Sequencing the *Phaseolus vulgaris* G19833 Genome

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Project overview

- Produce as good as possible reference sequence for PV with available funds that will serve as a directly useful tool for common bean improvement (when combined with ongoing Bean-CAP efforts) and a reference comparator for soybean
- The DOE Joint Genome Institute is producing a 454/Illumina based draft sequence for soybean comparative work
- USDA has funded the project "A sequence map of the common bean genome for bean improvement" to add longer range linking data and genetic mapping data to the draft in order to produce a reference PV genome sequence
- The overlap between the DOE-JGI portion and the USDA portion is coordinated by Jeremy Schmutz at HudsonAlpha, who is also funded as part of the JGI Plant Genome Program

Expected genome data for PV V1.0

- 12x 454 linear data
- 4-6x 454 paired data from multiple sized libraries (4kb and 8kb)
- 50x of Illumina data
- 200k fosmid Sanger sequenced pairs
- 80k BAC Sanger sequenced pairs (includes 40k from BeanMap efforts)
- Up to 1400 marker genetic map (Hyten & Cregan)
- BAC physical map (phaseolus.genomics.purdue.edu)

454 linear sequencing

- Collected 7.1 GB of linear data (~11x HQ bases)
- Includes 26 runs from 4 libraries
- Average HQ read length of 274 bps

| Phred20 0- 49 50- 99 100-149 150-199 200-249 250-299 300-349 | Reads 648713 2134679 2073312 2560947 3063228 3561945 4114373 | %ofReads 2.5% 8.2% 7.9% 9.8% 11.7% 13.7% 15.8% | X XXXX XXXX XXXXX XXXXXX XXXXXXX XXXXXX |
|---|---|---|---|
| 350-399 | 3769733 | 14.4% | |
| 400-449 | 2479550 | 9.5% | |
| 450-499 | 1418195 | 5.4% | |
| 500-549 | 264387 | 1.0% | |
| 550-599 | 4896 | 0.0% | |
| 600-649 | 19 | 0.0% | |
| 650-699 | 8 | 0.0% | |
| 700-749 | 3 | 0.0% | |

Number of reads: 26,093,988 Total bases: 8,881,905,934 Total Phred 20 bases: 7,159,549,663 Average length: 340.4 Phred average: 274.4 Phred average without failures: 276.9 Percent failed: 1.0%

454 paired sequencing

- Collected 3.4 Gb of total HQ raw data
- Includes 14 runs from 8 libraries
- Once true pairs are determined we only collect 724 Mb or ~1.1x of paired data
- Making good paired libraries has been the most difficult part of this project
- We have 4 more library attempts in progress

| Phred20 | Reads | %ofReads | |
|---------|---------|----------|-------------------|
| 0- 49 | 338969 | 6.6% | XXX |
| 50- 99 | 1506543 | 29.4% | XXXXXXXXXXXXXXXXX |
| 100-149 | 1218194 | 23.8% | XXXXXXXXXXXXX |
| 150-199 | 923676 | 18.0% | XXXXXXXXX |
| 200-249 | 601244 | 11.7% | XXXXXX |
| 250-299 | 329828 | 6.4% | XXX |
| 300-349 | 145060 | 2.8% | X |
| 350-399 | 47794 | 0.9% | İ |
| 400-449 | 6597 | 0.1% | İ |
| 450-499 | 87 | 0.0% | ĺ |

```
Number of reads: 5,117,992
Total bases: 840,722,607
Total Phred 20 bases: 723,932,906
Average length: 164.3
Phred average: 141.4
Phred average without failures: 145.2
Percent failed: 3.3%
```

Illumina sequencing

• We have collected several different GA2x flow cells for PV, most of the reads are paired 76mers that will be used to correct 454 read errors

```
Reads %ofReads
Phred20
 0-9 15837191 2.9%
                      IX
10-19 6520659 1.2%
                     IX
20-29 8564932 1.6%
                     X
30-39 12494229 2.3%
                     IX
40-49 18842458 3.4%
                    XX
50-59 31401672 5.7%
                     XXX
60-69 71041097 12.9%
                     IXXXXXX
70-79 383902008 70.0%
                     Number of reads: 548,604,246
Total bases: 41,693,922,696
Total Phred 20 bases: 36,746,552,154
Average length: 76.0
Phred average: 67.0
Phred average without failures: 71.2
Percent failed: 7.9%
```

Fosmid libraries

- Goal is to produce about 400k reads or 200k pairs from fosmid length libraries
- 2 libraries have been constructed
 - VUL 33,465 bp insert; 200 plates
 - VUK 35,558 bp insert; 260 plates
- We have sequenced a combined 152k reads, 100k more are in progress now at HudsonAlpha
- We are sequencing more BES from the new BAC library to replace some of the FES to beef up long range linking

New BAC library

- Dave Kudrna at Arizona Genomics created a new BAC library called PV_GBb with the goal of maximizing the insert length
- The first section is 120 plates with 149kb average
- The second section is 105 plates with a 136kb insert
- We are sequencing the entire first section and filling in additional inserts from the second section
- These will add to the 89K reads from PV_Gba and give us decent BAC coverage across the genome

| Ligations picked | into Lib. Plates# | QC plate Information | avg inserts | |
|------------------|-------------------|----------------------------------|--------------------|--|
| A2-1 | Plates 1-41 | | 148.4 kb | |
| A2-2-1 | Plates 42 - 46 | QC Plates 1 & 2: (Lib plts 1-95) | | |
| A2-1-1 | Plates 47 - 95 | | (plates 1 - 120) | |
| A2-2-1 | Plates 96 - 120 | QC Plate 3: (Lib plt 96 - 120) | | |
| | • | | | |
| A2-2-1 | Plates 121 - 141 | OC Plate 4: (85 at 121 216) | 136 kb | |
| 8-8 | Plates 142 - 226 | QC Plate 4. (10 pit 121 - 218) | (plates 121 - 216) | |

GC profiles of data sets

| Midpoint | Counts | | Midpoint | Counts | | Midpoint | Counts | |
|---------------------------|---------|--|--------------------------|---------|--|---------------------------|---------------------|---|
| 1.00 | 6 | # | 1.00 | 468 | # | 1.00 | 4747 | # |
| 3.00 | 5 | # | 3.00 | 953 | # | 3.00 | 4960 | # |
| 5.00 | 18 | # | 5.00 | 2460 | # | 5.00 | 9925 | # |
| 7.00 | 14 | # | 7.00 | 4608 | # | 7.00 | 16559 | # |
| 9.00 | 31 | # | 9.00 | 8565 | # | 9.00 | 27016 | # |
| 11.00 | 83 | # | 11.00 | 15891 | # | 11.00 | 4 8758 | # |
| 13.00 | 193 | # | 13.00 | 27067 | # | 13.00 | 89034 | # |
| 15.00 | 451 | # | 15.00 | 42345 | ## | 15.00 | 162697 | # |
| 17.00 | 968 | # | 17.00 | 64311 | ### | 17.00 | 292810 | ## |
| 19.00 | 1886 | # | 19.00 | 86994 | #### | 19.00 | 474258 | ### |
| 21.00 | 2986 | ## | 21.00 | 125829 | ###### | 21.00 | 714272 | ##### |
| 23.00 | 4564 | ### | 23.00 | 160890 | ####### | 23.00 | 911976 | ####### |
| 25.00 | 5768 | #### | 25.00 | 203194 | ######## | 25.00 | 1108337 | ######### |
| 27.00 | 7038 | ##### | 27.00 | 239978 | ########### | 27.00 | 1328012 | ########## |
| 29.00 | 9587 | ###### | 29.00 | 290801 | ####################################### | 29.00 | 1621897 | ####################################### |
| 31.00 | 13601 | ########### | 31.00 | 350680 | ####################################### | 31.00 | 1984717 | ####################################### |
| 33.00 | 20549 | ####################################### | 33.00 | 399716 | <i>#######################</i> ############# | 33.00 | 235288 4 | **** |
| 35.00 | 24395 | ####################################### | 35.00 | 413867 | ####################################### | 35.00 | 2445947 | ####################################### |
| 37.00 | 22343 | ####################################### | 37.00 | 411190 | ####################################### | 37.00 | 2326033 | ***** |
| 39.00 | 18384 | ####################################### | 39.00 | 364020 | ####################################### | 39.00 | 1943834 | ####################################### |
| 41.00 | 16116 | ####################################### | 41.00 | 340152 | ####################################### | 41.00 | 1577787 | ####################################### |
| 43.00 | 10211 | ######## | 43.00 | 254320 | ####################################### | 43.00 | 1140571 | ######### |
| 45.00 | 7084 | ##### | 45.00 | 203775 | ######## | 45.00 | 864689 | ####### |
| 47.00 | 6988 | ##### | 47.00 | 173552 | ####### | 47.00 | 736704 | ###### |
| 49.00 | 9497 | ###### | 49.00 | 151676 | ###### | 49.00 | 693994 | ##### |
| 51.00 | 12897 | ########## | 51.00 | 190870 | ######## | 51.00 | 855705 | ###### |
| 53.00 | 13547 | **** | 53.00 | 175463 | ######## | 53.00 | 868063 | ####### |
| 55.00 | 9033 | **** | 55.00 | 145752 | ####### | 55.00 | 650574 | ##### |
| 57.00 | 4691 | *** | 57.00 | 106204 | ##### | 57.00 | 398131 | ### |
| 59.00 | 2822 | ## | 59.00 | 66532 | ### | 59.00 | 221333 | # |
| 61.00 | 1234 | # | 61.00 | 42315 | ## | 61.00 | 112753 | # |
| 63.00 | 306 | # | 63.00 | 22964 | # | 63.00 | 51959 | # |
| 65.00 | 48 | | 65.00 | 13190 | # | 65.00 | 24374 | # |
| 67.00 | 25 | # | 67.00 | 7508 | # | 67.00 | 10622 | # |
| 69.00 | 19 | # | 69.00 | 4267 | # | 69.00 | 5995 | # |
| 71.00 | 13 | <i>#</i> | 71.00 | 2705 | # | 71.00 | 4164 | # |
| 73.00 | 3 | 1. The second se | 73.00 | 1534 | | 73.00 | 3266 | |
| 75.00 | 3 | 1 m | 75.00 | 797 | | 75.00 | 2247 | 1# |
| 77.00 | 3 | * | 77.00 | 364 | * | 77.00 | 1340 | * * |
| 79.00 | 2 | * | 79.00 | 127 | * | 79.00 | 639 | ** * |
| 81.00 | 2 | * | 81.00 | 50 | | 81.00 | 282 | * * |
| 03.00 | 0 | * | 03.00 | 30 | ** | 03.00 | 0 4 | # |
| 05.00 | 2 | * | 05.00 | 14 | * | 05.00 | 29 | |
| 07.00 | i c | ·* | 07.00 | 2 | 1 * | 01.00 | 4 | |
| 09.00 | 0 | * | 09.00 | 1 | * | 09.00 | 2 | 1# # |
| 91.00 | 1 | | 91.00 | 0 | | 91.00 | 2 | |
| 93.00 | 0 | | 93.00 | 1 | | 93.00 | 3 | |
| 93.00 | 8 | | 93.00 | 1 | | 93.00 | 8 | |
| 91.00 | 2 | # | 91.00 | 0 | | 91.00 | 6 | # |
| 99.00 | 2 | " | 99.00 | Ø | | 99.00 | 0 | " |
| Total: | 227426 | | Total: | 5117992 | | Total: | 26093975 | |
| SANGER.fna Average 60% | = 30 40 | | PAIRS.fna Average 60% | = 37 31 | | LINEAR.fna Average 60% | = 36 32 | |
| morage sca | 8.24 10 | | mon ago ocm | 01101 | | mon ago loca | 00102 | |

Kmer distributions

| 2.00 | 22.265 | 22.265 | **************************** | 2,08 | 24,548 | 24,540 | ********************** | 2.00 | 2,000 | 2,055 | |
|----------|--------|---------|--|----------|-----------------|--------------|--|-----------|--------|---------|--------------------------------|
| 3:88 | 9.384 | 31.649 | ******** | 3,88 | 13.066 | 30,214 | ********** | 4.00 | 1.000 | 4.075 | |
| 4 69 | 4 556 | 36.594 | ***** | 4,88 | 6.618 | 44,024 | 00000000 | 5,00 | 1.103 | 5.181 | |
| T.00 | 7.030 | 30.300 | 2222 C | 5,89 | 3,359 | 48,183 | 0000 | 6,00 | 1.469 | 15.654 | ********* |
| 5.66 | 3,991 | 331260 | | 6.88 | 2, 636 | 50.213 | 20 | 7,00 | 1, 977 | 0.627 | ********** |
| m.88 | 2-411 | 41.723 | | 7.89 | 6.453 | 51.665 | | 9.00 | 2.579 | 11.205 | *************** |
| 7.00 | 1.752 | 43.476 | ** | 8,98 | 1.456 | \$2,821 | | 10.00 | 31,769 | 14.099 | |
| 0.00 | 1,49# | #1,970 | ** | 0.00 | a 660 | 63.910 | | 11.00 | 4.153 | 22.291 | ****************************** |
| 9,88 | 1.282 | 96.252 | 1 | 10.00 | a. 699 | 50.000 | | 12,00 | 4.370 | 25,669 | ***************************** |
| 10,89 | 1,189 | \$7.368 | | 11 44 | 4. 244 | 88 44.7 | | 12,00 | 4.292 | 31.061 | ****************************** |
| 11,00 | 1,832 | 48, 392 | | 17.00 | 0,107 | - 100 - 1001 | - 1 2 | 14,00 | 4,219 | 33 4288 | |
| 12,89 | 8.944 | 60.335 | | 12,00 | 01123 | 30.199 | | 15.00 | 3.462 | 42.621 | ********** |
| 13.80 | B 881 | 50.217 | | 13.00 | 0,0(C) 1,100 | 30.002 | | 17,00 | 2.974 | 45,565 | ****************** |
| 14-99 | 4 812 | 51 694 | | 14.00 | 0.020 | 27. 107 | 12 | 10.00 | 2.400 | 40.091 | ************** |
| 17-00 | 0.001 | 11.00T | | 12.40 | 0.593 | 50.060 | | 19,00 | 2.840 | 58,131 | |
| 13.00 | 0.700 | 51.101 | - 12 | 10.00 | 8.335 | 28.033 | | 20.00 | 1.210 | 211,000 | ******** |
| 10+66 | 0.180 | 25.482 | 1 | 17.80 | 0.513 | 59,147 | | 22,00 | 1,061 | 54,159 | ******* |
| 17.08 | 8.672 | 53.167 | | 18.00 | 0.485 | 59,633 | | 22.00 | 0.050 | 55.017 | ***** |
| 10,08 | 8,626 | 53,793 | | 19.00 | 0.159 | 68.992 | | 24,00 | 0.783 | 55,719 | **** |
| 19.88 | 8.597 | 54.398 | 1 | 29,40 | 0.432 | \$0.524 | | 25.00 | 0.560 | 55,300 | |
| 28,88 | 8,564 | 54:954 | | 21.00 | 0.405 | \$8.931 | | 27,00 | 0.440 | 37.259 | |
| 21,89 | 8.536 | 55.498 | * | 22.88 | 8,377 | \$1.387 | | 29.09 | 0.300 | 57.657 | |
| 22,08 | 8.519 | 56,889 | | 23,68 | 8,354 | 61.662 | | 29,00 | 0.363 | 38.829 | |
| 23,88 | 8,489 | 56, 499 | * | 24,88 | 8,324 | 61.900 | | 30.00 | 6.306 | 55.355 | |
| 24.08 | 0.478 | 56.977 | | 25.88 | 8,362 | 62.200 | | 12.00 | 9.319 | 58,000 | |
| 35.89 | 0.460 | 57 444 | | 26,88 | 0.207 | 62.574 | | 30.00 | 0.269 | 59.223 | |
| 24.02 | 0.109 | 82.885 | | 27.98 | 0.273 | 62.847 | | 34.05 | 0.253 | 39.476 | |
| 20.00 | 0.433 | 50.002 | | 28,66 | 0.262 | 63.189 | | 35.00 | 0.237 | 39.714 | |
| 61.00 | 0.742 | 38.314 | | 29,88 | 0.252 | 63.36t | | 30.00 | 8.224 | 26.628 | |
| 20,08 | 8,424 | 55.738 | | 39.00 | 0.238 | 63,599 | | 30.02 | 0.202 | 68, 252 | |
| 29.88 | 0.412 | 59.158 | | 31.00 | 8.231 | 63,838 | | 39.00 | 0.192 | 68,544 | |
| 38,98 | 0.300 | 59.539 | | 32,00 | 8.222 | 64.051 | | 48,00 | 0,105 | 68,738 | |
| 31.00 | 0375 | 59.914 | 1 T | 37.94 | 8.216 | 55.257 | | 41.00 | 9.179 | 62.909 | |
| 32,00 | 8.369 | 68.203 | | 34.00 | 8.218 | 54.477 | | 45.00 | 0.184 | 01.077 | |
| 33.88 | 0.371 | 68.651 | | 15.48 | 0.797 | 55.578 | | 44.00 | 0.159 | 61.400 | |
| 34,00 | 8.358 | 61.884 | | 36.98 | 8,195 | 64.075 | | 45.00 | 0.153 | 61,553 | |
| 35,98 | 0.343 | 61.347 | | 17.98 | 8.104 | 65,979 | | 45.00 | 9.140 | 61.701 | |
| 16 88 | 0.174 | 61 671 | | 28 60 | 0.100 | 65.050 | | 40.00 | 0,104 | 61,040 | |
| 37.89 | 0.310 | 61 008 | | 30.40 | 8 194 | 65 440 | | 40.00 | 8.125 | 62.119 | |
| 37.00 | 0.217 | 01, 290 | | 49.99 | AF 4 2 9 7 | 46 410 | | 56.59 | 1.650 | 63,768 | |
| 30,00 | 0.010 | 02.300 | | 41 60 | 0.174 | 20.014 | | 72.49 | 1.425 | 65.203 | |
| 39.00 | 0.265 | 02,000 | | 47.00 | 99-317 | 60.040 | | 92.89 | 1,354 | 05-557 | |
| 40.88 | 0.385 | 62.918 | | 42.00 | 10 1 1 Call | 80,903 | | 152.35 | 1.287 | 69,117 | |
| 41.99 | 9.292 | 63,282 | | 93-00 | 0,105 | 50,1,34 | | 105.13 | 1-425 | 78,542 | ******** |
| 42.88 | 8_297 | 63.498 | | 44,00 | 84309 | 00.294 | | 249.97 | 1.060 | 72.403 | |
| 45,88 | 8.283 | 53.761 | • | 43.66 | 8,100 | 00.902 | | 328,19 | 1.492 | 73,894 | |
| 44.88 | 8.288 | 64.861 | | 40.88 | 81332 | 50.007 | | 410.15 | 1.210 | 23.104 | |
| 45.08 | 9,286 | 64.347 | * | +7.98 | 81322 | 66,762 | | 525.37 | 1.234 | 76,338 | |
| 46.82 | 0.276 | 64.623 | * | 10.00 | 9.151 | 60.914 | | 672.95 | 1.223 | 77.560 | ******* |
| 47,88 | 8,272 | 64, 895 | 2 | 44.88 | 8,195 | 67.458 | | 852.02 | 1.256 | 78.617 | |
| 48,88 | 0.252 | 65,147 | * | 58-21 | 2.23* | 69.292 | 100 | 1414.39 | 1.201 | 91,571 | |
| 45.89 | 8.251 | 65, 398 | * | 18.99 | 2.358 | 71+042 | | 1811.73 | 1,485 | 82,979 | |
| 58 21 | 9.670 | 60,360 | 80000 | 160.05 | 2.544 | 14.284 | | 2229.70 | 1.482 | 94.461 | ******* |
| 78 82 | 4 999 | 23 0.04 | ***** | 144,92 | 2,111 | 31-361 | | 2972.66 | 2,152 | 80,613 | |
| 10.07 | 0.4161 | 76 760 | 4744 | 196, 41 | 3,985 | 81.379 | No. of Contract of | 4977.49 | 1.613 | 91,025 | |
| 100-14 | 3-913 | 10.104 | and a second sec | 266,19 | 3,345 | 84,722 | | 6247,75 | 1,198 | 93,133 | ******* |
| 144.92 | 2.915 | 79.024 | Private Contraction of the Contr | 368.70 | 2,394 | 57.117 | 100 | 2002.91 | 2.459 | 95.593 | ****** |
| 196.41 | 2,562 | 82,185 | | 400.97 | 2.260 | 90.357 | | 18251.17 | 1.855 | 967647 | |
| 266.19 | 2,669 | 84,795 | | 662.70 | 1.702 | 92,887 | | +6010 07 | 0.005 | 97,200 | |
| 360,78 | 2.104 | 86.899 | ** | 696.18 | 1.357 | 93.443 | | 21849.22 | 1,231 | 92,482 | |
| 408.97 | 2.136 | 89,034 | 22 | 1217.31 | 5.198 | P9.64t | | 27597.64 | 0.414 | 99.216 | |
| 562.70 | 5.388 | 94,422 | ****** | 16+9.85 | 3,942 | P6.583 | | 35391 .46 | 0.100 | 99.916 | |
| 898.18 | 1.935 | 96,357 | ** | 2236.07 | 1.755 | 96.338 | | 45282.25 | 0.001 | 99.047 | |
| 1217.31 | 0.540 | 96,897 | | 3838.50 | \$.311 | 98.619 | | 74298-43 | 0.000 | 99.972 | |
| 1649.05 | 0.567 | 97,463 | | 4187.40 | \$,197 | 98.846 | | 95171.10 | 0.004 | 99.976 | |
| 2236.87 | 8-139 | 97.682 | * | 5966.84 | 8,246 | 99,892 | • | 121987,78 | 0.000 | 99.976 | |
| 1010 50 | 0.145 | 07 747 | | 7544.84 | 8,259 | 99.352 | | 156155.25 | 0.000 | 99.976 | |
| 4102 40 | 0.293 | 07 988 | | 18225.65 | 8,198 | 39.549 | • | 256217.25 | 0.000 | 99.976 | |
| TEG1. 10 | 0.233 | -DR 100 | | 13839.83 | 8.195 | 99.746 | | 329195.64 | 9.000 | 99.975 | |
| 2300.07 | 0_200 | 90.100 | | 38783137 | 8.287 | 99.953 | | 428397.26 | 0.824 | 108,008 | |
| 1099.09 | 8.017 | 90,991 | | 25457.43 | 0.047 | 108.000 | | 535492.00 | 0.000 | 108,000 | |
| 10225.05 | 0.840 | 49,631 | | 34582.92 | 0.000 | 108,808 | | | | | |
| 13859.01 | 8.363 | 20.000 | | | | | | | | | |

Sanger

188.888

0.000

18783.37

454 Pairs

454 Linear

Initial Newbler assemblies 454 only

• ~8x assembly

- ~12x assembly
- These builds are the basis for the genetic mapping effort

Main genome scaffold total: 20067 Main genome contig total: 61136 Main genome scaffold sequence total: 419.1 MB Main genome contig sequence total: 367.2 MB (-> 12.4% gap) Main genome scaffold N/L50: 2046/55.9 KB Main genome contig N/L50: 11467/9.1 KB Number of scaffolds > 50 KB: 2385 % main genome in scaffolds > 50 KB: 54.3% Main genome scaffold total: 10037 Main genome contig total: 47131 Main genome scaffold sequence total: 470.1 MB Main genome contig sequence total: 416.5 MB (-> 11.4% gap) Main genome scaffold N/L50: 520/214.4 KB Main genome contig N/L50: 7982/14.8 KB Number of scaffolds > 50 KB: 1998

| % main gen | ome in | scaffolds | > | 50 | KB: | 82.4% |
|------------|--------|-----------|---|----|-----|-------|
|------------|--------|-----------|---|----|-----|-------|

| Mini | imum | Number | Number | Total | Total | Scaffold |
|-------|------|-----------|---------|-------------|-------------|----------|
| Scaft | fold | of | of | Scaffold | Contig | Contig |
| Leng | gth | Scaffolds | Contigs | Length | Length | Coverage |
| | | | | | | |
| , A | 411 | 10,037 | 47,131 | 470,076,288 | 416,492,511 | 88.60% |
| 1 | kb | 10,037 | 47,131 | 470,076,288 | 416,492,511 | 88.60% |
| 2.5 | kb | 8,010 | 45,104 | 465,583,552 | 411,999,785 | 88.49% |
| 5 | kb | 5,753 | 42,714 | 458,127,389 | 404,765,693 | 88.35% |
| 10 | kb | 4,525 | 40,552 | 449,732,354 | 397,781,006 | 88.45% |
| 25 | kb | 3,071 | 36,351 | 425,878,517 | 378,081,319 | 88.78% |
| 50 | kb | 1,998 | 31,259 | 387,529,708 | 346,509,091 | 89.41% |
| 100 | kb | 1,157 | 24,832 | 328,052,126 | 295,902,874 | 90.20% |
| 250 | kb | 427 | 14,827 | 213,547,125 | 195,179,721 | 91.40% |
| 500 | kb | 145 | 7,558 | 115,721,896 | 106,708,733 | 92.21% |
| 1 | mb | 22 | 2,025 | 33,505,576 | 31,309,850 | 93.45% |

Latest Newbler assembly

• We are running several version of the compete data set to date, including BES and FES

Main genome scaffold total: 14932 Main genome contig total: 48818 Main genome scaffold sequence total: 469.0 MB Main genome contig sequence total: 398.5 MB (-> 15.0% gap) Main genome scaffold N/L50: 336/323.7 KB Main genome contig N/L50: 7908/13.8 KB Number of scaffolds > 50 KB: 1562 % main genome in scaffolds > 50 KB: 83.2%

| Minimum | Number | Number | Total | Total | Scaffold |
|----------|-----------|---------|-------------|-------------|----------|
| Scaffold | of | of | Scaffold | Contig | Contig |
| Length | Scaffolds | Contigs | Length | Length | Coverage |
| | | | | | |
| A11 | 14,932 | 48,818 | 469,034,573 | 398,491,214 | 84.96% |
| l kb | 14,932 | 48,818 | 469,034,573 | 398,491,214 | 84.96% |
| 2.5 kb | 10,284 | 44,170 | 458,708,951 | 388,165,740 | 84.62% |
| 5 kb | 5,008 | 38,690 | 441,366,896 | 371,170,537 | 84.10% |
| 10 kb | 3,285 | 35,737 | 430,037,215 | 361,639,508 | 84.09% |
| 25 kb | 2,189 | 32,594 | 412,689,007 | 347,700,588 | 84.25% |
| 50 kb | 1,562 | 29,642 | 390,023,800 | 330,043,578 | 84.62% |
| 100 kb | 951 | 25,234 | 346,755,218 | 296,695,458 | 85.56% |
| 250 kb | 450 | 18,194 | 267,049,160 | 232,736,465 | 87.15% |
| 500 kb | 185 | 11,205 | 175,356,909 | 155,374,306 | 88.60% |
| l mb | 56 | 5,205 | 86,489,208 | 77,731,920 | 89.87% |
| 2.5 mb | 5 | 779 | 14,735,915 | 13,561,325 | 92.03% |
| 5 mb | 0 | 0 | 0 | 0 | 0.00% |

New assembly pipeline

- Remove duplicate 454 pairs and unpaired reads
- Correct 454 bp and indel errors using Illumina reads
- Assemble using HA Arachne version including BES and FES and all of the 454 corrected sequence data
- Make scaffold breaks on misjoins by comparing to genetic map
- Order and orientate scaffolds based on genetic map and build chromosome scale assembly
- This same pipeline is being used to produce multiple plant genomes for the JGI Plant Genome Program

Annotation

• PV will be annotated using the same Phytozome pipeline as soybean, our goal is to have a comparable gene annotation between the two genomes



Timeline goals

- April 2011: Data collection complete
- July 2011: Chromosome scale assembly
- September 2011: Annotation complete and V1 PV publicly available