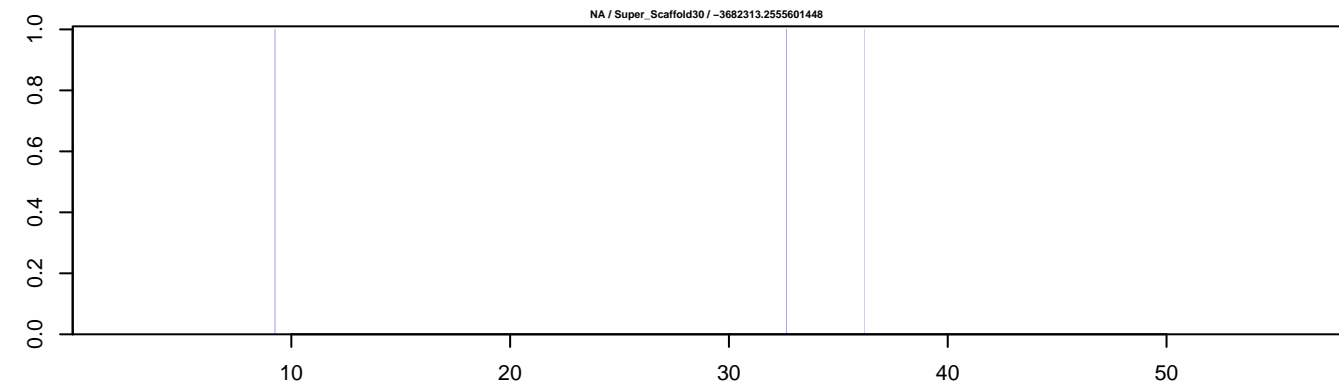
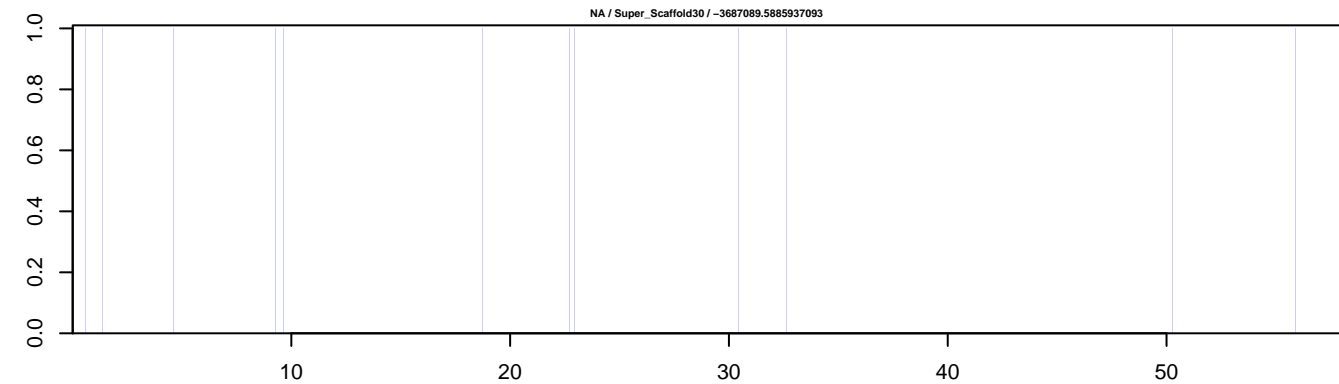
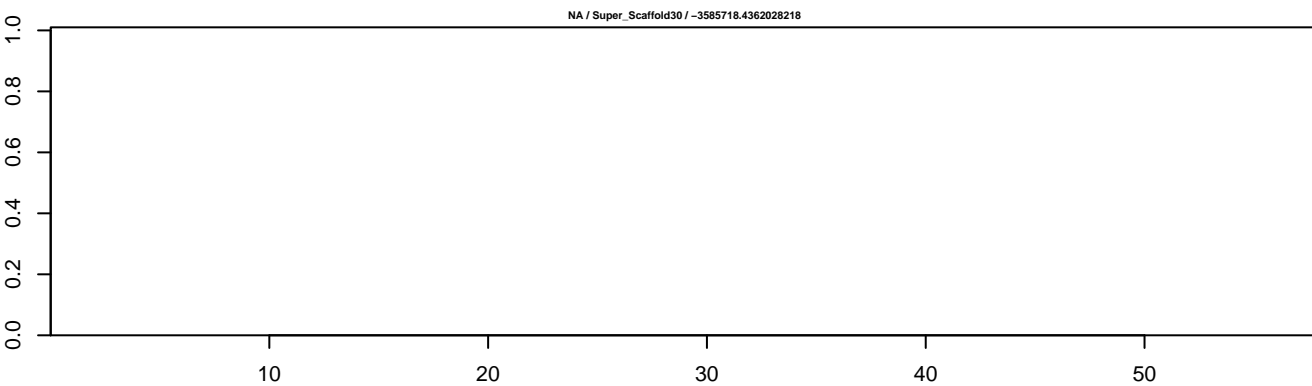
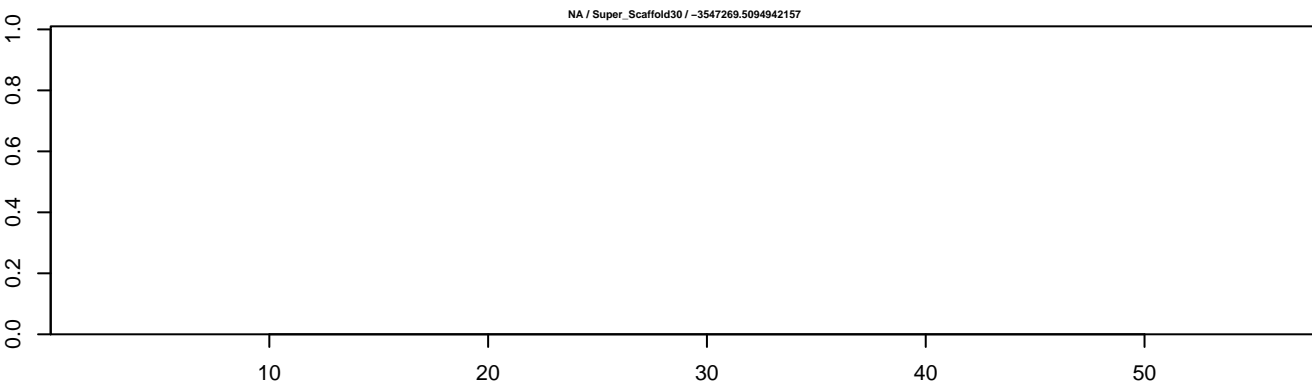
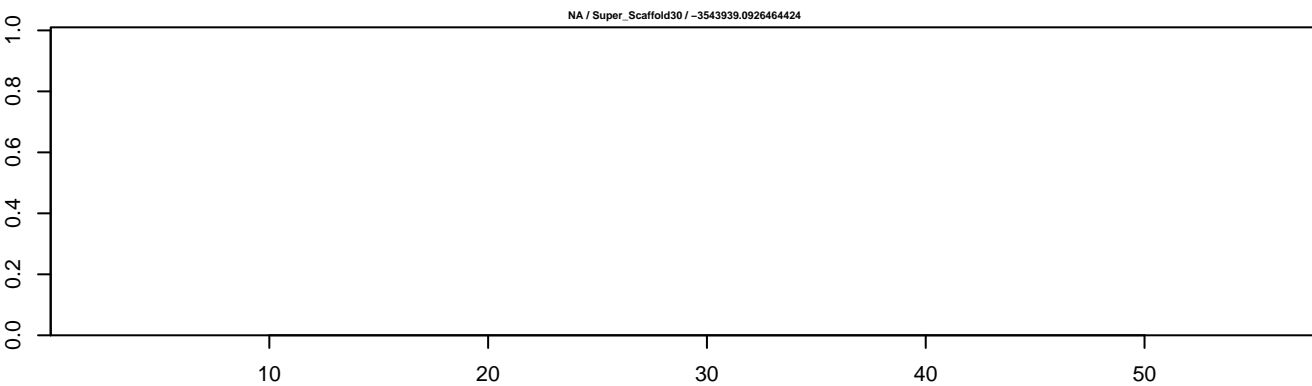
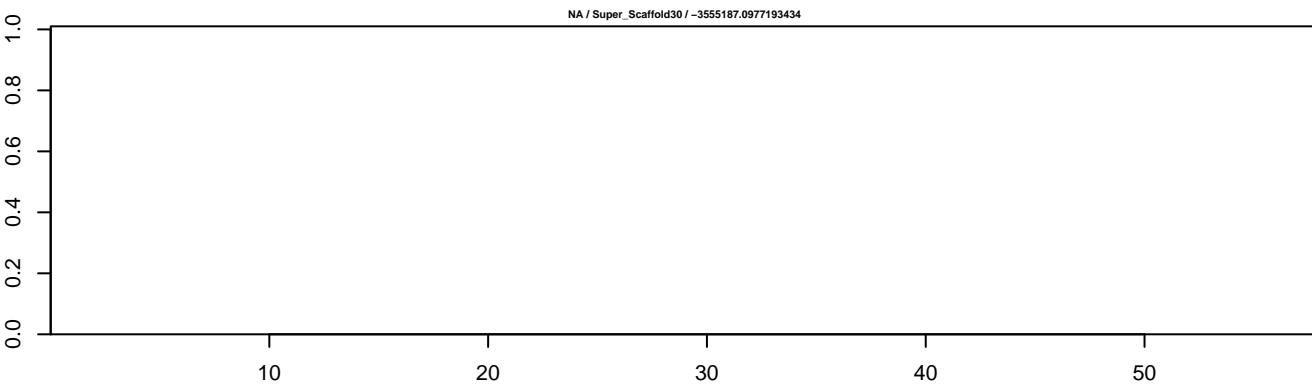
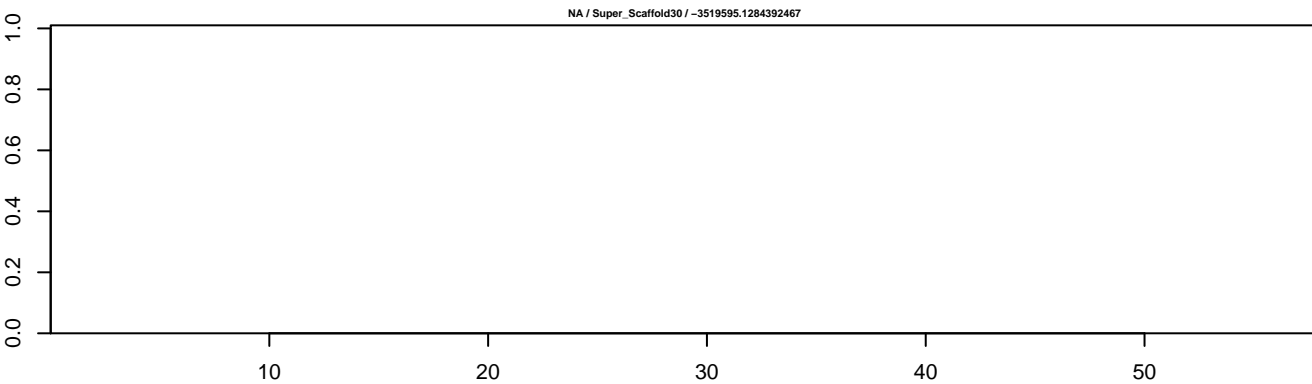
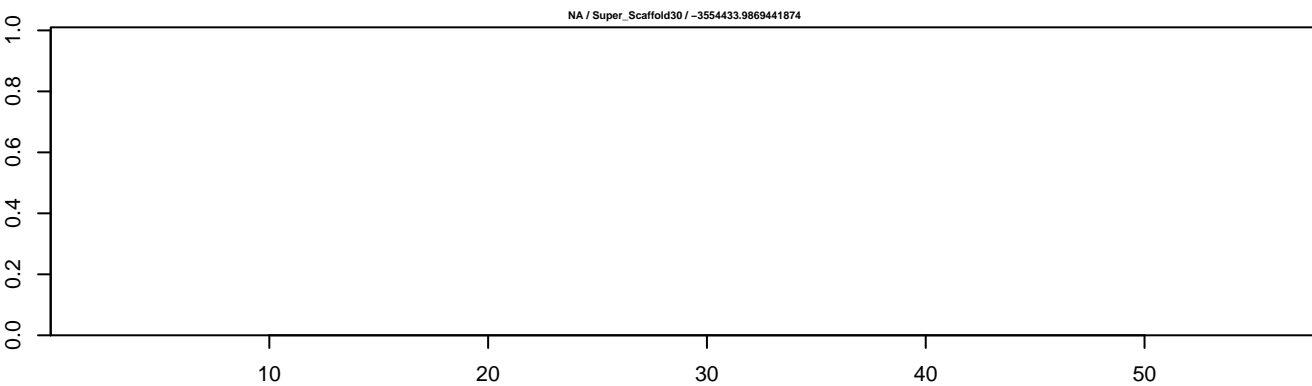
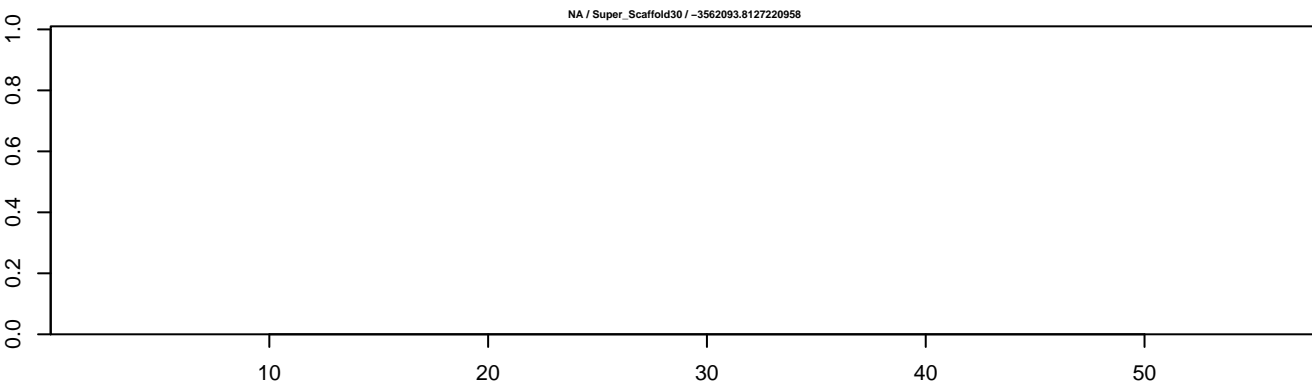
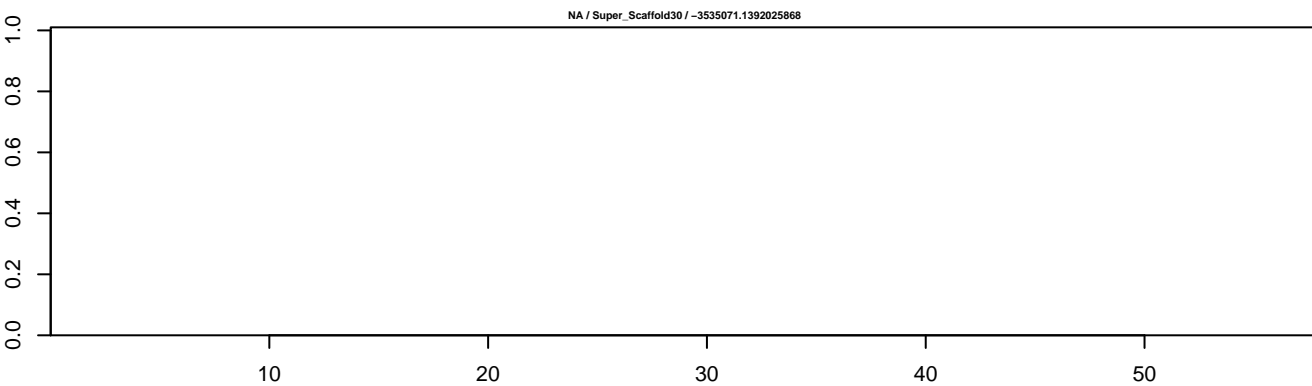
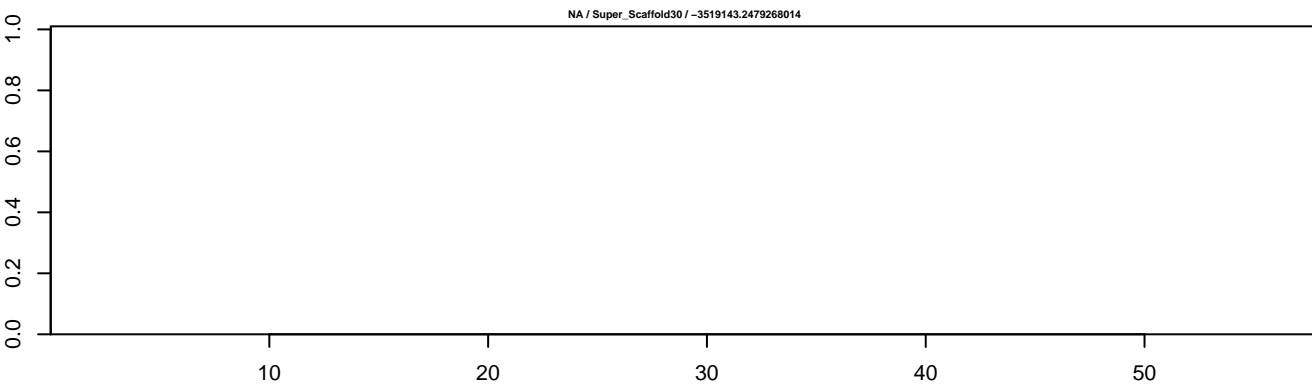
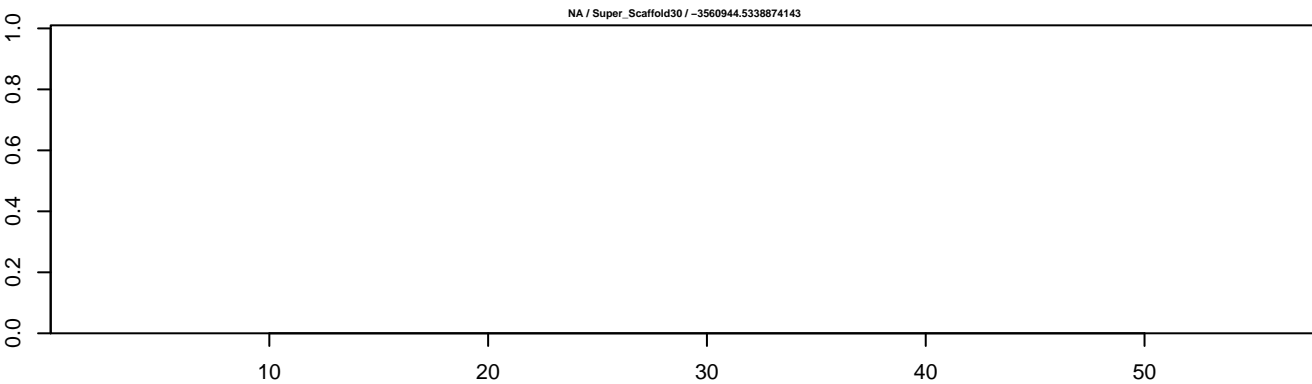
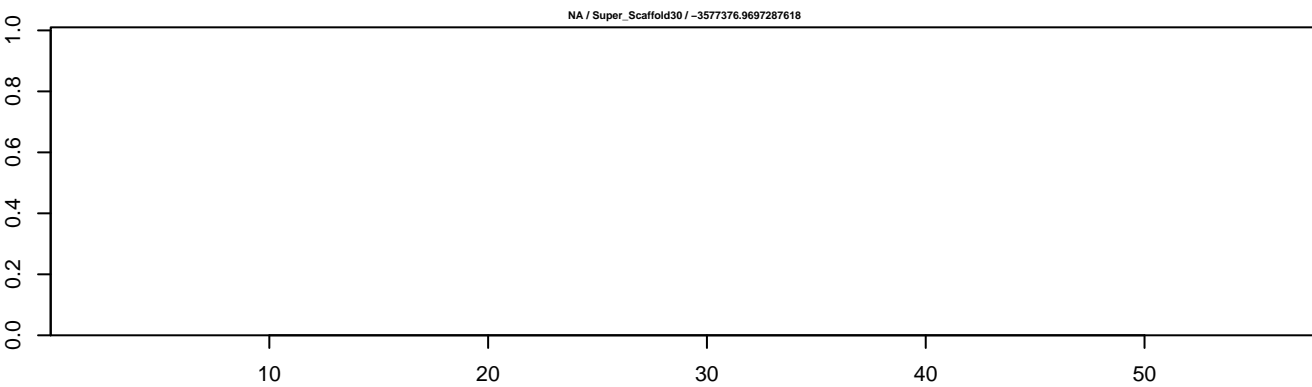
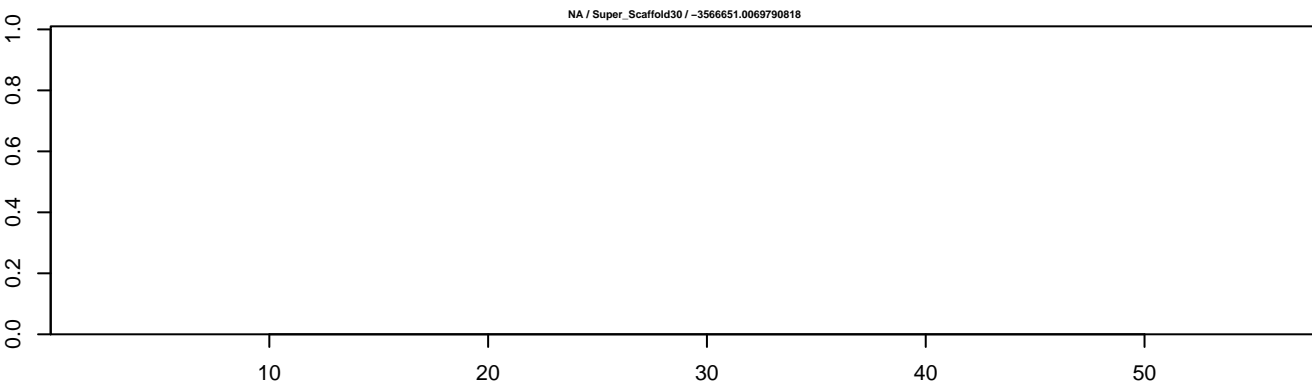
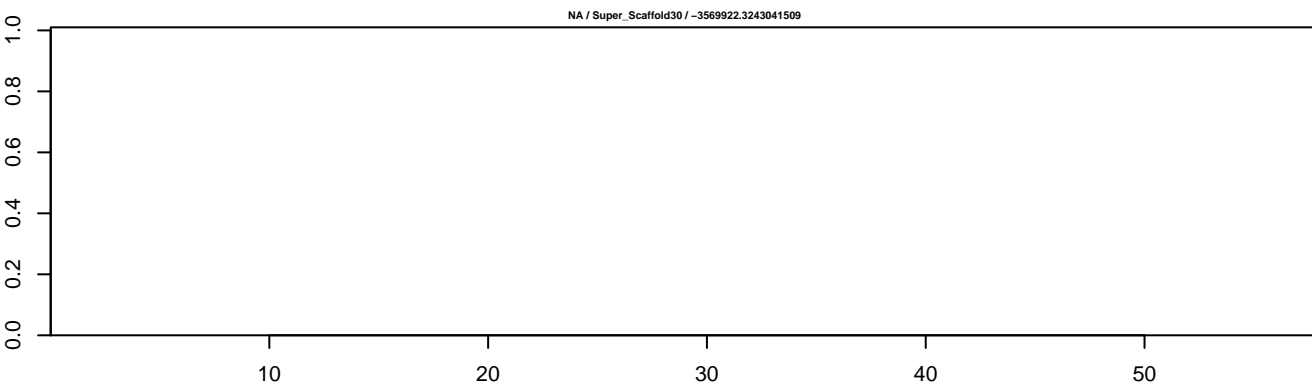
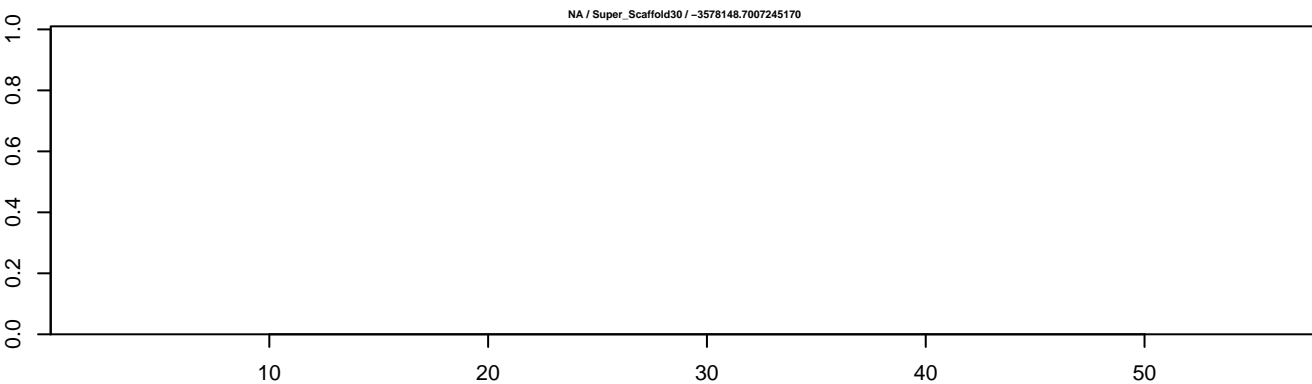
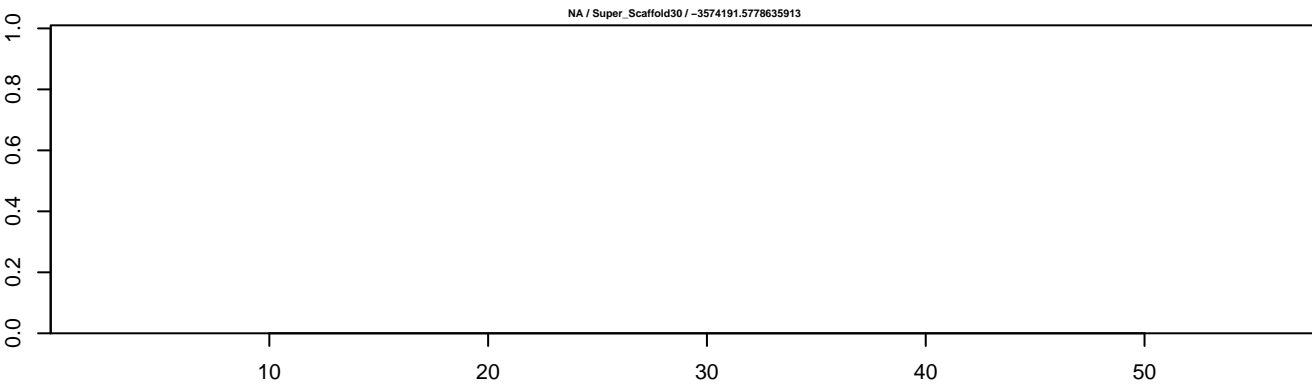
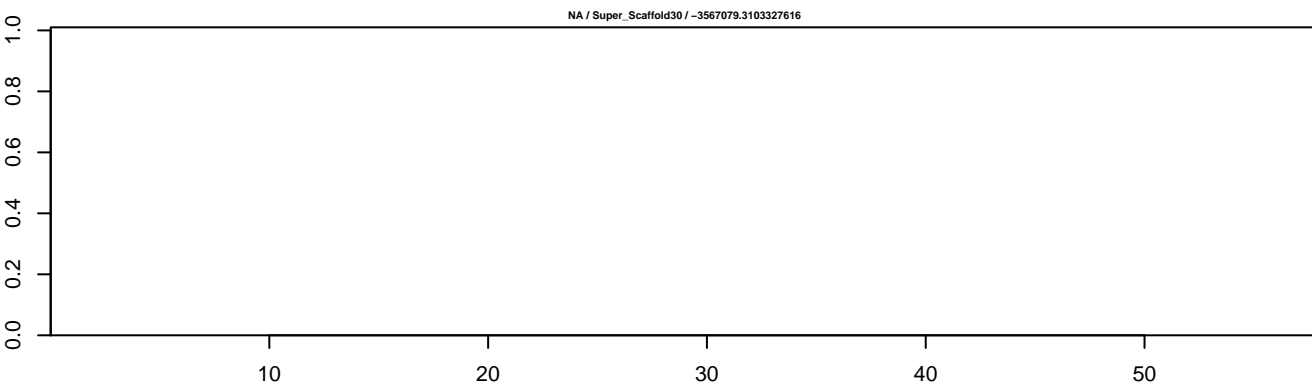
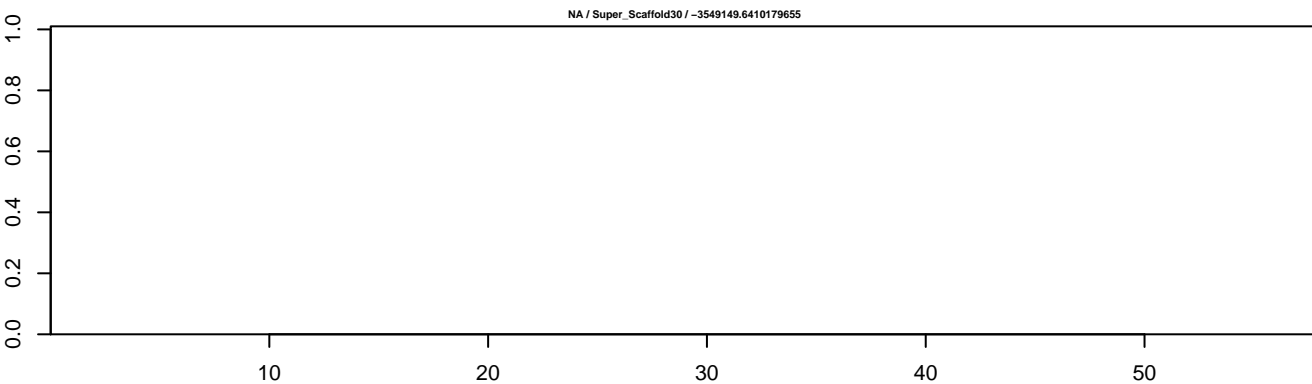
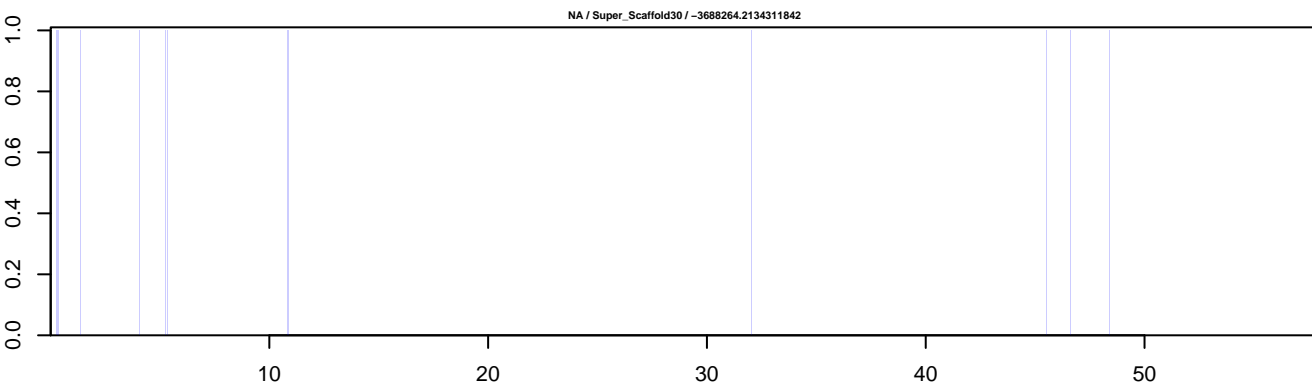
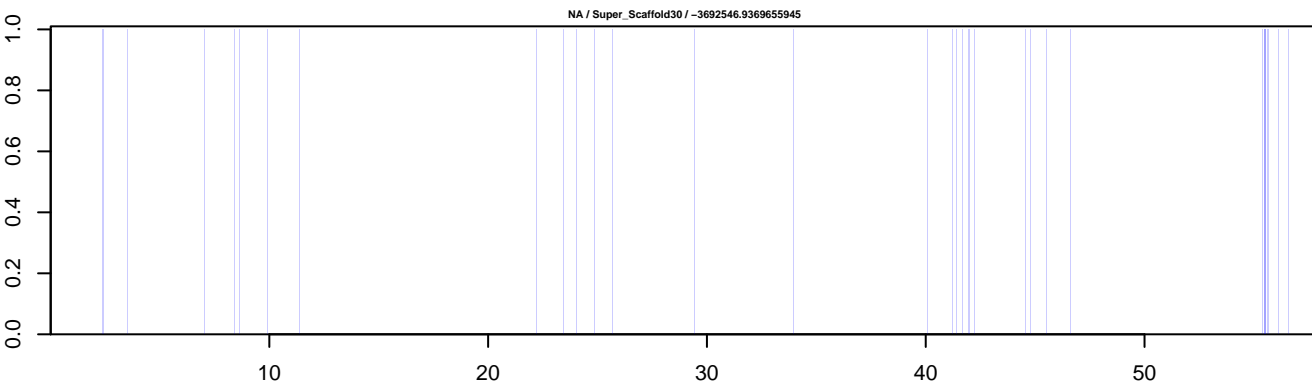
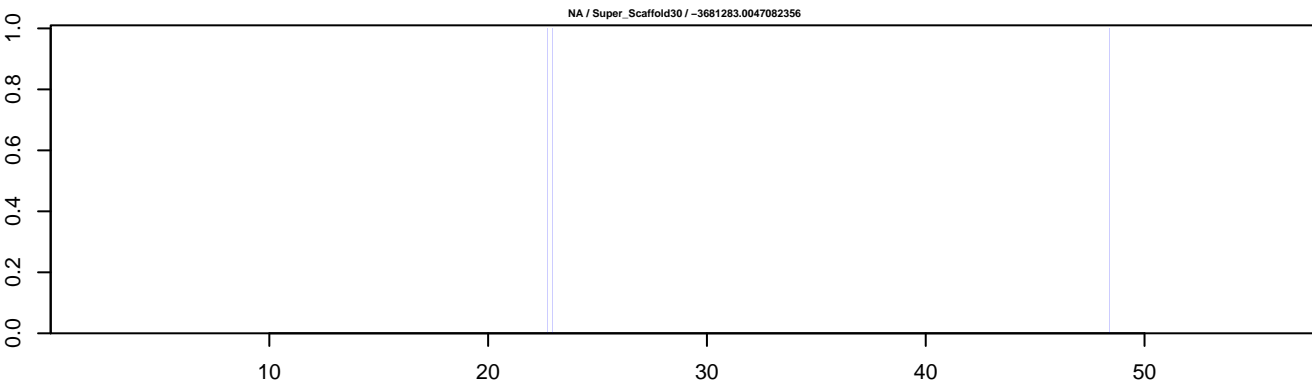


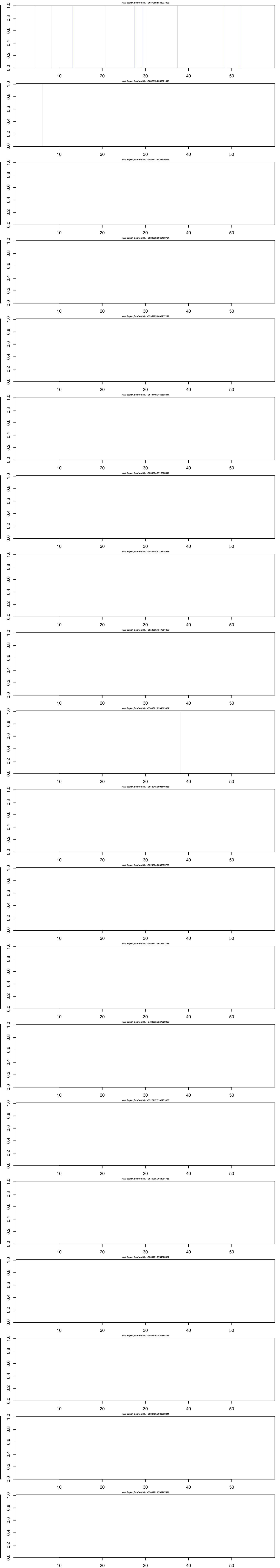
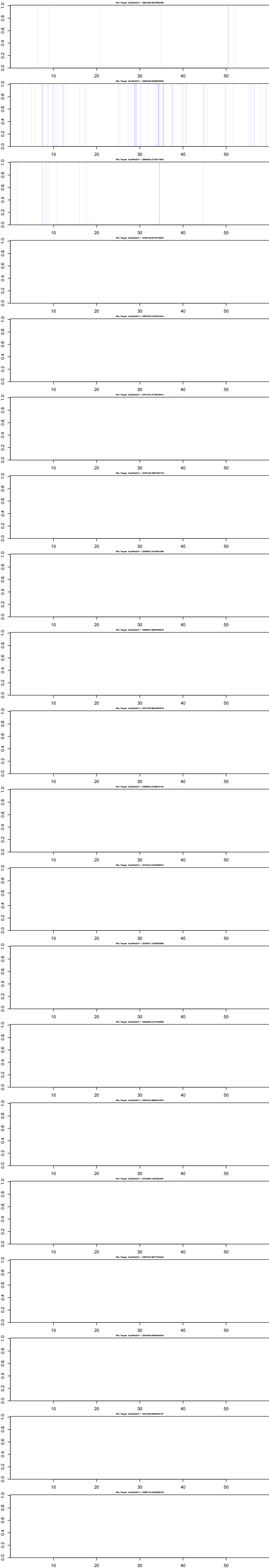


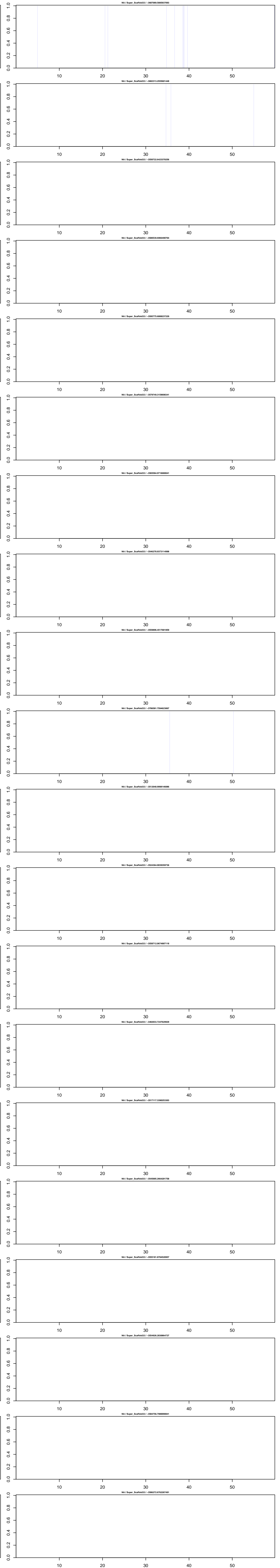
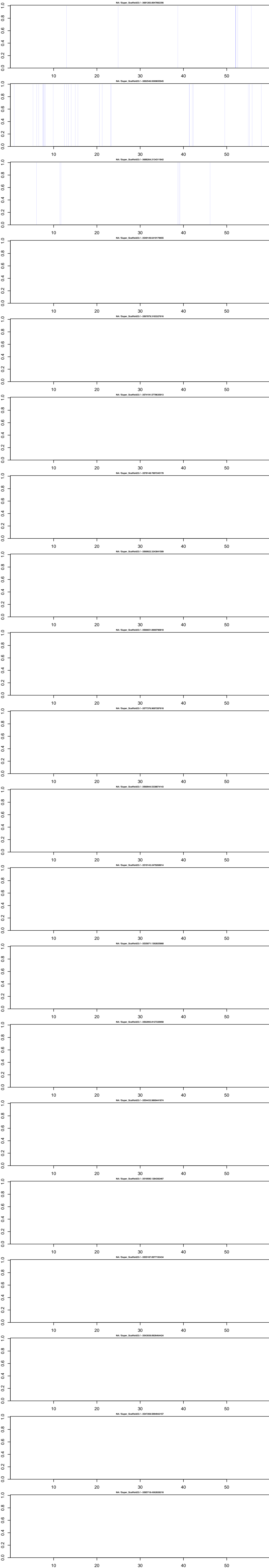


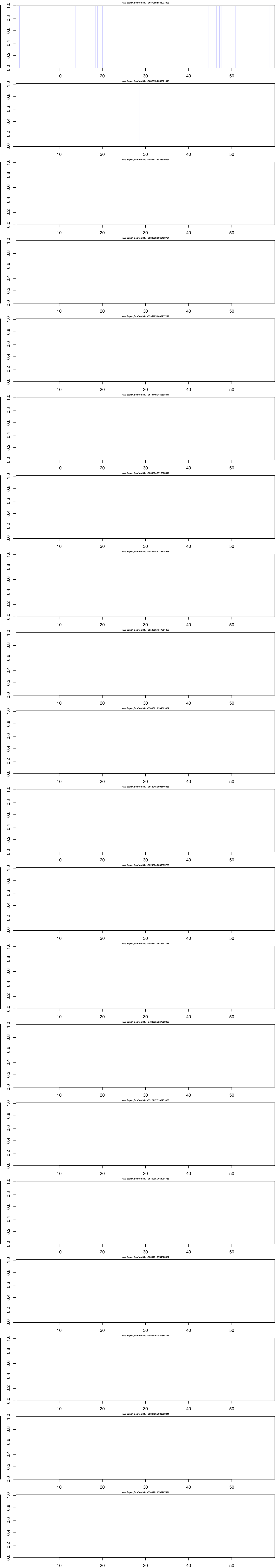
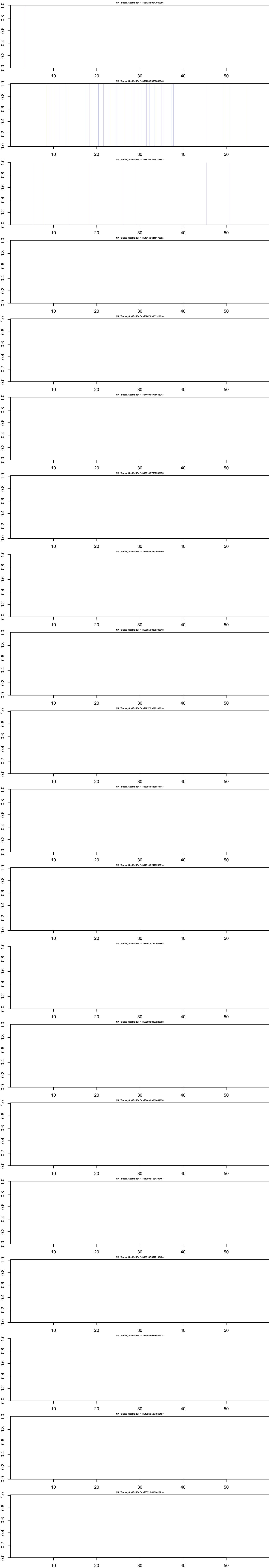


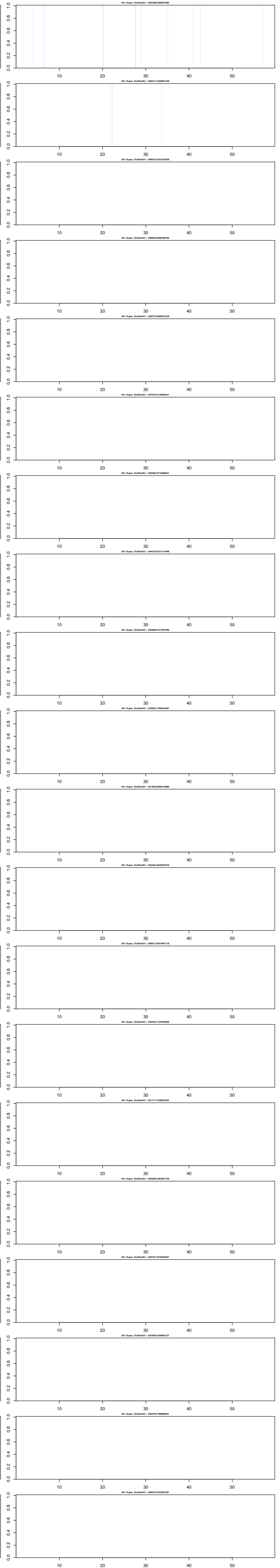
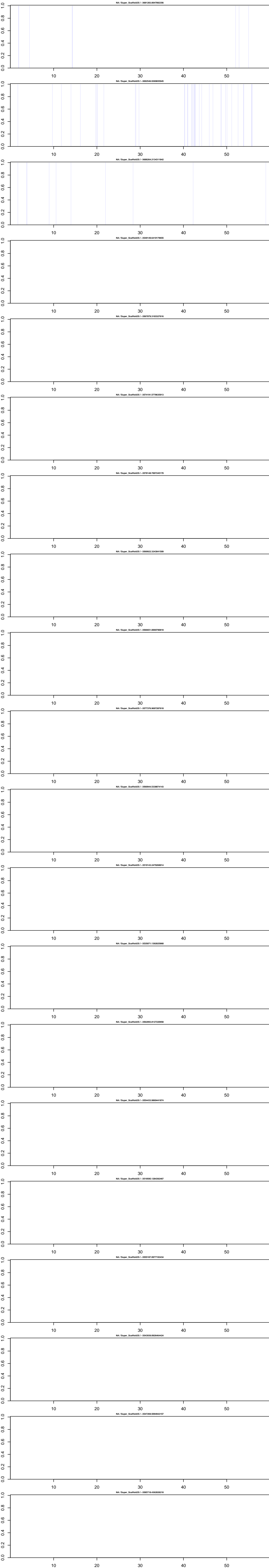


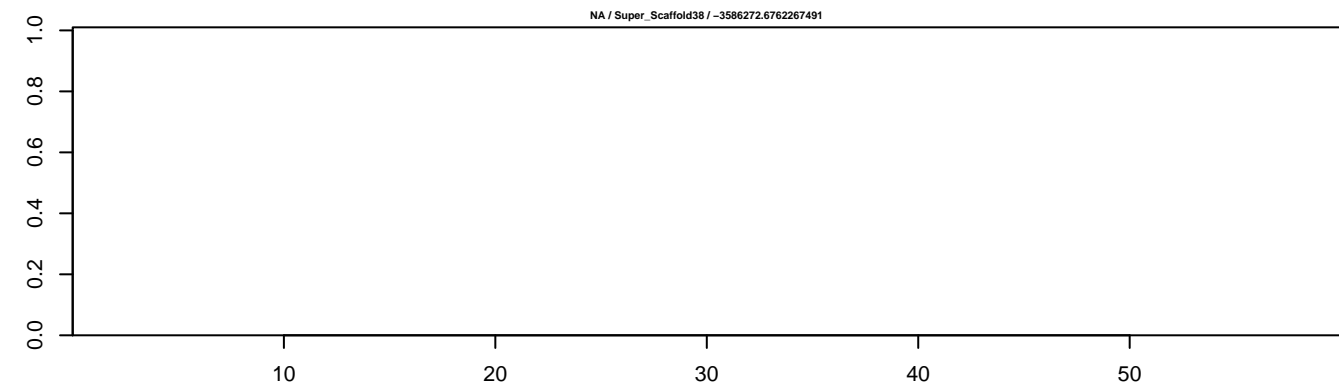
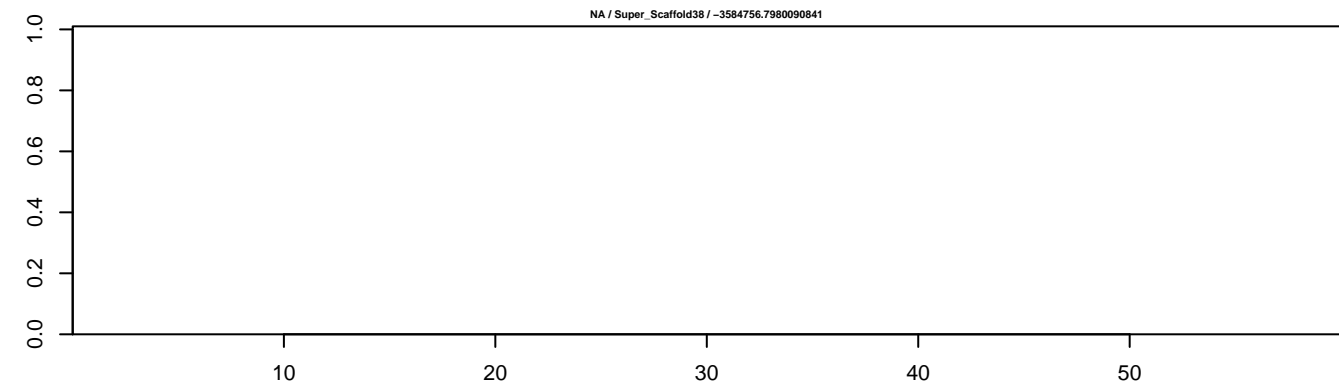
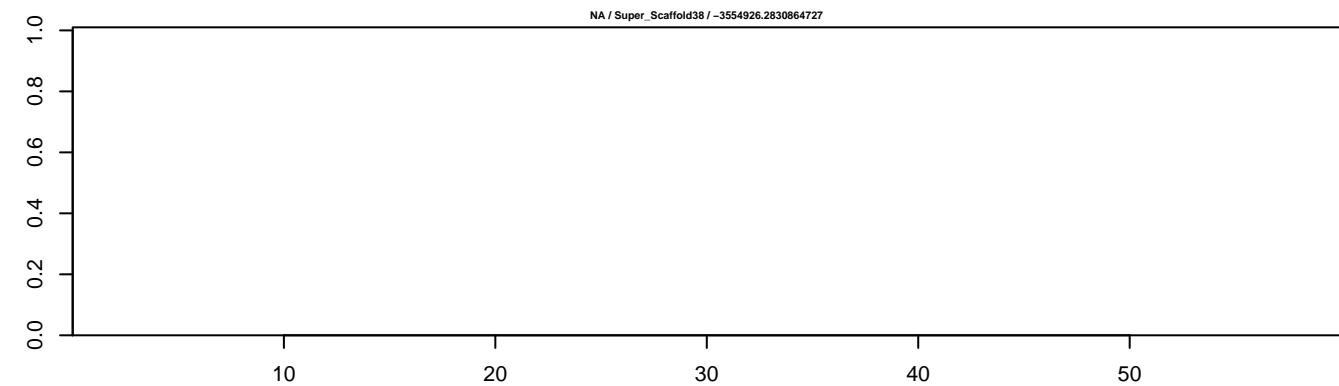
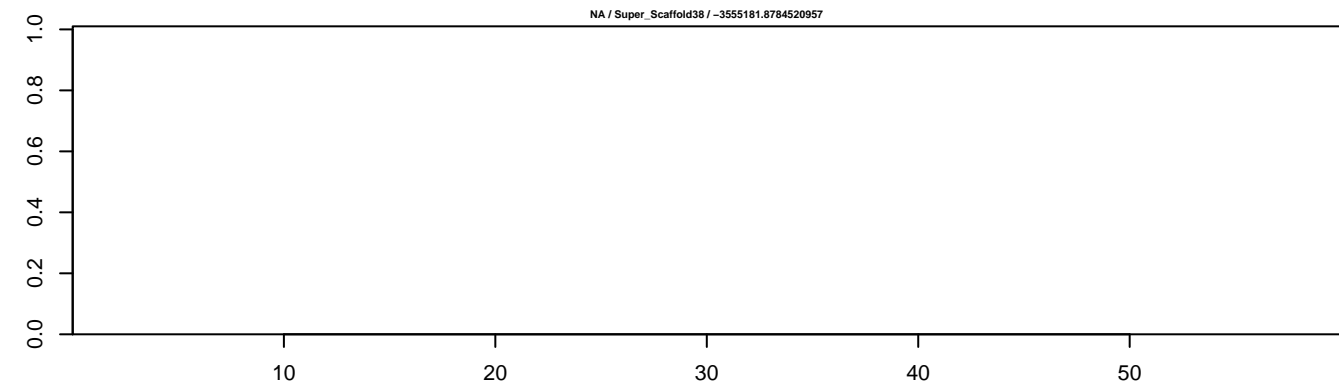
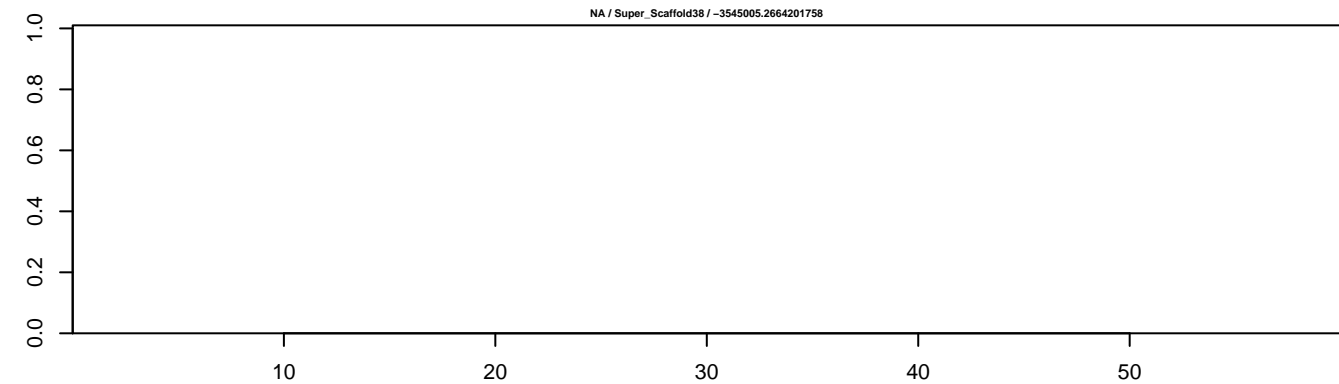
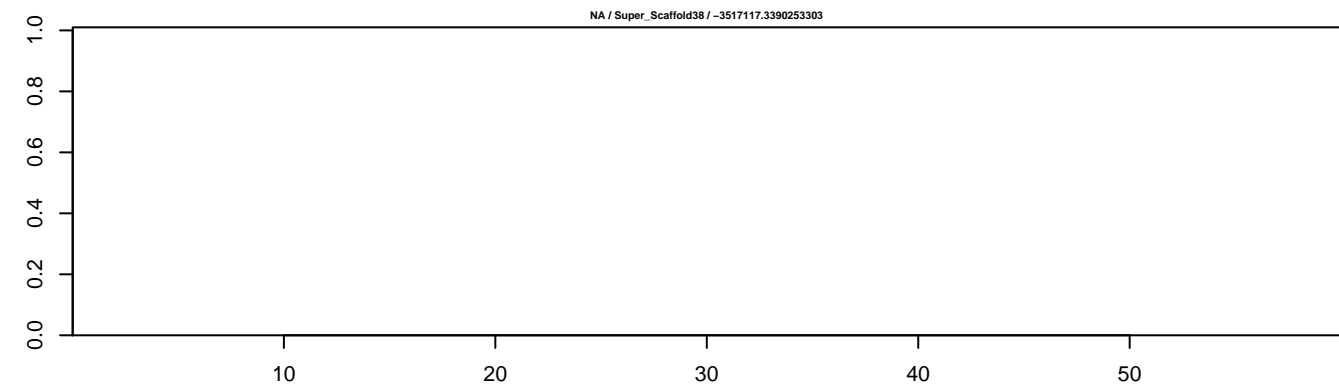
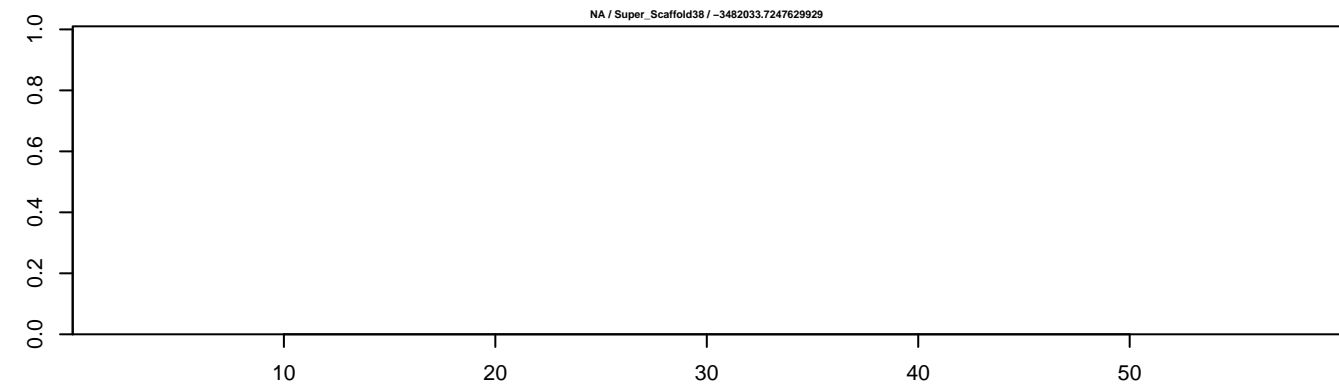
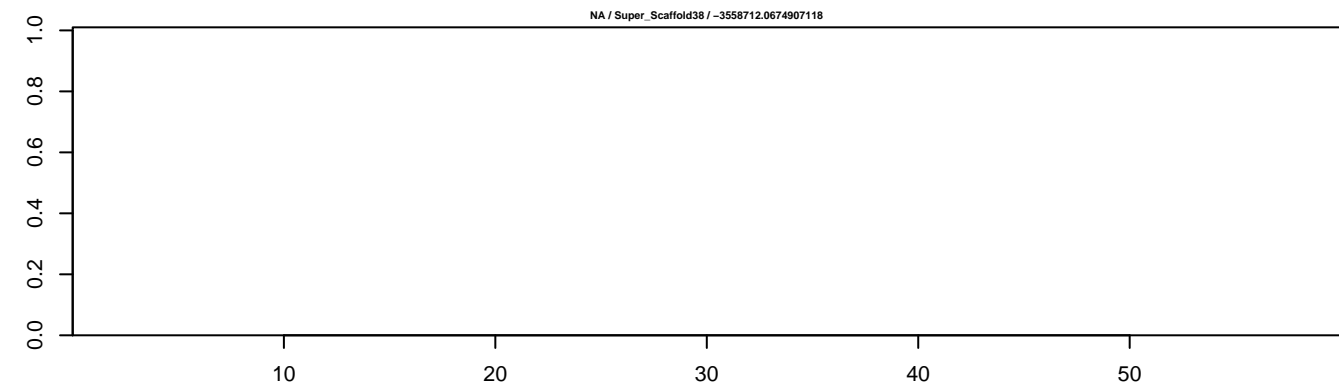
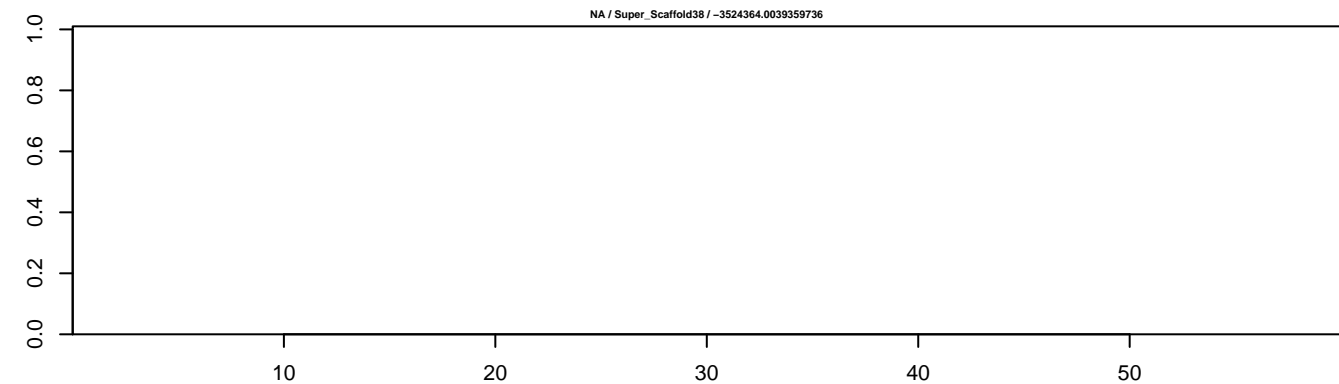
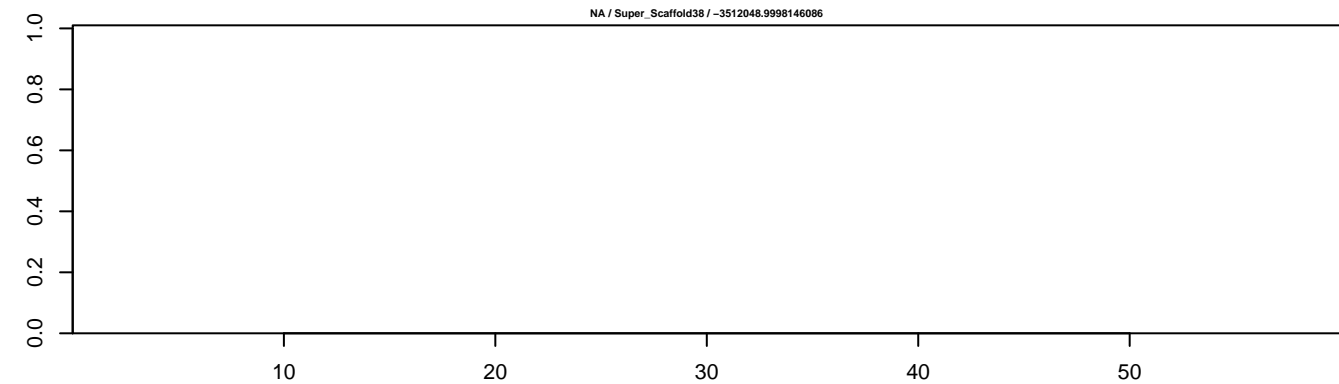
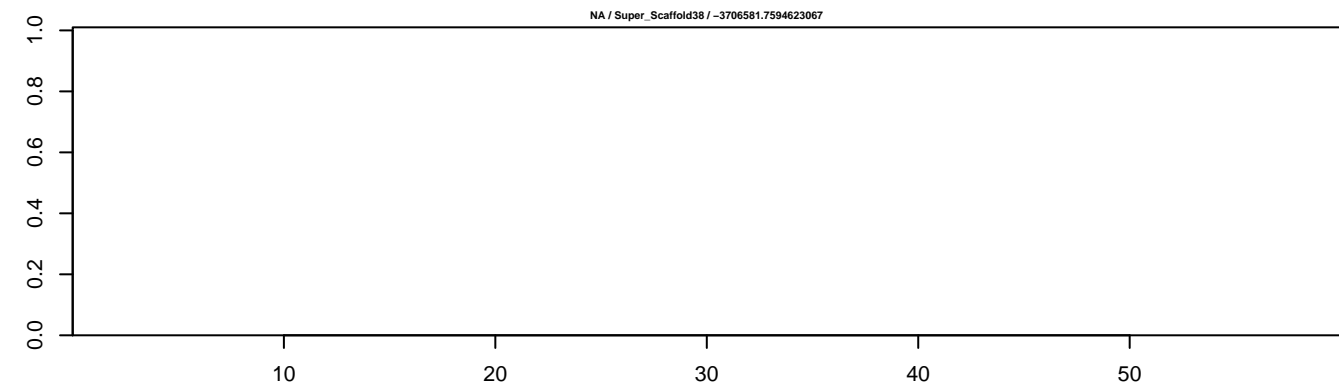
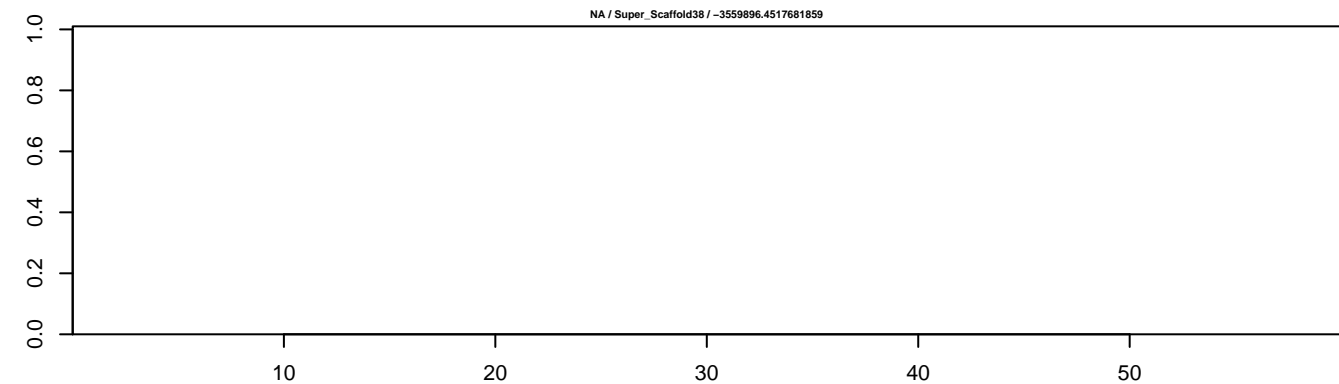
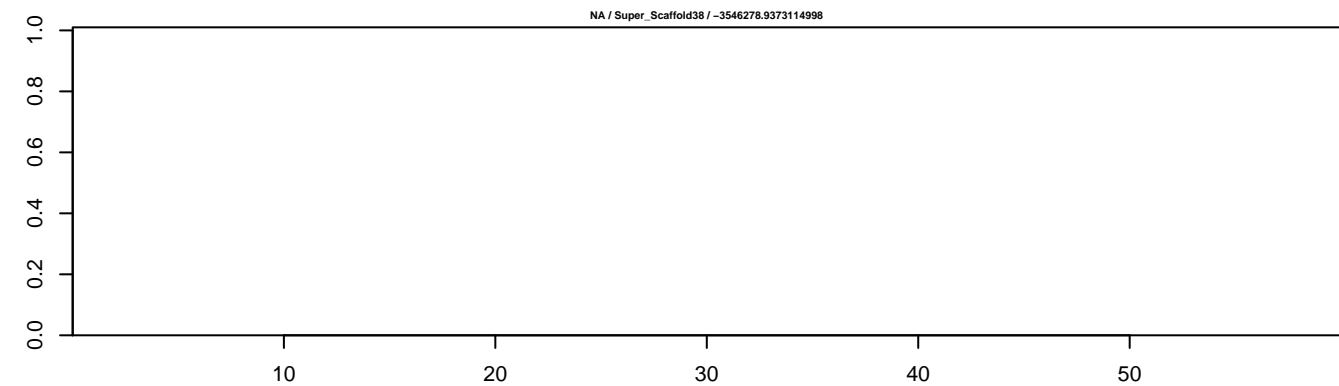
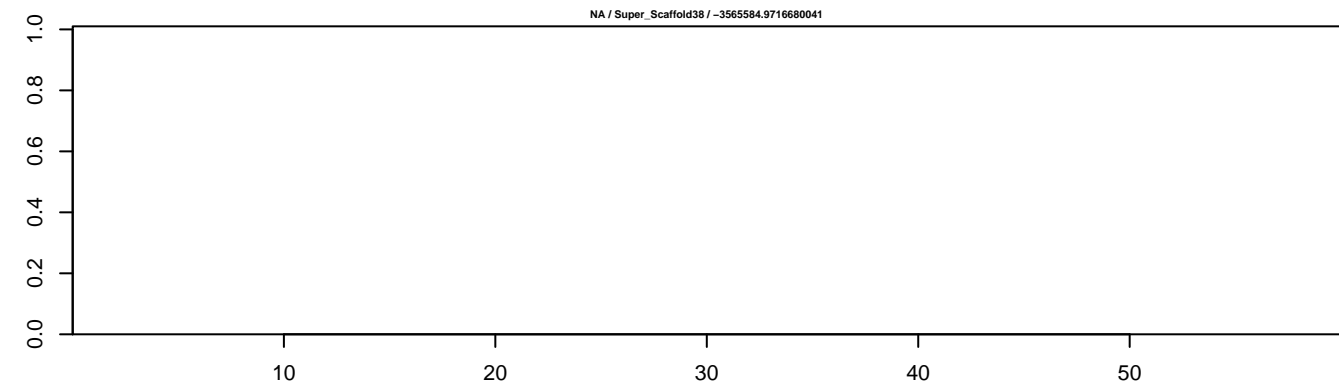
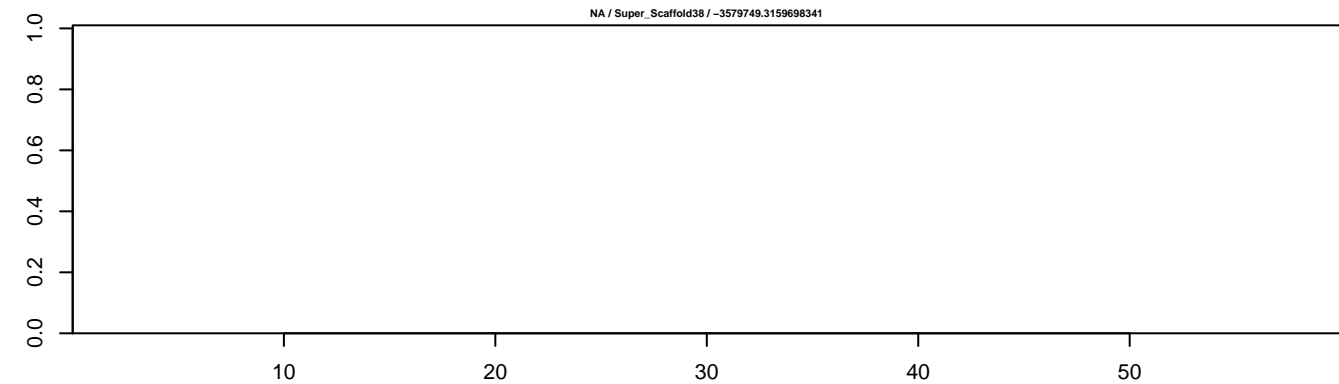
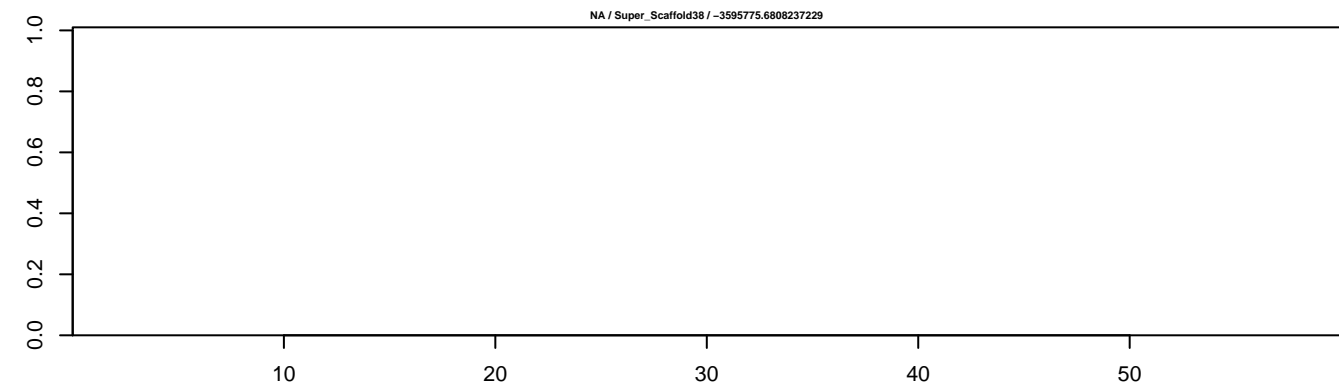
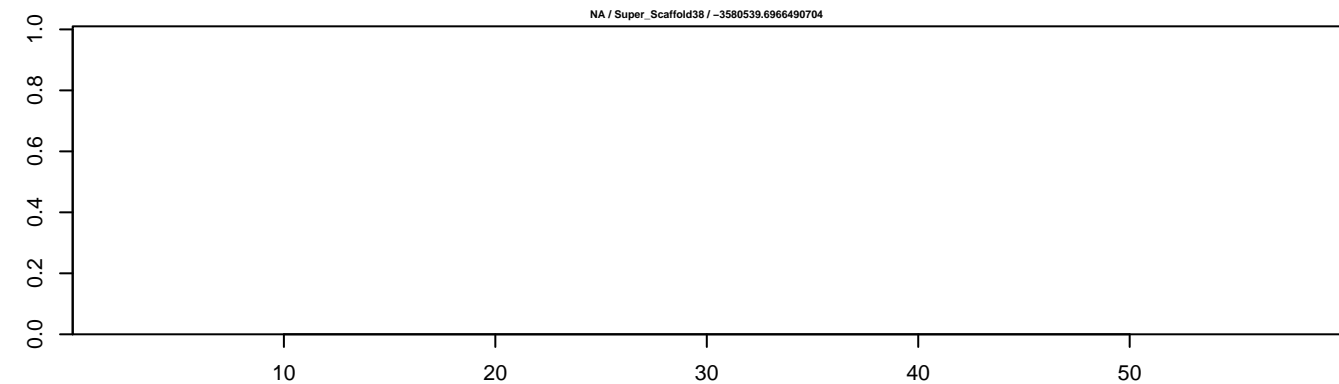
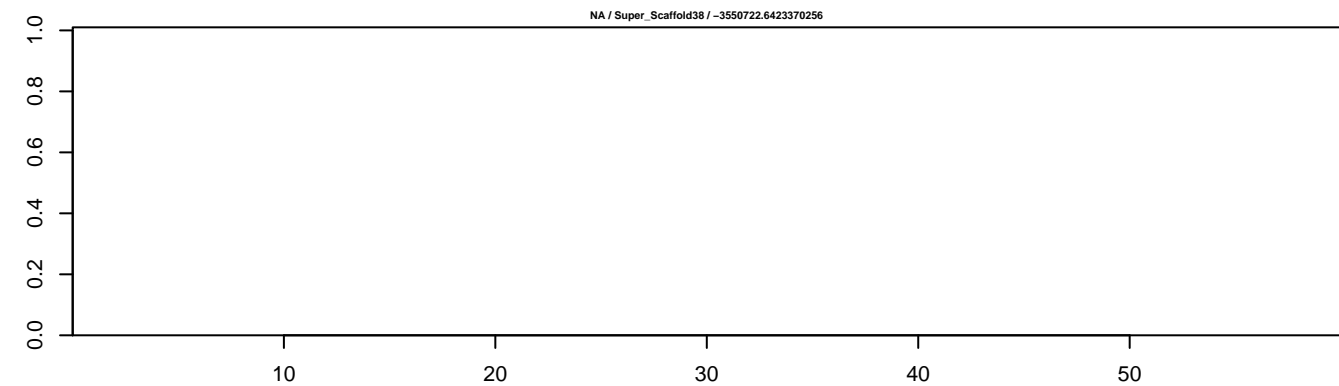
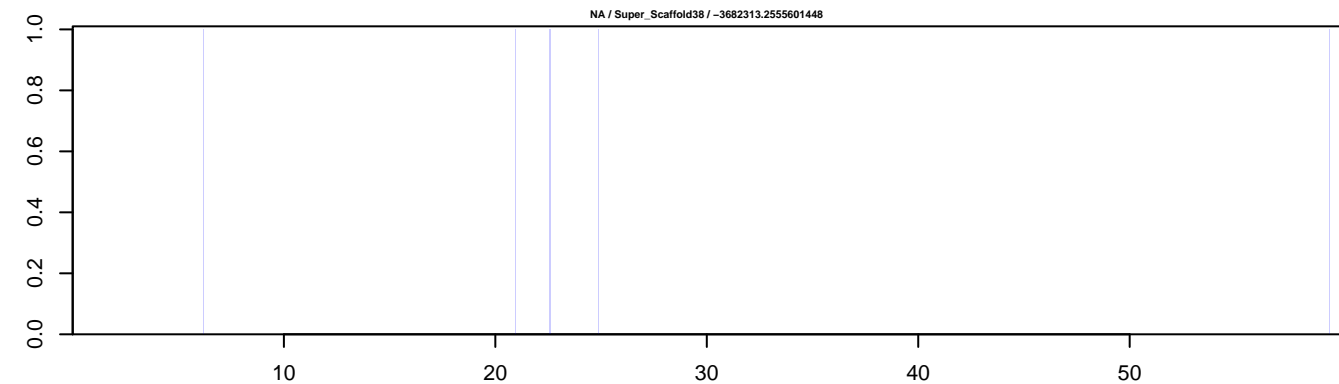
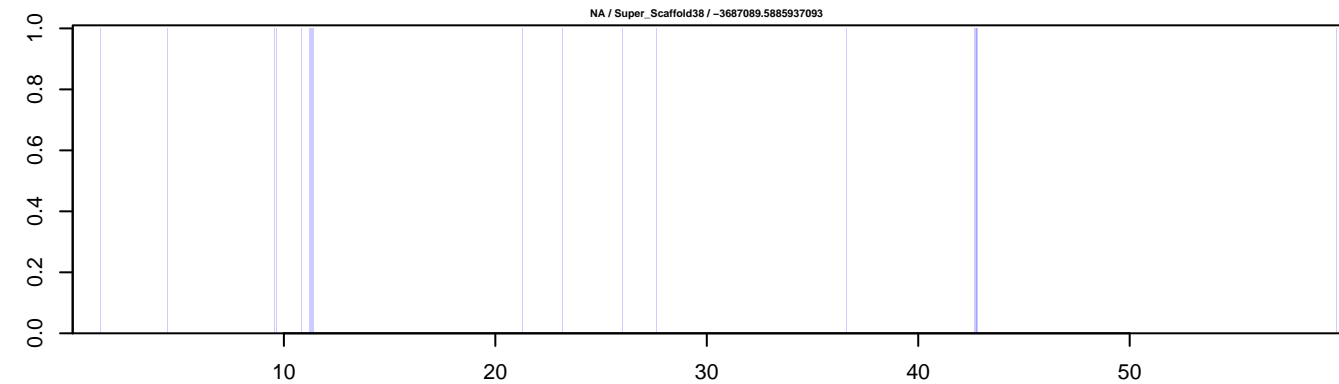
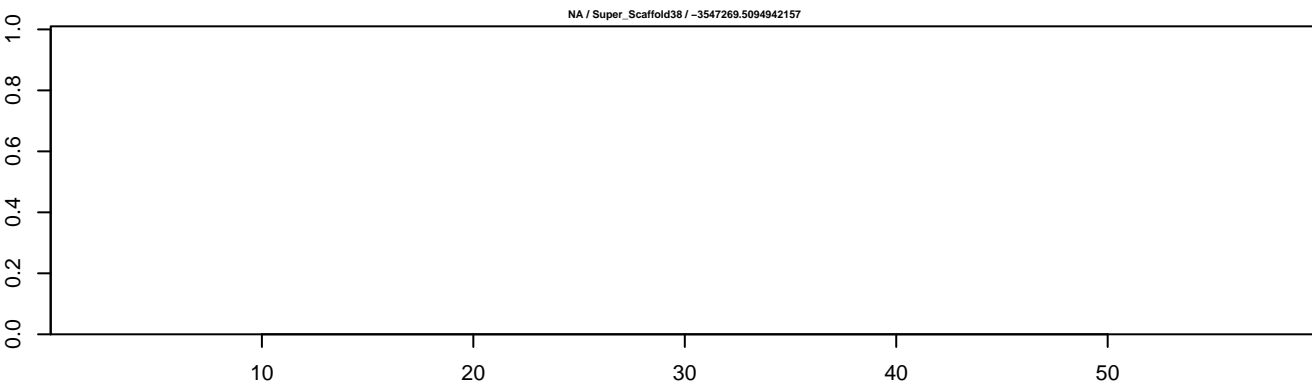
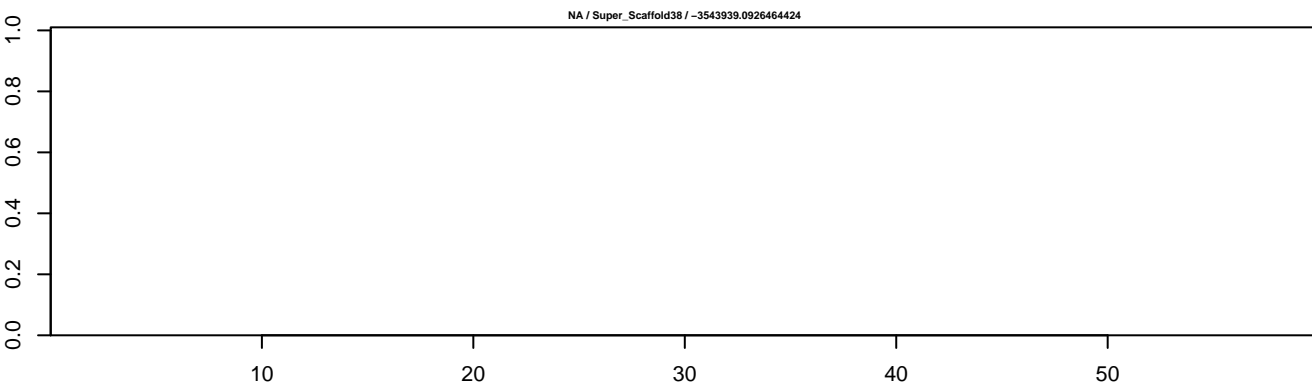
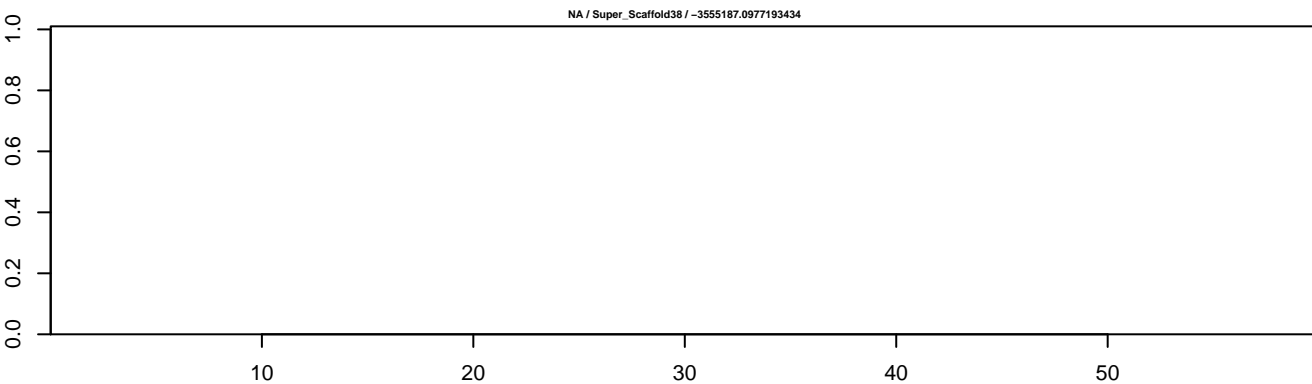
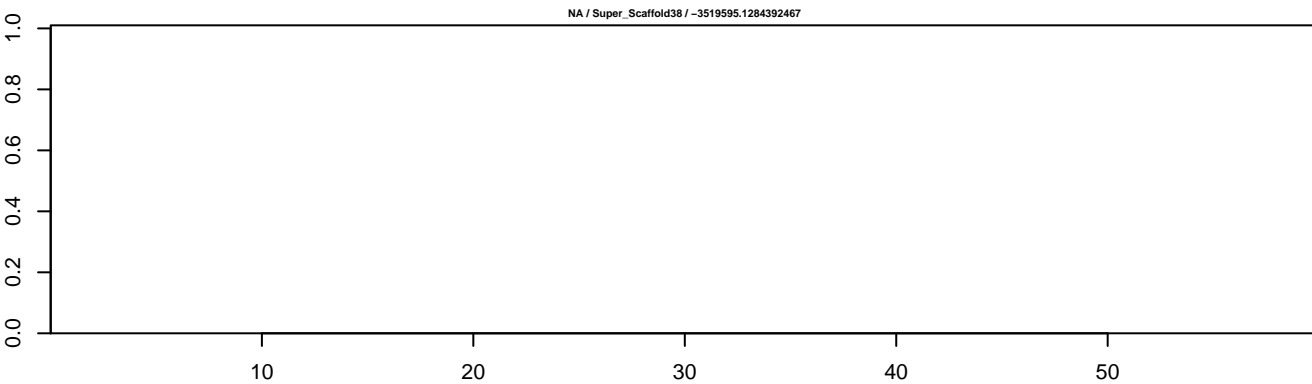
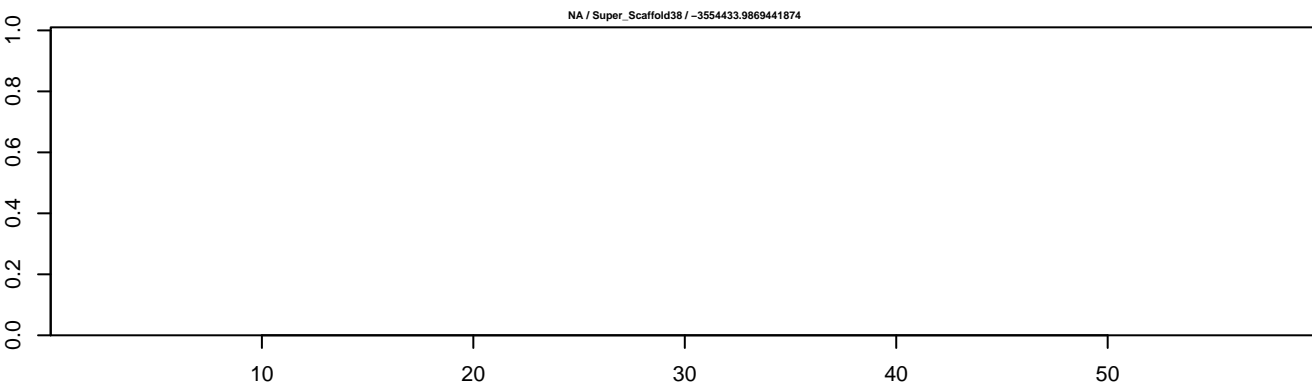
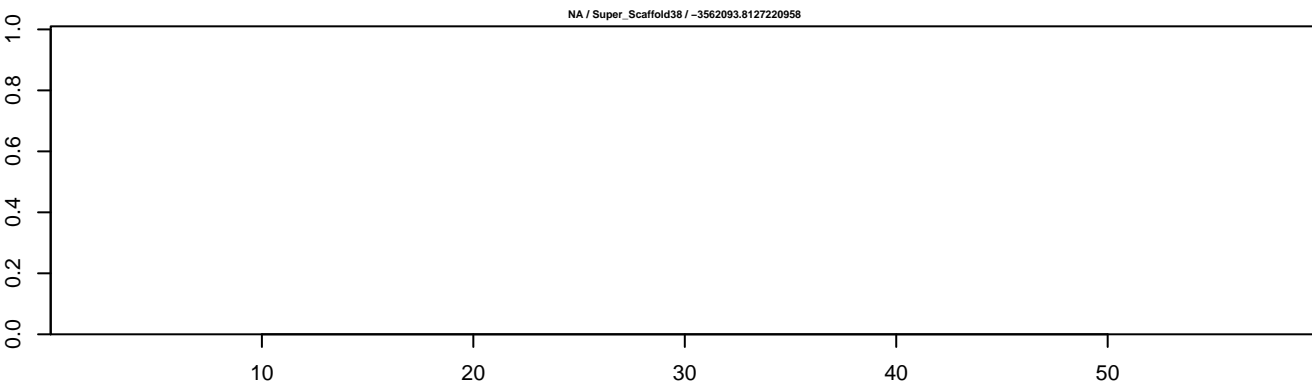
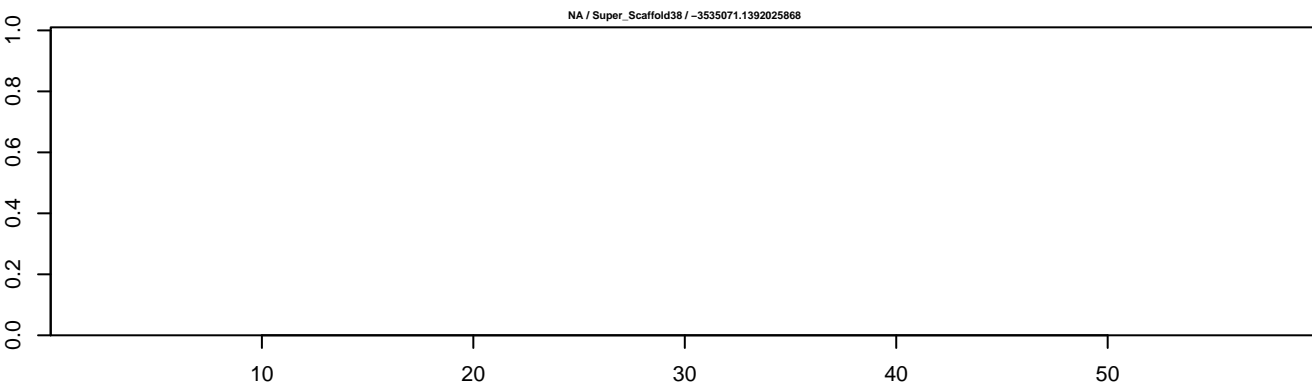
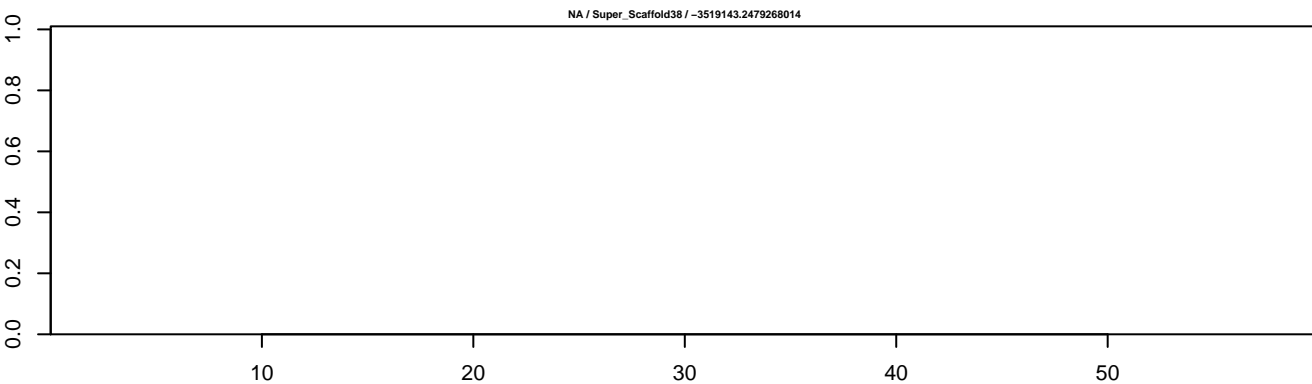
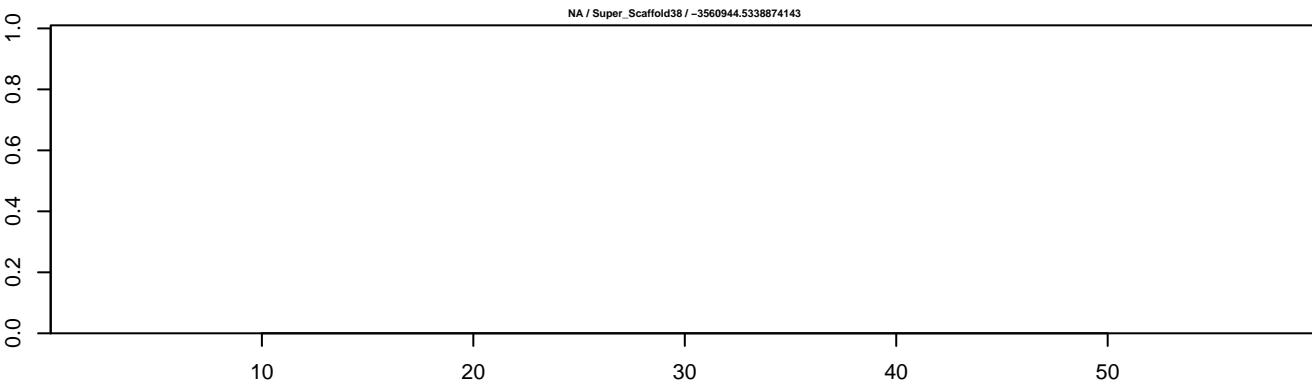
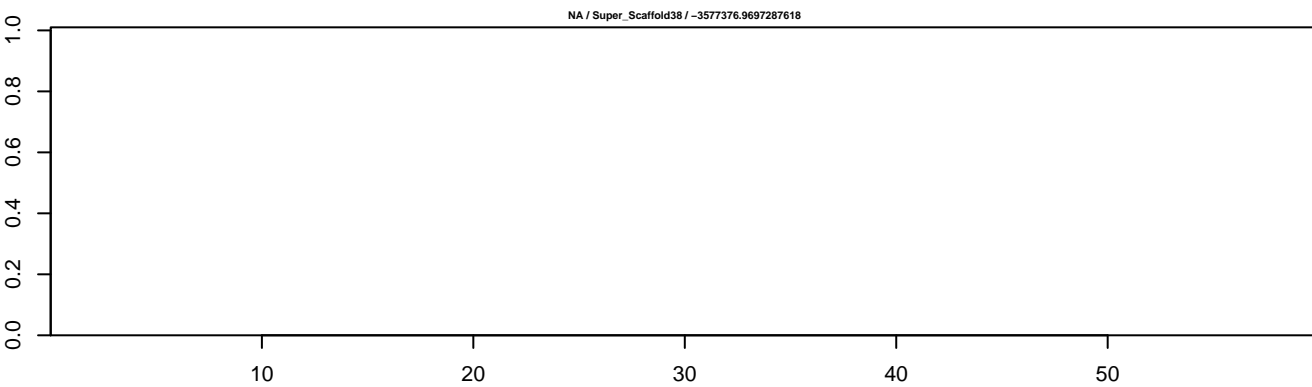
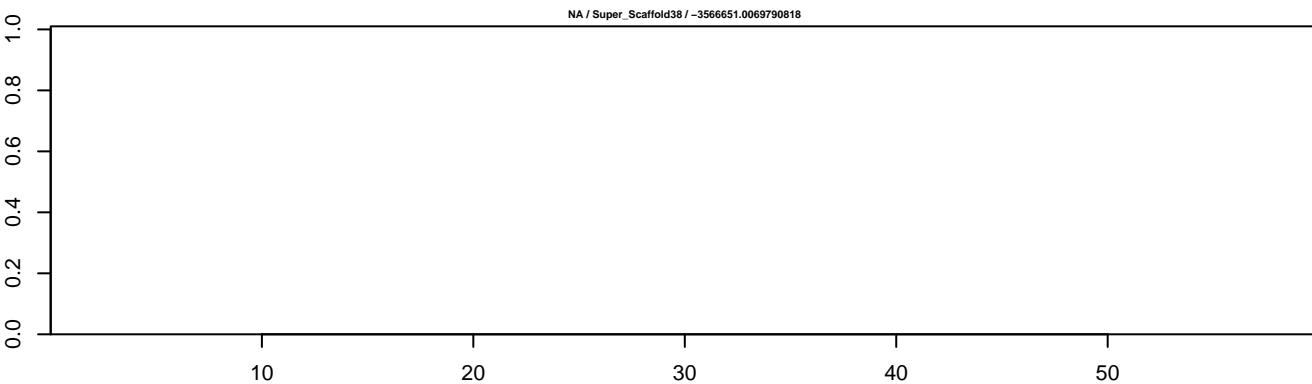
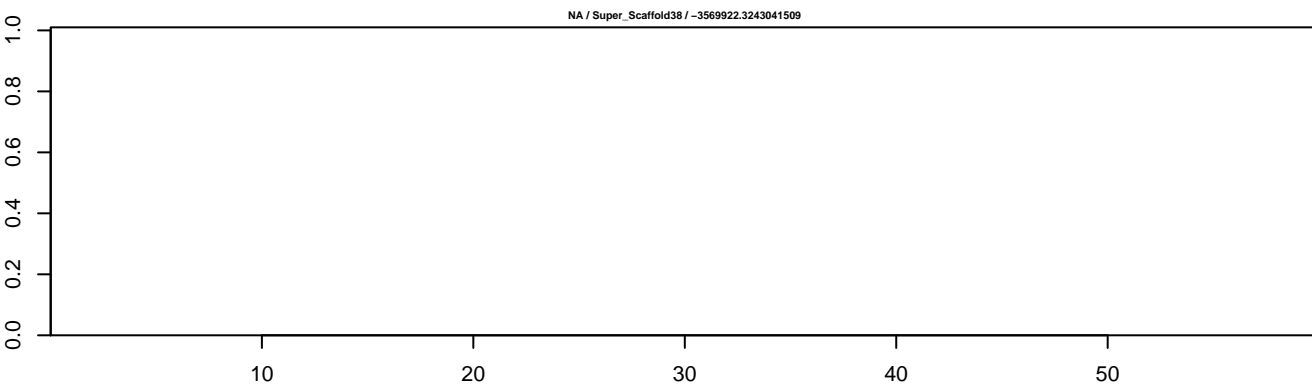
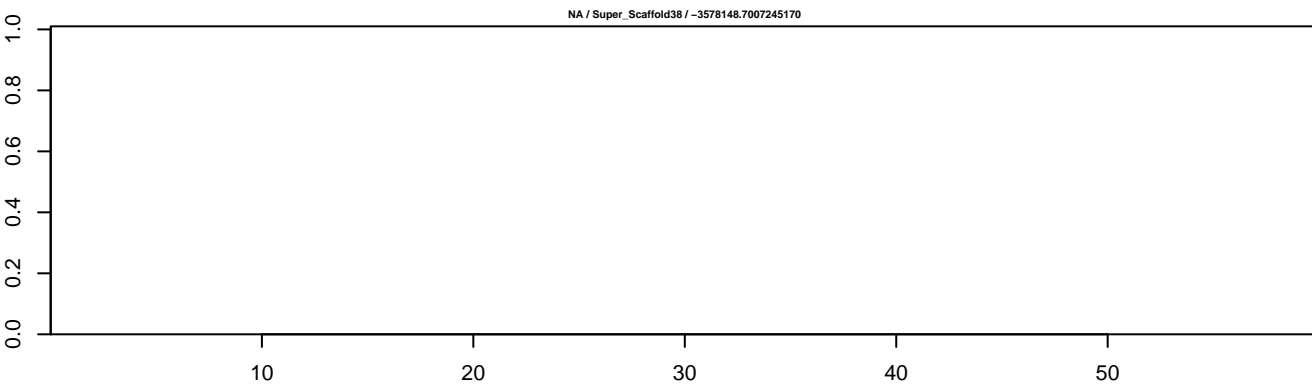
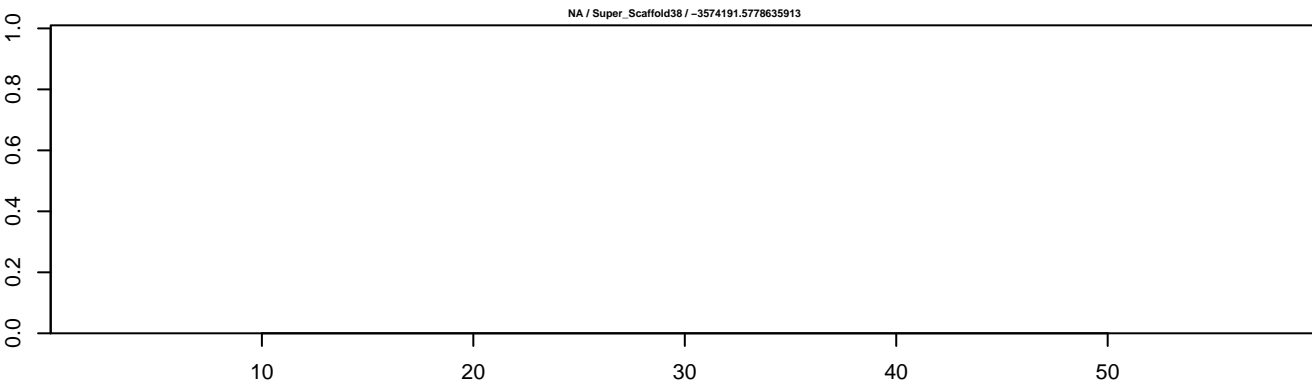
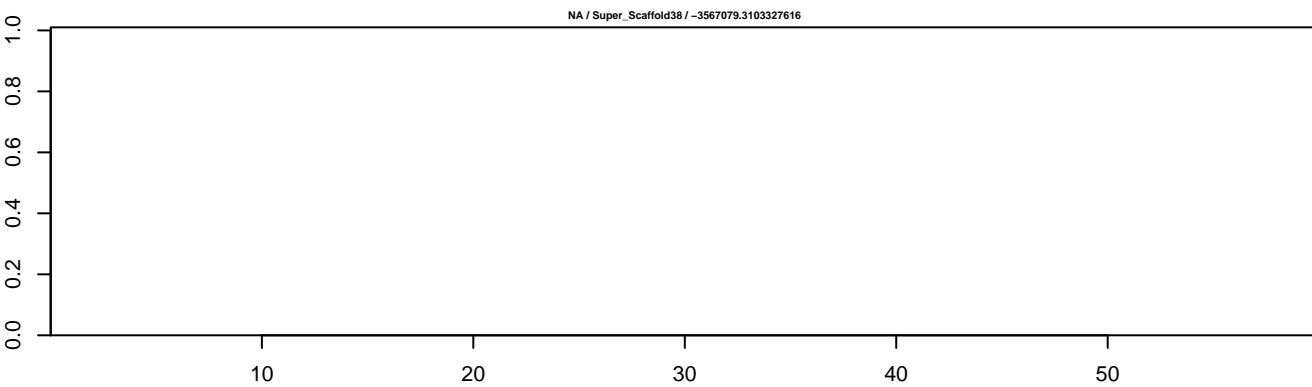
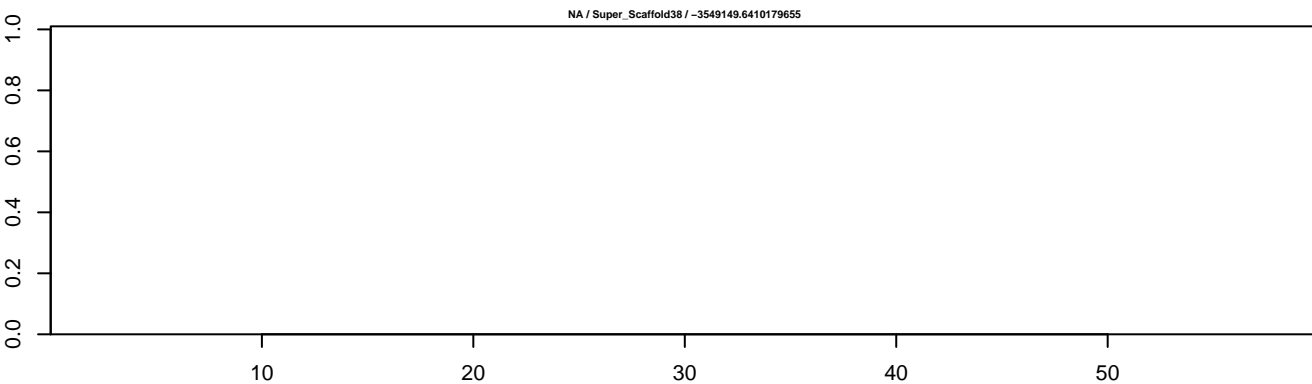
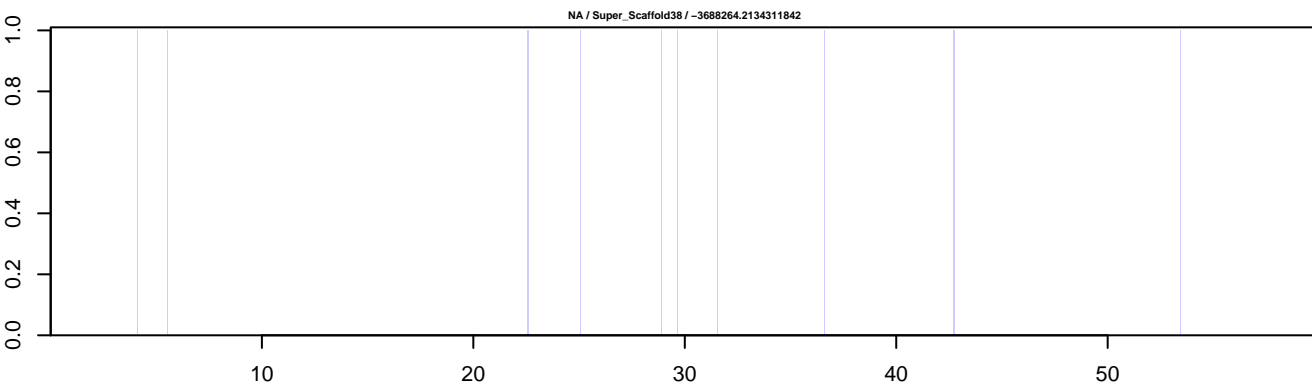
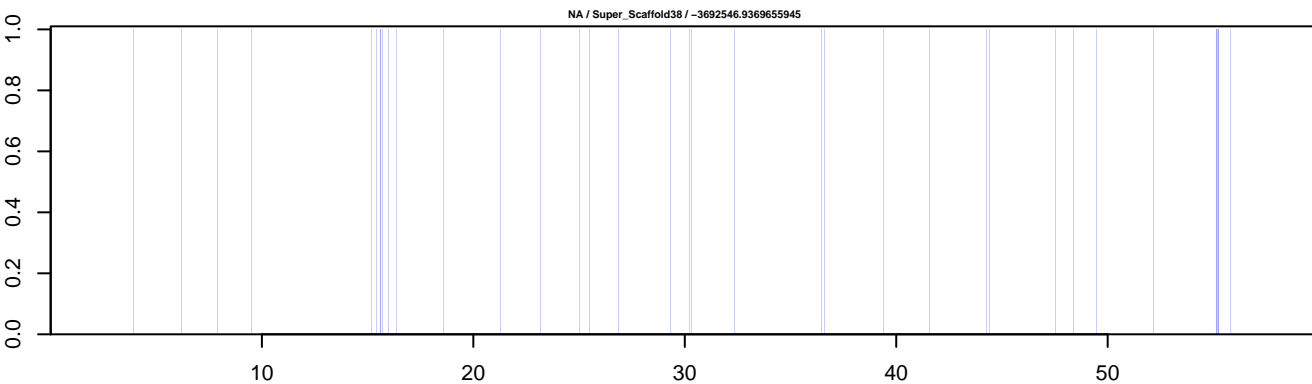
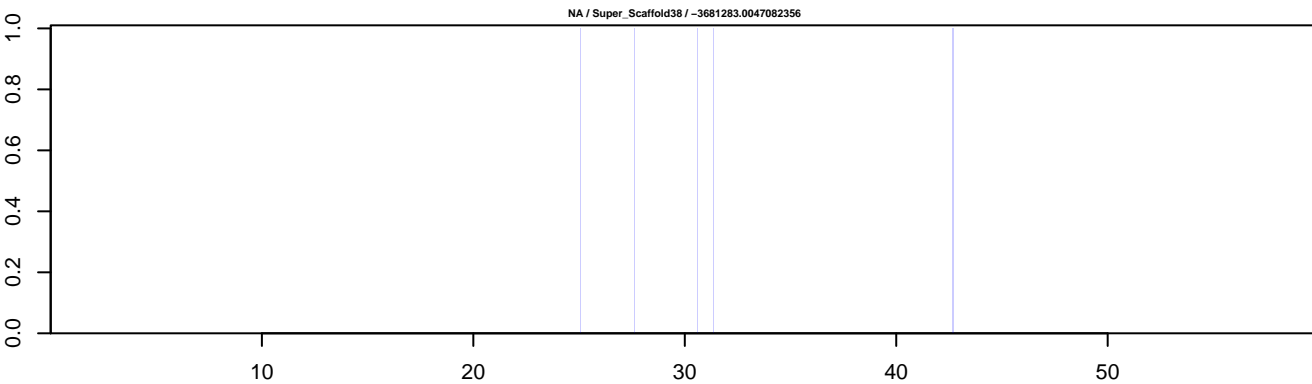


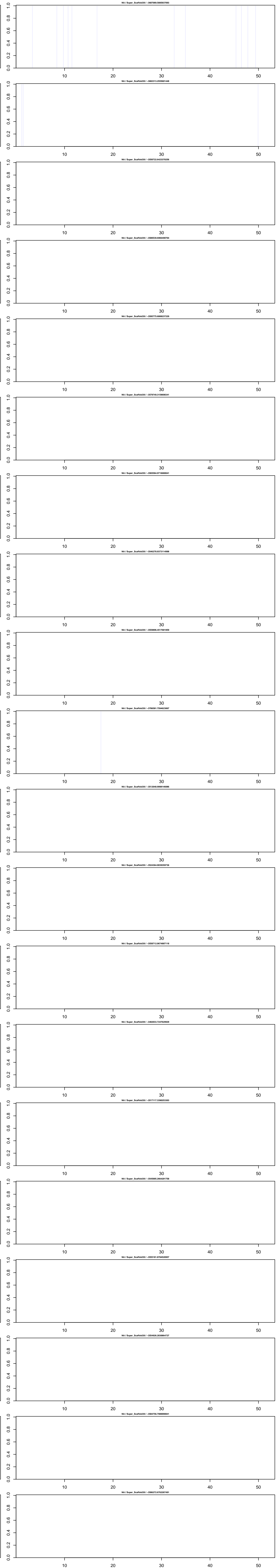
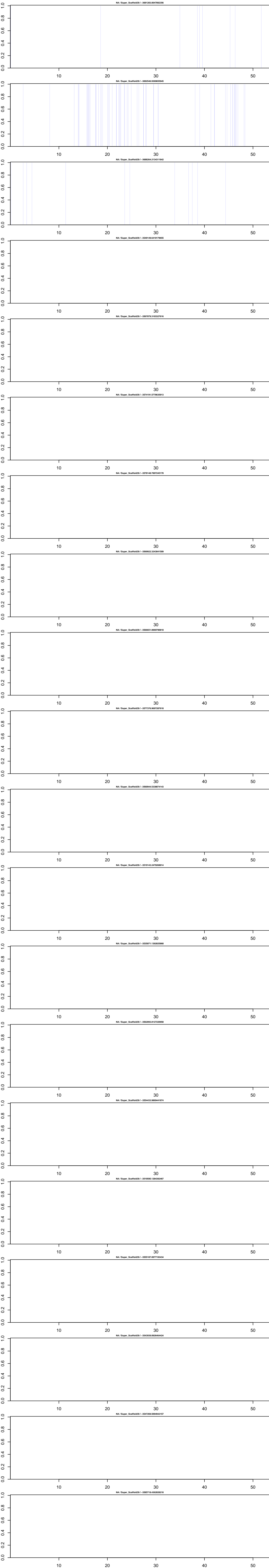


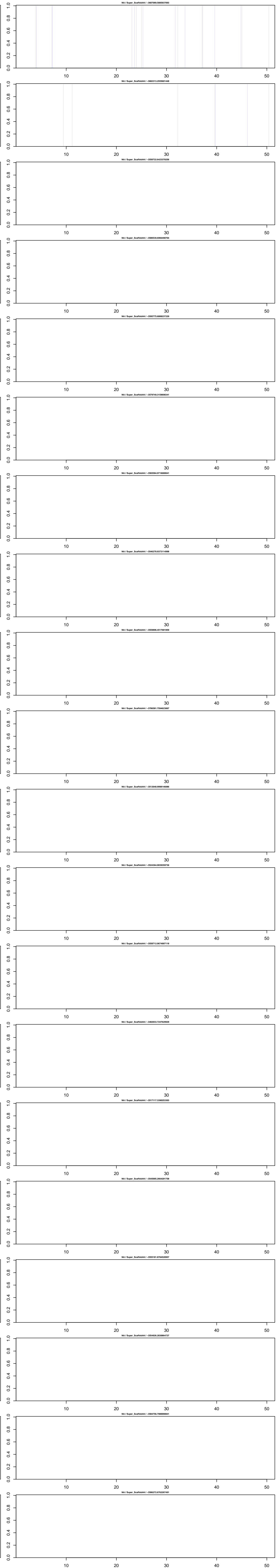
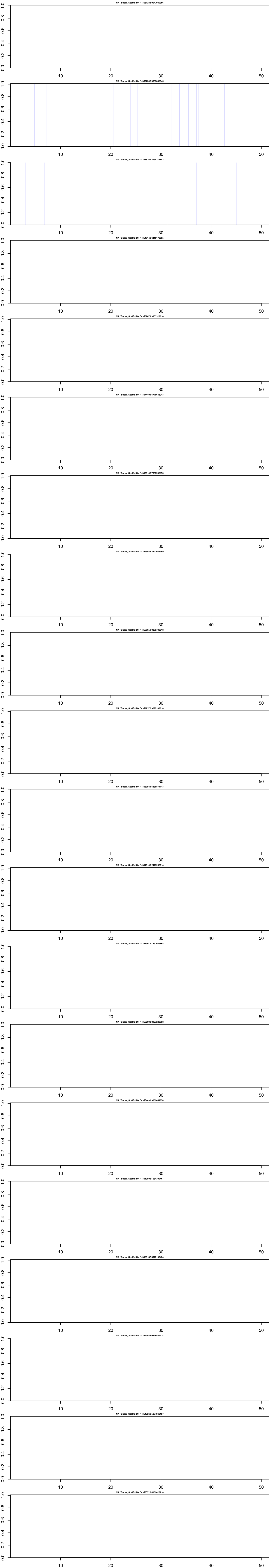


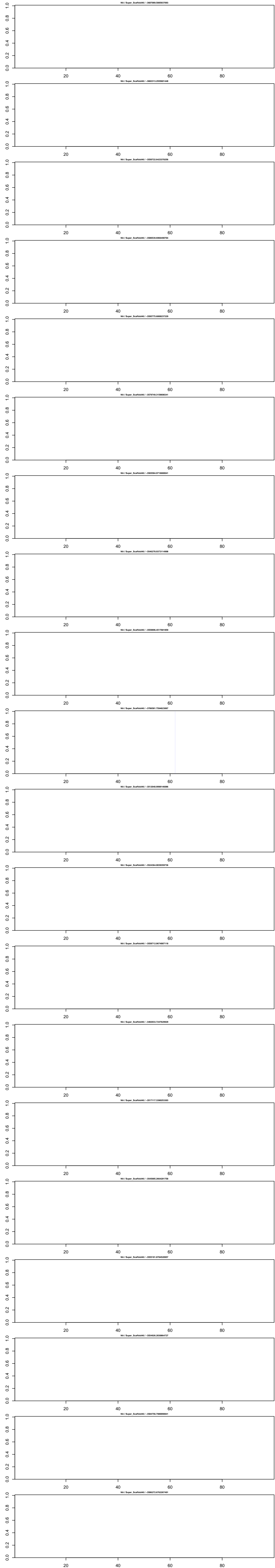
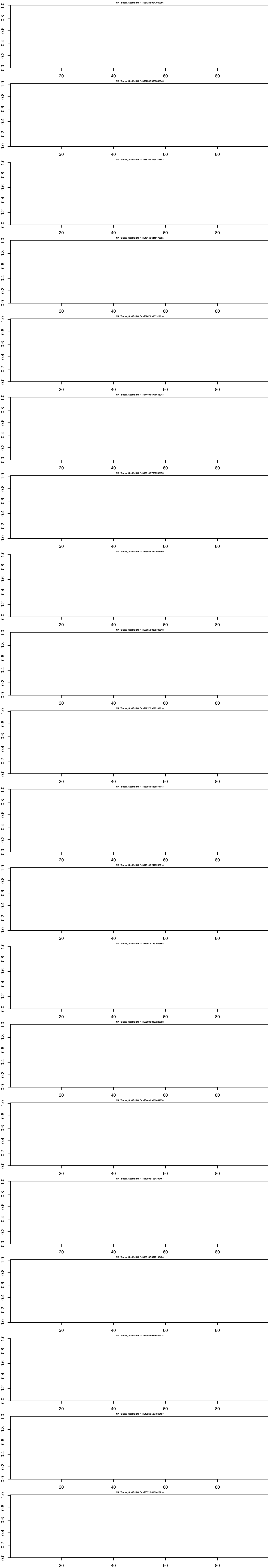


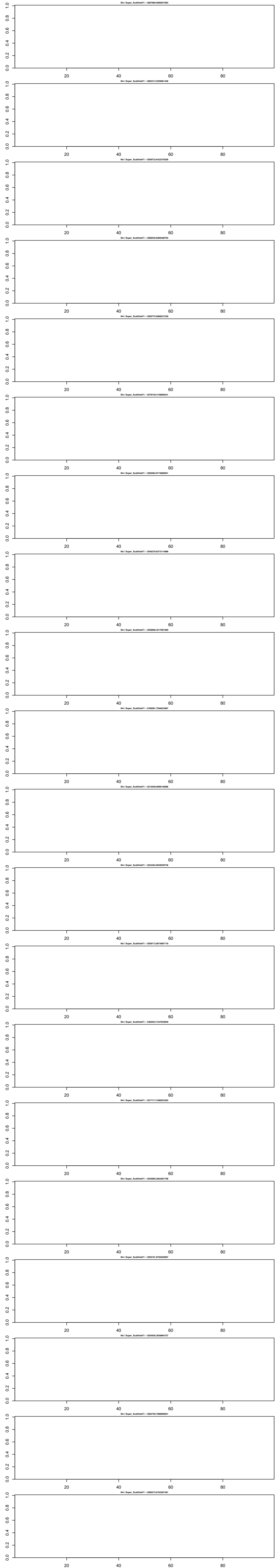
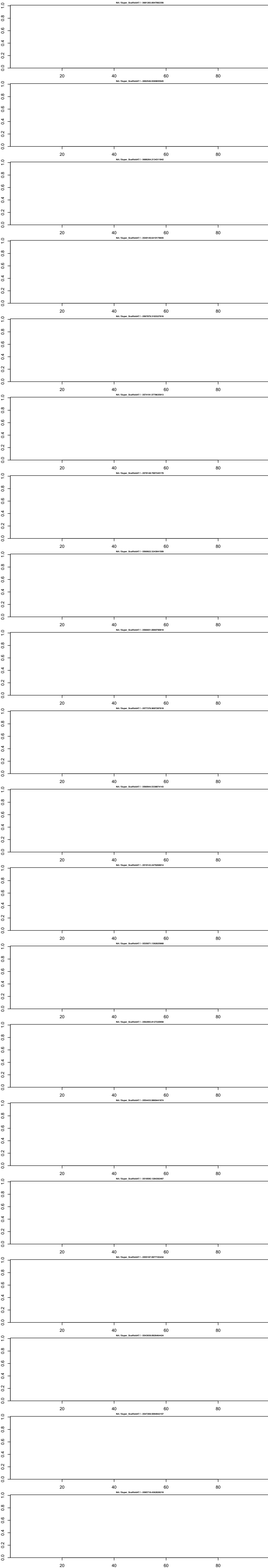


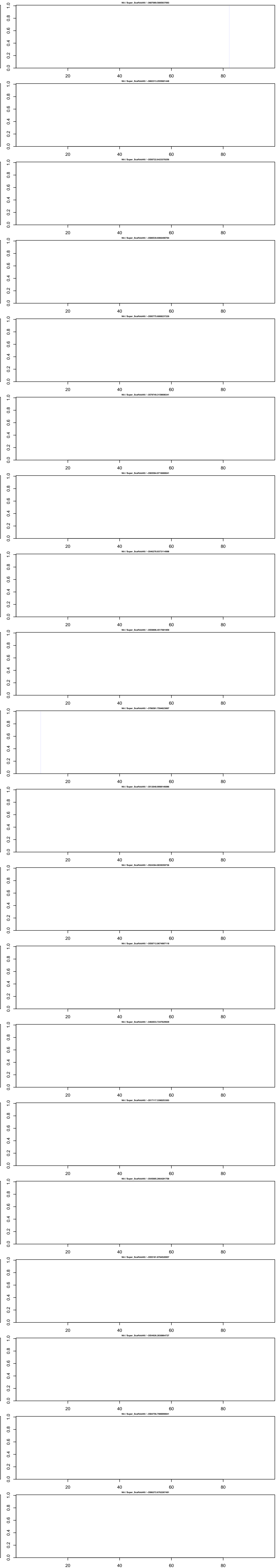
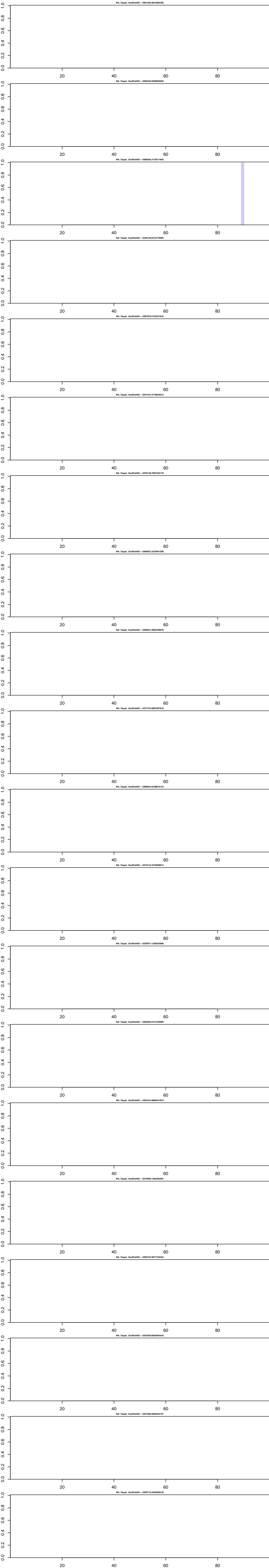


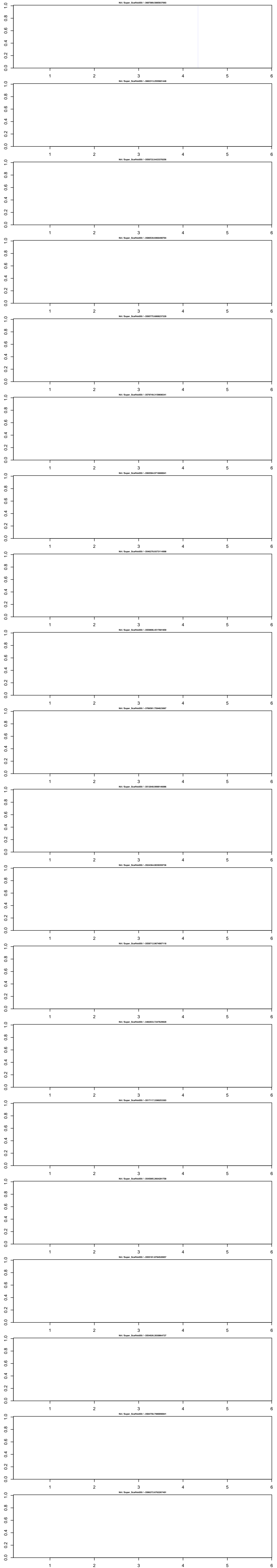
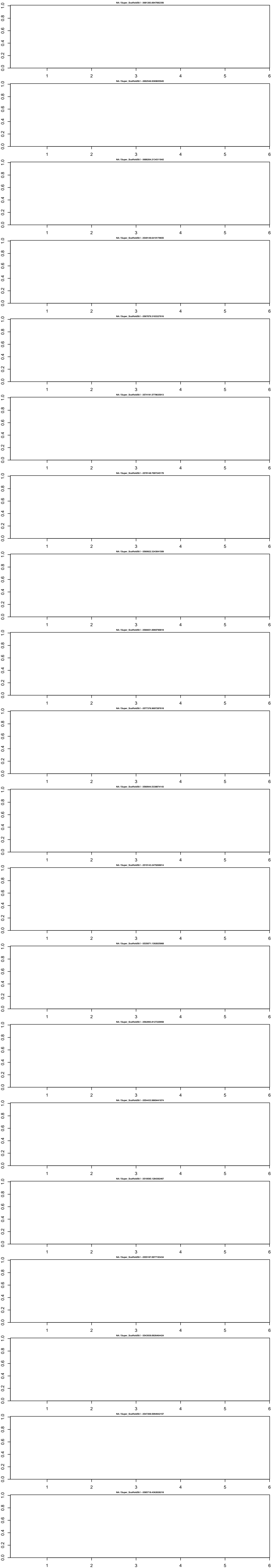




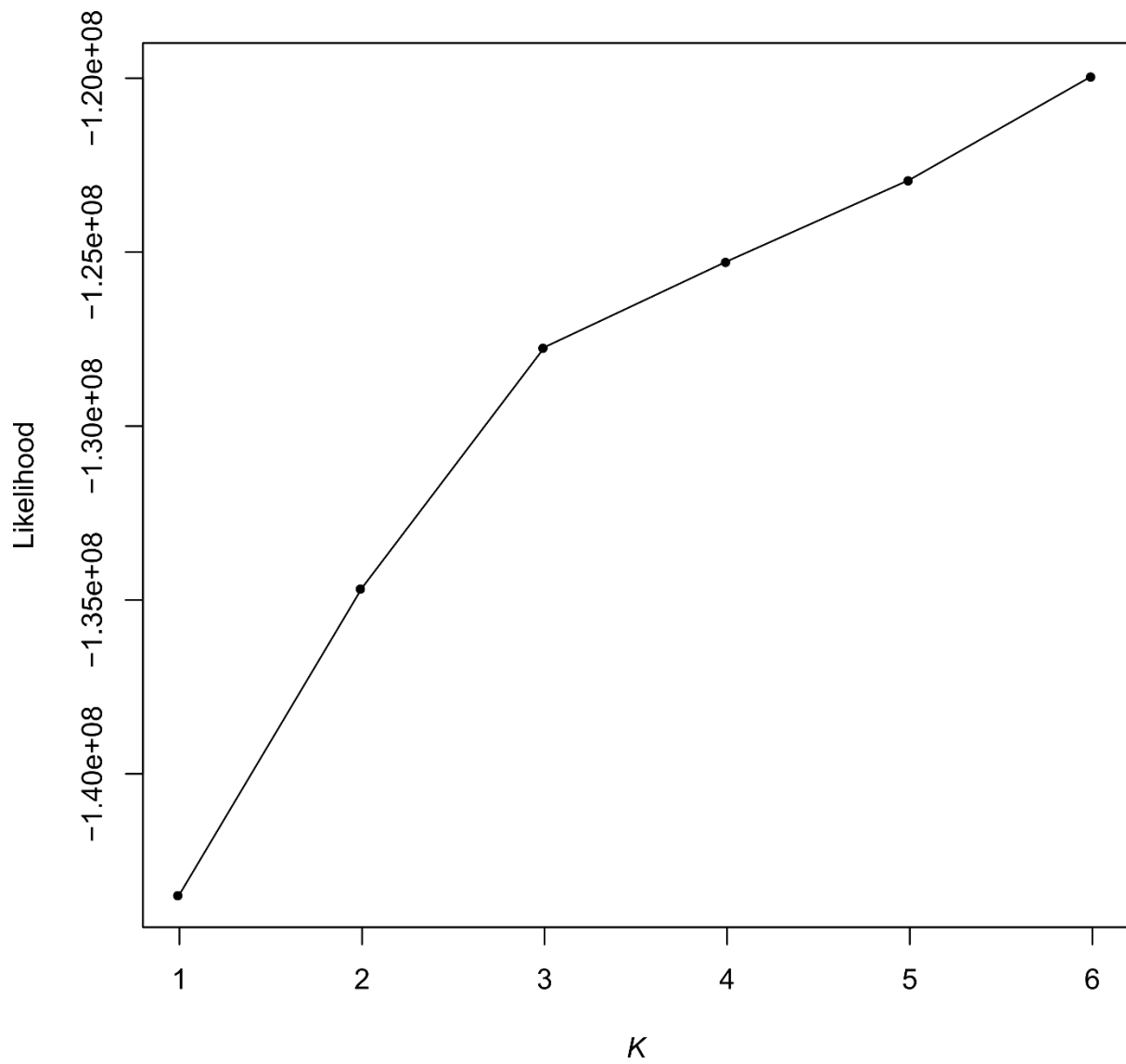




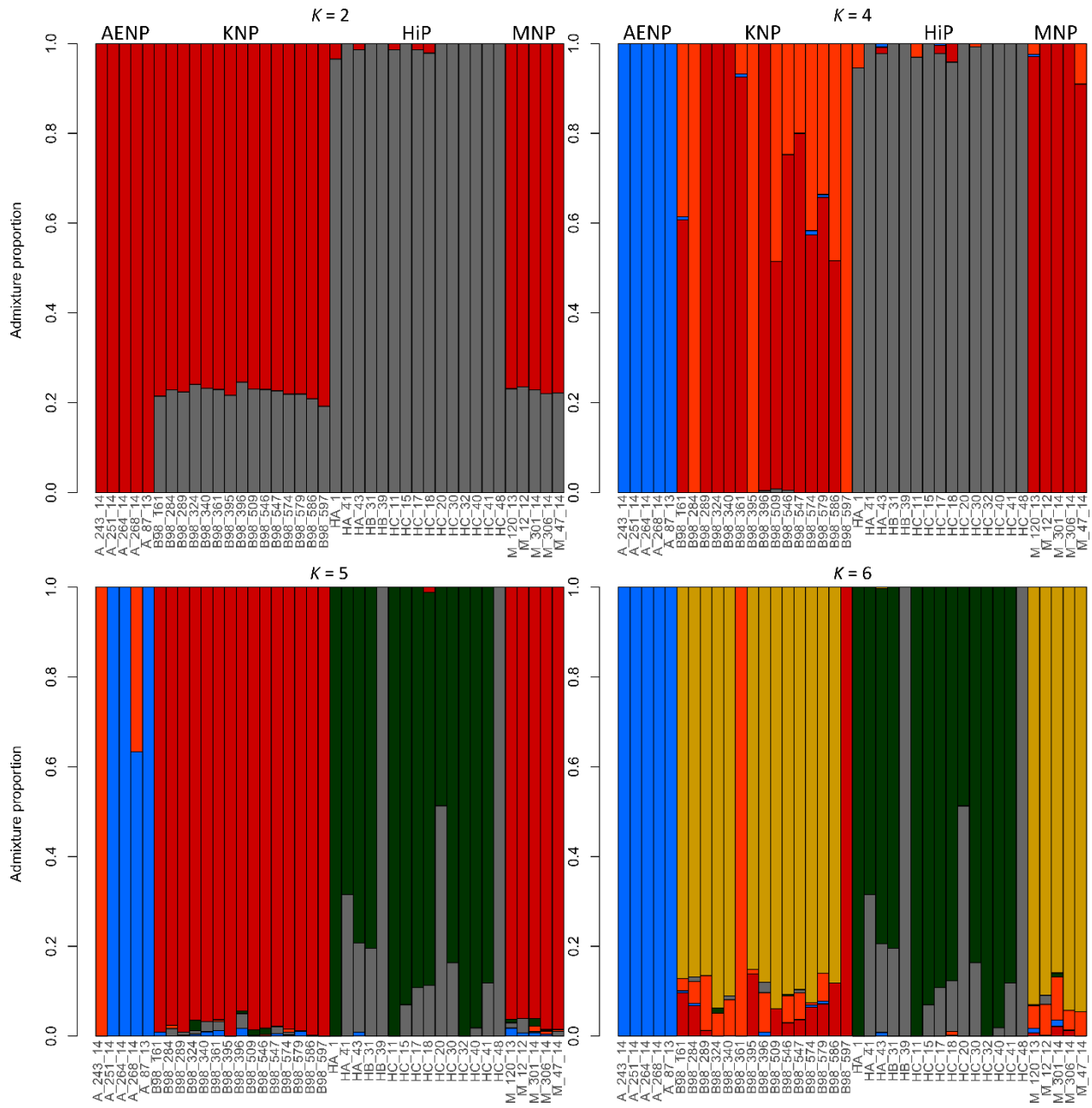




Supplementary Fig. 3. Inbreeding tracts, or identical by descent (IBD), plots. The plots were produced using the program ngsF-HMM for all super-scaffolds and all buffalo samples. The x-axis indicates the sites along the super-scaffold and the y-axis indicates whether the site was IBD (1) or not (0), as shown by the blue bars. Given the scale of the x-axis (~60 Mb), an extended IBD run is necessary in order for the blue bar to become visible.

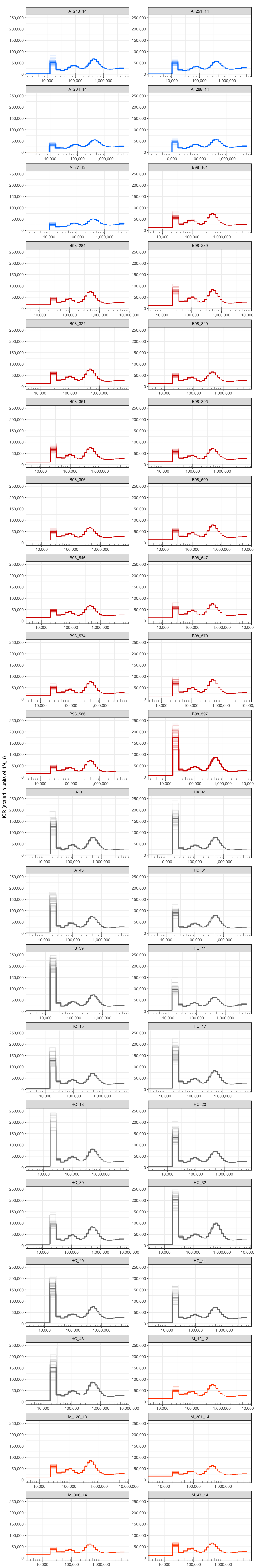


Supplementary Fig. 4. Best likelihood for $K = 1$ to $K = 6$ of the NGSadmixture analysis.

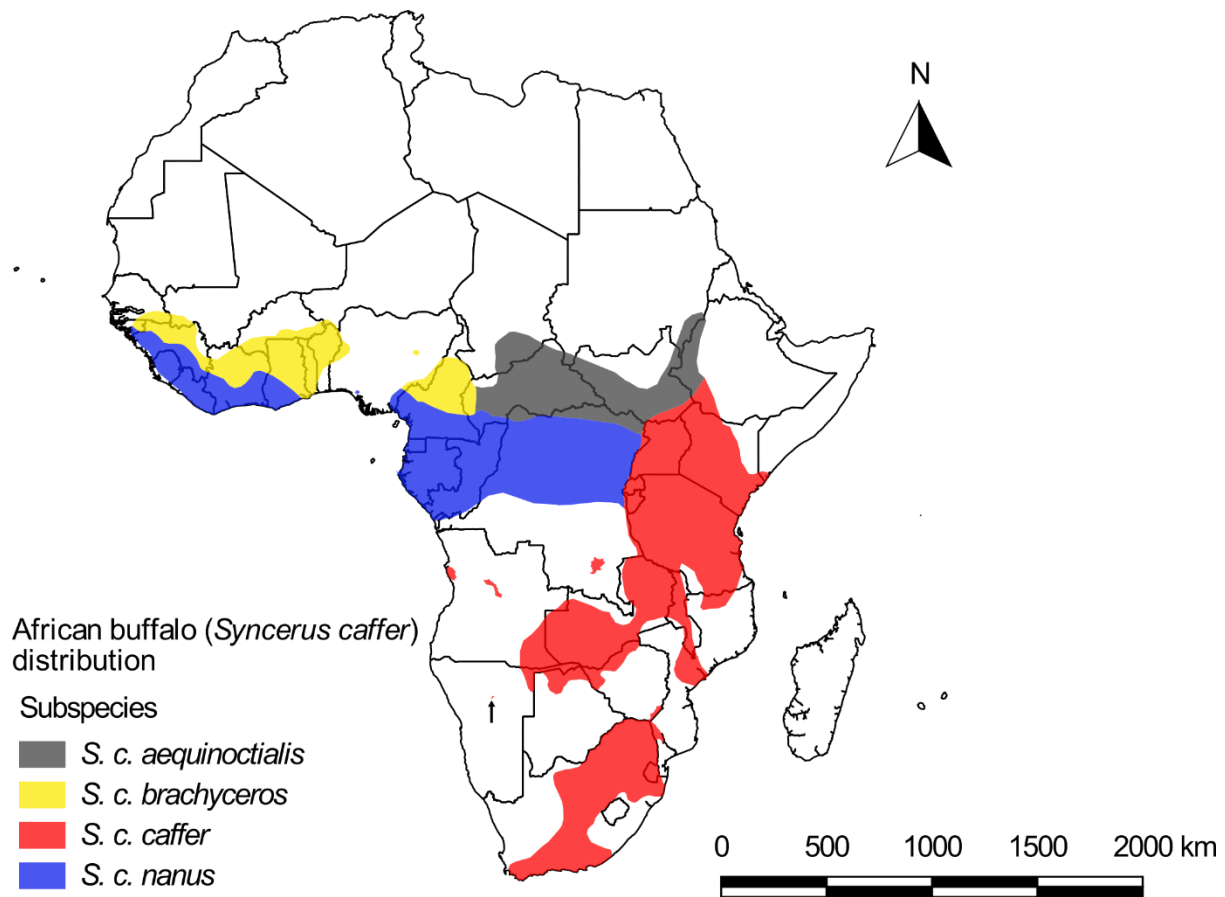


Supplementary Fig. 5. Individual assignment plots of the NGSadmixture analysis at $K = 2, 4, 5$ and 6 .

Population: — AENP — KNP — HIP — MNP



Supplementary Fig. 6. Pairwise sequentially Markovian coalescent (PSMC) inference of the inverse instantaneous coalescent rate (IICR) in each Cape buffalo sample, plotted by sampling locality. The x-axis represents time in years, calibrated using a generation time (g) of 7.5 years and a per site per generation mutation rate (μ) of $1.5e-8$. The y-axis shows IICR, which can be interpreted as N_e in an unstructured population. The faded lines show the 100 bootstrap replicates for each sample.



Supplementary Fig. 7. Distribution map of African buffalo (*Syncerus caffer*) subspecies. The arrow indicates an introduced population of Cape buffalo in Waterberg Plateau National Park, Namibia. Distribution data were obtained from the IUCN Red List database (<https://www.iucnredlist.org/species/21251/50195031>). The map was created in QGIS v3.4¹ (<https://www.qgis.org/en/site/>).

Supplementary Table 1. Summary of sequencing report from Novogene and individual NCBI accession numbers for BioProject PRJNA645266.

Sample	Sampling location	Raw data (Gb)	GC Content (%)	NCBI accession
A_243_14	Addo Elephant National Park	29.26	42.77	SAMN15501057
A_251_14	Addo Elephant National Park	27.4	42.91	SAMN15501058
A_264_14	Addo Elephant National Park	31	43.23	SAMN15501059
A_268_14	Addo Elephant National Park	28.44	43.13	SAMN15501060
A_87_13	Addo Elephant National Park	28.27	43.31	SAMN15501061
B98_161	Kruger National Park	29.72	42.17	SAMN15501062
B98_284	Kruger National Park	31.61	42.40	SAMN15501063
B98_289	Kruger National Park	33.23	42.09	SAMN15501064
B98_324	Kruger National Park	31.13	42.09	SAMN15501065
B98_340	Kruger National Park	28.94	41.82	SAMN15501066
B98_361	Kruger National Park	31.74	41.83	SAMN15501067
B98_395	Kruger National Park	32.97	41.62	SAMN15501068
B98_396	Kruger National Park	29.3	41.93	SAMN15501069
B98_509	Kruger National Park	34.36	41.65	SAMN15501070
B98_546	Kruger National Park	30.32	41.51	SAMN15501071
B98_547	Kruger National Park	31.25	41.68	SAMN15501072
B98_574	Kruger National Park	33.14	41.8	SAMN15501073
B98_579	Kruger National Park	31.57	43.14	SAMN15501074
B98_586	Kruger National Park	29.09	43.02	SAMN15501075
B98_597	Kruger National Park	32.4	42.33	SAMN15501076
HA_1	Hluhluwe-iMfolozi Park	31.1	42.82	SAMN15501077
HA_41	Hluhluwe-iMfolozi Park	30.91	42.86	SAMN15501078
HA_43	Hluhluwe-iMfolozi Park	29.33	42.77	SAMN15501079
HB_31	Hluhluwe-iMfolozi Park	31.88	42.61	SAMN15501080
HB_39	Hluhluwe-iMfolozi Park	29.32	42.57	SAMN15501081
HC_11	Hluhluwe-iMfolozi Park	28.15	42.56	SAMN15501082
HC_15	Hluhluwe-iMfolozi Park	29.52	42.37	SAMN15501083
HC_17	Hluhluwe-iMfolozi Park	30.6	42.67	SAMN15501084
HC_18	Hluhluwe-iMfolozi Park	30.99	42.09	SAMN15501085
HC_20	Hluhluwe-iMfolozi Park	28.56	42.11	SAMN15501086
HC_30	Hluhluwe-iMfolozi Park	31.86	42.47	SAMN15501087
HC_32	Hluhluwe-iMfolozi Park	36.5	42.96	SAMN15501088
HC_40	Hluhluwe-iMfolozi Park	29.78	42.74	SAMN15501089
HC_41	Hluhluwe-iMfolozi Park	31.23	42.15	SAMN15501090
HC_48	Hluhluwe-iMfolozi Park	32.5	42.52	SAMN15501091
M_120_13	Mokala National Park	32.64	42.00	SAMN15501092
M_12_12	Mokala National Park	30.8	42.23	SAMN15501093
M_301_14	Mokala National Park	27.51	42.89	SAMN15501094
M_306_14	Mokala National Park	26.93	42.84	SAMN15501095
M_47_14	Mokala National Park	26.67	42.69	SAMN15501096
Mean (SD)		30.55 (2.09)	42.43 (0.49)	

Supplementary Table 2. Number of sequences before and after read quality filtering and trimming. Each row represents one sequencing lane. Some samples were sequenced across multiple lanes or multiple sequencing machines and thus appear in multiple rows

Sample read pairs	#Raw paired sequences	#Paired sequences retained (%)	Forward only surviving (%)	Reverse only surviving (%)	#Sequences dropped (%)
A_243_14_DSW37619_HCT 32ALXX_L8	97 533 173	87 788 796 (90.01)	7 915 259 (8.12)	851 657 (0.87)	977 461 (1.00)
A_251_14_DSW37618_HCT 32ALXX_L7	91 325 771	82 363 634 (90.19)	7 180 128 (7.86)	835 079 (0.91)	946 930 (1.04)
A_264_14_DSW37616_HCT 32ALXX_L7	103 326 185	94 029 744 (91.00)	7 237 136 (7.00)	1 056 476 (1.02)	1 002 829 (0.97)
A_268_14_DSW37617_HCT 32ALXX_L7	94 791 680	82 081 893 (86.59)	10 807 890 (11.40)	673 365 (0.71)	1 228 532 (1.30)
A_87_13_DSW37615_HCT3 2ALXX_L7	94 233 009	84 333 051 (89.49)	8 020 895 (8.51)	832 411 (0.88)	1 046 652 (1.11)
B98_161_DSW37625_HJMJ MALXX_L2	48 942 673	45 009 136 (91.96)	3 166 596 (6.47)	338 485 (0.69)	428 456 (0.88)
B98_161_DSW37625_HJMJ MALXX_L3	50 107 493	46 911 732 (93.62)	2 559 724 (5.11)	319 490 (0.64)	316 547 (0.63)
B98_284_DSW37626_HJMJ MALXX_L2	50 869 584	46 844 232 (92.09)	3 246 197 (6.38)	348 159 (0.68)	430 996 (0.85)
B98_284_DSW37626_HJMJ MALXX_L3	54 509 792	51 143 499 (93.82)	2 692 956 (4.94)	343 118 (0.63)	330 219 (0.61)
B98_289_DSW37627_HJMJ MALXX_L2	53 090 353	49 389 067 (93.03)	2 926 266 (5.51)	376 481 (0.71)	398 539 (0.75)
B98_289_DSW37627_HJMJ MALXX_L3	57 678 152	54 415 043 (94.34)	2 557 446 (4.43)	381 722 (0.66)	323 941 (0.56)
B98_324_DSW37628_HJMJ MALXX_L2	49 603 030	45 577 523 (91.88)	3 305 833 (6.66)	314 237 (0.63)	405 437 (0.82)
B98_324_DSW37628_HJMJ MALXX_L3	54 175 329	50 695 077 (93.58)	2 820 210 (5.21)	327 054 (0.60)	332 988 (0.61)
B98_340_DSW37629_HJMJ MALXX_L1	48 219 143	45 193 442 (93.73)	2 536 668 (5.26)	230 810 (0.48)	258 223 (0.54)
B98_340_DSW37629_HJMJ MALXX_L4	48 253 442	45 055 218 (93.37)	2 604 881 (5.40)	291 167 (0.60)	302 176 (0.63)

Sample read pairs	#Raw paired sequences	#Paired sequences retained (%)	Forward only surviving (%)	Reverse only surviving (%)	#Sequences dropped (%)
B98_361_DSW37630_HJMJ MALXX_L1	50 884 775	47 864 456 (94.06)	2 518 558 (4.95)	238 121 (0.47)	263 640 (0.52)
B98_361_DSW37630_HJMJ MALXX_L4	54 904 545	51 453 130 (93.71)	2 793 255 (5.09)	335 926 (0.61)	322 234 (0.59)
B98_395_DSW37631_HJMJ MALXX_L1	55 533 629	52 792 974 (95.06)	2 228 778 (4.01)	264 591 (0.48)	247 286 (0.45)
B98_395_DSW37631_HJMJ MALXX_L4	54 352 594	51 541 305 (94.83)	2 201 629 (4.05)	337 271 (0.62)	272 389 (0.50)
B98_396_DSW37632_HJMJ MALXX_L1	46 512 118	43 832 604 (94.24)	2 224 207 (4.78)	218 861 (0.47)	236 446 (0.51)
B98_396_DSW37632_HJMJ MALXX_L4	51 159 167	48 069 745 (93.96)	2 478 159 (4.84)	316 909 (0.62)	294 354 (0.58)
B98_509_DSW37633_HJMJ MALXX_L1	59 669 150	56 481 893 (94.66)	2 625 253 (4.40)	279 387 (0.47)	282 617 (0.47)
B98_509_DSW37633_HJMJ MALXX_L4	54 877 165	51 845 358 (94.48)	2 405 529 (4.38)	335 310 (0.61)	290 968 (0.53)
B98_546_DSW37634_HJMJ MALXX_L1	48 766 165	46 123 916 (94.58)	2 175 626 (4.46)	228 207 (0.47)	238 416 (0.49)
B98_546_DSW37634_HJMJ MALXX_L4	52 286 079	49 281 350 (94.25)	2 393 054 (4.58)	321 829 (0.62)	289 846 (0.55)
B98_547_DSW37635_HJMJ MALXX_L3	52 097 331	48 991 406 (94.04)	2 453 293 (4.71)	349 813 (0.67)	302 819 (0.58)
B98_547_DSW37635_HJMJ MALXX_L4	52 064 264	49 195 161 (94.49)	2 271 495 (4.36)	323 927 (0.62)	273 681 (0.53)
B98_574_DSW37636_HJMJ MALXX_L3	56 336 753	53 029 657 (94.13)	2 591 456 (4.60)	386 063 (0.69)	329 577 (0.59)
B98_574_DSW37636_HJMJ MALXX_L4	54 144 293	51 112 158 (94.40)	2 383 110 (4.40)	351 552 (0.65)	297 473 (0.55)
B98_579_DSW37637_HG5K 3ALXX_L5	105 231 934	96 589 261 (91.79)	7 068 077 (6.72)	647 366 (0.62)	927 230 (0.88)
B98_586_DSW37638_HG5K 3ALXX_L5	96 969 332	89 640 909 (92.44)	5 875 744 (6.06)	638 136 (0.66)	814 543 (0.84)

Sample read pairs	#Raw paired sequences	#Paired sequences retained (%)	Forward only surviving (%)	Reverse only surviving (%)	#Sequences dropped (%)
B98_597_DSW37639_HG5K3ALXX_L5	107 991 879	101 215 035 (93.72)	5 232 495 (4.85)	744 545 (0.69)	799 804 (0.74)
HA_1_DSW37640_HG2LKA LXX_L1	103 658 620	96 376 518 (92.97)	5 598 608 (5.40)	806 454 (0.78)	877 040 (0.85)
HA_41_DSW37641_HG2LK ALXX_L1	103 033 897	96 258 628 (93.42)	5 175 531 (5.02)	774 810 (0.75)	824 928 (0.80)
HA_43_DSW37642_HG2LK ALXX_L4	97 771 592	90 406 297 (92.47)	5 602 794 (5.73)	839 587 (0.86)	922 914 (0.94)
HB_31_DSW37643_HG2LK ALXX_L4	106 264 773	97 379 753 (91.64)	6 926 439 (6.52)	877 442 (0.83)	1 081 139 (1.02)
HB_39_DSW37644_HG2LK ALXX_L4	97 747 948	88 975 121 (91.03)	6 992 484 (7.15)	732 297 (0.75)	1 048 046 (1.07)
HC_11_DSW37645_HG2LK ALXX_L5	93 834 066	89 053 854 (94.91)	3 545 228 (3.78)	635 837 (0.68)	599 147 (0.64)
HC_15_DSW37646_HG2LK ALXX_L5	98 409 683	92 351 308 (93.84)	4 757 265 (4.83)	586 152 (0.60)	714 958 (0.73)
HC_17_DSW37647_HG2LK ALXX_L7	101 996 967	94 310 754 (92.46)	5 876 710 (5.76)	867 914 (0.85)	941 589 (0.92)
HC_18_DSW37648_HG2LK ALXX_L7	103 294 056	94 595 060 (91.58)	6 799 725 (6.58)	855 991 (0.83)	1 043 280 (1.01)
HC_20_DSW37649_HG2LK ALXX_L7	95 208 985	87 894 702 (92.32)	5 678 820 (5.96)	781 698 (0.82)	853 765 (0.90)
HC_30_DSW37650_HG2LK ALXX_L8	73 421 834	66 575 994 (90.68)	5 500 040 (7.49)	525 306 (0.72)	820 494 (1.12)
HC_30_DSW37650_HGLY3 ALXX_L6	32 794 197	29 825 063 (90.95)	2 443 922 (7.45)	200 087 (0.61)	325 125 (0.99)
HC_32_DSW37651_HCT3H ALXX_L8	121 651 003	114 371 786 (94.02)	5 675 879 (4.67)	804 513 (0.66)	798 825 (0.66)
HC_40_DSW37652_HCT3H ALXX_L6	80 470 337	75 087 671 (93.31)	4 405 704 (5.47)	462 972 (0.58)	513 990 (0.64)
HC_40_DSW37652_HGLY3 ALXX_L6	18 797 213	17 035 796 (90.63)	1 462 655 (7.78)	116 155 (0.62)	182 607 (0.97)

Sample read pairs	#Raw paired sequences	#Paired sequences retained (%)	Forward only surviving (%)	Reverse only surviving (%)	#Sequences dropped (%)
HC_41_DSW37653_HJLV2 ALXX_L7	104 092 531	90 758 622 (87.19)	11 432 619 (10.98)	640 386 (0.62)	1 260 904 (1.21)
HC_48_DSW37654_HG2LK ALXX_L8	72 692 491	65 450 806 (90.04)	6 006 404 (8.26)	444 995 (0.61)	790 286 (1.09)
HC_48_DSW37654_HGLY3 ALXX_L6	35 649 538	32 142 444 (90.16)	2 949 865 (8.27)	198 022 (0.56)	359 207 (1.01)
M_120_13_DSW37623_HJM JMALXX_L2	52 526 467	48 071 690 (91.52)	3 613 215 (6.88)	355 607 (0.68)	485 955 (0.93)
M_120_13_DSW37623_HJM JMALXX_L3	56 272 060	52 609 116 (93.49)	2 953 811 (5.25)	347 986 (0.62)	361 147 (0.64)
M_12_12_DSW37624_HJMJ MALXX_L2	49 298 104	45 990 453 (93.29)	2 652 419 (5.38)	325 904 (0.66)	329 328 (0.67)
M_12_12_DSW37624_HJMJ MALXX_L3	53 382 105	50 377 468 (94.37)	2 366 625 (4.43)	344 059 (0.64)	293 953 (0.55)
M_301_14_DSW37621_HCT 32ALXX_L8	91 705 778	82 335 116 (89.78)	7 564 765 (8.25)	844 669 (0.92)	961 228 (1.05)
M_306_14_DSW37620_HCT 32ALXX_L8	89 764 545	81 003 388 (90.24)	7 126 699 (7.94)	782 212 (0.87)	852 246 (0.95)
M_47_14_DSW37622_HCT3 2ALXX_L8	88 910 066	80 321 009 (90.34)	6 914 488 (7.78)	799 374 (0.90)	875 195 (0.98)
Total	4 073 088 838	3 759 449 822 (92.30)	251 520 517 (6.18)	28 787 954 (0.71)	33 330 545 (0.82)

Supplementary Table 3. Summary of genome coverage before and after duplicates were marked (DM). Statistics generated via the CollectWgsMetrics tool in Picard.

Sample	Genome territory	Mean coverage	SD coverage	Exc dup (%)
A_243_14	2612863443	7.72	5.75	0
A_243_14_DM	2612863443	6.86	5.24	10.84
A_251_14	2612863443	7.20	5.72	0
A_251_14_DM	2612863443	6.42	5.23	10.50
A_264_14	2612863443	7.89	5.94	0
A_264_14_DM	2612863443	6.93	5.34	11.67
A_268_14	2612863443	7.02	5.33	0
A_268_14_DM	2612863443	6.30	4.87	9.83
A_87_13	2612863443	7.22	5.50	0
A_87_13_DM	2612863443	6.43	5.00	10.64
B98_161	2612863443	8.54	6.10	0
B98_161_DM*	2612863443	6.97	5.13	17.55
B98_284	2612863443	8.96	6.40	0
B98_284_DM*	2612863443	7.28	5.41	17.95
B98_289	2612863443	9.44	6.57	0
B98_289_DM*	2612863443	7.51	5.41	19.52
B98_324	2612863443	8.82	6.22	0
B98_324_DM*	2612863443	7.08	5.16	18.79
B98_340	2612863443	8.34	6.13	0
B98_340_DM*	2612863443	6.39	4.89	22.08
B98_361	2612863443	9.18	6.60	0
B98_361_DM*	2612863443	6.93	5.21	23.12
B98_395	2612863443	9.47	6.84	0
B98_395_DM*	2612863443	7.11	5.41	23.54
B98_396	2612863443	8.49	6.20	0
B98_396_DM*	2612863443	6.50	4.92	22.16
B98_509	2612863443	10.09	6.91	0
B98_509_DM*	2612863443	7.46	5.31	24.55
B98_546	2612863443	8.92	6.52	0
B98_546_DM*	2612863443	6.77	5.17	22.72
B98_547	2612863443	9.11	6.58	0
B98_547_DM*	2612863443	7.05	5.30	21.41
B98_574	2612863443	9.54	6.88	0
B98_574_DM*	2612863443	7.34	5.60	21.69
B98_579	2612863443	8.66	5.94	0
B98_579_DM	2612863443	7.71	5.39	10.88
B98_586	2612863443	8.06	5.68	0
B98_586_DM	2612863443	7.16	5.14	11.10
B98_597	2612863443	9.13	6.38	0
B98_597_DM	2612863443	8.07	5.78	11.35
HA_1	2612863443	8.56	6.12	0
HA_1_DM	2612863443	7.49	5.50	12.30

Sample	Genome territory	Mean coverage	SD coverage	Exc dup (%)
HA_41	2612863443	8.61	6.03	0
HA_41_DM	2612863443	7.51	5.39	12.46
HA_43	2612863443	7.97	5.84	0
HA_43_DM	2612863443	6.95	5.22	12.46
HB_31	2612863443	8.68	6.16	0
HB_31_DM	2612863443	7.57	5.51	12.35
HB_39	2612863443	7.91	5.82	0
HB_39_DM	2612863443	6.84	5.16	13.02
HC_11	2612863443	7.77	5.90	0
HC_11_DM	2612863443	6.39	5.03	17.05
HC_15	2612863443	8.20	6.15	0
HC_15_DM	2612863443	6.76	5.23	16.94
HC_17	2612863443	8.45	6.11	0
HC_17_DM	2612863443	7.55	5.59	10.61
HC_18	2612863443	8.52	6.20	0
HC_18_DM	2612863443	7.59	5.67	10.62
HC_20	2612863443	7.92	5.66	0
HC_20_DM	2612863443	7.10	5.15	10.14
HC_30	2612863443	8.78	6.04	0
HC_30_DM‡	2612863443	7.87	5.51	10.15
HC_32	2612863443	10.32	6.58	0
HC_32_DM	2612863443	9.06	5.89	12.00
HC_40	2612863443	8.35	6.13	0
HC_40_DM‡	2612863443	7.37	5.58	11.55
HC_41	2612863443	8.11	5.80	0
HC_41_DM	2612863443	7.25	5.28	10.23
HC_48	2612863443	8.85	6.27	0
HC_48_DM‡	2612863443	7.90	5.73	10.62
M_120_13	2612863443	9.35	6.61	0
M_120_13_DM*	2612863443	7.65	5.64	17.35
M_12_12	2612863443	8.84	6.47	0
M_12_12_DM*	2612863443	7.14	5.45	18.31
M_301_14	2612863443	7.29	5.48	0
M_301_14_DM	2612863443	6.50	5.00	10.61
M_306_14	2612863443	7.17	5.24	0
M_306_14_DM	2612863443	6.37	4.74	10.91
M_47_14	2612863443	7.16	5.41	0
M_47_14_DM	2612863443	6.40	4.93	10.40
Mean coverage before DM		8.47	6.11	
Mean coverage after DM		7.14	5.30	
Mean read duplicates (Exc Dup)				14.80

Genome territory: The number of non-N bases in the genome reference over which coverage was evaluated.

Mean coverage: The mean coverage in bases of the genome territory, after all filters were applied.
SD coverage: The standard deviation of coverage of the genome after all filters were applied.
Exc dup: The fraction of aligned bases that were filtered out because they were in reads marked as duplicates.

*Samples sequenced across two lanes of the same sequencing instrument.

‡Samples sequenced across two lanes, but on different sequencing instruments.

Supplementary Table 4. Alignment and coverage statistics per sampling locality.
Statistics generated using the AlignmentSummaryMetrics tool from Picard.

Sampling locality	Proportion reads aligned (SD)	Proportion HQ (Q20) reads aligned (SD)	Strand balance (SD)	Mean genome-wide coverage (mean SD)
AENP	0.994 (0.003)	0.909 (0.009)	0.50 (2.42652E-05)	6.59 (5.14)
KNP	0.997 (0.002)	0.921 (0.001)	0.50 (2.15592E-05)	7.15 (5.28)
HiP	0.997 (0.001)	0.919 (0.001)	0.50 (2.94245E-05)	7.41 (5.43)
MNP	0.998 (0.000)	0.919 (0.001)	0.50 (1.29306E-05)	6.81 (5.15)

Supplementary Table 5. Summary of variant metrics before and after filtering.

Data set	No. of SNPs	No. of INDELS	No. of multi-allelic SNPs	No. of singleton SNPs	Ti/Tv
Raw	49 139 319	6 265 707	1 030 363	8 153 097	1.90
Filtered	3 804 535	0	0	0	2.02

Supplementary Table 6. Individual genome-wide diversity indices.

Population	Sample	Heterozygosity (-GL 1)	Heterozygosity (-GL 2)	Inbreeding (<i>F</i>)
AENP	A_243_14	0.002291319	0.002774089	0.208155
	A_251_14	0.002178632	0.002688611	0.234317
	A_264_14	0.002102339	0.002626992	0.253398
	A_268_14	0.002283693	0.002855078	0.211124
	A_87_13	0.002224362	0.002762455	0.226621
KNP	B98_161	0.003295901	0.003789785	0.00004
	B98_284	0.003319184	0.003798951	0.000041
	B98_289	0.00324981	0.00370111	0.005002
	B98_324	0.003288107	0.003781846	0.000603
	B98_340	0.003206546	0.003751618	0.00647
	B98_361	0.003254793	0.003767767	0.000751
	B98_395	0.003217838	0.003696175	0.000555
	B98_396	0.003295896	0.003854604	0.000481
	B98_509	0.003232477	0.003699292	0.000602
	B98_546	0.003287116	0.00383712	0.000326
	B98_547	0.003356302	0.003903237	0.000046
	B98_574	0.003258123	0.003768387	0.000656
	B98_579	0.003338104	0.003879897	0.000327
	B98_586	0.003332227	0.003935346	0.00096
	B98_597	0.002687849	0.003145051	0.160587
HiP	HA_1	0.002633009	0.003085595	0.031488
	HA_41	0.002631377	0.003090141	0.005352
	HA_43	0.002670355	0.003093391	0.000698
	HB_31	0.00260152	0.002983572	0.01113
	HB_39	0.002484253	0.002918803	0.021197
	HC_11	0.002562633	0.003027731	0.029111
	HC_15	0.002554905	0.003004638	0.036178
	HC_17	0.002731626	0.003112482	0.000111
	HC_18	0.002600692	0.002980888	0.028988
	HC_20	0.002532242	0.002944969	0.008515
	HC_30	0.002710954	0.003079401	0.004374
	HC_32	0.002645481	0.002972926	0.036162
	HC_40	0.002543342	0.002993296	0.04519
	HC_41	0.002571964	0.003034663	0.038699
HC_48	0.002614778	0.002964487	0.025802	
MNP	M_120_13	0.003290583	0.003740989	0.000249
	M_12_12	0.003316097	0.00381499	0.000054
	M_301_14	0.003301199	0.0039377	0.002379
	M_306_14	0.00324949	0.003881643	0.003451
	M_47_14	0.003252709	0.003900671	0.002519

Supplementary Table 7. Genome-wide heterozygosity of buffalo populations and other mammal species included in Fig. 2c.

Species	Common name	Heterozygosity	Min_Het	Max_Het	Census*	IUCNstatus**	Reference
<i>Syncerus caffer caffer</i>	MNP (Cape buffalo)	0.003282016	0.00324949	0.003316097	400	NT	This study
<i>Syncerus caffer caffer</i>	KNP (Cape buffalo)	0.003241352	0.002687849	0.003356302	40,900	NT	This study
<i>Syncerus caffer caffer</i>	Cape buffalo	0.002880451	0.002102339	0.003356302	331,017	NT	This study
<i>Syncerus caffer caffer</i>	HiP (Cape buffalo)	0.002605942	0.002484253	0.002731626	4,000	NT	This study
<i>Ursus arctos</i>	Brown bear	0.0025	NA	NA	110,000	LC	Hailer et al. ²
<i>Syncerus caffer caffer</i>	AENP (Cape buffalo)	0.002216069	0.002102339	0.002291319	800	NT	This study
<i>Gorilla gorilla</i>	Western gorilla	0.0019	NA	NA	316,000	CR	Xue et al. ³
<i>Papio cynocephalus</i>	Yellow baboon	0.00168	NA	NA	1 [§]	LC	Westbury et al. ⁴
<i>Canis lupus</i>	Grey wolf	0.00144	0.000459252	0.002176767	300,000	LC	Fan et al. ⁵
<i>Tursiops truncatus</i>	Common bottlenose dolphin	0.00142	NA	NA	750,000	LC	Yim et al. ⁶
<i>Ailuropoda melanoleuca</i>	Giant panda	0.00135	NA	NA	750	VU	Li et al. ⁷
<i>Pongo abelii</i>	Sumatran orangutan	0.0012	NA	NA	13,846	CR	Cho et al. ⁸
<i>Panthera leo</i>	Lion	0.0012	NA	NA	31,000	VU	Armstrong et al. ⁹
<i>Pan troglodytes</i>	Chimpanzee	0.00117	0.0008	0.00176	236,200	EN	Waterson et al. ¹⁰
<i>Oryx dammah</i>	Scimitar-horned oryx	0.00097	0.00076	0.0011	15,000	EW	Humble et al. ¹¹
<i>Puma concolor</i>	Puma	0.000848	0.00033	0.00166	10,000	LC	Saremi et al. ¹²
<i>Pan paniscus</i>	Bonobo	0.0008	0.00065	0.00095	17,500	EN	Prado-Martinez et al. ¹³
<i>Homo sapiens</i>	Human (African)	0.000791	NA	NA	NA	NA	Westbury et al. ⁴
<i>Pongo pygmaeus</i>	Bornean orangutan	0.00065	NA	NA	104,700	CR	Cho et al. ⁸
<i>Gorilla beringei</i>	Eastern gorilla	0.00065	NA	NA	2,600	CR	Xue et al. ³
<i>Balaenoptera acutorostrata</i>	Minke whale	0.00061	NA	NA	200,000	LC	Yim et al. ⁶
<i>Panthera tigris altaica</i>	Siberian tiger	0.00061	0.00049	0.00073	360	EN	Cho et al. ⁸
<i>Homo sapiens</i>	Human (European)	0.000595	NA	NA	NA	NA	Westbury et al. ⁴

Species	Common name	Heterozygosity	Min_Het	Max_Het	Census*	IUCNstatus**	Reference
<i>Lynx lynx</i>	Eurasian lynx	0.0004	NA	NA	8,000	LC	Abascal et al. ¹⁴
<i>Ursus maritimus</i>	Polar bear	0.00032	NA	NA	26,000	VU	Westbury et al. ⁴
<i>Sarcophilus harrisi</i>	Tasmanian devil	0.00032	NA	NA	17,500	EN	Palkopoulou et al. ¹⁵
<i>Gulo gulo</i>	Wolverine	0.00028	0.00024	0.00032	580	LC	Ekblom et al. ¹⁶
<i>Panthera uncia</i>	Snow leopard	0.00023	NA	NA	3,048	EN	Cho et al. ⁸
<i>Lynx pardinus</i>	Iberian lynx	0.00022	0.00012	0.00022	156	EN	Abascal et al. ¹⁴
<i>Orcinus orca</i>	Orca	0.000214	NA	NA	50,000	DD	Westbury et al. ⁴
<i>Acinonyx jubatus</i>	Cheetah	0.0002	0.00019	0.00021	6,674	VU	Dobrynin et al. ¹⁷
<i>Urocyon littoralis</i>	Island fox	0.000125	0.0000142	0.000408	4,001	NT	Robinson et al. ¹⁸
<i>Lipotes vexillifer</i>	Baiji (dolphin)	0.000121	NA	NA	10	CR	Zhou et al. ¹⁹
<i>Hyaena brunnea</i>	Brown hyena	0.000121	NA	NA	7,238	NT	Westbury et al. ⁴

*Census size refers to mature individuals, if available (otherwise entire population size), as listed on the IUCN Red List website, accessed on 03/08/2020. Census size of individual populations are given for the Cape buffalo populations in this study and for the wolverine population from which the samples to calculate genome-wide heterozygosity originated.

**IUCN status is for entire distribution of species (as on 03/08/2020), not for local populations (thus the discrepancy between the status for wolverine here and in Ekblom et al.¹⁶).

§No census size for yellow baboon is available, thus a census of 1 was allocated, so it could still be included in Fig. 2c.

Cape buffalo mature individuals census size calculated as follows: Census size = 473,000*0.699 (the percentage of mature individuals- ratio as per the IUCN Red List calculation for Cape buffalo).

Scimitar-horned oryx census size obtained from Humble et al.¹¹.

Grey wolf census size obtained from Mech and Boitani²⁰.

Homo sapiens was not included in Fig. 2c.

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