Table S1. The tissues harvested into MID pools from *F.* ×*ananassa*.

Medley	A mixture of minor tissues presented in Table S2.
Leaf	Fully-expanded leaf blades without petiolules.
Petiole	Expanding and fully-expanded petioles, including petiolules.
Crown	The entire crown with roots and petioles excised as closely as possible.
Root	Complete roots from soil-grown plants, as well as root primordia from unrooted daughter plants and emerging roots from daughter plants placed onto moist media.
Fruit	Twelve stages of fruit development, from post-pollination to overripe were identified by level of expansion and color. Fruit RNA was harvested separately and then equal amounts were used in cDNA synthesis.
Flower	All stages of floral development, from earliest recognizable bud to flowers with abscising petals.
Stolon	All stages of stolons (expanding and fully expanded) with runner tips and inter-stolon removed.
Runner tip	The terminus of the stolon, from young emerging stolon to initiating daughter plant.

Table S2. Plant materials in 'Medley' pool

Dry achenes	Achenes were picked from ripe strawberry fruits and allowed to dry, then were stored at 4°C for at least 30 days.
Imbibed achenes	The aforementioned achenes were surface sterilized with 20% bleach for 30 min and rinsed with sterile water. The seeds were placed in sterile water on a shaker at room temperature for one week.
Fruit-resident achenes	Achenes were removed from fruits of all developmental stages and immediately ground.
Dormant buds	Axial buds were dissected from crowns by removing petioles to expose them, followed by immediate grinding.
Root tips	The terminal 2 mm of each root tip, both primary and lateral roots, were excised with a razor blade.
Apical buds	The entire apical region, comprising newly emerging leaves and meristem tissues was harvested from each crown, approximately the terminal 0.5 cm.
Vascular tissues	Individual leaf veins of all diameters were dissected from leaves of various levels of development.
Etiolated seedlings	Seeds were surface sterilized and germinated on 1x Murashige and Skoog media in complete darkness. Seedlings were harvested under a green safelight.

29. ABA 10-4 M (Liu et al. 1998)

F. Pharmacological Treatments: Whole plants were treated with atomized sprays (w/ 0.1% DMSO) and root drench where possible. In all cases a comparable set of tissues was dissected from the plant, cut to expose inner tissues, and placed into a sterile tall Petri dish containing the reagent.

30. Actinomycin D – 10 µg/ml (Barkley and Evans 1970) Transcription inhibitor, used to potentially bias the pool of resident RNA to extremely stable transcripts. Plant parts treated when detached from plant and incubated in phosphate buffer containing actinomycin D.
31. Cyclohexamide – 0.3 mM (Lam et al. 1989) Protein synthesis inhibitor, may stabilize some short lived transcripts by protecting them on the ribosome.
32. MG-132 – Proteosome inhibitor, may lead to changes in gene expression by stabilizing proteins associated with mRNA turnover (T. Madzima and K. Folta, unpublished) and may extend the activity of transcription factors normally destroyed through proteolysis.
33. Aphidicolin – 15 µM (Sedira et al. 2007) Cell cycle inhibitor, may lead to dramatic changes in gene expression associated with dividing cells and feedback loops in mitosis
34. Norfluorazon – 50 µM (Yurina et al. 2006) Chlorophyll synthesis inhibitor, implicated in alteration of retrograde signaling patterns, possibly presenting rare transcripts associated with plastid development.

Table S4. Sequencing statistics for individual MID pools.

MID Pool	Total Reads	Total Bases
Medley	153935	31500009
Leaf	100603	18924268
Petiole	118325	23749613
Crown	131311	27900172
Root	126485	25473780
Fruit	150639	28994640
Flower	146331	23282767
Stolon	126806	24559862
Runner tip	125424	24446229

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Table S5. The relative frequency of assembled contig sizes as assembled using Newbler and TGICL-based strategies.

Assembly with Newbler		**Assembly with TGICL**	
Contig Length Bin (bp)	**Number of Contigs**	**Contig Length Bin (bp)**	**Number of Contigs**
<100	61	<100	358
>= 100 && <200	6466	>= 100 && <200	2668
>= 200 && <300	7425	>= 200 && <300	16317
>= 300 && <400	4025	>= 300 && <400	11208
>= 400 && <500	2485	>= 400 && <500	5719
>= 500 && <900	4124	>= 500 && <900	6356
>= 900 && <1000	426	>= 900 && <1000	383
>= 1000 && <1100	354	>= 1000 && <1100	258
>= 1100 && <1200	262	>= 1100 && <1200	169
>= 1200 && <1300	170	>= 1200 && <1300	97
>= 1300 && <1400	166	>= 1300 && <1400	70
>= 1400	439	>= 1400	129

Table S6. The strategy used in removing non-strawberry reads from assembly.

Sequence Type	Genbank Search Type	Genbank Query	Number of Sequences Obtained
Bacterial	Nucleotide	Bacteria[organism] AND gene_in_genomic[PROP] AND complete[TITL] NOT partial[TITL] NOT pseudogene	75342
Insect	Nucleotide	Insecta[organism] AND gene_in_genomic[PROP] AND complete[TITL] NOT partial[TITL] NOT EST[All Fields] NOT pseudogene	75439
Mitochondrial	Nucleotide	Genbank Nucleotide Search: gene_in_mitochondrion[PROP] AND complete[TITL] NOT partial[All Fields] NOT pseudogene NOT EST[All Fields]	65137
Chloroplast	Nucleotide	Genbank Nucleotide Search: chloroplast[TITL] AND complete[TITL] NOT partial[TITL] NOT EST[All Fields]	14293

Table S7- Qualitative assessment of sequences identified as contamination of the strawberry EST reads.

	Newbler Assembly	**TGICL Assembly**
Total Contigs	26403	43732
Number of Contigs Got Hits	3290 (12.46%)	6739 (15.41%)
Contigs Passed Criteria	73 (.28%)	170 (.39%)
Mitochondrial Hits	25 (.09%)	44 (.1%)
Bacterial Hits	8 (.03%)	29 (.07%)
Chloroplast Hits	39 (.15%)	94 (.21%)
Insect Hits	1 (.003%)	2 (.004%)

Table S8. The total number of contigs assembled. *Single* refers to genome Cluster island position with only one contig. *Virtual* means genome Cluster island containing more than one contig but collapsed to a single contig (whose sequence belongs to that of longest contig).

Newbler	Single	24073
	Virtual	1082
TGICL	Single	6835
	Virtual	238
Total		32228

Table S9. GMAP analysis of Newbler-based contigs. "Cluster Size" indicates the number of individual contigs in a given cluster.

ClusterSize	#ofTheseClusterSizes	Total Contigs
1	17793	17793
2	2075	4150
3	602	1806
4	218	872
5	91	455
6	38	228
7	15	105
8	7	56
9	6	54
11	1	11
12	1	12
13	1	13
14	2	28
50	1	50

Table S10. GMAP analysis of TGICL -based contigs. "Cluster Size" indicates the number of individual contigs in a given cluster.

Cluster Size	# of this Cluster Size	Total Contigs
1	20572	20572
2	4098	8196
3	1543	4629
4	718	2872
5	360	1800
6	197	1182
7	112	784
8	72	576
9	38	342
10	19	190
11	21	231
12	19	228
13	12	156
14	7	98
15	4	60
16	7	112
18	5	90
19	1	19
20	3	60
21	3	63
22	3	66
24	1	24
25	2	50
26	2	52
27	2	54
31	1	31
40	1	40
44	1	44
53	1	53
61	1	61

Table S11. Allele-paralog detection using individual Newbler-derived contigs against the total Newbler-based assembly.

Cluster Size	# of this Cluster Size	Total Contigs
2	1335	2670
3	88	264
4	7	28
5	2	10
8	1	8
15	2	30
21	1	21
29	1	29
45	1	45
65	1	65

Table S12. Comparison of strawberry contigs to the apple and peach gene indices at various E value thresholds.

Total contigs = 32228	**Apple**	**Peach**	**Redundant between apple and peach**
E value <= 1e-10	17800 (55.23%)	13671 (42.42%)	12297 (38.16%)
E value <= 1e-20	13639 (42.32%)	10316 (32.01%)	9086 (28.19%)
E value <= 1e-50	5377 (16.68%)	4191 (13.00%)	3579 (11.11%)

Table S13. Blast2GO results distribution.

Category	Number of Sequences
Total contigs	32,228
No hits (E value = 1e-20)	19,500
BLAST hits (E value = 1e-20)	12,728
Map to GO ID	10,164
Do not map to GO ID	2,564
Annotation	7264
No annotation	2900